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Transcriptional characterization of *Vibrio fischeri* during colonization of juvenile *Euprymna scolopes*

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Summary

The marine bacterium *Vibrio fischeri* is the monospecific symbiont of the Hawaiian bobtail squid, *Euprymna scolopes*, and the establishment of this association involves a number of signaling pathways and transcriptional responses between both partners. We report here the first full RNA-Seq dataset representing host-associated *V. fischeri* cells from colonized juvenile *E. scolopes*, as well as comparative transcriptomes under both laboratory and simulated marine planktonic conditions. These data elucidate the broad transcriptional changes that these bacteria undergo during the early stages of symbiotic colonization. We report several previously undescribed and unexpected transcriptional responses within the early stages of this symbiosis, including gene expression patterns consistent with biochemical stresses inside the host, and metabolic patterns distinct from those reported in associations with adult animals. Integration of these transcriptional data with a recently developed metabolic model of *V. fischeri* provides us with a clearer picture of the metabolic state of symbionts within the juvenile host, including their possible carbon sources. Taken together, these results expand our understanding of the early stages of the squid–vibrio symbiosis, and more generally inform the transcriptional responses underlying the activities of marine microbes during host colonization.

Introduction

Bacterial colonization of host organisms has been studied in many different model systems, and in the context of both pathogenesis and beneficial symbiosis (Bry *et al*., 1996; Dedeine *et al*., 2001; Russell and Rychlik, 2001; Hongoh, 2010; Gilbert *et al*., 2012; Nyholm and Graf, 2012; Bulgarelli *et al*., 2013; McFall-Ngai *et al*., 2013; Almagro-Moreno *et al*., 2015; Uzal *et al*., 2015; Kao *et al*., 2016). Such interactions have strong transcriptional effects upon both host and symbiont, and there is a compelling interest towards better understanding these interactions and, in particular, the chemical dialogue that underlies their initial establishment (Montgomery and McFall-Ngai, 1994; Hughes and Sperandio, 2008; Mullard, 2009; Wier *et al*., 2010; Shin *et al*., 2011; Heath-Heckman *et al*., 2013; Kremer *et al*., 2013; Kabat *et al*., 2014; Penterman *et al*., 2014). The model symbiosis between the marine bioluminescent bacterium *Vibrio fischeri* and the Hawaiian bobtail squid *Euprymna scolopes* has served as an insightful window into host–microbe interactions over the past several decades, and provides an excellent system to study both the early and long-term interactions of a mutualistic symbiosis.

V. fischeri is the monospecific symbiont of the *E. scolopes* light-emitting organ. When first hatched, juvenile *E. scolopes* are aposymbiotic (i.e. they have no bacterial symbionts), and each generation must obtain their symbiotic bacteria from the surrounding seawater. Colonization of the squid light organ is both rapid and extremely specific, allowing *V. fischeri* to transition from being a minority member of the bacterioplankton (estimated at 0.01–0.15% of the ambient seawater bacteria) to being the sole resident of the host's light organ (Ruby and Lee, 1998). This transition from the seawater to the interior of this organ requires passage through several distinct microenvironments within the host's tissues (Nyholm and McFall-Ngai, 2004). During this process, bacterial cells must contend with chemical challenges (e.g. NO exposure) and recognize chemical cues (e.g. chitobiose, presented as a chemoattractant) used by the host to ensure colonization specificity, and to which *V. fischeri* is exquisitely adapted (DeLoney-Marino *et al*., 2003; Dunn *et al*., 2010; Wang *et al*., 2010; Kremer *et al*., 2013). Following aggregation on

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the host's epithelium, a small number of individual bacteria migrate into the inner tissues of the light organ where they colonize the deep crypts and multiply. This transition into the host leads to the establishment of a mutualistic symbiosis that continues for the duration of the squid's life, and is directly responsible for a large number of transcriptional and developmental changes within the host (Wier *et al*., 2010; Heath-Heckman *et al*., 2013; Kremer *et al*., 2013).

The functional foundation of this symbiosis is the provision of nutrients and a rich growth environment for the bacterial population, from which the squid host gains a source of light used for anti-predatory behaviour at night (Nyholm and McFall-Ngai, 2004). This relationship follows a strong diel rhythm, wherein the host expels up to 95% of the symbiont community each dawn and the population regrows while the animal is buried within the sand during the day. At night the host emerges and the bacterial population has grown sufficiently to luminesce, a process tightly regulated via quorum sensing (Miyashiro and Ruby, 2012). In adult animals, this process is concurrent with a strong transcriptional and metabolic rhythm between the symbionts and host tissues (Wier *et al*., 2010). During the day the host apparently presents glycerophospholipids to its symbionts, allowing them to undergo anaerobic respiration to maximize growth. However, at night the host withholds these metabolites and, instead, provides chitin, which the bacteria ferment under conditions that promote maximal production of light. This metabolic cycling, however, has been found to be distinct from that occurring during juvenile light-organ development, as host provision of chitin oligosaccharides at night only begins after about four weeks of host development (Schwartzman *et al*., 2015). These findings are consistent with developmental changes in the host, including within the light organ. Such changes are tightly tied to the initial contact between host and symbiont, with transcriptional responses evident in the light organ's tissues immediately following initial exposure to bacterial cells (Kremer *et al*., 2013).

The picture that arises of the establishment of the squid–vibrio symbiosis is one of tightly regulated developmental events within the host, and a well-adapted suite of tools for host colonization on the part of the bacterial symbionts. Prior studies have examined transcriptional patterns within this system in mature host animals, and within the host light organ during initial contact with bacterial symbionts; however, transcriptomics data on the bacteria in the juvenile light organ has thus far been missing because there are $<10^6$ symbionts per light organ during this early stage of development, below the input-biomass limit of standard RNA-Seq transcriptomics. In light of the strong and early response by the squid host to the initial presence of the symbiont (Kremer, *et al*., 2013), we asked what changes occur within the symbionts as they make the transition from the bacterioplankton to the host, a habitat switch similar to that made by most pathogenic *Vibrio* species. To this end, we performed RNA-Seq experiments on *V. fischeri* from three environments – (i) cells growing in rich medium, (ii) cells incubated in seawater and (iii) cells collected immediately after venting from the squid host – to identify transcriptional signals that could be directly associated with the early stages of host colonization (Fig. 1A). In particular, our comparisons of cells in seawater with those that had just exited the host's light organ revealed a large number of genes that were highly upregulated in response to host contact (Fig. 1B). These data fill an existing gap in our understanding of the early stages of symbiosis between *V. fischeri* and *E. scolopes*, addressing questions about both the metabolic state and the environmental responses of these bacteria during host colonization.

Results and discussion

Robust libraries made from ribo-depleted, low-biomass samples

This study depended upon the reliable measurement of the mRNA levels present in the small numbers of *V. fischeri* cells expelled from the juvenile squid's light organ each morning (Lee and Ruby, 1994). The yield of *V. fischeri* total RNA from 10 to 100 animals is typically less than 100 ng and, thus, efforts to deplete ribosomal RNA (ribo-depletion) might lead to high collateral loss of mRNA. Tests with the standard Illumina TruSeq library prep have shown reproducible results down to input levels of ~70 ng total RNA but, notably, these protocols do not employ ribo-depletion (Combs and Eisen, 2015). Therefore, we sought to establish the minimal number of juvenile squids necessary to create a reliable symbiont transcriptome. Specifically, we determined the lower limit of ribo-depleted RNA that would produce robust results when following the standard protocol of the TruSeq RNA Sample Preparation Kit (Illumina).

Using a single sample of *V. fischeri* total RNA from a culture grown in SWT medium, we made TruSeq libraries from three amounts of non-ribo-depleted total RNA (1000, 500 and 100 ng), and nine amounts of ribo-depleted RNA (1000, 500, 100, 50, 25, 10, 5, 2.5 and 1 ng) (Supporting Information Table S1). The 100-ng ribo-depleted sample from this experiment is the same as replicate no. 3 of the cultured-cell treatment in the comparison experiment. Libraries for the 5, 2.5 and 1 ng samples were amplified both with the standard 15 cycles as well as with 17 cycles.

We mapped and counted the reads from each library prep to the *V. fischeri* ES114 genome as described in the Experimental Procedures. Ribo-depletion using the Ribo-Zero Gold Epidemiology Kit (Epicentre) before library prep with the TruSeq kit reduced the percentage of rRNA in the

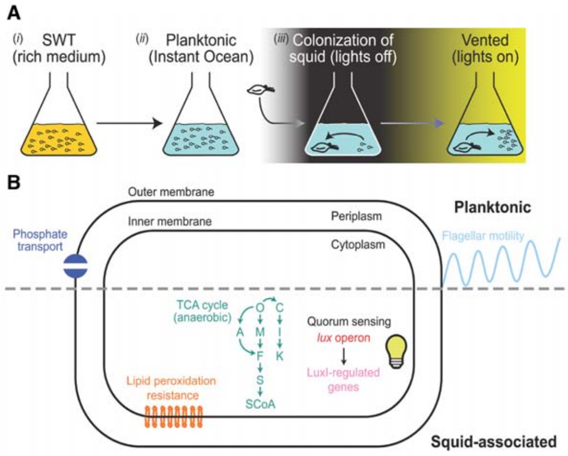

Fig. 1. Schematic cartoons of (A) the colonization of *E. scolopes* by *V. fischeri* during the study's 3-stage transcriptomic comparison, and (B) characteristic metabolic pathways that are differentially expressed in planktonic and squid-associated cells of *V. fischeri*. TCA cycle intermediates are indicated with one-letter codes: O, oxaloacetate; M, malate; F, fumarate; S, succinate; SCoA, succinyl-CoA; C, citrate; I, isocitrate; K, 2-ketoglutarate; A, aspartate.

sample from ~90% to ~1% (Supporting Information Fig. S1). Ribo-depletion did not appreciably affect the relative abundance of individual mRNAs detected, as shown by pairwise scatter plots between ribo-depleted and non-ribo-depleted samples, yielding *R*-squared values between 0.93 and 0.98 (Supporting Information Fig. S2). Contrasting the conditions represented in these scatter plots using DESeq2 did not identify any genes significantly differentially abundant between ribo-depleted and non-ribo-depleted samples (FDR-adjusted p-value < 0.05).

Having established that ribo-depletion removed ~99% of rRNA from as little as 100 ng total RNA without changing the relative abundance of mRNAs detected in a sample, we then determined how much the input RNA could be lowered, prior to ribo-depletion, without the loss of signal fidelity. Using the 100-ng ribo-depleted sample as a basis of comparison, pairwise scatter plots showed that the relative mRNA composition was maintained down to 10 ng, with *R*-squared values of 0.98 between the 100-ng and 10-ng samples (Supporting Information Fig. S3). Additional noise was introduced as the level of input RNA was decreased to 1 ng, but the *R*-squared values remained in the range of 0.91 to 0.95 (Supporting Information Fig. S4). Coverage of the *V. fischeri* ES114 genome, i.e. the fraction of CDS genes observed one or more times in the sample, was between 98 and 99% with samples as low as 50 ng of input total RNA; below this value, the coverage decreased to ~95% for samples down to 5 ng, and ~85% for input total RNA of 1 ng (Supporting Information Fig. S5A). Increasing the number of library amplification cycles increased the percent coverage somewhat (Supporting Information Fig. S5A); however, it did not necessarily bring the relative mRNA counts closer to those of the 100 ng standard (Supporting Information Fig. S4). As expected, those genes with the lowest relative mRNA abundance (when averaged across all samples from the 15 variations of preparation) were those most likely to be undetected in the low-input RNA samples (Supporting Information Fig. S5B). From these results, we concluded that the relative abundances of mRNA species could be reliably determined from an input level of 100 ng of total RNA (before ribo-depletion). In addition, input total RNA could be (i) reduced to 50 ng without loss of coverage, (ii) reduced further to 10 ng without loss of mRNA relative abundance fidelity and (iii) reduced further to 2.5 to 5 ng with ~10% reduction in coverage and mRNA relative abundance fidelity (Supporting Information Fig. S5).

Expelled bacteria show transcriptional patterns consistent with previous colonization data

To test how well the mRNA of expelled symbionts represents their transcriptional activity in the light organ, we first asked whether previously identified patterns of specific gene expression were found. Prior studies of the *V. fischeri*–*E. scolopes* mutualism have provided evidence of a number of genes that are involved with establishing a successful host colonization. Two such sets of genes include those responsive to quorum signaling, and those encoding flagellar motility (Ruby and Asato, 1993; Visick *et al*., 2000; Wier *et al*., 2010; Miyashiro *et al*., 2011). We found that, when compared with planktonic *V. fischeri*, the squid-associated symbionts regulate a number of genes consistent with previous physiological and morphological studies of these activities (Supporting Information Table S2). For example, one of the best characterized sets of genes in the squid–vibrio symbiosis is the LuxIR regulon, including both the *lux* operon, which regulates bacterial light production (Septer and Stabb, 2012), and a set of 21 other quorum signal-induced genes (Antunes *et al*., 2007). Specifically, relative to either cultured or planktonic cells, we observed at least a 16-fold upregulation of all the genes within the *lux* operon in the bacteria expelled from the light organ (Fig. 2), consistent with both the high population density within the symbiosis and previous physiological measurements of induced bioluminescence activity (Visick *et al*., 2000).

In contrast, while flagellar elaboration and motility are both critical during the initial step of host colonization, flagellation disappears once colonization has been established (Ruby and Asato, 1993; Graf *et al*. 1994), although no molecular evidence has indicated its control at the transcriptional level. Thus, we looked at genes involved in the assembly of both the flagellum and flagellar motor of *V.*

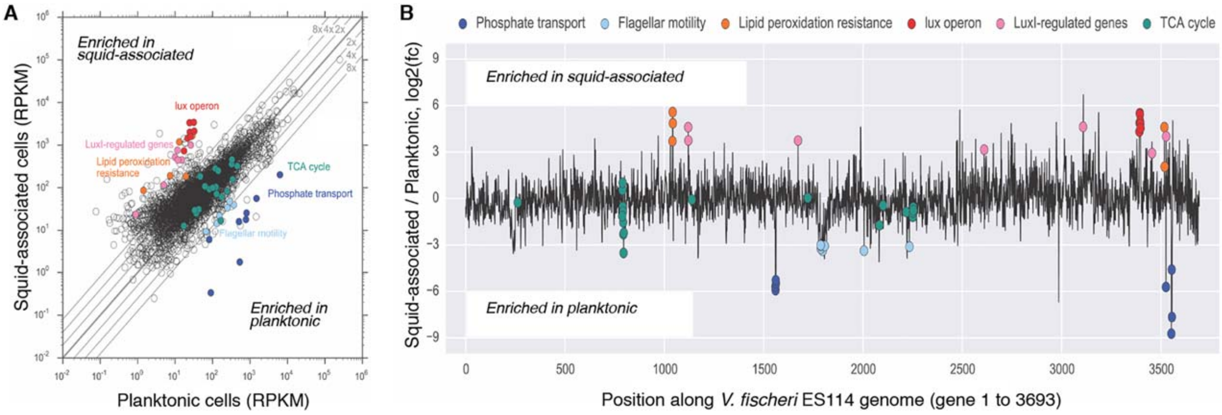

Fig. 2. Scatter plot and genome trace of gene transcript differential abundance between planktonic and squid-associated states, with genes belonging to pathways of interest highlighted. Color coding is from Fig. 1B.
A. Scatter plot showing log-scale differences in relative (RPKM) transcript abundances between planktonic (pre-squid colonization) and vented (post-squid colonization) states. Parallel lines show unity (log2 of fold change, log2(fc) = 0), 2x fold change (log2(fc) = ±1), 4x fold change (log2(fc) = ±2), and 8x fold change (log2(fc) = ±3).
B. Genome trace of log2(fc) between squid-associated and planktonic states. Genes are plotted in their order on the *V. fischeri* ES114 genome, which consists of Chromosome 1 (genes 1–2527), Chromosome 2 (genes 2528–3641), and a conjugative plasmid (genes 3642–3693).

fischeri (Brennan *et al*., 2013), and observed significantly lower expression ($|\log2(fc)| > 1$, $p_{adj} < .01$) of 30 of 42 of these genes among the squid-associated symbionts (Supporting Information Table S2; Fig. 2). The focus here is on the habitat transition between the transcriptomes of planktonic and squid-associated bacteria, as these are the conditions most relevant to the life history of the symbiosis. However, the comparison of the SWT-cultured and squid-associated samples corroborates many of these results, and serves as a control for the rich growth conditions within the light organ (Graf and Ruby, 1998). Taken together, the expression of genes involved in these two symbiosis-driven physiological activities (Supporting Information Table S2) is both consistent with previous studies, and provides evidence that our samples of expelled symbionts are likely to faithfully report transcriptional activity within the host light organ.

Insight into symbiont metabolism within the juvenile host

Prior work has demonstrated that the symbiosis between *V. fischeri* and *E. scolopes* follows a well-regulated diel metabolic cycle (Wier *et al*., 2010). These studies also demonstrated that at least some of the metabolic pathways characteristic of symbionts in adult light organs are not established until the host has matured to approximately 4 weeks of age (Schwartzman *et al*., 2015). Most notably, a major nocturnal activity of symbionts in adult animals is the fermentation of chitin and its monomer *N*-acetylglucosamine (GlcNAc), while during the day they appear to anaerobically respire glycerol and glycerol-3-phosphate (G3P) using nitrate as the terminal electron acceptor (Wier *et al*., 2010). However, regardless of the time of day, GlcNAc is not a significant nutrient source for symbionts of juvenile squid; i.e. even when defective in GlcNAc catabolism, *V. fischeri* cells maintain a robust population until the symbiosis has matured, around 28 days (Miyashiro *et al*., 2011; Schwartzman *et al*., 2015). Thus, while the primary catabolic activity(s) of bacteria in the juvenile crypts has not been established, the transcriptomic signature of the released symbionts may provide some clues.

One such clue comes from an analysis of tricarboxylic acid (TCA) cycle gene expression within the squid-associated bacteria, which revealed distinct regulatory patterns consistent with fermentation rather than respiration. Specifically, we observed a significant down-regulation confined to the cycle's *sucABCD* and *acnB* genes, encoding the enzymes responsible for converting citrate to succinate (Table 1). This weakening of the oxidative side of the TCA cycle (Fig. 1B) leaves the reductive side in a position to support fermentation (Neidhardt, 1996); in addition, the resulting buildup in citrate is expected to enhance bioluminescence (Septer *et al*., 2015). Consistent with, and perhaps responsible for, this signature of fermentative activity is an upregulation of VF_1068, a homologue of the regulatory protein pirin (Table 1), whose induction switches the flow of glycolysis-derived pyruvate from respiration to fermentation (Soo *et al*., 2007; Hansen *et al*., 2012).

In addition, genes associated with the extracellular breakdown of glycerophosphodiester to G3P and an alcohol (i.e. *glpQ*), and the subsequent catabolism of G3P (i.e. *glpAB*/*glpD*) were upregulated in the squid-associated samples (Table 1). This transcriptional pattern is reminiscent of the morning upregulation of genes associated with

Table 1. Differentially expressed *V. fischeri* genes indicating symbiont metabolism in the juvenile host.

Gene*	Vnt/Plk log2(fc)[a]	FDR-adjusted *p*-value[a]	Description
Tricarboxylic Acid (TCA) cycle interruption			
sucA (VF_0823)	−1.5	2.2 E −03	α-ketoglutarate dehydrogenase E1
sucB (VF_0824)	−2.3	1.1 E −06	Dihydrolipoamide succinyltransferase
sucC (VF_0825)	−3.5	1.1 E −05	Succinyl-CoA synthetase subunit beta
sucD (VF_0826)	−2.2	1.9 E −03	Succinyl-CoA synthetase subunit alpha
acnB (VF_2158)	−1.7	1.3 E −02	Bifunctional aconitate hydratase
Respiration/fermentation switch regulator			
VF_1068	3.5	9.5 E −09	Pirin
Phospholipid/G3P catabolism			
pldA (VF_1556)	1.8	7.7 E −03	Outer membrane phospholipase A
glpD (VF_A0239)	3.1	1.3 E −04	Glycerol-3-phosphate (G3P) dehydrogenase
glpC (VF_A0248)	0.5	0.69	Anaerobic G3P dehydrogenase subunit C
glpB (VF_A0249)	2.3	8.4 E −03	Anaerobic G3P dehydrogenase subunit B
glpA (VF_A0250)	1.7	1.8 E −02	Anaerobic G3P dehydrogenase subunit A
glpQ (VF_A0958)	3.2	2.8 E −21	Glycerophosphoryl diester phosphodiesterase GlpQ
Formate dehydrogenase subunits			
fdnI (VF_1358)	−2.1	3.2 E −05	Formate dehydrogenase N subunit gamma
fdnH (VF_1359)	−2.7	1.3 E −03	Formate dehydrogenase N subunit beta
fdnG (VF_1360)	−2.9	5.9 E −08	Formate dehydrogenase N subunit alpha
fdhD (VF_1366)	−0.6	0.34	Formate dehydrogenase subunit delta
fdhF (VF_A0251)	−1.7	2.1 E −02	Formate dehydrogenase-H
Phosphate transport			
pstB (VF_1983)	−0.3	0.52	Phosphate ABC transporter ATP-binding protein
pstA (VF_1984)	−1.2	4.8 E −02	Phosphate ABC transporter permease
pstC (VF_1985)	−1.2	1.6 E −02	Phosphate ABC transporter permease
pstS (VF_1986)	1.8	1.3 E −05	Phosphate-binding protein
phoR (VF_1987)	2.1	1.7 E −07	Phosphate regulon sensor
phoB (VF_1988)	2.5	1.8 E −02	DNA-binding response regulator with PhoR
pstS2 (VF_1610)	−5.7	1.8 E −24	Phosphate-binding protein
pstC2 (VF_1611)	−5.9	2.3 E −24	Phosphate ABC transporter permease
pstA2 (VF_1612)	−5.3	2.5 E −16	Phosphate ABC transporter permease
pstB2 (VF_1613)	−5.5	1.3 E −41	Phosphate ABC transporter ATP-binding protein
VF_A0555	−1.7	1.8 E −04	Phosphate-binding protein

*Orange: upregulated; Blue: down-regulated in squid relative to seawater.

a. Genes listed showed differential expression between squid-associated (Vnt) and planktonic (Plk) *V. fischeri* of at least abs(log 2(fc) $>$ 1) and FDR-adjusted p-value < 0.01.

the anaerobic respiration of glycerol/G3P observed in the symbionts of adult squid (Wier *et al*., 2010); however, other, anaerobic respiration-linked genes upregulated by these symbionts (e.g. those encoding formate dehydrogenase; Table 1) were instead down-regulated in the symbionts of juveniles. These results indicate that, within the pre-dawn juvenile host, *V. fischeri* is likely to be fermenting G3P, distinct from its daytime respiration and, the nighttime fermentation of GlcNAc, in the mature symbiosis (Schwartzman *et al*., 2015).

To further investigate which nutrients might be used by the symbionts of juvenile animals, we applied flux coupling analysis (Burgard *et al*., 2004) using a new genome-scale metabolic model for *V. fischeri*. This analysis can identify metabolic genes that are linked to the utilization of specific carbohydrates, such that flux through the reactions catalyzed by these genes will indicate that a particular substrate is being used by the bacteria. This flux coupling analysis identified *N*-acetylneuraminic acid (NANA) as a possible carbon source for *V. fischeri* in juvenile animals based on an apparent upregulation of several genes involved in NANA uptake and utilization (Supporting Information Table S3). Independent support for NANA as a symbiont substrate comes from a high-throughput insertion sequencing study (Brooks *et al*., 2014) predicting genes encoding the putative transporter and lyase of NANA (*nanT* and *nanA*) to be colonization factors. In addition, NANA is a component of squid mucus, and a chemoattractant of *V. fischeri* (DeLoney-Marino *et al*., 2003; Schwartzman *et al*., 2015). The analysis also suggested glycerophosphodiester as a potential carbon source for *V. fischeri* in juvenile animals based on the upregulation in the symbionts of *glpQ*, as mentioned above. In the analysis, *glpQ* is the only gene specifically connected to the utilization of glycerophosphodiesters, because other genes involved in glycerol and G3P catabolism also play a role in the use of other nutrients. Overall, these results support the conclusion that nutrients such as NANA and

Table 2. Differentially expressed *V. fischeri* genes indicating potential stress in the juvenile symbiosis.

Gene[a]	Vnt/Plk log2(fc)[b]	FDR-adjusted *p*-value[b]	Description
Detoxification of peroxidized lipids			
acrR (VF_1081)	3.7	3.5 E −13	TetR family transcriptional regulator
yfcG (VF_1082)	5.6	2.9 E −28	glutathione S-transferase
yghU (VF_1083)	4.9	1.8 E −38	glutathione S-transferase YghU
nemA (VF_A1049)	4.6	2.5 E −11	*N*-ethylmaleimide reductase FMN-linked
VF_A1050	2.1	1.8 E −02	ABC transporter domain protein
RND family exporters			
VF_1161	4.6	5.9 E −19	periplasmic protein of efflux system
tolC (VF_1162)	3.7	1.1 E −10	outer membrane protein TolC
VF_1163	2.0	5.9 E −06	export ABC transporter permease
VF_1164	1.5	1.9 E −04	export ABC transporter permease
macB (VF_1165)	2.8	3.1 E −06	macrolide ABC transporter ATP-binding membrane protein
VF_A0742	2.7	7.6 E −03	hypothetical protein
VF_A0743	3.0	1.7 E −03	multidrug resistance protein A
VF_A0904	2.0	*0.08*	transporter
VF_A0905	3.8	1.9 E −03	hypothetical protein
VF_A0906	3.0	7.7 E −03	acriflavin resistance periplasmic protein
VF_A0907	2.2	1.2 E −02	acriflavin resistance plasma membrane protein
VF_A0044	3.8	3.8 E −04	acriflavin resistance periplasmic protein
Colonization regulators			
tcpP (VF_A0473)	3.3	1.8 E −05	transcriptional regulatory protein TcpP
tcpH (VF_A0474)	4.9	3.5 E −05	transcriptional regulatory protein TcpH
Outer membrane proteins			
ompU (VF_0475)	1.6	6.5 E −03	outer membrane protein U porin
ompU2 (VF_A0487)	−6.7	2.9 E −33	outer membrane protein U paralog

a. Orange: upregulated; Blue: down-regulated in squid relative to seawater.
b. Genes listed showed differential expression between squid-associated (Vnt) and planktonic (Plk) *V. fischeri* of at least abs(log2(fc) > 1) and FDR-adjusted *p*-value < 0.01; *p*-value >0.05 in black italics.

glycerophosphodiester may be used as carbon sources by symbionts in the juvenile light organ (Pan *et al.*, 2015). Future metabolomics studies aimed at detecting these and other potential carbon sources in the host will help refine comparisons between our flux coupling analysis and transcriptomic results.

Finally, while no specific mechanism has yet been established to explain what limits the growth of bacterial symbionts as they repopulate the light organ each day (Ruby, 1996), one hypothesis has been that the host controls symbiont growth by limiting access to a specific nutrient, such as phosphate. However, we observed that genes encoding for phosphate transporters were consistently more highly transcribed in both fast-growing cultured and slow-growing planktonic cells than in the squid-associated cells (Table 1), inconsistent with the notion that the symbiont population is phosphate-limited.

Clues to other conditions within the host

We observed several examples of genes that were relatively upregulated in the squid-associated bacteria, and that could represent responses to two specific classes of host-derived biochemical stress: reactive oxygen species (ROS) and antimicrobial peptides. The symbiont transcriptome indicated a relatively high expression of several genes predicted to be involved in the detoxification of peroxidized membrane lipids (Table 2; Fig. 2), a condition arising from exposure to ROS. Two of these genes are predicted to be glutathione S-transferases (GST). While the enzymatic activity of these putative GSTs has not been characterized, one (*yfcG*, VF_1082) shows strong sequence and domain homology to *yfcG* from *Escherichia coli* (blastp E-value $< 10^{-54}$, amino acid identity = 46%), a GST with an important role in ROS resistance (Kanai *et al.*, 2006; Stourman *et al.*, 2011). Furthermore, we also observed significant upregulation of the *N*-ethylmaleimide reductase gene, *nemA*. This gene has similarly been linked to lipid-peroxidation stress in *E. coli* (Miura *et al.*, 1997; Williams and Bruce, 2002). The NemA homologue of *V. fischeri* ES114 shows significant identity to YqjM from *Bacillus subtilis* (blastp E-value $< 10^{-43}$, amino acid identity = 32%), which is involved in the oxidative stress response induced by hydrogen peroxide (Fitzpatrick *et al.*, 2003). These results lead to the conclusion that *V. fischeri* is exposed to ROS stress within its eukaryotic host, a notion that is supported by previous analyses of the host tissue and symbiont genetics (Visick and Ruby, 1998; Ruby and McFall-Ngai, 1999; Mone *et al.*, 2014; Schwartzman and Ruby, 2016).

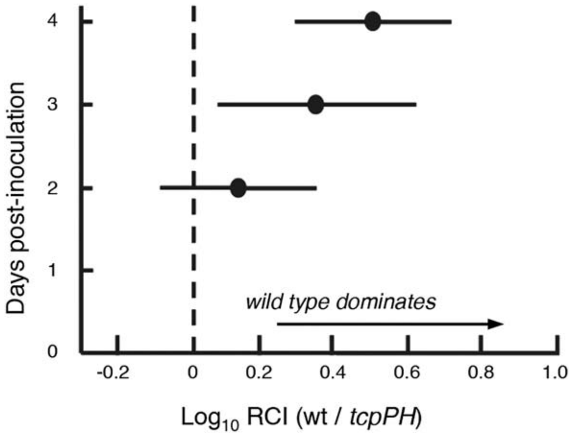

Fig. 3. Colonization defect of a *tcpPH* deletion mutant of *V. fischeri*. Newly hatched juvenile squid were placed into seawater inoculated with an equal number of wild-type and mutant cells. After 2, 3 and 4 days, the composition of the symbiont population in the light organ was determined and calculated as a relative colonization index (RCI). The *tcpPH* mutant was increasingly out-competed over the course of the colonization. Data are from two independent trials.

It was of particular interest to find three sets of genes that were annotated as encoding RND-family multidrug efflux pumps (Table 2). Such proteins share a domain structure predicted to be involved in the extrusion of antimicrobial small molecules and peptides (Koronakis *et al.*, 2000), and are required by *Vibrio cholerae* for effective colonization (Bina *et al.*, 2008). The relatively high expression of these genes suggests that *V. fischeri* cells are exposed to antimicrobial compounds that the symbionts are actively pumping out while they are within the light-organ crypts (Heath-Heckman *et al.*, 2014). One locus (VF_1161–1165) has homology to a polyketide efflux system, and is regulated via quorum signaling (Antunes *et al.*, 2007); thus, its induction is likely driven by the high density the symbiont population achieves within the crypts (McFall-Ngai, 2014). The basis for the 4- to 14-fold increase in expression of the two other putative RND-family gene sets (VF_A0742–0743) and (VF_ A0044; A0904–0907) is not clear; however, in *V. cholerae* there is a linkage between antimicrobial resistance and the increased expression of the membrane-bound regulatory proteins TcpP/H (Bina *et al.*, 2008); these regulators are 8- and 30-fold induced within the light organ relative to seawater (Table 2). This high level of expression led us to ask whether *tcpP/H* plays a role in early colonization, perhaps by regulating important symbiosis determinants. Interestingly, while a *tcpP/H* deletion mutant colonized about as well as wild-type parent over the first 48 h, it increasingly lost the ability to compete over time (Fig. 3). Although *V. fischeri* does not encode ToxT, the best-known target of TcpP/H in *V. cholerae*, we predict that the regulon of TcpP/H in *V. fischeri* includes important colonization genes, whose identities are under investigation.

Finally, the major outer membrane porin OmpU senses and protects *V. cholerae* from bactericidal/permeability-increasing peptides (Mathur and Waldor, 2004; Mathur *et al.*, 2007), like those induced by *V. fischeri* during colonization of its squid host (Krasity *et al.*, 2011). Much as in *V. cholerae*, the threefold to fourfold increase in *ompU* expression by symbiotic *V. fischeri* (Table 2) may be triggered by the surfeit of amino acids in the crypt matrix (Graf and Ruby, 1998; Mey *et al.*, 2012). Taken together, these patterns of symbiont gene expression indicate that the environment of the light-organ crypt presents *V. fischeri* with the ongoing challenge of host-produced antimicrobial compounds. The recognition that OmpU is a protecting colonization factor for both pathogenic (Duperthuy *et al.*, 2010) and beneficial (Aeckersberg *et al.*, 2001) species of *Vibrio* emphasizes the context-dependency of host-microbe interaction (Hentschel *et al.*, 2000)

Recent work with other symbioses has revealed that host-derived stresses are a common theme, not only between *V. fischeri* and its pathogenic congeners, but also among the microbiota of several vertebrate and invertebrate mutualisms (Schwartzman and Ruby, 2016). In each of these other associations, by presenting a particular mixture of antimicrobial peptides on its epithelial surfaces, the host apparently manages the composition of its epithelium-associated microbiota, selecting for particular communities of beneficial microbes while excluding pathogens (Duerkop *et al.*, 2009; Vaishnava *et al.*, 2011; Franzenburg *et al.*, 2013). Perhaps the synergistic activity of these kinds of RND multidrug effluxers (Bohnert *et al.*, 2011) induced by the symbionts (Table 2) allow them to target the squid's specific antimicrobial peptide, galaxin (Heath-Heckman *et al.*, 2014), and/or other compounds, contributing to the strict specificity of the symbiosis (McFall-Ngai, 2014).

Conclusions

We have reported here the first full RNA-Seq datasets of *Vibrio fischeri*, including one that is representative of the bacteria during colonization of the juvenile host. The gene expression patterns of bacteria making the habitat transition from seawater to host tissue have provided previously unavailable information suggesting that, once within the juvenile host, *V. fischeri* switches from a respiratory metabolism to one characteristic of G3P fermentation. Further, a flux coupled analysis using these transcriptional datasets and a newly developed genome-scale metabolic model for *V. fischeri* (Pan *et al.*, in review) have also provided us with predictive details about symbiont metabolism that would be inaccessible through conventional gene-expression analysis alone. Finally, this study identified the *V. cholerae* virulence determinants *tcpPH* as candidate regulators during the habitat transition of *V. fischeri*, and went on to experimentally demonstrate their importance to the success of a beneficial microbial symbioses.

Experimental procedures

Bacterial strains and growth conditions

The wild-type bacterium used in this study was *V. fischeri* strain ES114, isolated from an *E. scolopes* light organ (Boettcher and Ruby, 1990). Mutant *V. fischeri* cells were derived from strain ES114. The *Escherichia coli* cells used for cloning were strain DH5α λpir (Hanahan, 1983). Deletion mutants and fluorescently labelled strains were constructed as described previously (Stabb and Ruby, 2002; Dunn *et al.*, 2006; Le Roux *et al.*, 2007; Shibata and Visick, 2012). Primers were designed to generate homology regions upstream and downstream of the *tcpPH* locus (tcpPH_H1_Fwd: 5′- TCA GCC GTC GAC TGT TTA CTT CAA ATT AAT GAA GAG; tcpPH_H1_Rev: 5′- TCA GCC GCA TGC AAC CAT ATC ATC CTG ACT TAA; tcpPH_H2_Fwd: 5′- TCA GCC GCA TGC AAA TAC AAT AAT TAA TTT ATT TTC AAT AAT TTG; tcpPH_H2_Rev: 5′- TCA GCC ACT AGT ATT AAG ATA TGA TTT GAA AAA CAA ATT TTC), and the genotype of the mutant was confirmed via PCR (tcpPH_Conf_Fwd: 5′- ATT GCC AAA AAT CGG TTT; tcpPH_Conf_Rev: 5′- AAC CAT CCA CTT TGA TTT CAT). *V. fischeri* cells were grown at 28°C with shaking in either Luria-Bertani salt (LBS) broth (per liter, 10 g tryptone, 5 g yeast extract and 20 g NaCl) or a dilute artificial seawater-based tryptone (SWT) broth (5 g tryptone, 3 g yeast extract, 3 mL glycerol, 700 mL Instant Ocean (IO; Aquarium Systems, Mentor, OH, USA) at 33 ppt, and 300 mL water) as indicated. *E. coli* cells were grown in Luria-Bertani (LB) broth (10 g/L tryptone, 5 g/L yeast extract, 10 g/L NaCl) at 37°C with shaking. Planktonic conditions were simulated by culturing *V. fischeri* cells to mid-log phase in SWT medium, then inoculating filter-sterilized IO (FSIO) with approximately 2×10^8 CFU, and allowing the suspension to incubate at room temperature (~23°C) for 18 h. Antibiotics were used at the following concentrations when appropriate: erythromycin at 5 mg/mL for *V. fischeri* and 150 mg/mL for *E. coli*, and chloramphenicol at 2.5 mg/mL for *V. fischeri* and 25 mg/mL for *E. coli*.

Collection of bacterial RNA

Bacterial RNA was obtained from *V. fischeri* cells either grown in SWT to an OD_{600} of ~0.5 (‘cultured’), or cultured in SWT to an OD_{600} of ~0.5, then incubated in artificial seawater for 18 h (‘planktonic’), as described above (Fig. 1A). In both cases, the bacteria were collected by centrifugation at 12 000 rpm for 2 min (Model 5254R, Eppendorf) immediately prior to RNA extraction and purification using a ZR RNA MicroPrep Kit (Zymo Research).

To obtain squid-associated bacteria, freshly hatched juvenile squid from the University of Wisconsin-Madison aquarium facility were collected into *V. fischeri*-free IO. Animals were subsequently exposed for 3 h to approximately 5000 CFU of *V. fischeri* per mL, and then transferred to fresh *V. fischeri*-free IO. Animals were maintained on a 12:12 hour day:night cycle in batches of approximately 30 to 35 animals to optimize uniformity of colonization timing between individual animals. After ~36 h, colonization of the animals was verified by determining their production of bioluminescence using a luminometer (Turner TD 20/20). At approximately 48 h post-colonization, equivalent to the end of night time, animals were collected in batches of 100 into 80 mL of filter-sterilized IO, and exposed to light for 15 min to induce the normal dawn-cued expulsion of their bacterial population (Boettcher and Ruby, 1990). Squid were subsequently removed, and the expelled bacteria were collected by centrifugation at 12 000 rpm for 10 min at room temperature in an SS-34 rotor (Thermo Fisher Scientific). The supernatant was discarded, and total bacterial RNA was immediately extracted and purified using a ZR RNA MicroPrep Kit. In all cases, the time from initial light exposure to RNA extraction was $<$ 30 min.

RNA-seq library preparation and sequencing

Three (3) replicate RNA samples for each condition (squid-associated, planktonic, or cultured) were processed for RNA-Seq transcriptome analysis. Starting with total RNA, ribosomal RNA was removed using the Ribo-Zero Gold Epidemiology Kit (Epicentre), which removed prokaryotic (*V. fischeri*) rRNA as well as any contaminating eukaryotic (*E. scolopes*) rRNA. The resulting ribo-depleted RNA was then used for library preparation using the TruSeq RNA sample preparation kit (Illumina). Libraries were sequenced using Illumina HiSeq 2500 with high output, V4 chemistry, and 100-bp single-end reads. Fastq files were de-multiplexed, yielding on average 18M reads per sample (range: 5 to 26M reads per sample). Per-sample raw fastq files and processed CDS and rRNA count tables have been submitted to NCBI Gene Expression Omnibus (GEO) with accession number GSE80607.

Sequence read processing and mapping

Single-end fastq files were trimmed with Trimmomatic v.0.33, using the parameters ILLUMINACLIP:TruSeq3-SE.fa:2:30:10 LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:36 (the file TruSeq3-SE.fa contained TruSeq3 indexed and universal adapters as well as poly-A and poly-T sequences) (Bolger *et al.*, 2014). Reads from each sample were mapped to the *V. fischeri* ES114 genome (NC_006840.2) using bwa v.0.6.2 (Burrows–Wheeler Aligner), applying commands index, aln, and samse. The resulting SAM files were processed with SAMtools v.0.1.19 to generate BAM files (Li *et al.*, 2009). The numbers of reads mapping to protein-coding (CDS) or rRNA genes were calculated using the htseq-count command of HTSeq v.0.6.1p1 (Anders *et al.*, 2015). Ribo-depleted samples for the primary three-treatment comparison yielded an average of 10.0M CDS reads mapped per sample; ribo-depleted samples for the low-biomass comparison yielded an average of 5.3M CDS reads mapped per sample; in addition, ~34 000 rRNA reads were mapped per sample across both sets of ribo-depleted samples.

Differential expression analysis

Detection of genes differentially expressed (i.e. relative transcript abundance) between conditions was performed using the R packages DESeq2 and NOISeq from the Bioconductor program (Anders and Huber, 2010; Tarazona *et al.*, 2011). Low counts were removed using the NOISeq command filtered.data, with norm = FALSE, depth = NULL, method = 1, cv.cutoff = 10 and cpm = 5. After loading data into a data frame, DESeq2 was run using the commands DESeqDataSetFromMatrix, estimateSizeFactors, estimateDispersions and nbinomWaldTest. The three conditions (squid-associated, planktonic and cultured) were contrasted pairwise for all genes, and results exported as Benjamini–Hochberg adjusted *p*-values and log2(fold change). Differentially expressed genes were identified using tiered cutoffs of these values, with the most stringent cutoff being an adjusted p-value < 0.001 and abs(log2(fold change)) > 3.0 (three replicates per condition). All code used in data analysis and manuscript preparation is available at https://github.com/cuttlefishh/papers/tree/master/vibrio-fischeri-transcriptomics.

Light-organ colonization assay

To determine the relative colonization effectiveness of the *tcpP/H* deletion mutant, inocula were prepared that contained a 1:1 mixture of wild-type and mutant cells, differentially labelled with either green- (GFP) or red-fluorescent protein (RFP) (Dunn *et al.*, 2006). The inocula were prepared by growing each strain in SWT medium to mid-exponential phase (OD_{600} ~0.3) before diluting them in FSIO. Newly hatched squid were then transferred into the inoculated FSIO containing a pair of strains, with a total inoculum of around 5000 colony-forming unit (CFU) per mL. After 3 h of exposure to the inoculum, each squid was removed to a vial containing 4 mL of bacteria-free FSIO; at 24 h the FSIO was changed, and at 48, 72 and 96 h, 20 squids were homogenized, dilutions spread on LBS agar, and the number of GFP and RFP CFUs were counted using a fluorescence dissecting scope. The extent of a colonization defect in the *tcpP/H* mutant was determined by a relative competitive index (RCI), calculated as the ratio of the mutant to wild type in the light organ divided by the ratio in the inoculum (RCI = log[(CFU mutant)/(CFU wild type)]/[(inoculum CFU mutant)/(inoculum CFU wild type)]).

Flux-coupling analysis of symbiont sugar uptake

We analysed the transcriptome data using a constraint-based genome-scale metabolic model developed for *V. fischeri* ES114 (Pan *et al.*, in review). Flux-coupling analysis was performed on the model to identify which reactions (and their associated genes) are fully, partially, or directionally coupled to nutrient uptake (Burgard *et al.*, 2004). These types of reaction–nutrient coupling indicate that if the coupled reaction is active (i.e. carries a non-zero flux) then the nutrient must be consumed. As a result, the genes associated with these coupled reactions might serve as biomarkers for nutrient uptake. Flux-coupling analysis was performed assuming all sugars, amino acids, nucleotides and inorganic nutrients were available (by making the lower limits for all the exchange reactions in the model negative). The genes associated with reactions coupled to only one nutrient were compared with the list of differentially regulated genes to allow us to determine which nutrients could be used by *V. fischeri*. This metabolic model is included within the supplemental materials (Supporting Information Table S4).

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References

Aeckersberg, F., Lupp, C., Feliciano, B., and Ruby, E.G. (2001) *Vibrio fischeri* outer membrane protein OmpU plays a role in normal symbiotic colonization. *J Bacteriol* **183:** 6590–6597.

Almagro-Moreno, S., Pruss, K., and Taylor, R.K. (2015) Intestinal colonization dynamics of *Vibrio cholerae*. *PLoS Pathog* **11:** e1004787.

Anders, S., and Huber, W. (2010) Differential expression analysis for sequence count data. *Genome Biol* **11:** R106.

Anders, S., Pyl, P.T., and Huber, W. (2015) HTSeq–a Python framework to work with high-throughput sequencing data. *Bioinformatics (Oxford, England)* **31:** 166–169.

Antunes, L.C., Schaefer, A.L., Ferreira, R.B., Qin, N., Stevens, A.M., Ruby, E.G., and Greenberg, E.P. (2007) Transcriptome analysis of the *Vibrio fischeri* LuxR-LuxI regulon. *J Bacteriol* **189:** 8387–8391.

Bina, X.R., Provenzano, D., Nguyen, N., and Bina, J.E. (2008) *Vibrio cholerae* RND family efflux systems are required for antimicrobial resistance, optimal virulence factor production, and colonization of the infant mouse small intestine. *Infect Immun* **76:** 3595–3605.

Boettcher, K.J., and Ruby, E.G. (1990) Depressed light emission by symbiotic *Vibrio fischeri* of the sepiolid squid Euprymna scolopes. *J Bacteriol* **172:** 3701–3706.

Bohnert, J.A., Szymaniak-Vits, M., Schuster, S., and Kern, W.V. (2011) Efflux inhibition by selective serotonin reuptake inhibitors in *Escherichia coli*. *J Antimicrob Chemother* **66:** 2057–2060.

Bolger, A.M., Lohse, M., and Usadel, B. (2014) Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics (Oxford, England)* **30:** 2114–2120.

Brennan, C.A., Mandel, M.J., Gyllborg, M.C., Thomasgard, K.A., and Ruby, E.G. (2013) Genetic determinants of swimming motility in the squid light-organ symbiont *Vibrio fischeri*. *MicrobiologyOpen* **2:** 576–594.

Brooks, J.F., Gyllborg, M.C., Cronin, D.C., Quillin, S.J., Mallama, C.A., Foxall, R., *et al.* (2014) Global discovery of colonization determinants in the squid symbiont *Vibrio fischeri*. *Proc Natl Acad Sci U S A* **111:** 17284–17289.

Bry, L., Falk, P.G., Midtvedt, T., and Gordon, J.I. (1996) A model of host-microbial interactions in an open mammalian ecosystem. *Science* **273:** 1380–1383.

Bulgarelli, D., Schlaeppi, K., Spaepen, S., Ver Loren van Themaat, E., and Schulze-Lefert, P. (2013) Structure and functions of the bacterial microbiota of plants. *Annu Rev Plant Biol* **64:** 807–838.

Burgard, A.P., Nikolaev, E.V., Schilling, C.H., and Maranas, C.D. (2004) Flux coupling analysis of genome-scale metabolic network reconstructions. *Genome Res* **14:** 301–312.

Combs, P.A., and Eisen, M.B. (2015) Low-cost, low-input RNA-seq protocols perform nearly as well as high-input protocols. *PeerJ* **3:** e869–e869.

Dedeine, F., Vavre, F., Fleury, F., Loppin, B., Hochberg, M.E., and Bouletreau, M. (2001) Removing symbiotic Wolbachia bacteria specifically inhibits oogenesis in a parasitic wasp. *Proc Natl Acad Sci USA* **98:** 6247–6252.

Deloney-Marino, C.R., Wolfe, A.J., and Visick, K.L. (2003) Chemoattraction of *Vibrio fischeri* to serine, nucleosides, and *N*-acetylneuraminic acid, a component of squid light-organ mucus. *Appl Environ Microbiol* **69:** 7527–7530.

Duerkop, B.A., Vaishnava, S., and Hooper, L.V. (2009) Immune responses to the microbiota at the intestinal mucosal surface. *Immunity* **31:** 368–376.

Dunn, A.K., Karr, E.A., Wang, Y., Batton, A.R., Ruby, E.G., and Stabb, E.V. (2010) The alternative oxidase (AOX) gene in *Vibrio fischeri* is controlled by NsrR and upregulated in response to nitric oxide. *Mol Microbiol* **77:** 44–55.

Dunn, A.K., Millikan, D.S., Adin, D.M., Bose, J.L., and Stabb, E.V. (2006) New rfp- and pES213-derived tools for analyzing symbiotic *Vibrio fischeri* reveal patterns of infection and *lux* expression *in situ*. *Appl Environ Microbiol* **72:** 802–810.

Duperthuy, M., Binesse, J., LeRoux, F., Romestand, B., Caro, A., Got, P., *et al*. (2010) The major outer membrane protein OmpU of *Vibrio splendidus* contributes to host antimicrobial peptide resistance and is required for virulence in the oyster Crassostrea gigas. *Environ Microbiol* **12:** 951–963.

Fitzpatrick, T.B., Amrhein, N., and Macheroux, P. (2003) Characterization of YqjM, an Old Yellow Enzyme homolog from *Bacillus subtilis* involved in the oxidative stress response. *J Biol Chem* **278:** 19891–19897.

Franzenburg, S., Walter, J., Kunzel, S., Wang, J., Baines, J.F., Bosch, T.C., and Fraune, S. (2013) Distinct antimicrobial peptide expression determines host species-specific bacterial associations. *Proc Natl Acad Sci USA* **110:** E3730–E3738.

Gilbert, S.F., Sapp, J., and Tauber, A.I. (2012) A symbiotic view of life: we have never been individuals. *Q Rev Biol* **87:** 325–341.

Graf, J., Dunlap, P.V., and Ruby, E.G. (1994) Effect of transposon-induced motility mutations on colonization of the host light organ by *Vibrio fischeri*. *J Bacteriol* **176:** 6986–6991.

Graf, J., and Ruby, E.G. (1998) Characterization of the nutritional environment of a symbiotic light organ using bacterial mutants and biochemical analyses. *Proc Natl Acad Sci USA* **95:** 1818–1822.

Hanahan, D. (1983) Studies on transformation of *Escherichia coli* with plasmids. *J Mol Biol* **166:** 557–580.

Hansen, G.A., Ahmad, R., Hjerde, E., Fenton, C.G., Willassen, N.P., and Haugen, P. (2012) Expression profiling reveals Spot 42 small RNA as a key regulator in the central metabolism of *Aliivibrio salmonicida*. *BMC Genomics* **13:** 37.

Heath-Heckman, E.A., Gillette, A.A., Augustin, R., Gillette, M.X., Goldman, W.E., and McFall-Ngai, M.J. (2014) Shaping the microenvironment: evidence for the influence of a host galaxin on symbiont acquisition and maintenance in the squid-*Vibrio* symbiosis. *Environ Microbiol* **16:** 3669–3682.

Heath-Heckman, E.A., Peyer, S.M., Whistler, C.A., Apicella, M.A., Goldman, W.E., and McFall-Ngai, M.J. (2013) Bacterial bioluminescence regulates expression of a host cryptochrome gene in the squid-*Vibrio* symbiosis. *mBio* **4:** e00167–e00113.

Hentschel, U., Steinert, M., and Hacker, J. (2000) Common molecular mechanisms of symbiosis and pathogenesis. *Trends Microbiol* **8:** 226–231.

Hongoh, Y. (2010) Diversity and genomes of uncultured microbial symbionts in the termite gut. *Biosci Biotechnol Biochem* **74:** 1145–1151.

Hughes, D.T., and Sperandio, V. (2008) Inter-kingdom signalling: communication between bacteria and their hosts. *Nat Rev Microbiol* **6:** 111–120.

Kabat, A.M., Srinivasan, N., and Maloy, K.J. (2014) Modulation of immune development and function by intestinal microbiota. *Trends Immunol* **35:** 507–517.

Kanai, T., Takahashi, K., and Inoue, H. (2006) Three distinct-type glutathione S-transferases from *Escherichia coli* important for defense against oxidative stress. *J Biochem* **140:** 703–711.

Kao, C.Y., Sheu, B.S., and Wu, J.J. (2016) *Helicobacter pylori* infection: An overview of bacterial virulence factors and pathogenesis. *Biomed J* **39:** 14–23.

Koronakis, V., Sharff, A., Koronakis, E., Luisi, B., and Hughes, C. (2000) Crystal structure of the bacterial membrane protein TolC central to multidrug efflux and protein export. *Nature* **405:** 914–919.

Krasity, B.C., Troll, J.V., Weiss, J.P., and McFall-Ngai, M.J. (2011) LBP/BPI proteins and their relatives: conservation over evolution and roles in mutualism. *Biochem Soc Trans* **39:** 1039–1044.

Kremer, N., Philipp, E.E., Carpentier, M.C., Brennan, C.A., Kraemer, L., Altura, M.A., *et al*. (2013) Initial symbiont contact orchestrates host-organ-wide transcriptional changes that prime tissue colonization. *Cell Host Microbe* **14:** 183–194.

Lee, K.H., and Ruby, E.G. (1994) Effect of the squid host on the abundance and distribution of symbiotic *Vibrio fischeri* in nature. *Appl Environ Microbiol* **60:** 1565–1571.

Le Roux, F., Binesse, J., Saulnier, D., and Mazel, D. (2007) Construction of a *Vibrio splendidus* mutant lacking the metalloprotease gene *vsm* by use of a novel counterselectable suicide vector. *Appl Environ Microbiol* **73:** 777–784.

Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., Homer, N., *et al*. (2009) The sequence alignment/map format and SAMtools. *Bioinformatics (Oxford, England)* **25:** 2078–2079.

Mathur, J., Davis, B.M., and Waldor, M.K. (2007) Antimicrobial peptides activate the *Vibrio cholerae* sigmaE regulon through an OmpU-dependent signalling pathway. *Mol Microbiol* **63:** 848–858.

Mathur, J., and Waldor, M.K. (2004) The *Vibrio cholerae* ToxR-regulated porin OmpU confers resistance to antimicrobial peptides. *Infect Immun* **72:** 3577–3583.

McFall-Ngai, M., Hadfield, M.G., Bosch, T.C., Carey, H.V., Domazet-Loso, T., Douglas, A.E., *et al*. (2013) Animals in a bacterial world, a new imperative for the life sciences. *Proc Natl Acad Sci USA* **110:** 3229–3236.

McFall-Ngai, M.J. (2014) The importance of microbes in animal development: lessons from the squid-vibrio symbiosis. *Annu Rev Microbiol* **68:** 177–194.

Mey, A.R., Craig, S.A., and Payne, S.M. (2012) Effects of amino acid supplementation on porin expression and ToxR levels in *Vibrio cholerae*. *Infect Immun* **80:** 518–528.

Miura, K., Tomioka, Y., Hoshi, Y., Suzuki, H., Yonezawa, M., Hishinuma, T., and Mizugaki, M. (1997) The effects of unsaturated fatty acids, oxidizing agents and Michael reaction acceptors on the induction of *N*-ethylmaleimide reductase in *Escherichia coli*: possible application for drug design of chemoprotectors. *Methods Find Exp Clin Pharmacol* **19:** 147–151.

Miyashiro, T., Klein, W., Oehlert, D., Cao, X., Schwartzman, J., and Ruby, E.G. (2011) The *N*-acetyl-D-glucosamine repressor NagC of *Vibrio fischeri* facilitates colonization of *Euprymna scolopes*. *Mol Microbiol* **82:** 894–903.

Miyashiro, T., and Ruby, E.G.E. (2012) Shedding light on bioluminescence regulation in *Vibrio fischeri*. *Mol Microbiol* **84:** 795–806.

Mone, Y., Monnin, D., and Kremer, N. (2014) The oxidative environment: a mediator of interspecies communication that drives symbiosis evolution. *Proc R Soc B* **281:** 20133112.

Montgomery, M.K., and McFall-Ngai, M. (1994) Bacterial symbionts induce host organ morphogenesis during early postembryonic development of the squid *Euprymna scolopes*. *Development* **120:** 1719–1729.

Mullard, A. (2009) Microbiology: Tinker, bacteria, eukaryote, spy. *Nature* **459:** 159–161.

Neidhardt, F.C. (1996) *Escherichia Coli and Salmonella: Cellular and Molecular Biology*. Washington, DC: ASM Press.

Nyholm, S.V., and Graf, J. (2012) Knowing your friends: invertebrate innate immunity fosters beneficial bacterial symbioses. *Nat Rev Microbiol* **10:** 815–827.

Nyholm, S.V., and McFall-Ngai, M. (2004) The winnowing: establishing the squid–vibrio symbiosis. *Nat Rev Microbiol* **2:** 632–642.

Pan, M., Schwartzman, J.A., Dunn, A.K., Lu, Z., and Ruby, E.G. (2015) A Single host-derived glycan impacts key regulatory nodes of symbiont metabolism in a coevolved mutualism. *mBio* **6:** e00811–e00815.

Penterman, J., Abo, R.P., De Nisco, N.J., Arnold, M.F., Longhi, R., Zanda, M., and Walker, G.C. (2014) Host plant peptides elicit a transcriptional response to control the *Sinorhizobium meliloti* cell cycle during symbiosis. *Proc Natl Acad Sci USA* **111:** 3561–3566.

Ruby, E.G. (1996) Lessons from a cooperative, bacterial-animal association: the *Vibrio fischeri-Euprymna scolopes* light organ symbiosis. *Annu Rev Microbiol* **50:** 591–624.

Ruby, E.G., and Asato, L.M. (1993) Growth and flagellation of *Vibrio fischeri* during initiation of the sepiolid squid light organ symbiosis. *Arch Microbiol* **159:** 160–167.

Ruby, E.G., and Lee, K.H. (1998) The *Vibrio fischeri-Euprymna scolopes* light organ association: current ecological paradigms. *Appl Environ Microbiol* **64:** 805–812.

Ruby, E.G., and McFall-Ngai, M.J. (1999) Oxygen-utilizing reactions and symbiotic colonization of the squid light organ by *Vibrio fischeri*. *Trends Microbiol* **7:** 414–420.

Russell, J.B., and Rychlik, J.L. (2001) Factors that alter rumen microbial ecology. *Science* **292:** 1119–1122.

Schwartzman, J.A., Koch, E., Heath-Heckman, E.A., Zhou, L., Kremer, N., McFall-Ngai, M.J., and Ruby, E.G. (2015) The chemistry of negotiation: rhythmic, glycan-driven acidification in a symbiotic conversation. *Proc Natl Acad Sci USA* **112:** 566–571.

Schwartzman, J.A., and Ruby, E.G. (2016) Stress as a normal cue in the symbiotic environment. *Trends Microbiol*. **24:** 414–424. doi: 10.1016/j.tim.2016.02.012

Septer, A.N., and Stabb, E.V. (2012) Coordination of the *arc* regulatory system and pheromone-mediated positive feedback in controlling the *Vibrio fischeri lux* operon. *PLoS ONE* **7:** e49590.

Septer, A.N., Bose, J.L., Lipzen, A., Martin, J., Whistler, C., and Stabb, E.V. (2015) Bright luminescence of *Vibrio fischeri* aconitase mutants reveals a connection between citrate and the Gac/Csr regulatory system. *Mol Microbiol* **95:** 283–296.

Shibata, S., and Visick, K.L. (2012) Sensor kinase RscS induces the production of antigenically distinct outer membrane vesicles that depend on the symbiosis polysaccharide locus in *Vibrio fischeri*. *J Bacteriol* **194:** 185–194.

Shin, S.C., Kim, S.H., You, H., Kim, B., Kim, A.C., Lee, K.A., *et al*. (2011) *Drosophila* microbiome modulates host developmental and metabolic homeostasis via insulin signaling. *Science* **334:** 670–674.

Soo, P.C., Horng, Y.T., Lai, M.J., Wei, J.R., Hsieh, S.C., Chang, Y.L., *et al*. (2007) Pirin regulates pyruvate catabolism by interacting with the pyruvate dehydrogenase E1 subunit and modulating pyruvate dehydrogenase activity. *J Bacteriol* **189:** 109–118.

Stabb, E.V., and Ruby, E.G. (2002) RP4-based plasmids for conjugation between *Escherichia coli* and members of the *Vibrionaceae*. *Methods Enzymol* **358:** 413–426.

Stourman, N.V., Branch, M.C., Schaab, M.R., Harp, J.M., Ladner, J.E., and Armstrong, R.N. (2011) Structure and function of YghU, a nu-class glutathione transferase related to YfcG from *Escherichia coli*. *Biochemistry* **50:** 1274–1281.

Tarazona, S., Garcia-Alcalde, F., Dopazo, J., Ferrer, A., and Conesa, A. (2011) Differential expression in RNA-seq: A matter of depth. *Genome Res* **21:** 2213–2223.

Uzal, F.A., McClane, B.A., Cheung, J.K., Theoret, J., Garcia, J.P., Moore, R.J., and Rood, J.I. (2015) Animal models to study the pathogenesis of human and animal *Clostridium perfringens* infections. *Vet Microbiol* **179:** 23–33.

Vaishnava, S., Yamamoto, M., Severson, K.M., Ruhn, K.A., Yu, X., Koren, O., *et al*. (2011) The antibacterial lectin RegIII-gamma promotes the spatial segregation of microbiota and host in the intestine. *Science* **334:** 255–258.

Visick, K.L., Foster, J., Doino, J., McFall-Ngai, M., and Ruby, E.G. (2000) *Vibrio fischeri lux* genes play an important role in colonization and development of the host light organ. *J Bacteriol* **182:** 4578–4586.

Visick, K.L., and Ruby, E.G. (1998) The periplasmic, group III catalase of *Vibrio fischeri* is required for normal symbiotic competence and is induced both by oxidative stress and by approach to stationary phase. *J Bacteriol* **180:** 2087–2092.

Wang, Y., Dufour, Y.S., Carlson, H.K., Donohue, T.J., Marletta, M.A., and Ruby, E.G. (2010) H-NOX-mediated nitric oxide sensing modulates symbiotic colonization by *Vibrio fischeri*. *Proc Natl Acad Sci USA* **107:** 8375–8380.

Wier, A.M., Nyholm, S.V., Mandel, M.J., Massengo-Tiasse, R.P., Schaefer, A.L., Koroleva, I., *et al*. (2010) Transcriptional patterns in both host and bacterium underlie a daily rhythm of anatomical and metabolic change in a beneficial symbiosis. *Proc Natl Acad Sci USA* **107:** 2259–2264.

Williams, R.E., and Bruce, N.C. (2002) 'New uses for an Old Enzyme'–the Old Yellow Enzyme family of flavoenzymes. *Microbiology* **148:** 1607–1614.

Supporting information

Additional Supporting Information may be found in the online version of this article at the publisher's website:

Fig. S1. Effectiveness of ribo-depletion for enrichment of CDS transcripts over rRNA transcripts. (A) Proportions of reads assigned to CDS and rRNA in ribo-depleted and non-ribo-depleted samples. (B) Distribution of read assignments to CDS and rRNA among "sum good alignments", "not aligned", "ambiguous", and "no feature" groupings.

Fig. S2. Pairwise scatter plots of CDS transcript counts between ribo-depleted and non-ribo-depleted samples, in relative abundance units (counts per million total CDS counts).

Fig. S3. Pairwise scatter plots of low-biomass (between 10 and 1000 ng) total-RNA library-prep counts versus counts from the 100-ng total-RNA sample. All samples shown were ribo-depleted. Transcript counts are in relative abundance units (counts per million total CDS counts).

Fig. S4. Pairwise scatter plots of low-biomass (between 1 and 5 ng) total-RNA library-prep counts versus counts from the 100-ng total RNA sample. All samples shown were ribo-depleted. Transcript counts are in relative abundance units (counts per million total CDS counts).

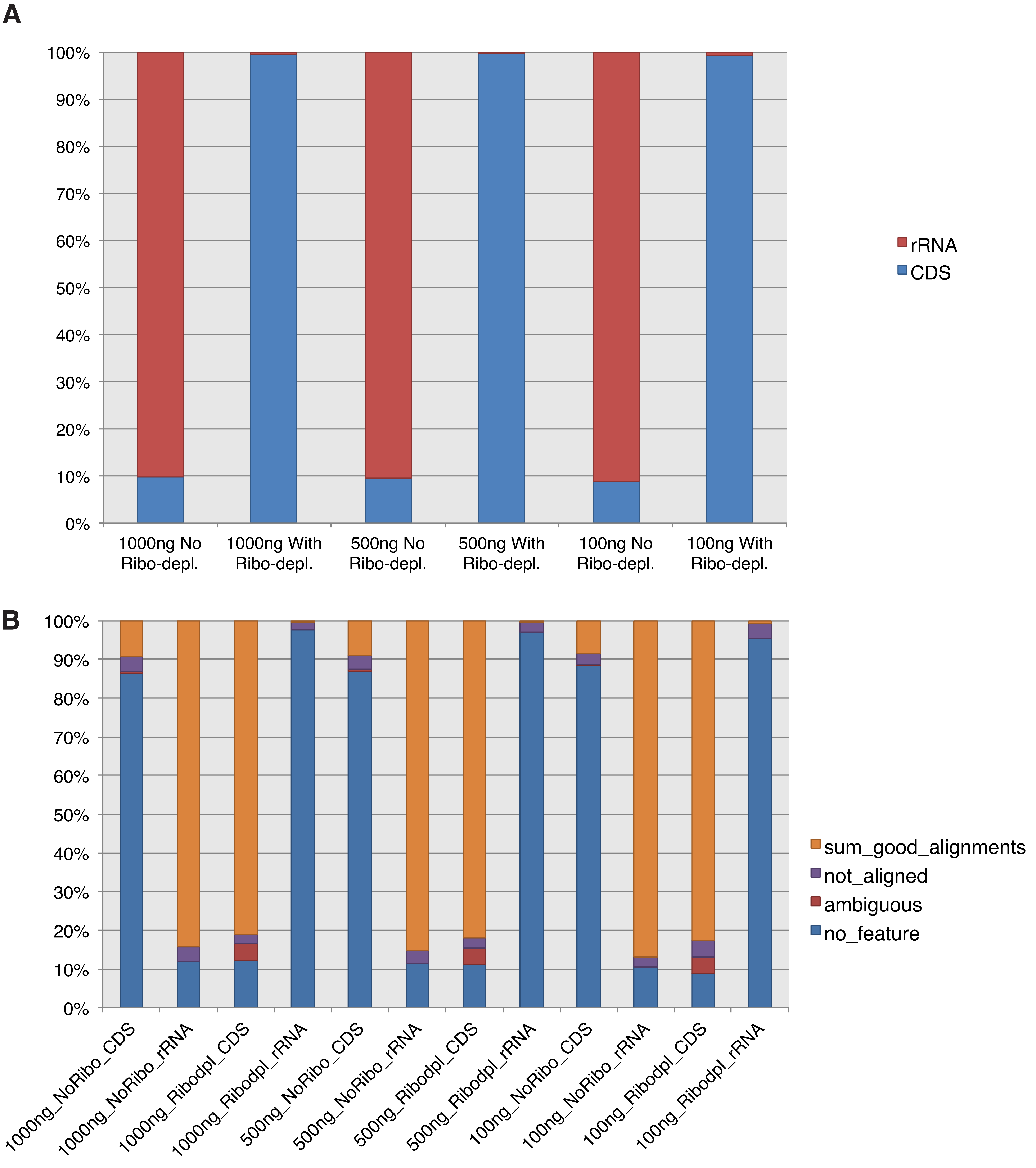
Fig. S5. Effectiveness of low-biomass analyses to detect rare transcripts. (A) Percent coverage of the *V. fischeri* genome as function of total RNA input and the number of library amplification cycles. (B) Fraction of library preps a transcript is detected in (out of 15 total) as a function of total RNA input amount.

Table S1. Summary of *V. fischeri* samples analyzed by RNA-Seq. For each sample name the following information is provided: accession number (NCBI GEO SRA), description and source name (low-biomass test or replicate #1–3 of the planktonic, SWT or vented treatments), organism, growth medium, total RNA input, ribo-depletion status, library PCR amplification cycles, replicate number, and molecule type. Full study data including CDS and rRNA count tables are available using the main GEO accession number GSE80607 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE80607). *Note*: the sample for the 100-ng ribo-depleted test (*i.e.*, 100ng_Ribodpl) is identical to SWT replicate 3 (Swt3_Ribodpl).

Table S2. Relative expression levels of bioluminescence and motility genes in *V. fischeri*. Genes listed showed differential expression between squid-associated (Vnt) and planktonic (Plk) *V. fischeri* of at least abs(log2(fc) $>$ 1) and FDR-adjusted *p*-value < 0.01

Table S3. Differentially expressed genes appearing during both the comparisons of squid-associated *V. fischeri* (Vnt), seawater-suspended *V. fischeri* (Plk) and SWT medium-grown *V. fischeri*(SWT). Differential expression cutoffs used $|\log2(fc)| > 3$ and FDR-adjusted *p*-value $< .001$. Those genes whose relative level of expression is in the same direction for Vnt/Plk and Vnt/SWT comparisons are indicated by a check mark.

Table S4.


A
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
1000ng No Ribo-depl.
1000ng With Ribo-depl.
500ng No Ribo-depl.
500ng With Ribo-depl.
100ng No Ribo-depl.
100ng With Ribo-depl.
rRNA
CDS
B
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
1000ng_NoRibo_CDS
1000ng_NoRibo_rRNA
1000ng_Ribodpl_CDS
1000ng_Ribodpl_rRNA
500ng_NoRibo_CDS
500ng_NoRibo_rRNA
500ng_Ribodpl_CDS
500ng_Ribodpl_rRNA
100ng_NoRibo_CDS
100ng_NoRibo_rRNA
100ng_Ribodpl_CDS
100ng_Ribodpl_rRNA
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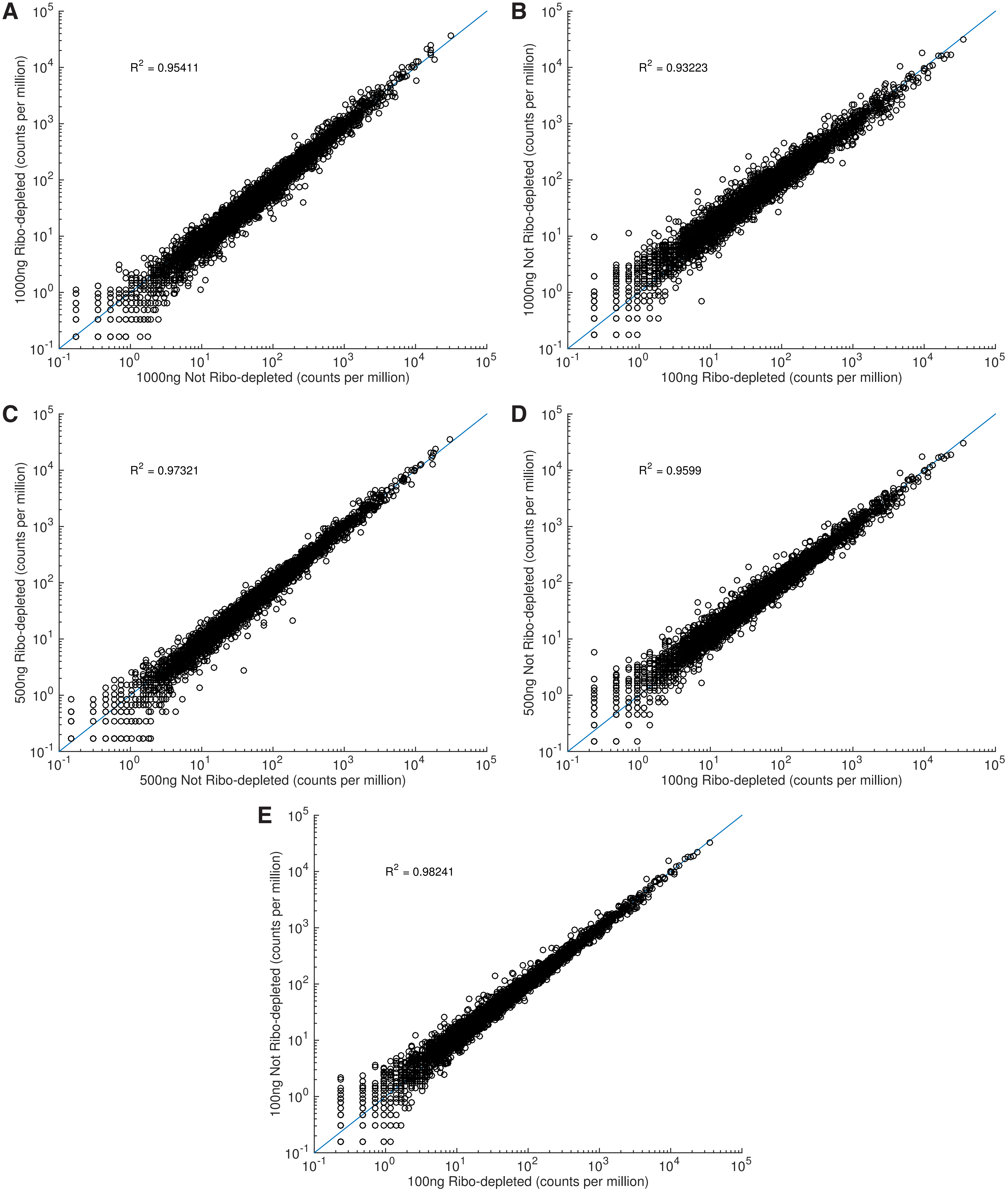
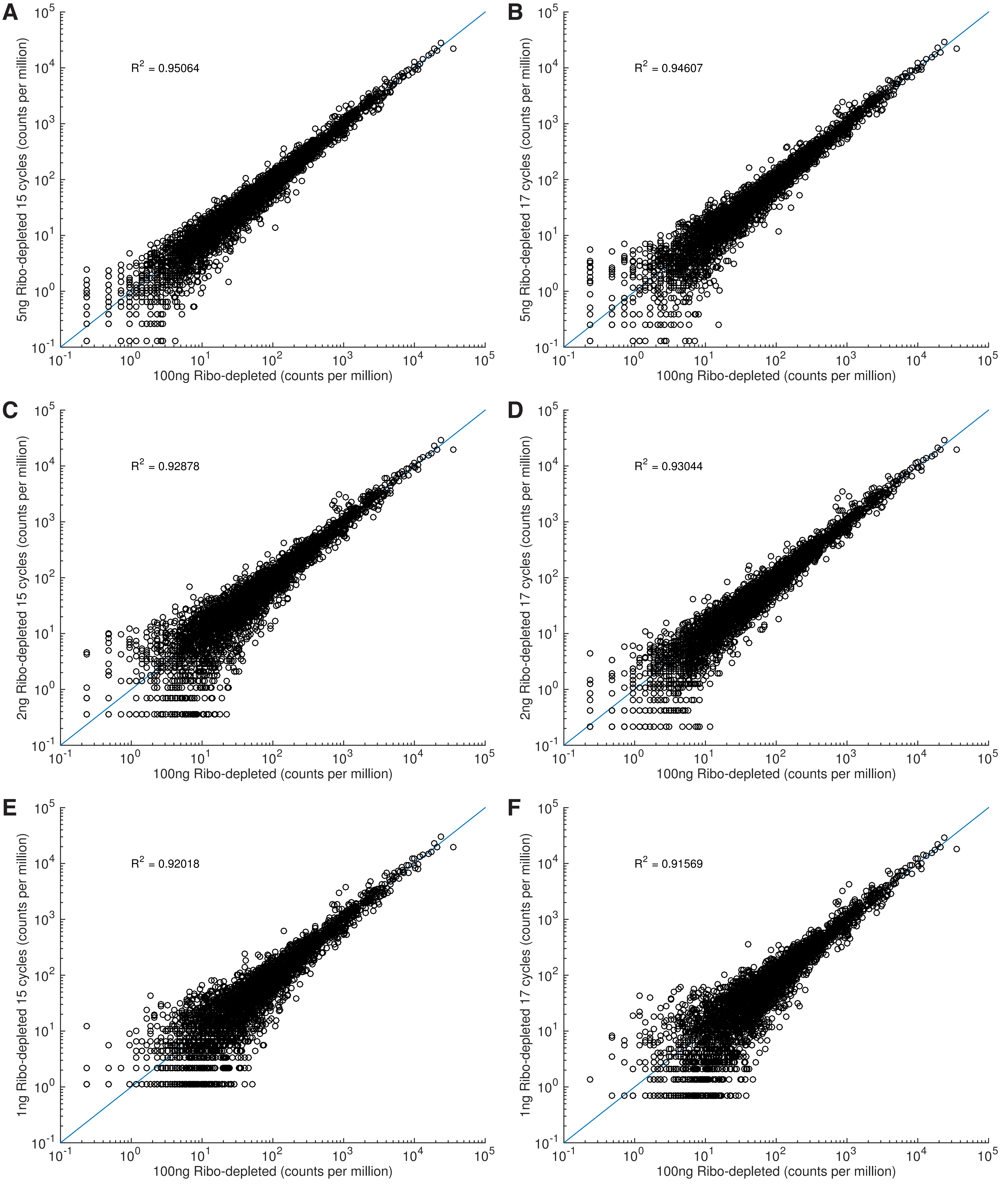
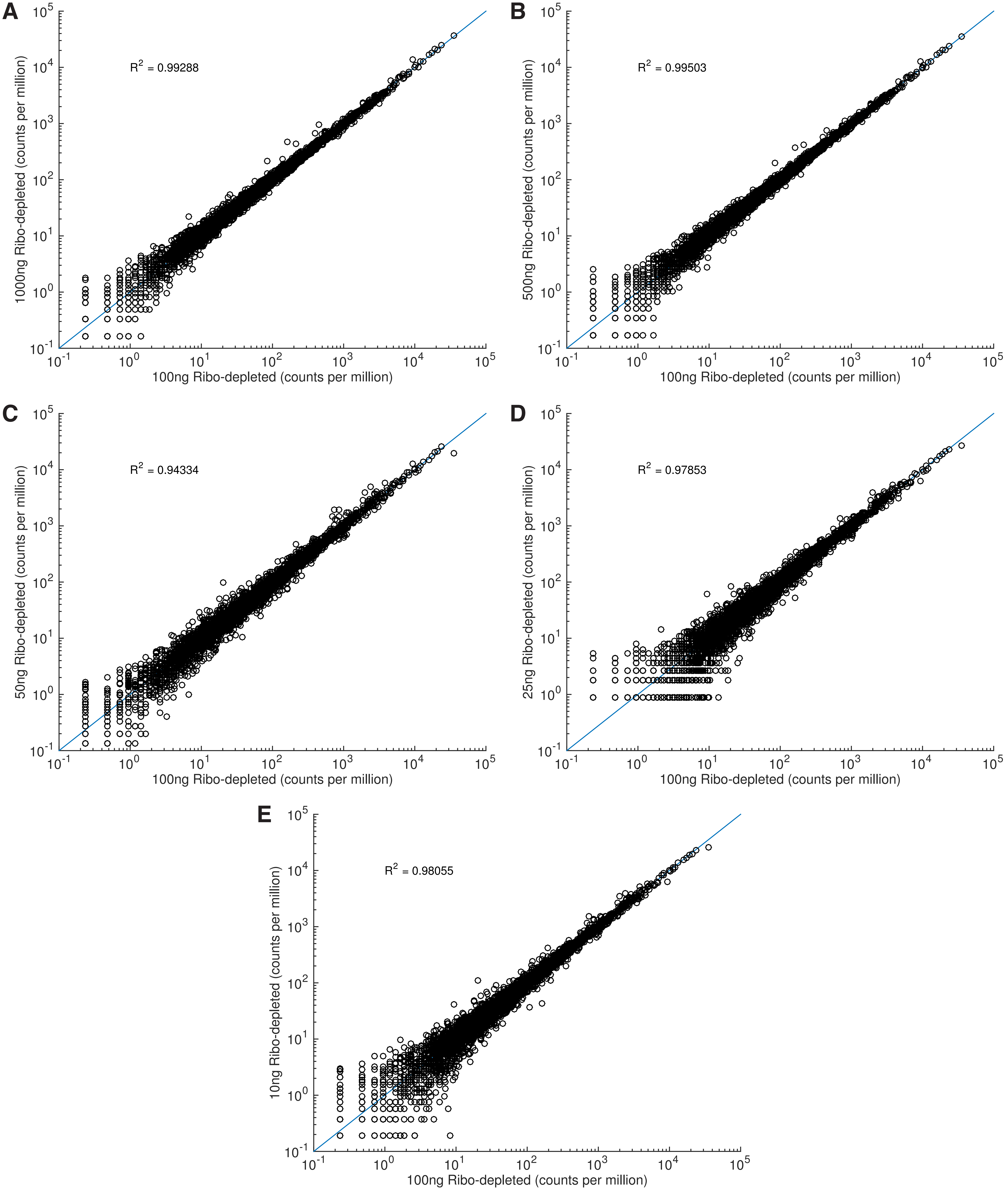
not_aligned
ambiguous
no_feature


A
R^2 = 0.95411
1000ng Ribo-depleted (counts per million)
1000ng Not Ribo-depleted (counts per million)
B
R^2 = 0.93223
1000ng Not Ribo-depleted (counts per million)
100ng Ribo-depleted (counts per million)
C
R^2 = 0.97321
500ng Ribo-depleted (counts per million)
500ng Not Ribo-depleted (counts per million)
D
R^2 = 0.9599
500ng Not Ribo-depleted (counts per million)
100ng Ribo-depleted (counts per million)
E
R^2 = 0.98241
100ng Not Ribo-depleted (counts per million)
100ng Ribo-depleted (counts per million)
10^-1
10^0
10^1
10^2
10^3
10^4
10^5


A
R^2 = 0.95064
5ng Ribo-depleted 15 cycles (counts per million)
100ng Ribo-depleted (counts per million)
B
R^2 = 0.94607
5ng Ribo-depleted 17 cycles (counts per million)
100ng Ribo-depleted (counts per million)
C
R^2 = 0.92878
2ng Ribo-depleted 15 cycles (counts per million)
100ng Ribo-depleted (counts per million)
D
R^2 = 0.93044
2ng Ribo-depleted 17 cycles (counts per million)
100ng Ribo-depleted (counts per million)
E
R^2 = 0.92018
1ng Ribo-depleted 15 cycles (counts per million)
100ng Ribo-depleted (counts per million)
F
R^2 = 0.91569
1ng Ribo-depleted 17 cycles (counts per million)
100ng Ribo-depleted (counts per million)
10^-1
10^0
10^1
10^2
10^3
10^4
10^5


A
R^2 = 0.99288
1000ng Ribo-depleted (counts per million)
100ng Ribo-depleted (counts per million)
B
R^2 = 0.99503
500ng Ribo-depleted (counts per million)
100ng Ribo-depleted (counts per million)
C
R^2 = 0.94334
50ng Ribo-depleted (counts per million)
100ng Ribo-depleted (counts per million)
D
R^2 = 0.97853
25ng Ribo-depleted (counts per million)
100ng Ribo-depleted (counts per million)
E
R^2 = 0.98055
10ng Ribo-depleted (counts per million)
100ng Ribo-depleted (counts per million)
10^{-1}
10^0
10^1
10^2
10^3
10^4
10^5

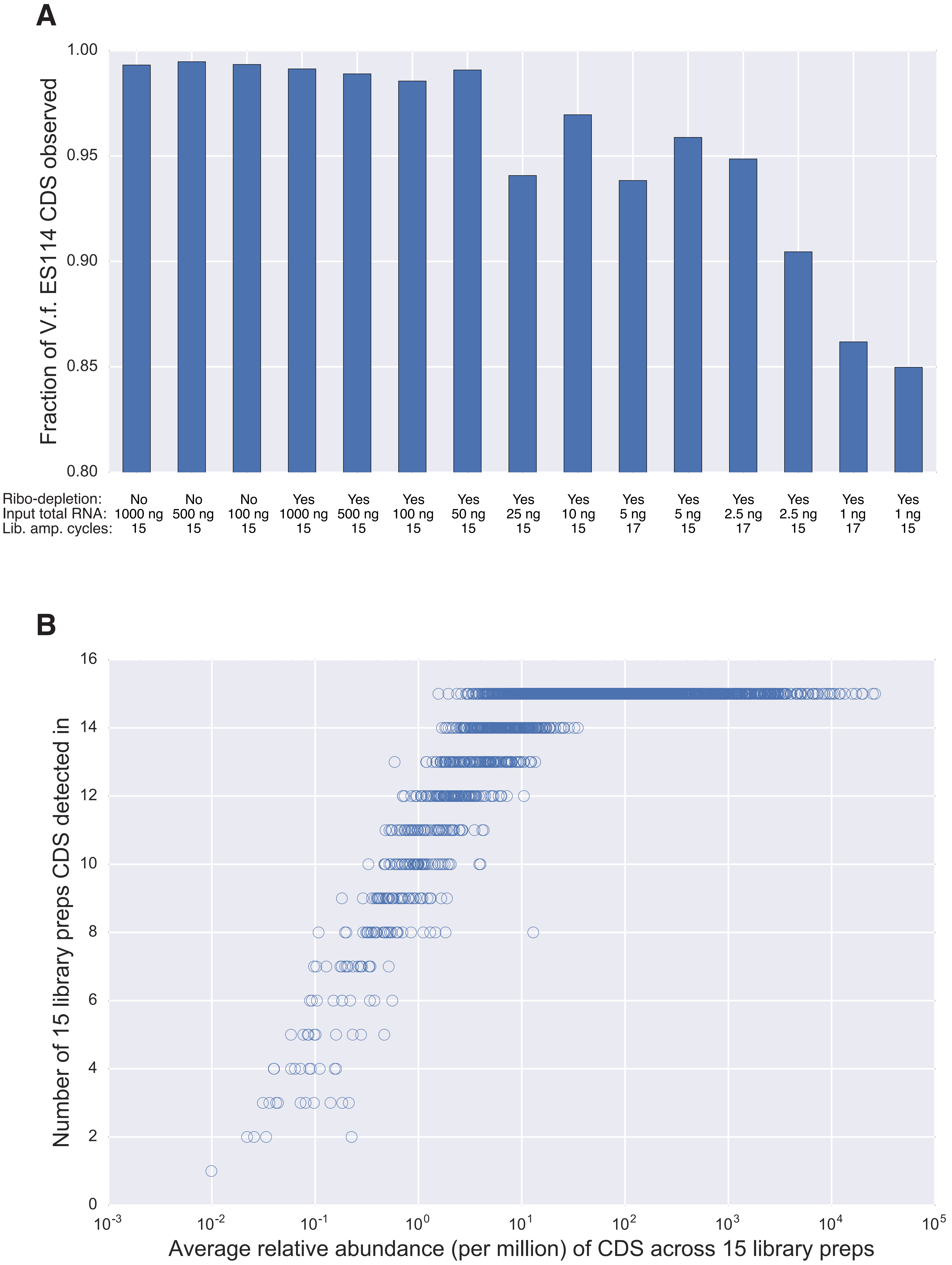

A
Fraction of V.f. ES114 CDS observed
1.00
0.95
0.90
0.85
0.80
Ribo-depletion: No No No Yes Yes Yes Yes Yes Yes Yes Yes Yes Yes Yes Yes
Input total RNA: 1000 ng 500 ng 100 ng 1000 ng 500 ng 100 ng 50 ng 25 ng 10 ng 5 ng 5 ng 2.5 ng 2.5 ng 1 ng 1 ng
Lib. amp. cycles: 15 15 15 15 15 15 15 15 15 17 15 17 15 17 15
B
Number of 15 library preps CDS detected in
16
14
12
10
8
6
4
2
0
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
10^{5}
Average relative abundance (per million) of CDS across 15 library preps

Table S1. Summary of *V. fischeri* samples analyzed by RNA-Seq.

Sample name	Accession no.	Description
1000ng_NoRibo	GSM2131511	Low-biomass test with 1000ng total RNA and no ribodepletion
500ng_NoRibo	GSM2131512	Low-biomass test with 500ng total RNA and no ribodepletion
100ng_NoRibo	GSM2131513	Low-biomass test with 100ng total RNA and no ribodepletion
1000ng_Ribodpl	GSM2131514	Low-biomass test with 1000ng total RNA and ribodepletion
500ng_Ribodpl	GSM2131515	Low-biomass test with 500ng total RNA and ribodepletion
50ng_Ribodpl	GSM2131516	Low-biomass test with 50ng total RNA and ribodepletion
25ng_Ribodpl	GSM2131517	Low-biomass test with 25ng total RNA and ribodepletion
10ng_Ribodpl	GSM2131518	Low-biomass test with 10ng total RNA and ribodepletion
5ng_Ribodpl_17cyc	GSM2131519	Low-biomass test with 5ng total RNA and ribodepletion (2 additional cycles)
5ng_Ribodpl_15cyc	GSM2131520	Low-biomass test with 5ng total RNA and ribodepletion
2ng_Ribodpl_17cyc	GSM2131521	Low-biomass test with 2.5ng total RNA and ribodepletion (2 additional cycles)
2ng_Ribodpl_15cyc	GSM2131522	Low-biomass test with 2.5ng total RNA and ribodepletion
1ng_Ribodpl_17cyc	GSM2131523	Low-biomass test with 1ng total RNA and ribodepletion (2 additional cycles)
1ng_Ribodpl_15cyc	GSM2131524	Low-biomass test with 1ng total RNA and ribodepletion
Plk1_Ribodpl	GSM2131525	Planktonic replicate 1 (100ng total RNA and ribodepletion)
Plk2_Ribodpl	GSM2131526	Planktonic replicate 2 (100ng total RNA and ribodepletion)
Plk3_Ribodpl	GSM2131527	Planktonic replicate 3 (100ng total RNA and ribodepletion)
Swt1_Ribodpl	GSM2131528	SWT replicate 1 (100ng total RNA and ribodepletion)
Swt2_Ribodpl	GSM2131529	SWT replicate 2 (100ng total RNA and ribodepletion)
Swt3_Ribodpl	GSM2131530	SWT replicate 3 (100ng total RNA and ribodepletion)
Vnt1_Ribodpl	GSM2131531	Vented replicate 1 (100ng total RNA and ribodepletion)
Vnt2_Ribodpl	GSM2131532	Vented replicate 2 (100ng total RNA and ribodepletion)
Vnt3_Ribodpl	GSM2131533	Vented replicate 3 (100ng total RNA and ribodepletion)

Table S2. Relative expression levels of bioluminescence and motility genes in *V. fischeri*

Gene*	**Vnt / Plk log2(fc)†**	**FDR-adjusted *p*-value†**	**Description**
Bioluminescence			
***luxR* (VF_A0925)**	2.3	1.7 E-06	LuxR family transcriptional regulator
***luxI* (VF_A0924)**	4.5	6.0 E-09	3-oxo-C6-HSL autoinducer synthesis protein
***luxC* (VF_A0923)**	4.8	1.8 E-12	acyl-CoA reductase
***luxD* (VF_A0922)**	5.0	9.5 E-14	acyl transferase
***luxA* (VF_A0921)**	5.4	1.5 E-14	luciferase alpha chain
***luxB* (VF_A0920)**	5.5	4.6 E-11	luciferase beta chain
***luxE* (VF_A0919)**	4.9	3.9 E-10	long-chain-fatty-acid ligase
***luxG* (VF_A0918)**	4.3	9.1 E-15	FMN reductase
Flagellar motility			
***motA* (VF_0714)**	-2.2	1.5 E-05	flagellar motor protein
***motB* (VF_0715)**	-2.8	9.6 E-07	flagellar motor protein
***flhA* (VF_1837)**	-2.2	6.0 E-03	flagellar biosynthesis protein
***flhB* (VF_1839)**	-3.0	9.0 E-05	flagellar biosynthesis protein
***fliR* (VF_1840)**	-2.6	2.0 E-06	flagellar biosynthesis protein
***fliQ* (VF_1841)**	-3.0	4.4 E-05	flagellar biosynthesis protein
***fliP* (VF_1842)**	-3.2	1.4 E-04	flagellar biosynthesis protein
***fliO* (VF_1843)**	-3.1	4.8 E-04	flagellar biosynthesis protein
***fliN* (VF_1844)**	-2.9	3.2 E-03	flagellar motor switch protein
***fliM* (VF_1845)**	-2.7	7.1 E-04	flagellar motor switch protein
***fliK* (VF_1847)**	-2.6	9.5 E-06	flagellar hook length control protein
***fliJ* (VF_1848)**	-2.5	1.2 E-03	flagellar biosynthesis chaperone
***fliI* (VF_1849)**	-1.7	2.4 E-03	flagellum-specific ATP synthase
***fliG* (VF_1851)**	-3.4	1.1 E-03	flagellar motor switch protein
***fliF* (VF_1852)**	-3.6	4.4 E-07	flagellar MS-ring protein
***fliE* (VF_1853)**	-2.6	4.0 E-05	flagellar hook-basal body protein
***flrC* (VF_1854)**	-3.5	9.0 E-04	two-component response regulator
***flrB* (VF_1855)**	-2.8	7.9 E-04	sensory histidine kinase
***fliD* (VF_1860)**	-3.0	7.5 E-09	flagellar capping protein
***flaG* (VF_1861)**	-3.9	9.8 E-10	flagellin
***flaE* (VF_1862)**	-2.4	3.8 E-03	flagellin
***flaD* (VF_1863)**	-3.1	3.9 E-05	flagellin
***flaA* (VF_1866)**	-2.2	7.7 E-03	flagellin
***flgK* (VF_1868)**	-1.3	7.0 E-03	flagellar hook-associated protein
***flgI* (VF_1870)**	-2.3	2.0 E-04	flagellar basal body P-ring biosynthesis protein
***flgG* (VF_1872)**	-2.7	3.0 E-05	flagellar basal body rod protein
***flgM* (VF_1881)**	-1.4	2.9 E-03	flagellar anti-sigma-28 factor
***flgN* (VF_1882)**	-2.0	3.1 E-04	chaperone
***flaF* (VF_2079)**	-3.4	2.7 E-04	flagellin
***motX* (VF_2317)**	-3.1	9.6 E-04	flagellar motor protein

* Orange: upregulated; Blue: down-regulated in squid relative to seawater.

† Genes listed showed differential expression between squid-associated (Vnt) and planktonic (Plk) *V. fischeri* of at least abs(log2(fc) > 1) and FDR-adjusted *p*-value < 0.01.

Table S3. Differentially expressed genes appearing during both the comparisons of sq

VF_number	CDS_number	Plk1_rpkm	Plk2_rpkm	Plk3_rpkm	Plk_rpkm_	Plk_rpkm_	SWT1_rpk
VF_0001	c1cds0	26.7	14.3	10.4	17.1	8.5	85.1
VF_0002	c1cds1	126.8	95.0	112.9	111.6	16.0	113.2
VF_0003	c1cds2	115.2	225.2	306.0	215.5	95.8	753.5
VF_0004	c1cds3	39.0	106.1	142.3	95.8	52.4	305.8
VF_0005	c1cds4	5483.9	5720.1	3946.2	5050.1	963.3	7467.4
VF_0006	c1cds5	177.9	49.2	68.4	98.5	69.4	11.1
VF_0007	c1cds6	98.7	28.1	35.5	54.1	38.8	4.9
VF_0008	c1cds7	1127.2	161.1	223.6	504.0	540.6	16.2
VF_0009	c1cds8	14.3	32.0	37.6	28.0	12.2	149.0
VF_0010	c1cds9	31.5	47.4	53.6	44.2	11.4	187.0
VF_0011	c1cds10	74.4	76.0	90.2	80.2	8.7	257.3
VF_0012	c1cds11	75.5	108.2	130.4	104.7	27.6	674.3
VF_0013	c1cds12	548.8	516.5	376.9	480.7	91.4	115.0
VF_0014	c1cds13	12.1	19.9	21.9	18.0	5.2	43.6
VF_0015	c1cds14	37.7	45.6	60.1	47.8	11.3	564.2
VF_0016	c1cds15	52.6	67.5	92.3	70.8	20.1	537.1
VF_0017	c1cds16	122.8	88.9	105.7	105.8	16.9	118.9
VF_0018	c1cds17	2648.5	1285.4	949.5	1627.8	899.8	546.3
VF_0019	c1cds18	37.0	103.8	124.5	88.5	45.7	29.4
VF_0020	c1cds19	1746.5	2918.4	1492.6	2052.5	760.6	77.2
VF_0021	c1cds20	50.1	66.8	57.6	58.1	8.4	29.1
VF_0022	c1cds21	24.7	25.4	17.3	22.4	4.5	14.3
VF_0023	c1cds22	661.0	353.5	353.5	456.0	177.5	148.9
VF_0024	c1cds23	843.0	775.1	609.0	742.3	120.4	7.2
VF_0025	c1cds24	937.3	545.7	674.7	719.3	199.6	7.1
VF_0026	c1cds25	28.2	37.4	34.1	33.2	4.7	35.7
VF_0027	c1cds26	15.4	20.7	16.0	17.4	2.9	25.8
VF_0028	c1cds27	16.2	17.1	18.3	17.2	1.0	40.2
VF_0029	c1cds28	38.6	24.7	24.3	29.2	8.2	204.0
VF_0030	c1cds29	61.6	29.9	17.5	36.3	22.7	139.8
VF_0031	c1cds30	93.4	41.5	38.1	57.7	31.0	13.0
VF_0032	c1cds31	2.3	2.3	2.3	2.3	0.0	3.6
VF_0033	c1cds32	3.2	2.4	2.1	2.6	0.6	3.2
VF_0034	c1cds33	4.5	2.1	3.6	3.4	1.2	4.0
VF_0035	c1cds35	6.2	2.7	3.5	4.1	1.8	5.6
VF_0036	c1cds36	7.3	4.6	5.6	5.8	1.4	5.2
VF_0037	c1cds37	25.7	22.2	25.3	24.4	1.9	28.2
VF_0038	c1cds38	57.7	59.7	71.8	63.1	7.6	215.3
VF_0040	c1cds39	17.7	7.1	7.8	10.8	5.9	14.9
VF_0041	c1cds40	37.8	69.4	58.1	55.1	16.0	239.9

VF_0042	c1cds41	149.4	159.9	154.0	154.4	5.3	178.8
VF_0043	c1cds42	26.1	25.1	25.2	25.5	0.5	12.5
VF_0044	c1cds43	8.5	7.8	7.8	8.0	0.4	27.7
VF_0046	c1cds44	28.2	39.9	49.2	39.1	10.5	248.4
VF_0047	c1cds45	6.8	16.4	16.3	13.2	5.5	64.7
VF_0048	c1cds46	179.6	127.2	140.8	149.2	27.2	127.3
VF_0049	c1cds47	1438.9	550.3	512.0	833.8	524.4	603.3
VF_0050	c1cds48	804.2	553.5	714.7	690.8	127.1	367.1
VF_0051	c1cds49	821.3	410.2	470.1	567.2	222.1	307.9
VF_0052	c1cds50	11.8	12.5	20.2	14.8	4.7	33.4
VF_0053	c1cds51	119.8	87.6	100.3	102.6	16.2	290.6
VF_0054	c1cds52	56.4	84.5	106.5	82.5	25.1	218.8
VF_0056	c1cds53	72.6	120.9	136.7	110.1	33.4	432.5
VF_0057	c1cds54	672.3	690.3	647.1	669.9	21.7	861.5
VF_0058	c1cds55	408.4	479.6	628.1	505.4	112.1	605.3
VF_0059	c1cds56	402.2	175.6	213.8	263.9	121.3	34.8
VF_0060	c1cds57	131.1	142.2	168.5	147.3	19.2	122.7
VF_0061	c1cds58	64.3	74.5	63.8	67.5	6.1	82.9
VF_0062	c1cds59	63.5	64.0	90.8	72.7	15.6	237.9
VF_0063	c1cds60	61.5	42.1	47.4	50.3	10.0	151.5
VF_0064	c1cds61	61.8	46.6	47.9	52.1	8.4	163.7
VF_0065	c1cds62	54.9	30.4	28.0	37.8	14.9	78.6
VF_0066	c1cds63	38.1	61.4	75.4	58.3	18.9	244.6
VF_0067	c1cds64	51.3	49.2	60.5	53.7	6.0	35.8
VF_0068	c1cds65	26.4	37.6	50.6	38.2	12.1	81.0
VF_0069	c1cds66	11.4	9.8	8.8	10.0	1.3	8.3
VF_0070	c1cds67	6.6	16.9	20.6	14.7	7.3	31.1
VF_0071	c1cds68	11.2	17.5	20.2	16.3	4.7	32.2
VF_0072	c1cds69	7.0	12.8	13.0	11.0	3.4	1156.3
VF_0073	c1cds70	24.4	21.4	22.9	22.9	1.5	30.5
VF_0074	c1cds71	35.7	45.1	48.6	43.2	6.7	154.7
VF_0075	c1cds72	97.9	100.4	116.8	105.0	10.3	213.7
VF_0076	c1cds73	177.2	294.1	346.3	272.5	86.6	494.6
VF_0077	c1cds74	88.6	82.9	95.2	88.9	6.2	65.6
VF_0078	c1cds75	116.8	163.6	157.6	146.0	25.5	102.2
VF_0079	c1cds76	86.8	102.6	117.7	102.4	15.5	105.6
VF_0080	c1cds77	86.8	105.8	134.4	109.0	24.0	150.3
VF_0081	c1cds78	63.9	66.7	80.1	70.2	8.6	75.0
VF_0082	c1cds79	23.3	21.1	26.2	23.5	2.6	44.1
VF_0083	c1cds80	990.7	898.8	630.5	840.0	187.2	1556.5
VF_0084	c1cds81	1395.8	940.4	790.7	1042.3	315.2	926.4
VF_0085	c1cds82	1177.7	724.7	496.7	799.7	346.6	125.7
VF_0086	c1cds83	251.4	148.2	144.8	181.5	60.6	41.7

VF_0087	c1cds84	181.8	70.7	64.0	105.5	66.2	27.3
VF_0088	c1cds85	45.7	25.4	34.0	35.0	10.2	23.4
VF_0089	c1cds86	47.4	31.2	39.8	39.5	8.1	20.8
VF_0090	c1cds87	26.6	50.9	65.6	47.7	19.7	72.5
VF_0091	c1cds88	1.2	0.6	0.6	0.8	0.3	1.2
VF_0093	c1cds90	269.7	177.3	193.6	213.5	49.3	222.7
VF_0094	c1cds91	12.0	24.1	22.8	19.7	6.6	32.5
VF_0095	c1cds92	6.9	7.5	7.4	7.3	0.3	32.3
VF_0096	c1cds93	4.1	5.4	7.0	5.5	1.5	25.8
VF_0097	c1cds94	22.6	22.1	19.4	21.3	1.7	31.3
VF_0098	c1cds95	113.0	144.1	206.3	154.5	47.5	489.2
VF_0099	c1cds96	868.6	949.7	1512.3	1110.2	350.6	712.3
VF_0100	c1cds97	27.7	26.1	25.1	26.3	1.3	35.6
VF_0101	c1cds98	89.2	43.9	61.2	64.8	22.9	84.4
VF_0102	c1cds99	63.6	37.0	49.6	50.1	13.3	87.8
VF_0103	c1cds100	15.4	11.0	13.4	13.3	2.2	31.0
VF_0104	c1cds101	192.2	160.4	182.5	178.3	16.3	182.2
VF_0105	c1cds102	1225.3	815.4	871.9	970.9	222.2	831.2
VF_0106	c1cds103	166.8	212.2	261.4	213.5	47.3	192.3
VF_0107	c1cds104	125.1	93.6	103.3	107.3	16.2	10.4
VF_0108	c1cds105	26.4	7.2	5.4	13.0	11.6	17.6
VF_0109	c1cds106	13.4	3.1	1.9	6.2	6.3	0.9
VF_0110	c1cds107	68.0	101.1	117.9	95.7	25.4	185.6
VF_0111	c1cds108	127.8	191.1	228.0	182.3	50.7	180.3
VF_0112	c1cds109	47.4	46.1	54.8	49.5	4.7	77.4
VF_0113	c1cds110	8.5	24.2	21.5	18.1	8.4	14.7
VF_0114	c1cds111	336.5	142.7	163.0	214.1	106.5	200.3
VF_0115	c1cds112	13.6	8.0	11.1	10.9	2.8	20.3
VF_0116	c1cds113	1.6	2.9	2.2	2.2	0.7	4.6
VF_0117	c1cds114	4.2	2.1	4.0	3.4	1.2	1.9
VF_0118	c1cds115	23.2	37.6	37.2	32.6	8.2	55.2
VF_0119	c1cds116	87.8	85.4	80.1	84.4	3.9	98.6
VF_0120	c1cds117	10.2	6.2	8.5	8.3	2.0	161.6
VF_0121	c1cds118	34.5	13.4	18.2	22.0	11.0	88.0
VF_0122	c1cds119	53.8	21.9	24.6	33.4	17.7	51.7
VF_0124	c1cds120	44.3	27.8	26.2	32.8	10.0	52.1
VF_0125	c1cds121	41.9	14.1	14.3	23.5	16.0	92.2
VF_0126	c1cds122	78.1	95.0	72.8	82.0	11.6	102.8
VF_0127	c1cds123	1730.4	5043.6	4245.8	3673.3	1729.2	3612.5
VF_0128	c1cds124	1817.7	4276.4	4946.2	3680.1	1647.2	3600.5
VF_0129	c1cds125	70.4	42.2	47.5	53.4	15.0	51.9
VF_0130	c1cds126	29.2	15.9	18.7	21.3	7.0	23.6
VF_0131	c1cds127	55.5	34.4	34.5	41.5	12.2	60.8

VF_0132	c1cds128	41.9	43.9	46.7	44.1	2.4	49.9
VF_0133	c1cds129	29.1	37.5	50.5	39.1	10.8	76.1
VF_0134	c1cds130	32.0	43.3	57.9	44.4	13.0	77.3
VF_0135	c1cds131	30.9	70.3	103.9	68.4	36.5	80.7
VF_0136	c1cds132	39.6	43.9	52.4	45.3	6.5	58.3
VF_0137	c1cds133	92.9	54.8	59.1	68.9	20.9	119.8
VF_0138	c1cds134	50.4	35.1	36.7	40.7	8.4	60.3
VF_0139	c1cds135	83.4	60.7	65.7	69.9	11.9	85.1
VF_0140	c1cds136	284.5	209.8	213.2	235.9	42.2	436.5
VF_0141	c1cds137	173.2	190.6	212.2	192.0	19.6	323.1
VF_0142	c1cds138	234.2	167.1	182.9	194.7	35.0	289.3
VF_0143	c1cds139	207.6	143.7	135.3	162.2	39.6	260.1
VF_0144	c1cds140	113.1	106.3	93.5	104.3	9.9	164.2
VF_0145	c1cds141	156.2	158.4	147.6	154.1	5.7	283.9
VF_0146	c1cds142	139.9	129.0	134.2	134.3	5.5	267.2
VF_0147	c1cds143	128.0	111.7	117.7	119.1	8.2	219.7
VF_0148	c1cds144	190.3	94.3	73.4	119.3	62.3	345.5
VF_0149	c1cds145	46.5	33.8	21.1	33.8	12.7	80.0
VF_0150	c1cds146	26.9	42.8	20.6	30.1	11.4	15.1
VF_0151	c1cds147	41.6	61.0	36.6	46.4	12.9	20.9
VF_0152	c1cds148	233.3	189.5	199.4	207.4	23.0	230.5
VF_0153	c1cds149	57.2	7.6	7.4	24.1	28.7	3.1
VF_0154	c1cds150	37.3	11.1	4.9	17.8	17.2	10.1
VF_0155	c1cds151	78.7	64.2	74.5	72.5	7.5	87.3
VF_0157	c1cds152	9.5	5.1	5.8	6.8	2.3	37.0
VF_0158	c1cds153	1.3	0.6	0.4	0.8	0.5	15.7
VF_0160	c1cds154	0.5	0.3	0.6	0.5	0.1	7.8
VF_0161	c1cds155	2185.5	348.0	351.9	961.8	1059.8	4978.6
VF_0162	c1cds156	7.0	5.9	9.8	7.6	2.0	98.6
VF_0163	c1cds157	24.2	13.7	12.8	16.9	6.4	127.0
VF_0164	c1cds158	8.5	7.0	10.4	8.6	1.7	139.6
VF_0165	c1cds159	9.7	5.5	7.4	7.5	2.1	108.6
VF_0166	c1cds160	28.6	15.3	15.9	20.0	7.5	155.5
VF_0167	c1cds161	22.7	10.1	11.5	14.8	6.9	92.8
VF_0168	c1cds162	30.7	7.1	8.8	15.5	13.2	79.0
VF_0169	c1cds163	20.7	7.3	3.8	10.6	8.9	39.6
VF_0170	c1cds164	15.0	3.8	2.2	7.0	6.9	6.8
VF_0171	c1cds165	22.5	3.6	1.8	9.3	11.4	3.8
VF_0172	c1cds166	125.7	8.6	6.0	46.8	68.4	95.5
VF_0173	c1cds167	10.6	2.3	1.1	4.6	5.2	1.8
VF_0174	c1cds169	60.6	3.8	2.3	22.3	33.2	39.0
VF_0175	c1cds170	76.7	7.4	4.7	29.6	40.8	87.7
VF_0176	c1cds171	161.2	20.5	19.9	67.2	81.4	380.4

VF_0177	c1cds172	78.3	16.3	12.5	35.7	36.9	134.0
VF_0178	c1cds173	105.0	21.2	20.4	48.9	48.6	249.3
VF_0179	c1cds174	106.3	15.3	14.1	45.2	52.9	419.5
VF_0180	c1cds175	55.4	33.7	37.6	42.2	11.6	240.5
VF_0181	c1cds176	298.2	323.9	276.7	299.6	23.6	179.0
VF_0182	c1cds177	318.3	412.3	426.8	385.8	58.9	243.0
VF_0183	c1cds178	315.2	404.2	428.4	382.6	59.6	258.5
VF_0184	c1cds179	377.4	429.5	458.2	421.7	41.0	455.4
VF_0185	c1cds180	288.6	378.1	313.9	326.8	46.2	202.8
VF_0186	c1cds181	238.5	278.7	169.9	229.0	55.0	113.4
VF_0187	c1cds182	228.2	320.9	211.1	253.4	59.1	90.3
VF_0188	c1cds183	144.9	195.0	132.0	157.3	33.3	81.2
VF_0189	c1cds184	53.2	88.9	45.3	62.4	23.2	9.1
VF_0190	c1cds185	87.2	75.8	42.7	68.6	23.1	24.0
VF_0191	c1cds186	273.5	206.5	222.9	234.3	34.9	309.7
VF_0192	c1cds187	227.5	166.1	199.7	197.8	30.7	283.9
VF_0193	c1cds188	140.6	113.3	128.4	127.4	13.7	201.2
VF_0194	c1cds189	149.3	174.5	191.1	171.7	21.0	134.0
VF_0195	c1cds190	183.4	191.8	224.3	199.8	21.6	152.0
VF_0196	c1cds191	142.8	187.5	165.7	165.3	22.3	89.2
VF_0197	c1cds192	98.3	161.5	160.3	140.0	36.1	65.3
VF_0200	c1cds193	69.8	55.2	51.9	58.9	9.5	53.1
VF_0201	c1cds194	252.2	226.5	252.5	243.8	14.9	261.9
VF_0202	c1cds195	322.0	311.8	367.6	333.8	29.7	609.8
VF_0203	c1cds196	12.2	8.1	7.7	9.3	2.5	8.6
VF_0204	c1cds197	298.7	145.0	165.0	202.9	83.6	580.7
VF_0205	c1cds198	347.7	142.7	195.0	228.4	106.5	955.3
VF_0206	c1cds199	879.2	722.7	828.6	810.1	79.9	993.5
VF_0207	c1cds200	117.3	78.7	97.4	97.8	19.3	84.5
VF_0208	c1cds201	114.0	37.5	49.9	67.1	41.1	0.3
VF_0209	c1cds202	9.4	29.4	38.0	25.6	14.7	158.6
VF_0210	c1cds203	302.6	137.2	179.5	206.4	85.9	617.8
VF_0211	c1cds204	314.0	214.2	278.6	268.9	50.6	199.9
VF_0212	c1cds205	98.3	132.0	132.7	121.0	19.7	45.6
VF_0214	c1cds206	46.2	68.9	95.2	70.1	24.6	147.3
VF_0215	c1cds207	26.1	30.2	21.1	25.8	4.5	27.5
VF_0216	c1cds208	26.7	36.7	28.1	30.5	5.4	16.3
VF_0217	c1cds209	5.3	2.4	2.9	3.5	1.5	10.1
VF_0218	c1cds210	16.2	14.5	18.9	16.5	2.2	36.5
VF_0219	c1cds211	40.7	47.5	44.9	44.4	3.4	35.2
VF_0220	c1cds212	55.3	51.0	60.9	55.7	5.0	36.5
VF_0222	c1cds213	482.8	292.8	369.2	381.6	95.6	326.1
VF_0223	c1cds214	539.7	326.0	410.8	425.5	107.6	655.5

VF_0224	c1cds215	94.9	47.8	44.3	62.4	28.2	95.8
VF_0225	c1cds216	70.1	21.0	25.7	39.0	27.1	34.4
VF_0226	c1cds217	382.0	237.0	253.3	290.8	79.4	831.5
VF_0227	c1cds218	54.4	47.7	41.3	47.8	6.6	75.8
VF_0228	c1cds219	37.5	34.2	37.2	36.3	1.9	51.7
VF_0229	c1cds220	34.1	33.1	26.8	31.3	4.0	41.0
VF_0230	c1cds222	1799.9	3142.4	4250.2	3064.1	1227.0	8011.3
VF_0231	c1cds223	1701.1	2678.3	3739.9	2706.5	1019.7	6508.6
VF_0232	c1cds225	405.0	478.5	661.1	514.9	131.8	1064.8
VF_0233	c1cds226	3792.3	3154.5	3465.4	3470.7	318.9	16150.6
VF_0234	c1cds227	2190.4	2049.2	1591.2	1943.6	313.3	7500.6
VF_0235	c1cds228	1633.0	1822.9	1738.9	1731.6	95.1	5675.9
VF_0237	c1cds229	1336.3	1206.2	1170.5	1237.7	87.3	4595.9
VF_0238	c1cds230	800.4	963.7	789.3	851.2	97.7	2571.5
VF_0239	c1cds231	1779.1	1677.1	1757.7	1737.9	53.8	4679.1
VF_0240	c1cds232	2001.5	2026.5	1850.3	1959.4	95.3	4884.0
VF_0241	c1cds233	2160.2	1741.1	1592.0	1831.1	294.6	4565.3
VF_0242	c1cds234	1741.0	1293.0	1289.2	1441.0	259.7	3042.0
VF_0243	c1cds235	2273.1	1384.0	1496.3	1717.8	484.2	3159.0
VF_0244	c1cds236	2162.5	1318.4	997.7	1492.9	601.7	3475.2
VF_0245	c1cds237	5332.2	5223.6	4410.6	4988.8	503.7	6788.0
VF_0246	c1cds238	1785.7	3247.6	4477.8	3170.4	1347.7	7827.8
VF_0248	c1cds239	2484.0	5305.6	6661.6	4817.1	2131.2	8940.9
VF_0249	c1cds240	2011.7	4326.3	5800.3	4046.1	1909.8	8014.7
VF_0250	c1cds241	1112.0	2743.6	3917.0	2590.9	1408.7	4147.1
VF_0251	c1cds242	1928.1	3607.0	4636.5	3390.6	1367.1	6768.5
VF_0252	c1cds243	1753.7	3831.9	4933.8	3506.5	1614.9	6856.4
VF_0253	c1cds244	1210.0	2119.2	2959.6	2096.3	875.0	4427.8
VF_0254	c1cds245	1988.2	3639.2	4553.3	3393.6	1300.0	6199.8
VF_0255	c1cds246	1721.8	2653.5	3575.3	2650.2	926.8	3596.1
VF_0256	c1cds247	3255.5	4229.5	5406.7	4297.2	1077.2	6192.3
VF_0257	c1cds248	2560.6	3156.4	4157.6	3291.5	807.0	5169.1
VF_0258	c1cds249	4921.1	3599.8	5798.3	4773.1	1106.7	5246.1
VF_0259	c1cds250	3206.2	2227.7	4199.2	3211.0	985.8	5919.8
VF_0260	c1cds251	2590.2	2032.4	3452.2	2691.6	715.3	5408.5
VF_0261	c1cds252	3193.6	2243.4	3821.1	3086.0	794.3	5739.3
VF_0262	c1cds253	3535.1	2802.7	4550.5	3629.5	877.7	5779.9
VF_0263	c1cds254	3079.4	2456.5	4296.4	3277.4	935.8	3359.8
VF_0264	c1cds255	367.2	118.9	126.4	204.2	141.2	304.0
VF_0265	c1cds256	60.6	64.2	71.7	65.5	5.7	85.6
VF_0266	c1cds257	131.0	258.9	227.1	205.7	66.6	69.5
VF_0267	c1cds258	23.5	23.2	17.1	21.3	3.6	27.4
VF_0268	c1cds259	8.1	4.8	3.0	5.3	2.6	4.1

VF_0269	c1cds260	7.1	4.5	3.5	5.0	1.8	8.1
VF_0270	c1cds261	363.2	201.0	212.5	258.9	90.5	53.3
VF_0271	c1cds262	373.5	206.6	217.7	265.9	93.3	55.3
VF_0272	c1cds263	146.2	70.5	91.3	102.7	39.1	146.5
VF_0273	c1cds264	89.1	71.9	72.7	77.9	9.7	129.4
VF_0274	c1cds265	1000.0	538.6	593.4	710.7	252.1	958.3
VF_0275	c1cds266	52.2	183.9	274.4	170.2	111.7	189.5
VF_0276	c1cds267	259.6	400.0	323.6	327.7	70.3	1587.3
VF_0277	c1cds268	132.0	96.3	150.7	126.3	27.7	175.6
VF_0278	c1cds269	2850.6	3746.2	4920.2	3839.0	1037.9	4493.4
VF_0279	c1cds270	4126.9	7729.9	10290.5	7382.4	3096.5	4957.8
VF_0280	c1cds271	275.6	156.3	161.8	197.9	67.3	113.0
VF_0281	c1cds272	12.2	5.2	6.9	8.1	3.6	9.9
VF_0283	c1cds273	6.4	5.7	4.3	5.5	1.1	6.7
VF_0284	c1cds274	38.0	20.3	22.2	26.8	9.7	73.2
VF_0285	c1cds275	13.3	6.0	7.9	9.0	3.8	11.1
VF_0286	c1cds276	253.0	217.5	272.8	247.8	28.0	217.2
VF_0287	c1cds277	59.4	46.4	56.5	54.1	6.8	124.7
VF_0288	c1cds278	49.7	38.7	53.2	47.2	7.6	112.5
VF_0289	c1cds279	95.4	64.8	73.2	77.8	15.8	133.7
VF_0290	c1cds280	102.3	67.2	79.0	82.8	17.9	72.9
VF_0291	c1cds281	325.9	74.7	68.4	156.4	146.9	28.7
VF_0292	c1cds282	70.1	63.5	80.7	71.4	8.7	235.2
VF_0293	c1cds283	63.8	42.9	74.1	60.3	15.9	219.3
VF_0294	c1cds284	53.6	46.1	65.3	55.0	9.7	217.7
VF_0295	c1cds285	49.8	67.7	110.6	76.0	31.2	183.1
VF_0296	c1cds286	46.8	13.0	9.9	23.2	20.5	17.6
VF_0297	c1cds287	66.2	34.2	31.0	43.8	19.5	34.4
VF_0298	c1cds288	63.4	18.5	18.9	33.6	25.8	24.1
VF_0300	c1cds289	12.2	4.3	5.8	7.4	4.2	26.0
VF_0301	c1cds290	58.8	46.5	50.9	52.1	6.2	69.0
VF_0302	c1cds291	87.5	64.1	89.4	80.3	14.1	74.9
VF_0303	c1cds292	25.7	18.0	17.7	20.5	4.6	4.6
VF_0304	c1cds293	478.8	264.0	269.8	337.5	122.4	124.0
VF_0305	c1cds294	37.2	62.0	63.4	54.2	14.8	138.8
VF_0306	c1cds295	29.9	56.1	42.6	42.9	13.1	119.2
VF_0307	c1cds296	119.3	188.4	272.2	193.3	76.6	88.3
VF_0308	c1cds297	195.0	312.3	375.6	294.3	91.7	211.6
VF_0309	c1cds298	411.6	235.8	276.9	308.1	91.9	23.2
VF_0310	c1cds299	51.3	14.5	20.0	28.6	19.8	3.3
VF_0311	c1cds300	59.7	16.3	22.8	32.9	23.4	11.2
VF_0312	c1cds301	124.3	39.0	45.5	69.6	47.5	13.4
VF_0313	c1cds302	475.6	163.1	160.4	266.4	181.2	26.3

VF_0314	c1cds303	272.5	290.5	346.6	303.2	38.7	2064.2
VF_0315	c1cds304	245.8	126.4	127.4	166.5	68.6	103.0
VF_0316	c1cds305	4.8	23.0	4.4	10.7	10.6	4.3
VF_0317	c1cds306	14.9	116.9	19.9	50.6	57.5	19.3
VF_0318	c1cds307	7.9	4.7	2.4	5.0	2.8	6.9
VF_0319	c1cds308	45.6	140.2	150.1	112.0	57.7	1361.1
VF_0320	c1cds309	134.9	17.7	24.2	58.9	65.9	4.8
VF_0321	c1cds310	151.6	19.7	29.5	66.9	73.5	5.0
VF_0322	c1cds311	55.8	7.2	9.6	24.2	27.4	1.6
VF_0323	c1cds312	54.2	8.0	9.4	23.9	26.2	5.2
VF_0324	c1cds313	24.2	51.6	45.3	40.4	14.3	121.7
VF_0325	c1cds314	112.0	45.5	53.0	70.2	36.5	52.8
VF_0326	c1cds315	98.3	51.3	45.8	65.2	28.9	25.6
VF_0327	c1cds316	64.6	42.1	25.3	44.0	19.8	7.9
VF_0328	c1cds317	207.5	90.6	71.3	123.1	73.7	28.1
VF_0329	c1cds320	132.4	93.4	72.5	99.5	30.4	639.5
VF_0330	c1cds321	3701.7	290.3	159.7	1383.9	2008.3	136.2
VF_0331	c1cds322	250.6	128.9	97.7	159.1	80.8	51.6
VF_0332	c1cds323	29.1	19.2	15.2	21.2	7.1	25.0
VF_0333	c1cds324	22.9	13.0	10.1	15.3	6.7	17.3
VF_0336	c1cds325	199.5	129.9	98.0	142.5	51.9	85.8
VF_0337	c1cds326	49.0	33.8	35.1	39.3	8.4	58.2
VF_0338	c1cds327	37.0	22.7	24.5	28.1	7.8	56.4
VF_0339	c1cds328	26.3	27.6	16.0	23.3	6.3	32.6
VF_0340	c1cds329	7.7	10.0	7.7	8.4	1.3	20.9
VF_0341	c1cds330	32.7	39.4	42.2	38.1	4.9	108.3
VF_0342	c1cds331	103.2	139.6	147.3	130.0	23.5	468.3
VF_0343	c1cds332	25.5	15.2	12.5	17.7	6.8	22.1
VF_0344	c1cds333	70.0	28.2	25.1	41.1	25.1	75.2
VF_0345	c1cds334	50.7	23.2	21.3	31.7	16.4	49.5
VF_0346	c1cds335	23.5	9.3	9.4	14.0	8.2	25.9
VF_0347	c1cds336	19.7	12.8	7.0	13.2	6.4	11.6
VF_0348	c1cds337	27.3	11.8	5.8	15.0	11.1	9.3
VF_0349	c1cds338	80.7	27.7	21.7	43.4	32.4	31.2
VF_0350	c1cds339	115.3	45.6	32.8	64.6	44.4	41.6
VF_0351	c1cds340	131.1	37.7	27.8	65.5	57.0	37.8
VF_0352	c1cds341	153.2	55.6	44.9	84.6	59.7	26.7
VF_0353	c1cds343	136.9	153.7	221.4	170.7	44.7	424.3
VF_0354	c1cds344	69.1	37.3	26.9	44.5	22.0	14.7
VF_0355	c1cds345	38.4	33.3	31.4	34.4	3.6	32.5
VF_0356	c1cds346	16.8	29.8	26.9	24.5	6.8	86.2
VF_0357	c1cds347	7.3	11.4	12.7	10.5	2.9	53.4
VF_0358	c1cds348	6.6	14.0	9.8	10.1	3.7	45.7

VF_0359	c1cds349	16.9	27.5	30.0	24.8	7.0	90.8
VF_0360	c1cds350	9.4	15.8	15.2	13.4	3.5	52.4
VF_0361	c1cds351	13.0	21.1	23.0	19.0	5.3	77.9
VF_0362	c1cds352	18.8	19.2	18.4	18.8	0.4	89.7
VF_0363	c1cds353	18.4	15.1	14.8	16.1	2.0	56.2
VF_0364	c1cds354	16.6	11.8	9.9	12.8	3.5	46.7
VF_0365	c1cds355	39.2	29.1	29.6	32.6	5.7	163.1
VF_0366	c1cds356	181.4	73.4	85.8	113.5	59.1	991.6
VF_0367	c1cds357	15.6	8.4	9.5	11.2	3.9	18.2
VF_0368	c1cds358	9.1	6.8	8.5	8.1	1.2	10.8
VF_0369	c1cds359	8.4	4.8	5.8	6.3	1.8	5.5
VF_0370	c1cds360	9.8	5.1	6.5	7.2	2.4	6.1
VF_0371	c1cds361	42.6	21.5	18.4	27.5	13.1	14.3
VF_0372	c1cds362	217.4	149.1	170.5	179.0	35.0	442.6
VF_0373	c1cds363	32.9	16.2	20.2	23.1	8.8	138.8
VF_0374	c1cds364	41.2	15.1	21.2	25.8	13.7	116.4
VF_0375	c1cds365	52.7	31.3	44.6	42.9	10.8	82.1
VF_0376	c1cds366	108.7	69.4	69.1	82.4	22.8	139.0
VF_0377	c1cds367	74.9	46.4	46.1	55.8	16.5	50.7
VF_0378	c1cds368	345.4	174.2	194.2	238.0	93.6	90.5
VF_0379	c1cds369	111.1	81.5	88.8	93.8	15.4	102.7
VF_0380	c1cds370	855.0	538.0	590.5	661.2	169.9	234.7
VF_0381	c1cds371	38.9	41.4	54.5	44.9	8.4	110.3
VF_0382	c1cds372	194.1	112.8	128.7	145.2	43.1	45.6
VF_0383	c1cds373	9.8	5.3	5.2	6.7	2.6	33.9
VF_0384	c1cds374	8.9	12.3	9.2	10.1	1.8	65.0
VF_0385	c1cds375	37.3	32.9	27.2	32.5	5.1	102.2
VF_0386	c1cds376	1517.4	765.8	574.6	952.6	498.4	506.0
VF_0387	c1cds377	458.0	302.4	293.0	351.1	92.6	259.3
VF_0388	c1cds378	178.5	102.5	96.1	125.7	45.8	107.4
VF_0389	c1cds379	257.1	135.4	137.2	176.6	69.7	99.7
VF_0390	c1cds380	390.0	181.3	206.2	259.1	114.0	111.9
VF_0391	c1cds381	357.4	180.8	189.4	242.5	99.6	139.0
VF_0392	c1cds382	105.4	81.0	77.4	87.9	15.3	140.2
VF_0393	c1cds383	27.5	49.5	58.7	45.2	16.0	75.3
VF_0394	c1cds384	93.0	45.6	44.7	61.1	27.6	39.7
VF_0395	c1cds385	65.6	30.6	28.2	41.5	21.0	20.0
VF_0396	c1cds386	52.3	21.7	28.6	34.2	16.0	24.1
VF_0397	c1cds387	84.2	36.9	29.9	50.3	29.6	49.2
VF_0399	c1cds388	48.5	22.6	23.9	31.7	14.6	33.1
VF_0400	c1cds389	428.1	507.5	467.0	467.5	39.7	380.8
VF_0401	c1cds390	198.3	205.0	229.2	210.8	16.3	347.3
VF_0402	c1cds391	48.0	48.1	70.8	55.7	13.1	116.0

VF_0403	c1cds392	7.6	7.3	6.0	7.0	0.8	12.3
VF_0404	c1cds393	247.9	229.2	252.2	243.1	12.2	1079.2
VF_0405	c1cds394	109.5	44.7	44.5	66.3	37.5	31.5
VF_0406	c1cds395	70.7	28.5	39.4	46.2	21.9	36.4
VF_0407	c1cds397	61.2	79.3	221.7	120.7	87.9	65.7
VF_0408	c1cds398	21.6	7.9	8.0	12.5	7.9	33.2
VF_0409	c1cds399	393.7	374.2	445.3	404.4	36.7	247.7
VF_0410	c1cds400	95.7	55.4	62.1	71.0	21.6	29.6
VF_0411	c1cds401	108.8	136.7	199.5	148.3	46.5	599.3
VF_0412	c1cds402	21.0	19.4	19.9	20.1	0.8	97.2
VF_0413	c1cds403	218.3	195.1	227.3	213.6	16.6	714.0
VF_0414	c1cds404	80.4	85.6	101.0	89.0	10.8	74.9
VF_0415	c1cds405	75.5	66.6	88.4	76.8	11.0	66.0
VF_0416	c1cds406	35.0	31.1	34.2	33.4	2.1	75.7
VF_0417	c1cds407	33.6	50.5	39.8	41.3	8.6	63.9
VF_0418	c1cds408	18.7	42.1	37.1	32.6	12.3	36.6
VF_0420	c1cds409	9.0	8.6	7.3	8.3	0.9	35.0
VF_0421	c1cds410	142.4	173.1	211.2	175.6	34.4	363.6
VF_0422	c1cds411	14.9	12.5	15.6	14.3	1.6	46.0
VF_0423	c1cds413	31.5	20.7	19.1	23.7	6.7	32.8
VF_0424	c1cds414	48.3	32.0	37.5	39.3	8.3	52.6
VF_0425	c1cds415	41.5	39.8	43.8	41.7	2.0	83.6
VF_0426	c1cds416	18.4	13.5	13.4	15.1	2.9	25.3
VF_0427	c1cds417	85.2	123.4	116.7	108.4	20.4	58.8
VF_0428	c1cds418	74.8	77.9	72.4	75.0	2.8	80.6
VF_0429	c1cds419	69.8	72.1	83.8	75.2	7.5	76.2
VF_0430	c1cds420	40.0	47.5	53.3	46.9	6.6	62.5
VF_0431	c1cds421	74.9	49.4	53.0	59.1	13.8	83.4
VF_0432	c1cds422	69.4	49.4	53.1	57.3	10.6	68.5
VF_0433	c1cds423	109.3	75.0	70.4	84.9	21.3	49.5
VF_0434	c1cds424	142.8	86.9	72.6	100.8	37.1	61.5
VF_0435	c1cds425	312.8	159.2	167.7	213.2	86.4	264.9
VF_0436	c1cds426	171.2	79.8	80.5	110.5	52.5	128.9
VF_0437	c1cds427	9.6	23.5	22.4	18.5	7.8	5.3
VF_0438	c1cds428	0.8	2.1	1.4	1.4	0.6	17.1
VF_0439	c1cds429	22.9	22.1	27.9	24.3	3.2	189.3
VF_0440	c1cds430	23.5	80.2	107.0	70.2	42.6	825.2
VF_0441	c1cds431	43.9	84.3	93.3	73.8	26.3	58.0
VF_0442	c1cds432	666.9	477.5	633.7	592.7	101.1	982.2
VF_0443	c1cds433	795.7	661.6	766.8	741.4	70.6	3035.6
VF_0444	c1cds434	53.5	69.5	97.4	73.5	22.2	125.8
VF_0445	c1cds435	6.1	4.4	4.5	5.0	0.9	13.6
VF_0446	c1cds436	67.8	56.3	65.5	63.2	6.1	18.3

VF_0447	c1cds437	45.9	34.3	46.1	42.1	6.8	93.5
VF_0448	c1cds438	13.9	13.9	11.8	13.2	1.3	34.3
VF_0449	c1cds439	385.9	342.5	329.7	352.7	29.5	147.9
VF_0450	c1cds440	26.8	23.7	20.7	23.7	3.1	27.2
VF_0452	c1cds441	1183.8	2021.6	2784.5	1996.6	800.7	4874.5
VF_0452	c1cds441	86.8	148.2	204.1	146.4	58.7	357.4
VF_0453	c1cds442	200.9	223.0	350.6	258.2	80.8	727.2
VF_0454	c1cds443	88.6	158.9	146.6	131.4	37.5	112.2
VF_0455	c1cds444	24.9	37.8	42.6	35.1	9.2	32.5
VF_0456	c1cds445	117.5	163.1	169.3	150.0	28.3	265.4
VF_0457	c1cds446	37.2	31.1	30.1	32.8	3.8	51.4
VF_0458	c1cds447	52.8	43.5	48.5	48.3	4.7	28.0
VF_0459	c1cds448	78.0	92.9	97.4	89.5	10.2	86.5
VF_0460	c1cds449	82.6	76.0	84.7	81.1	4.5	84.6
VF_0461	c1cds450	49.6	244.0	292.9	195.5	128.7	3.7
VF_0462	c1cds451	16.0	18.1	11.1	15.1	3.6	40.8
VF_0463	c1cds452	62.1	40.0	32.1	44.7	15.6	73.9
VF_0464	c1cds453	2790.1	3623.6	3496.8	3303.5	449.1	2358.5
VF_0465	c1cds454	20.2	30.7	25.6	25.5	5.3	22.4
VF_0466	c1cds455	82.4	111.9	122.4	105.6	20.7	164.4
VF_0467	c1cds456	105.9	126.8	170.8	134.5	33.1	551.1
VF_0468	c1cds457	204.9	188.3	196.8	196.7	8.3	364.5
VF_0469	c1cds458	66.7	75.8	82.0	74.8	7.7	67.1
VF_0470	c1cds459	61.3	72.8	73.7	69.3	6.9	74.2
VF_0471	c1cds460	114.8	89.1	108.4	104.1	13.4	100.2
VF_0472	c1cds461	27.0	27.5	60.1	38.2	19.0	235.2
VF_0473	c1cds462	53.0	36.2	72.2	53.8	18.0	321.1
VF_0474	c1cds463	7.6	11.0	9.5	9.3	1.7	28.9
VF_0475	c1cds464	997.1	697.8	906.7	867.2	153.5	6017.4
VF_0476	c1cds465	575.1	427.8	390.8	464.5	97.5	843.1
VF_0477	c1cds466	295.8	347.0	267.9	303.6	40.1	122.8
VF_0478	c1cds467	518.3	347.7	313.4	393.1	109.8	259.7
VF_0479	c1cds468	444.1	386.5	488.1	439.6	51.0	636.9
VF_0480	c1cds469	19.2	23.5	21.3	21.3	2.2	49.1
VF_0481	c1cds470	62.9	83.9	90.3	79.0	14.3	262.9
VF_0483	c1cds471	290.0	305.7	321.3	305.7	15.6	1088.2
VF_0484	c1cds472	204.4	210.5	310.8	241.9	59.8	570.6
VF_0485	c1cds473	191.1	209.3	298.8	233.1	57.6	596.6
VF_0486	c1cds474	287.8	325.6	459.5	357.6	90.2	699.3
VF_0487	c1cds475	286.1	166.9	219.9	224.3	59.7	162.5
VF_0488	c1cds476	239.8	200.9	241.8	227.5	23.1	143.5
VF_0489	c1cds477	4486.2	3626.1	3255.5	3789.2	631.4	4211.7
VF_0490	c1cds478	211.3	413.8	555.4	393.5	173.0	1263.8

VF_0491	c1cds479	69.0	90.7	98.4	86.0	15.2	154.3
VF_0492	c1cds480	27.3	19.6	24.5	23.8	3.9	12.6
VF_0493	c1cds481	15.1	16.7	23.2	18.3	4.3	11.1
VF_0494	c1cds482	9.6	21.9	17.4	16.3	6.2	40.9
VF_0495	c1cds483	44.5	44.5	41.4	43.5	1.8	84.1
VF_0496	c1cds484	70.4	85.2	103.5	86.3	16.6	83.5
VF_0497	c1cds485	1.9	0.8	0.3	1.0	0.8	0.5
VF_0498	c1cds486	28.9	28.7	31.4	29.7	1.5	62.8
VF_0499	c1cds487	15.1	29.1	28.3	24.2	7.9	31.2
VF_0500	c1cds488	55.0	92.8	135.9	94.6	40.5	240.5
VF_0501	c1cds490	88.9	44.6	46.6	60.0	25.0	23.2
VF_0502	c1cds491	158.7	497.5	522.7	393.0	203.3	2494.1
VF_0503	c1cds492	2153.4	3521.4	2821.6	2832.1	684.1	355.9
VF_0504	c1cds493	1486.0	1721.0	1730.2	1645.7	138.4	501.6
VF_0505	c1cds494	179.7	192.8	250.1	207.6	37.5	219.8
VF_0506	c1cds495	255.6	264.4	361.8	293.9	58.9	400.0
VF_0507	c1cds496	427.6	314.6	399.1	380.4	58.8	248.5
VF_0508	c1cds497	428.6	208.9	232.8	290.1	120.5	93.1
VF_0509	c1cds498	73.4	90.1	103.5	89.0	15.0	96.7
VF_0511	c1cds500	0.5	0.3	0.1	0.3	0.2	0.0
VF_0512	c1cds501	2.0	1.7	1.2	1.6	0.4	0.6
VF_0513	c1cds502	3.5	1.5	1.7	2.2	1.1	1.3
VF_0515	c1cds504	7.3	4.1	3.6	5.0	2.0	2.5
VF_0516	c1cds505	7.2	3.2	4.0	4.8	2.1	2.9
VF_0517	c1cds506	5.7	3.8	2.1	3.9	1.8	2.1
VF_0518	c1cds507	6.0	2.5	2.2	3.6	2.1	1.2
VF_0519	c1cds508	5.0	2.6	2.3	3.3	1.5	2.5
VF_0520	c1cds509	7.3	3.8	3.3	4.8	2.2	2.3
VF_0521	c1cds510	6.1	2.9	4.4	4.5	1.6	1.7
VF_0522	c1cds511	8.3	6.0	5.4	6.6	1.5	3.9
VF_0523	c1cds512	50.8	19.3	18.2	29.4	18.5	12.6
VF_0524	c1cds513	23.7	8.3	4.6	12.2	10.1	11.1
VF_0525	c1cds514	16.5	6.3	4.5	9.1	6.4	11.4
VF_0526	c1cds515	44.1	22.3	14.7	27.0	15.2	38.3
VF_0527	c1cds516	74.0	41.8	35.0	50.3	20.8	97.3
VF_0528	c1cds517	19.4	20.4	21.1	20.3	0.9	49.6
VF_0529	c1cds518	2066.0	2465.8	3539.9	2690.6	762.2	4647.8
VF_0530	c1cds519	187.6	26.7	22.3	78.9	94.2	28.7
VF_0531	c1cds520	21.9	16.7	19.6	19.4	2.6	35.0
VF_0532	c1cds521	8.1	3.0	4.1	5.1	2.7	6.6
VF_0533	c1cds522	1098.2	313.7	251.3	554.4	472.0	27.1
VF_0534	c1cds523	15.5	15.5	16.6	15.9	0.6	58.3
VF_0535	c1cds525	77.1	71.9	93.9	80.9	11.5	1001.3

VF_0536	c1cds526	98.7	112.9	137.6	116.4	19.7	343.9
VF_0537	c1cds527	300.9	172.7	190.8	221.4	69.4	466.9
VF_0538	c1cds528	1030.4	766.3	743.3	846.7	159.5	1717.9
VF_0539	c1cds530	72.9	49.1	74.2	65.4	14.1	53.9
VF_0540	c1cds531	134.3	86.0	117.1	112.5	24.5	42.7
VF_0541	c1cds532	101.0	32.9	23.6	52.5	42.3	42.8
VF_0542	c1cds533	326.1	133.1	143.0	200.8	108.7	103.9
VF_0543	c1cds534	178.2	136.8	147.2	154.1	21.5	199.6
VF_0544	c1cds535	62.1	39.7	44.0	48.6	11.9	75.1
VF_0545	c1cds536	241.5	251.3	257.1	250.0	7.9	282.5
VF_0546	c1cds537	37.8	38.9	40.6	39.1	1.4	53.6
VF_0547	c1cds538	122.3	69.2	59.1	83.5	34.0	80.2
VF_0548	c1cds539	224.8	223.5	290.7	246.3	38.5	209.9
VF_0549	c1cds540	1801.4	1707.9	1703.5	1737.6	55.3	3525.9
VF_0550	c1cds541	1598.6	2137.0	3096.5	2277.3	758.7	3910.7
VF_0551	c1cds542	1150.9	1842.3	2635.2	1876.1	742.7	2855.1
VF_0552	c1cds543	1797.8	2602.1	3522.3	2640.8	862.9	4720.2
VF_0553	c1cds544	13.5	8.9	6.1	9.5	3.7	40.7
VF_0554	c1cds545	37.9	30.1	29.5	32.5	4.7	67.8
VF_0555	c1cds546	20.1	29.9	28.0	26.0	5.2	58.0
VF_0556	c1cds547	34.2	46.7	33.5	38.1	7.4	92.6
VF_0557	c1cds548	416.0	245.9	320.9	327.6	85.2	493.8
VF_0558	c1cds549	52.4	37.8	36.3	42.2	8.9	51.4
VF_0559	c1cds550	31.8	20.4	19.8	24.0	6.8	25.6
VF_0560	c1cds551	24.8	24.6	23.2	24.2	0.9	50.9
VF_0561	c1cds552	40.4	36.1	35.0	37.1	2.8	107.1
VF_0562	c1cds553	8285.0	3912.5	4411.1	5536.2	2393.6	7073.5
VF_0563	c1cds554	101.1	99.4	92.0	97.5	4.9	149.9
VF_0564	c1cds555	111.0	103.9	116.1	110.4	6.1	221.4
VF_0565	c1cds556	25.1	20.3	27.2	24.2	3.5	74.5
VF_0566	c1cds557	129.6	67.2	53.4	83.4	40.6	133.4
VF_0568	c1cds558	53.6	11.1	8.3	24.3	25.4	2.7
VF_0569	c1cds559	4.8	1.1	1.3	2.4	2.1	1.4
VF_0571	c1cds561	2.1	0.5	0.6	1.1	0.9	1.2
VF_0572	c1cds562	8.1	3.2	2.4	4.6	3.1	9.8
VF_0573	c1cds563	6.0	4.0	3.2	4.4	1.4	6.6
VF_0574	c1cds564	10.6	7.5	5.3	7.8	2.7	16.5
VF_0576	c1cds566	38.4	41.3	49.1	42.9	5.5	321.9
VF_0577	c1cds567	96.9	110.2	106.6	104.6	6.9	360.2
VF_0578	c1cds568	10.5	7.6	7.5	8.5	1.7	9.3
VF_0579	c1cds569	29.2	8.4	6.6	14.7	12.5	16.0
VF_0580	c1cds570	6.0	9.9	9.7	8.5	2.2	12.2
VF_0581	c1cds571	11.0	7.8	9.6	9.5	1.6	30.4

VF_0582	c1cds572	20.0	21.0	19.2	20.1	0.9	36.8
VF_0583	c1cds573	23.4	16.8	18.1	19.4	3.5	32.7
VF_0584	c1cds574	16.9	16.8	19.0	17.6	1.3	8.9
VF_0585	c1cds575	5.0	21.0	69.1	31.7	33.4	3.7
VF_0586	c1cds576	34.2	31.9	34.6	33.6	1.4	63.5
VF_0587	c1cds577	6.0	4.6	6.8	5.8	1.1	13.8
VF_0588	c1cds578	3.2	5.7	6.3	5.1	1.6	27.0
VF_0589	c1cds579	29.9	16.8	19.9	22.2	6.9	38.3
VF_0590	c1cds580	11.5	14.5	14.8	13.6	1.8	23.3
VF_0591	c1cds581	23.5	27.0	22.0	24.2	2.5	42.8
VF_0592	c1cds582	20.9	15.7	13.5	16.7	3.8	35.8
VF_0593	c1cds583	76.9	64.1	91.4	77.5	13.7	110.4
VF_0594	c1cds584	52.3	49.9	47.9	50.0	2.2	44.9
VF_0595	c1cds585	285.6	123.0	138.8	182.4	89.7	488.7
VF_0596	c1cds586	16.8	17.5	13.3	15.9	2.2	79.5
VF_0597	c1cds587	23.7	18.3	14.1	18.7	4.8	33.1
VF_0598	c1cds588	61.1	52.2	55.8	56.4	4.5	92.5
VF_0599	c1cds589	31.0	42.4	50.6	41.3	9.8	59.1
VF_0600	c1cds590	10.0	12.3	17.6	13.3	3.9	36.8
VF_0601	c1cds591	55.5	68.1	94.2	72.6	19.8	57.1
VF_0602	c1cds592	39.7	55.3	62.9	52.7	11.8	51.0
VF_0603	c1cds593	6.1	3.3	3.7	4.4	1.5	9.2
VF_0604	c1cds594	10.8	2.5	3.2	5.5	4.6	26.6
VF_0605	c1cds595	27.0	8.0	9.9	15.0	10.5	28.6
VF_0606	c1cds596	16.5	7.0	9.5	11.0	4.9	21.0
VF_0607	c1cds597	20.4	11.8	11.8	14.6	5.0	30.1
VF_0608	c1cds598	22.8	17.9	15.6	18.8	3.7	26.0
VF_0609	c1cds599	5.9	5.0	5.0	5.3	0.6	12.8
VF_0610	c1cds600	34.0	24.2	29.9	29.4	4.9	53.5
VF_0611	c1cds601	45.9	44.3	52.0	47.4	4.1	91.9
VF_0612	c1cds602	28.8	31.2	37.9	32.7	4.7	34.0
VF_0613	c1cds603	47.9	34.0	45.9	42.6	7.5	50.8
VF_0614	c1cds604	17.6	67.7	116.0	67.1	49.2	128.0
VF_0615	c1cds605	25.1	42.5	41.1	36.2	9.7	157.7
VF_0616	c1cds606	525.9	415.6	247.7	396.4	140.1	161.4
VF_0617	c1cds607	1451.3	742.7	537.0	910.4	479.7	365.6
VF_0618	c1cds608	3093.9	2810.6	2224.5	2709.7	443.4	469.9
VF_0619	c1cds609	2111.0	1756.5	1286.6	1718.0	413.5	276.4
VF_0620	c1cds610	120.5	176.1	125.0	140.5	30.9	77.8
VF_0621	c1cds611	217.3	335.9	270.0	274.4	59.4	142.5
VF_0622	c1cds612	394.1	690.7	561.9	548.9	148.7	284.6
VF_0623	c1cds613	469.4	527.1	296.8	431.1	119.8	70.2
VF_0624	c1cds614	304.9	377.3	383.3	355.2	43.6	446.1

VF_0625	c1cds615	165.2	74.9	62.3	100.8	56.1	643.6
VF_0626	c1cds616	9.9	30.8	41.5	27.4	16.1	91.0
VF_0627	c1cds617	33.8	44.4	57.9	45.4	12.1	67.9
VF_0628	c1cds618	60.5	67.8	87.6	72.0	14.1	155.7
VF_0629	c1cds619	77.5	72.4	99.3	83.0	14.3	146.4
VF_0630	c1cds620	152.5	134.5	167.4	151.5	16.5	231.3
VF_0631	c1cds621	205.1	189.3	245.5	213.3	29.0	315.9
VF_0632	c1cds622	301.7	234.9	289.9	275.5	35.7	345.8
VF_0633	c1cds623	126.5	105.2	124.0	118.6	11.7	154.7
VF_0634	c1cds624	29.5	15.1	15.4	20.0	8.3	21.2
VF_0635	c1cds625	254.3	165.7	110.8	176.9	72.4	172.9
VF_0636	c1cds626	26.5	59.2	55.3	47.0	17.8	29.5
VF_0637	c1cds627	37.3	95.7	116.3	83.1	41.0	193.2
VF_0638	c1cds628	62.1	83.3	106.3	83.9	22.1	205.6
VF_0639	c1cds629	18.0	7.8	10.6	12.2	5.3	33.7
VF_0640	c1cds630	18.4	28.2	26.7	24.4	5.3	35.9
VF_0641	c1cds631	9.2	6.6	6.3	7.4	1.6	47.4
VF_0642	c1cds632	2.6	3.8	1.5	2.6	1.2	104.7
VF_0643	c1cds633	7.0	6.3	4.1	5.8	1.5	14.3
VF_0644	c1cds634	187.4	125.6	115.3	142.8	39.0	31.1
VF_0645	c1cds635	644.6	290.7	308.7	414.7	199.3	35.7
VF_0646	c1cds637	151.3	52.0	49.2	84.2	58.2	91.6
VF_0647	c1cds638	35.6	20.7	18.3	24.9	9.4	4.6
VF_0648	c1cds639	664.6	313.2	352.7	443.5	192.5	32.3
VF_0649	c1cds640	11.4	15.9	14.9	14.1	2.4	42.1
VF_0650	c1cds641	56.6	36.4	54.5	49.1	11.1	32.2
VF_0651	c1cds642	16.9	22.8	22.0	20.5	3.2	95.2
VF_0652	c1cds643	4.1	5.5	6.6	5.4	1.3	57.1
VF_0653	c1cds644	47.5	56.0	68.0	57.2	10.3	59.0
VF_0654	c1cds645	161.4	212.0	286.8	220.1	63.1	168.6
VF_0655	c1cds646	125.8	36.2	55.3	72.4	47.2	7.2
VF_0656	c1cds647	7.6	15.2	17.8	13.5	5.3	21.8
VF_0657	c1cds648	313.7	230.4	288.3	277.5	42.7	153.7
VF_0658	c1cds649	235.6	231.7	275.4	247.6	24.2	67.1
VF_0659	c1cds650	283.7	270.1	250.3	268.1	16.8	51.2
VF_0660	c1cds651	10.7	8.6	6.1	8.5	2.3	4.0
VF_0661	c1cds652	137.8	57.6	58.6	84.6	46.0	60.5
VF_0662	c1cds653	36.7	13.2	9.8	19.9	14.7	38.0
VF_0663	c1cds654	11.9	21.7	18.1	17.2	5.0	491.6
VF_0664	c1cds655	32.8	60.7	53.4	49.0	14.4	107.3
VF_0665	c1cds656	12.8	15.2	14.7	14.2	1.3	175.9
VF_0666	c1cds657	1.0	3.8	3.2	2.7	1.5	136.4
VF_0667	c1cds658	1.4	2.8	2.1	2.1	0.7	63.7

VF_0668	c1cds659	2.2	2.7	2.3	2.4	0.3	118.2
VF_0669	c1cds660	12.6	14.3	10.9	12.6	1.7	182.9
VF_0670	c1cds661	5.9	4.4	5.3	5.2	0.7	32.9
VF_0671	c1cds662	2.7	2.4	3.9	3.0	0.8	17.6
VF_0672	c1cds663	5.6	1.9	3.5	3.6	1.8	27.1
VF_0673	c1cds664	5.5	2.8	3.6	4.0	1.4	23.4
VF_0674	c1cds665	3.9	1.1	2.4	2.5	1.4	8.8
VF_0675	c1cds666	6.0	0.4	2.2	2.8	2.8	12.9
VF_0676	c1cds667	0.5	0.6	0.4	0.5	0.1	4.6
VF_0678	c1cds669	2.1	2.8	2.9	2.6	0.4	4.1
VF_0680	c1cds671	0.8	0.5	0.6	0.7	0.2	1.5
VF_0681	c1cds672	1.2	0.6	0.5	0.8	0.4	2.5
VF_0682	c1cds673	225.6	233.0	374.8	277.8	84.1	478.2
VF_0683	c1cds674	5.1	9.4	10.2	8.2	2.8	19.4
VF_0684	c1cds675	332.6	208.8	203.5	248.3	73.1	454.5
VF_0685	c1cds676	28.8	45.7	55.7	43.4	13.6	44.8
VF_0686	c1cds677	28.3	52.3	49.6	43.4	13.1	49.1
VF_0687	c1cds678	71.8	88.2	126.5	95.5	28.1	78.6
VF_0688	c1cds680	15.6	12.6	10.6	12.9	2.5	10.4
VF_0689	c1cds681	18.2	11.7	13.5	14.5	3.4	14.8
VF_0690	c1cds682	28.7	18.5	21.0	22.7	5.3	36.1
VF_0691	c1cds683	27.9	13.4	16.3	19.2	7.7	30.7
VF_0692	c1cds684	15.6	7.2	8.1	10.3	4.6	20.4
VF_0693	c1cds685	322.5	149.3	133.0	201.6	105.0	47.8
VF_0694	c1cds686	5.4	16.8	17.3	13.2	6.7	9.8
VF_0695	c1cds687	594.9	428.2	549.3	524.1	86.1	1927.1
VF_0696	c1cds688	16.0	11.6	12.1	13.2	2.4	86.1
VF_0697	c1cds689	870.0	541.9	319.1	577.0	277.2	475.4
VF_0698	c1cds690	7.5	22.3	17.9	15.9	7.6	4.4
VF_0699	c1cds691	106.4	108.2	108.5	107.7	1.1	78.8
VF_0700	c1cds692	77.9	91.8	98.7	89.5	10.6	66.2
VF_0701	c1cds693	96.1	105.3	129.0	110.2	17.0	85.4
VF_0702	c1cds694	282.6	281.7	283.9	282.7	1.1	350.2
VF_0703	c1cds695	174.9	280.3	304.1	253.1	68.7	457.9
VF_0704	c1cds696	150.2	197.8	272.6	206.9	61.7	315.4
VF_0705	c1cds697	12.0	11.7	9.2	11.0	1.5	24.0
VF_0706	c1cds698	19.7	55.3	41.5	38.9	17.9	50.5
VF_0707	c1cds699	15.0	20.8	10.2	15.3	5.3	17.9
VF_0708	c1cds700	4.2	4.1	2.0	3.4	1.2	4.4
VF_0709	c1cds701	42.9	11.9	10.4	21.7	18.3	11.8
VF_0710	c1cds702	75.6	21.1	16.3	37.7	33.0	42.4
VF_0711	c1cds703	130.4	71.8	86.9	96.4	30.4	155.2
VF_0712	c1cds704	19.8	27.7	28.7	25.4	4.9	110.9

VF_0713	c1cds705	13.4	43.8	40.3	32.5	16.7	60.8
VF_0714	c1cds706	50.9	121.6	94.4	89.0	35.7	85.1
VF_0715	c1cds707	75.1	218.0	190.9	161.3	75.9	130.6
VF_0716	c1cds708	38.5	116.3	169.5	108.1	65.9	110.6
VF_0717	c1cds709	277.2	79.9	85.6	147.6	112.3	75.5
VF_0718	c1cds710	5.3	4.3	4.5	4.7	0.6	8.7
VF_0719	c1cds711	116.6	116.2	148.3	127.0	18.4	4095.0
VF_0720	c1cds712	24.9	28.1	31.6	28.2	3.4	39.4
VF_0721	c1cds713	240.2	288.4	360.5	296.4	60.5	281.4
VF_0722	c1cds714	67.8	39.3	32.9	46.7	18.6	206.7
VF_0723	c1cds715	32.9	31.5	35.8	33.4	2.2	86.1
VF_0724	c1cds716	125.4	119.3	100.4	115.0	13.0	206.0
VF_0725	c1cds717	460.4	789.2	1116.1	788.6	327.9	2315.4
VF_0726	c1cds718	276.4	444.1	708.9	476.5	218.1	1357.4
VF_0727	c1cds719	511.9	779.2	1208.9	833.3	351.6	1988.6
VF_0728	c1cds720	454.4	668.6	867.7	663.6	206.7	1615.5
VF_0729	c1cds721	679.5	702.6	809.4	730.5	69.3	1997.4
VF_0731	c1cds722	616.3	926.6	1146.8	896.6	266.5	1594.4
VF_0732	c1cds723	304.1	224.7	235.3	254.7	43.1	201.3
VF_0733	c1cds724	586.1	483.9	446.3	505.4	72.3	84.2
VF_0734	c1cds725	10.0	7.8	6.6	8.2	1.7	22.0
VF_0735	c1cds726	67.6	46.9	47.2	53.9	11.9	130.1
VF_0736	c1cds727	111.3	48.8	66.8	75.6	32.1	573.7
VF_0737	c1cds728	19.3	12.8	11.2	14.4	4.3	92.4
VF_0738	c1cds729	242.0	242.8	344.2	276.3	58.8	353.6
VF_0739	c1cds730	50.4	38.8	41.3	43.5	6.1	76.6
VF_0740	c1cds731	79.1	47.2	47.6	58.0	18.3	126.0
VF_0741	c1cds732	65.0	42.1	48.7	51.9	11.8	155.2
VF_0742	c1cds733	96.7	113.8	149.5	120.0	27.0	212.4
VF_0743	c1cds734	48.8	62.8	75.9	62.5	13.6	123.3
VF_0744	c1cds735	1138.9	464.1	390.7	664.6	412.4	323.0
VF_0745	c1cds736	174.5	244.3	292.1	237.0	59.2	378.9
VF_0746	c1cds737	11.9	9.6	8.1	9.9	1.9	43.3
VF_0747	c1cds738	11.5	7.0	7.3	8.6	2.5	30.8
VF_0748	c1cds739	19.9	11.4	12.8	14.7	4.6	29.7
VF_0749	c1cds740	30.7	23.4	34.0	29.4	5.4	68.6
VF_0750	c1cds741	79.2	32.4	30.3	47.3	27.7	112.7
VF_0751	c1cds742	15.9	11.1	11.5	12.8	2.6	59.8
VF_0752	c1cds743	55.6	41.8	37.4	45.0	9.5	97.3
VF_0753	c1cds744	102.5	111.1	150.6	121.4	25.7	446.0
VF_0754	c1cds745	499.5	502.5	348.4	450.1	88.1	256.4
VF_0755	c1cds746	19.1	16.2	16.8	17.4	1.5	19.2
VF_0756	c1cds747	534.0	556.2	701.0	597.1	90.7	461.8

VF_0757	c1cds748	235.4	110.1	128.1	157.8	67.7	206.2
VF_0758	c1cds749	112.9	61.1	58.2	77.4	30.8	177.1
VF_0759	c1cds750	21.9	62.6	96.0	60.2	37.1	249.0
VF_0760	c1cds751	67.7	41.8	42.5	50.7	14.8	39.2
VF_0762	c1cds752	136.0	107.5	157.3	133.6	25.0	294.7
VF_0763	c1cds753	90.7	72.5	115.5	92.9	21.6	121.2
VF_0764	c1cds754	143.7	215.6	295.3	218.2	75.8	468.0
VF_0765	c1cds755	37.4	19.7	22.2	26.4	9.6	35.1
VF_0766	c1cds756	31.8	15.6	16.6	21.4	9.1	16.9
VF_0767	c1cds757	20.3	33.1	36.9	30.1	8.7	66.5
VF_0768	c1cds758	37.7	44.2	53.8	45.2	8.1	212.3
VF_0769	c1cds759	37.2	37.0	43.8	39.4	3.9	148.3
VF_0770	c1cds760	36.3	25.6	13.8	25.2	11.2	98.0
VF_0771	c1cds761	73.3	57.3	61.4	64.0	8.3	134.3
VF_0772	c1cds762	126.5	120.3	146.2	131.0	13.5	435.7
VF_0773	c1cds763	45.5	19.4	19.5	28.1	15.1	21.2
VF_0774	c1cds764	9.1	5.3	5.6	6.7	2.1	8.6
VF_0775	c1cds765	16.6	12.5	16.1	15.1	2.2	30.9
VF_0776	c1cds766	7.5	8.4	12.5	9.4	2.7	69.6
VF_0777	c1cds767	73.2	78.4	79.8	77.1	3.5	869.8
VF_0778	c1cds768	257.8	305.3	333.9	299.0	38.4	1967.3
VF_0779	c1cds769	156.7	21.8	23.0	67.2	77.5	30.9
VF_0780	c1cds770	5852.6	31.6	46.5	1976.9	3356.4	78.5
VF_0781	c1cds771	1854.0	9.6	23.2	628.9	1061.0	21.0
VF_0782	c1cds772	44.2	12.1	12.2	22.8	18.5	22.5
VF_0783	c1cds773	141.5	73.0	68.7	94.4	40.9	130.4
VF_0784	c1cds774	12.0	6.0	5.9	8.0	3.5	11.8
VF_0785	c1cds775	20.5	21.6	24.5	22.2	2.0	35.8
VF_0786	c1cds776	4.2	6.9	10.1	7.0	2.9	13.5
VF_0787	c1cds777	4.3	8.4	11.8	8.2	3.7	21.4
VF_0788	c1cds778	291.7	101.8	82.7	158.7	115.5	39.1
VF_0789	c1cds779	148.0	56.5	52.4	85.6	54.0	65.0
VF_0790	c1cds780	225.4	124.8	122.1	157.4	58.9	204.8
VF_0791	c1cds781	175.0	106.9	106.9	129.6	39.4	215.5
VF_0792	c1cds782	170.0	63.2	63.0	98.7	61.8	623.8
VF_0793	c1cds783	220.4	497.3	312.0	343.2	141.1	784.6
VF_0794	c1cds784	23.8	28.6	34.3	28.9	5.2	144.8
VF_0795	c1cds785	302.2	305.4	473.2	360.3	97.8	2121.5
VF_0796	c1cds786	339.3	155.3	175.7	223.5	100.9	1019.4
VF_0797	c1cds787	1941.2	1050.2	1147.6	1379.7	488.7	1157.2
VF_0798	c1cds788	230.6	115.3	112.0	152.6	67.5	625.6
VF_0799	c1cds789	851.7	509.5	509.1	623.4	197.7	2981.2
VF_0800	c1cds790	158.9	103.6	137.3	133.3	27.9	316.8

VF_0801	c1cds791	46.8	4.6	5.8	19.1	24.0	4.7
VF_0802	c1cds792	57.9	48.8	55.3	54.0	4.7	51.6
VF_0803	c1cds793	123.8	128.8	108.5	120.4	10.6	99.9
VF_0804	c1cds794	21.4	12.3	14.1	15.9	4.8	92.4
VF_0805	c1cds795	32.3	24.8	25.5	27.5	4.1	38.3
VF_0806	c1cds796	108.6	163.9	174.8	149.1	35.5	248.6
VF_0807	c1cds797	28.3	37.4	44.0	36.6	7.8	69.6
VF_0808	c1cds798	75.7	165.5	138.9	126.7	46.1	890.3
VF_0809	c1cds799	139.9	132.5	157.5	143.3	12.9	568.5
VF_0810	c1cds800	509.3	222.4	283.9	338.5	151.1	305.9
VF_0811	c1cds801	57.9	29.0	45.8	44.2	14.5	9.4
VF_0812	c1cds802	237.7	294.8	313.5	282.0	39.5	422.7
VF_0813	c1cds803	195.6	256.7	194.2	215.5	35.7	135.9
VF_0814	c1cds804	142.3	70.6	60.6	91.2	44.6	32.0
VF_0815	c1cds805	54.2	160.9	171.4	128.9	64.9	206.1
VF_0816	c1cds806	71.1	122.9	165.0	119.7	47.1	446.6
VF_0817	c1cds807	41.4	20.6	22.1	28.0	11.6	60.9
VF_0818	c1cds808	233.7	572.1	562.0	455.9	192.5	1120.5
VF_0819	c1cds809	107.5	127.7	119.5	118.2	10.2	893.6
VF_0820	c1cds810	46.7	47.3	46.0	46.7	0.7	411.0
VF_0821	c1cds811	50.3	92.3	102.6	81.7	27.7	493.7
VF_0822	c1cds812	122.3	123.8	121.5	122.5	1.2	670.9
VF_0823	c1cds813	164.9	96.1	120.5	127.2	34.9	1703.9
VF_0824	c1cds814	273.5	118.3	132.4	174.7	85.8	1987.2
VF_0825	c1cds815	285.6	95.0	116.4	165.7	104.4	2055.2
VF_0826	c1cds816	498.4	98.1	132.7	243.1	221.8	2467.6
VF_0827	c1cds817	18.3	8.3	8.1	11.5	5.8	9.5
VF_0828	c1cds818	7.4	13.3	11.6	10.8	3.0	6.9
VF_0829	c1cds819	9.3	17.0	14.4	13.6	3.9	15.3
VF_0830	c1cds820	16.2	24.0	14.2	18.1	5.2	35.4
VF_0831	c1cds821	19.1	23.3	24.4	22.3	2.8	48.5
VF_0832	c1cds822	34.1	20.7	16.5	23.8	9.2	18.4
VF_0833	c1cds823	284.7	476.0	406.1	388.9	96.8	362.2
VF_0834	c1cds824	278.1	554.9	460.8	431.3	140.8	363.1
VF_0835	c1cds825	227.5	582.5	462.9	424.3	180.6	120.6
VF_0836	c1cds826	126.4	33.2	49.5	69.7	49.8	556.7
VF_0837	c1cds827	432.2	599.7	965.2	665.7	272.5	602.6
VF_0838	c1cds828	2167.5	1210.4	1061.1	1479.7	600.3	293.6
VF_0839	c1cds829	81.2	153.0	237.0	157.0	78.0	281.7
VF_0840	c1cds830	38.0	51.1	60.1	49.7	11.1	46.5
VF_0841	c1cds831	12.4	6.2	6.1	8.3	3.6	42.2
VF_0842	c1cds832	21.3	21.5	15.7	19.5	3.3	122.3
VF_0843	c1cds833	24.9	27.7	20.3	24.3	3.7	140.5

VF_0844	c1cds834	33.4	22.4	26.9	27.6	5.5	71.1
VF_0845	c1cds835	37.8	30.5	30.6	33.0	4.2	24.1
VF_0846	c1cds836	68.4	80.9	59.4	69.6	10.8	104.3
VF_0847	c1cds837	213.4	81.5	72.3	122.4	79.0	198.7
VF_0848	c1cds838	18.1	16.5	16.2	16.9	1.0	42.3
VF_0849	c1cds839	8.6	7.9	7.0	7.8	0.8	22.3
VF_0850	c1cds840	29.3	16.8	13.6	19.9	8.3	24.1
VF_0851	c1cds841	37.2	29.7	29.4	32.1	4.4	65.2
VF_0852	c1cds842	72.0	36.7	46.8	51.8	18.2	166.9
VF_0853	c1cds843	53.3	39.5	40.6	44.5	7.6	90.5
VF_0854	c1cds844	58.5	28.2	28.6	38.4	17.4	72.8
VF_0855	c1cds845	24.8	15.4	15.4	18.5	5.4	26.3
VF_0856	c1cds846	47.4	22.1	23.7	31.1	14.2	39.1
VF_0857	c1cds847	34.2	20.2	25.6	26.7	7.1	54.9
VF_0858	c1cds848	44.8	18.3	21.9	28.3	14.4	69.9
VF_0859	c1cds849	76.7	49.3	57.2	61.0	14.1	134.5
VF_0860	c1cds850	66.3	38.0	49.0	51.1	14.3	147.5
VF_0861	c1cds851	2540.9	1600.2	1631.6	1924.2	534.3	1015.6
VF_0862	c1cds852	3300.3	6284.8	5745.5	5110.2	1590.4	3266.6
VF_0863	c1cds853	236.7	194.4	199.5	210.2	23.1	87.5
VF_0864	c1cds854	3.6	3.6	5.2	4.1	0.9	13.4
VF_0865	c1cds855	59.9	30.9	31.2	40.7	16.6	17.2
VF_0866	c1cds856	1.5	0.6	1.0	1.0	0.4	0.7
VF_0867	c1cds857	6.6	3.5	4.1	4.7	1.6	1.6
VF_0868	c1cds858	27.8	26.6	31.0	28.5	2.3	30.7
VF_0869	c1cds859	9.5	5.6	4.4	6.5	2.6	9.4
VF_0870	c1cds860	0.8	0.9	0.7	0.8	0.1	7.8
VF_0871	c1cds861	6.4	9.1	8.4	8.0	1.4	36.0
VF_0872	c1cds862	8.9	4.1	4.0	5.7	2.8	5.4
VF_0873	c1cds863	14.4	9.8	6.9	10.4	3.8	148.3
VF_0874	c1cds864	6.5	3.4	5.1	5.0	1.5	2.6
VF_0875	c1cds865	1.7	1.2	1.3	1.4	0.3	2.1
VF_0876	c1cds866	8.8	10.5	15.1	11.5	3.2	30.7
VF_0877	c1cds867	153.3	46.3	48.5	82.7	61.1	7.5
VF_0878	c1cds868	4.7	3.8	4.7	4.4	0.5	23.1
VF_0879	c1cds869	1.6	2.0	2.1	1.9	0.2	11.6
VF_0880	c1cds870	28.5	62.7	95.0	62.1	33.3	72.0
VF_0881	c1cds871	9.3	14.6	16.3	13.4	3.7	18.8
VF_0882	c1cds872	28.5	29.6	25.3	27.8	2.2	43.3
VF_0883	c1cds873	144.7	79.5	66.5	96.9	41.9	19.2
VF_0884	c1cds874	22.2	18.9	27.0	22.7	4.1	33.2
VF_0885	c1cds875	11.3	9.8	12.2	11.1	1.2	11.7
VF_0886	c1cds876	26.5	22.7	20.9	23.4	2.8	17.7

VF_0887	c1cds877	102.9	143.8	142.2	129.6	23.1	120.2
VF_0888	c1cds878	432.3	309.2	307.6	349.7	71.5	1031.2
VF_0889	c1cds879	63.9	64.8	91.4	73.4	15.6	30.1
VF_0890	c1cds880	223.6	128.0	112.3	154.7	60.2	254.1
VF_0891	c1cds881	80.5	86.5	86.0	84.3	3.3	111.4
VF_0892	c1cds882	31.5	72.6	88.6	64.2	29.5	74.9
VF_0893	c1cds883	31.6	60.1	51.8	47.8	14.7	138.0
VF_0894	c1cds884	6.0	11.6	8.9	8.8	2.8	14.5
VF_0895	c1cds885	28.0	22.4	20.6	23.6	3.8	61.6
VF_0896	c1cds886	49.4	123.8	79.1	84.1	37.4	74.3
VF_0897	c1cds887	145.2	445.3	395.5	328.6	160.8	716.5
VF_0898	c1cds888	54.4	43.3	37.5	45.0	8.6	150.1
VF_0899	c1cds889	88.5	107.0	136.3	110.6	24.1	145.2
VF_0900	c1cds890	33.0	31.0	37.6	33.9	3.4	89.9
VF_0901	c1cds891	29.6	35.9	41.5	35.7	5.9	82.6
VF_0902	c1cds892	205.4	142.1	161.9	169.8	32.4	302.2
VF_0903	c1cds893	153.8	19.5	30.8	68.0	74.5	720.0
VF_0904	c1cds894	131.6	102.6	107.4	113.9	15.5	448.0
VF_0905	c1cds895	53.1	45.0	44.7	47.6	4.8	73.6
VF_0906	c1cds896	160.8	127.0	126.1	138.0	19.8	136.6
VF_0907	c1cds897	40.1	24.3	26.8	30.4	8.5	41.6
VF_0908	c1cds898	137.9	196.0	256.8	196.9	59.4	799.6
VF_0909	c1cds899	154.1	50.6	72.1	92.3	54.6	209.4
VF_0910	c1cds900	197.8	387.5	389.2	324.8	110.0	131.0
VF_0911	c1cds901	75.9	98.3	116.9	97.0	20.5	75.2
VF_0912	c1cds902	48.1	42.5	41.4	44.0	3.6	45.7
VF_0913	c1cds903	1276.3	905.6	1034.7	1072.2	188.1	4751.4
VF_0914	c1cds904	256.5	169.1	133.7	186.4	63.2	105.7
VF_0915	c1cds905	17.7	31.7	21.0	23.5	7.3	77.2
VF_0916	c1cds906	42.6	55.6	32.4	43.5	11.6	49.1
VF_0917	c1cds908	25.3	31.5	22.1	26.3	4.8	18.5
VF_0918	c1cds909	288.1	464.4	521.9	424.8	121.8	507.0
VF_0919	c1cds910	495.7	196.5	152.9	281.7	186.6	52.3
VF_0920	c1cds911	17.6	69.6	45.1	44.1	26.0	157.3
VF_0921	c1cds912	1430.1	551.7	612.1	864.6	490.6	3293.1
VF_0922	c1cds913	705.7	452.7	476.9	545.1	139.6	899.4
VF_0923	c1cds914	9.7	9.2	11.8	10.3	1.4	27.1
VF_0924	c1cds915	27.5	25.7	27.3	26.9	1.0	45.9
VF_0925	c1cds916	26.3	23.4	28.1	25.9	2.4	32.4
VF_0926	c1cds917	56.6	183.4	136.2	125.4	64.1	49.3
VF_0927	c1cds918	73.7	180.1	59.7	104.5	65.9	174.7
VF_0928	c1cds919	221.7	104.4	110.0	145.4	66.2	321.3
VF_0929	c1cds920	64.7	61.9	54.1	60.2	5.5	72.1

VF_0930	c1cds921	47.6	51.4	55.1	51.4	3.7	46.3
VF_0931	c1cds922	44.8	31.9	36.3	37.7	6.5	58.2
VF_0932	c1cds923	51.5	18.4	18.2	29.4	19.2	74.0
VF_0933	c1cds924	37.5	15.6	23.5	25.5	11.1	68.0
VF_0934	c1cds925	21.3	28.2	24.1	24.6	3.5	48.4
VF_0935	c1cds926	34.4	24.2	25.8	28.1	5.5	43.5
VF_0936	c1cds927	35.0	32.6	36.2	34.6	1.8	58.0
VF_0937	c1cds928	16.8	13.6	10.5	13.6	3.2	23.7
VF_0938	c1cds929	73.5	21.7	22.1	39.1	29.8	41.4
VF_0939	c1cds930	53.3	53.0	48.5	51.6	2.7	97.3
VF_0940	c1cds931	229.0	104.3	79.3	137.5	80.2	64.8
VF_0941	c1cds932	42.1	31.0	26.7	33.3	8.0	109.7
VF_0942	c1cds933	26.0	28.4	18.6	24.3	5.1	46.1
VF_0943	c1cds934	50.5	36.8	38.7	42.0	7.4	70.7
VF_0944	c1cds935	580.9	294.1	360.8	411.9	150.1	346.6
VF_0945	c1cds936	448.8	233.0	221.8	301.2	128.0	310.7
VF_0946	c1cds937	20.3	18.0	18.2	18.8	1.3	92.7
VF_0947	c1cds938	50.0	63.4	63.8	59.1	7.9	101.6
VF_0948	c1cds939	20.7	31.4	30.5	27.5	5.9	45.3
VF_0949	c1cds940	267.6	321.1	434.5	341.1	85.2	472.0
VF_0950	c1cds941	14.6	3.5	3.2	7.1	6.5	5.9
VF_0951	c1cds942	40.3	36.3	32.2	36.3	4.1	82.4
VF_0952	c1cds943	39.2	46.1	39.7	41.7	3.8	48.8
VF_0953	c1cds944	464.1	667.1	778.2	636.5	159.3	1083.7
VF_0954	c1cds945	551.4	513.7	667.1	577.4	79.9	1069.1
VF_0955	c1cds946	309.8	113.6	70.8	164.8	127.4	390.9
VF_0956	c1cds947	2364.5	1430.1	1529.9	1774.9	513.1	1404.3
VF_0957	c1cds948	55.1	47.7	35.7	46.1	9.8	73.5
VF_0958	c1cds949	66.6	49.0	48.7	54.7	10.2	72.0
VF_0959	c1cds950	42.1	49.8	43.1	45.0	4.2	46.6
VF_0960	c1cds951	174.4	107.2	138.1	139.9	33.6	37.8
VF_0962	c1cds952	745.3	522.4	522.5	596.7	128.6	526.0
VF_0963	c1cds953	3326.6	2066.8	1759.2	2384.2	830.5	4123.1
VF_0964	c1cds954	625.0	440.8	403.0	489.6	118.7	500.4
VF_0965	c1cds955	49.6	96.3	118.7	88.2	35.3	110.7
VF_0966	c1cds956	43.4	44.5	59.4	49.1	8.9	153.2
VF_0967	c1cds957	2.7	0.9	0.2	1.3	1.3	103.5
VF_0968	c1cds958	21.8	9.4	10.7	14.0	6.8	7.6
VF_0969	c1cds959	135.9	199.2	108.9	148.0	46.4	18.8
VF_0970	c1cds960	61.8	87.5	68.1	72.5	13.4	11.4
VF_0971	c1cds961	19.0	28.0	26.7	24.6	4.9	20.5
VF_0972	c1cds962	50.3	42.0	44.7	45.7	4.3	39.1
VF_0973	c1cds963	31.7	46.3	32.8	36.9	8.1	2.3

VF_0974	c1cds964	29.0	36.6	30.5	32.0	4.0	4.6
VF_0975	c1cds965	25.2	22.6	22.4	23.4	1.6	5.5
VF_0976	c1cds966	41.0	36.5	34.2	37.2	3.4	33.3
VF_0977	c1cds968	41.4	45.9	50.3	45.9	4.4	34.4
VF_0978	c1cds969	18.7	8.4	5.8	11.0	6.8	30.1
VF_0979	c1cds970	60.5	51.8	62.1	58.1	5.5	27.8
VF_0980	c1cds971	4.5	2.7	3.5	3.6	0.9	8.2
VF_0981	c1cds972	83.7	86.3	49.3	73.1	20.7	8.8
VF_0982	c1cds973	14.7	16.2	9.0	13.3	3.8	33.6
VF_0983	c1cds974	423.4	166.6	190.6	260.2	141.8	123.3
VF_0984	c1cds975	138.9	66.3	57.5	87.6	44.7	48.4
VF_0985	c1cds976	34.2	27.4	18.0	26.5	8.1	6.5
VF_0986	c1cds977	49.2	9.9	15.9	25.0	21.2	8.7
VF_0987	c1cds978	49.3	29.2	26.0	34.8	12.6	4.2
VF_0988	c1cds979	35.7	22.4	19.6	25.9	8.6	11.0
VF_0989	c1cds980	13.7	22.6	13.2	16.5	5.3	18.8
VF_0990	c1cds981	7.5	3.7	2.4	4.5	2.6	3.7
VF_0991	c1cds982	3.8	2.9	2.5	3.1	0.6	3.1
VF_0993	c1cds983	4.5	2.1	1.8	2.8	1.5	3.7
VF_0994	c1cds984	4.3	1.6	2.0	2.6	1.4	4.1
VF_0995	c1cds985	4.1	1.4	1.4	2.3	1.5	5.5
VF_0997	c1cds987	5.2	1.5	1.7	2.8	2.1	6.4
VF_0998	c1cds989	1.9	0.5	0.7	1.0	0.7	4.1
VF_0999	c1cds990	2.7	0.6	1.2	1.5	1.1	6.3
VF_1001	c1cds992	1.5	0.2	0.2	0.6	0.8	1.5
VF_1003	c1cds994	5.0	1.5	1.1	2.5	2.1	11.3
VF_1005	c1cds996	1.3	0.4	0.4	0.7	0.5	1.7
VF_1006	c1cds997	3.7	4.7	2.4	3.6	1.1	15.0
VF_1007	c1cds998	4.7	7.7	7.9	6.8	1.8	14.2
VF_1008	c1cds999	10.6	13.2	12.6	12.1	1.3	12.9
VF_1009	c1cds1000	11.7	13.4	13.4	12.9	1.0	11.5
VF_1010	c1cds1001	1156.4	1965.7	2298.0	1806.7	587.2	3336.4
VF_1011	c1cds1002	528.4	792.0	1025.5	782.0	248.7	24833.7
VF_1012	c1cds1003	32.6	39.4	51.2	41.1	9.4	49.1
VF_1013	c1cds1004	25.6	33.0	48.7	35.8	11.8	30.4
VF_1014	c1cds1005	40.5	35.0	56.3	43.9	11.0	39.8
VF_1015	c1cds1006	29.9	42.4	62.6	45.0	16.5	38.9
VF_1016	c1cds1007	31.5	45.7	67.5	48.2	18.1	23.2
VF_1017	c1cds1008	29.3	40.2	55.4	41.6	13.1	31.4
VF_1018	c1cds1009	26.8	31.6	44.8	34.4	9.4	26.6
VF_1019	c1cds1010	63.2	46.9	56.2	55.4	8.2	54.1
VF_1020	c1cds1011	3.8	9.3	8.9	7.3	3.1	11.3
VF_1021	c1cds1012	27.8	20.8	24.9	24.5	3.5	23.8

VF_1022	c1cds1013	78.7	44.4	46.2	56.4	19.3	101.1
VF_1023	c1cds1014	53.1	43.2	50.0	48.8	5.1	97.7
VF_1024	c1cds1015	51.8	73.8	104.9	76.8	26.7	23.9
VF_1025	c1cds1016	37.9	23.0	22.5	27.8	8.7	12.2
VF_1026	c1cds1017	15.3	17.6	26.8	19.9	6.1	15.5
VF_1027	c1cds1018	108.5	69.8	87.3	88.5	19.4	142.6
VF_1028	c1cds1019	49.5	31.2	40.4	40.4	9.2	99.4
VF_1029	c1cds1020	29.9	17.0	18.8	21.9	7.0	42.7
VF_1031	c1cds1021	31.7	16.3	19.8	22.6	8.0	41.4
VF_1032	c1cds1022	19.2	13.2	17.4	16.6	3.1	26.3
VF_1033	c1cds1023	15.8	11.1	13.7	13.5	2.4	22.1
VF_1034	c1cds1026	61.0	41.7	45.4	49.4	10.2	59.0
VF_1035	c1cds1027	178.5	122.0	125.3	141.9	31.7	191.5
VF_1036	c1cds1028	64.4	40.9	21.2	42.2	21.6	8.6
VF_1037	c1cds1029	69.7	18.4	9.0	32.4	32.7	9.6
VF_1038	c1cds1030	150.6	301.8	415.0	289.1	132.7	246.7
VF_1039	c1cds1031	27.8	44.3	37.4	36.5	8.3	111.2
VF_1040	c1cds1032	19.7	25.6	23.3	22.9	3.0	47.8
VF_1041	c1cds1033	10.3	2.1	0.8	4.4	5.1	3.6
VF_1042	c1cds1034	51.0	15.2	11.5	25.9	21.8	25.0
VF_1043	c1cds1035	43.3	27.4	15.3	28.7	14.0	68.0
VF_1044	c1cds1036	14.8	7.7	6.3	9.6	4.5	30.6
VF_1045	c1cds1037	6.5	3.6	1.4	3.8	2.6	4.4
VF_1046	c1cds1038	14.1	7.8	4.0	8.6	5.1	31.2
VF_1047	c1cds1039	16.3	8.4	5.5	10.1	5.6	66.6
VF_1048	c1cds1041	31.3	10.6	6.7	16.2	13.2	8.9
VF_1049	c1cds1042	2.0	1.0	1.0	1.4	0.6	1.4
VF_1050	c1cds1043	187.6	85.9	52.9	108.8	70.2	127.3
VF_1051	c1cds1044	301.1	179.2	191.7	224.0	67.0	334.1
VF_1052	c1cds1045	5.1	7.7	11.4	8.1	3.2	22.0
VF_1053	c1cds1046	17.1	17.5	19.6	18.1	1.3	9.6
VF_1054	c1cds1047	86.7	34.1	42.2	54.3	28.3	12.0
VF_1055	c1cds1048	232.2	187.0	136.4	185.2	47.9	159.0
VF_1056	c1cds1049	719.5	762.7	518.7	667.0	130.2	281.6
VF_1057	c1cds1050	5.4	7.5	7.8	6.9	1.3	5.9
VF_1058	c1cds1051	53.9	17.4	21.3	30.9	20.0	8.6
VF_1059	c1cds1052	279.4	59.3	108.4	149.1	115.5	135.3
VF_1060	c1cds1053	1.1	12.5	11.6	8.4	6.3	1.9
VF_1061	c1cds1054	7.3	4.3	4.8	5.5	1.6	1.8
VF_1062	c1cds1055	12.6	15.8	26.8	18.4	7.4	89.9
VF_1063	c1cds1056	317.2	156.7	109.6	194.5	108.9	19.6
VF_1064	c1cds1057	1463.7	493.7	462.7	806.7	569.2	418.4
VF_1065	c1cds1058	597.8	155.8	127.3	293.6	263.8	117.9

VF_1066	c1cds1059	10.1	6.7	4.8	7.2	2.7	8.7
VF_1067	c1cds1060	12.5	8.4	7.4	9.4	2.7	7.1
VF_1068	c1cds1061	26.0	22.3	21.0	23.1	2.6	11.3
VF_1070	c1cds1063	32.9	9.1	8.9	16.9	13.8	2.6
VF_1071	c1cds1064	4.1	2.1	2.3	2.8	1.1	0.8
VF_1072	c1cds1065	23.6	22.4	17.2	21.1	3.4	9.0
VF_1073	c1cds1066	88.9	42.8	45.9	59.2	25.8	138.6
VF_1074	c1cds1067	17.5	23.2	15.4	18.7	4.1	37.3
VF_1075	c1cds1068	27.1	8.3	7.7	14.4	11.0	3.8
VF_1076	c1cds1069	5.0	1.9	2.1	3.0	1.7	3.4
VF_1077	c1cds1070	2.5	0.8	1.8	1.7	0.9	2.8
VF_1080	c1cds1073	13.1	12.7	8.0	11.3	2.8	4.3
VF_1081	c1cds1074	3.6	8.6	9.8	7.3	3.3	12.9
VF_1082	c1cds1075	9.7	18.2	10.7	12.9	4.6	10.3
VF_1083	c1cds1076	36.0	30.3	19.6	28.7	8.3	18.9
VF_1084	c1cds1077	14.2	11.6	17.2	14.3	2.8	33.0
VF_1085	c1cds1078	154.8	195.0	219.9	189.9	32.9	841.8
VF_1086	c1cds1080	8.9	12.7	8.5	10.0	2.3	6.4
VF_1087	c1cds1081	4.3	5.5	1.6	3.8	2.0	0.9
VF_1088	c1cds1082	32.3	31.2	30.4	31.3	0.9	48.0
VF_1089	c1cds1083	141.4	196.5	181.8	173.2	28.5	28.7
VF_1090	c1cds1084	42.0	45.1	39.9	42.3	2.6	4.8
VF_1091	c1cds1085	11.8	4.3	4.8	7.0	4.2	37.0
VF_1092	c1cds1086	12.6	12.8	9.8	11.7	1.7	11.7
VF_1093	c1cds1087	206.9	80.0	53.6	113.5	82.0	1.7
VF_1094	c1cds1088	166.6	73.0	51.7	97.1	61.1	15.8
VF_1095	c1cds1089	15.8	13.3	9.6	12.9	3.1	9.1
VF_1096	c1cds1090	11.1	6.2	6.5	7.9	2.7	2.5
VF_1097	c1cds1091	7.8	3.5	3.5	4.9	2.5	8.7
VF_1098	c1cds1092	7.6	3.9	3.8	5.1	2.2	30.1
VF_1099	c1cds1093	5.5	5.8	5.2	5.5	0.3	21.0
VF_1100	c1cds1094	4.8	7.5	5.5	5.9	1.4	22.9
VF_1101	c1cds1095	87.0	105.6	112.9	101.8	13.4	116.6
VF_1102	c1cds1096	4.2	9.5	9.9	7.9	3.2	17.2
VF_1103	c1cds1097	64.1	27.0	22.9	38.0	22.7	8.3
VF_1104	c1cds1098	107.8	204.3	195.7	169.2	53.4	136.2
VF_1105	c1cds1099	37.4	59.9	55.5	50.9	11.9	19.1
VF_1106	c1cds1100	73.2	61.8	53.5	62.8	9.9	13.7
VF_1107	c1cds1101	142.0	103.5	78.5	108.0	32.0	37.7
VF_1108	c1cds1102	77.6	88.0	77.4	81.0	6.1	47.8
VF_1109	c1cds1103	17.6	13.5	10.7	13.9	3.5	7.6
VF_1111	c1cds1105	15.2	14.8	13.7	14.6	0.8	8.6
VF_1112	c1cds1106	547.5	237.3	227.5	337.4	182.0	57.4

VF_1113	c1cds1107	8.4	22.1	20.9	17.1	7.6	33.1
VF_1114	c1cds1108	5.0	14.2	16.4	11.8	6.0	21.8
VF_1115	c1cds1109	6.5	17.7	18.7	14.3	6.8	16.2
VF_1116	c1cds1111	6.4	4.2	2.7	4.5	1.9	0.4
VF_1117	c1cds1112	14.1	14.3	11.5	13.3	1.5	4.5
VF_1118	c1cds1113	5.1	5.5	4.1	4.9	0.8	12.6
VF_1119	c1cds1114	4.9	4.6	3.3	4.3	0.8	5.8
VF_1120	c1cds1115	150.1	90.2	77.9	106.1	38.7	10.1
VF_1121	c1cds1116	3.0	3.5	4.0	3.5	0.5	26.0
VF_1122	c1cds1117	88.6	41.4	36.4	55.4	28.8	66.0
VF_1123	c1cds1118	34.8	16.1	17.5	22.8	10.4	8.0
VF_1124	c1cds1119	1.5	0.4	0.5	0.8	0.6	29.1
VF_1125	c1cds1120	82.0	26.5	23.1	43.9	33.1	7.2
VF_1126	c1cds1121	13.2	10.2	7.8	10.4	2.7	79.7
VF_1127	c1cds1122	17.1	10.8	6.9	11.6	5.2	70.1
VF_1128	c1cds1123	29.0	18.8	10.8	19.5	9.1	76.6
VF_1129	c1cds1124	3.3	2.6	4.4	3.4	0.9	5.3
VF_1130	c1cds1125	8.1	17.1	18.2	14.5	5.5	29.9
VF_1131	c1cds1126	43.0	31.6	24.5	33.0	9.3	25.3
VF_1132	c1cds1127	23.1	11.1	11.8	15.3	6.7	12.5
VF_1133	c1cds1128	25.5	127.0	141.2	97.9	63.1	87.0
VF_1134	c1cds1129	362.5	169.4	184.2	238.7	107.5	195.8
VF_1135	c1cds1130	197.5	157.0	139.1	164.5	29.9	74.1
VF_1136	c1cds1131	1326.6	470.5	634.4	810.5	454.4	342.5
VF_1137	c1cds1132	1303.5	615.1	701.4	873.3	375.1	710.3
VF_1138	c1cds1133	9.5	5.9	5.3	6.9	2.3	1.5
VF_1139	c1cds1134	101.0	68.4	55.6	75.0	23.4	109.8
VF_1140	c1cds1135	3.3	1.7	2.1	2.4	0.9	1.2
VF_1141	c1cds1136	4.5	7.3	5.4	5.7	1.4	6.1
VF_1142	c1cds1137	74.7	70.0	81.1	75.2	5.6	207.6
VF_1143	c1cds1138	58.1	62.3	59.8	60.0	2.1	68.5
VF_1144	c1cds1139	12.5	26.6	27.9	22.3	8.5	36.0
VF_1145	c1cds1140	19.3	26.6	28.8	24.9	5.0	27.5
VF_1146	c1cds1141	23.4	18.9	19.8	20.7	2.4	23.2
VF_1147	c1cds1142	96.5	341.2	530.8	322.8	217.7	8.3
VF_1148	c1cds1143	27.9	10.0	11.2	16.4	10.0	14.4
VF_1149	c1cds1144	63.4	30.1	29.8	41.1	19.3	7.2
VF_1150	c1cds1145	6.6	6.0	6.7	6.4	0.4	13.9
VF_1151	c1cds1146	2114.5	1040.2	451.8	1202.2	843.1	134.3
VF_1152	c1cds1147	552.1	241.2	306.3	366.6	164.0	145.0
VF_1153	c1cds1148	63.8	83.4	63.7	70.3	11.3	60.2
VF_1154	c1cds1149	14.6	20.8	14.0	16.5	3.7	30.9
VF_1155	c1cds1150	16.7	200.2	234.2	150.4	117.0	9.6

VF_1156	c1cds1151	15.2	23.5	26.8	21.9	6.0	28.0
VF_1157	c1cds1152	608.3	225.4	160.1	331.3	242.1	2.0
VF_1158	c1cds1153	60.2	142.7	136.2	113.0	45.9	2.0
VF_1159	c1cds1154	77.8	127.1	180.9	128.6	51.5	915.7
VF_1160	c1cds1155	177.3	184.4	210.4	190.7	17.4	66.5
VF_1161	c1cds1156	15.3	9.7	5.1	10.0	5.1	10.0
VF_1162	c1cds1157	23.0	11.9	10.4	15.1	6.9	13.2
VF_1163	c1cds1158	58.2	31.1	28.4	39.2	16.5	13.9
VF_1164	c1cds1159	39.7	22.5	20.5	27.5	10.6	11.9
VF_1165	c1cds1160	42.0	20.0	18.3	26.8	13.2	27.1
VF_1166	c1cds1161	18.9	5.8	5.2	10.0	7.8	8.3
VF_1167	c1cds1162	10.4	9.7	11.8	10.6	1.1	24.0
VF_1168	c1cds1163	17.1	16.3	19.3	17.6	1.6	32.8
VF_1169	c1cds1164	81.7	108.2	109.0	99.6	15.6	93.6
VF_1170	c1cds1165	26.4	14.5	12.4	17.7	7.5	18.3
VF_1171	c1cds1166	9.2	8.5	7.6	8.4	0.8	21.7
VF_1172	c1cds1167	12.8	8.8	5.7	9.1	3.6	17.7
VF_1173	c1cds1168	2305.0	1878.2	897.7	1693.6	721.6	79.7
VF_1174	c1cds1169	6128.9	4820.0	3052.6	4667.2	1543.8	194.2
VF_1175	c1cds1170	221.7	192.1	170.1	194.6	25.9	7.8
VF_1176	c1cds1171	21.7	100.4	98.5	73.5	44.9	378.5
VF_1177	c1cds1172	22.8	188.6	146.4	119.3	86.1	493.9
VF_1178	c1cds1173	17.3	8.5	5.2	10.3	6.2	4.2
VF_1179	c1cds1174	7.6	10.0	10.9	9.5	1.7	19.4
VF_1180	c1cds1175	47.3	66.7	74.1	62.7	13.8	274.1
VF_1181	c1cds1176	138.5	87.6	58.8	95.0	40.4	59.9
VF_1182	c1cds1177	290.8	165.3	153.9	203.3	75.9	50.9
VF_1183	c1cds1178	274.1	125.4	120.6	173.4	87.2	53.8
VF_1184	c1cds1179	222.8	135.1	127.2	161.7	53.0	53.5
VF_1185	c1cds1180	119.9	100.2	105.0	108.4	10.3	92.5
VF_1186	c1cds1181	49.4	57.9	67.6	58.3	9.1	93.3
VF_1187	c1cds1182	197.9	169.6	144.2	170.5	26.9	93.6
VF_1188	c1cds1183	31.6	42.9	59.4	44.6	14.0	278.5
VF_1189	c1cds1184	120.0	218.7	156.3	165.0	49.9	52.4
VF_1190	c1cds1185	65.1	275.8	165.4	168.7	105.4	1415.5
VF_1191	c1cds1186	7.6	15.8	9.7	11.0	4.2	239.1
VF_1192	c1cds1187	17.8	31.7	21.0	23.5	7.3	276.7
VF_1193	c1cds1188	21.8	31.7	23.1	25.5	5.3	165.9
VF_1194	c1cds1189	336.7	295.4	329.2	320.5	22.0	191.0
VF_1195	c1cds1190	246.5	221.1	211.4	226.3	18.1	141.8
VF_1196	c1cds1191	50.8	52.8	53.5	52.4	1.4	94.4
VF_1197	c1cds1192	45.4	12.3	9.1	22.3	20.1	19.6
VF_1198	c1cds1193	294.4	227.9	272.4	264.9	33.9	101.8

VF_1199	c1cds1194	412.7	159.9	134.3	235.6	153.8	65.0
VF_1200	c1cds1195	71.3	23.2	17.6	37.4	29.5	50.0
VF_1201	c1cds1197	103.3	124.2	117.8	115.1	10.8	330.5
VF_1202	c1cds1198	106.6	80.4	112.2	99.7	17.0	568.9
VF_1203	c1cds1199	27.7	21.3	27.2	25.4	3.6	77.4
VF_1204	c1cds1200	184.7	167.6	243.8	198.7	39.9	1181.5
VF_1205	c1cds1202	56.2	120.4	47.0	74.5	40.0	335.8
VF_1206	c1cds1203	13.6	8.4	9.5	10.5	2.7	14.7
VF_1207	c1cds1204	8.2	10.5	13.8	10.8	2.8	33.6
VF_1208	c1cds1205	2.8	4.1	2.9	3.3	0.8	23.6
VF_1209	c1cds1206	13.9	13.6	10.9	12.8	1.7	21.3
VF_1210	c1cds1207	97.5	78.7	73.0	83.0	12.8	87.2
VF_1211	c1cds1208	2451.8	24.0	12.4	829.4	1405.1	346.7
VF_1212	c1cds1209	1620.3	18.2	6.1	548.2	928.5	222.5
VF_1213	c1cds1210	9.4	5.7	6.9	7.3	1.9	9.7
VF_1214	c1cds1211	408.6	596.4	719.3	574.8	156.4	556.6
VF_1216	c1cds1212	12100.2	14960.6	16345.7	14468.8	2165.1	5874.0
VF_1217	c1cds1213	12195.6	11420.9	10074.4	11230.3	1073.4	12159.4
VF_1218	c1cds1214	5493.6	6660.6	6459.0	6204.4	623.8	3792.8
VF_1219	c1cds1215	29.1	11.9	7.7	16.2	11.3	1.0
VF_1220	c1cds1216	70.5	102.4	33.3	68.7	34.6	170.0
VF_1221	c1cds1217	11.9	51.3	18.2	27.2	21.1	127.8
VF_1222	c1cds1218	14.0	55.5	17.4	29.0	23.0	286.0
VF_1223	c1cds1219	9.5	49.5	15.4	24.8	21.6	119.0
VF_1224	c1cds1220	22.9	93.0	32.9	49.6	37.9	219.6
VF_1225	c1cds1221	36.2	140.6	55.3	77.4	55.6	225.3
VF_1226	c1cds1222	35.5	147.0	57.9	80.1	59.0	409.7
VF_1227	c1cds1223	48.9	87.0	25.1	53.7	31.2	603.9
VF_1228	c1cds1224	541.0	242.4	104.2	295.9	223.2	1726.5
VF_1229	c1cds1225	2.7	1.8	1.2	1.9	0.7	2.4
VF_1230	c1cds1226	2.1	1.1	1.0	1.4	0.6	1.6
VF_1231	c1cds1227	5.4	3.1	2.5	3.7	1.5	4.4
VF_1232	c1cds1228	16.2	17.2	14.4	15.9	1.4	13.5
VF_1233	c1cds1229	33.9	25.1	16.4	25.1	8.7	11.7
VF_1234	c1cds1230	101.7	100.7	23.0	75.2	45.2	251.8
VF_1235	c1cds1231	67.5	87.9	107.6	87.7	20.1	524.8
VF_1236	c1cds1232	109.8	124.2	202.3	145.4	49.7	591.2
VF_1237	c1cds1233	6437.5	1754.3	1564.9	3252.3	2760.2	1182.8
VF_1238	c1cds1234	57.6	71.4	67.9	65.6	7.2	37.3
VF_1239	c1cds1235	52.9	43.8	53.0	49.9	5.3	46.9
VF_1240	c1cds1236	314.3	154.4	201.6	223.4	82.1	267.2
VF_1241	c1cds1237	97.8	97.3	138.0	111.0	23.3	210.3
VF_1242	c1cds1238	33.6	28.1	29.1	30.3	2.9	78.7

VF_1243	c1cds1239	83.7	45.7	46.4	58.6	21.7	67.6
VF_1244	c1cds1240	145.8	214.2	245.6	201.9	51.0	195.7
VF_1245	c1cds1241	58.7	46.9	42.9	49.5	8.2	33.2
VF_1246	c1cds1242	86.7	29.9	23.6	46.7	34.7	6.0
VF_1247	c1cds1243	275.7	207.3	172.4	218.5	52.6	312.6
VF_1248	c1cds1244	46.6	26.1	31.2	34.6	10.7	1.3
VF_1249	c1cds1246	44.0	56.3	39.0	46.4	8.9	9.0
VF_1250	c1cds1247	27.3	34.9	17.6	26.6	8.7	1.0
VF_1251	c1cds1248	118.4	75.2	44.2	79.3	37.3	24.7
VF_1252	c1cds1249	118.3	68.0	51.8	79.4	34.7	23.3
VF_1253	c1cds1250	4.9	5.3	4.7	5.0	0.3	8.6
VF_1255	c1cds1252	24.0	46.8	51.1	40.6	14.6	20.1
VF_1256	c1cds1253	106.8	50.2	45.3	67.4	34.1	18.9
VF_1257	c1cds1254	19.5	10.2	9.8	13.2	5.5	28.9
VF_1258	c1cds1255	56.5	25.7	25.5	35.9	17.8	6.6
VF_1259	c1cds1256	5.0	2.1	2.1	3.1	1.7	10.8
VF_1260	c1cds1257	16.7	13.6	10.4	13.6	3.1	14.8
VF_1261	c1cds1258	10.0	10.2	9.1	9.8	0.6	11.4
VF_1262	c1cds1259	128.6	72.3	54.1	85.0	38.9	9.1
VF_1263	c1cds1260	118.0	60.7	38.9	72.5	40.8	6.7
VF_1264	c1cds1261	9.4	13.1	12.7	11.7	2.0	16.2
VF_1265	c1cds1262	25.2	13.2	7.8	15.4	8.9	8.9
VF_1266	c1cds1263	4.0	7.9	7.0	6.3	2.0	4.2
VF_1269	c1cds1264	6.3	7.2	6.6	6.7	0.4	22.5
VF_1270	c1cds1265	3.4	8.6	6.2	6.1	2.6	10.2
VF_1271	c1cds1266	10.1	9.5	7.2	8.9	1.6	4.3
VF_1272	c1cds1267	202.1	221.0	292.1	238.4	47.5	346.7
VF_1273	c1cds1268	28.0	34.5	34.9	32.5	3.8	16.5
VF_1274	c1cds1269	29.3	42.3	50.4	40.6	10.6	29.2
VF_1275	c1cds1270	148.0	90.4	89.9	109.4	33.4	32.4
VF_1276	c1cds1271	54.0	42.4	30.7	42.4	11.7	9.7
VF_1277	c1cds1272	51.8	31.9	24.1	35.9	14.3	44.6
VF_1278	c1cds1273	143.2	124.9	115.8	128.0	13.9	105.9
VF_1279	c1cds1274	1015.3	571.6	646.6	744.5	237.5	989.5
VF_1280	c1cds1275	324.3	225.6	263.1	271.0	49.8	418.4
VF_1281	c1cds1276	330.5	155.6	83.7	189.9	126.9	2.8
VF_1282	c1cds1277	216.5	118.2	104.9	146.5	60.9	223.7
VF_1283	c1cds1278	49.3	16.6	13.5	26.5	19.8	17.4
VF_1284	c1cds1279	477.6	246.4	258.6	327.6	130.1	887.5
VF_1285	c1cds1280	33.5	36.0	48.5	39.3	8.0	202.8
VF_1286	c1cds1281	65.8	76.7	53.7	65.4	11.5	61.0
VF_1287	c1cds1282	45.4	99.4	130.6	91.8	43.1	128.0
VF_1288	c1cds1283	23.6	54.5	74.6	50.9	25.7	61.2

VF_1289	c1cds1284	89.4	113.0	135.1	112.5	22.8	103.1
VF_1290	c1cds1285	399.4	292.5	348.1	346.7	53.5	150.3
VF_1291	c1cds1286	24157.5	19367.2	19020.7	20848.5	2871.0	1029.1
VF_1292	c1cds1287	279.1	346.4	231.5	285.6	57.8	494.3
VF_1293	c1cds1288	28.2	26.2	23.3	25.9	2.5	57.3
VF_1294	c1cds1289	103.6	136.8	97.3	112.5	21.2	173.0
VF_1295	c1cds1290	2.3	2.6	2.2	2.4	0.2	3.9
VF_1296	c1cds1291	11.4	5.3	4.6	7.1	3.8	11.2
VF_1297	c1cds1292	13.4	9.9	7.0	10.1	3.2	16.5
VF_1298	c1cds1293	26.1	28.4	18.0	24.2	5.5	57.4
VF_1299	c1cds1294	210.5	223.6	217.0	217.0	6.5	497.6
VF_1300	c1cds1295	260.3	279.8	289.6	276.6	14.9	738.9
VF_1301	c1cds1296	274.7	197.0	172.7	214.8	53.3	413.9
VF_1302	c1cds1297	533.5	452.9	424.9	470.4	56.4	624.7
VF_1303	c1cds1298	17.9	27.1	11.2	18.8	8.0	59.7
VF_1304	c1cds1299	7.5	10.1	7.7	8.4	1.4	41.6
VF_1306	c1cds1300	2.9	3.3	1.8	2.7	0.8	8.6
VF_1307	c1cds1301	5.0	3.8	3.4	4.1	0.8	10.7
VF_1308	c1cds1302	496.1	593.8	614.2	568.0	63.1	239.2
VF_1310	c1cds1303	1757.3	1568.7	1264.5	1530.2	248.6	408.9
VF_1311	c1cds1304	27.2	46.1	56.8	43.3	15.0	80.9
VF_1312	c1cds1305	114.7	118.7	140.8	124.7	14.0	76.6
VF_1313	c1cds1306	96.9	79.2	92.2	89.4	9.2	78.1
VF_1314	c1cds1307	20.4	11.8	10.4	14.2	5.4	17.7
VF_1315	c1cds1308	96.3	56.7	50.0	67.7	25.0	98.1
VF_1316	c1cds1309	45.0	23.1	19.9	29.4	13.7	61.9
VF_1317	c1cds1310	294.6	112.1	96.8	167.8	110.0	54.6
VF_1318	c1cds1311	308.4	82.7	78.2	156.4	131.6	80.2
VF_1319	c1cds1312	96.3	206.9	262.6	188.6	84.6	259.2
VF_1320	c1cds1313	72.1	379.0	111.7	187.6	166.9	18.5
VF_1321	c1cds1314	16.7	11.0	11.9	13.2	3.1	22.4
VF_1322	c1cds1315	5.2	5.0	4.0	4.8	0.6	1.0
VF_1323	c1cds1316	245.2	139.5	93.5	159.4	77.8	61.8
VF_1324	c1cds1317	162.1	114.9	70.0	115.7	46.0	42.0
VF_1325	c1cds1318	503.3	248.9	140.9	297.7	186.1	94.9
VF_1326	c1cds1319	163.3	83.2	93.7	113.4	43.5	19.3
VF_1327	c1cds1320	69.5	29.4	26.3	41.7	24.1	15.0
VF_1328	c1cds1321	73.4	43.4	43.0	53.3	17.5	5.1
VF_1329	c1cds1322	244.5	87.9	93.8	142.1	88.8	5.5
VF_1330	c1cds1323	52.7	17.2	17.7	29.2	20.3	3.2
VF_1331	c1cds1324	64.4	88.1	77.0	76.5	11.9	150.7
VF_1332	c1cds1325	2.3	2.1	1.3	1.9	0.5	2.1
VF_1333	c1cds1326	3.1	4.4	3.2	3.5	0.7	11.1

VF_1334	c1cds1327	39.2	30.6	34.8	34.8	4.3	41.5
VF_1335	c1cds1328	24.3	16.9	14.4	18.5	5.1	10.2
VF_1336	c1cds1329	12.0	13.0	8.1	11.1	2.6	3.4
VF_1337	c1cds1330	262.8	334.9	355.1	317.6	48.5	55.6
VF_1338	c1cds1331	258.9	190.8	189.4	213.0	39.8	3.3
VF_1339	c1cds1332	30.8	20.8	19.4	23.6	6.2	19.0
VF_1340	c1cds1333	10.3	6.7	7.4	8.2	1.9	8.9
VF_1341	c1cds1334	67.5	64.9	67.4	66.6	1.5	105.5
VF_1342	c1cds1335	17.8	11.0	11.2	13.4	3.9	13.8
VF_1343	c1cds1336	20.5	17.4	13.0	16.9	3.8	19.5
VF_1344	c1cds1337	21.2	14.8	16.0	17.3	3.4	10.1
VF_1345	c1cds1338	25.1	24.3	24.1	24.5	0.5	14.8
VF_1346	c1cds1339	50.8	33.3	39.0	41.0	8.9	33.3
VF_1347	c1cds1340	45.6	43.6	37.9	42.4	4.0	36.6
VF_1348	c1cds1341	26.3	37.9	40.1	34.8	7.4	38.9
VF_1349	c1cds1342	164.2	83.0	82.5	109.9	47.0	97.9
VF_1350	c1cds1343	8.9	15.7	9.6	11.4	3.7	10.5
VF_1351	c1cds1344	11.1	9.1	5.8	8.7	2.7	8.3
VF_1352	c1cds1345	54.7	59.0	55.4	56.4	2.3	14.9
VF_1353	c1cds1347	115.4	48.7	59.7	74.6	35.7	102.8
VF_1354	c1cds1348	38.8	26.6	20.8	28.7	9.2	197.5
VF_1355	c1cds1349	36.1	17.1	12.5	21.9	12.5	79.6
VF_1356	c1cds1351	17.5	12.3	10.3	13.3	3.7	40.0
VF_1358	c1cds1352	204.1	105.3	238.5	182.7	69.1	154.1
VF_1359	c1cds1353	221.4	81.3	203.4	168.7	76.2	212.9
VF_1360	c1cds1354	150.8	80.3	189.3	140.1	55.3	182.4
VF_1361	c1cds1355	175.2	90.6	150.5	138.8	43.5	198.5
VF_1362	c1cds1356	53.4	65.5	134.7	84.5	43.9	83.8
VF_1363	c1cds1357	31.8	63.2	144.7	79.9	58.3	81.3
VF_1364	c1cds1358	31.0	51.0	74.7	52.2	21.9	66.1
VF_1365	c1cds1359	40.9	46.1	48.8	45.3	4.0	98.3
VF_1366	c1cds1360	110.4	80.5	98.0	96.3	15.0	99.5
VF_1367	c1cds1361	6.4	4.8	3.2	4.8	1.6	6.9
VF_1368	c1cds1362	1.0	1.2	0.6	0.9	0.3	5.8
VF_1369	c1cds1363	11.6	16.3	14.4	14.1	2.4	266.4
VF_1370	c1cds1364	82.9	51.1	54.4	62.8	17.5	125.9
VF_1371	c1cds1365	31.1	18.4	23.8	24.4	6.3	64.3
VF_1372	c1cds1366	44.0	14.9	17.2	25.3	16.2	53.2
VF_1373	c1cds1367	23.6	23.1	16.1	20.9	4.2	25.0
VF_1374	c1cds1368	23.7	18.3	16.0	19.3	3.9	15.9
VF_1375	c1cds1369	9.6	6.0	7.1	7.6	1.9	17.3
VF_1376	c1cds1370	5.8	9.4	8.8	8.0	2.0	16.0
VF_1377	c1cds1371	9.4	14.7	11.1	11.7	2.7	23.5

VF_1378	c1cds1372	5.0	2.9	3.4	3.8	1.1	4.7
VF_1379	c1cds1373	87.4	33.3	36.0	52.2	30.5	26.1
VF_1380	c1cds1374	98.0	28.7	28.3	51.7	40.1	8.3
VF_1381	c1cds1375	358.4	168.4	123.9	216.9	124.6	47.0
VF_1382	c1cds1376	1117.1	236.6	197.1	516.9	520.1	76.9
VF_1383	c1cds1377	16.7	53.0	59.8	43.2	23.1	52.7
VF_1384	c1cds1378	34.5	33.6	28.8	32.3	3.1	31.7
VF_1385	c1cds1379	450.4	214.3	172.4	279.1	149.9	28.7
VF_1386	c1cds1380	26.1	24.6	26.2	25.6	0.9	68.0
VF_1387	c1cds1383	31.0	25.6	25.7	27.4	3.1	53.6
VF_1388	c1cds1384	23.6	16.9	18.9	19.8	3.4	36.8
VF_1389	c1cds1385	8.6	10.1	11.2	10.0	1.3	33.9
VF_1390	c1cds1386	21.6	15.1	17.1	17.9	3.3	26.8
VF_1391	c1cds1387	15.5	8.6	5.0	9.7	5.3	1.4
VF_1392	c1cds1388	19.1	12.1	7.9	13.0	5.7	6.5
VF_1393	c1cds1390	31.7	39.8	28.9	33.4	5.6	90.6
VF_1394	c1cds1391	8.4	20.5	33.4	20.8	12.5	45.4
VF_1395	c1cds1392	51.0	32.8	39.9	41.2	9.2	28.5
VF_1396	c1cds1393	54.4	34.9	37.6	42.3	10.5	35.4
VF_1397	c1cds1394	44.4	15.3	16.0	25.2	16.6	15.3
VF_1398	c1cds1395	9.0	6.9	3.9	6.6	2.6	4.5
VF_1399	c1cds1396	11.9	9.3	7.9	9.7	2.0	6.5
VF_1400	c1cds1398	15.0	24.3	23.1	20.8	5.1	12.2
VF_1401	c1cds1399	17.9	44.2	44.2	35.5	15.2	22.3
VF_1402	c1cds1400	43.0	99.7	140.1	94.3	48.8	978.6
VF_1403	c1cds1401	18.3	23.5	31.4	24.4	6.6	103.6
VF_1404	c1cds1402	38.6	34.3	43.9	39.0	4.8	82.3
VF_1405	c1cds1403	25.7	30.9	36.6	31.1	5.5	39.2
VF_1406	c1cds1404	93.2	63.4	80.7	79.1	15.0	111.1
VF_1407	c1cds1405	55.6	65.2	80.7	67.2	12.7	20.1
VF_1408	c1cds1406	31.7	60.8	61.3	51.3	17.0	238.8
VF_1409	c1cds1407	6.9	5.8	6.2	6.3	0.6	8.9
VF_1410	c1cds1409	28.8	48.8	46.2	41.2	10.9	122.8
VF_1411	c1cds1410	53.8	42.0	33.4	43.0	10.2	24.9
VF_1412	c1cds1411	90.1	212.8	190.6	164.5	65.4	128.6
VF_1413	c1cds1412	1085.5	854.3	584.9	841.6	250.6	179.3
VF_1414	c1cds1414	25.8	35.1	29.1	30.0	4.7	54.5
VF_1415	c1cds1415	6.5	25.7	30.6	20.9	12.7	18.7
VF_1416	c1cds1416	20.3	16.5	16.2	17.7	2.3	26.2
VF_1417	c1cds1417	16.2	28.6	21.0	22.0	6.2	46.6
VF_1418	c1cds1418	26.4	10.7	10.2	15.8	9.2	3.2
VF_1419	c1cds1419	59.0	54.7	61.5	58.4	3.4	60.5
VF_1420	c1cds1420	34.8	13.4	11.1	19.8	13.1	6.2

VF_1421	c1cds1421	33.9	14.1	11.9	20.0	12.1	4.6
VF_1422	c1cds1422	51.0	18.0	20.2	29.7	18.4	5.8
VF_1423	c1cds1423	50.6	14.3	12.2	25.7	21.6	4.3
VF_1424	c1cds1424	84.3	24.2	21.2	43.3	35.6	5.7
VF_1425	c1cds1425	138.2	47.0	47.4	77.5	52.5	10.7
VF_1426	c1cds1426	128.2	49.8	48.2	75.4	45.7	4.5
VF_1427	c1cds1427	3317.8	1222.7	1099.0	1879.9	1246.8	46.7
VF_1428	c1cds1428	7.3	4.7	6.0	6.0	1.3	2.5
VF_1429	c1cds1429	1.4	0.7	1.2	1.1	0.4	0.6
VF_1430	c1cds1430	12.8	9.8	10.2	10.9	1.6	16.8
VF_1431	c1cds1432	20.2	30.2	23.3	24.6	5.1	25.5
VF_1432	c1cds1433	13.9	9.3	7.8	10.4	3.2	15.6
VF_1433	c1cds1434	13.8	11.4	7.2	10.8	3.3	21.1
VF_1434	c1cds1435	14.1	10.9	7.7	10.9	3.2	7.7
VF_1435	c1cds1436	90.3	88.8	67.5	82.2	12.8	36.0
VF_1436	c1cds1437	87.0	83.7	86.4	85.7	1.7	30.9
VF_1437	c1cds1439	76.4	38.1	45.6	53.4	20.3	131.4
VF_1438	c1cds1440	120.5	52.2	38.4	70.4	44.0	18.2
VF_1439	c1cds1441	41.9	23.3	22.4	29.2	11.0	28.3
VF_1440	c1cds1442	20.5	11.6	10.3	14.1	5.5	7.3
VF_1441	c1cds1443	12.6	7.3	4.7	8.2	4.1	2.2
VF_1442	c1cds1444	231.9	144.8	139.0	171.9	52.0	10.8
VF_1443	c1cds1445	62.2	74.2	64.8	67.0	6.3	16.4
VF_1444	c1cds1446	14.7	25.4	40.0	26.7	12.7	15.4
VF_1445	c1cds1447	6.4	19.3	22.1	15.9	8.4	9.1
VF_1446	c1cds1448	7.1	30.7	32.2	23.3	14.1	10.4
VF_1447	c1cds1449	80.3	165.9	111.6	119.3	43.3	97.6
VF_1448	c1cds1450	8.8	29.6	25.4	21.3	11.0	22.4
VF_1449	c1cds1451	8.6	29.5	24.1	20.7	10.8	24.3
VF_1450	c1cds1452	12.0	9.5	10.8	10.8	1.2	5.0
VF_1451	c1cds1453	431.8	108.2	215.3	251.8	164.9	2173.9
VF_1452	c1cds1454	221.4	141.1	136.7	166.4	47.7	12.7
VF_1453	c1cds1455	255.1	216.4	183.2	218.2	36.0	106.6
VF_1454	c1cds1457	40.4	98.2	100.2	79.6	34.0	12.9
VF_1455	c1cds1459	74.8	47.3	50.1	57.4	15.1	27.1
VF_1456	c1cds1460	46.9	48.7	59.0	51.5	6.5	24.3
VF_1457	c1cds1462	65.1	44.4	44.0	51.2	12.1	53.7
VF_1460	c1cds1465	5.4	4.4	4.2	4.6	0.6	11.6
VF_1461	c1cds1466	42.3	20.3	12.8	25.1	15.3	230.8
VF_1462	c1cds1467	10.3	6.3	3.1	6.6	3.6	94.4
VF_1463	c1cds1468	11.9	10.6	8.6	10.4	1.7	77.1
VF_1464	c1cds1469	4.2	5.5	6.3	5.3	1.0	13.7
VF_1465	c1cds1470	1.9	1.5	1.6	1.7	0.2	4.7

VF_1466	c1cds1471	16.3	44.0	87.6	49.3	35.9	34.9
VF_1467	c1cds1472	15.1	48.8	129.3	64.4	58.7	16.8
VF_1468	c1cds1473	14.0	14.5	11.7	13.4	1.5	12.9
VF_1470	c1cds1475	9.1	3.5	3.7	5.4	3.2	12.6
VF_1471	c1cds1476	39.8	41.2	26.9	35.9	7.9	3.0
VF_1472	c1cds1477	20.2	38.6	19.1	26.0	10.9	2.1
VF_1473	c1cds1478	83.1	120.4	61.3	88.3	29.8	9.7
VF_1474	c1cds1479	44.2	68.6	59.0	57.3	12.3	4.1
VF_1475	c1cds1480	3.5	2.3	3.3	3.0	0.6	25.9
VF_1476	c1cds1481	1.4	1.4	1.6	1.5	0.1	1.6
VF_1477	c1cds1482	5.8	6.6	6.4	6.2	0.4	10.8
VF_1478	c1cds1483	217.7	350.4	208.5	258.8	79.4	12.3
VF_1479	c1cds1484	436.0	166.1	168.9	257.0	155.1	69.1
VF_1480	c1cds1485	234.6	34.5	34.1	101.1	115.6	145.6
VF_1481	c1cds1486	6.0	3.5	2.4	4.0	1.8	1.5
VF_1482	c1cds1487	108.3	51.5	52.3	70.7	32.6	44.8
VF_1483	c1cds1488	38.6	25.2	13.6	25.8	12.5	28.9
VF_1484	c1cds1489	26.4	16.1	13.1	18.5	7.0	30.7
VF_1485	c1cds1490	51.3	53.4	55.1	53.3	1.9	437.7
VF_1486	c1cds1491	4.7	16.4	11.1	10.7	5.9	28.2
VF_1487	c1cds1492	1.1	4.8	5.0	3.6	2.2	19.1
VF_1488	c1cds1493	41.7	37.4	44.9	41.3	3.8	251.3
VF_1489	c1cds1494	5.7	5.2	8.3	6.4	1.7	6.4
VF_1490	c1cds1495	189.5	96.8	111.2	132.5	49.9	143.0
VF_1491	c1cds1496	38.1	50.9	47.8	45.6	6.7	125.9
VF_1492	c1cds1497	43.1	54.2	55.2	50.9	6.7	39.9
VF_1493	c1cds1498	14.1	12.7	8.0	11.6	3.2	142.2
VF_1494	c1cds1499	16.8	5.8	9.8	10.8	5.6	98.6
VF_1495	c1cds1500	167.5	206.4	262.6	212.2	47.8	144.5
VF_1496	c1cds1501	35.3	36.6	21.9	31.3	8.1	77.2
VF_1497	c1cds1502	20.8	21.6	21.1	21.2	0.4	88.3
VF_1498	c1cds1503	5.0	11.1	9.5	8.5	3.1	61.4
VF_1499	c1cds1504	522.2	496.5	456.4	491.7	33.2	794.4
VF_1500	c1cds1505	67.8	71.8	94.3	78.0	14.3	83.3
VF_1501	c1cds1506	237.3	125.4	125.6	162.8	64.5	83.9
VF_1502	c1cds1507	440.4	98.9	74.8	204.7	204.5	20.0
VF_1503	c1cds1508	10.8	29.8	29.6	23.4	10.9	171.0
VF_1504	c1cds1509	6.9	11.3	10.5	9.6	2.4	1.7
VF_1505	c1cds1510	27.0	57.6	75.8	53.5	24.6	55.9
VF_1506	c1cds1511	596.6	420.5	458.5	491.9	92.7	90.9
VF_1507	c1cds1512	1087.6	378.4	265.6	577.2	445.6	408.5
VF_1508	c1cds1513	35.5	13.3	9.4	19.4	14.1	6.1
VF_1509	c1cds1514	4.5	4.6	3.3	4.1	0.7	4.1

VF_1510	c1cds1515	6.3	9.9	12.5	9.6	3.1	2.2
VF_1511	c1cds1516	35.4	41.1	47.4	41.3	6.0	823.2
VF_1512	c1cds1517	46.5	35.3	42.2	41.3	5.7	121.7
VF_1513	c1cds1518	111.7	91.7	104.8	102.7	10.1	11.8
VF_1514	c1cds1519	37.8	50.5	44.2	44.2	6.4	30.6
VF_1515	c1cds1520	101.8	41.7	30.4	58.0	38.4	20.6
VF_1516	c1cds1521	93.1	98.2	93.0	94.8	3.0	89.6
VF_1517	c1cds1522	113.3	100.4	131.1	114.9	15.4	140.8
VF_1518	c1cds1523	21.9	14.8	18.6	18.4	3.6	39.8
VF_1519	c1cds1525	187.0	137.8	150.0	158.3	25.6	126.0
VF_1520	c1cds1526	110.7	52.9	58.5	74.0	31.9	71.6
VF_1521	c1cds1527	217.4	546.3	717.8	493.8	254.3	2429.5
VF_1522	c1cds1528	222.5	49.2	42.0	104.6	102.2	35.9
VF_1523	c1cds1529	4801.0	1070.6	1215.4	2362.3	2113.2	61.7
VF_1524	c1cds1530	46.0	45.5	32.7	41.4	7.5	43.0
VF_1525	c1cds1531	24.1	23.6	21.4	23.0	1.4	28.4
VF_1526	c1cds1532	77.4	86.8	64.9	76.4	11.0	139.8
VF_1527	c1cds1533	43.8	27.4	26.9	32.7	9.6	109.5
VF_1528	c1cds1534	4.6	17.2	16.5	12.8	7.1	15.0
VF_1529	c1cds1535	59.7	124.2	130.6	104.8	39.2	24.8
VF_1530	c1cds1536	23.9	31.5	24.4	26.6	4.3	37.4
VF_1531	c1cds1537	20.7	24.5	20.7	22.0	2.2	47.6
VF_1532	c1cds1538	1190.9	904.9	825.8	973.8	192.1	1.6
VF_1533	c1cds1539	243.8	207.7	156.1	202.6	44.1	0.4
VF_1534	c1cds1540	229.8	201.6	165.6	199.0	32.2	0.7
VF_1535	c1cds1541	314.0	312.3	243.0	289.8	40.5	2.4
VF_1536	c1cds1542	2817.9	1399.6	1475.2	1897.6	797.9	425.9
VF_1537	c1cds1543	22.7	26.4	29.6	26.2	3.4	12.5
VF_1538	c1cds1544	357.8	181.0	144.9	227.9	114.0	15.0
VF_1539	c1cds1545	263.9	123.2	108.8	165.3	85.7	12.6
VF_1540	c1cds1546	98.2	58.8	51.1	69.3	25.2	121.1
VF_1541	c1cds1547	34.2	36.1	27.0	32.4	4.8	35.5
VF_1542	c1cds1548	7.0	14.4	13.2	11.5	3.9	11.2
VF_1543	c1cds1549	10.4	6.5	7.4	8.1	2.0	7.4
VF_1544	c1cds1550	31.4	32.9	21.7	28.6	6.1	7.2
VF_1545	c1cds1551	6.0	8.0	6.4	6.8	1.1	20.3
VF_1546	c1cds1552	1.3	2.1	3.0	2.1	0.8	0.5
VF_1547	c1cds1553	2.3	1.5	5.0	2.9	1.8	1.1
VF_1548	c1cds1554	25.6	15.9	12.0	17.8	7.0	16.5
VF_1549	c1cds1555	26.9	18.5	17.4	20.9	5.2	11.3
VF_1550	c1cds1556	11.2	5.1	5.1	7.1	3.5	5.5
VF_1551	c1cds1557	11.9	10.5	14.1	12.1	1.8	14.2
VF_1552	c1cds1558	20.6	18.0	33.1	23.9	8.1	40.6

VF_1553	c1cds1559	33.1	40.3	72.7	48.7	21.1	113.9
VF_1554	c1cds1560	26.7	28.3	55.0	36.7	15.9	78.7
VF_1555	c1cds1561	30.2	142.3	140.8	104.4	64.3	49.0
VF_1556	c1cds1563	58.3	112.6	79.7	83.6	27.4	55.5
VF_1557	c1cds1564	16.2	12.0	10.7	12.9	2.8	20.4
VF_1558	c1cds1565	64.5	139.5	211.4	138.5	73.4	277.6
VF_1559	c1cds1566	6.8	8.9	3.7	6.5	2.6	57.3
VF_1560	c1cds1567	16.3	11.3	12.5	13.4	2.6	33.3
VF_1561	c1cds1568	24.1	22.5	15.5	20.7	4.6	7.5
VF_1562	c1cds1569	79.1	39.3	22.8	47.1	28.9	7.6
VF_1563	c1cds1570	23.8	43.3	21.2	29.4	12.1	20.3
VF_1564	c1cds1571	5.8	6.3	4.8	5.6	0.8	5.0
VF_1565	c1cds1572	13.5	9.8	8.3	10.5	2.7	22.1
VF_1566	c1cds1573	5.3	13.1	10.0	9.5	3.9	11.3
VF_1567	c1cds1574	39.2	17.4	13.7	23.5	13.8	2.3
VF_1568	c1cds1575	22.5	64.8	70.7	52.7	26.3	61.6
VF_1569	c1cds1576	125.2	84.4	87.6	99.1	22.6	367.7
VF_1570	c1cds1577	466.5	308.9	342.5	372.6	83.0	199.3
VF_1571	c1cds1578	51.9	61.0	54.8	55.9	4.7	56.3
VF_1572	c1cds1579	86.1	63.0	60.5	69.9	14.1	214.4
VF_1573	c1cds1580	318.6	523.1	399.4	413.7	103.0	190.8
VF_1574	c1cds1581	357.3	182.7	158.4	232.8	108.5	47.0
VF_1575	c1cds1582	19.2	21.4	13.5	18.0	4.1	23.5
VF_1576	c1cds1583	107.3	68.4	67.7	81.1	22.7	110.4
VF_1577	c1cds1584	89.5	70.9	74.5	78.3	9.9	121.0
VF_1578	c1cds1585	28.5	6.5	6.0	13.7	12.9	13.3
VF_1579	c1cds1586	7.2	6.2	5.4	6.3	0.9	12.2
VF_1580	c1cds1587	47.3	39.7	44.8	43.9	3.9	62.8
VF_1581	c1cds1588	22.6	22.1	27.9	24.2	3.2	20.6
VF_1582	c1cds1589	15.5	17.8	18.7	17.3	1.6	18.0
VF_1583	c1cds1590	50.9	39.7	52.0	47.5	6.8	223.8
VF_1584	c1cds1591	153.3	68.3	58.1	93.2	52.3	176.1
VF_1585	c1cds1592	100.3	120.3	82.6	101.1	18.9	9.9
VF_1586	c1cds1593	135.1	164.8	141.1	147.0	15.7	15.4
VF_1587	c1cds1594	472.0	340.1	344.9	385.7	74.8	65.2
VF_1588	c1cds1595	285.7	322.7	343.6	317.3	29.3	42.5
VF_1589	c1cds1596	79.5	106.3	149.2	111.7	35.2	66.5
VF_1590	c1cds1597	728.8	580.1	625.4	644.8	76.2	1878.4
VF_1591	c1cds1598	172.3	150.3	179.2	167.3	15.1	154.1
VF_1592	c1cds1599	3.4	3.6	3.5	3.5	0.1	15.9
VF_1593	c1cds1600	55.4	52.4	74.9	60.9	12.2	252.4
VF_1594	c1cds1601	32.9	38.6	63.4	45.0	16.2	203.7
VF_1595	c1cds1602	18.2	24.1	36.0	26.1	9.1	115.5

VF_1596	c1cds1603	17.4	17.1	25.9	20.1	5.0	150.1
VF_1597	c1cds1604	197.3	251.2	361.8	270.1	83.8	950.8
VF_1598	c1cds1605	129.7	28.8	80.0	79.5	50.5	3.6
VF_1599	c1cds1606	18.7	12.7	16.4	15.9	3.0	34.6
VF_1600	c1cds1607	65.9	83.1	95.1	81.4	14.7	190.5
VF_1601	c1cds1608	793.3	437.0	475.7	568.7	195.5	872.4
VF_1602	c1cds1609	10.0	15.1	11.4	12.2	2.6	32.3
VF_1603	c1cds1610	32.0	61.9	53.8	49.2	15.5	83.7
VF_1604	c1cds1611	69.9	51.3	48.5	56.6	11.6	79.4
VF_1605	c1cds1612	53.3	93.9	59.6	68.9	21.9	24.4
VF_1606	c1cds1613	166.9	182.4	184.0	177.8	9.4	25.8
VF_1607	c1cds1614	121.2	159.6	214.8	165.2	47.1	141.2
VF_1608	c1cds1615	52.9	51.4	74.7	59.7	13.1	77.5
VF_1609	c1cds1616	69.3	56.5	78.9	68.2	11.2	58.2
VF_1610	c1cds1617	8108.3	3540.3	7153.0	6267.2	2409.4	2.6
VF_1611	c1cds1618	795.0	501.0	1023.6	773.2	262.0	0.5
VF_1612	c1cds1619	543.6	322.8	652.6	506.4	168.0	2.0
VF_1613	c1cds1620	1648.2	884.4	1907.7	1480.1	531.9	12.9
VF_1614	c1cds1621	80.8	38.3	27.4	48.8	28.2	13.1
VF_1615	c1cds1622	44.1	15.4	13.6	24.4	17.1	6.6
VF_1616	c1cds1623	36.7	20.7	14.7	24.0	11.4	79.9
VF_1617	c1cds1624	11.3	8.9	7.1	9.1	2.1	30.1
VF_1618	c1cds1625	49.0	53.4	52.0	51.4	2.3	18.2
VF_1619	c1cds1626	19.2	24.9	23.9	22.7	3.0	18.6
VF_1620	c1cds1627	10.2	12.3	13.4	12.0	1.6	21.9
VF_1621	c1cds1628	152.6	64.1	73.6	96.8	48.6	203.3
VF_1622	c1cds1629	29.7	34.2	34.8	32.9	2.8	40.0
VF_1623	c1cds1630	5.3	4.4	4.4	4.7	0.5	13.2
VF_1624	c1cds1631	1046.9	498.2	358.8	634.6	363.8	136.8
VF_1625	c1cds1632	122.4	141.0	136.5	133.3	9.7	56.8
VF_1626	c1cds1633	48.8	39.6	33.3	40.5	7.8	67.1
VF_1627	c1cds1634	137.9	183.1	184.9	168.6	26.6	269.5
VF_1628	c1cds1635	14.1	8.9	6.8	9.9	3.8	12.1
VF_1629	c1cds1636	8.6	11.7	9.1	9.8	1.7	19.4
VF_1630	c1cds1637	12.3	37.9	39.4	29.9	15.2	46.3
VF_1631	c1cds1638	563.0	620.1	429.7	537.6	97.7	969.5
VF_1632	c1cds1639	2.5	3.2	2.9	2.8	0.4	3.9
VF_1633	c1cds1640	54.6	63.2	71.6	63.1	8.5	104.6
VF_1634	c1cds1641	13.2	26.5	26.9	22.2	7.8	161.7
VF_1635	c1cds1642	12.4	7.1	5.0	8.2	3.8	6.2
VF_1636	c1cds1643	41.2	43.2	58.0	47.5	9.1	18.7
VF_1637	c1cds1644	31.8	44.3	44.9	40.3	7.4	71.0
VF_1638	c1cds1645	5.1	8.1	8.4	7.2	1.8	18.6

VF_1639	c1cds1646	8.6	12.1	6.6	9.1	2.8	23.0
VF_1640	c1cds1647	8.6	16.0	12.6	12.4	3.7	69.9
VF_1641	c1cds1648	6.0	8.6	8.6	7.7	1.5	30.6
VF_1642	c1cds1649	134.1	67.1	99.7	100.3	33.5	6.0
VF_1643	c1cds1650	65.6	51.9	53.0	56.8	7.6	109.3
VF_1644	c1cds1651	30.5	95.3	108.8	78.2	41.9	180.2
VF_1645	c1cds1652	261.6	231.4	243.6	245.5	15.2	189.6
VF_1646	c1cds1653	8.7	6.4	7.3	7.5	1.2	351.7
VF_1647	c1cds1654	31.9	17.3	17.4	22.2	8.4	24.1
VF_1648	c1cds1655	50.8	33.5	32.7	39.0	10.2	140.4
VF_1649	c1cds1656	211.9	176.5	142.6	177.0	34.7	194.2
VF_1650	c1cds1657	258.1	121.5	129.3	169.7	76.7	59.2
VF_1651	c1cds1658	14.8	10.2	11.2	12.1	2.4	26.3
VF_1652	c1cds1659	1.6	1.3	0.8	1.2	0.4	0.2
VF_1653	c1cds1660	43.9	39.2	34.5	39.2	4.7	27.3
VF_1654	c1cds1661	236.9	136.8	115.3	163.0	64.9	78.6
VF_1655	c1cds1662	2.3	1.4	1.2	1.6	0.6	0.5
VF_1656	c1cds1663	4.2	3.1	3.9	3.7	0.6	1.3
VF_1657	c1cds1664	81.2	77.2	86.4	81.6	4.6	214.9
VF_1658	c1cds1665	17.2	14.7	11.5	14.5	2.9	24.8
VF_1659	c1cds1666	6.5	19.0	23.6	16.4	8.8	17.7
VF_1660	c1cds1667	5.4	21.8	23.5	16.9	10.0	37.7
VF_1661	c1cds1668	6.1	4.1	5.7	5.3	1.1	4.9
VF_1662	c1cds1669	618.3	436.2	367.4	474.0	129.6	2163.6
VF_1663	c1cds1670	453.7	223.8	244.8	307.4	127.1	213.0
VF_1664	c1cds1671	26.4	18.2	14.7	19.8	6.0	20.6
VF_1665	c1cds1672	62.6	53.8	34.6	50.4	14.3	16.7
VF_1666	c1cds1673	9.7	13.5	14.7	12.6	2.6	47.6
VF_1667	c1cds1674	11.6	17.6	15.5	14.9	3.0	71.8
VF_1669	c1cds1675	36.8	90.2	113.9	80.3	39.5	198.1
VF_1670	c1cds1676	22.9	18.4	21.7	21.0	2.3	48.0
VF_1671	c1cds1677	39.8	31.8	36.3	36.0	4.0	33.1
VF_1672	c1cds1678	103.0	83.2	77.4	87.9	13.4	71.1
VF_1673	c1cds1679	65.5	81.6	96.9	81.3	15.7	94.7
VF_1674	c1cds1680	10.9	7.2	6.0	8.0	2.6	14.6
VF_1675	c1cds1682	8.6	6.4	6.7	7.3	1.2	29.3
VF_1676	c1cds1683	6.1	4.7	5.1	5.3	0.7	13.2
VF_1677	c1cds1684	39.3	21.7	21.4	27.5	10.3	24.9
VF_1678	c1cds1685	356.9	241.5	229.8	276.1	70.2	707.7
VF_1679	c1cds1686	22.2	7.8	5.8	11.9	9.0	2.6
VF_1680	c1cds1687	11.6	23.3	25.5	20.1	7.5	12.1
VF_1681	c1cds1688	32.0	33.8	35.2	33.7	1.6	71.2
VF_1682	c1cds1689	38.9	25.1	27.4	30.5	7.4	79.4

VF_1683	c1cds1690	9.1	4.4	4.1	5.9	2.8	17.9
VF_1684	c1cds1691	19.7	13.6	11.6	14.9	4.2	14.7
VF_1685	c1cds1692	23.3	22.3	20.6	22.1	1.3	91.3
VF_1686	c1cds1693	247.7	249.0	231.1	242.6	10.0	637.8
VF_1687	c1cds1694	25.1	36.8	46.0	35.9	10.4	119.2
VF_1688	c1cds1695	41.9	152.7	133.4	109.3	59.2	243.4
VF_1689	c1cds1698	815.9	484.5	360.7	553.7	235.4	10.4
VF_1690	c1cds1699	47.0	49.0	55.0	50.4	4.2	55.5
VF_1691	c1cds1700	16.3	13.8	12.2	14.1	2.1	67.1
VF_1692	c1cds1701	47.6	36.9	42.0	42.1	5.4	68.1
VF_1693	c1cds1702	67.6	52.6	56.9	59.1	7.7	118.3
VF_1694	c1cds1703	37.2	33.1	37.5	36.0	2.5	76.7
VF_1695	c1cds1704	256.6	295.6	305.1	285.8	25.7	606.6
VF_1696	c1cds1706	190.0	122.0	134.9	148.9	36.2	82.2
VF_1697	c1cds1707	112.5	86.6	106.2	101.8	13.5	223.4
VF_1698	c1cds1708	146.2	182.0	253.3	193.9	54.5	234.3
VF_1699	c1cds1709	61.5	50.1	46.1	52.6	7.9	69.3
VF_1700	c1cds1710	498.9	464.5	617.1	526.8	80.0	1200.1
VF_1701	c1cds1711	22.2	21.5	27.3	23.7	3.2	31.6
VF_1702	c1cds1712	59.7	50.8	64.2	58.2	6.8	153.1
VF_1703	c1cds1713	46.2	56.9	51.7	51.6	5.3	85.7
VF_1704	c1cds1714	49.0	48.4	50.4	49.3	1.0	130.7
VF_1705	c1cds1715	62.7	55.1	59.7	59.2	3.8	328.5
VF_1706	c1cds1716	68.7	65.9	53.4	62.7	8.2	152.0
VF_1707	c1cds1717	25.8	20.7	25.9	24.1	3.0	35.3
VF_1708	c1cds1718	60.3	51.1	55.0	55.5	4.6	125.8
VF_1709	c1cds1719	43.9	46.7	50.4	47.0	3.3	25.5
VF_1710	c1cds1720	130.7	114.9	101.8	115.8	14.5	48.9
VF_1711	c1cds1721	79.2	108.3	129.3	105.6	25.1	88.1
VF_1712	c1cds1722	75.4	112.5	136.2	108.0	30.6	126.0
VF_1713	c1cds1723	41.2	65.1	84.8	63.7	21.8	37.2
VF_1714	c1cds1724	31.3	23.9	32.8	29.3	4.8	68.4
VF_1715	c1cds1725	119.4	104.7	100.5	108.2	9.9	43.9
VF_1716	c1cds1726	9.5	8.7	6.2	8.1	1.7	10.7
VF_1717	c1cds1727	33.7	14.1	11.8	19.9	12.1	1.7
VF_1718	c1cds1728	8.2	8.2	6.5	7.6	1.0	22.1
VF_1719	c1cds1729	2.9	7.9	6.5	5.8	2.6	22.6
VF_1720	c1cds1730	7.4	6.2	7.5	7.0	0.7	27.2
VF_1721	c1cds1732	78.1	22.7	31.5	44.1	29.8	2.6
VF_1722	c1cds1733	19.4	10.0	17.0	15.5	4.9	11.3
VF_1723	c1cds1735	18.8	17.1	12.3	16.0	3.4	25.8
VF_1724	c1cds1736	5.2	5.9	7.6	6.2	1.3	163.8
VF_1725	c1cds1737	20.0	8.9	6.8	11.9	7.1	12.4

VF_1726	c1cds1738	14.3	23.5	28.4	22.1	7.2	59.4
VF_1727	c1cds1739	31.2	67.6	75.0	57.9	23.4	365.6
VF_1728	c1cds1740	586.1	238.7	234.1	353.0	201.9	377.7
VF_1729	c1cds1742	61.4	31.9	31.8	41.7	17.1	22.8
VF_1730	c1cds1743	35.0	48.1	35.9	39.7	7.3	3.7
VF_1731	c1cds1745	17.1	12.2	10.9	13.4	3.3	11.8
VF_1732	c1cds1746	718.6	528.4	408.6	551.9	156.3	121.4
VF_1733	c1cds1747	149.5	77.9	81.3	102.9	40.4	64.8
VF_1734	c1cds1748	102.4	52.2	48.6	67.7	30.1	49.4
VF_1735	c1cds1749	105.2	72.2	70.2	82.5	19.6	57.2
VF_1736	c1cds1750	34.7	29.1	29.4	31.1	3.1	36.4
VF_1737	c1cds1751	39.0	24.5	27.9	30.5	7.6	20.0
VF_1738	c1cds1752	101.4	146.0	178.3	141.9	38.6	879.0
VF_1739	c1cds1753	5503.3	3472.0	3235.4	4070.3	1246.7	13897.2
VF_1740	c1cds1754	524.7	448.3	493.2	488.7	38.4	1710.0
VF_1741	c1cds1755	347.9	250.8	250.2	283.0	56.3	743.9
VF_1742	c1cds1756	402.9	273.7	264.9	313.9	77.2	385.0
VF_1743	c1cds1757	211.7	102.5	92.6	135.6	66.1	86.8
VF_1744	c1cds1758	1676.4	2478.6	1999.5	2051.5	403.6	2045.6
VF_1745	c1cds1759	1112.9	1840.0	1938.1	1630.3	450.8	1722.3
VF_1746	c1cds1760	12.1	5.5	5.8	7.8	3.7	19.0
VF_1747	c1cds1761	131.2	130.9	151.4	137.9	11.7	156.8
VF_1748	c1cds1762	163.4	287.0	381.7	277.4	109.4	528.1
VF_1749	c1cds1763	26.2	62.1	73.9	54.1	24.9	37.2
VF_1750	c1cds1764	43.9	47.8	56.3	49.3	6.3	32.4
VF_1751	c1cds1765	471.3	202.1	171.7	281.7	164.9	118.3
VF_1752	c1cds1766	686.9	406.8	467.5	520.4	147.3	207.6
VF_1753	c1cds1767	49.4	41.3	50.3	47.0	5.0	42.6
VF_1754	c1cds1768	47.3	59.6	78.5	61.8	15.7	308.9
VF_1755	c1cds1769	105.9	30.3	28.4	54.8	44.2	89.5
VF_1756	c1cds1770	91.8	76.8	86.4	85.0	7.6	34.2
VF_1757	c1cds1771	236.0	102.9	74.2	137.7	86.3	199.9
VF_1758	c1cds1772	28019.7	10248.9	8868.2	15712.3	10680.9	9939.7
VF_1759	c1cds1773	9770.7	8608.1	9091.5	9156.8	584.1	9482.3
VF_1760	c1cds1774	836.5	1008.9	703.1	849.5	153.3	1126.3
VF_1761	c1cds1775	44.2	27.6	27.0	32.9	9.7	143.1
VF_1762	c1cds1776	22.3	15.2	15.0	17.5	4.2	22.2
VF_1763	c1cds1777	43.0	31.2	29.0	34.4	7.5	22.5
VF_1764	c1cds1778	737.6	709.4	756.1	734.4	23.5	518.1
VF_1765	c1cds1779	1625.2	503.1	546.9	891.7	635.6	356.9
VF_1766	c1cds1780	2448.5	515.0	370.1	1111.2	1160.4	658.7
VF_1767	c1cds1781	5790.3	1747.1	1850.0	3129.1	2305.3	479.4
VF_1768	c1cds1782	60.1	30.1	22.5	37.6	19.9	14.1

VF_1769	c1cds1783	73.0	36.0	36.4	48.5	21.3	27.7
VF_1770	c1cds1784	38.0	42.7	54.5	45.1	8.5	119.3
VF_1771	c1cds1785	1866.7	594.6	434.7	965.3	784.7	31.1
VF_1773	c1cds1786	855.7	342.6	251.3	483.2	325.8	14.9
VF_1774	c1cds1787	1004.2	286.7	213.9	501.6	436.8	15.3
VF_1775	c1cds1788	100.4	144.9	179.1	141.5	39.5	794.5
VF_1776	c1cds1789	27.7	23.8	25.7	25.7	2.0	29.6
VF_1777	c1cds1791	61.0	83.8	83.7	76.2	13.1	64.1
VF_1778	c1cds1792	1.6	1.4	1.2	1.4	0.2	1.4
VF_1779	c1cds1793	108.3	31.8	20.8	53.6	47.7	13.4
VF_1780	c1cds1794	119.2	36.4	33.0	62.9	48.8	9.5
VF_1781	c1cds1795	53.9	15.9	12.8	27.5	22.9	4.9
VF_1782	c1cds1796	3.2	3.4	3.1	3.2	0.2	1.8
VF_1783	c1cds1797	14.7	8.3	6.7	9.9	4.3	12.4
VF_1784	c1cds1798	94.3	212.7	268.9	192.0	89.1	194.0
VF_1785	c1cds1799	167.5	258.1	381.6	269.1	107.5	189.3
VF_1786	c1cds1800	43.2	46.6	62.6	50.8	10.3	397.4
VF_1787	c1cds1801	31.6	15.3	14.4	20.4	9.7	11.2
VF_1788	c1cds1803	114.4	54.0	53.8	74.1	34.9	113.7
VF_1789	c1cds1804	8.1	15.7	14.2	12.7	4.0	100.7
VF_1790	c1cds1805	35.6	42.7	45.5	41.3	5.1	55.2
VF_1791	c1cds1806	71.8	94.9	85.6	84.1	11.6	51.6
VF_1792	c1cds1807	64.3	79.7	71.0	71.6	7.7	49.7
VF_1793	c1cds1808	9.1	14.8	18.4	14.1	4.7	41.1
VF_1794	c1cds1809	193.3	86.0	97.9	125.7	58.8	226.9
VF_1795	c1cds1810	4.8	7.8	5.9	6.2	1.5	16.8
VF_1796	c1cds1811	29.9	19.4	17.8	22.4	6.6	23.4
VF_1797	c1cds1812	57.5	12.5	10.8	26.9	26.5	2.0
VF_1798	c1cds1813	13.7	22.2	15.1	17.0	4.6	25.0
VF_1799	c1cds1814	89.5	115.0	115.3	106.6	14.8	127.9
VF_1800	c1cds1815	103.1	59.0	52.1	71.4	27.7	105.1
VF_1801	c1cds1816	209.8	152.0	123.6	161.8	43.9	88.3
VF_1802	c1cds1817	14.2	19.9	19.7	17.9	3.2	22.2
VF_1803	c1cds1818	2.0	2.0	1.5	1.8	0.3	1.8
VF_1804	c1cds1819	6.3	4.6	5.3	5.4	0.9	39.0
VF_1805	c1cds1820	146.0	82.6	111.2	113.3	31.8	175.2
VF_1806	c1cds1822	55.7	66.4	91.2	71.1	18.2	157.8
VF_1807	c1cds1823	167.2	153.3	172.3	164.3	9.8	51.0
VF_1808	c1cds1824	199.8	210.3	239.9	216.6	20.8	119.9
VF_1809	c1cds1825	117.6	54.1	46.0	72.6	39.2	43.5
VF_1810	c1cds1826	472.6	549.2	590.9	537.6	60.0	13.7
VF_1811	c1cds1827	250.3	358.0	500.5	369.6	125.5	14.0
VF_1812	c1cds1828	963.4	443.8	654.1	687.1	261.4	1391.7

VF_1813	c1cds1829	8.4	6.8	7.0	7.4	0.9	5.2
VF_1814	c1cds1830	57.4	20.8	13.1	30.4	23.7	18.6
VF_1815	c1cds1831	59.2	23.8	21.8	34.9	21.0	35.2
VF_1816	c1cds1832	391.2	244.9	257.9	298.0	81.0	189.7
VF_1817	c1cds1833	277.5	163.7	154.4	198.5	68.5	182.6
VF_1818	c1cds1834	215.3	167.6	165.9	182.9	28.0	139.7
VF_1819	c1cds1835	132.3	103.5	126.3	120.7	15.2	133.7
VF_1820	c1cds1836	132.6	135.3	151.8	139.9	10.4	178.3
VF_1821	c1cds1837	65.0	111.5	71.2	82.6	25.2	78.8
VF_1822	c1cds1838	46.6	45.2	52.1	48.0	3.6	69.1
VF_1823	c1cds1839	28.4	33.8	29.7	30.6	2.8	35.4
VF_1824	c1cds1840	39.6	80.0	80.0	66.6	23.4	88.8
VF_1825	c1cds1841	251.0	314.2	304.5	289.9	34.1	773.1
VF_1826	c1cds1842	169.9	153.6	155.6	159.7	8.9	773.9
VF_1828	c1cds1843	77.9	127.9	118.7	108.2	26.6	159.8
VF_1829	c1cds1844	85.2	160.5	154.9	133.5	42.0	219.7
VF_1830	c1cds1845	111.6	269.2	257.7	212.8	87.8	343.0
VF_1831	c1cds1846	202.3	460.5	407.6	356.8	136.4	433.0
VF_1832	c1cds1847	206.0	410.2	384.8	333.7	111.3	418.5
VF_1833	c1cds1848	274.1	612.2	521.2	469.2	174.9	365.7
VF_1834	c1cds1849	345.6	615.0	624.8	528.5	158.4	374.0
VF_1835	c1cds1850	371.4	647.6	623.3	547.5	153.0	336.4
VF_1836	c1cds1851	205.8	534.5	535.7	425.3	190.1	161.9
VF_1837	c1cds1852	110.8	266.7	232.4	203.3	81.9	68.4
VF_1838	c1cds1853	20.7	27.5	24.8	24.3	3.4	21.6
VF_1839	c1cds1854	27.3	69.3	45.5	47.4	21.0	12.4
VF_1840	c1cds1855	35.4	89.3	74.6	66.4	27.9	18.7
VF_1841	c1cds1856	35.3	87.2	76.3	66.3	27.3	35.9
VF_1842	c1cds1857	43.1	85.8	83.4	70.8	24.0	43.3
VF_1843	c1cds1858	89.8	192.5	174.8	152.4	54.9	89.4
VF_1844	c1cds1859	146.2	277.5	291.9	238.5	80.3	248.5
VF_1845	c1cds1860	80.7	171.5	170.0	140.7	52.0	160.0
VF_1846	c1cds1861	58.9	169.2	141.8	123.3	57.5	100.1
VF_1847	c1cds1862	84.1	225.5	216.3	175.3	79.1	94.9
VF_1848	c1cds1863	40.2	76.4	62.6	59.7	18.3	32.6
VF_1849	c1cds1864	55.4	108.3	105.0	89.6	29.6	49.7
VF_1850	c1cds1865	57.8	141.2	125.0	108.0	44.2	47.8
VF_1851	c1cds1866	165.2	454.9	492.0	370.7	178.9	153.2
VF_1852	c1cds1867	140.9	384.3	419.9	315.0	151.9	127.4
VF_1853	c1cds1868	186.4	403.2	423.6	337.7	131.4	163.7
VF_1854	c1cds1869	102.4	216.3	235.7	184.8	72.0	124.3
VF_1855	c1cds1870	93.2	245.0	275.4	204.5	97.6	103.1
VF_1856	c1cds1871	338.8	338.5	367.7	348.3	16.7	319.1

VF_1858	c1cds1872	91.5	350.1	311.2	250.9	139.5	404.5
VF_1859	c1cds1873	43.1	113.5	64.7	73.7	36.1	110.6
VF_1860	c1cds1874	32.0	78.3	73.0	61.1	25.3	120.1
VF_1861	c1cds1875	74.4	150.4	128.7	117.8	39.1	300.4
VF_1862	c1cds1876	182.7	480.6	392.4	351.9	153.0	4504.4
VF_1863	c1cds1877	118.6	392.7	344.8	285.4	146.4	1345.4
VF_1864	c1cds1878	78.2	96.5	108.5	94.4	15.3	1717.1
VF_1865	c1cds1879	26.6	78.1	77.5	60.7	29.6	100.8
VF_1866	c1cds1880	69.5	171.0	221.0	153.8	77.2	1864.9
VF_1867	c1cds1881	26.3	21.0	24.7	24.0	2.7	163.2
VF_1868	c1cds1882	16.8	18.1	21.0	18.6	2.1	322.6
VF_1869	c1cds1883	21.0	75.1	70.6	55.6	30.0	177.7
VF_1870	c1cds1884	91.4	200.4	227.2	173.0	72.0	122.6
VF_1871	c1cds1885	15.5	24.6	26.2	22.1	5.8	165.1
VF_1872	c1cds1886	15.0	20.7	26.5	20.8	5.8	272.2
VF_1873	c1cds1887	6.9	18.2	22.1	15.8	7.9	225.0
VF_1874	c1cds1888	190.2	242.4	266.6	233.0	39.1	498.7
VF_1875	c1cds1889	401.9	535.4	560.9	499.4	85.4	1669.4
VF_1876	c1cds1890	275.8	455.2	440.9	390.6	99.7	1368.7
VF_1877	c1cds1891	458.3	520.9	413.0	464.1	54.2	1940.9
VF_1878	c1cds1892	76.6	148.1	141.5	122.1	39.5	245.0
VF_1879	c1cds1893	59.1	205.4	175.4	146.6	77.3	289.2
VF_1880	c1cds1894	76.5	98.3	72.1	82.3	14.0	32.2
VF_1881	c1cds1895	1247.8	2033.4	1454.3	1578.5	407.2	832.9
VF_1882	c1cds1896	1063.7	1830.1	1773.3	1555.7	427.0	345.8
VF_1883	c1cds1897	31.5	129.2	164.6	108.5	68.9	212.7
VF_1884	c1cds1898	27.6	88.3	95.5	70.5	37.3	273.1
VF_1885	c1cds1899	72.0	80.7	71.1	74.6	5.3	98.2
VF_1886	c1cds1900	2.6	2.4	0.8	1.9	1.0	11.5
VF_1887	c1cds1902	102.2	183.7	250.0	178.6	74.0	459.4
VF_1888	c1cds1903	77.7	82.9	65.5	75.4	8.9	164.1
VF_1889	c1cds1904	57.0	45.9	48.4	50.5	5.8	31.2
VF_1890	c1cds1905	62.6	34.4	37.7	44.9	15.4	44.6
VF_1891	c1cds1906	411.9	303.3	362.8	359.4	54.4	238.1
VF_1892	c1cds1907	73.4	38.6	35.0	49.0	21.2	51.2
VF_1893	c1cds1908	1288.0	274.0	354.3	638.8	563.7	228.7
VF_1894	c1cds1909	343.9	338.1	275.2	319.1	38.1	1168.3
VF_1895	c1cds1910	168.3	164.0	183.5	171.9	10.2	559.5
VF_1897	c1cds1911	715.0	560.6	678.0	651.2	80.6	1828.7
VF_1898	c1cds1912	80.6	59.0	55.1	64.9	13.7	149.3
VF_1899	c1cds1913	65.7	179.1	113.6	119.5	56.9	90.9
VF_1900	c1cds1914	64.3	227.7	184.1	158.7	84.6	114.9
VF_1901	c1cds1915	45.1	22.5	29.1	32.2	11.6	40.5

VF_1902	c1cds1916	186.7	240.8	345.9	257.8	81.0	91.3
VF_1903	c1cds1917	673.3	346.6	410.5	476.8	173.1	473.0
VF_1904	c1cds1918	678.2	296.5	378.6	451.1	200.9	607.4
VF_1905	c1cds1919	569.3	318.5	439.6	442.5	125.4	583.8
VF_1906	c1cds1920	658.3	319.9	416.8	465.0	174.3	564.5
VF_1907	c1cds1921	455.9	270.4	279.8	335.4	104.5	144.7
VF_1908	c1cds1922	84.1	23.8	19.1	42.3	36.2	23.5
VF_1909	c1cds1923	205.1	132.0	145.4	160.8	38.9	98.4
VF_1910	c1cds1924	529.8	390.7	258.0	392.8	135.9	38.8
VF_1911	c1cds1925	408.1	188.4	195.4	264.0	124.9	121.4
VF_1912	c1cds1926	22.6	27.6	21.4	23.9	3.3	20.8
VF_1913	c1cds1927	83.6	33.2	33.7	50.2	29.0	124.8
VF_1914	c1cds1928	81.8	63.6	71.0	72.1	9.2	178.5
VF_1915	c1cds1929	28.7	15.9	16.9	20.5	7.1	37.8
VF_1916	c1cds1930	253.9	44.3	24.5	107.6	127.1	58.5
VF_1917	c1cds1931	217.0	186.9	242.6	215.5	27.9	237.0
VF_1918	c1cds1932	277.1	196.1	233.5	235.5	40.5	352.6
VF_1919	c1cds1933	78.9	79.1	60.8	72.9	10.5	120.3
VF_1920	c1cds1934	446.6	358.7	310.7	372.0	68.9	434.1
VF_1921	c1cds1935	54.9	38.7	30.5	41.4	12.4	31.0
VF_1922	c1cds1937	37.9	28.6	24.2	30.3	7.0	46.0
VF_1923	c1cds1938	181.6	52.5	51.4	95.2	74.8	553.5
VF_1924	c1cds1939	74.2	26.6	26.0	42.2	27.6	151.7
VF_1925	c1cds1940	146.8	101.4	113.2	120.5	23.6	85.3
VF_1926	c1cds1941	47.7	45.9	62.0	51.9	8.8	71.5
VF_1927	c1cds1942	677.6	477.6	615.3	590.2	102.3	582.8
VF_1928	c1cds1943	8.4	12.4	14.1	11.6	3.0	66.9
VF_1929	c1cds1944	64.7	31.4	29.0	41.7	20.0	77.2
VF_1930	c1cds1945	104.0	123.3	128.0	118.4	12.7	240.5
VF_1931	c1cds1946	119.9	131.4	122.7	124.7	6.0	395.6
VF_1932	c1cds1947	1338.0	992.4	1059.2	1129.9	183.3	41.4
VF_1934	c1cds1949	55.6	66.4	70.9	64.3	7.8	71.8
VF_1935	c1cds1950	60.2	71.6	84.1	72.0	12.0	65.9
VF_1936	c1cds1951	31.3	33.7	42.2	35.7	5.7	34.1
VF_1937	c1cds1952	132.6	92.7	86.3	103.9	25.1	52.6
VF_1938	c1cds1953	45.4	40.3	36.0	40.6	4.7	77.5
VF_1939	c1cds1954	12.2	10.6	13.8	12.2	1.6	47.9
VF_1940	c1cds1955	20.9	28.4	29.8	26.4	4.8	76.0
VF_1941	c1cds1956	38.1	20.7	22.2	27.0	9.6	22.9
VF_1942	c1cds1957	407.3	159.1	209.0	258.5	131.3	230.7
VF_1943	c1cds1958	397.3	448.7	383.4	409.8	34.4	139.9
VF_1945	c1cds1959	175.1	128.6	133.3	145.7	25.6	37.9
VF_1946	c1cds1960	132.4	219.0	239.1	196.8	56.7	443.0

VF_1947	c1cds1961	63.9	57.2	59.9	60.3	3.4	99.7
VF_1948	c1cds1962	34.6	45.4	41.4	40.5	5.5	61.5
VF_1949	c1cds1963	33.8	39.6	43.5	38.9	4.8	54.3
VF_1950	c1cds1964	334.4	295.1	315.8	315.1	19.7	564.7
VF_1951	c1cds1965	364.0	249.4	210.5	274.6	79.8	488.0
VF_1952	c1cds1966	511.4	334.4	455.1	433.7	90.4	479.2
VF_1953	c1cds1967	496.7	440.7	406.6	448.0	45.5	591.1
VF_1954	c1cds1968	107.7	71.5	90.2	89.8	18.1	139.2
VF_1955	c1cds1969	109.0	58.8	71.1	79.7	26.2	69.6
VF_1956	c1cds1970	8.7	12.6	11.9	11.0	2.1	42.4
VF_1957	c1cds1971	32.5	65.1	53.4	50.3	16.5	61.9
VF_1958	c1cds1972	57.8	80.8	86.6	75.1	15.2	111.6
VF_1959	c1cds1973	161.6	182.8	240.5	195.0	40.8	749.8
VF_1960	c1cds1974	74.0	59.6	66.1	66.6	7.2	486.8
VF_1961	c1cds1975	995.3	917.4	1022.1	978.3	54.4	2649.9
VF_1962	c1cds1976	2823.9	3499.9	2962.1	3095.3	357.2	4742.3
VF_1963	c1cds1977	170.4	141.8	173.4	161.9	17.5	317.0
VF_1964	c1cds1978	27.9	8.7	10.4	15.7	10.7	37.1
VF_1965	c1cds1979	144.5	49.2	29.8	74.5	61.4	77.8
VF_1966	c1cds1980	112.1	103.6	95.7	103.8	8.2	345.7
VF_1967	c1cds1981	36.4	48.6	55.7	46.9	9.7	258.8
VF_1968	c1cds1982	249.4	310.1	303.0	287.5	33.2	637.2
VF_1969	c1cds1983	81.7	92.9	113.0	95.8	15.9	203.2
VF_1970	c1cds1984	15.8	19.2	21.8	18.9	3.0	102.7
VF_1971	c1cds1985	428.7	219.7	273.4	307.3	108.6	211.6
VF_1972	c1cds1986	1652.1	924.8	553.1	1043.3	559.0	4.3
VF_1973	c1cds1987	875.8	542.5	383.1	600.4	251.4	1.9
VF_1974	c1cds1988	20.9	19.8	23.3	21.3	1.8	70.6
VF_1975	c1cds1989	3128.3	1422.5	1795.6	2115.4	896.8	9286.8
VF_1976	c1cds1990	63.5	59.9	61.3	61.6	1.8	112.8
VF_1977	c1cds1991	100.0	68.2	76.9	81.7	16.4	42.0
VF_1978	c1cds1992	20.2	16.9	11.5	16.2	4.4	6.5
VF_1979	c1cds1993	19.6	8.1	6.4	11.4	7.1	25.4
VF_1980	c1cds1994	6.3	2.6	2.4	3.8	2.2	1.8
VF_1981	c1cds1995	4363.4	1257.3	1304.3	2308.3	1779.9	970.3
VF_1982	c1cds1996	160.1	84.1	95.7	113.3	41.0	79.9
VF_1983	c1cds1997	119.9	58.1	62.6	80.2	34.4	61.8
VF_1984	c1cds1998	70.5	28.2	31.7	43.5	23.5	16.3
VF_1985	c1cds1999	59.1	22.8	28.0	36.6	19.7	12.4
VF_1986	c1cds2000	8.9	6.5	7.1	7.5	1.2	15.3
VF_1987	c1cds2001	17.3	8.8	9.5	11.9	4.7	29.5
VF_1988	c1cds2002	21.5	5.8	6.6	11.3	8.8	58.2
VF_1989	c1cds2003	27.8	31.4	35.2	31.4	3.7	98.3

VF_1990	c1cds2004	18.0	94.4	139.0	83.8	61.2	277.7
VF_1991	c1cds2005	46.9	281.0	373.1	233.6	168.1	157.9
VF_1992	c1cds2006	38.9	57.4	65.1	53.8	13.5	37.6
VF_1993	c1cds2007	153.9	96.2	123.1	124.4	28.9	174.1
VF_1994	c1cds2008	830.5	631.5	762.9	741.6	101.2	2713.3
VF_1995	c1cds2009	185.3	87.7	112.5	128.5	50.7	38.9
VF_1996	c1cds2010	367.8	322.0	434.3	374.7	56.5	616.7
VF_1997	c1cds2011	33.7	33.0	37.0	34.6	2.2	63.0
VF_1998	c1cds2012	17.9	13.1	12.3	14.4	3.0	217.7
VF_1999	c1cds2013	299.5	175.7	231.2	235.5	62.0	91.6
VF_2000	c1cds2014	49.6	26.7	31.8	36.0	12.0	45.7
VF_2001	c1cds2015	25.3	18.7	21.1	21.7	3.4	30.8
VF_2002	c1cds2016	264.6	266.8	401.0	310.8	78.1	344.3
VF_2003	c1cds2017	41.9	49.2	57.3	49.5	7.7	16.8
VF_2004	c1cds2018	13.2	7.1	6.8	9.0	3.6	3.1
VF_2005	c1cds2019	15.1	7.9	8.0	10.3	4.1	16.8
VF_2006	c1cds2020	11.4	6.2	5.3	7.7	3.3	8.3
VF_2007	c1cds2021	9.2	2.0	4.7	5.3	3.6	9.9
VF_2008	c1cds2022	3.3	1.9	2.2	2.5	0.7	3.4
VF_2012	c1cds2027	2.9	0.9	1.4	1.7	1.1	4.8
VF_2013	c1cds2028	1.5	0.9	0.8	1.0	0.4	2.1
VF_2015	c1cds2030	2.5	1.7	1.4	1.9	0.6	1.4
VF_2019	c1cds2035	29.8	14.9	21.2	22.0	7.5	9.2
VF_2020	c1cds2036	16.8	8.2	8.6	11.2	4.9	7.6
VF_2022	c1cds2039	4.9	3.1	3.1	3.7	1.0	4.1
VF_2026	c1cds2043	0.6	0.7	0.9	0.8	0.2	1.5
VF_2027	c1cds2044	2.4	1.1	1.2	1.5	0.7	1.4
VF_2028	c1cds2045	15.2	8.9	6.2	10.1	4.6	5.8
VF_2029	c1cds2046	12.3	5.9	6.4	8.2	3.6	8.6
VF_2030	c1cds2047	24.2	5.5	4.6	11.4	11.1	16.2
VF_2031	c1cds2049	4.0	1.9	2.1	2.7	1.1	2.0
VF_2032	c1cds2050	27.5	17.3	10.0	18.3	8.8	52.1
VF_2035	c1cds2055	4.3	1.4	0.6	2.1	1.9	2.1
VF_2036	c1cds2056	1.8	0.4	0.9	1.0	0.7	1.1
VF_2037	c1cds2059	159.7	459.1	427.2	348.7	164.4	293.2
VF_2038	c1cds2061	180.0	355.0	283.2	272.7	88.0	263.1
VF_2039	c1cds2062	77.2	100.6	68.9	82.2	16.4	199.9
VF_2040	c1cds2063	110.6	125.3	102.2	112.7	11.7	171.8
VF_2041	c1cds2065	7.9	9.3	9.6	8.9	0.9	28.5
VF_2042	c1cds2066	7.5	147.8	74.9	76.7	70.2	9.5
VF_2043	c1cds2067	5.0	5.6	4.7	5.1	0.5	17.8
VF_2044	c1cds2068	1.7	1.2	1.1	1.3	0.3	4.7
VF_2046	c1cds2070	3.5	2.5	2.1	2.7	0.7	6.8

VF_2047	c1cds2071	2.0	1.4	1.3	1.6	0.4	4.4
VF_2048	c1cds2072	4.4	1.9	1.9	2.7	1.4	8.6
VF_2049	c1cds2073	7.1	3.2	3.3	4.5	2.2	10.6
VF_2051	c1cds2074	3.4	1.7	2.3	2.5	0.9	18.4
VF_2052	c1cds2075	1.4	3.7	1.9	2.3	1.2	1.5
VF_2053	c1cds2076	15.9	7.3	6.6	10.0	5.2	28.0
VF_2054	c1cds2077	8.7	2.2	3.6	4.8	3.4	9.0
VF_2055	c1cds2078	13.6	6.7	9.1	9.8	3.5	6.0
VF_2056	c1cds2079	38.7	24.9	28.3	30.6	7.2	39.2
VF_2057	c1cds2080	1.1	0.7	1.3	1.0	0.3	1.3
VF_2058	c1cds2081	0.5	0.4	0.7	0.6	0.2	0.3
VF_2059	c1cds2082	47.1	78.6	107.2	77.7	30.1	222.1
VF_2060	c1cds2083	13.6	21.0	13.7	16.1	4.3	2.1
VF_2061	c1cds2084	35.2	9.3	7.5	17.4	15.5	7.2
VF_2062	c1cds2085	30.2	10.7	13.7	18.2	10.5	18.6
VF_2063	c1cds2086	9.4	5.3	5.2	6.6	2.4	19.4
VF_2064	c1cds2087	7.4	6.7	9.5	7.9	1.4	40.5
VF_2065	c1cds2088	2.1	3.4	4.2	3.3	1.1	1.7
VF_2066	c1cds2089	269.7	167.9	109.7	182.4	81.0	17.0
VF_2067	c1cds2090	4572.7	1828.6	2891.8	3097.7	1383.6	35.8
VF_2068	c1cds2091	2526.4	1069.2	1138.5	1578.0	822.0	99.3
VF_2069	c1cds2092	28.0	19.0	16.3	21.1	6.1	52.8
VF_2070	c1cds2093	28.2	20.2	23.9	24.1	4.0	77.8
VF_2071	c1cds2094	44.4	38.0	38.7	40.4	3.5	102.9
VF_2072	c1cds2095	32.1	26.6	31.3	30.0	3.0	62.3
VF_2073	c1cds2096	15.5	20.1	20.6	18.7	2.8	42.9
VF_2074	c1cds2097	16.1	12.6	14.6	14.4	1.8	34.9
VF_2075	c1cds2098	1634.3	1205.8	1562.1	1467.4	229.4	3340.6
VF_2076	c1cds2099	503.2	373.8	512.8	463.3	77.7	573.1
VF_2078	c1cds2100	175.9	35.6	39.3	83.6	79.9	24.0
VF_2079	c1cds2101	46.4	177.7	162.7	129.0	71.9	170.9
VF_2080	c1cds2102	332.3	195.9	265.2	264.4	68.2	198.6
VF_2081	c1cds2103	148.8	112.6	138.5	133.3	18.7	64.1
VF_2082	c1cds2104	24.7	35.8	48.6	36.4	12.0	51.3
VF_2083	c1cds2105	49.4	64.1	62.1	58.5	8.0	122.6
VF_2084	c1cds2106	72.6	83.6	90.0	82.1	8.8	215.3
VF_2085	c1cds2107	34.2	27.8	26.1	29.4	4.2	33.7
VF_2086	c1cds2108	332.3	235.2	244.5	270.6	53.6	170.1
VF_2087	c1cds2109	253.2	203.4	196.7	217.8	30.9	154.8
VF_2088	c1cds2110	358.1	171.6	166.1	231.9	109.3	277.1
VF_2089	c1cds2111	141.1	165.5	202.2	169.6	30.8	419.6
VF_2090	c1cds2112	342.8	109.9	117.1	189.9	132.4	60.5
VF_2091	c1cds2113	212.4	118.6	109.5	146.8	57.0	44.2

VF_2092	c1cds2114	1419.8	736.6	881.1	1012.5	360.1	236.0
VF_2093	c1cds2115	1352.6	790.2	745.0	962.6	338.5	238.3
VF_2094	c1cds2116	126.5	182.7	231.8	180.3	52.7	174.3
VF_2095	c1cds2117	3.0	6.6	5.9	5.2	1.9	8.5
VF_2096	c1cds2118	60.3	43.3	30.8	44.8	14.8	145.1
VF_2097	c1cds2119	44.6	31.0	33.7	36.4	7.2	80.2
VF_2098	c1cds2120	2.3	3.0	4.7	3.3	1.2	13.9
VF_2099	c1cds2122	1328.1	248.7	324.8	633.9	602.5	68.0
VF_2100	c1cds2123	31.6	33.6	34.6	33.3	1.5	68.1
VF_2101	c1cds2124	34.6	41.6	42.0	39.4	4.1	89.1
VF_2102	c1cds2125	91.4	74.7	99.6	88.6	12.7	164.3
VF_2103	c1cds2126	304.8	364.0	344.7	337.8	30.2	329.5
VF_2104	c1cds2127	23.1	15.4	22.4	20.3	4.2	45.7
VF_2105	c1cds2128	71.7	104.1	128.9	101.6	28.7	201.4
VF_2106	c1cds2129	74.4	29.9	33.6	46.0	24.7	89.3
VF_2107	c1cds2130	277.9	106.5	101.1	161.8	100.5	64.8
VF_2108	c1cds2131	288.4	176.0	198.9	221.1	59.4	315.4
VF_2109	c1cds2132	76.9	53.1	54.1	61.3	13.5	152.5
VF_2110	c1cds2133	16.6	18.4	17.6	17.5	0.9	18.7
VF_2111	c1cds2134	7556.2	677.9	704.0	2979.4	3963.7	116.6
VF_2112	c1cds2135	371.5	205.5	166.5	247.8	108.8	22.2
VF_2113	c1cds2136	66.6	53.6	49.2	56.4	9.1	53.9
VF_2114	c1cds2137	65.1	50.2	42.7	52.6	11.4	64.0
VF_2115	c1cds2138	5175.5	1622.6	2027.3	2941.8	1945.0	700.0
VF_2116	c1cds2139	73.6	56.5	62.7	64.3	8.7	282.7
VF_2117	c1cds2140	60.9	44.5	58.5	54.6	8.8	235.5
VF_2118	c1cds2141	41.8	30.5	46.5	39.6	8.2	186.7
VF_2119	c1cds2143	442.2	193.4	194.6	276.7	143.3	64.8
VF_2120	c1cds2144	412.3	540.1	681.2	544.5	134.5	460.1
VF_2121	c1cds2145	109.9	59.8	63.4	77.7	27.9	177.0
VF_2122	c1cds2146	34.9	37.6	38.0	36.8	1.7	58.2
VF_2123	c1cds2147	3.0	3.8	5.4	4.1	1.3	2.9
VF_2124	c1cds2148	34.5	58.7	118.8	70.7	43.4	116.1
VF_2125	c1cds2149	102.9	98.8	141.1	114.3	23.3	98.3
VF_2126	c1cds2150	643.8	410.1	328.5	460.8	163.6	96.0
VF_2128	c1cds2151	61.4	60.0	74.5	65.3	8.0	250.5
VF_2129	c1cds2152	8.4	8.3	6.7	7.8	1.0	18.8
VF_2130	c1cds2153	11.1	17.7	18.0	15.6	3.9	34.8
VF_2131	c1cds2154	35.7	35.3	31.1	34.0	2.6	87.0
VF_2132	c1cds2155	323.7	125.4	187.6	212.2	101.4	11.9
VF_2133	c1cds2156	323.7	138.5	189.2	217.1	95.7	14.3
VF_2134	c1cds2157	1057.3	529.2	661.5	749.3	274.8	197.8
VF_2135	c1cds2158	123.8	122.4	167.6	137.9	25.7	282.5

VF_2136	c1cds2159	29.7	48.7	37.6	38.7	9.5	41.4
VF_2137	c1cds2160	14.0	19.8	20.7	18.2	3.6	51.8
VF_2138	c1cds2161	14.2	17.1	17.8	16.4	1.9	50.1
VF_2139	c1cds2162	46.1	117.7	148.5	104.1	52.5	49.4
VF_2140	c1cds2163	1.5	3.0	6.8	3.8	2.7	3.7
VF_2141	c1cds2164	2.0	6.6	9.0	5.9	3.6	6.9
VF_2142	c1cds2165	3.9	8.7	11.5	8.0	3.8	13.3
VF_2143	c1cds2166	11.0	14.0	17.7	14.2	3.4	17.1
VF_2144	c1cds2167	9.8	19.2	18.4	15.8	5.2	16.8
VF_2145	c1cds2168	4.8	4.5	6.4	5.2	1.0	7.9
VF_2146	c1cds2169	11.4	9.7	9.6	10.2	1.0	16.2
VF_2147	c1cds2170	19.1	15.3	19.0	17.8	2.2	70.0
VF_2148	c1cds2171	74.1	43.8	48.1	55.3	16.4	47.2
VF_2149	c1cds2172	42.6	66.6	34.1	47.8	16.8	92.4
VF_2150	c1cds2173	26.7	41.7	16.9	28.4	12.5	31.7
VF_2151	c1cds2174	628.2	982.3	466.0	692.2	264.0	1659.3
VF_2152	c1cds2175	16.9	12.7	10.5	13.3	3.3	2.0
VF_2153	c1cds2176	5.5	4.7	3.5	4.6	1.0	2.0
VF_2154	c1cds2177	148.9	76.5	81.1	102.2	40.5	59.9
VF_2155	c1cds2178	3.9	5.8	4.7	4.8	0.9	12.6
VF_2156	c1cds2179	14.5	86.7	89.8	63.6	42.6	5.4
VF_2157	c1cds2180	15.8	77.3	30.7	41.3	32.0	8.7
VF_2158	c1cds2181	219.8	344.4	468.1	344.1	124.1	755.2
VF_2159	c1cds2182	34.0	29.8	31.3	31.7	2.1	53.9
VF_2161	c1cds2183	19.5	48.0	43.0	36.8	15.2	132.9
VF_2162	c1cds2184	23.9	20.5	22.0	22.1	1.7	37.0
VF_2163	c1cds2185	15.3	12.3	14.5	14.0	1.5	28.7
VF_2164	c1cds2186	549.4	314.3	269.4	377.7	150.4	133.0
VF_2165	c1cds2187	944.7	1158.0	1273.8	1125.5	167.0	563.5
VF_2166	c1cds2189	47.0	46.3	45.6	46.3	0.7	75.3
VF_2168	c1cds2190	19.4	26.3	26.4	24.0	4.0	73.0
VF_2169	c1cds2191	23.9	27.4	34.1	28.4	5.2	109.9
VF_2170	c1cds2192	46.0	64.7	80.8	63.8	17.4	151.2
VF_2171	c1cds2193	25.0	16.6	15.7	19.1	5.1	40.9
VF_2172	c1cds2194	23.1	12.4	12.9	16.1	6.0	52.2
VF_2173	c1cds2195	23.3	13.2	10.6	15.7	6.7	14.2
VF_2174	c1cds2196	103.5	65.5	52.5	73.8	26.5	441.6
VF_2175	c1cds2197	583.5	181.1	213.0	325.9	223.7	30.5
VF_2176	c1cds2198	164.4	98.1	112.7	125.1	34.8	342.3
VF_2177	c1cds2199	1231.8	702.0	631.1	855.0	328.3	1008.7
VF_2178	c1cds2200	293.9	314.4	357.4	321.9	32.4	2171.3
VF_2179	c1cds2201	445.6	319.1	368.6	377.8	63.8	1535.2
VF_2181	c1cds2202	483.1	313.8	366.9	387.9	86.6	1650.8

VF_2182	c1cds2203	255.5	198.2	182.7	212.1	38.4	426.4
VF_2183	c1cds2204	29.6	35.4	25.6	30.2	4.9	27.4
VF_2184	c1cds2205	122.3	99.6	126.4	116.1	14.4	108.6
VF_2186	c1cds2207	0.3	0.2	0.2	0.2	0.0	0.2
VF_2188	c1cds2209	46.2	29.5	32.4	36.0	8.9	23.0
VF_2189	c1cds2210	153.2	79.8	72.2	101.7	44.7	66.1
VF_2190	c1cds2211	136.7	113.8	108.2	119.6	15.1	105.9
VF_2191	c1cds2212	208.2	138.3	128.9	158.5	43.3	105.6
VF_2192	c1cds2213	26.2	9.7	7.7	14.5	10.1	48.8
VF_2193	c1cds2214	183.1	143.1	164.0	163.4	20.0	471.7
VF_2194	c1cds2215	110.9	67.1	59.4	79.1	27.8	60.2
VF_2195	c1cds2216	2365.4	2823.6	3599.3	2929.4	623.7	1585.0
VF_2196	c1cds2217	1043.8	811.1	865.7	906.9	121.7	918.2
VF_2197	c1cds2218	355.9	260.2	301.9	306.0	48.0	222.0
VF_2199	c1cds2219	393.6	191.0	203.0	262.5	113.7	122.7
VF_2200	c1cds2220	47.9	67.2	64.3	59.8	10.4	146.2
VF_2201	c1cds2221	15.7	16.7	18.3	16.9	1.3	65.9
VF_2202	c1cds2222	17.4	17.2	16.8	17.1	0.3	25.2
VF_2203	c1cds2223	51.7	55.8	62.5	56.7	5.4	104.9
VF_2204	c1cds2224	55.2	83.4	78.2	72.3	15.0	107.1
VF_2205	c1cds2225	41.8	53.7	57.5	51.0	8.2	64.1
VF_2206	c1cds2226	38.7	38.7	47.3	41.6	4.9	77.0
VF_2207	c1cds2227	33.2	18.6	24.5	25.4	7.4	41.2
VF_2208	c1cds2228	23.8	21.9	26.2	24.0	2.1	13.5
VF_2209	c1cds2229	42.0	68.1	82.7	64.3	20.6	64.2
VF_2210	c1cds2230	133.1	35.7	39.2	69.4	55.2	97.6
VF_2211	c1cds2231	150.2	132.5	147.7	143.4	9.6	143.9
VF_2212	c1cds2232	31.5	23.5	26.4	27.1	4.0	39.6
VF_2213	c1cds2233	24.1	32.6	34.8	30.5	5.7	59.6
VF_2214	c1cds2234	43.3	30.6	38.3	37.4	6.4	122.4
VF_2215	c1cds2235	772.2	950.6	1250.4	991.1	241.7	979.2
VF_2216	c1cds2236	520.0	450.1	633.1	534.4	92.3	1099.4
VF_2217	c1cds2237	233.9	246.2	260.6	246.9	13.4	498.2
VF_2218	c1cds2238	91.3	128.4	143.5	121.1	26.9	243.1
VF_2220	c1cds2239	97.8	109.4	151.1	119.4	28.0	220.9
VF_2221	c1cds2240	1025.7	902.2	1352.1	1093.3	232.4	4842.8
VF_2222	c1cds2241	1027.1	685.5	993.6	902.1	188.3	6143.2
VF_2223	c1cds2242	49.5	27.6	21.3	32.8	14.8	79.9
VF_2224	c1cds2243	144.0	103.7	110.6	119.5	21.6	306.9
VF_2225	c1cds2244	447.0	135.4	128.4	236.9	182.0	27.4
VF_2226	c1cds2245	32.4	32.9	38.0	34.4	3.1	25.7
VF_2227	c1cds2246	41.6	51.8	62.3	51.9	10.3	314.0
VF_2228	c1cds2247	22.0	30.3	35.8	29.4	7.0	209.7

VF_2229	c1cds2248	111.5	53.0	52.1	72.2	34.0	119.2
VF_2230	c1cds2249	96.1	62.4	64.4	74.3	18.9	125.4
VF_2231	c1cds2250	127.6	99.0	91.6	106.1	19.0	82.6
VF_2232	c1cds2251	146.5	111.2	113.6	123.7	19.8	94.1
VF_2233	c1cds2252	434.4	274.5	322.3	343.7	82.0	525.0
VF_2234	c1cds2253	160.2	116.6	128.2	135.0	22.6	170.0
VF_2235	c1cds2254	39.8	25.9	30.8	32.1	7.0	53.0
VF_2236	c1cds2255	75.3	107.4	109.3	97.4	19.1	219.3
VF_2237	c1cds2256	43.8	18.8	14.0	25.5	16.0	41.3
VF_2238	c1cds2257	97.9	62.3	65.9	75.3	19.6	115.7
VF_2239	c1cds2258	471.1	332.0	369.2	390.8	72.0	326.0
VF_2240	c1cds2259	374.2	342.0	445.0	387.1	52.7	313.0
VF_2241	c1cds2260	156.6	174.0	218.0	182.9	31.6	324.3
VF_2242	c1cds2261	33.2	13.7	13.6	20.1	11.3	20.5
VF_2243	c1cds2262	28.2	18.6	17.5	21.4	5.9	22.6
VF_2244	c1cds2263	40.9	25.2	31.7	32.6	7.9	33.6
VF_2245	c1cds2264	4.1	6.1	4.6	4.9	1.0	41.9
VF_2246	c1cds2265	11.6	22.8	24.9	19.8	7.1	50.6
VF_2247	c1cds2266	33.4	46.4	44.0	41.3	7.0	91.2
VF_2248	c1cds2267	19.0	21.3	17.5	19.3	1.9	64.6
VF_2249	c1cds2268	61.1	87.1	109.3	85.9	24.1	68.2
VF_2250	c1cds2269	702.0	1603.2	2321.7	1542.3	811.6	2160.3
VF_2251	c1cds2270	1265.3	3017.3	4676.9	2986.5	1706.0	2781.5
VF_2252	c1cds2271	178.9	146.8	139.3	155.0	21.0	115.6
VF_2254	c1cds2272	605.7	629.3	741.6	658.9	72.6	1029.8
VF_2255	c1cds2274	317.7	146.9	144.8	203.1	99.2	86.5
VF_2256	c1cds2275	119.2	60.0	59.3	79.5	34.4	68.3
VF_2257	c1cds2276	291.3	225.1	169.5	228.6	61.0	57.7
VF_2258	c1cds2277	485.5	622.1	776.2	627.9	145.4	1063.9
VF_2259	c1cds2278	10.3	5.3	5.4	7.0	2.8	18.8
VF_2260	c1cds2279	380.4	38.0	24.0	147.5	201.9	4.7
VF_2261	c1cds2280	15.3	12.1	8.8	12.1	3.2	9.2
VF_2262	c1cds2281	303.0	218.5	229.0	250.2	46.0	113.7
VF_2263	c1cds2282	210.7	248.1	278.2	245.7	33.8	118.5
VF_2264	c1cds2283	56.4	95.2	112.7	88.1	28.8	180.8
VF_2265	c1cds2284	33.9	48.8	59.1	47.3	12.7	62.1
VF_2266	c1cds2285	29.3	23.1	25.8	26.1	3.1	39.6
VF_2267	c1cds2286	23.7	20.5	22.0	22.1	1.6	44.9
VF_2268	c1cds2287	33.2	34.5	33.7	33.8	0.6	63.3
VF_2269	c1cds2288	13.0	1.9	2.7	5.9	6.2	13.0
VF_2270	c1cds2289	140.0	5.5	6.3	50.6	77.4	60.3
VF_2271	c1cds2290	31.5	23.6	18.2	24.5	6.7	32.2
VF_2272	c1cds2291	155.6	184.8	208.4	182.9	26.4	289.7

VF_2273	c1cds2292	1560.2	3024.6	2627.2	2404.0	757.3	5348.6
VF_2274	c1cds2293	14.9	14.2	15.8	15.0	0.8	29.8
VF_2275	c1cds2294	15.5	18.1	19.6	17.7	2.1	195.4
VF_2276	c1cds2295	33.6	60.4	86.7	60.2	26.6	130.3
VF_2277	c1cds2296	94.1	105.2	101.6	100.3	5.7	287.5
VF_2278	c1cds2297	185.8	123.2	153.5	154.2	31.3	466.9
VF_2279	c1cds2298	280.1	232.0	240.7	250.9	25.6	149.7
VF_2280	c1cds2299	234.3	380.3	474.8	363.1	121.1	1915.9
VF_2281	c1cds2300	1784.5	549.4	454.0	929.3	742.2	118.2
VF_2282	c1cds2301	474.1	152.3	179.0	268.5	178.6	94.9
VF_2283	c1cds2302	142.2	100.6	103.4	115.4	23.2	76.4
VF_2284	c1cds2303	420.2	499.7	382.6	434.2	59.8	200.6
VF_2285	c1cds2304	1.6	1.3	1.5	1.5	0.1	19.3
VF_2286	c1cds2305	69.6	97.5	116.7	94.6	23.7	358.9
VF_2287	c1cds2306	15.5	40.3	51.4	35.7	18.4	135.9
VF_2288	c1cds2307	30.3	68.9	89.2	62.8	29.9	297.5
VF_2289	c1cds2308	18.7	19.5	17.5	18.6	1.0	51.9
VF_2290	c1cds2309	70.1	68.7	76.3	71.7	4.0	141.6
VF_2291	c1cds2310	89.1	97.4	108.9	98.4	9.9	261.9
VF_2292	c1cds2311	250.9	290.4	425.3	322.2	91.4	498.7
VF_2293	c1cds2312	6.8	3.9	4.4	5.0	1.5	6.8
VF_2294	c1cds2313	6.6	3.6	3.2	4.5	1.8	4.8
VF_2295	c1cds2314	3.5	1.4	0.8	1.9	1.4	2.1
VF_2296	c1cds2315	3.0	1.1	1.4	1.8	1.0	1.4
VF_2297	c1cds2316	3.7	2.7	2.7	3.0	0.6	2.6
VF_2298	c1cds2317	89.8	84.8	96.5	90.3	5.9	149.3
VF_2299	c1cds2318	10.8	14.8	14.6	13.4	2.3	44.4
VF_2300	c1cds2319	57.6	84.5	53.6	65.2	16.8	369.5
VF_2301	c1cds2320	13.8	16.8	20.5	17.1	3.3	33.0
VF_2302	c1cds2321	17.2	24.6	23.5	21.8	4.0	12.7
VF_2303	c1cds2322	23.8	60.3	151.8	78.7	66.0	31.8
VF_2304	c1cds2323	40.0	132.4	364.3	178.9	167.1	38.8
VF_2305	c1cds2324	15.5	62.5	230.1	102.7	112.8	8.8
VF_2306	c1cds2325	10.3	81.9	315.6	135.9	159.6	7.2
VF_2307	c1cds2326	10.7	21.1	36.6	22.8	13.0	90.4
VF_2308	c1cds2327	48.9	89.9	114.0	84.3	32.9	185.2
VF_2309	c1cds2328	161.8	55.5	92.8	103.4	53.9	25.0
VF_2310	c1cds2329	1972.7	3017.8	3251.1	2747.2	680.8	4421.8
VF_2311	c1cds2330	1458.6	2497.9	3157.4	2371.3	856.5	4492.8
VF_2312	c1cds2332	1686.4	2661.9	2919.7	2422.7	650.5	5255.6
VF_2313	c1cds2333	123.0	110.6	138.8	124.1	14.1	137.9
VF_2314	c1cds2334	174.8	157.2	184.1	172.0	13.6	137.5
VF_2315	c1cds2335	47.3	35.2	41.6	41.4	6.1	57.4

VF_2316	c1cds2336	15.3	12.6	12.2	13.4	1.7	52.0
VF_2317	c1cds2337	99.7	342.5	304.1	248.7	130.5	371.4
VF_2318	c1cds2338	245.5	296.1	300.3	280.6	30.5	983.4
VF_2319	c1cds2339	26.6	11.2	12.7	16.8	8.5	23.9
VF_2320	c1cds2340	588.1	211.4	238.0	345.9	210.2	867.3
VF_2321	c1cds2341	558.6	268.9	276.8	368.1	165.0	944.8
VF_2322	c1cds2342	468.2	260.7	261.1	330.0	119.7	504.0
VF_2323	c1cds2343	1226.8	495.0	407.5	709.8	449.9	1154.0
VF_2324	c1cds2344	722.5	305.7	293.9	440.7	244.1	467.4
VF_2325	c1cds2345	99.8	40.7	39.1	59.9	34.6	60.6
VF_2326	c1cds2346	37.9	32.2	36.4	35.5	3.0	81.3
VF_2327	c1cds2347	83.5	81.8	77.4	80.9	3.1	141.8
VF_2328	c1cds2348	44.3	32.8	38.0	38.4	5.7	31.8
VF_2329	c1cds2349	85.4	103.4	105.8	98.2	11.2	228.3
VF_2330	c1cds2350	167.6	149.6	146.7	154.6	11.3	120.3
VF_2331	c1cds2351	144.4	139.4	157.9	147.2	9.6	258.1
VF_2332	c1cds2352	2.7	2.0	1.6	2.1	0.6	4.0
VF_2333	c1cds2353	23.8	18.8	21.7	21.5	2.5	39.8
VF_2334	c1cds2354	26.7	31.0	51.9	36.5	13.5	176.7
VF_2335	c1cds2355	37.1	39.3	51.4	42.6	7.7	141.6
VF_2336	c1cds2356	25.4	28.0	46.1	33.2	11.3	85.2
VF_2337	c1cds2357	147.5	63.9	91.2	100.9	42.6	210.0
VF_2338	c1cds2358	604.2	692.9	716.2	671.1	59.1	901.4
VF_2339	c1cds2359	10.8	13.0	11.6	11.8	1.1	17.0
VF_2340	c1cds2360	670.5	424.1	474.1	522.9	130.2	486.0
VF_2341	c1cds2361	74.0	55.7	56.7	62.1	10.3	52.1
VF_2342	c1cds2362	808.7	425.6	268.6	500.9	277.8	91.4
VF_2343	c1cds2363	108.2	40.9	55.4	68.1	35.4	45.6
VF_2344	c1cds2364	47.5	13.6	16.4	25.8	18.8	20.1
VF_2345	c1cds2365	35.9	38.7	47.2	40.6	5.9	58.8
VF_2347	c1cds2366	146.0	88.3	95.8	110.0	31.3	135.7
VF_2348	c1cds2367	106.3	69.5	73.1	82.9	20.3	136.2
VF_2349	c1cds2368	107.2	113.6	131.3	117.4	12.5	1242.6
VF_2350	c1cds2369	33.2	65.5	68.5	55.7	19.6	295.8
VF_2351	c1cds2370	22.9	29.9	33.4	28.7	5.3	60.7
VF_2352	c1cds2371	274.0	146.4	151.4	190.6	72.2	77.4
VF_2353	c1cds2372	335.6	858.6	837.3	677.1	296.0	1567.9
VF_2354	c1cds2373	60.7	339.4	234.8	211.6	140.8	145.5
VF_2355	c1cds2374	1701.8	1214.1	775.2	1230.4	463.5	185.5
VF_2356	c1cds2375	76.5	62.5	71.7	70.2	7.1	32.7
VF_2357	c1cds2376	161.4	109.0	124.5	131.6	26.9	186.1
VF_2358	c1cds2377	60.0	16.9	15.8	30.9	25.2	9.6
VF_2359	c1cds2378	359.4	68.5	66.1	164.6	168.6	65.2

VF_2360	c1cds2379	181.0	22.1	21.4	74.8	92.0	43.1
VF_2361	c1cds2380	111.2	11.7	9.9	44.3	58.0	13.0
VF_2362	c1cds2381	187.7	76.1	72.3	112.0	65.5	36.5
VF_2363	c1cds2382	85.8	37.1	35.6	52.8	28.6	10.6
VF_2364	c1cds2383	9.5	4.3	4.9	6.2	2.9	2.3
VF_2366	c1cds2384	26.5	14.9	15.2	18.9	6.6	3.8
VF_2370	c1cds2388	10.1	5.0	4.8	6.6	3.0	6.2
VF_2372	c1cds2389	215.3	148.6	209.2	191.0	36.9	239.2
VF_2373	c1cds2390	44.9	63.5	71.6	60.0	13.7	66.7
VF_2374	c1cds2391	107.5	55.3	74.3	79.0	26.4	76.3
VF_2375	c1cds2392	32.8	15.8	12.3	20.3	11.0	11.6
VF_2376	c1cds2393	138.3	429.1	46.6	204.7	199.7	0.2
VF_2377	c1cds2394	223.9	894.0	180.6	432.8	400.0	1.9
VF_2379	c1cds2395	15.9	19.1	21.4	18.8	2.8	10.8
VF_2380	c1cds2396	1.4	2.3	2.5	2.1	0.6	27.1
VF_2381	c1cds2397	9.6	77.9	9.3	32.2	39.5	1.6
VF_2382	c1cds2398	3.1	31.0	7.2	13.8	15.1	0.9
VF_2383	c1cds2399	438.4	619.1	307.7	455.0	156.4	17.7
VF_2385	c1cds2400	74.4	52.2	33.4	53.4	20.5	225.9
VF_2386	c1cds2401	94.5	51.7	47.2	64.4	26.1	503.6
VF_2387	c1cds2402	80.5	54.1	57.1	63.9	14.5	424.2
VF_2388	c1cds2403	17.3	20.7	24.7	20.9	3.7	154.0
VF_2389	c1cds2404	13.4	30.1	61.1	34.8	24.2	80.8
VF_2391	c1cds2405	60.6	69.9	137.1	89.2	41.7	130.9
VF_2392	c1cds2406	133.0	261.4	290.2	228.2	83.7	103.2
VF_2393	c1cds2407	27.7	19.3	9.0	18.7	9.4	24.1
VF_2394	c1cds2408	12.0	11.9	16.5	13.5	2.6	89.5
VF_2395	c1cds2409	18.0	11.4	16.3	15.2	3.4	87.6
VF_2396	c1cds2410	163.4	78.4	66.1	102.6	53.0	66.7
VF_2397	c1cds2411	997.2	696.0	620.5	771.2	199.3	4411.5
VF_2398	c1cds2412	49.8	36.1	42.6	42.8	6.9	127.9
VF_2399	c1cds2413	380.9	230.8	231.4	281.0	86.5	216.0
VF_2400	c1cds2414	26.9	28.0	21.5	25.5	3.5	39.3
VF_2401	c1cds2415	178.1	165.4	143.2	162.2	17.7	23.1
VF_2402	c1cds2416	217.0	247.8	309.6	258.2	47.1	541.8
VF_2403	c1cds2417	60.6	38.9	44.1	47.9	11.3	53.9
VF_2404	c1cds2418	646.7	456.3	357.0	486.7	147.2	482.8
VF_2405	c1cds2419	82.3	111.3	91.6	95.1	14.8	4.0
VF_2406	c1cds2420	121.2	103.6	90.4	105.1	15.4	5.0
VF_2407	c1cds2421	135.3	204.7	106.4	148.8	50.5	3.1
VF_2408	c1cds2422	64.3	75.2	31.9	57.1	22.6	0.0
VF_2409	c1cds2423	9.5	8.0	7.7	8.4	1.0	0.3
VF_2410	c1cds2424	39.0	29.2	35.2	34.4	4.9	2.5

VF_2412	c1cds2425	1335.6	1355.8	1759.8	1483.7	239.3	2609.0
VF_2414	c1cds2426	1153.1	1486.5	2033.1	1557.5	444.3	2890.7
VF_2415	c1cds2427	1549.3	4737.2	5310.1	3865.5	2026.3	4279.4
VF_2416	c1cds2428	1129.3	4671.4	5580.2	3793.7	2351.7	4567.7
VF_2418	c1cds2429	665.4	1821.7	2708.3	1731.8	1024.4	4556.3
VF_2419	c1cds2430	556.8	1736.6	2245.1	1512.8	866.1	4849.7
VF_2421	c1cds2431	1131.3	1220.0	1643.4	1331.6	273.7	1428.4
VF_2422	c1cds2432	626.9	547.3	621.4	598.5	44.5	730.9
VF_2423	c1cds2434	3336.6	2610.2	2869.1	2938.6	368.1	12763.0
VF_2424	c1cds2435	13.3	25.5	18.4	19.1	6.1	78.6
VF_2425	c1cds2436	31.3	33.7	29.0	31.4	2.4	50.6
VF_2426	c1cds2437	51.0	40.9	36.8	42.9	7.3	76.9
VF_2427	c1cds2438	3.8	3.4	2.9	3.4	0.4	19.1
VF_2428	c1cds2439	49.2	72.7	64.9	62.2	12.0	227.7
VF_2432	c1cds2440	152.3	151.0	114.4	139.3	21.5	535.9
VF_2433	c1cds2441	16.8	14.6	13.5	15.0	1.7	37.9
VF_2434	c1cds2442	5.4	3.7	2.6	3.9	1.4	19.5
VF_2435	c1cds2443	15.8	14.2	14.6	14.9	0.8	227.2
VF_2436	c1cds2444	250.1	152.8	151.6	184.8	56.5	59.3
VF_2437	c1cds2445	372.9	160.2	207.1	246.7	111.7	179.5
VF_2438	c1cds2446	110.8	73.7	78.8	87.8	20.1	159.7
VF_2439	c1cds2447	22.0	38.2	33.9	31.4	8.4	133.9
VF_2440	c1cds2448	15.8	35.2	14.5	21.8	11.6	17.2
VF_2441	c1cds2449	49.8	156.4	52.5	86.2	60.8	201.4
VF_2442	c1cds2450	154.8	151.1	131.0	145.6	12.8	358.3
VF_2443	c1cds2451	49.8	48.7	60.7	53.1	6.6	37.7
VF_2444	c1cds2452	67.4	48.7	56.6	57.6	9.4	32.0
VF_2445	c1cds2453	53.5	40.7	54.7	49.6	7.7	36.4
VF_2446	c1cds2454	105.4	72.0	69.1	82.1	20.2	75.3
VF_2447	c1cds2455	32.4	28.4	33.4	31.4	2.6	55.7
VF_2448	c1cds2456	51.1	24.4	22.2	32.6	16.1	103.7
VF_2450	c1cds2457	1450.8	1244.8	1550.9	1415.5	156.1	451.7
VF_2451	c1cds2458	90.0	82.5	101.2	91.2	9.4	73.8
VF_2452	c1cds2459	49.9	67.0	73.9	63.6	12.4	77.3
VF_2453	c1cds2460	54.3	64.8	73.9	64.3	9.8	106.6
VF_2454	c1cds2461	42.3	51.6	53.0	49.0	5.8	55.8
VF_2455	c1cds2462	61.8	49.9	39.7	50.5	11.0	51.6
VF_2456	c1cds2463	11.7	11.0	11.9	11.5	0.5	22.5
VF_2457	c1cds2464	31.6	41.6	30.6	34.6	6.1	42.5
VF_2458	c1cds2466	509.5	218.6	193.8	307.3	175.6	123.3
VF_2459	c1cds2467	22.1	14.6	6.9	14.5	7.6	34.7
VF_2460	c1cds2468	25.3	17.1	17.0	19.8	4.8	34.2
VF_2461	c1cds2469	526.0	563.2	538.5	542.6	18.9	427.3

VF_2462	c1cds2470	76.3	41.1	40.4	52.6	20.5	114.5
VF_2463	c1cds2471	68.5	43.2	46.6	52.8	13.7	127.2
VF_2464	c1cds2472	38.8	22.3	20.9	27.3	10.0	61.3
VF_2465	c1cds2473	18.7	13.3	12.8	14.9	3.3	25.3
VF_2466	c1cds2474	27.1	16.2	15.8	19.7	6.4	53.3
VF_2467	c1cds2475	41.5	17.0	20.5	26.4	13.2	26.6
VF_2468	c1cds2476	24.5	18.0	13.4	18.6	5.6	12.7
VF_2469	c1cds2477	26.7	14.5	11.8	17.7	7.9	19.6
VF_2470	c1cds2478	75.2	23.9	30.7	43.3	27.9	64.2
VF_2471	c1cds2479	230.2	68.8	78.6	125.9	90.5	171.1
VF_2472	c1cds2480	110.3	42.0	47.0	66.5	38.1	46.5
VF_2473	c1cds2481	72.7	27.1	33.9	44.6	24.6	44.5
VF_2474	c1cds2482	115.8	47.4	58.0	73.8	36.8	78.8
VF_2475	c1cds2483	160.3	50.3	56.3	88.9	61.9	36.8
VF_2476	c1cds2484	96.4	46.1	54.9	65.8	26.9	95.2
VF_2477	c1cds2485	774.2	307.3	380.1	487.2	251.2	483.5
VF_2478	c1cds2486	1465.9	937.9	1045.1	1149.6	279.1	974.2
VF_2479	c1cds2487	40.7	19.7	22.6	27.7	11.4	28.3
VF_2480	c1cds2488	25.1	50.7	54.3	43.4	15.9	70.3
VF_2481	c1cds2489	23.7	21.4	22.1	22.4	1.2	34.7
VF_2482	c1cds2490	10.7	13.9	12.7	12.4	1.6	1113.3
VF_2483	c1cds2491	17.2	9.6	10.6	12.5	4.1	47.3
VF_2484	c1cds2493	37.3	20.3	22.3	26.6	9.3	110.1
VF_2485	c1cds2494	52.1	50.4	58.2	53.6	4.1	170.2
VF_2486	c1cds2496	63.2	37.4	42.3	47.6	13.7	120.2
VF_2487	c1cds2497	173.1	80.1	81.9	111.7	53.2	320.9
VF_2488	c1cds2498	29.6	23.4	34.7	29.2	5.7	93.2
VF_2489	c1cds2499	320.0	222.6	271.9	271.5	48.7	608.6
VF_2490	c1cds2500	18.9	13.8	12.9	15.2	3.3	68.6
VF_2491	c1cds2501	9.0	7.8	8.2	8.3	0.6	6.2
VF_2492	c1cds2502	134.1	23.6	21.9	59.9	64.3	5.8
VF_2493	c1cds2503	29.5	1.8	3.3	11.5	15.6	1.8
VF_2494	c1cds2504	25.0	3.0	3.6	10.5	12.5	2.4
VF_2495	c1cds2506	294.9	161.2	111.1	189.1	95.0	35.1
VF_2496	c1cds2507	1.4	1.7	1.5	1.5	0.1	17.3
VF_2497	c1cds2508	1.4	0.7	0.7	1.0	0.4	20.1
VF_2498	c1cds2509	1.3	1.0	0.7	1.0	0.3	30.8
VF_2499	c1cds2510	6.8	2.2	2.4	3.8	2.6	18.4
VF_2500	c1cds2511	13.7	11.9	14.0	13.2	1.1	7.0
VF_2501	c1cds2512	5.5	5.0	4.4	5.0	0.5	16.3
VF_2502	c1cds2513	2.2	11.4	5.0	6.2	4.7	3.7
VF_2503	c1cds2514	12.9	55.1	38.9	35.6	21.3	21.1
VF_2504	c1cds2515	3.8	27.7	17.0	16.2	11.9	0.5

VF_2505	c1cds2516	4.4	21.2	20.4	15.3	9.4	9.4
VF_2506	c1cds2517	5.9	24.0	19.6	16.5	9.4	12.0
VF_2507	c1cds2518	12.4	21.3	21.2	18.3	5.1	9.2
VF_2508	c1cds2519	25.3	40.5	34.2	33.3	7.6	19.7
VF_2509	c1cds2520	36.6	39.5	47.0	41.0	5.3	39.2
VF_2510	c1cds2521	6.2	21.3	19.8	15.8	8.3	6.8
VF_2511	c1cds2522	206.8	91.6	93.5	130.6	66.0	55.2
VF_2512	c1cds2523	144.4	55.8	56.6	85.6	50.9	38.9
VF_2513	c1cds2524	122.4	24.9	29.1	58.8	55.1	43.8
VF_2514	c1cds2525	132.2	46.5	47.4	75.3	49.2	45.4
VF_2515	c1cds2526	341.7	196.0	174.9	237.6	90.8	127.5
VF_2516	c1cds2527	99.3	167.5	136.5	134.5	34.2	17.6
VF_2517	c1cds2528	87.0	180.3	149.6	139.0	47.5	13.2
VF_2518	c1cds2529	376.3	395.3	463.0	411.5	45.6	62.1
VF_2519	c1cds2530	194.6	267.4	318.8	260.3	62.4	37.8
VF_2520	c1cds2531	265.4	144.0	156.1	188.5	66.9	305.6
VF_2521	c1cds2532	26.5	32.4	34.1	31.0	4.0	42.4
VF_2522	c1cds2533	502.7	202.2	145.1	283.3	192.1	54.2
VF_2523	c1cds2534	398.5	214.3	185.9	266.2	115.4	192.2
VF_2524	c1cds2535	282.1	171.0	167.4	206.8	65.2	186.2
VF_2525	c1cds2536	686.0	219.1	192.2	365.8	277.7	329.6
VF_2528	c1cds2537	76.1	67.9	62.7	68.9	6.7	116.4
VF_2529	c1cds2538	17.8	20.4	15.2	17.8	2.6	15.3
VF_2533	c1cds2539	11.3	5.1	5.6	7.3	3.5	49.3
VF_2534	c1cds2540	13.9	14.6	10.3	12.9	2.3	21.2
VF_2535	c1cds2541	21.4	19.1	20.1	20.2	1.2	49.6
VF_2536	c1cds2542	22.5	16.1	18.1	18.9	3.2	40.0
VF_2537	c1cds2543	3.9	4.8	4.8	4.5	0.5	31.0
VF_2538	c1cds2544	11.4	8.5	7.0	9.0	2.2	51.3
VF_2539	c1cds2545	40.2	30.8	38.0	36.3	4.9	52.8
VF_2540	c1cds2546	47.8	60.6	54.4	54.3	6.4	90.0
VF_2541	c1cds2547	12.4	3.6	5.1	7.0	4.7	22.3
VF_2542	c1cds2548	8.8	7.6	11.0	9.1	1.8	19.0
VF_2543	c1cds2549	320.4	223.0	205.8	249.7	61.8	293.4
VF_2544	c1cds2550	160.4	156.6	174.7	163.9	9.6	230.1
VF_2545	c1cds2551	45.1	48.4	47.9	47.2	1.8	93.3
VF_2546	c1cds2552	48.2	38.6	43.0	43.2	4.8	82.8
VF_2547	c1cds2553	25.5	25.7	22.2	24.5	1.9	31.4
VF_2548	c1cds2554	35.6	33.6	26.3	31.8	4.9	35.0
VF_2549	c1cds2555	302.6	249.3	240.0	264.0	33.8	239.1
VF_2550	c1cds2557	430.6	67.8	46.7	181.7	215.8	133.7
VF_2551	c1cds2558	78.2	90.8	94.4	87.8	8.5	88.8
VF_2552	c1cds2559	68.6	31.8	40.6	47.0	19.2	41.0

VF_2553	c1cds2560	576.1	166.9	210.6	317.9	224.7	391.9
VF_2554	c1cds2561	124.5	78.7	77.4	93.5	26.8	57.6
VF_2555	c1cds2562	23.6	13.8	13.1	16.8	5.8	19.8
VF_2556	c1cds2564	10.6	11.0	20.3	14.0	5.5	106.8
VF_2557	c1cds2565	19.5	7.5	14.0	13.7	6.0	139.0
VF_2558	c1cds2566	20.3	17.4	27.6	21.8	5.2	173.1
VF_2559	c1cds2567	26.1	39.1	53.7	39.6	13.8	251.8
VF_2560	c1cds2568	27.0	41.8	46.0	38.3	10.0	221.0
VF_2561	c1cds2569	704.9	1680.4	1821.4	1402.2	608.0	7102.8
VF_2562	c1cds2570	224.0	136.7	171.5	177.4	43.9	234.6
VF_2563	c1cds2571	1729.1	497.7	751.2	992.7	650.2	6306.6
VF_2564	c1cds2572	1286.1	415.5	574.3	758.6	463.6	6024.9
VF_2565	c1cds2573	1159.4	515.4	645.0	773.2	340.6	5547.1
VF_2566	c1cds2574	1010.4	475.8	606.8	697.7	278.6	5299.1
VF_2567	c1cds2575	989.8	443.9	504.7	646.1	299.2	4010.8
VF_2568	c1cds2576	1104.8	537.7	588.9	743.8	313.7	4329.5
VF_2569	c1cds2577	1423.7	814.4	843.9	1027.3	343.6	4809.4
VF_2570	c1cds2578	1436.2	734.9	806.1	992.4	386.0	4752.8
VF_2571	c1cds2579	1767.8	755.9	670.9	1064.9	610.2	3667.4
VF_2572	c1cds2580	91.2	145.1	190.3	142.2	49.6	168.6
VF_2573	c1cds2581	114.0	150.4	266.7	177.0	79.7	182.6
VF_2574	c1cds2582	131.5	180.6	256.0	189.4	62.7	160.5
VF_2575	c1cds2583	93.2	208.2	294.1	198.5	100.8	156.0
VF_2576	c1cds34	5.3	2.9	1.5	3.2	1.9	5.8
VF_2580	c1cds89	32.2	17.7	14.3	21.4	9.5	12.7
VF_2581	c1cds168	28.0	1.9	0.8	10.2	15.4	8.6
VF_2582	c1cds221	102.2	26.1	12.2	46.9	48.5	88.9
VF_2583	c1cds224	0.3	0.6	1.1	0.7	0.4	3.3
VF_2585	c1cds318	4.2	1.7	1.0	2.3	1.7	3.9
VF_2588	c1cds396	45.3	117.0	232.3	131.5	94.4	18.1
VF_2589	c1cds412	222.1	160.2	168.1	183.5	33.7	126.7
VF_2590	c1cds489	124.4	8.8	4.3	45.8	68.1	23.1
VF_2591	c1cds524	17.3	11.0	14.7	14.3	3.2	18.8
VF_2592	c1cds529	91.5	86.5	92.6	90.2	3.3	78.7
VF_2594	c1cds636	23.5	10.5	9.8	14.6	7.7	28.3
VF_2595	c1cds679	42.4	23.2	18.7	28.1	12.6	25.3
VF_2596	c1cds907	42.6	44.8	33.1	40.2	6.2	117.3
VF_2598	c1cds967	29.7	22.4	16.4	22.9	6.7	23.1
VF_2602	c1cds1024	13.1	7.6	8.4	9.7	3.0	19.8
VF_2603	c1cds1025	0.0	0.0	0.5	0.2	0.3	0.0
VF_2604	c1cds1040	271.9	168.5	123.2	187.8	76.2	157.8
VF_2605	c1cds1079	8.4	7.3	8.1	7.9	0.6	7.8
VF_2608	c1cds1201	365.6	135.4	69.7	190.2	155.4	250.7

VF_2610	c1cds1346	71.0	48.6	21.2	46.9	25.0	7.8
VF_2611	c1cds1350	23.7	20.1	19.3	21.0	2.4	56.7
VF_2614	c1cds1389	28.1	27.6	18.8	24.8	5.2	39.6
VF_2615	c1cds1397	58.3	681.8	460.5	400.2	316.1	292.4
VF_2616	c1cds1408	76.2	28.0	18.5	40.9	30.9	11.2
VF_2617	c1cds1413	1454.8	681.4	386.8	841.0	551.6	487.0
VF_2618	c1cds1431	12.3	20.1	21.7	18.1	5.0	11.4
VF_2619	c1cds1438	51.9	30.5	18.1	33.5	17.1	9.1
VF_2620	c1cds1456	155.3	18.9	12.6	62.3	80.6	64.4
VF_2621	c1cds1458	2.5	2.2	0.7	1.8	1.0	0.5
VF_2622	c1cds1461	23.0	52.9	41.9	39.3	15.1	4.7
VF_2623	c1cds1524	255.1	259.4	186.7	233.7	40.8	42.6
VF_2625	c1cds1681	7.0	1.3	0.2	2.8	3.7	0.8
VF_2626	c1cds1696	5.5	3.8	3.0	4.1	1.3	4.5
VF_2628	c1cds1705	73.5	33.3	29.2	45.3	24.5	15.7
VF_2629	c1cds1731	172.8	81.8	57.7	104.1	60.7	33.7
VF_2630	c1cds1734	145375.7	311592.1	285558.2	247508.7	89402.4	3779.5
VF_2631	c1cds1741	595.2	60.4	36.4	230.7	315.9	43.6
VF_2632	c1cds1744	9.1	28.1	29.4	22.2	11.3	0.0
VF_2633	c1cds1790	124.2	51.7	45.4	73.7	43.8	55.2
VF_2635	c1cds1821	44.4	53.2	19.7	39.1	17.4	31.1
VF_2636	c1cds1901	4376.5	5134.7	1317.2	3609.5	2021.1	20.9
VF_2637	c1cds1936	35.1	33.9	20.5	29.8	8.1	18.1
VF_2638	c1cds1948	51.6	59.1	25.7	45.4	17.5	17.0
VF_2648	c1cds2060	187.2	374.6	234.8	265.5	97.4	368.8
VF_2649	c1cds2064	85.5	53.5	29.5	56.2	28.1	78.0
VF_2650	c1cds2121	6.0	3.8	3.2	4.3	1.5	3.9
VF_2652	c1cds2142	508.9	408.2	281.1	399.4	114.2	65.1
VF_2653	c1cds2188	15.4	6.0	5.0	8.8	5.7	14.7
VF_2656	c1cds2331	1802.9	2885.1	3318.2	2668.7	780.5	5392.8
VF_2657	c1cds2433	25.5	8.8	8.4	14.2	9.8	87.4
VF_2659	c1cds2492	23.0	13.6	13.0	16.5	5.6	54.1
VF_2660	c1cds2495	78.6	55.6	48.5	60.9	15.8	254.2
VF_2661	c1cds2505	96.0	49.9	37.4	61.1	30.9	16.1
VF_2662	c1cds2556	18250.2	14974.6	9265.2	14163.3	4547.1	1043.1
VF_2663	c1cds2563	33.2	33.9	18.8	28.6	8.5	87.1
VF_A0001	c2cds0	59.7	130.9	117.9	102.8	37.9	183.3
VF_A0002	c2cds1	31.9	13.2	15.0	20.0	10.3	37.8
VF_A0003	c2cds2	1.4	1.1	1.5	1.3	0.2	3.1
VF_A0004	c2cds3	19.1	24.7	30.4	24.7	5.6	45.4
VF_A0005	c2cds4	714.0	214.5	202.9	377.2	291.8	12.7
VF_A0006	c2cds5	330.1	111.2	81.1	174.1	135.9	27.9
VF_A0007	c2cds6	11.6	8.1	10.6	10.1	1.8	4.7

VF_A0008	c2cds7	53.1	36.5	23.5	37.7	14.8	11.9
VF_A0009	c2cds8	278.7	186.0	146.3	203.7	67.9	282.6
VF_A0011	c2cds10	24.2	13.9	9.9	16.0	7.3	30.2
VF_A0013	c2cds12	314.8	52.4	64.4	143.9	148.2	13.1
VF_A0014	c2cds13	1025.5	801.8	591.7	806.3	217.0	12.3
VF_A0015	c2cds14	4.6	7.5	8.6	6.9	2.1	12.7
VF_A0016	c2cds15	3.4	2.8	3.6	3.3	0.4	5.5
VF_A0017	c2cds16	106.7	51.0	48.7	68.8	32.8	8.3
VF_A0018	c2cds17	168.8	150.5	203.6	174.3	26.9	183.1
VF_A0019	c2cds18	138.5	41.9	37.5	72.6	57.1	59.6
VF_A0020	c2cds19	90.4	41.3	43.4	58.4	27.8	64.3
VF_A0021	c2cds23	5.3	2.4	3.1	3.6	1.6	4.6
VF_A0023	c2cds25	1.3	2.3	1.8	1.8	0.5	4.4
VF_A0024	c2cds26	5.9	4.7	4.4	5.0	0.8	9.8
VF_A0025	c2cds27	1.2	1.4	2.6	1.7	0.8	21.1
VF_A0026	c2cds28	9.4	9.7	5.5	8.2	2.3	12.5
VF_A0027	c2cds29	50.4	40.1	42.8	44.4	5.3	15.9
VF_A0028	c2cds30	8.3	5.5	6.8	6.9	1.4	4.3
VF_A0029	c2cds31	35.6	21.2	15.2	24.0	10.5	22.4
VF_A0030	c2cds32	35.5	37.2	31.6	34.8	2.9	12.5
VF_A0031	c2cds33	4.0	2.7	2.9	3.2	0.7	10.4
VF_A0032	c2cds34	17.5	20.4	19.3	19.1	1.5	6.0
VF_A0033	c2cds35	97.2	53.0	56.6	68.9	24.5	135.2
VF_A0034	c2cds36	27.8	25.1	23.8	25.6	2.0	23.5
VF_A0035	c2cds37	6.8	3.9	4.8	5.2	1.5	6.0
VF_A0036	c2cds38	23.9	8.1	11.0	14.3	8.4	22.6
VF_A0037	c2cds39	23.9	11.1	12.8	15.9	7.0	30.2
VF_A0038	c2cds40	8.7	7.0	11.6	9.1	2.3	17.3
VF_A0039	c2cds42	3.6	4.5	4.8	4.3	0.7	5.4
VF_A0040	c2cds43	2.1	3.0	2.9	2.7	0.5	4.1
VF_A0041	c2cds44	6.0	13.8	16.6	12.1	5.5	12.9
VF_A0042	c2cds45	2.8	1.4	1.3	1.8	0.8	3.2
VF_A0043	c2cds46	22.9	21.4	20.4	21.6	1.3	47.7
VF_A0044	c2cds47	0.1	0.3	0.5	0.3	0.2	28.8
VF_A0045	c2cds48	1.1	1.3	1.0	1.2	0.2	18.3
VF_A0046	c2cds49	7.0	5.0	4.6	5.5	1.3	24.4
VF_A0048	c2cds50	27.7	17.1	15.6	20.1	6.6	29.7
VF_A0049	c2cds51	21.6	14.2	19.6	18.5	3.8	31.3
VF_A0050	c2cds52	4.4	4.3	3.2	4.0	0.7	4.9
VF_A0051	c2cds53	45.3	31.1	41.9	39.4	7.4	26.5
VF_A0052	c2cds54	500.0	485.3	322.5	435.9	98.5	19.7
VF_A0053	c2cds55	2.5	4.0	2.9	3.1	0.8	6.8
VF_A0054	c2cds56	36.1	20.0	18.8	25.0	9.6	39.6

VF_A0055	c2cds57	5.6	5.3	3.2	4.7	1.3	11.4
VF_A0056	c2cds58	17.8	84.4	66.1	56.1	34.4	5.5
VF_A0057	c2cds59	6.0	3.7	2.3	4.0	1.8	4.6
VF_A0058	c2cds60	11.3	5.6	3.2	6.7	4.2	3.9
VF_A0059	c2cds61	6.3	3.0	3.2	4.2	1.8	8.3
VF_A0060	c2cds62	13.1	43.0	28.0	28.0	14.9	6.1
VF_A0061	c2cds63	18.8	36.4	26.9	27.3	8.8	6.0
VF_A0062	c2cds64	28.5	41.4	30.3	33.4	7.0	11.9
VF_A0063	c2cds65	12.5	24.7	16.4	17.9	6.2	35.8
VF_A0064	c2cds66	44.3	24.0	17.6	28.6	13.9	19.6
VF_A0065	c2cds68	77.7	41.1	35.0	51.3	23.1	24.8
VF_A0067	c2cds69	1.1	0.4	0.8	0.8	0.3	0.8
VF_A0069	c2cds71	16.1	9.0	7.9	11.0	4.4	7.0
VF_A0070	c2cds72	30.1	11.9	9.8	17.3	11.2	5.3
VF_A0071	c2cds73	334.3	138.7	95.5	189.5	127.2	21.0
VF_A0072	c2cds74	321.6	117.2	77.6	172.2	131.0	16.9
VF_A0073	c2cds75	31.6	28.2	44.6	34.8	8.6	132.1
VF_A0074	c2cds76	46.8	61.7	55.9	54.8	7.5	228.8
VF_A0075	c2cds77	19.5	29.0	23.8	24.1	4.8	61.7
VF_A0076	c2cds78	5.6	10.6	13.8	10.0	4.1	47.7
VF_A0077	c2cds79	7.2	14.1	16.2	12.5	4.7	34.7
VF_A0078	c2cds80	5.6	13.3	10.9	9.9	4.0	20.4
VF_A0079	c2cds81	6.2	15.4	11.3	11.0	4.6	19.0
VF_A0080	c2cds82	8.6	9.9	14.9	11.1	3.3	2.4
VF_A0081	c2cds83	6.0	8.0	10.0	8.0	2.0	2.3
VF_A0082	c2cds84	2.0	2.9	5.9	3.6	2.0	1.1
VF_A0083	c2cds85	5.7	8.6	11.3	8.6	2.8	0.7
VF_A0084	c2cds86	9.1	11.8	8.5	9.8	1.8	2.3
VF_A0085	c2cds87	112.0	97.2	118.9	109.4	11.1	323.3
VF_A0086	c2cds88	54.8	27.8	44.2	42.3	13.6	90.7
VF_A0087	c2cds89	105.5	47.0	47.4	66.6	33.7	39.2
VF_A0088	c2cds90	12.4	14.3	14.8	13.9	1.3	40.7
VF_A0089	c2cds91	55.7	31.7	27.9	38.4	15.1	18.2
VF_A0090	c2cds92	7.7	4.6	2.6	5.0	2.6	1.4
VF_A0091	c2cds93	103.6	42.1	50.5	65.4	33.3	65.7
VF_A0092	c2cds94	2.0	1.7	1.4	1.7	0.3	8.3
VF_A0093	c2cds95	5.3	12.9	13.3	10.5	4.5	22.3
VF_A0094	c2cds96	29.9	13.2	12.3	18.4	9.9	9.4
VF_A0095	c2cds97	23.8	13.6	11.8	16.4	6.5	12.6
VF_A0096	c2cds98	53.9	21.6	22.7	32.7	18.4	14.1
VF_A0097	c2cds99	151.1	55.8	66.6	91.2	52.2	43.4
VF_A0098	c2cds100	3.6	2.0	1.8	2.5	1.0	1.6
VF_A0099	c2cds101	2.1	1.8	1.5	1.8	0.3	0.7

VF_A0101	c2cds103	1.3	0.4	0.3	0.7	0.6	0.2
VF_A0102	c2cds104	1.7	1.3	1.3	1.4	0.2	2.6
VF_A0103	c2cds105	4.7	4.2	4.0	4.3	0.4	9.4
VF_A0104	c2cds106	337.4	136.0	144.7	206.0	113.8	24.6
VF_A0105	c2cds107	287.8	163.8	157.9	203.2	73.3	15.2
VF_A0106	c2cds108	19.6	26.8	23.0	23.2	3.6	46.6
VF_A0107	c2cds109	14.3	12.6	11.8	12.9	1.3	26.5
VF_A0108	c2cds110	503.6	552.4	296.9	451.0	135.7	106.0
VF_A0109	c2cds111	70.5	28.6	18.4	39.2	27.7	2.4
VF_A0110	c2cds112	36.6	49.3	51.2	45.7	7.9	52.2
VF_A0111	c2cds113	25.7	39.1	39.1	34.6	7.7	34.7
VF_A0112	c2cds114	20.3	30.9	26.8	26.0	5.3	23.2
VF_A0113	c2cds116	213.5	433.2	555.0	400.6	173.1	176.6
VF_A0114	c2cds117	8.2	6.3	6.2	6.9	1.2	8.6
VF_A0115	c2cds118	38.3	13.9	11.4	21.2	14.9	22.3
VF_A0116	c2cds119	20.8	19.8	15.2	18.6	3.0	104.9
VF_A0117	c2cds120	3.5	6.6	3.3	4.5	1.9	1.7
VF_A0118	c2cds121	25.4	23.5	28.4	25.8	2.5	15.2
VF_A0119	c2cds122	21.6	19.9	17.3	19.6	2.2	18.5
VF_A0120	c2cds123	15.5	12.3	11.5	13.1	2.1	2.2
VF_A0121	c2cds124	32.4	24.8	19.6	25.6	6.4	3.8
VF_A0122	c2cds125	7.5	15.8	24.1	15.8	8.3	21.0
VF_A0123	c2cds126	1.4	18.3	17.7	12.5	9.6	1.8
VF_A0124	c2cds127	10.5	54.0	37.0	33.8	21.9	48.1
VF_A0125	c2cds128	17.6	18.8	16.7	17.7	1.1	19.1
VF_A0126	c2cds129	20.7	23.9	24.0	22.9	1.9	56.1
VF_A0127	c2cds130	53.5	19.7	19.1	30.7	19.7	37.2
VF_A0128	c2cds131	8.4	27.4	34.9	23.6	13.6	131.4
VF_A0129	c2cds132	8.2	29.6	24.4	20.7	11.1	120.4
VF_A0130	c2cds133	23.4	41.1	40.7	35.1	10.1	238.3
VF_A0131	c2cds134	3.4	4.9	5.5	4.6	1.1	30.2
VF_A0132	c2cds135	270.8	81.4	65.0	139.1	114.4	67.2
VF_A0133	c2cds136	17.8	13.9	8.2	13.3	4.8	12.2
VF_A0135	c2cds138	4.9	5.8	3.3	4.7	1.3	31.4
VF_A0136	c2cds139	17.5	19.9	10.1	15.8	5.1	40.0
VF_A0137	c2cds140	3.4	4.0	2.4	3.3	0.8	11.1
VF_A0138	c2cds141	2.9	0.6	0.7	1.4	1.3	14.8
VF_A0139	c2cds142	3.2	1.9	1.4	2.2	0.9	0.5
VF_A0140	c2cds143	11.9	10.5	14.2	12.2	1.9	10.9
VF_A0142	c2cds144	2.0	1.8	2.5	2.1	0.4	2.1
VF_A0143	c2cds145	1.7	1.4	1.9	1.7	0.3	3.3
VF_A0144	c2cds146	8.3	1.5	1.4	3.7	4.0	3.4
VF_A0145	c2cds147	18.9	14.1	14.0	15.7	2.8	19.0

VF_A0146	c2cds148	11.8	19.8	22.9	18.2	5.7	9.9
VF_A0147	c2cds149	8038.9	5211.1	3037.5	5429.2	2507.8	809.9
VF_A0148	c2cds150	10.0	47.7	46.6	34.8	21.5	7.4
VF_A0149	c2cds151	83.1	143.0	125.2	117.1	30.8	199.3
VF_A0150	c2cds152	102.5	232.8	296.5	210.6	98.9	415.3
VF_A0151	c2cds153	2.4	4.4	3.5	3.4	1.0	15.1
VF_A0152	c2cds154	2.6	5.0	3.4	3.7	1.2	2.5
VF_A0153	c2cds155	1.9	1.4	1.9	1.7	0.3	21.3
VF_A0154	c2cds156	53.9	92.4	103.4	83.2	26.0	25.9
VF_A0155	c2cds157	4.2	4.5	2.3	3.6	1.2	4.9
VF_A0156	c2cds158	12.7	44.9	13.2	23.6	18.4	64.2
VF_A0157	c2cds159	5.0	6.9	2.1	4.7	2.4	11.9
VF_A0158	c2cds160	3.6	10.1	4.2	6.0	3.6	40.6
VF_A0159	c2cds161	4.8	10.0	5.6	6.8	2.8	81.3
VF_A0160	c2cds162	4.4	8.1	3.6	5.4	2.4	38.0
VF_A0161	c2cds163	8.2	45.5	7.7	20.5	21.7	212.1
VF_A0162	c2cds164	9.5	32.1	5.3	15.6	14.4	240.4
VF_A0163	c2cds165	8.7	29.0	4.7	14.1	13.0	152.3
VF_A0164	c2cds166	14.4	34.3	4.2	17.7	15.3	258.2
VF_A0165	c2cds167	22.8	31.4	6.7	20.3	12.5	487.8
VF_A0166	c2cds168	198.6	127.9	106.3	144.3	48.3	303.4
VF_A0167	c2cds169	310.1	279.9	272.5	287.5	19.9	163.9
VF_A0168	c2cds170	17.8	24.6	18.7	20.4	3.7	23.2
VF_A0169	c2cds171	23.4	20.5	23.3	22.4	1.6	14.2
VF_A0170	c2cds172	11.8	12.0	11.4	11.7	0.3	24.1
VF_A0173	c2cds175	127.3	93.2	95.1	105.2	19.2	182.2
VF_A0174	c2cds176	95.4	31.8	21.1	49.4	40.1	10.7
VF_A0175	c2cds177	5.4	5.4	5.6	5.5	0.1	2.2
VF_A0176	c2cds178	24.8	6.4	5.1	12.1	11.0	17.3
VF_A0177	c2cds179	56.5	62.9	50.5	56.6	6.2	19.5
VF_A0178	c2cds180	93.6	17.0	12.2	40.9	45.7	3.4
VF_A0179	c2cds181	167.4	59.8	49.0	92.0	65.5	16.4
VF_A0180	c2cds182	26.4	21.1	9.3	18.9	8.8	23.7
VF_A0181	c2cds183	9.6	19.6	11.4	13.5	5.3	12.3
VF_A0182	c2cds184	3.7	7.0	5.4	5.4	1.6	10.6
VF_A0183	c2cds185	2.9	0.7	0.6	1.4	1.3	0.3
VF_A0184	c2cds186	5.1	2.0	1.9	3.0	1.8	0.4
VF_A0185	c2cds187	19.6	10.6	8.1	12.8	6.0	1.8
VF_A0186	c2cds188	21.7	12.5	6.7	13.6	7.5	1.3
VF_A0187	c2cds189	18.7	14.3	11.1	14.7	3.8	1.2
VF_A0188	c2cds190	16.3	30.5	61.0	36.0	22.9	11.3
VF_A0189	c2cds191	7.8	18.7	25.3	17.3	8.8	14.3
VF_A0191	c2cds193	31.2	29.0	11.5	23.9	10.8	26.0

VF_A0192	c2cds194	10.9	10.0	4.1	8.4	3.7	11.6
VF_A0193	c2cds195	11.5	8.2	5.1	8.3	3.2	9.8
VF_A0194	c2cds196	10.2	9.1	4.8	8.0	2.9	4.4
VF_A0195	c2cds197	11.6	9.9	4.6	8.7	3.6	6.1
VF_A0196	c2cds198	10.3	5.2	4.2	6.6	3.3	4.6
VF_A0197	c2cds199	10.2	4.8	4.4	6.5	3.2	6.1
VF_A0198	c2cds200	540.9	205.0	178.9	308.3	201.9	40.7
VF_A0199	c2cds201	17.2	44.8	9.5	23.8	18.6	37.5
VF_A0200	c2cds202	6.1	39.1	6.4	17.2	18.9	33.8
VF_A0201	c2cds203	14.6	15.5	7.7	12.6	4.3	74.4
VF_A0202	c2cds204	134.1	74.2	101.8	103.4	30.0	2.5
VF_A0204	c2cds206	2.4	3.7	2.7	3.0	0.7	3.7
VF_A0205	c2cds207	19.0	32.7	26.8	26.2	6.9	18.4
VF_A0206	c2cds208	49.4	27.0	26.0	34.1	13.3	9.9
VF_A0207	c2cds209	112.6	33.1	32.8	59.5	46.0	1.9
VF_A0208	c2cds210	6.9	3.7	3.1	4.6	2.0	6.4
VF_A0209	c2cds211	7.9	4.1	2.9	4.9	2.6	1.8
VF_A0210	c2cds212	6.3	7.2	7.7	7.1	0.7	10.9
VF_A0211	c2cds213	29.9	36.4	30.9	32.4	3.5	22.8
VF_A0212	c2cds214	23.0	19.9	15.9	19.6	3.6	12.0
VF_A0213	c2cds215	5.4	2.9	3.0	3.8	1.4	1.4
VF_A0214	c2cds217	17.5	16.1	11.4	15.0	3.2	18.3
VF_A0215	c2cds218	2.2	2.1	1.7	2.0	0.3	1.4
VF_A0216	c2cds219	5.7	3.2	2.1	3.7	1.8	4.8
VF_A0217	c2cds220	38.4	18.9	18.6	25.3	11.4	9.2
VF_A0218	c2cds221	30.1	10.4	6.9	15.8	12.5	3.5
VF_A0219	c2cds223	0.5	0.4	0.3	0.4	0.1	0.5
VF_A0220	c2cds224	2.0	1.5	1.1	1.6	0.5	0.4
VF_A0222	c2cds226	5.9	3.2	3.1	4.1	1.6	2.0
VF_A0223	c2cds227	6.3	5.1	5.4	5.6	0.6	3.3
VF_A0224	c2cds228	11.2	7.5	5.1	7.9	3.1	1.3
VF_A0225	c2cds229	11.1	6.6	4.4	7.4	3.4	1.9
VF_A0226	c2cds230	7.4	5.9	2.9	5.4	2.3	0.8
VF_A0227	c2cds231	16.1	5.9	6.1	9.4	5.8	2.7
VF_A0228	c2cds232	23.6	11.4	11.6	15.5	7.0	4.1
VF_A0229	c2cds233	35.7	23.1	18.5	25.8	8.9	5.2
VF_A0230	c2cds234	29.0	14.9	8.8	17.6	10.3	11.4
VF_A0231	c2cds235	1.3	1.6	0.4	1.1	0.6	2.3
VF_A0232	c2cds236	0.1	1.6	1.1	0.9	0.7	0.1
VF_A0233	c2cds237	4.9	1.7	1.1	2.6	2.0	1.7
VF_A0234	c2cds238	0.5	0.1	0.5	0.4	0.2	0.6
VF_A0235	c2cds239	96.2	28.8	34.5	53.2	37.4	1545.8
VF_A0236	c2cds240	317.3	106.7	120.4	181.5	117.8	3885.2

VF_A0237	c2cds241	24.8	9.9	7.8	14.2	9.3	3.9
VF_A0238	c2cds242	36.7	23.4	19.1	26.4	9.2	89.5
VF_A0239	c2cds243	26.5	9.2	23.0	19.6	9.2	2885.2
VF_A0240	c2cds244	0.1	0.4	0.0	0.2	0.2	0.3
VF_A0241	c2cds245	31.7	45.3	40.7	39.2	6.9	71.2
VF_A0244	c2cds246	52.9	34.6	20.1	35.9	16.5	6.8
VF_A0245	c2cds247	3.3	2.9	1.2	2.5	1.1	0.3
VF_A0246	c2cds248	46.3	20.9	17.0	28.1	16.0	6.2
VF_A0247	c2cds249	15.5	13.1	11.6	13.4	2.0	3.9
VF_A0248	c2cds250	2.6	1.4	1.1	1.7	0.8	101.5
VF_A0249	c2cds251	0.9	0.6	0.5	0.7	0.2	123.4
VF_A0250	c2cds252	1.3	1.4	1.6	1.4	0.1	308.8
VF_A0251	c2cds253	41.3	65.9	122.9	76.7	41.9	23.2
VF_A0253	c2cds254	11.2	24.0	21.7	19.0	6.8	83.2
VF_A0254	c2cds255	7.0	17.4	15.8	13.4	5.6	7.5
VF_A0255	c2cds256	19.6	14.2	9.5	14.4	5.0	24.2
VF_A0256	c2cds257	24.7	16.3	11.4	17.5	6.8	23.0
VF_A0257	c2cds258	4498.3	1313.0	1648.0	2486.4	1750.4	1.6
VF_A0258	c2cds259	108.4	64.7	45.5	72.9	32.2	6.3
VF_A0259	c2cds260	22.4	21.0	17.1	20.2	2.8	4.8
VF_A0260	c2cds261	105.8	45.5	41.1	64.1	36.1	64.5
VF_A0261	c2cds262	78.8	33.9	29.3	47.3	27.3	49.7
VF_A0263	c2cds264	57.4	40.4	54.4	50.7	9.1	43.2
VF_A0264	c2cds265	30.0	28.1	37.4	31.8	4.9	59.5
VF_A0265	c2cds266	28.7	23.3	24.4	25.5	2.8	12.5
VF_A0266	c2cds267	23.2	24.2	29.8	25.7	3.5	24.1
VF_A0267	c2cds268	23.5	19.8	16.8	20.0	3.4	10.6
VF_A0268	c2cds269	74.4	29.8	26.3	43.5	26.8	23.1
VF_A0269	c2cds270	413.4	180.8	138.0	244.1	148.2	8.3
VF_A0272	c2cds271	173.9	111.0	86.3	123.7	45.1	28.9
VF_A0273	c2cds272	206.2	112.2	93.9	137.4	60.3	10.8
VF_A0274	c2cds273	78.9	32.9	30.5	47.4	27.3	64.4
VF_A0275	c2cds274	62.0	21.8	16.7	33.5	24.8	18.2
VF_A0276	c2cds275	17.9	31.2	24.0	24.4	6.7	41.9
VF_A0277	c2cds276	419.9	263.7	207.7	297.1	110.0	17.6
VF_A0278	c2cds277	26.4	17.4	14.0	19.3	6.4	7.0
VF_A0279	c2cds278	204.7	84.7	90.2	126.5	67.7	76.3
VF_A0280	c2cds279	10.9	5.7	5.2	7.2	3.2	5.8
VF_A0281	c2cds280	6.3	5.7	7.9	6.7	1.1	17.1
VF_A0282	c2cds281	4.7	4.7	4.7	4.7	0.0	5.1
VF_A0283	c2cds282	47.7	30.3	41.3	39.8	8.8	70.7
VF_A0284	c2cds283	1319.2	598.3	492.7	803.4	449.8	370.0
VF_A0285	c2cds284	450.5	222.8	219.7	297.7	132.3	3.9

VF_A0286	c2cds285	3.7	2.1	1.7	2.5	1.1	1.5
VF_A0287	c2cds286	11.0	24.9	28.0	21.3	9.1	79.2
VF_A0288	c2cds287	63.6	41.9	28.0	44.5	17.9	31.4
VF_A0289	c2cds288	8.6	10.8	12.3	10.6	1.9	19.0
VF_A0290	c2cds289	23.8	22.0	20.8	22.2	1.5	32.5
VF_A0291	c2cds290	14.3	15.5	17.3	15.7	1.5	11.6
VF_A0292	c2cds291	14.5	14.6	16.6	15.3	1.2	22.7
VF_A0293	c2cds292	69.4	66.3	69.7	68.5	1.9	61.3
VF_A0294	c2cds293	236.5	172.4	240.2	216.4	38.1	167.5
VF_A0295	c2cds294	90.9	116.9	147.2	118.3	28.2	106.9
VF_A0296	c2cds295	7.6	15.1	14.7	12.4	4.2	14.3
VF_A0297	c2cds296	403.7	257.4	155.2	272.1	124.9	24.6
VF_A0298	c2cds297	524.7	396.0	415.1	445.3	69.4	75.2
VF_A0299	c2cds298	672.4	514.6	663.5	616.8	88.7	116.9
VF_A0300	c2cds299	33.9	15.3	22.7	24.0	9.3	1.6
VF_A0301	c2cds300	47.9	57.4	53.8	53.0	4.8	50.2
VF_A0302	c2cds301	6.9	5.6	4.1	5.6	1.4	0.7
VF_A0304	c2cds303	62.6	51.7	24.2	46.2	19.8	9.4
VF_A0305	c2cds304	112.4	85.0	71.4	89.6	20.9	47.2
VF_A0306	c2cds305	92.7	92.0	101.8	95.5	5.5	46.3
VF_A0307	c2cds306	100.2	66.6	64.4	77.1	20.1	36.8
VF_A0308	c2cds307	114.3	98.1	70.7	94.4	22.0	28.3
VF_A0309	c2cds308	121.6	110.7	104.6	112.3	8.6	30.3
VF_A0310	c2cds309	43.0	16.4	13.8	24.4	16.2	12.2
VF_A0311	c2cds310	406.2	648.0	449.2	501.1	129.0	87.4
VF_A0312	c2cds311	215.2	339.3	227.2	260.6	68.5	52.5
VF_A0313	c2cds312	295.1	490.2	480.3	421.9	109.9	63.4
VF_A0314	c2cds313	56.2	110.1	100.3	88.9	28.7	29.1
VF_A0315	c2cds314	72.2	101.4	94.2	89.2	15.2	36.6
VF_A0316	c2cds315	2.4	3.3	2.5	2.7	0.5	4.6
VF_A0317	c2cds316	1.4	1.1	1.4	1.3	0.2	2.4
VF_A0318	c2cds317	2.8	1.9	1.9	2.2	0.5	2.2
VF_A0319	c2cds318	7.8	4.8	4.5	5.7	1.9	7.5
VF_A0320	c2cds319	11.9	7.9	6.2	8.7	2.9	6.2
VF_A0321	c2cds320	22.2	11.2	12.0	15.1	6.1	9.8
VF_A0322	c2cds321	26.1	17.4	18.2	20.5	4.8	9.0
VF_A0323	c2cds322	3.1	2.4	1.3	2.3	0.9	1.5
VF_A0324	c2cds323	10.7	5.0	5.6	7.1	3.2	4.8
VF_A0325	c2cds324	32.5	80.6	80.7	64.6	27.8	133.7
VF_A0326	c2cds325	1.5	0.8	0.2	0.8	0.7	2.0
VF_A0327	c2cds326	29.2	71.1	47.4	49.2	21.0	5.9
VF_A0328	c2cds327	1.8	8.4	9.0	6.4	4.0	25.3
VF_A0329	c2cds328	6.6	4.1	2.6	4.4	2.0	232.9

VF_A0330	c2cds329	2.2	3.3	0.7	2.1	1.3	238.6
VF_A0331	c2cds330	0.9	2.8	0.4	1.4	1.3	79.5
VF_A0332	c2cds331	1.2	2.0	0.6	1.3	0.7	135.5
VF_A0333	c2cds332	1.8	7.3	1.6	3.6	3.2	81.0
VF_A0334	c2cds333	5.0	4.2	3.2	4.1	0.9	9.4
VF_A0335	c2cds334	104.9	89.0	61.7	85.2	21.9	47.6
VF_A0336	c2cds335	94.4	68.3	57.3	73.3	19.1	28.4
VF_A0338	c2cds336	2.7	3.1	4.7	3.5	1.1	25.2
VF_A0339	c2cds337	1.6	1.2	1.3	1.4	0.2	4.4
VF_A0340	c2cds338	7.8	7.9	7.8	7.8	0.1	10.6
VF_A0341	c2cds339	0.0	0.0	0.0	0.0	0.0	0.0
VF_A0342	c2cds340	0.3	0.4	0.3	0.4	0.1	0.0
VF_A0343	c2cds341	0.5	0.5	0.4	0.5	0.1	0.3
VF_A0344	c2cds342	6.9	6.1	4.2	5.7	1.4	1.7
VF_A0345	c2cds343	19.3	5.9	7.0	10.7	7.4	5.2
VF_A0346	c2cds344	0.7	0.9	1.2	0.9	0.2	8.0
VF_A0347	c2cds345	0.7	0.6	0.8	0.7	0.1	6.2
VF_A0348	c2cds346	22.4	25.3	22.2	23.3	1.7	65.5
VF_A0349	c2cds347	1.0	1.7	1.0	1.2	0.4	5.9
VF_A0350	c2cds348	2.6	3.0	2.5	2.7	0.3	16.4
VF_A0351	c2cds349	4.2	12.2	8.9	8.5	4.1	165.5
VF_A0352	c2cds350	1.6	3.8	4.2	3.2	1.4	34.0
VF_A0353	c2cds351	1.4	1.5	1.9	1.6	0.3	55.4
VF_A0355	c2cds352	3.3	4.6	3.4	3.8	0.7	68.6
VF_A0356	c2cds353	18.7	9.6	8.4	12.2	5.7	90.3
VF_A0357	c2cds354	16.3	10.6	11.5	12.8	3.1	4.4
VF_A0358	c2cds355	0.7	0.6	1.1	0.8	0.3	3.5
VF_A0359	c2cds356	8.2	4.4	4.0	5.5	2.3	7.6
VF_A0360	c2cds357	398.6	133.7	108.2	213.5	160.8	22.0
VF_A0361	c2cds358	8.8	5.2	3.8	5.9	2.6	37.1
VF_A0362	c2cds359	8.4	8.6	3.9	7.0	2.6	146.9
VF_A0363	c2cds360	126.5	234.6	216.3	192.4	57.9	9.5
VF_A0364	c2cds361	18.1	10.2	11.6	13.3	4.2	9.4
VF_A0365	c2cds362	39.1	71.2	60.2	56.8	16.3	65.1
VF_A0366	c2cds363	5.3	11.0	16.6	11.0	5.6	42.7
VF_A0367	c2cds364	4.9	3.2	3.4	3.9	0.9	6.1
VF_A0368	c2cds365	3.8	1.7	1.2	2.3	1.4	1.0
VF_A0370	c2cds367	6.9	2.3	3.1	4.1	2.5	15.9
VF_A0371	c2cds368	111.6	107.6	67.8	95.7	24.2	6.1
VF_A0372	c2cds369	68.1	26.2	20.5	38.3	26.0	15.7
VF_A0373	c2cds370	6.5	6.2	3.1	5.2	1.9	2.9
VF_A0374	c2cds371	7.6	6.9	7.1	7.2	0.4	17.5
VF_A0375	c2cds372	32.0	31.5	24.0	29.2	4.5	4.6

VF_A0376	c2cds373	5.5	10.7	8.7	8.3	2.6	4.3
VF_A0377	c2cds374	23.1	14.9	12.6	16.9	5.5	10.1
VF_A0378	c2cds375	34.9	83.3	82.5	66.9	27.8	87.1
VF_A0379	c2cds376	178.2	74.2	82.6	111.7	57.7	114.9
VF_A0380	c2cds377	152.1	73.1	60.8	95.3	49.5	103.7
VF_A0381	c2cds378	21.6	19.6	13.9	18.4	4.0	19.2
VF_A0382	c2cds380	119.6	36.9	29.2	61.9	50.1	53.0
VF_A0383	c2cds381	50.6	62.5	79.0	64.0	14.2	111.1
VF_A0384	c2cds382	178.2	158.3	195.1	177.2	18.4	83.9
VF_A0385	c2cds383	96.0	47.1	37.6	60.2	31.4	114.4
VF_A0386	c2cds384	4.8	1.6	1.9	2.7	1.8	156.9
VF_A0387	c2cds385	11.7	17.7	15.3	14.9	3.0	29.5
VF_A0388	c2cds386	89.9	77.1	45.4	70.8	22.9	52.2
VF_A0389	c2cds387	34.5	133.9	117.9	95.4	53.4	43.9
VF_A0390	c2cds388	105.8	71.0	60.0	78.9	23.9	38.2
VF_A0391	c2cds389	153.1	116.2	107.6	125.6	24.2	102.2
VF_A0392	c2cds390	12.6	3.8	3.3	6.5	5.2	18.7
VF_A0393	c2cds391	4.1	3.0	4.8	4.0	0.9	33.6
VF_A0394	c2cds392	120.2	99.4	142.8	120.8	21.7	501.6
VF_A0395	c2cds393	148.5	87.4	59.3	98.4	45.6	39.5
VF_A0396	c2cds394	17.2	22.2	20.8	20.1	2.5	16.9
VF_A0397	c2cds395	5.5	6.7	6.9	6.4	0.8	66.5
VF_A0398	c2cds396	4.0	2.6	1.7	2.8	1.2	30.2
VF_A0399	c2cds397	3.0	3.6	3.2	3.2	0.3	43.8
VF_A0400	c2cds398	34.3	35.0	31.9	33.7	1.6	58.1
VF_A0401	c2cds399	89.5	82.9	71.2	81.2	9.3	119.9
VF_A0402	c2cds400	484.2	498.6	350.4	444.4	81.7	887.5
VF_A0403	c2cds401	317.7	194.2	177.8	229.9	76.5	33.4
VF_A0404	c2cds402	158.5	97.4	73.9	109.9	43.7	18.1
VF_A0405	c2cds403	31.5	25.5	28.0	28.3	3.0	23.1
VF_A0406	c2cds404	87.3	87.4	98.4	91.0	6.4	40.7
VF_A0407	c2cds405	623.1	408.2	385.1	472.2	131.2	190.2
VF_A0408	c2cds406	48.5	74.2	67.0	63.3	13.3	65.3
VF_A0409	c2cds407	48.5	73.0	58.9	60.2	12.3	47.0
VF_A0410	c2cds408	20.3	15.8	13.6	16.6	3.4	23.1
VF_A0411	c2cds409	38.2	98.8	82.3	73.1	31.3	47.0
VF_A0412	c2cds410	20.0	25.4	24.8	23.4	3.0	132.8
VF_A0413	c2cds411	22.9	23.4	22.1	22.8	0.7	16.4
VF_A0414	c2cds412	164.5	118.3	91.2	124.7	37.1	141.7
VF_A0415	c2cds413	119.1	157.0	130.5	135.6	19.5	80.5
VF_A0416	c2cds414	274.1	165.3	95.0	178.1	90.2	29.5
VF_A0417	c2cds415	30.4	54.2	57.1	47.2	14.6	495.8
VF_A0418	c2cds416	21.2	61.4	58.5	47.0	22.4	357.3

VF_A0419	c2cds417	10.0	14.6	14.7	13.1	2.7	13.6
VF_A0420	c2cds418	22.9	21.4	11.6	18.6	6.2	12.1
VF_A0421	c2cds419	119.9	209.4	295.2	208.2	87.7	360.8
VF_A0422	c2cds421	113.3	69.0	49.4	77.2	32.8	73.4
VF_A0423	c2cds422	5.1	3.4	2.2	3.5	1.5	1.0
VF_A0424	c2cds423	147.9	165.3	181.4	164.9	16.7	89.7
VF_A0425	c2cds424	71.0	90.6	102.9	88.2	16.1	76.5
VF_A0426	c2cds425	18.7	25.7	31.9	25.4	6.6	38.6
VF_A0427	c2cds426	150.1	126.2	157.5	144.6	16.4	135.7
VF_A0428	c2cds427	52.8	166.2	179.7	132.9	69.7	62.3
VF_A0429	c2cds428	23.9	30.8	32.6	29.1	4.6	51.2
VF_A0430	c2cds429	19.9	33.3	39.0	30.7	9.8	127.2
VF_A0431	c2cds430	14.0	16.9	23.1	18.0	4.6	137.2
VF_A0432	c2cds431	37.6	66.5	78.6	60.9	21.0	274.1
VF_A0434	c2cds432	21.8	37.9	24.8	28.2	8.6	13.5
VF_A0435	c2cds433	16.9	12.5	11.2	13.5	3.0	6.7
VF_A0436	c2cds434	14.5	13.5	10.1	12.7	2.3	11.7
VF_A0437	c2cds435	2.3	2.0	2.5	2.3	0.2	2.1
VF_A0438	c2cds436	11.7	4.3	3.8	6.6	4.4	0.7
VF_A0439	c2cds437	75.0	62.7	59.7	65.8	8.1	7.8
VF_A0440	c2cds438	63.3	51.3	44.8	53.1	9.4	39.8
VF_A0441	c2cds439	1.9	4.1	2.6	2.9	1.1	4.9
VF_A0442	c2cds440	1732.2	2.7	5.3	580.0	997.8	5.3
VF_A0443	c2cds441	1278.3	0.3	0.7	426.4	737.8	0.6
VF_A0444	c2cds442	1487.9	0.4	0.9	496.4	858.6	0.5
VF_A0445	c2cds443	1701.3	1.0	1.9	568.1	981.4	0.8
VF_A0446	c2cds444	5271.4	20.9	14.8	1769.0	3033.1	20.8
VF_A0447	c2cds445	10.6	11.7	12.4	11.6	0.9	3.0
VF_A0448	c2cds446	58.7	45.0	53.8	52.5	7.0	47.6
VF_A0449	c2cds447	31.9	7.7	5.0	14.9	14.8	44.9
VF_A0450	c2cds448	24.1	12.3	18.9	18.4	5.9	70.4
VF_A0451	c2cds449	29.0	10.8	13.0	17.6	9.9	52.4
VF_A0452	c2cds450	29.8	7.9	6.0	14.5	13.2	11.2
VF_A0453	c2cds451	74.0	17.1	15.7	35.6	33.3	27.0
VF_A0454	c2cds452	16.9	4.6	3.9	8.5	7.3	49.9
VF_A0455	c2cds453	19.0	24.2	19.8	21.0	2.8	8.0
VF_A0456	c2cds454	130.5	121.7	135.2	129.1	6.9	110.1
VF_A0457	c2cds455	27.1	28.6	29.9	28.5	1.4	72.5
VF_A0458	c2cds456	227.8	131.0	129.7	162.8	56.3	137.8
VF_A0460	c2cds457	88.8	49.0	55.9	64.5	21.3	81.1
VF_A0461	c2cds458	123.4	85.1	76.6	95.1	24.9	82.0
VF_A0462	c2cds459	27.4	20.2	24.7	24.1	3.6	23.8
VF_A0463	c2cds460	30.1	18.9	26.4	25.1	5.7	18.5

VF_A0464	c2cds461	52.3	39.2	41.5	44.3	7.0	25.3
VF_A0465	c2cds462	873.8	635.6	439.1	649.5	217.7	2.3
VF_A0467	c2cds463	25.9	44.0	23.6	31.2	11.2	0.5
VF_A0468	c2cds464	35.6	22.0	23.4	27.0	7.5	26.8
VF_A0469	c2cds465	53.8	34.4	30.1	39.4	12.6	50.5
VF_A0470	c2cds466	65.8	46.8	54.2	55.6	9.6	81.4
VF_A0471	c2cds467	25.7	21.9	19.1	22.2	3.3	13.9
VF_A0472	c2cds468	69.4	27.9	17.7	38.3	27.4	6.2
VF_A0473	c2cds469	2.5	3.5	2.0	2.7	0.7	9.3
VF_A0474	c2cds470	0.3	0.4	0.7	0.5	0.2	0.5
VF_A0475	c2cds471	1.2	0.9	0.8	1.0	0.2	5.7
VF_A0476	c2cds472	0.6	0.5	0.4	0.5	0.1	2.8
VF_A0477	c2cds473	2.0	0.8	0.5	1.1	0.8	6.6
VF_A0478	c2cds474	3.8	2.3	1.7	2.6	1.1	4.0
VF_A0479	c2cds475	4.0	2.1	1.7	2.6	1.2	5.5
VF_A0481	c2cds477	7.2	5.4	3.9	5.5	1.6	17.3
VF_A0482	c2cds478	10.2	16.4	11.1	12.5	3.3	8.0
VF_A0483	c2cds479	5.9	6.5	7.3	6.6	0.7	12.8
VF_A0484	c2cds480	4.2	2.2	3.3	3.2	1.0	12.2
VF_A0485	c2cds481	4.3	3.1	3.8	3.7	0.6	13.4
VF_A0486	c2cds482	430.5	391.8	322.8	381.7	54.5	63.3
VF_A0487	c2cds483	2258.1	770.0	1322.6	1450.3	752.2	0.7
VF_A0488	c2cds484	355.0	202.8	159.0	238.9	102.9	28.9
VF_A0489	c2cds485	2.3	3.5	1.9	2.6	0.8	3.6
VF_A0490	c2cds486	11.5	5.6	5.0	7.4	3.6	4.3
VF_A0491	c2cds487	26.1	14.2	11.2	17.2	7.8	4.4
VF_A0492	c2cds488	65.5	44.0	38.4	49.3	14.3	96.8
VF_A0493	c2cds489	22.2	26.7	27.8	25.6	3.0	80.4
VF_A0494	c2cds490	179.6	103.9	147.6	143.7	38.0	496.7
VF_A0495	c2cds491	4.2	13.7	13.9	10.6	5.5	27.2
VF_A0496	c2cds492	25.0	28.2	26.3	26.5	1.6	54.9
VF_A0497	c2cds493	37.9	40.5	40.9	39.8	1.6	79.4
VF_A0498	c2cds494	85.6	49.8	40.7	58.7	23.7	78.6
VF_A0499	c2cds495	61.9	42.8	35.6	46.8	13.6	34.1
VF_A0500	c2cds496	84.9	76.7	63.4	75.0	10.8	206.0
VF_A0501	c2cds497	131.7	139.9	152.0	141.2	10.2	191.3
VF_A0502	c2cds498	26.6	89.0	87.5	67.7	35.6	109.4
VF_A0503	c2cds499	805.4	215.9	209.4	410.2	342.3	154.0
VF_A0504	c2cds500	270.2	183.5	122.9	192.2	74.0	155.3
VF_A0505	c2cds501	128.9	85.6	68.4	94.3	31.2	71.4
VF_A0506	c2cds502	22.0	17.2	14.8	18.0	3.6	12.8
VF_A0507	c2cds503	186.7	141.1	113.7	147.2	36.9	36.1
VF_A0508	c2cds504	21.9	7.3	5.7	11.6	8.9	12.5

VF_A0509	c2cds505	46.9	37.0	35.9	39.9	6.1	73.4
VF_A0510	c2cds506	45.7	39.4	43.6	42.9	3.2	67.8
VF_A0511	c2cds507	72.9	80.2	93.9	82.3	10.6	114.5
VF_A0514	c2cds510	1.8	10.5	2.9	5.1	4.7	6.4
VF_A0515	c2cds511	3.1	2.7	1.9	2.6	0.6	0.5
VF_A0516	c2cds512	6.2	2.9	2.4	3.8	2.1	3.0
VF_A0517	c2cds513	0.5	0.0	0.0	0.2	0.3	0.0
VF_A0522	c2cds518	0.9	0.3	0.4	0.5	0.3	0.3
VF_A0525	c2cds521	3.0	1.8	1.5	2.1	0.8	0.6
VF_A0526	c2cds522	0.3	1.0	0.6	0.7	0.4	0.3
VF_A0527	c2cds523	0.6	0.3	0.5	0.5	0.2	4.4
VF_A0528	c2cds524	4.7	2.3	1.6	2.9	1.7	3.9
VF_A0529	c2cds525	12.6	10.7	8.4	10.6	2.1	6.0
VF_A0530	c2cds526	61.8	33.5	33.5	42.9	16.3	11.1
VF_A0531	c2cds527	29.2	19.9	16.5	21.9	6.6	12.9
VF_A0532	c2cds528	10.7	12.3	7.6	10.2	2.4	16.3
VF_A0533	c2cds529	24.4	11.8	11.6	15.9	7.3	13.2
VF_A0534	c2cds530	30.2	1.8	0.4	10.8	16.8	30.5
VF_A0535	c2cds531	38.6	8.9	9.8	19.1	16.9	70.8
VF_A0536	c2cds532	30.5	17.2	19.6	22.4	7.1	65.9
VF_A0537	c2cds533	36.3	23.5	22.9	27.6	7.5	69.9
VF_A0538	c2cds534	55.4	30.1	25.6	37.1	16.0	57.5
VF_A0539	c2cds535	62.7	38.5	50.8	50.7	12.1	68.8
VF_A0540	c2cds536	42.9	18.5	19.1	26.8	13.9	44.3
VF_A0541	c2cds537	10.4	6.1	5.9	7.5	2.5	46.4
VF_A0542	c2cds538	20.1	8.8	8.5	12.5	6.6	59.6
VF_A0543	c2cds539	19.5	12.2	12.6	14.8	4.1	41.1
VF_A0544	c2cds540	11.0	7.1	12.3	10.1	2.7	26.3
VF_A0545	c2cds541	20.9	13.0	13.7	15.9	4.3	35.1
VF_A0546	c2cds542	33.8	19.4	20.0	24.4	8.1	44.5
VF_A0547	c2cds543	108.5	37.8	34.7	60.3	41.8	77.7
VF_A0548	c2cds544	38.3	32.6	38.2	36.3	3.3	21.2
VF_A0549	c2cds545	24.1	29.1	32.6	28.6	4.3	2.3
VF_A0550	c2cds546	16.4	16.0	19.8	17.4	2.1	3.6
VF_A0551	c2cds547	20.0	9.2	7.1	12.1	6.9	11.6
VF_A0552	c2cds548	18.4	15.5	19.3	17.7	2.0	50.8
VF_A0553	c2cds549	82.8	93.5	124.8	100.4	21.8	145.9
VF_A0554	c2cds550	411.4	298.0	361.6	357.0	56.8	230.8
VF_A0555	c2cds551	216.1	110.0	196.7	174.2	56.5	31.9
VF_A0556	c2cds552	18.0	13.3	14.5	15.3	2.4	42.1
VF_A0557	c2cds553	53.6	37.7	31.2	40.8	11.6	29.9
VF_A0558	c2cds554	28.1	13.3	12.8	18.1	8.7	39.5
VF_A0559	c2cds555	12.2	15.5	14.0	13.9	1.7	8.4

VF_A0560	c2cds556	49.4	29.6	28.5	35.8	11.8	31.3
VF_A0561	c2cds557	79.7	50.7	55.1	61.8	15.7	105.6
VF_A0562	c2cds558	39.8	33.3	30.8	34.6	4.7	41.8
VF_A0563	c2cds559	283.3	204.8	142.1	210.1	70.7	30.1
VF_A0564	c2cds560	19.6	93.6	76.7	63.3	38.8	74.3
VF_A0565	c2cds561	211.4	167.3	143.8	174.2	34.3	180.2
VF_A0566	c2cds562	14.4	2.4	2.0	6.3	7.1	1.5
VF_A0567	c2cds563	114.3	62.6	45.1	74.0	36.0	18.7
VF_A0568	c2cds564	144.4	80.5	63.8	96.2	42.5	24.5
VF_A0569	c2cds565	200.3	242.1	250.0	230.8	26.7	312.1
VF_A0570	c2cds566	17.9	23.2	19.0	20.0	2.8	119.2
VF_A0571	c2cds567	8.1	7.2	5.2	6.8	1.5	14.7
VF_A0572	c2cds568	15.3	12.1	11.8	13.0	1.9	54.9
VF_A0573	c2cds569	239.8	117.0	103.6	153.5	75.1	60.4
VF_A0576	c2cds572	26.7	20.4	16.2	21.1	5.2	1.8
VF_A0578	c2cds574	0.7	0.9	0.4	0.6	0.3	0.0
VF_A0580	c2cds576	8.2	4.0	3.3	5.2	2.6	0.7
VF_A0581	c2cds577	1.6	1.0	0.9	1.2	0.3	0.5
VF_A0582	c2cds578	350.9	106.9	78.7	178.8	149.7	72.1
VF_A0583	c2cds581	415.7	257.6	288.7	320.6	83.7	260.9
VF_A0584	c2cds582	30.5	18.7	16.2	21.8	7.7	3.4
VF_A0585	c2cds583	150.8	163.6	171.3	161.9	10.3	441.0
VF_A0586	c2cds584	142.6	168.0	170.1	160.2	15.3	531.6
VF_A0587	c2cds585	51.7	76.3	63.4	63.8	12.3	88.0
VF_A0588	c2cds586	45.3	26.2	25.7	32.4	11.2	6.6
VF_A0589	c2cds587	38.5	36.8	28.8	34.7	5.2	4.0
VF_A0590	c2cds588	56.9	34.8	34.6	42.1	12.8	5.7
VF_A0591	c2cds589	144.2	76.5	73.8	98.2	39.9	13.8
VF_A0592	c2cds590	111.6	85.8	82.2	93.2	16.0	11.4
VF_A0593	c2cds591	185.6	181.9	200.9	189.5	10.1	373.3
VF_A0594	c2cds592	293.4	229.5	204.9	242.6	45.7	130.6
VF_A0595	c2cds593	10153.5	9273.2	11228.3	10218.3	979.1	3723.0
VF_A0596	c2cds594	19.4	31.3	22.3	24.4	6.2	31.9
VF_A0597	c2cds595	26.6	34.1	33.4	31.4	4.2	28.9
VF_A0598	c2cds596	8.2	17.4	12.3	12.6	4.6	123.2
VF_A0599	c2cds597	6.8	6.2	5.9	6.3	0.5	15.1
VF_A0600	c2cds598	86.2	126.0	122.4	111.6	22.0	85.3
VF_A0601	c2cds599	82.8	45.5	37.2	55.2	24.3	51.6
VF_A0602	c2cds600	75.6	68.8	81.9	75.4	6.6	140.3
VF_A0603	c2cds601	33.1	19.0	16.5	22.8	9.0	36.6
VF_A0604	c2cds602	50.1	33.6	33.1	38.9	9.7	106.6
VF_A0605	c2cds603	61.3	96.6	95.0	84.3	20.0	81.1
VF_A0606	c2cds604	523.1	308.9	265.8	365.9	137.8	1662.8

VF_A0607	c2cds605	86.0	46.1	51.5	61.2	21.7	22.9
VF_A0608	c2cds606	19.5	29.1	26.7	25.1	5.0	22.6
VF_A0609	c2cds607	359.6	140.9	100.6	200.4	139.4	260.6
VF_A0610	c2cds608	9.0	11.5	12.5	11.0	1.8	484.3
VF_A0611	c2cds609	8.4	15.9	20.5	14.9	6.1	12.6
VF_A0612	c2cds610	236.2	141.4	116.1	164.6	63.3	57.3
VF_A0613	c2cds611	27.2	18.9	12.9	19.7	7.2	33.7
VF_A0614	c2cds612	120.2	100.4	92.3	104.3	14.3	55.6
VF_A0615	c2cds613	9.8	19.6	13.7	14.4	4.9	22.9
VF_A0616	c2cds614	91.0	39.1	8.6	46.2	41.7	3.1
VF_A0617	c2cds615	50.2	54.4	66.3	57.0	8.4	46.4
VF_A0618	c2cds616	18.6	177.4	269.1	155.0	126.7	21.0
VF_A0619	c2cds617	53.4	81.5	72.6	69.2	14.4	104.7
VF_A0620	c2cds618	457.2	199.3	116.3	257.6	177.8	91.6
VF_A0621	c2cds619	34.7	15.8	13.8	21.4	11.5	66.6
VF_A0622	c2cds620	11.8	12.7	9.9	11.5	1.5	5.6
VF_A0623	c2cds621	3.0	7.2	1.4	3.9	3.0	0.0
VF_A0624	c2cds622	71.8	33.5	23.4	42.9	25.6	21.4
VF_A0625	c2cds623	88.1	50.8	27.1	55.3	30.8	12.9
VF_A0626	c2cds624	73.5	18.2	9.6	33.8	34.7	29.6
VF_A0627	c2cds625	5.5	6.5	3.3	5.1	1.6	12.5
VF_A0628	c2cds626	10.0	4.3	5.1	6.5	3.1	10.9
VF_A0629	c2cds628	28.4	20.4	11.4	20.1	8.5	52.3
VF_A0630	c2cds629	35.0	54.2	29.2	39.5	13.1	76.5
VF_A0631	c2cds630	35.9	37.4	19.1	30.8	10.1	33.7
VF_A0632	c2cds631	28.0	21.1	16.6	21.9	5.8	79.9
VF_A0633	c2cds632	4.6	4.4	4.1	4.3	0.3	13.7
VF_A0634	c2cds633	44.5	18.9	11.0	24.8	17.5	32.3
VF_A0635	c2cds634	13.8	15.5	7.1	12.1	4.4	72.5
VF_A0636	c2cds635	17.9	16.9	15.7	16.8	1.1	53.5
VF_A0637	c2cds636	10.0	22.6	20.6	17.7	6.8	63.8
VF_A0638	c2cds637	3.4	3.5	2.0	3.0	0.9	22.6
VF_A0639	c2cds638	20.8	19.2	19.3	19.8	0.9	116.8
VF_A0640	c2cds639	10.9	35.1	26.0	24.0	12.2	54.6
VF_A0641	c2cds640	92.9	295.3	230.4	206.2	103.3	137.6
VF_A0642	c2cds641	92.1	54.6	34.6	60.4	29.2	29.7
VF_A0643	c2cds642	14.4	19.2	16.8	16.8	2.4	26.5
VF_A0644	c2cds643	2.4	5.5	3.2	3.7	1.6	2.5
VF_A0645	c2cds644	12.7	12.1	8.9	11.2	2.0	61.1
VF_A0646	c2cds645	34.5	22.4	15.4	24.1	9.7	80.5
VF_A0647	c2cds646	9.9	4.5	2.9	5.8	3.7	11.8
VF_A0648	c2cds647	17.3	7.9	8.3	11.2	5.3	32.8
VF_A0649	c2cds648	14.6	16.0	8.5	13.0	4.0	26.4

VF_A0650	c2cds649	15.4	14.7	8.8	13.0	3.6	29.3
VF_A0651	c2cds650	129.8	84.2	52.4	88.8	38.9	212.8
VF_A0652	c2cds651	58.8	30.8	15.1	34.9	22.1	55.7
VF_A0653	c2cds652	5.1	3.0	2.3	3.5	1.5	30.7
VF_A0654	c2cds653	9.4	5.5	4.0	6.3	2.8	51.2
VF_A0655	c2cds654	10.1	5.0	3.1	6.1	3.6	49.7
VF_A0656	c2cds655	17.2	11.4	10.7	13.1	3.5	30.3
VF_A0658	c2cds657	6.8	4.1	3.8	4.9	1.6	17.0
VF_A0659	c2cds658	1.2	2.0	1.3	1.5	0.5	1.1
VF_A0660	c2cds659	65.4	150.5	99.4	105.1	42.9	51.3
VF_A0661	c2cds660	60.2	53.9	37.4	50.5	11.7	158.5
VF_A0662	c2cds661	23.4	15.6	14.9	17.9	4.7	29.4
VF_A0663	c2cds662	31.9	7.1	7.8	15.6	14.1	1.7
VF_A0664	c2cds663	11.9	33.5	25.3	23.6	10.9	11.0
VF_A0665	c2cds664	33.6	47.4	47.2	42.8	7.9	57.5
VF_A0666	c2cds665	37.6	38.7	46.8	41.1	5.0	55.4
VF_A0667	c2cds666	15.2	18.2	20.4	17.9	2.6	31.0
VF_A0668	c2cds667	49.5	42.2	36.8	42.9	6.4	36.9
VF_A0669	c2cds668	7.4	7.7	2.9	6.0	2.7	16.9
VF_A0670	c2cds669	57.7	44.4	23.3	41.8	17.4	20.9
VF_A0671	c2cds670	26.2	17.0	11.8	18.3	7.3	5.6
VF_A0672	c2cds671	4.9	3.2	2.8	3.6	1.1	6.6
VF_A0673	c2cds672	3.5	3.2	2.1	2.9	0.7	4.6
VF_A0674	c2cds673	3.0	1.9	2.4	2.4	0.6	7.5
VF_A0675	c2cds674	5.6	4.9	3.8	4.8	0.9	4.2
VF_A0676	c2cds675	138.5	132.5	135.0	135.3	3.0	101.7
VF_A0677	c2cds676	13.1	47.5	41.8	34.1	18.4	269.0
VF_A0678	c2cds677	146.8	65.1	81.8	97.9	43.2	51.9
VF_A0679	c2cds678	92.4	35.8	50.5	59.6	29.4	35.8
VF_A0680	c2cds679	32.1	12.3	15.6	20.0	10.6	7.7
VF_A0681	c2cds680	60.8	19.2	24.5	34.8	22.6	16.0
VF_A0682	c2cds681	92.6	18.4	23.1	44.7	41.6	29.9
VF_A0683	c2cds682	169.0	28.0	27.2	74.7	81.6	43.9
VF_A0684	c2cds683	1.0	0.4	0.4	0.6	0.4	0.0
VF_A0685	c2cds684	465.3	547.3	489.8	500.8	42.1	102.3
VF_A0686	c2cds685	107.2	163.2	157.5	142.6	30.8	75.1
VF_A0687	c2cds686	273.5	187.6	179.6	213.6	52.1	16.7
VF_A0688	c2cds687	20.0	13.7	10.9	14.9	4.6	18.0
VF_A0689	c2cds688	2.5	0.6	0.4	1.2	1.1	0.4
VF_A0690	c2cds689	4.6	3.4	3.0	3.7	0.8	1.1
VF_A0691	c2cds690	66.6	60.3	50.7	59.2	8.0	87.9
VF_A0692	c2cds691	36.3	18.5	14.4	23.1	11.6	14.3
VF_A0693	c2cds692	1293.4	894.0	664.6	950.6	318.2	381.5

VF_A0694	c2cds693	105.9	81.1	92.2	93.1	12.4	12.4
VF_A0695	c2cds694	43.9	20.6	21.4	28.6	13.2	163.4
VF_A0696	c2cds695	29.6	21.4	29.9	26.9	4.8	58.6
VF_A0697	c2cds696	175.0	112.1	130.0	139.1	32.4	63.1
VF_A0698	c2cds697	230.8	178.8	158.3	189.3	37.4	74.3
VF_A0699	c2cds698	1176.8	1230.7	997.4	1135.0	122.1	209.5
VF_A0700	c2cds699	29.8	15.9	15.2	20.3	8.2	399.9
VF_A0701	c2cds700	1.5	2.4	1.7	1.9	0.5	137.0
VF_A0702	c2cds701	9.3	10.6	9.7	9.9	0.7	1170.5
VF_A0703	c2cds702	8.0	7.5	9.1	8.2	0.8	1111.1
VF_A0704	c2cds703	60.1	36.4	27.2	41.2	17.0	66.3
VF_A0705	c2cds704	42.9	33.4	33.3	36.5	5.5	70.0
VF_A0706	c2cds705	1.5	2.1	1.2	1.6	0.4	7.7
VF_A0707	c2cds706	8.9	7.2	6.7	7.6	1.1	6.3
VF_A0708	c2cds707	7.2	30.8	26.4	21.5	12.5	8.9
VF_A0709	c2cds709	11.2	17.4	20.9	16.5	4.9	14.3
VF_A0710	c2cds710	22.4	46.9	43.0	37.4	13.1	126.1
VF_A0711	c2cds711	7.3	5.6	3.5	5.5	1.9	20.0
VF_A0712	c2cds712	16.8	16.3	12.0	15.1	2.7	56.3
VF_A0713	c2cds713	17.6	18.1	20.8	18.8	1.7	7.9
VF_A0714	c2cds714	9.5	8.1	6.7	8.1	1.4	3.5
VF_A0715	c2cds715	18.6	34.4	76.3	43.1	29.8	183.4
VF_A0716	c2cds716	53.7	20.7	18.9	31.1	19.5	9.1
VF_A0717	c2cds717	17.2	8.2	7.3	10.9	5.5	8.1
VF_A0718	c2cds718	14.8	8.5	8.3	10.5	3.7	7.2
VF_A0719	c2cds719	31.1	12.4	11.7	18.4	11.0	9.3
VF_A0720	c2cds720	8.5	3.8	2.8	5.0	3.0	4.2
VF_A0721	c2cds721	1.1	0.9	1.0	1.0	0.1	1.8
VF_A0722	c2cds722	3.8	11.4	32.9	16.0	15.1	0.5
VF_A0724	c2cds724	2.5	4.0	4.4	3.6	1.0	11.1
VF_A0725	c2cds725	7.5	5.8	4.4	5.9	1.5	2.0
VF_A0726	c2cds726	53.8	40.6	38.2	44.2	8.4	83.8
VF_A0727	c2cds727	83.3	61.5	50.4	65.0	16.7	73.1
VF_A0728	c2cds728	138.8	129.4	123.8	130.7	7.5	97.0
VF_A0729	c2cds729	18.1	22.6	16.4	19.1	3.2	20.1
VF_A0730	c2cds730	4.2	6.1	3.7	4.7	1.3	11.4
VF_A0731	c2cds731	1.0	2.0	1.9	1.7	0.5	7.4
VF_A0732	c2cds732	48.0	19.8	16.1	28.0	17.5	20.0
VF_A0733	c2cds733	28.8	26.4	21.8	25.7	3.6	10.5
VF_A0734	c2cds734	8.3	8.7	6.5	7.8	1.2	1.3
VF_A0735	c2cds735	5.6	4.3	5.6	5.2	0.7	1.6
VF_A0736	c2cds736	5.2	4.0	5.1	4.8	0.7	1.4
VF_A0738	c2cds738	3.9	2.8	2.9	3.2	0.6	1.2

VF_A0739	c2cds739	34.0	38.1	40.7	37.6	3.4	45.3
VF_A0740	c2cds740	4.4	5.0	5.0	4.8	0.3	3.4
VF_A0741	c2cds741	10.3	12.9	11.9	11.7	1.3	23.2
VF_A0742	c2cds742	2.6	1.2	1.1	1.6	0.9	0.3
VF_A0743	c2cds743	0.9	1.2	1.4	1.1	0.3	0.6
VF_A0744	c2cds744	4.6	4.5	4.9	4.7	0.2	9.8
VF_A0745	c2cds745	92.1	93.7	104.5	96.8	6.8	7.2
VF_A0746	c2cds746	28.2	42.6	33.4	34.7	7.3	2.7
VF_A0747	c2cds747	16.4	67.5	44.8	42.9	25.6	2.6
VF_A0748	c2cds749	26.2	83.8	68.0	59.4	29.7	6.1
VF_A0749	c2cds750	863.0	354.6	177.5	465.0	355.9	112.7
VF_A0750	c2cds751	61.7	49.1	47.6	52.8	7.8	80.5
VF_A0751	c2cds752	13.8	18.8	20.9	17.8	3.6	36.4
VF_A0752	c2cds753	1010.9	1078.6	706.2	931.9	198.4	63.1
VF_A0753	c2cds754	384.7	356.6	210.8	317.4	93.4	29.2
VF_A0754	c2cds755	19.0	14.7	13.0	15.6	3.1	16.5
VF_A0755	c2cds756	3142.1	941.9	643.6	1575.8	1364.6	283.8
VF_A0756	c2cds757	86.7	143.1	62.3	97.4	41.5	179.2
VF_A0757	c2cds758	1229.9	1251.8	922.2	1134.6	184.3	28.7
VF_A0758	c2cds759	1011.4	1054.0	643.5	903.0	225.7	31.6
VF_A0759	c2cds760	337.1	460.4	209.2	335.6	125.6	10.4
VF_A0760	c2cds761	1295.4	1414.6	911.1	1207.0	263.1	90.2
VF_A0761	c2cds762	384.3	298.8	207.8	296.9	88.3	39.3
VF_A0762	c2cds763	689.1	588.9	400.9	559.6	146.3	65.8
VF_A0763	c2cds764	591.6	602.8	451.9	548.7	84.1	33.1
VF_A0764	c2cds765	796.6	566.7	248.0	537.1	275.5	42.0
VF_A0765	c2cds766	1947.5	1745.9	1345.7	1679.7	306.3	125.2
VF_A0766	c2cds767	695.8	997.1	643.1	778.7	191.0	67.3
VF_A0768	c2cds769	427.9	183.1	230.3	280.4	129.8	83.5
VF_A0769	c2cds770	748.8	210.3	257.2	405.4	298.3	139.6
VF_A0770	c2cds771	5.9	5.7	6.1	5.9	0.2	4.5
VF_A0771	c2cds772	6.4	5.1	5.2	5.6	0.7	10.7
VF_A0772	c2cds773	7.6	26.2	25.3	19.7	10.5	9.5
VF_A0773	c2cds774	745.5	487.3	352.6	528.4	199.6	36.4
VF_A0774	c2cds775	189.9	133.5	119.8	147.7	37.2	102.2
VF_A0775	c2cds776	50.3	54.2	54.6	53.0	2.4	20.5
VF_A0776	c2cds777	26.4	25.7	25.0	25.7	0.7	18.1
VF_A0777	c2cds778	29.3	38.1	25.9	31.1	6.3	22.3
VF_A0778	c2cds779	18.4	30.4	25.8	24.9	6.0	15.9
VF_A0779	c2cds780	25.0	43.7	32.7	33.8	9.4	28.7
VF_A0780	c2cds781	22.0	41.0	27.1	30.0	9.8	29.1
VF_A0781	c2cds782	13.5	34.8	20.2	22.8	10.9	4.4
VF_A0782	c2cds783	10.5	39.7	23.8	24.7	14.6	5.8

VF_A0783	c2cds784	23.9	61.2	35.9	40.4	19.1	12.0
VF_A0784	c2cds785	40.4	147.2	83.4	90.3	53.7	36.2
VF_A0785	c2cds786	79.6	33.7	23.6	45.6	29.8	15.8
VF_A0786	c2cds787	5.2	10.1	8.3	7.9	2.4	30.9
VF_A0787	c2cds788	185.3	293.9	426.5	301.9	120.8	99.0
VF_A0788	c2cds789	57.7	14.4	9.5	27.2	26.5	2.4
VF_A0789	c2cds790	11.2	8.6	8.6	9.5	1.5	3.0
VF_A0790	c2cds791	8.5	9.3	8.3	8.7	0.5	2.8
VF_A0791	c2cds792	45.4	8.5	8.2	20.7	21.4	13.3
VF_A0792	c2cds793	15.1	10.5	13.4	13.0	2.3	4.2
VF_A0793	c2cds794	9.4	12.5	11.3	11.1	1.6	13.2
VF_A0794	c2cds795	40.7	41.5	47.0	43.1	3.4	402.0
VF_A0795	c2cds796	5.2	3.1	1.9	3.4	1.7	4.5
VF_A0796	c2cds797	8.4	2.1	4.2	4.9	3.2	6.5
VF_A0797	c2cds798	167.2	96.4	98.2	120.6	40.4	52.8
VF_A0798	c2cds799	20.0	12.1	10.6	14.2	5.1	25.2
VF_A0799	c2cds800	95.7	38.0	32.0	55.2	35.1	654.9
VF_A0800	c2cds801	42.3	19.7	21.1	27.7	12.7	42.5
VF_A0801	c2cds802	53.6	31.9	26.9	37.5	14.2	26.8
VF_A0802	c2cds803	56.3	92.2	92.9	80.5	20.9	154.6
VF_A0803	c2cds804	151.9	251.8	233.4	212.4	53.1	148.1
VF_A0804	c2cds805	16.7	26.5	18.3	20.5	5.3	6.2
VF_A0805	c2cds806	532.7	116.9	154.6	268.1	229.9	121.2
VF_A0806	c2cds807	273.4	101.5	103.8	159.6	98.6	76.1
VF_A0807	c2cds808	121.9	40.2	34.8	65.6	48.8	37.9
VF_A0808	c2cds809	40.4	22.3	21.2	28.0	10.8	188.9
VF_A0809	c2cds810	44.3	18.1	17.9	26.8	15.2	133.3
VF_A0810	c2cds811	27.9	12.2	12.7	17.6	8.9	67.7
VF_A0811	c2cds812	21.1	14.0	10.9	15.4	5.2	54.0
VF_A0812	c2cds813	28.6	31.8	28.6	29.7	1.8	90.3
VF_A0813	c2cds814	8.3	20.0	16.6	15.0	6.0	23.3
VF_A0814	c2cds815	354.8	199.7	142.4	232.3	109.9	14.7
VF_A0815	c2cds816	41.3	23.6	18.7	27.9	11.9	24.7
VF_A0816	c2cds817	9.5	10.4	10.8	10.2	0.7	8.6
VF_A0817	c2cds818	11.5	9.7	9.2	10.1	1.2	13.0
VF_A0818	c2cds819	202.4	62.3	43.4	102.7	86.8	272.2
VF_A0819	c2cds820	19.2	28.6	29.2	25.7	5.6	18.1
VF_A0820	c2cds821	153.8	54.7	39.1	82.5	62.2	21.7
VF_A0821	c2cds822	37.3	39.4	31.7	36.2	4.0	9.8
VF_A0822	c2cds823	1646.7	608.6	372.4	875.9	677.9	314.5
VF_A0823	c2cds824	14.1	15.1	11.8	13.7	1.7	14.3
VF_A0824	c2cds825	5.8	12.5	4.7	7.6	4.2	8.6
VF_A0825	c2cds826	2.3	5.6	2.4	3.4	1.9	2.8

VF_A0826	c2cds827	3.6	7.6	2.8	4.7	2.6	4.2
VF_A0827	c2cds828	35.0	40.0	19.3	31.4	10.8	24.9
VF_A0828	c2cds830	226.3	240.9	208.6	225.3	16.2	124.1
VF_A0829	c2cds831	188.9	300.7	227.2	239.0	56.8	97.3
VF_A0830	c2cds832	203.7	329.4	230.8	254.6	66.2	84.6
VF_A0832	c2cds833	108.5	238.1	168.3	171.6	64.9	95.3
VF_A0833	c2cds834	92.1	57.7	34.8	61.5	28.8	18.1
VF_A0834	c2cds835	119.0	272.8	272.7	221.5	88.8	226.3
VF_A0835	c2cds836	5.7	5.7	5.3	5.6	0.2	6.6
VF_A0836	c2cds837	19.0	12.6	17.4	16.3	3.4	80.2
VF_A0837	c2cds838	20.0	35.1	31.7	28.9	7.9	27.8
VF_A0838	c2cds839	13.2	7.8	11.6	10.9	2.8	27.8
VF_A0839	c2cds840	300.5	239.7	273.1	271.1	30.4	38.5
VF_A0840	c2cds841	341.2	219.5	239.0	266.6	65.3	26.6
VF_A0841	c2cds842	7.5	9.0	10.7	9.0	1.6	14.3
VF_A0842	c2cds843	178.2	133.2	95.6	135.6	41.4	72.7
VF_A0844	c2cds845	7.7	4.6	5.2	5.8	1.6	3.2
VF_A0845	c2cds846	27.7	16.3	13.9	19.3	7.4	3.1
VF_A0846	c2cds847	14.6	10.6	11.1	12.1	2.2	25.9
VF_A0847	c2cds848	81.1	148.7	120.8	116.8	33.9	71.5
VF_A0848	c2cds849	21.6	95.6	18.1	45.1	43.8	41.2
VF_A0849	c2cds850	1754.1	710.0	613.5	1025.9	632.5	31.8
VF_A0850	c2cds851	6.6	7.0	5.2	6.2	0.9	5.3
VF_A0851	c2cds852	67.4	92.7	43.6	67.9	24.6	7.1
VF_A0852	c2cds853	4.4	3.2	7.9	5.1	2.4	84.3
VF_A0853	c2cds854	299.5	204.3	220.5	241.4	51.0	199.8
VF_A0854	c2cds855	25.2	31.1	20.2	25.5	5.5	27.7
VF_A0856	c2cds856	6.0	16.2	12.2	11.5	5.1	19.5
VF_A0857	c2cds857	76.6	34.9	23.1	44.8	28.1	38.0
VF_A0858	c2cds858	46.0	14.7	11.0	23.9	19.2	11.1
VF_A0859	c2cds859	56.5	67.4	74.4	66.1	9.1	6.4
VF_A0860	c2cds860	44.0	184.2	96.7	108.3	70.8	1.6
VF_A0861	c2cds861	34.7	79.0	41.3	51.7	23.9	2.5
VF_A0862	c2cds862	16.9	33.7	29.6	26.8	8.8	13.3
VF_A0863	c2cds863	14.9	26.6	21.8	21.1	5.9	4.9
VF_A0864	c2cds864	1.6	2.5	1.4	1.8	0.6	0.8
VF_A0865	c2cds865	7.1	6.7	5.0	6.3	1.1	6.9
VF_A0866	c2cds866	23.5	14.4	10.5	16.1	6.7	11.3
VF_A0867	c2cds867	5.8	6.0	2.8	4.8	1.8	4.2
VF_A0868	c2cds868	5.8	4.0	3.8	4.5	1.1	8.8
VF_A0869	c2cds869	2.6	1.5	0.7	1.6	1.0	3.1
VF_A0870	c2cds870	1.6	0.5	0.4	0.8	0.7	1.0
VF_A0871	c2cds871	0.6	1.2	0.6	0.8	0.3	0.7

VF_A0872	c2cds872	9.0	5.4	3.9	6.1	2.6	10.6
VF_A0873	c2cds873	9.5	5.0	4.3	6.3	2.8	10.3
VF_A0874	c2cds874	7.4	5.9	5.7	6.3	0.9	5.4
VF_A0875	c2cds875	9.2	5.4	2.5	5.7	3.4	15.3
VF_A0876	c2cds876	2.9	3.7	3.0	3.2	0.5	2.0
VF_A0877	c2cds877	3.2	3.6	1.7	2.8	1.0	5.1
VF_A0879	c2cds879	1.3	0.7	0.4	0.8	0.5	1.0
VF_A0880	c2cds880	0.0	1.7	0.6	0.8	0.9	0.2
VF_A0881	c2cds881	6.4	3.5	3.8	4.6	1.6	4.4
VF_A0882	c2cds882	6.5	5.1	4.0	5.2	1.3	3.9
VF_A0883	c2cds883	4.7	2.9	2.6	3.4	1.1	3.6
VF_A0884	c2cds884	2.4	1.2	1.6	1.7	0.6	1.2
VF_A0885	c2cds885	1.6	1.1	0.8	1.2	0.4	2.0
VF_A0886	c2cds886	6.8	2.6	1.7	3.7	2.8	1.6
VF_A0887	c2cds888	6.8	5.1	4.3	5.4	1.3	4.1
VF_A0888	c2cds889	30.2	32.3	14.8	25.8	9.5	6.3
VF_A0889	c2cds890	44.4	17.5	12.4	24.8	17.2	52.4
VF_A0890	c2cds891	67.1	38.5	24.4	43.3	21.7	44.8
VF_A0891	c2cds892	11.9	7.9	4.5	8.1	3.7	5.7
VF_A0892	c2cds893	30.1	11.0	11.7	17.6	10.8	40.7
VF_A0893	c2cds894	30.1	18.3	16.7	21.7	7.3	18.1
VF_A0894	c2cds895	21.9	13.9	13.0	16.3	4.9	8.6
VF_A0895	c2cds896	5.7	5.1	7.2	6.0	1.1	5.4
VF_A0896	c2cds897	2.7	5.7	6.4	4.9	2.0	2.3
VF_A0897	c2cds898	25.3	25.5	17.3	22.7	4.7	18.9
VF_A0899	c2cds900	3.8	1.4	2.0	2.4	1.3	2.1
VF_A0904	c2cds906	1.7	1.0	0.8	1.2	0.5	0.3
VF_A0905	c2cds907	0.9	0.6	0.3	0.6	0.3	0.4
VF_A0906	c2cds908	1.4	0.5	0.7	0.9	0.5	1.0
VF_A0907	c2cds909	3.0	1.6	2.1	2.3	0.7	1.4
VF_A0908	c2cds910	8.7	10.3	10.2	9.8	0.9	3.2
VF_A0909	c2cds911	33.7	15.0	9.4	19.4	12.7	13.6
VF_A0910	c2cds912	1.9	0.8	0.6	1.1	0.7	0.5
VF_A0911	c2cds913	7.5	4.6	3.8	5.3	1.9	9.6
VF_A0912	c2cds915	21.7	11.2	11.8	14.9	5.9	14.4
VF_A0913	c2cds916	46.2	17.2	10.5	24.6	19.0	16.2
VF_A0914	c2cds917	14.4	11.6	12.5	12.8	1.5	50.3
VF_A0915	c2cds918	31.8	26.1	18.7	25.5	6.6	465.0
VF_A0916	c2cds919	4.8	8.7	7.7	7.1	2.0	30.0
VF_A0917	c2cds920	280.8	124.0	134.0	179.6	87.8	122.2
VF_A0918	c2cds921	32.7	10.4	8.7	17.2	13.4	38.1
VF_A0919	c2cds922	44.4	17.1	12.4	24.6	17.3	35.6
VF_A0920	c2cds923	51.0	14.7	6.9	24.2	23.5	50.9

VF_A0921	c2cds924	65.8	15.1	13.4	31.4	29.7	70.9
VF_A0922	c2cds925	73.0	13.4	10.9	32.5	35.2	45.2
VF_A0923	c2cds926	42.2	11.5	10.5	21.4	18.0	20.4
VF_A0924	c2cds927	46.3	16.0	14.9	25.7	17.9	13.3
VF_A0925	c2cds928	32.2	38.1	26.4	32.2	5.9	36.0
VF_A0926	c2cds929	24.6	39.1	33.7	32.5	7.3	52.6
VF_A0927	c2cds930	119.5	72.0	25.1	72.2	47.2	23.3
VF_A0928	c2cds931	1.9	3.2	4.4	3.2	1.3	7.8
VF_A0929	c2cds932	3.4	4.1	3.7	3.7	0.4	6.7
VF_A0930	c2cds933	7.6	5.9	9.1	7.5	1.6	6.0
VF_A0931	c2cds934	54.2	29.4	31.6	38.4	13.8	11.6
VF_A0932	c2cds935	116.9	73.7	83.6	91.4	22.7	21.4
VF_A0933	c2cds936	28.3	10.7	4.4	14.5	12.4	18.0
VF_A0934	c2cds937	24.3	20.4	24.1	22.9	2.2	10.9
VF_A0935	c2cds938	46.5	30.4	30.8	35.9	9.2	11.1
VF_A0936	c2cds939	94.2	48.4	40.6	61.1	29.0	30.5
VF_A0937	c2cds940	52.4	61.6	79.7	64.6	13.9	340.8
VF_A0938	c2cds941	15.3	24.8	23.0	21.0	5.1	14.2
VF_A0939	c2cds942	11.1	25.7	33.3	23.4	11.3	39.9
VF_A0940	c2cds943	73.0	37.8	43.6	51.5	18.9	8.9
VF_A0941	c2cds944	41.4	16.6	18.4	25.4	13.8	3.2
VF_A0942	c2cds945	45.8	18.9	18.1	27.6	15.8	3.5
VF_A0943	c2cds947	7.1	5.8	4.3	5.7	1.4	2.4
VF_A0945	c2cds948	8.7	5.1	2.4	5.4	3.2	2.2
VF_A0946	c2cds949	4.6	4.2	1.9	3.6	1.5	0.9
VF_A0948	c2cds951	7.5	3.8	2.8	4.7	2.5	0.7
VF_A0949	c2cds952	24.4	10.9	6.8	14.0	9.2	5.0
VF_A0950	c2cds953	10.4	4.5	2.8	5.9	3.9	1.4
VF_A0951	c2cds954	5.9	4.8	2.2	4.3	1.9	4.1
VF_A0952	c2cds955	0.5	0.4	0.5	0.5	0.0	0.8
VF_A0953	c2cds956	0.2	0.5	0.7	0.5	0.3	0.5
VF_A0954	c2cds957	7.4	9.0	8.9	8.4	0.9	9.8
VF_A0955	c2cds958	18.0	18.7	17.1	17.9	0.8	19.8
VF_A0956	c2cds959	69.9	51.3	64.1	61.8	9.6	61.1
VF_A0957	c2cds960	20.5	10.6	12.9	14.7	5.2	1255.7
VF_A0958	c2cds961	9.0	5.9	8.5	7.8	1.7	1749.2
VF_A0959	c2cds962	33.0	47.1	50.7	43.6	9.4	9.8
VF_A0960	c2cds963	25.7	66.2	69.7	53.8	24.5	9.6
VF_A0961	c2cds964	10.5	37.0	26.2	24.6	13.3	210.3
VF_A0962	c2cds965	7.3	15.5	9.8	10.9	4.2	71.9
VF_A0963	c2cds966	72.9	84.0	77.5	78.1	5.6	18.8
VF_A0964	c2cds967	5.0	9.7	6.8	7.2	2.4	9.4
VF_A0965	c2cds968	47.9	15.1	16.0	26.3	18.7	51.5

VF_A0966	c2cds969	183.7	133.8	120.8	146.1	33.2	1.3
VF_A0967	c2cds970	5.1	6.9	6.2	6.1	0.9	0.8
VF_A0968	c2cds971	19.3	21.2	17.8	19.4	1.7	6.1
VF_A0969	c2cds972	4.9	4.6	4.1	4.5	0.4	1.3
VF_A0970	c2cds973	11.5	9.4	6.5	9.1	2.5	8.4
VF_A0971	c2cds974	6.4	3.1	3.2	4.2	1.9	20.1
VF_A0972	c2cds975	2.6	2.1	1.9	2.2	0.4	7.1
VF_A0973	c2cds976	9.8	9.9	7.8	9.2	1.2	22.6
VF_A0975	c2cds978	4.8	3.2	4.5	4.1	0.9	7.3
VF_A0976	c2cds979	4.2	2.8	1.7	2.9	1.2	1.7
VF_A0977	c2cds980	15.8	20.9	5.8	14.1	7.7	2.1
VF_A0978	c2cds981	3.4	2.4	2.4	2.7	0.6	12.8
VF_A0979	c2cds982	16.9	38.4	39.1	31.5	12.6	25.7
VF_A0980	c2cds983	500.5	94.2	45.0	213.3	250.0	32.5
VF_A0981	c2cds984	149.6	35.3	17.0	67.3	71.8	23.6
VF_A0982	c2cds985	64.8	27.8	19.9	37.5	23.9	20.3
VF_A0983	c2cds986	4.7	4.8	2.6	4.1	1.2	1.3
VF_A0984	c2cds987	0.3	0.3	0.1	0.2	0.1	0.1
VF_A0985	c2cds988	1.3	1.0	0.4	0.9	0.4	0.5
VF_A0986	c2cds989	30.9	11.3	12.2	18.2	11.1	7.7
VF_A0987	c2cds990	19.1	10.4	8.4	12.7	5.7	9.3
VF_A0988	c2cds991	9.2	6.2	4.2	6.6	2.5	4.1
VF_A0989	c2cds992	6.9	17.7	15.6	13.4	5.7	9.2
VF_A0990	c2cds993	7.0	5.0	5.1	5.7	1.1	3.1
VF_A0991	c2cds994	5.6	5.4	2.8	4.6	1.6	2.5
VF_A0992	c2cds995	5.1	5.9	6.3	5.7	0.6	9.5
VF_A0993	c2cds996	1.1	3.8	3.8	2.9	1.6	1.2
VF_A0994	c2cds997	12.9	10.1	6.9	10.0	3.0	2.3
VF_A0995	c2cds998	26.8	366.4	58.5	150.6	187.6	59.8
VF_A0996	c2cds999	21.4	14.0	17.2	17.6	3.7	34.5
VF_A0997	c2cds1000	7.4	6.6	7.4	7.1	0.5	35.5
VF_A0998	c2cds1001	6.0	9.3	8.3	7.9	1.7	44.2
VF_A0999	c2cds1002	3.5	8.1	8.4	6.7	2.7	12.7
VF_A1000	c2cds1003	3.9	11.5	10.9	8.8	4.2	15.6
VF_A1001	c2cds1004	11.9	24.6	24.5	20.3	7.3	19.1
VF_A1002	c2cds1005	7.4	15.0	18.2	13.6	5.6	16.1
VF_A1003	c2cds1006	6.2	19.0	16.0	13.7	6.7	12.6
VF_A1004	c2cds1007	2.6	4.8	4.4	4.0	1.2	4.2
VF_A1005	c2cds1008	2.0	2.2	1.4	1.8	0.4	5.4
VF_A1006	c2cds1009	23.4	34.9	31.0	29.8	5.8	182.8
VF_A1007	c2cds1010	0.5	3.4	3.2	2.4	1.6	1.1
VF_A1008	c2cds1011	47.0	27.9	26.5	33.8	11.4	3.9
VF_A1010	c2cds1012	5.9	7.7	6.6	6.7	0.9	37.7

VF_A1011	c2cds1013	33.3	25.4	27.3	28.6	4.1	202.8
VF_A1012	c2cds1014	111.6	94.8	60.0	88.8	26.3	89.4
VF_A1013	c2cds1015	192.8	43.7	26.7	87.7	91.4	20.6
VF_A1014	c2cds1016	661.1	298.1	186.0	381.7	248.3	61.2
VF_A1015	c2cds1017	2461.4	749.5	507.8	1239.6	1065.0	335.3
VF_A1016	c2cds1018	391.1	51.0	30.7	157.6	202.5	14.9
VF_A1017	c2cds1019	280.9	41.6	19.8	114.1	144.9	15.6
VF_A1018	c2cds1020	42.8	39.0	33.7	38.5	4.6	8.1
VF_A1019	c2cds1021	9.4	12.0	12.4	11.3	1.7	4.2
VF_A1020	c2cds1022	19.6	15.2	12.5	15.8	3.6	2.4
VF_A1021	c2cds1023	13.0	11.6	13.5	12.7	1.0	2.0
VF_A1022	c2cds1024	10.7	7.1	7.5	8.4	2.0	1.6
VF_A1023	c2cds1025	8.7	2.6	4.0	5.1	3.2	3.0
VF_A1024	c2cds1026	39.1	18.9	13.8	23.9	13.4	7.8
VF_A1025	c2cds1027	64.4	34.2	26.6	41.7	20.0	21.2
VF_A1026	c2cds1028	375.7	183.1	183.6	247.4	111.0	37.7
VF_A1027	c2cds1029	51.9	22.7	19.0	31.2	18.0	5.3
VF_A1028	c2cds1030	4.6	3.9	4.0	4.2	0.4	0.5
VF_A1029	c2cds1031	3.1	3.0	3.4	3.2	0.2	0.0
VF_A1030	c2cds1032	3.4	1.8	1.6	2.3	1.0	0.5
VF_A1031	c2cds1033	4.9	4.1	3.3	4.1	0.8	1.6
VF_A1032	c2cds1034	3.1	3.3	4.5	3.6	0.8	0.9
VF_A1034	c2cds1036	2.5	1.4	2.4	2.1	0.7	0.2
VF_A1035	c2cds1037	7.2	4.7	4.2	5.4	1.6	1.0
VF_A1036	c2cds1038	9.2	3.9	3.9	5.7	3.0	1.2
VF_A1037	c2cds1039	9.9	7.4	6.2	7.8	1.9	2.1
VF_A1038	c2cds1040	52.8	23.8	19.5	32.0	18.1	19.6
VF_A1039	c2cds1041	25.9	29.8	29.8	28.5	2.3	23.6
VF_A1040	c2cds1042	18.1	26.1	26.3	23.5	4.7	12.4
VF_A1041	c2cds1043	87.0	54.2	20.8	54.0	33.1	26.6
VF_A1042	c2cds1044	44.8	41.5	40.4	42.2	2.3	14.6
VF_A1043	c2cds1045	46.8	64.9	54.0	55.2	9.1	17.9
VF_A1044	c2cds1046	99.3	58.7	59.2	72.4	23.3	27.4
VF_A1045	c2cds1047	23.0	13.7	14.7	17.1	5.1	63.8
VF_A1046	c2cds1048	37.0	55.0	61.5	51.2	12.7	64.0
VF_A1047	c2cds1049	64.2	35.5	36.7	45.5	16.2	51.4
VF_A1048	c2cds1050	11.4	3.8	2.9	6.0	4.6	5.9
VF_A1049	c2cds1051	1.8	1.4	1.0	1.4	0.4	1.4
VF_A1050	c2cds1052	37.1	10.2	10.4	19.3	15.5	2.4
VF_A1051	c2cds1053	128.7	64.5	79.5	90.9	33.6	13.7
VF_A1052	c2cds1054	37.9	14.6	12.8	21.8	14.0	3.0
VF_A1053	c2cds1055	289.1	118.7	129.4	179.1	95.5	26.6
VF_A1054	c2cds1056	177.7	117.1	105.7	133.5	38.7	89.2

VF_A1055	c2cds1057	8.2	11.1	7.6	9.0	1.9	2.3
VF_A1056	c2cds1058	19.3	11.8	14.1	15.1	3.9	14.3
VF_A1057	c2cds1059	1314.0	346.8	750.5	803.8	485.8	2.9
VF_A1058	c2cds1060	47.7	16.5	14.1	26.1	18.7	51.2
VF_A1059	c2cds1061	26.2	12.3	12.5	17.0	8.0	2.6
VF_A1060	c2cds1062	2.7	2.7	2.6	2.7	0.1	1.6
VF_A1061	c2cds1063	8.6	4.7	3.8	5.7	2.6	8.8
VF_A1062	c2cds1064	37.0	52.3	48.6	45.9	8.0	10.9
VF_A1063	c2cds1065	26.4	27.8	43.5	32.6	9.5	37.0
VF_A1064	c2cds1066	9.0	11.6	8.6	9.7	1.6	5.6
VF_A1065	c2cds1067	14.9	13.6	13.4	14.0	0.8	67.3
VF_A1066	c2cds1068	17.9	7.8	6.5	10.7	6.3	12.4
VF_A1067	c2cds1069	2.1	1.1	0.6	1.3	0.8	1.7
VF_A1068	c2cds1070	75.9	204.2	165.7	148.6	65.8	302.8
VF_A1069	c2cds1071	2.4	2.0	1.4	2.0	0.5	7.7
VF_A1070	c2cds1072	0.6	1.4	0.6	0.9	0.5	2.6
VF_A1071	c2cds1073	2.0	1.1	0.6	1.2	0.7	2.8
VF_A1072	c2cds1074	3.6	2.2	3.0	2.9	0.7	5.6
VF_A1073	c2cds1075	1.2	1.3	0.7	1.1	0.3	2.2
VF_A1074	c2cds1076	32.1	16.9	8.7	19.2	11.9	23.2
VF_A1075	c2cds1077	0.7	0.5	0.7	0.6	0.1	0.8
VF_A1077	c2cds1079	68.1	43.1	41.3	50.8	15.0	6.3
VF_A1078	c2cds1080	38.4	14.9	15.6	23.0	13.3	23.3
VF_A1079	c2cds1081	86.7	30.9	21.9	46.5	35.1	13.0
VF_A1080	c2cds1082	10.4	6.7	5.8	7.6	2.5	5.4
VF_A1082	c2cds1084	6.8	3.2	1.0	3.7	2.9	1.4
VF_A1084	c2cds1086	3.2	1.9	0.8	2.0	1.2	0.8
VF_A1085	c2cds1087	14.5	14.9	10.1	13.2	2.7	4.5
VF_A1086	c2cds1088	5.8	8.1	7.1	7.0	1.2	13.5
VF_A1087	c2cds1090	1045.7	220.5	327.4	531.2	448.8	0.5
VF_A1088	c2cds1091	165.2	65.9	117.0	116.0	49.7	0.2
VF_A1089	c2cds1092	122.3	49.9	71.6	81.3	37.2	0.3
VF_A1090	c2cds1093	135.8	55.4	77.5	89.5	41.5	0.0
VF_A1091	c2cds1094	307.5	79.0	127.9	171.5	120.3	1.5
VF_A1092	c2cds1095	320.0	59.0	77.7	152.2	145.6	4.3
VF_A1093	c2cds1096	64.9	7.1	6.4	26.1	33.6	8.3
VF_A1094	c2cds1097	11.8	5.5	5.5	7.6	3.6	305.1
VF_A1095	c2cds1098	17.6	6.3	5.4	9.8	6.8	19.3
VF_A1096	c2cds1099	1.1	0.6	0.5	0.7	0.3	2.6
VF_A1097	c2cds1100	0.5	0.6	0.6	0.6	0.0	0.7
VF_A1098	c2cds1101	39.8	30.1	25.5	31.8	7.3	29.7
VF_A1099	c2cds1102	2.6	1.8	1.0	1.8	0.8	1.3
VF_A1100	c2cds1103	2.3	0.9	0.9	1.4	0.8	0.8

VF_A1102	c2cds1105	14.1	8.7	6.8	9.9	3.8	10.6
VF_A1103	c2cds1106	1.7	0.3	0.3	0.8	0.8	0.5
VF_A1104	c2cds1107	0.8	0.7	0.4	0.6	0.2	0.4
VF_A1105	c2cds1108	18.1	11.2	11.3	13.6	4.0	7.1
VF_A1106	c2cds1109	10.0	44.3	17.8	24.0	18.0	6.4
VF_A1107	c2cds1110	68.1	63.2	59.1	63.5	4.5	103.6
VF_A1108	c2cds1111	501.9	448.8	408.5	453.0	46.8	79.9
VF_A1109	c2cds1113	6.0	4.5	3.9	4.8	1.1	8.7
VF_A1110	c2cds1112	1.0	1.9	3.8	2.2	1.4	1.4
VF_A1111	c2cds1114	82.4	36.6	36.9	51.9	26.4	32.7
VF_A1112	c2cds1115	10.9	12.9	21.6	15.1	5.7	5.6
VF_A1113	c2cds1116	10.9	9.9	9.4	10.1	0.8	44.5
VF_A1114	c2cds1117	2.3	3.8	4.3	3.5	1.1	6.9
VF_A1115	c2cds1118	4.1	8.7	9.6	7.5	3.0	16.7
VF_A1116	c2cds1119	12.4	10.7	15.1	12.7	2.2	14.7
VF_A1117	c2cds1120	20.4	36.2	39.2	31.9	10.1	6.6
VF_A1118	c2cds1121	25.8	45.4	58.7	43.3	16.5	22.4
VF_A1121	c2cds1124	24.1	15.1	12.5	17.2	6.1	38.2
VF_A1123	c2cds1126	1.3	1.8	1.9	1.6	0.3	1.9
VF_A1125	c2cds1128	1.0	0.9	1.5	1.1	0.3	1.6
VF_A1127	c2cds1130	11.5	8.3	2.7	7.5	4.5	3.6
VF_A1128	c2cds1131	29.3	9.5	4.6	14.5	13.0	8.2
VF_A1129	c2cds1133	15.0	6.8	6.2	9.3	4.9	10.4
VF_A1132	c2cds1136	25.1	21.7	14.3	20.4	5.5	23.1
VF_A1133	c2cds1137	7.2	8.4	4.8	6.8	1.8	7.9
VF_A1134	c2cds1138	2.8	4.5	2.3	3.2	1.2	4.8
VF_A1135	c2cds1139	4.4	3.9	1.3	3.2	1.7	5.0
VF_A1138	c2cds1142	0.1	0.6	0.0	0.2	0.3	0.1
VF_A1140	c2cds1144	40.7	10.0	6.6	19.1	18.8	11.3
VF_A1142	c2cds1146	3.4	4.3	5.0	4.2	0.8	6.8
VF_A1143	c2cds1147	1.5	0.7	1.4	1.2	0.4	1.2
VF_A1144	c2cds1148	87.8	50.6	34.1	57.5	27.5	53.9
VF_A1145	c2cds1149	38.2	16.8	16.5	23.9	12.5	38.6
VF_A1146	c2cds1150	1.2	1.8	2.8	1.9	0.8	4.7
VF_A1147	c2cds1151	38.9	32.8	33.6	35.1	3.3	78.6
VF_A1148	c2cds1152	28.1	27.6	36.2	30.6	4.8	22.8
VF_A1149	c2cds1153	16.5	5.5	5.1	9.1	6.5	2.5
VF_A1152	c2cds1154	15.9	8.1	3.6	9.2	6.3	1.8
VF_A1153	c2cds1155	7.7	5.0	6.2	6.3	1.4	13.2
VF_A1154	c2cds1156	418.5	511.7	550.8	493.7	68.0	132.2
VF_A1155	c2cds1157	9.3	11.7	19.2	13.4	5.2	18.6
VF_A1156	c2cds1158	14.3	14.6	13.4	14.1	0.6	24.0
VF_A1158	c2cds1159	80.8	70.7	61.9	71.1	9.5	269.2

VF_A1159	c2cds1160	15.0	5.1	10.1	10.1	5.0	38.6
VF_A1160	c2cds1161	24.6	19.5	24.0	22.7	2.8	17.4
VF_A1161	c2cds1162	109.8	123.7	121.5	118.3	7.5	76.8
VF_A1162	c2cds1163	69.2	23.2	21.6	38.0	27.0	31.4
VF_A1163	c2cds1164	381.3	116.2	103.8	200.4	156.8	218.4
VF_A1164	c2cds1165	596.2	142.9	171.9	303.7	253.7	282.0
VF_A1165	c2cds1166	70.3	42.0	32.4	48.2	19.7	44.2
VF_A1166	c2cds1167	66.0	41.0	27.9	45.0	19.4	40.6
VF_A1167	c2cds1168	130.5	53.0	36.3	73.3	50.3	38.4
VF_A1168	c2cds1169	147.9	44.2	32.5	74.9	63.5	43.1
VF_A1169	c2cds1170	14.8	14.6	13.9	14.4	0.5	21.1
VF_A1170	c2cds1171	218.6	87.1	104.8	136.8	71.3	156.7
VF_A1171	c2cds1172	49.6	111.8	129.5	97.0	42.0	172.2
VF_A1172	c2cds1173	34.3	71.6	76.1	60.7	22.9	134.0
VF_A1173	c2cds20	0.7	3.0	3.2	2.3	1.4	2.8
VF_A1174	c2cds21	1.6	3.0	0.8	1.8	1.1	1.7
VF_A1175	c2cds22	18.6	12.2	10.4	13.7	4.3	64.8
VF_A1176	c2cds41	4.1	4.4	2.0	3.5	1.3	17.6
VF_A1177	c2cds115	170.2	78.4	87.1	111.9	50.7	89.8
VF_A1180	c2cds379	43.1	6.3	5.6	18.3	21.5	2.2
VF_A1181	c2cds420	334.3	63.0	51.9	149.7	159.9	54.4
VF_A1184	c2cds575	47.6	31.1	21.4	33.3	13.3	15.2
VF_A1185	c2cds579	554.8	140.1	86.3	260.4	256.4	28.3
VF_A1186	c2cds580	47.1	6.4	2.8	18.8	24.6	25.5
VF_A1187	c2cds627	63.9	13.2	4.4	27.2	32.1	45.9
VF_A1188	c2cds708	0.0	0.0	0.2	0.1	0.1	0.3
VF_A1189	c2cds748	26.5	121.9	87.9	78.8	48.4	5.5
VF_A1190	c2cds829	3439.7	936.0	1014.5	1796.7	1423.4	221.1
VF_A1192	c2cds905	1.0	0.5	0.4	0.6	0.3	0.0
VF_A1193	c2cds914	4.1	3.3	2.8	3.4	0.7	0.9
VF_A1195	c2cds1089	91.3	54.5	65.7	70.5	18.8	489.1
VF_A1196	c2cds1132	0.3	0.4	0.2	0.3	0.1	0.7
VF_B0001	p1cds0	10.2	1.2	0.7	4.0	5.4	9.5
VF_B0002	p1cds1	17.9	5.8	4.8	9.5	7.3	7.1
VF_B0003	p1cds2	65.7	96.1	69.3	77.0	16.6	122.8
VF_B0004	p1cds3	52.7	46.3	39.9	46.3	6.4	97.2
VF_B0005	p1cds4	41.1	51.6	30.1	40.9	10.8	110.8
VF_B0006	p1cds5	28.5	39.2	37.7	35.1	5.8	102.2
VF_B0007	p1cds6	44.0	50.7	49.0	47.9	3.5	76.5
VF_B0008	p1cds7	3.5	2.5	3.1	3.1	0.5	3.3
VF_B0009	p1cds8	774.5	213.1	169.1	385.6	337.5	43.2
VF_B0010	p1cds9	280.2	126.7	91.7	166.2	100.3	29.0
VF_B0011	p1cds10	51.9	30.1	22.2	34.7	15.4	9.4

VF_B0012	p1cds11	358.9	193.7	147.7	233.4	111.0	176.5
VF_B0013	p1cds12	81.5	74.5	53.6	69.9	14.5	95.0
VF_B0015	p1cds14	26.5	34.2	41.5	34.0	7.5	13.9
VF_B0016	p1cds15	85.0	38.6	28.1	50.6	30.3	179.9
VF_B0017	p1cds16	38.9	25.3	16.4	26.9	11.4	50.5
VF_B0018	p1cds17	1128.6	1247.8	742.6	1039.6	264.1	379.9
VF_B0020	p1cds19	183.3	76.1	46.8	102.1	71.9	196.6
VF_B0021	p1cds20	67.1	23.2	35.9	42.1	22.6	133.7
VF_B0022	p1cds21	67.3	45.9	32.7	48.6	17.5	95.3
VF_B0023	p1cds22	78.8	25.1	11.9	38.6	35.4	88.1
VF_B0024	p1cds23	38.5	7.3	9.8	18.5	17.3	102.5
VF_B0025	p1cds24	21.3	6.6	8.1	12.0	8.1	91.6
VF_B0026	p1cds25	18.2	6.6	8.7	11.1	6.2	87.0
VF_B0027	p1cds26	18.0	5.6	7.3	10.3	6.7	82.9
VF_B0028	p1cds27	12.4	4.3	6.2	7.6	4.3	76.4
VF_B0029	p1cds28	11.7	4.7	6.3	7.6	3.6	66.7
VF_B0030	p1cds29	28.8	8.1	9.8	15.6	11.5	81.7
VF_B0031	p1cds30	37.7	12.6	13.8	21.4	14.1	115.2
VF_B0032	p1cds31	17.1	9.2	10.7	12.3	4.2	60.5
VF_B0033	p1cds32	59.7	25.5	23.8	36.3	20.3	125.5
VF_B0034	p1cds33	154.2	72.0	46.5	90.9	56.3	193.7
VF_B0035	p1cds34	282.0	84.6	94.8	153.8	111.1	186.5
VF_B0036	p1cds35	466.8	65.6	88.2	206.9	225.4	233.5
VF_B0037	p1cds36	6.9	2.3	2.4	3.9	2.7	8.9
VF_B0038	p1cds37	15.2	3.4	4.7	7.7	6.5	42.7
VF_B0039	p1cds39	20.4	9.3	10.7	13.5	6.0	31.1
VF_B0040	p1cds41	10.4	4.6	5.6	6.9	3.1	18.3
VF_B0041	p1cds42	11.3	2.6	3.8	5.9	4.7	18.5
VF_B0042	p1cds43	13.5	4.3	4.9	7.6	5.1	18.7
VF_B0043	p1cds44	15.2	2.8	4.4	7.5	6.8	16.1
VF_B0044	p1cds45	20.7	6.4	5.1	10.8	8.6	17.1
VF_B0045	p1cds46	92.1	20.7	16.4	43.0	42.5	38.3
VF_B0046	p1cds47	7.4	1.2	1.7	3.4	3.5	22.9
VF_B0047	p1cds48	10.0	0.9	2.1	4.3	5.0	32.0
VF_B0048	p1cds49	5.4	1.0	1.9	2.8	2.3	21.1
VF_B0050	p1cds51	12.7	2.0	2.6	5.8	6.0	13.7
VF_B0051	p1cds52	22.9	4.0	4.3	10.4	10.8	18.6
VF_B0052	p1cds53	17.4	5.3	2.2	8.3	8.0	16.6
VF_B0053	p1cds54	20.3	7.5	7.6	11.8	7.4	20.1
VF_B0054	p1cds55	4.7	1.5	1.9	2.7	1.8	12.3
VF_B0055	p1cds56	34.1	23.2	23.1	26.8	6.3	17.8

uid-associated V. fischeri (Vnt), seawater-suspended V. fischeri (Plk) and SWT medium-grown V.

SWT2_rpkn	SWT3_rpkn	SWT_rpkm	SWT_rpkm	Vnt1_rpkm	Vnt2_rpkm	Vnt3_rpkm	Vnt_rpkm_
93.6	80.1	86.3	6.8	0.0	24.7	20.9	15.2
145.9	131.4	130.2	16.4	39.3	85.1	93.9	72.8
335.2	384.5	491.1	228.6	306.1	220.9	137.8	221.6
114.7	134.3	184.9	105.1	259.7	148.2	127.2	178.3
6323.8	4406.6	6065.9	1546.6	473.3	5099.6	5001.5	3524.8
8.4	9.5	9.7	1.4	127.6	95.9	82.3	101.9
2.7	3.1	3.6	1.2	146.8	134.0	74.8	118.5
18.3	19.9	18.1	1.8	2730.3	1770.5	1104.6	1868.5
110.7	133.8	131.2	19.3	58.0	137.4	98.3	97.9
124.6	142.0	151.2	32.2	73.3	150.0	117.2	113.5
219.5	206.1	227.6	26.5	278.2	162.4	154.7	198.4
416.2	435.4	508.6	143.8	35.2	93.3	87.5	72.0
306.6	654.6	358.7	273.6	159.8	386.1	281.5	275.8
39.5	48.1	43.7	4.3	63.8	36.4	26.1	42.1
229.9	273.4	355.8	181.8	36.5	83.8	60.6	60.3
276.1	366.4	393.2	132.5	32.0	70.6	58.6	53.7
143.4	158.1	140.1	19.8	183.1	166.7	173.8	174.5
1734.5	1416.4	1232.4	615.1	115.7	994.4	612.1	574.1
32.1	24.1	28.5	4.1	106.8	89.0	82.4	92.7
560.2	193.4	276.9	252.1	1699.0	2617.3	1596.3	1970.9
64.6	48.5	47.4	17.8	152.3	93.2	79.5	108.3
22.5	30.1	22.3	7.9	45.1	44.7	27.3	39.0
226.3	185.2	186.8	38.7	208.0	318.3	428.4	318.2
10.2	7.4	8.3	1.7	685.4	1416.5	1917.4	1339.7
12.3	5.9	8.4	3.4	1444.8	2167.6	2475.4	2029.2
106.7	99.0	80.5	38.9	1.8	42.4	56.2	33.5
35.1	38.9	33.3	6.7	63.0	35.9	32.4	43.8
58.2	63.9	54.1	12.4	0.0	44.3	30.3	24.9
22.3	30.2	85.5	102.7	88.7	52.5	28.3	56.5
19.1	33.0	64.0	66.0	0.0	73.6	14.6	29.4
10.9	14.3	12.7	1.7	190.9	94.1	94.7	126.6
3.7	5.8	4.3	1.3	55.6	44.9	29.4	43.3
4.5	5.2	4.3	1.0	88.3	21.0	14.5	41.3
5.7	7.0	5.6	1.5	0.0	25.1	16.0	13.7
10.8	9.8	8.7	2.8	0.0	32.3	27.5	19.9
6.6	7.1	6.3	1.0	38.2	21.6	16.0	25.2
17.6	15.3	20.4	6.9	49.9	39.1	32.7	40.6
161.4	187.0	187.9	27.0	133.7	99.9	95.4	109.7
7.9	11.2	11.3	3.5	112.6	8.7	9.8	43.7
112.2	91.2	147.7	80.5	150.4	327.8	241.9	240.0

140.5	145.8	155.0	20.7	504.6	339.0	241.2	361.6
8.0	10.4	10.3	2.3	19.3	15.8	14.2	16.4
21.0	19.6	22.8	4.4	19.2	14.1	10.3	14.5
135.3	143.6	175.8	63.0	167.1	148.8	116.4	144.1
51.0	38.6	51.4	13.1	0.0	37.0	20.3	19.1
77.1	92.7	99.0	25.7	251.6	153.8	215.6	207.0
527.9	819.4	650.2	151.3	1850.3	523.4	456.4	943.4
578.6	576.3	507.3	121.5	829.7	417.4	589.4	612.2
313.2	267.1	296.1	25.2	286.2	297.7	350.0	311.3
29.6	34.8	32.6	2.7	0.0	33.6	20.1	17.9
409.7	454.0	384.8	84.5	327.4	70.4	83.8	160.5
220.3	225.6	221.6	3.6	101.3	23.9	27.9	51.0
481.7	435.8	450.0	27.5	163.1	58.9	55.6	92.5
552.5	522.6	645.5	187.7	761.1	972.7	774.6	836.1
368.0	380.7	451.3	133.5	438.6	475.4	404.2	439.4
26.8	27.4	29.7	4.5	291.5	279.1	270.6	280.4
136.3	115.6	124.9	10.5	109.4	104.6	86.1	100.0
84.3	83.2	83.5	0.7	233.5	58.7	42.5	111.6
164.1	164.9	189.0	42.4	26.8	97.5	67.3	63.9
169.5	167.7	162.9	9.9	89.9	68.9	90.6	83.1
244.3	239.8	216.0	45.3	107.0	63.6	79.0	83.2
50.7	57.9	62.4	14.5	54.4	26.0	43.2	41.2
327.2	265.2	279.0	43.0	80.2	65.2	57.1	67.5
31.3	33.9	33.7	2.2	63.2	41.6	29.3	44.7
46.7	51.9	59.9	18.5	17.8	28.4	20.9	22.4
7.6	7.3	7.7	0.5	3.0	13.9	13.7	10.2
19.4	18.1	22.8	7.2	22.6	21.7	19.0	21.1
11.2	7.8	17.1	13.2	0.0	11.3	6.0	5.8
1461.3	1159.6	1259.1	175.2	23.8	25.0	36.5	28.5
26.1	24.2	26.9	3.2	11.7	73.4	48.9	44.7
130.9	153.9	146.5	13.5	109.7	75.7	59.3	81.6
130.9	153.2	165.9	42.8	160.9	141.0	115.0	139.0
595.2	317.6	469.1	140.5	888.8	634.8	586.9	703.5
45.0	36.6	49.1	14.9	377.2	80.9	96.6	184.9
62.5	53.1	72.6	26.1	188.9	95.8	129.1	137.9
54.6	55.1	71.8	29.3	52.4	101.6	107.0	87.0
121.6	111.4	127.8	20.2	75.9	90.9	86.3	84.3
140.4	124.3	113.2	34.0	150.4	68.9	79.7	99.7
54.7	48.1	49.0	5.3	93.4	57.5	50.6	67.2
9285.2	5489.3	5443.7	3864.6	363.1	1353.5	1287.8	1001.5
1255.9	1061.0	1081.1	165.7	416.1	1647.9	1861.4	1308.5
280.1	226.4	210.8	78.4	1064.0	1266.2	1431.9	1254.0
49.2	40.4	43.8	4.8	437.1	399.7	580.0	472.3

15.5	16.6	19.8	6.5	179.6	162.7	165.6	169.3
13.2	16.1	17.6	5.3	0.0	43.4	41.7	28.4
16.1	17.4	18.1	2.4	105.3	35.2	57.5	66.0
35.1	48.6	52.1	18.9	0.0	57.6	54.6	37.4
2.2	2.1	1.8	0.6	0.0	5.5	2.9	2.8
279.3	240.9	247.6	28.9	351.3	294.1	340.5	328.6
25.1	28.9	28.8	3.7	13.6	10.2	8.6	10.8
40.5	34.3	35.7	4.3	13.6	7.2	8.1	9.6
17.3	17.5	20.2	4.8	46.6	11.5	10.4	22.8
61.5	36.0	42.9	16.2	4.2	88.5	102.0	64.9
472.1	458.6	473.3	15.4	221.8	153.9	113.1	162.9
304.6	277.2	431.3	243.7	531.5	681.1	835.5	682.7
40.7	54.8	43.7	10.0	94.9	56.8	40.3	64.0
126.1	127.2	112.5	24.4	7.7	37.5	62.7	36.0
115.1	83.1	95.4	17.3	158.2	31.7	43.4	77.8
15.3	22.2	22.8	7.9	0.0	12.2	15.7	9.3
178.0	139.6	166.6	23.5	174.2	102.2	117.7	131.4
665.8	663.4	720.2	96.2	1716.4	997.1	1088.0	1267.2
174.2	159.7	175.4	16.3	75.5	291.1	290.4	219.0
11.6	9.3	10.5	1.1	55.3	91.8	89.1	78.7
15.6	11.9	15.0	2.9	0.0	50.2	44.1	31.5
2.0	1.8	1.6	0.6	67.3	28.1	22.0	39.1
120.6	123.5	143.2	36.7	80.4	132.3	124.3	112.4
104.4	85.3	123.3	50.2	29.7	254.9	295.9	193.5
41.6	42.1	53.7	20.5	5.2	66.7	73.7	48.5
15.5	17.6	15.9	1.5	39.6	28.3	23.4	30.4
479.5	413.1	364.3	145.9	264.7	124.6	160.3	183.2
34.1	38.0	30.8	9.3	61.0	13.9	13.2	29.4
2.9	1.9	3.1	1.3	30.6	6.8	5.2	14.2
1.7	2.4	2.0	0.4	0.0	7.1	8.8	5.3
61.6	55.8	57.5	3.5	102.8	57.5	50.3	70.2
168.1	158.7	141.8	37.7	341.0	83.2	92.6	172.3
104.4	127.2	131.0	28.8	13.1	5.4	5.8	8.1
60.9	71.9	73.6	13.6	0.0	18.8	23.3	14.0
32.6	38.5	40.9	9.8	75.2	19.5	29.5	41.4
42.4	44.6	46.3	5.1	0.0	24.6	31.9	18.8
48.2	63.6	68.0	22.3	41.9	18.9	23.8	28.2
87.2	105.3	98.4	9.8	0.0	60.6	67.6	42.8
2938.6	2355.8	2969.0	628.9	1111.6	3335.0	3469.2	2638.6
2590.2	3640.2	3277.0	595.1	3436.4	3641.3	3976.4	3684.7
83.3	81.4	72.2	17.6	9.8	46.3	34.9	30.3
33.3	35.4	30.7	6.3	0.0	18.7	16.0	11.6
30.7	32.7	41.4	16.9	54.4	25.2	18.6	32.7

47.4	33.3	43.5	8.9	112.3	41.8	49.0	67.7
38.8	44.9	53.3	20.0	41.4	25.3	27.7	31.5
46.5	53.8	59.2	16.1	4.3	30.9	29.5	21.5
54.7	60.2	65.2	13.7	0.0	49.8	45.3	31.7
104.1	90.8	84.4	23.6	50.9	33.7	27.1	37.2
72.0	73.6	88.5	27.2	160.3	60.8	57.6	92.9
53.5	62.7	58.8	4.8	32.1	45.0	47.9	41.7
112.5	93.1	96.9	14.1	0.0	66.6	73.3	46.6
556.3	683.7	558.8	123.6	1057.9	383.8	273.5	571.8
402.1	413.5	379.6	49.3	690.6	178.8	176.9	348.8
258.9	300.3	282.8	21.4	65.3	161.2	202.4	143.0
296.3	310.1	288.8	25.8	103.3	123.2	139.1	121.9
166.4	183.9	171.5	10.8	29.5	106.7	94.7	77.0
312.2	325.6	307.2	21.3	142.9	139.7	148.2	143.6
221.0	270.2	252.8	27.6	176.0	150.3	145.9	157.4
280.0	235.6	245.1	31.2	180.3	139.4	140.3	153.4
450.3	392.2	396.0	52.5	706.6	163.1	110.7	326.8
91.0	79.0	83.3	6.6	115.9	76.4	36.8	76.4
64.8	29.4	36.5	25.6	84.8	12.0	5.7	34.2
32.9	17.8	23.9	7.9	71.8	26.6	14.7	37.7
272.7	273.5	258.9	24.6	46.4	195.4	181.3	141.1
4.5	3.9	3.8	0.7	25.1	6.7	7.2	13.0
6.1	9.1	8.4	2.1	247.0	26.6	12.7	95.4
69.7	75.5	77.5	8.9	368.5	75.2	74.5	172.7
15.9	24.4	25.8	10.6	19.9	9.0	10.6	13.2
2.3	2.7	6.9	7.6	0.0	1.1	1.0	0.7
2.6	5.1	5.2	2.6	0.0	2.7	1.2	1.3
9989.8	6378.3	7115.6	2585.7	6239.8	2467.4	3765.1	4157.4
47.4	51.3	65.8	28.5	57.4	23.1	23.0	34.5
60.2	81.0	89.4	34.1	124.6	49.4	27.0	67.0
54.7	64.0	86.1	46.6	0.0	15.3	9.8	8.4
48.7	73.9	77.1	30.1	39.9	5.8	7.0	17.6
115.5	181.8	151.0	33.4	20.5	25.0	24.7	23.4
68.0	145.0	101.9	39.3	43.6	19.4	15.6	26.2
58.9	114.4	84.1	28.1	0.0	23.1	21.4	14.8
45.8	46.4	44.0	3.8	64.6	15.0	9.9	29.8
19.2	17.1	14.4	6.7	53.6	6.8	4.2	21.6
23.9	21.1	16.3	10.9	67.9	7.6	3.0	26.2
90.2	205.0	130.2	64.8	345.3	36.0	16.5	132.6
16.2	8.2	8.7	7.2	97.0	6.3	2.1	35.1
81.7	94.6	71.8	29.1	158.0	21.3	5.8	61.7
135.7	166.5	130.0	39.7	48.1	36.2	8.6	30.9
523.8	579.8	494.7	102.8	15.5	75.9	55.1	48.8

229.2	207.6	190.3	49.9	117.3	65.2	29.6	70.7
240.0	273.2	254.2	17.2	145.9	70.1	47.3	87.8
273.6	302.4	331.8	77.3	61.3	73.9	40.4	58.5
184.6	169.5	198.2	37.4	169.4	121.3	51.8	114.2
165.9	205.3	183.4	20.1	205.4	348.4	215.7	256.5
423.8	340.7	335.8	90.5	282.4	268.8	249.0	266.7
333.2	307.4	299.7	37.9	339.5	147.6	161.6	216.2
565.6	524.4	515.1	55.7	374.5	267.7	291.4	311.2
227.2	229.1	219.7	14.7	238.6	223.8	197.7	220.0
107.0	86.7	102.4	14.0	339.7	105.1	65.3	170.0
283.6	168.9	180.9	97.2	583.4	182.7	109.0	291.7
144.3	93.4	106.3	33.4	215.1	128.1	82.7	142.0
24.6	11.6	15.1	8.3	103.5	43.0	23.7	56.7
67.4	40.8	44.1	21.9	530.0	60.1	26.6	205.6
395.8	347.7	351.1	43.1	324.0	240.8	179.9	248.2
166.2	173.5	207.8	66.0	295.5	101.6	80.1	159.1
177.4	162.0	180.2	19.8	88.2	72.1	62.7	74.3
142.0	122.5	132.8	9.8	174.7	95.0	88.1	119.3
182.4	182.6	172.3	17.6	99.6	127.9	145.4	124.3
96.5	100.1	95.3	5.6	445.1	111.8	84.8	213.9
91.4	76.0	77.5	13.1	134.5	112.6	88.8	112.0
56.5	54.4	54.7	1.7	62.3	77.8	67.3	69.1
318.0	297.0	292.3	28.4	179.1	181.0	228.2	196.1
912.5	1109.0	877.1	251.5	145.5	352.8	364.7	287.7
4.9	5.3	6.3	2.0	0.7	7.6	6.7	5.0
489.0	516.3	528.7	47.1	242.7	277.2	348.9	289.6
836.7	827.4	873.2	71.3	196.0	231.3	366.8	264.7
1266.4	1571.4	1277.1	289.1	458.0	1139.0	1542.3	1046.4
143.7	144.4	124.2	34.4	126.7	163.5	140.9	143.7
0.7	1.1	0.7	0.4	3.2	64.3	88.0	51.8
98.6	85.1	114.1	39.1	27.8	82.5	72.9	61.1
804.1	805.4	742.4	107.9	664.3	568.3	329.3	520.6
534.0	639.1	457.7	229.3	240.9	199.4	167.5	202.6
33.7	34.4	37.9	6.7	149.2	58.6	64.3	90.7
114.1	75.6	112.3	35.9	69.6	107.9	96.7	91.4
26.3	30.5	28.1	2.1	4.3	54.4	25.7	28.1
21.9	22.5	20.2	3.4	87.9	25.0	23.9	45.6
2.5	3.4	5.3	4.2	2.2	8.8	11.4	7.5
24.9	24.1	28.5	6.9	38.3	17.8	21.8	26.0
33.4	29.7	32.8	2.8	258.1	41.9	42.0	114.0
39.1	38.4	38.0	1.3	52.6	50.2	57.6	53.5
357.3	371.1	351.5	23.1	626.6	318.1	387.3	444.0
531.0	511.3	565.9	78.2	222.8	399.8	503.8	375.5

130.4	83.4	103.2	24.3	0.0	41.8	51.0	30.9
40.8	48.4	41.2	7.0	78.5	35.0	33.5	49.0
808.0	924.9	854.8	61.8	627.5	625.7	720.8	658.0
104.6	140.5	107.0	32.4	165.4	140.4	121.7	142.5
117.4	120.0	96.4	38.7	587.6	111.7	149.2	282.8
107.9	95.0	81.3	35.5	125.6	100.7	101.7	109.3
5740.7	6194.4	6648.8	1201.6	2552.9	3276.6	2883.7	2904.4
4942.1	4148.3	5199.7	1201.0	802.1	2371.3	2162.7	1778.7
775.4	836.2	892.2	152.6	443.2	547.6	644.5	545.1
13633.2	15851.4	15211.7	1375.2	2500.3	2947.6	3082.5	2843.4
4546.4	5505.1	5850.7	1507.1	1649.2	2140.5	1865.5	1885.0
4514.4	5716.4	5302.2	682.6	1021.4	1342.3	1420.9	1261.5
2955.5	4749.9	4100.4	994.5	238.0	686.4	638.3	520.9
2394.6	3742.8	2903.0	732.7	1631.6	338.1	275.6	748.4
4655.0	6718.0	5350.7	1184.2	380.5	561.3	586.0	509.3
5518.2	6665.6	5689.2	903.0	265.2	565.9	614.8	482.0
4583.1	8966.4	6038.3	2535.8	700.2	629.2	618.6	649.3
3532.0	6006.7	4193.6	1589.2	492.3	661.8	596.7	583.6
3705.8	6814.8	4559.9	1971.9	679.2	898.3	1014.0	863.8
3422.7	5379.7	4092.5	1115.1	3999.4	662.5	764.2	1808.7
9840.0	12802.0	9810.0	3007.1	848.5	4086.9	3972.3	2969.2
3540.3	4065.6	5144.6	2338.6	693.1	1728.7	1876.0	1432.6
5298.6	4981.2	6406.9	2200.2	1199.3	2032.6	1970.8	1734.2
4610.9	4274.9	5633.5	2069.0	868.4	1271.3	1303.0	1147.6
3281.7	3350.1	3593.0	481.1	329.7	796.3	790.3	638.8
4284.6	4930.6	5327.9	1288.7	861.4	806.4	878.5	848.8
5116.3	5413.7	5795.5	930.8	478.6	711.5	767.5	652.6
2989.5	3215.9	3544.4	773.3	177.3	422.7	392.4	330.8
5007.7	4844.1	5350.5	740.0	284.2	508.1	497.7	430.0
3410.4	4576.4	3861.0	626.5	18.7	483.9	551.8	351.5
6396.0	7090.8	6559.7	471.1	427.8	1000.5	1050.3	826.2
4334.8	5043.0	4849.0	449.7	643.0	901.8	1013.0	852.6
4731.6	5972.8	5316.8	623.6	1062.0	2004.3	2114.8	1727.0
2833.8	3099.2	3950.9	1710.3	609.2	1215.4	1081.2	968.6
2715.9	3055.6	3726.6	1466.4	126.5	508.9	493.5	376.3
3287.1	3683.2	4236.5	1316.4	543.4	488.0	417.7	483.0
3892.0	4523.8	4731.9	961.0	380.5	767.7	748.5	632.2
2797.4	3576.3	3244.5	402.0	182.4	1011.1	851.7	681.7
359.4	239.9	301.1	59.8	678.6	193.2	210.7	360.8
106.8	105.3	99.2	11.8	190.9	104.1	84.9	126.6
86.9	70.8	75.7	9.7	507.9	194.1	189.4	297.1
22.3	23.1	24.3	2.7	68.3	74.6	59.3	67.4
3.0	3.1	3.4	0.6	35.6	22.3	11.8	23.3

6.7	6.7	7.2	0.8	25.4	20.8	12.4	19.5
44.0	47.2	48.2	4.7	300.0	259.9	364.6	308.1
48.8	48.8	50.9	3.7	495.2	315.9	496.9	436.0
270.3	329.6	248.8	93.4	345.5	129.2	137.2	204.0
72.0	55.4	85.6	38.9	152.1	73.0	70.4	98.5
565.6	283.3	602.4	339.0	735.8	846.9	817.2	800.0
150.3	162.9	167.6	20.0	33.3	114.5	132.3	93.4
3000.5	1984.2	2190.7	728.8	392.8	501.1	477.8	457.3
200.3	220.6	198.8	22.6	178.8	139.5	140.9	153.1
2460.3	3081.7	3345.1	1041.9	4387.0	2195.4	2153.5	2912.0
4338.1	4285.5	4527.1	373.9	1494.7	4304.1	3890.8	3229.9
72.6	76.4	87.3	22.3	149.1	162.6	208.5	173.4
24.4	25.1	19.8	8.6	0.0	5.6	3.9	3.2
17.7	12.3	12.2	5.5	0.0	7.0	4.7	3.9
73.0	75.3	73.8	1.3	76.7	51.8	44.0	57.5
11.4	10.4	11.0	0.5	17.9	7.9	6.3	10.7
169.5	187.4	191.4	24.1	106.8	199.2	228.1	178.0
114.8	100.1	113.2	12.4	65.8	36.1	38.4	46.8
112.8	108.9	111.4	2.2	47.8	43.4	52.9	48.0
105.9	129.8	123.1	15.1	125.8	94.6	86.9	102.5
50.3	58.7	60.6	11.4	427.6	92.0	90.6	203.4
16.1	13.8	19.6	8.0	392.4	107.7	143.9	214.7
157.4	87.0	159.9	74.1	0.0	17.2	10.2	9.1
171.4	123.4	171.4	48.0	26.9	16.8	16.2	20.0
176.6	122.1	172.2	47.9	0.0	38.8	27.2	22.0
170.6	138.8	164.2	22.8	33.3	60.0	50.7	48.0
18.9	21.1	19.2	1.8	0.0	29.2	42.7	24.0
60.3	54.4	49.7	13.6	37.4	43.2	49.8	43.5
24.8	23.3	24.1	0.7	155.2	16.5	22.5	64.8
21.1	22.5	23.2	2.5	99.6	18.9	24.8	47.8
65.0	63.0	65.7	3.0	46.5	58.5	63.4	56.1
43.6	53.2	57.2	16.0	55.9	46.6	61.8	54.8
3.0	4.4	4.0	0.9	16.6	18.2	24.4	19.7
134.1	202.8	153.6	42.8	457.8	462.9	613.3	511.3
87.2	86.9	104.3	29.9	2.4	92.5	71.2	55.4
65.9	66.5	83.9	30.6	495.7	119.1	87.0	234.0
64.9	76.6	76.6	11.7	196.5	97.9	100.2	131.5
181.8	184.1	192.5	16.6	138.9	152.5	115.4	135.6
51.8	44.3	39.8	14.8	315.4	437.8	577.1	443.4
2.9	3.4	3.2	0.3	67.9	91.0	62.6	73.8
19.7	17.1	16.0	4.3	187.2	71.6	54.8	104.5
27.1	16.7	19.0	7.1	86.8	101.8	82.1	90.2
32.5	21.6	26.8	5.5	122.9	288.1	300.5	237.2

1611.1	1407.9	1694.4	335.9	454.9	525.2	487.9	489.3
193.0	165.0	153.7	46.1	203.2	138.9	134.1	158.7
1.7	2.5	2.8	1.3	0.0	3.7	1.9	1.9
14.4	10.5	14.7	4.4	0.0	11.7	8.3	6.7
4.7	2.0	4.5	2.4	64.9	16.2	10.3	30.5
794.3	805.4	986.9	324.1	162.2	203.7	176.6	180.8
2.7	3.1	3.6	1.1	296.0	316.9	214.1	275.6
4.6	3.0	4.2	1.0	156.8	191.3	161.4	169.8
1.2	1.2	1.3	0.2	183.6	90.0	61.8	111.8
4.9	2.8	4.3	1.3	242.4	63.6	59.5	121.8
267.9	227.9	205.8	75.6	73.1	37.5	33.5	48.0
46.0	64.3	54.4	9.3	32.3	68.6	59.4	53.4
27.9	34.6	29.4	4.7	58.7	48.3	52.8	53.3
6.9	6.6	7.1	0.7	9.8	36.5	34.5	26.9
44.7	29.7	34.1	9.1	250.3	159.9	221.9	210.7
624.3	471.6	578.5	92.9	164.5	81.6	84.1	110.0
103.2	147.1	128.8	22.8	9672.7	1598.7	495.3	3922.2
44.9	25.8	40.8	13.4	381.4	143.6	142.2	222.4
28.6	34.5	29.4	4.8	198.6	41.4	35.0	91.6
15.8	20.5	17.9	2.4	103.8	15.5	13.9	44.4
45.0	41.7	57.5	24.6	331.6	175.8	121.8	209.7
60.6	62.4	60.4	2.1	336.5	104.4	92.2	177.7
40.4	43.1	46.6	8.6	171.5	107.4	62.4	113.8
17.0	17.9	22.5	8.8	89.6	77.2	54.5	73.8
10.8	9.4	13.7	6.3	31.8	11.2	5.7	16.3
73.5	76.4	86.0	19.4	39.3	27.6	26.6	31.2
356.9	297.9	374.4	86.5	168.8	321.2	283.8	257.9
19.0	15.0	18.7	3.6	72.0	37.1	29.0	46.0
46.1	39.3	53.5	19.1	104.8	49.6	55.7	70.0
40.9	36.6	42.3	6.6	67.9	26.3	36.9	43.7
17.6	19.2	20.9	4.4	25.8	12.1	12.9	16.9
6.7	6.3	8.2	3.0	0.0	11.1	5.9	5.7
3.6	5.8	6.2	2.9	68.8	19.0	8.0	31.9
27.6	27.7	28.8	2.0	111.0	40.6	38.3	63.3
47.7	55.1	48.1	6.8	343.2	76.6	90.8	170.2
50.9	56.0	48.2	9.4	243.4	70.7	67.3	127.1
49.1	42.5	39.4	11.5	145.2	67.5	86.0	99.6
320.8	331.4	358.8	57.0	56.7	100.1	79.1	78.6
14.0	19.9	16.2	3.2	58.0	128.8	76.1	87.6
29.5	23.4	28.5	4.6	67.9	53.8	42.0	54.6
60.5	57.8	68.2	15.7	83.5	77.2	44.6	68.4
27.9	37.7	39.7	12.9	50.9	34.6	13.7	33.0
33.4	30.5	36.5	8.1	0.0	19.8	14.2	11.3

66.7	77.8	78.4	12.1	79.9	32.8	30.2	47.6
32.6	51.3	45.4	11.2	31.7	29.1	16.1	25.7
71.4	88.1	79.1	8.4	63.6	38.6	29.5	43.9
65.9	80.2	78.6	12.0	83.8	30.4	24.1	46.1
53.6	46.0	51.9	5.3	82.2	26.5	22.2	43.7
43.0	42.4	44.0	2.3	159.8	24.6	14.9	66.4
178.3	203.2	181.6	20.3	0.0	72.5	50.7	41.1
1951.7	1733.6	1559.0	503.3	188.0	239.1	167.4	198.2
20.1	16.5	18.3	1.8	0.0	15.8	13.1	9.6
19.0	19.5	16.5	4.9	0.0	13.3	13.6	9.0
3.3	8.9	5.9	2.8	0.0	6.4	4.0	3.5
8.8	6.7	7.2	1.4	28.5	6.7	5.1	13.5
21.7	21.1	19.1	4.1	129.1	28.4	38.2	65.2
430.3	402.5	425.2	20.6	469.2	319.5	343.5	377.4
74.2	80.7	97.9	35.6	64.5	43.0	38.7	48.7
55.6	58.1	76.7	34.4	0.0	25.8	20.9	15.6
96.5	87.2	88.6	7.3	50.6	42.1	44.3	45.7
266.0	216.6	207.2	64.0	132.7	107.5	88.4	109.5
52.0	63.5	55.4	7.0	126.3	54.2	45.5	75.3
119.3	81.7	97.1	19.7	290.2	141.6	191.8	207.9
130.3	118.6	117.2	13.8	13.2	106.6	109.3	76.4
303.1	290.5	276.1	36.4	560.5	293.6	509.9	454.7
96.5	114.2	107.0	9.3	66.7	78.6	63.7	69.7
52.0	32.8	43.5	9.7	90.9	86.3	87.3	88.2
18.1	37.3	29.8	10.3	0.0	18.3	8.2	8.9
50.3	58.1	57.8	7.3	0.0	29.1	25.9	18.3
89.3	113.5	101.7	12.1	73.2	141.6	160.6	125.1
1803.3	1105.8	1138.4	649.3	1654.3	1565.6	1502.2	1574.0
370.7	319.1	316.3	55.7	244.8	367.9	494.5	369.1
82.9	94.2	94.8	12.2	146.7	167.7	207.2	173.9
84.6	117.2	100.5	16.3	182.3	187.8	263.5	211.2
95.5	113.9	107.1	10.1	616.2	288.1	432.3	445.5
101.4	120.2	120.2	18.8	277.8	246.1	345.1	289.7
91.9	118.7	116.9	24.2	85.1	158.5	133.4	125.7
45.6	42.7	54.5	18.0	75.0	73.8	60.8	69.9
44.0	34.3	39.4	4.9	91.4	50.0	64.4	68.6
19.7	19.5	19.8	0.2	122.7	21.2	28.8	57.5
28.1	22.6	24.9	2.8	79.3	31.7	33.0	48.0
48.7	48.7	48.9	0.3	701.9	66.3	36.5	268.2
33.8	40.1	35.7	3.9	164.1	66.3	49.5	93.3
287.2	216.6	294.9	82.4	2289.8	666.3	834.7	1263.6
214.7	242.6	268.2	69.9	290.6	352.7	432.2	358.5
65.3	60.7	80.6	30.7	220.7	119.5	76.4	138.9

8.9	6.9	9.4	2.7	51.3	15.1	9.8	25.4
466.7	452.3	666.1	357.9	184.0	407.8	351.5	314.4
58.0	37.1	42.2	14.0	101.3	111.0	94.6	102.3
39.6	32.6	36.2	3.5	172.4	98.8	107.1	126.1
97.9	63.9	75.8	19.1	27.9	23.6	19.8	23.8
26.6	24.2	28.0	4.7	33.1	6.6	3.7	14.5
221.0	176.3	215.0	36.1	513.5	353.7	369.9	412.4
26.1	34.4	30.0	4.1	61.2	103.5	84.4	83.0
319.3	315.8	411.5	162.7	175.5	132.0	119.0	142.2
48.0	61.0	68.7	25.5	55.5	23.4	16.1	31.7
553.1	581.8	616.3	85.8	86.2	217.9	259.4	187.8
98.1	87.7	86.9	11.6	371.5	96.3	76.6	181.5
71.3	68.8	68.7	2.7	74.9	47.2	45.0	55.7
55.7	40.9	57.4	17.5	0.0	66.4	53.4	39.9
56.5	49.2	56.6	7.4	0.0	160.5	94.0	84.8
30.9	20.1	29.2	8.4	69.5	95.1	73.4	79.3
25.8	34.6	31.8	5.2	46.3	9.5	6.6	20.8
325.6	290.1	326.4	36.8	1145.6	340.2	292.1	592.7
18.6	22.7	29.1	14.8	101.1	15.5	12.4	43.0
28.8	36.2	32.6	3.7	34.1	61.6	43.9	46.5
31.3	33.8	39.2	11.7	127.5	38.1	37.0	67.5
65.4	52.0	67.0	15.8	18.8	44.8	60.6	41.4
17.1	20.2	20.9	4.2	122.0	28.3	22.5	57.6
95.8	94.7	83.1	21.1	303.6	97.4	78.5	159.8
93.9	79.5	84.7	8.0	68.7	80.6	70.7	73.3
101.0	109.9	95.7	17.5	139.6	105.1	98.2	114.3
88.3	73.8	74.8	12.9	110.4	42.2	52.9	68.5
106.2	104.2	97.9	12.6	111.2	122.9	117.5	117.2
87.3	89.1	81.6	11.4	245.4	68.8	81.1	131.8
80.4	64.0	64.7	15.5	102.6	103.0	162.0	122.5
107.6	93.4	87.5	23.6	202.7	127.8	159.0	163.2
291.8	297.0	284.6	17.2	191.6	174.9	259.4	208.6
103.6	120.1	117.5	12.8	42.9	88.8	101.5	77.7
7.0	7.8	6.7	1.3	0.0	11.7	10.2	7.3
7.2	15.1	13.1	5.2	64.9	4.3	3.1	24.1
70.8	164.9	141.7	62.6	135.9	331.0	295.4	254.1
372.8	370.6	522.9	261.8	108.4	187.8	142.3	146.2
67.8	50.0	58.6	8.9	147.3	82.6	66.8	98.9
831.8	1331.6	1048.5	256.4	653.0	915.0	1198.6	922.2
2402.9	3395.1	2944.5	502.3	653.7	1418.3	1541.3	1204.4
65.7	64.1	85.2	35.2	38.8	133.8	112.1	94.9
19.8	15.9	16.4	3.2	19.1	22.9	13.8	18.6
31.1	23.1	24.1	6.5	134.8	118.5	76.4	109.9

101.0	115.7	103.4	11.3	47.5	101.1	57.0	68.5
19.5	21.3	25.1	8.1	91.2	34.0	20.6	48.6
104.9	124.8	125.9	21.5	422.7	372.2	335.1	376.7
18.7	16.1	20.7	5.8	114.0	45.0	55.0	71.3
2342.3	2225.5	3147.4	1496.8	2242.0	2927.8	2594.6	2588.1
171.7	163.2	230.7	109.7	164.4	214.6	190.2	189.7
582.8	660.7	656.9	72.3	152.6	216.7	170.5	179.9
156.9	160.6	143.2	26.9	143.3	431.6	262.6	279.2
47.1	50.1	43.3	9.4	189.3	49.8	50.4	96.5
585.2	466.8	439.1	161.6	185.7	412.0	432.2	343.3
59.9	50.8	54.0	5.1	87.2	61.3	52.1	66.9
22.5	27.1	25.9	2.9	92.0	92.1	93.8	92.7
64.2	47.7	66.2	19.5	135.8	127.2	116.8	126.6
80.3	79.3	81.4	2.9	196.0	95.8	86.5	126.1
2.2	3.5	3.1	0.8	168.2	641.0	355.6	388.3
44.7	50.8	45.4	5.1	95.6	61.3	43.8	66.9
91.0	114.2	93.0	20.2	324.6	140.5	140.1	201.8
1855.4	1565.3	1926.4	401.3	1672.3	3710.6	3343.7	2908.9
15.2	14.2	17.3	4.5	56.8	40.4	30.8	42.7
130.8	128.3	141.2	20.2	259.5	276.4	248.6	261.5
308.7	325.4	395.1	135.4	159.2	172.4	177.0	169.5
214.4	223.2	267.4	84.3	262.9	331.2	270.3	288.1
65.7	49.0	60.6	10.1	135.9	70.8	75.8	94.2
82.0	76.0	77.4	4.1	74.7	58.5	52.9	62.0
104.8	106.7	103.9	3.3	275.4	70.1	64.9	136.8
86.0	78.5	133.2	88.4	1.0	57.4	53.5	37.3
154.7	128.2	201.3	104.6	57.9	51.2	54.2	54.5
15.2	18.0	20.7	7.2	34.3	21.8	15.9	24.0
6174.8	5128.2	5773.5	564.3	2773.0	3936.9	6112.2	4274.0
821.9	908.1	857.7	44.9	2109.6	767.8	769.1	1215.5
93.8	69.5	95.4	26.7	332.2	429.9	291.7	351.3
277.4	279.7	272.3	10.9	3073.0	427.4	610.5	1370.3
623.1	588.9	616.3	24.7	553.1	565.4	751.2	623.2
43.5	43.0	45.2	3.4	6.7	29.4	33.0	23.0
320.8	329.4	304.4	36.1	96.3	93.1	90.7	93.4
672.7	644.0	801.6	248.6	430.9	625.2	519.3	525.1
439.9	431.7	480.7	78.0	228.6	250.7	212.8	230.7
587.3	560.1	581.3	19.0	161.2	205.0	182.1	182.8
987.8	886.0	857.7	146.3	186.8	143.3	150.3	160.2
169.0	171.8	167.8	4.7	137.4	242.6	240.9	207.0
159.7	136.9	146.7	11.7	147.3	219.6	242.5	203.2
3806.9	3476.8	3831.8	368.0	2320.9	5282.3	4437.9	4013.7
819.6	889.0	990.8	238.9	227.9	420.6	398.9	349.1

203.0	165.8	174.4	25.5	225.6	115.5	88.0	143.0
27.7	37.3	25.9	12.4	25.5	40.5	35.5	33.9
21.2	26.5	19.6	7.8	32.4	10.5	9.4	17.4
25.1	28.9	31.6	8.2	44.8	28.6	17.6	30.3
200.5	256.1	180.2	87.8	340.3	76.8	57.7	158.2
280.7	263.5	209.2	109.2	102.3	146.3	138.2	128.9
0.3	0.8	0.6	0.2	76.7	0.4	1.2	26.1
39.4	49.5	50.6	11.7	407.1	106.3	73.6	195.7
37.2	42.0	36.8	5.4	95.3	78.6	56.1	76.7
137.3	131.9	169.9	61.2	130.5	199.3	136.9	155.5
29.9	35.1	29.4	6.0	151.5	120.0	105.5	125.6
2314.6	3060.1	2622.9	389.1	211.4	838.4	627.5	559.1
1259.0	855.3	823.4	452.4	491.7	1501.2	1148.2	1047.0
1370.2	1430.1	1100.6	519.6	826.7	727.6	580.7	711.7
722.5	696.1	546.2	282.9	52.2	127.4	103.4	94.3
899.5	890.9	730.1	285.9	79.1	57.0	63.5	66.5
399.9	618.3	422.2	185.9	162.6	119.4	161.2	147.7
45.7	82.5	73.8	24.9	307.9	305.4	212.4	275.2
93.0	62.0	83.9	19.0	151.3	92.4	64.0	102.6
0.1	0.4	0.2	0.2	23.0	4.9	0.6	9.5
0.8	0.9	0.8	0.1	0.0	4.3	3.7	2.7
1.3	0.9	1.2	0.3	14.5	6.2	5.5	8.7
2.5	2.3	2.4	0.1	64.2	11.5	6.7	27.5
2.4	3.1	2.8	0.4	54.7	4.5	3.8	21.0
2.2	3.5	2.6	0.8	39.1	5.8	5.8	16.9
1.6	2.2	1.6	0.5	77.0	8.3	6.4	30.6
1.7	3.6	2.6	0.9	0.0	8.7	5.6	4.8
1.4	4.3	2.7	1.5	71.5	9.8	4.5	28.6
2.2	1.0	1.6	0.6	0.0	11.4	6.9	6.1
4.8	3.9	4.2	0.5	61.7	10.0	7.2	26.3
14.5	20.1	15.7	3.9	56.1	24.0	22.3	34.1
7.8	13.6	10.8	2.9	45.4	20.0	16.8	27.4
12.3	9.7	11.2	1.3	103.4	20.3	15.4	46.4
33.6	35.3	35.8	2.4	230.5	54.5	42.1	109.0
76.6	94.3	89.4	11.2	136.7	81.8	70.1	96.2
59.0	58.1	55.6	5.2	16.2	50.0	40.1	35.4
2305.9	2707.9	3220.5	1252.3	1519.9	3367.2	4289.9	3059.0
8.4	17.9	18.4	10.2	161.5	36.0	21.2	72.9
31.6	35.9	34.2	2.3	56.1	55.1	32.0	47.8
4.2	4.0	4.9	1.4	90.3	18.9	11.3	40.1
47.9	37.2	37.4	10.4	310.8	196.5	263.0	256.8
30.6	31.4	40.1	15.8	31.0	14.3	13.3	19.5
551.0	475.5	676.0	284.3	124.2	182.6	128.8	145.2

193.4	225.6	254.3	79.3	156.4	155.6	122.5	144.8
293.5	337.5	366.0	90.2	734.9	331.9	284.7	450.5
1839.4	1519.5	1692.3	161.5	1024.8	1444.0	1075.6	1181.4
102.7	44.6	67.1	31.2	50.8	69.2	49.5	56.5
54.3	32.7	43.2	10.8	191.3	114.5	104.5	136.8
43.1	52.8	46.3	5.7	36.2	40.0	29.5	35.2
199.3	148.6	150.6	47.8	1088.4	150.8	206.6	481.9
173.4	148.3	173.8	25.7	250.5	163.9	180.3	198.3
126.5	123.5	108.3	28.8	123.3	61.9	74.3	86.5
430.1	259.9	324.2	92.4	516.2	319.8	246.2	360.7
37.2	48.9	46.6	8.4	65.3	39.7	34.2	46.4
45.1	66.2	63.9	17.6	87.4	107.1	62.4	85.6
188.8	184.1	194.2	13.7	292.9	158.1	190.8	213.9
2863.4	4164.2	3517.8	650.4	742.8	1617.3	1260.8	1207.0
4198.9	5666.4	4592.0	941.6	2405.5	2150.3	1933.2	2163.0
3958.2	5191.1	4001.5	1168.6	535.1	1478.6	1203.9	1072.6
6282.4	6133.7	5712.1	862.2	1279.3	1926.6	1418.1	1541.3
27.8	29.8	32.8	7.0	129.4	45.8	37.3	70.8
71.2	69.5	69.5	1.7	188.8	118.4	79.6	129.0
46.5	53.8	52.8	5.9	44.2	49.0	41.3	44.8
74.0	63.7	76.8	14.7	404.6	102.7	66.3	191.2
360.3	359.6	404.6	77.3	86.0	137.9	161.9	128.6
67.7	66.9	62.0	9.2	165.7	58.4	48.0	90.7
25.4	27.2	26.1	1.0	17.1	89.8	52.5	53.2
37.8	36.6	41.8	7.9	190.1	55.3	31.9	92.4
67.0	82.8	85.6	20.2	175.9	122.6	74.0	124.2
23617.1	21656.2	17448.9	9038.7	2115.4	2711.4	2332.2	2386.3
110.6	160.2	140.2	26.2	441.6	252.7	157.8	284.0
225.7	222.9	223.3	2.2	144.9	230.6	205.4	193.6
78.4	65.5	72.8	6.6	61.0	51.0	34.4	48.8
307.8	251.9	231.0	89.1	104.0	115.2	150.6	123.3
3.6	3.7	3.3	0.6	266.5	23.5	28.6	106.2
1.3	2.2	1.6	0.5	143.1	5.7	3.2	50.7
1.9	4.0	2.4	1.5	34.8	6.7	2.1	14.5
15.0	17.3	14.0	3.8	0.0	21.1	9.4	10.2
3.8	3.1	4.5	1.8	13.6	11.5	8.5	11.2
17.4	19.5	17.8	1.5	179.5	27.1	14.4	73.7
162.2	206.7	230.3	82.4	82.6	101.5	80.7	88.3
201.6	194.0	251.9	93.8	0.0	167.2	95.3	87.5
18.6	14.3	14.1	4.6	176.3	25.4	20.2	74.0
15.6	20.9	17.5	2.9	45.9	36.6	29.7	37.4
21.3	20.5	18.0	5.1	84.9	37.7	22.2	48.3
34.7	32.9	32.7	2.2	19.3	8.9	7.5	11.9

51.4	48.0	45.4	7.6	47.6	17.0	16.2	26.9
36.6	36.7	35.3	2.3	8.9	17.7	16.3	14.3
9.3	10.2	9.5	0.6	107.7	75.0	41.5	74.7
3.1	2.8	3.2	0.4	0.0	4.6	5.5	3.4
73.8	56.2	64.5	8.8	0.0	52.8	51.4	34.8
9.8	7.6	10.4	3.1	46.8	18.9	13.4	26.4
22.9	22.5	24.1	2.5	40.1	33.0	27.4	33.5
28.9	23.6	30.3	7.4	0.0	48.8	41.2	30.0
13.9	14.1	17.1	5.4	22.7	27.0	23.3	24.4
26.3	31.7	33.6	8.4	0.0	83.3	80.6	54.6
18.7	20.1	24.9	9.5	113.0	74.2	51.3	79.5
56.0	69.7	78.7	28.3	154.0	161.4	179.3	164.9
57.0	49.1	50.3	6.1	60.4	47.8	38.8	49.0
763.3	607.8	619.9	137.7	62.7	77.5	81.5	73.9
60.1	72.8	70.8	9.8	83.9	56.0	31.7	57.2
14.4	21.7	23.0	9.4	107.8	18.3	13.2	46.4
105.9	80.4	92.9	12.8	64.9	81.1	78.1	74.7
36.7	47.7	47.8	11.2	71.1	81.6	53.3	68.6
26.2	23.5	28.8	7.0	53.6	33.0	27.3	38.0
42.7	38.3	46.0	9.8	109.6	67.8	54.1	77.2
49.0	38.6	46.2	6.7	0.0	78.8	54.8	44.5
5.9	8.4	7.8	1.7	73.6	6.6	5.8	28.6
22.3	40.2	29.7	9.4	62.3	5.4	6.6	24.8
34.5	35.2	32.7	3.6	22.3	11.9	15.6	16.6
21.2	22.9	21.7	1.0	91.0	21.0	21.0	44.3
49.9	45.6	41.9	10.4	128.0	14.3	22.1	54.8
24.8	24.9	25.2	0.7	56.9	48.9	38.4	48.1
7.1	10.7	10.2	2.9	71.9	9.8	11.1	30.9
25.5	42.3	40.4	14.1	58.0	40.0	20.8	39.6
75.4	104.6	90.6	14.7	112.3	93.0	80.1	95.1
23.0	30.1	29.0	5.6	284.7	67.0	64.5	138.7
33.3	43.5	42.5	8.8	158.1	67.3	58.5	94.6
67.3	50.7	82.0	40.7	343.0	574.1	320.2	412.4
118.2	122.4	132.8	21.7	43.2	159.1	151.2	117.8
186.1	189.8	179.1	15.5	614.7	1098.5	862.6	858.6
222.9	241.2	276.6	77.7	875.5	1244.7	828.3	982.8
485.6	399.1	451.6	46.1	1118.1	2442.8	2261.5	1940.8
169.2	152.6	199.4	67.2	809.6	867.1	738.4	805.1
44.4	49.9	57.4	17.9	17.4	118.3	84.4	73.4
91.8	92.9	109.1	28.9	73.9	200.7	121.2	131.9
232.5	204.0	240.4	40.9	1140.9	302.2	186.2	543.1
72.3	46.2	62.9	14.5	11.2	221.6	117.0	116.6
561.1	519.9	509.0	58.3	190.8	172.4	154.1	172.4

590.3	682.5	638.8	46.3	103.1	240.1	122.1	155.1
64.6	67.9	74.5	14.4	104.2	133.7	105.5	114.5
73.8	77.5	73.1	4.8	23.0	84.4	63.3	56.9
152.1	163.2	157.0	5.7	350.4	140.8	120.9	204.0
130.5	142.2	139.7	8.2	48.1	75.3	70.0	64.5
225.8	209.0	222.0	11.6	151.9	172.1	218.4	180.8
305.8	318.5	313.4	6.7	229.0	273.9	356.1	286.3
314.7	270.6	310.4	37.8	153.0	274.8	379.2	269.0
84.0	75.4	104.7	43.5	156.6	175.1	207.1	179.6
18.0	25.1	21.4	3.5	81.9	27.5	30.3	46.6
676.1	592.7	480.5	269.7	225.2	422.3	341.6	329.7
14.2	12.8	18.8	9.3	26.6	80.5	47.7	51.6
138.3	99.1	143.5	47.3	98.8	192.1	112.8	134.6
140.1	89.1	145.0	58.4	125.5	192.5	89.0	135.7
14.4	20.5	22.9	9.9	63.2	19.4	12.1	31.6
33.2	43.8	37.6	5.5	121.6	41.2	28.5	63.8
56.1	70.4	58.0	11.6	30.7	20.5	20.8	24.0
50.1	67.1	74.0	27.9	0.0	10.0	4.8	4.9
11.3	22.9	16.2	6.1	40.4	18.3	9.6	22.8
31.5	29.0	30.5	1.4	130.3	234.1	279.1	214.5
56.8	44.5	45.7	10.6	108.3	294.6	480.0	294.3
121.1	124.4	112.4	18.1	420.4	194.1	176.4	263.6
3.8	3.7	4.0	0.5	43.9	21.3	24.4	29.8
51.0	41.2	41.5	9.3	130.7	295.2	517.2	314.4
46.3	38.4	42.3	3.9	70.6	36.7	29.8	45.7
28.7	38.9	33.3	5.2	143.4	56.0	51.3	83.5
48.6	60.9	68.2	24.2	37.7	50.3	37.8	41.9
39.4	33.3	43.3	12.3	35.2	17.8	14.6	22.6
49.9	50.5	53.1	5.1	151.7	163.7	125.2	146.9
98.1	121.0	129.2	36.0	356.2	381.9	261.9	333.3
7.0	8.4	7.5	0.8	107.6	51.9	63.5	74.3
22.5	21.1	21.8	0.7	43.8	47.2	41.8	44.3
141.2	129.6	141.5	12.1	334.8	341.7	398.0	358.2
74.9	54.4	65.4	10.4	384.8	265.9	351.3	334.0
65.3	61.0	59.2	7.3	279.6	301.5	382.9	321.4
4.1	4.4	4.2	0.2	99.3	28.0	19.0	48.7
94.4	103.2	86.0	22.6	89.0	150.1	76.3	105.1
29.9	30.3	32.7	4.5	0.0	26.4	14.3	13.5
465.4	648.3	535.1	98.9	2.5	53.3	44.3	33.4
132.0	175.2	138.2	34.4	99.5	102.9	66.5	89.6
193.7	206.8	192.1	15.5	105.2	30.7	26.1	54.0
340.1	484.7	320.4	175.0	53.2	10.7	6.8	23.6
157.6	205.0	142.1	71.9	28.2	4.3	3.6	12.0

145.0	149.8	137.6	17.0	28.8	8.2	5.7	14.2
223.8	142.8	183.2	40.5	54.7	22.4	21.5	32.9
37.0	43.6	37.8	5.4	0.0	7.7	3.8	3.9
17.6	20.2	18.5	1.5	0.0	5.2	4.0	3.1
21.3	27.0	25.1	3.3	0.0	6.7	3.7	3.5
25.7	24.9	24.7	1.2	0.7	5.3	2.5	2.8
13.7	11.1	11.2	2.4	0.0	3.2	2.6	1.9
19.9	15.6	16.2	3.5	0.0	8.7	3.6	4.1
13.4	11.6	9.9	4.6	37.6	13.0	6.1	18.9
5.5	7.0	5.5	1.5	90.8	5.9	5.2	34.0
0.7	0.8	1.0	0.5	33.8	4.8	3.9	14.1
2.0	1.7	2.1	0.4	24.2	12.3	6.2	14.2
263.3	284.1	341.9	118.5	193.3	313.0	271.4	259.2
15.3	16.5	17.1	2.1	0.0	16.4	10.9	9.1
363.1	303.1	373.6	76.2	496.8	317.5	255.0	356.5
28.9	20.4	31.4	12.4	14.9	116.6	71.7	67.7
22.7	29.2	33.7	13.8	188.9	187.7	146.6	174.4
57.6	70.7	69.0	10.6	60.9	144.4	121.3	108.9
7.3	3.5	7.1	3.5	0.0	40.4	14.5	18.3
10.3	5.2	10.1	4.8	154.4	27.3	11.9	64.5
41.7	26.8	34.9	7.5	45.6	25.9	14.6	28.7
34.3	23.8	29.6	5.3	58.0	17.7	14.2	30.0
20.7	14.7	18.6	3.4	0.0	19.9	8.1	9.3
59.6	33.9	47.1	12.9	173.2	122.0	152.0	149.1
12.8	14.6	12.4	2.4	93.9	21.1	11.2	42.1
907.5	687.6	1174.1	661.4	526.9	488.6	405.3	473.6
46.2	58.6	63.6	20.4	39.5	30.9	28.4	32.9
580.4	292.6	449.4	145.6	929.0	609.5	523.4	687.3
31.6	22.3	19.4	13.8	85.7	16.1	10.9	37.6
172.7	124.6	125.4	46.9	22.4	187.3	164.6	124.8
76.7	87.0	76.6	10.4	43.1	79.5	71.9	64.8
99.2	90.0	91.5	7.0	209.9	89.6	78.5	126.0
495.2	436.9	427.5	73.0	363.6	370.4	338.1	357.4
341.6	284.0	361.2	88.6	223.7	437.1	375.7	345.5
223.0	273.3	270.5	46.3	280.3	320.1	276.4	292.2
16.7	28.1	22.9	5.8	138.0	46.2	11.5	65.3
109.7	62.4	74.2	31.3	0.0	155.8	100.3	85.4
19.6	24.5	20.7	3.5	30.1	75.3	40.2	48.5
2.4	3.2	3.3	1.0	45.6	12.0	4.1	20.6
6.0	12.2	10.0	3.5	474.1	57.4	24.4	185.3
23.5	37.2	34.4	9.8	153.3	109.0	34.0	98.8
64.3	70.9	96.8	50.7	88.7	96.8	98.1	94.5
52.7	57.3	73.6	32.4	193.0	154.1	113.8	153.6

33.0	36.6	43.5	15.1	0.0	145.3	129.7	91.7
91.6	99.8	92.2	7.4	52.8	33.9	20.7	35.8
126.6	109.8	122.3	11.0	31.3	43.3	33.5	36.0
71.7	67.6	83.3	23.7	204.2	267.1	169.4	213.6
101.7	83.7	86.9	13.4	127.1	119.8	161.2	136.0
3.9	6.9	6.5	2.4	11.1	9.1	8.1	9.5
1690.5	1560.9	2448.8	1427.1	650.3	502.6	321.8	491.6
22.6	28.3	30.1	8.5	39.2	48.7	27.6	38.5
289.2	343.8	304.8	34.0	153.9	417.6	371.4	314.3
101.4	229.7	179.3	68.4	106.2	192.5	59.8	119.5
86.3	91.5	88.0	3.1	74.1	55.1	49.5	59.6
190.9	205.1	200.7	8.5	398.6	324.2	170.0	297.6
1345.5	1427.6	1696.1	537.9	643.9	1070.1	1071.0	928.3
780.2	833.8	990.5	318.9	357.5	335.9	357.0	350.1
1245.4	1245.8	1493.2	429.0	630.6	438.4	516.2	528.4
1066.8	976.9	1219.7	345.7	194.8	383.1	373.6	317.2
1085.4	1147.8	1410.2	509.5	379.3	400.1	323.2	367.5
1634.3	1421.0	1549.9	113.4	217.4	416.9	410.3	348.2
105.1	84.4	130.3	62.4	214.5	161.0	244.7	206.7
60.1	42.1	62.1	21.1	268.3	542.2	512.4	440.9
14.2	12.9	16.4	4.9	19.4	15.3	13.0	15.9
65.9	82.4	92.8	33.3	145.2	92.4	86.2	107.9
511.4	461.6	515.6	56.2	144.1	91.0	83.4	106.2
40.5	49.5	60.8	27.7	22.5	58.7	36.7	39.3
253.6	243.1	283.4	61.0	214.9	524.8	551.5	430.4
135.5	121.6	111.2	30.8	45.2	64.0	68.2	59.2
183.1	192.4	167.1	36.0	199.0	75.8	67.0	113.9
159.9	155.4	156.8	2.6	137.2	84.5	69.7	97.1
100.7	91.4	134.8	67.4	2.3	62.3	62.9	42.5
67.7	67.6	86.2	32.1	322.4	152.3	123.9	199.5
186.0	221.7	243.6	71.1	153.6	544.4	440.0	379.3
200.0	206.2	261.7	101.5	439.4	389.9	336.9	388.7
20.5	32.7	32.2	11.4	51.2	19.6	15.0	28.6
12.6	16.5	20.0	9.6	40.0	17.1	15.1	24.1
16.2	25.0	23.6	6.9	8.9	16.9	15.0	13.6
54.5	60.3	61.1	7.1	35.7	44.5	54.0	44.7
75.1	97.1	95.0	18.9	20.8	97.8	69.5	62.7
33.1	39.0	44.0	14.0	265.4	47.5	51.9	121.6
60.6	66.2	74.7	19.8	596.7	81.3	100.3	259.4
219.2	226.4	297.2	128.9	142.7	181.2	164.6	162.8
988.9	682.9	642.7	367.9	921.4	908.9	1152.0	994.1
14.7	17.3	17.0	2.3	14.8	17.7	17.2	16.6
521.9	481.1	488.3	30.7	478.2	692.6	786.0	652.3

153.7	228.8	196.2	38.6	252.3	218.9	222.7	231.3
176.0	234.9	196.0	33.7	59.6	123.2	125.9	102.9
130.1	119.4	166.1	71.9	155.8	120.2	103.8	126.6
55.2	56.9	50.5	9.8	92.0	56.4	46.6	65.0
144.2	152.3	197.1	84.6	50.3	211.2	162.7	141.4
79.4	90.5	97.0	21.6	80.9	155.9	137.1	124.6
306.4	270.2	348.2	105.3	175.1	334.2	291.3	266.9
23.0	33.2	30.4	6.5	56.9	13.5	14.4	28.3
15.1	18.7	16.9	1.8	300.4	30.5	44.4	125.1
34.8	42.8	48.0	16.5	248.8	165.5	115.2	176.5
105.7	101.4	139.8	62.8	53.5	108.5	90.9	84.3
68.0	79.3	98.5	43.4	165.2	91.8	85.5	114.2
37.3	57.2	64.2	30.9	186.8	93.7	24.6	101.7
76.5	99.5	103.4	29.1	217.9	143.5	110.7	157.4
346.7	323.3	368.6	59.3	267.5	290.0	250.5	269.3
24.9	24.9	23.7	2.1	67.8	28.9	29.0	41.9
17.3	32.7	19.5	12.2	34.6	19.8	11.6	22.0
88.7	213.0	110.9	93.1	0.0	23.0	20.9	14.6
13.6	42.6	41.9	28.0	0.0	8.6	9.2	5.9
691.0	626.7	729.2	126.0	59.2	30.4	36.1	41.9
1342.0	1348.9	1552.7	359.0	869.6	504.8	398.6	591.0
26.6	24.3	27.3	3.3	203.1	21.7	23.9	82.9
114.6	78.3	90.5	20.9	1615.0	712.6	979.0	1102.2
92.4	70.8	61.4	36.6	1122.7	611.1	782.5	838.8
30.4	37.2	30.0	7.4	231.5	62.8	48.9	114.4
63.6	79.3	91.1	34.9	59.0	70.4	92.4	73.9
7.9	9.4	9.7	2.0	113.7	12.6	15.4	47.2
15.0	10.0	20.3	13.7	74.5	34.5	10.9	40.0
2.1	2.1	5.9	6.6	70.4	9.3	2.6	27.4
5.7	5.9	11.0	9.0	62.3	60.8	19.7	47.6
30.5	29.1	32.9	5.4	186.8	112.4	113.5	137.6
28.7	43.9	45.9	18.2	144.2	77.7	87.2	103.0
192.6	214.8	204.1	11.1	47.2	185.8	133.4	122.2
204.3	201.1	206.9	7.6	744.8	190.0	194.4	376.4
508.9	580.9	571.2	58.0	165.0	201.6	220.3	195.6
438.5	389.8	537.6	215.3	163.4	521.5	366.9	350.6
82.5	76.6	101.3	37.8	155.0	76.8	58.9	96.9
818.5	933.7	1291.2	721.3	302.9	657.6	703.0	554.5
987.9	1066.6	1024.6	39.6	244.3	479.9	410.2	378.1
1028.7	1041.6	1075.8	70.7	1339.6	1477.7	1724.7	1514.0
402.4	460.3	496.1	115.8	441.7	233.8	290.2	321.9
2129.2	1767.6	2292.7	623.1	1464.5	2014.2	1469.4	1649.3
160.5	184.0	220.5	84.3	237.2	249.6	213.1	233.3

4.0	1.3	3.3	1.8	0.0	16.9	9.7	8.9
36.1	52.1	46.6	9.1	19.8	40.3	44.6	34.9
90.4	95.3	95.2	4.7	49.8	167.3	107.8	108.3
68.2	67.5	76.0	14.2	84.0	61.0	42.2	62.4
27.0	23.8	29.7	7.6	45.4	25.0	20.0	30.1
284.9	267.6	267.0	18.2	123.6	299.1	259.4	227.4
82.0	82.0	77.8	7.2	586.6	109.5	117.3	271.2
765.0	676.5	777.3	107.4	285.9	526.4	566.9	459.7
481.4	498.5	516.1	46.2	237.9	383.6	270.4	297.3
112.6	170.3	196.3	99.3	345.9	642.1	499.3	495.8
8.6	7.3	8.4	1.0	1241.5	230.6	142.1	538.1
255.5	234.3	304.2	103.2	70.1	542.7	448.6	353.8
104.0	87.0	109.0	24.8	666.5	503.1	310.0	493.2
21.1	20.2	24.4	6.6	180.3	108.1	107.8	132.1
204.4	190.2	200.2	8.8	315.9	226.3	174.3	238.8
409.5	398.8	418.3	25.0	185.1	133.8	96.7	138.6
54.8	53.4	56.4	4.0	50.4	27.3	16.3	31.3
1039.1	514.6	891.4	328.9	177.3	413.3	379.3	323.3
985.9	481.6	787.0	268.5	167.3	394.0	288.0	283.1
312.1	184.0	302.4	113.8	306.0	137.5	108.5	184.0
841.2	373.8	569.6	242.8	74.7	106.5	97.1	92.8
879.8	364.1	638.3	259.4	61.2	124.8	126.2	104.1
1128.6	642.8	1158.4	531.2	73.6	74.8	65.7	71.4
1724.0	885.5	1532.2	575.3	89.7	52.5	39.5	60.6
1564.7	557.5	1392.5	763.6	3.8	26.9	19.6	16.8
1981.5	694.0	1714.4	916.5	120.7	70.5	55.0	82.1
16.3	19.6	15.1	5.1	63.6	34.0	17.7	38.4
5.3	6.7	6.3	0.9	135.5	17.0	10.8	54.4
7.4	9.3	10.7	4.1	0.0	28.2	19.8	16.0
14.1	18.2	22.6	11.3	198.1	68.8	46.1	104.4
19.1	28.5	32.0	15.0	107.8	74.6	55.4	79.3
12.3	17.4	16.0	3.3	134.2	44.3	31.8	70.1
14.7	10.0	129.0	202.0	172.1	91.2	94.7	119.3
28.7	26.0	139.3	193.9	242.2	170.3	143.9	185.5
33.0	13.3	55.6	57.1	193.8	222.7	239.3	218.6
115.1	216.2	296.0	231.3	83.3	57.7	70.9	70.6
356.2	445.2	468.0	124.8	222.0	649.7	755.5	542.4
589.2	485.0	455.9	149.9	5672.3	1090.3	1302.2	2688.3
143.7	156.3	193.9	76.3	57.5	169.7	147.3	124.9
25.0	31.1	34.2	11.1	65.7	53.1	47.7	55.5
29.2	30.0	33.8	7.3	24.5	14.5	14.2	17.7
130.1	107.1	119.9	11.7	90.3	47.1	40.9	59.4
60.0	67.4	89.3	44.5	190.7	66.2	43.1	100.0

50.0	67.6	62.9	11.3	35.4	98.2	61.9	65.2
19.1	23.7	22.3	2.8	16.9	72.2	48.0	45.7
117.0	111.0	110.8	6.3	252.9	118.9	123.4	165.1
157.4	225.4	193.8	34.3	338.9	215.5	177.3	243.9
55.4	32.4	43.4	11.5	40.0	55.0	60.4	51.8
17.8	12.7	17.6	4.8	9.6	14.3	13.5	12.5
7.1	22.2	17.8	9.3	146.5	37.8	31.6	72.0
39.1	39.7	48.0	14.9	42.4	30.5	35.5	36.1
134.0	158.5	153.1	17.1	9.5	62.2	70.0	47.2
116.7	93.2	100.1	14.4	85.3	57.9	82.0	75.1
61.1	70.8	68.2	6.3	83.0	55.5	51.5	63.3
12.4	15.9	18.2	7.2	0.0	11.1	9.7	6.9
31.3	31.7	34.0	4.4	125.2	26.6	39.3	63.7
59.6	50.6	55.0	4.5	42.5	13.9	18.3	24.9
65.1	74.4	69.8	4.7	0.0	14.7	18.3	11.0
156.8	184.0	158.4	24.8	128.2	56.6	67.1	83.9
172.2	172.6	164.1	14.4	43.5	41.8	34.9	40.1
857.5	705.8	859.6	154.9	2552.6	2357.6	3124.6	2678.3
5472.6	6743.6	5161.0	1759.4	7678.3	5771.2	5616.6	6355.4
116.3	90.3	98.0	15.9	478.9	230.4	176.4	295.3
6.9	5.6	8.6	4.2	17.5	5.9	5.3	9.6
19.4	18.0	18.2	1.1	39.1	45.2	55.6	46.6
0.8	0.6	0.7	0.1	29.9	1.7	2.0	11.2
3.3	3.0	2.6	0.9	0.0	7.4	13.3	6.9
33.5	32.0	32.1	1.4	0.0	59.6	33.5	31.0
9.3	8.4	9.0	0.6	0.0	14.0	7.8	7.3
2.9	3.6	4.8	2.7	0.0	4.3	1.1	1.8
19.9	15.7	23.9	10.7	0.0	27.3	12.9	13.4
3.8	5.0	4.7	0.8	48.4	11.1	8.1	22.5
45.0	38.2	77.2	61.7	72.4	31.5	24.0	42.6
3.4	10.7	5.6	4.5	0.0	8.8	9.0	5.9
1.9	6.9	3.6	2.8	25.2	5.4	3.7	11.4
16.0	13.8	20.2	9.2	225.5	43.6	35.9	101.7
5.6	5.9	6.3	1.1	68.1	37.9	63.5	56.5
20.4	18.9	20.8	2.1	21.5	10.9	12.2	14.9
8.6	9.9	10.1	1.5	0.0	6.1	4.9	3.7
50.9	48.1	57.0	13.1	160.6	118.9	99.7	126.4
18.5	16.0	17.8	1.5	0.0	12.3	8.7	7.0
36.8	45.3	41.8	4.5	232.1	50.1	35.1	105.8
20.4	16.3	18.6	2.1	135.2	39.7	53.9	76.3
23.0	15.5	23.9	8.9	21.7	67.0	49.9	46.2
5.6	5.7	7.6	3.5	16.0	10.6	7.5	11.3
9.2	12.2	13.0	4.3	68.9	27.2	22.6	39.6

172.4	144.8	145.8	26.1	164.9	256.7	212.2	211.3
795.4	776.7	867.8	141.8	313.1	534.6	667.6	505.1
14.5	15.1	19.9	8.9	49.3	36.9	33.9	40.0
255.6	259.1	256.3	2.5	314.2	445.6	309.4	356.4
54.8	75.1	80.4	28.7	190.8	270.5	288.2	249.8
43.4	43.1	53.8	18.3	44.3	92.4	69.8	68.8
126.5	109.3	124.6	14.5	111.4	173.3	133.2	139.3
10.5	6.9	10.6	3.8	5.0	42.0	32.0	26.3
50.2	46.1	52.6	8.0	152.9	44.3	40.7	79.3
125.8	89.3	96.5	26.5	1893.3	219.7	163.6	758.9
279.9	264.7	420.4	256.6	85.8	482.3	395.3	321.1
113.0	135.5	132.8	18.7	197.2	123.8	71.8	130.9
136.3	89.2	123.6	30.1	89.0	167.7	143.2	133.3
55.4	70.5	71.9	17.3	19.5	29.2	20.8	23.2
46.2	49.4	59.4	20.2	48.7	35.4	27.0	37.0
376.1	302.6	327.0	42.6	235.6	230.9	181.5	216.0
1328.5	732.3	926.9	347.9	36.1	26.5	17.4	26.7
323.6	260.7	344.1	95.3	205.1	163.3	92.8	153.7
51.8	53.5	59.7	12.1	107.0	61.1	69.6	79.3
100.2	95.2	110.7	22.6	163.4	102.5	106.0	124.0
31.6	31.8	35.0	5.7	92.4	53.8	63.2	69.8
660.1	670.0	709.9	77.8	89.1	354.4	312.1	251.9
122.9	152.4	161.6	44.0	414.9	149.0	144.5	236.1
75.1	66.7	90.9	35.0	179.9	459.3	426.2	355.1
49.2	43.4	55.9	16.9	189.0	175.7	186.3	183.7
64.8	95.2	68.6	24.9	119.0	61.4	71.1	83.8
5357.8	8899.8	6336.3	2240.6	893.7	1844.2	1688.0	1475.3
155.9	128.2	129.9	25.1	667.7	280.2	234.4	394.1
45.1	87.4	69.9	22.1	194.1	24.1	7.2	75.1
43.5	42.1	44.9	3.7	2942.7	128.9	104.6	1058.7
12.7	11.7	14.3	3.7	59.9	50.4	34.7	48.3
2570.8	3164.6	2080.8	1395.0	898.8	982.9	1361.7	1081.1
67.6	110.2	76.7	30.0	160.1	559.7	341.1	353.7
217.5	100.9	158.6	58.3	81.8	17.9	7.4	35.7
4206.2	3367.4	3622.2	507.1	1134.4	1094.2	1135.8	1121.5
342.3	425.1	555.6	300.6	276.9	596.1	372.7	415.2
12.9	15.4	18.4	7.6	11.9	21.2	12.5	15.2
28.4	27.1	33.8	10.5	28.7	35.9	22.0	28.8
18.8	16.1	22.4	8.7	53.6	51.5	40.9	48.7
32.1	29.1	36.8	10.9	58.7	58.2	33.9	50.2
5.8	5.2	61.9	97.7	533.4	128.6	75.8	245.9
329.7	273.5	308.2	30.3	623.7	162.2	159.7	315.2
56.5	83.1	70.6	13.4	371.9	41.0	47.5	153.5

36.3	37.1	39.9	5.5	83.6	40.3	44.5	56.1
32.0	45.8	45.3	13.1	51.4	31.0	33.1	38.5
22.0	32.1	42.7	27.6	121.6	31.5	29.8	60.9
24.9	24.7	39.2	24.9	21.2	19.4	22.4	21.0
23.9	24.6	32.3	13.9	21.1	41.7	36.3	33.0
19.5	26.4	29.8	12.3	53.9	100.9	63.0	72.6
48.8	53.0	53.3	4.6	167.8	52.6	44.8	88.4
24.3	29.9	26.0	3.4	114.4	43.9	41.2	66.5
27.3	39.8	36.2	7.7	612.3	95.2	70.0	259.2
116.5	121.6	111.8	12.8	45.9	78.1	79.2	67.7
52.9	32.3	50.0	16.4	402.0	310.1	342.0	351.4
32.6	43.4	61.9	41.7	14.0	172.2	161.9	116.0
21.3	27.0	31.4	13.0	109.4	116.0	113.9	113.1
32.3	27.1	43.4	23.8	120.4	151.7	126.8	133.0
338.8	274.6	320.0	39.5	515.2	376.9	543.3	478.5
307.8	265.3	294.6	25.4	114.4	281.4	317.8	237.9
47.9	60.4	67.0	23.1	36.3	54.6	42.4	44.4
102.2	98.3	100.7	2.1	264.4	143.7	119.9	176.0
24.4	28.6	32.8	11.1	24.6	87.8	67.0	59.8
368.3	351.2	397.2	65.4	253.1	396.0	323.8	324.3
2.8	4.0	4.2	1.5	0.0	3.8	4.2	2.7
48.0	48.6	59.7	19.7	208.4	59.8	52.3	106.8
28.4	26.2	34.4	12.5	132.7	53.2	46.6	77.5
1179.6	1078.1	1113.8	57.0	345.5	565.0	579.9	496.8
1291.5	1417.5	1259.4	176.4	521.6	362.5	418.8	434.3
195.8	340.3	309.0	101.3	10.4	110.0	63.0	61.1
1857.5	1486.3	1582.7	241.5	566.1	1145.0	1224.7	978.6
66.5	61.3	67.1	6.1	144.6	118.8	85.8	116.4
58.2	75.0	68.4	9.0	102.8	124.9	111.0	112.9
49.5	50.4	48.9	2.0	245.8	88.6	69.1	134.5
31.5	34.9	34.7	3.2	161.5	130.6	189.7	160.6
532.4	430.4	496.3	57.1	794.6	656.6	892.4	781.2
5471.4	3823.8	4472.8	877.7	1061.7	3389.7	4008.0	2819.8
285.8	323.7	370.0	114.5	332.3	384.5	452.0	389.6
87.7	83.7	94.0	14.6	75.8	133.9	98.4	102.7
131.0	133.0	139.1	12.3	111.9	80.1	61.6	84.5
98.1	98.3	100.0	3.1	71.8	11.3	2.6	28.6
6.2	5.4	6.4	1.1	39.3	25.6	21.7	28.9
25.5	32.8	25.7	7.0	663.3	133.0	115.4	303.9
19.7	22.4	17.8	5.7	848.2	123.0	105.1	358.8
20.3	20.9	20.6	0.3	52.0	83.9	36.0	57.3
52.8	37.8	43.2	8.3	166.3	71.3	55.0	97.5
2.7	2.1	2.4	0.3	31.5	18.3	16.9	22.2

3.6	4.1	4.1	0.5	54.8	25.5	23.0	34.4
4.0	7.4	5.6	1.7	53.0	20.8	17.7	30.5
32.3	32.9	32.8	0.5	97.4	66.3	57.0	73.6
26.7	33.1	31.4	4.1	95.4	81.1	49.5	75.3
12.4	14.5	19.0	9.7	30.9	14.8	12.3	19.3
17.5	17.3	20.9	6.0	0.0	118.8	70.5	63.1
10.1	8.0	8.8	1.1	2.9	46.2	51.6	33.6
12.3	10.2	10.4	1.8	110.8	114.7	101.1	108.9
8.9	9.5	17.3	14.1	58.8	36.9	16.2	37.3
119.4	116.4	119.7	3.5	886.3	229.5	279.2	465.0
51.0	58.3	52.6	5.1	66.1	94.8	76.6	79.1
5.4	4.5	5.5	1.0	136.3	83.4	40.4	86.7
5.5	3.7	6.0	2.5	25.5	23.2	31.2	26.7
5.3	5.6	5.0	0.7	435.7	46.9	55.3	179.3
17.7	14.9	14.5	3.4	142.0	55.7	37.5	78.4
18.3	22.5	19.9	2.3	174.4	39.9	17.9	77.4
1.9	4.5	3.4	1.4	37.4	11.7	7.7	18.9
3.4	2.3	2.9	0.6	11.7	5.9	6.4	8.0
1.8	1.7	2.4	1.1	45.8	3.3	3.6	17.6
4.0	2.7	3.6	0.8	52.4	2.0	2.0	18.8
3.5	2.9	4.0	1.4	66.1	1.5	2.6	23.4
5.5	4.5	5.5	1.0	41.0	2.9	3.2	15.7
1.8	1.7	2.5	1.4	31.4	1.2	1.8	11.5
2.9	3.3	4.2	1.8	15.2	2.2	1.7	6.4
0.3	0.4	0.8	0.6	17.9	0.8	0.8	6.5
6.2	3.5	7.0	4.0	15.9	6.6	4.7	9.1
1.2	1.2	1.4	0.3	123.6	3.0	2.0	42.9
10.6	11.9	12.5	2.2	205.8	7.2	3.6	72.2
13.9	11.7	13.3	1.4	0.0	15.8	15.1	10.3
9.9	11.8	11.5	1.5	8.7	19.3	16.2	14.7
8.8	11.2	10.5	1.5	36.6	17.9	9.6	21.3
1058.9	602.8	1666.0	1464.5	5102.8	6014.4	3611.0	4909.4
19652.0	26603.3	23696.4	3612.5	856.4	1055.6	719.6	877.2
66.6	55.1	57.0	8.9	221.2	86.3	50.2	119.2
55.4	33.3	39.7	13.7	33.1	44.7	25.3	34.4
68.2	50.4	52.8	14.3	37.7	24.6	16.2	26.1
62.2	39.5	46.9	13.3	37.6	27.5	25.2	30.1
48.6	33.0	34.9	12.8	45.6	23.3	20.2	29.7
48.2	38.8	39.5	8.4	44.1	19.2	15.7	26.3
40.0	24.5	30.3	8.4	59.4	23.4	19.5	34.1
92.4	47.6	64.7	24.2	119.1	56.3	37.7	71.1
7.3	8.8	9.2	2.0	37.5	34.1	33.8	35.2
19.7	16.1	19.9	3.9	34.2	59.8	44.8	46.3

73.6	85.5	86.8	13.8	11.2	128.6	66.1	68.6
88.7	93.2	93.2	4.5	247.9	159.5	91.9	166.4
18.8	14.9	19.2	4.5	0.0	119.9	97.2	72.4
7.5	9.4	9.7	2.4	82.1	87.0	33.8	67.7
19.5	11.6	15.5	3.9	35.7	112.3	74.5	74.2
167.9	116.7	142.4	25.6	26.4	53.8	52.3	44.1
107.1	92.4	99.7	7.4	86.6	26.9	25.2	46.2
36.9	33.1	37.6	4.8	19.0	35.4	24.9	26.4
46.1	35.5	41.0	5.3	0.0	22.6	18.5	13.7
34.9	30.2	30.5	4.3	55.8	9.8	7.3	24.3
25.2	23.6	23.6	1.5	11.5	13.7	8.6	11.3
87.6	85.7	77.4	16.0	128.1	50.1	46.3	74.8
672.3	434.4	432.7	240.4	207.6	137.3	119.7	154.9
8.4	6.4	7.8	1.2	199.1	56.9	39.9	98.6
7.1	7.3	8.0	1.4	133.4	69.0	36.5	79.6
220.1	187.0	217.9	30.0	283.1	444.9	476.2	401.4
65.1	60.1	78.8	28.2	77.2	113.5	96.3	95.7
47.0	53.5	49.4	3.6	220.6	45.0	33.9	99.9
3.0	5.0	3.9	1.0	61.8	13.1	3.1	26.0
20.3	22.8	22.7	2.3	484.5	71.8	54.7	203.7
102.8	110.6	93.8	22.7	331.2	56.1	30.9	139.4
24.5	27.4	27.5	3.1	54.7	39.2	31.6	41.8
6.9	4.4	5.3	1.5	18.5	28.6	7.6	18.3
22.1	32.4	28.6	5.6	45.5	55.6	18.3	39.8
77.1	71.2	71.6	5.3	0.0	66.2	27.7	31.3
11.1	13.1	11.1	2.1	123.1	62.6	14.5	66.8
1.2	1.1	1.2	0.1	0.0	5.0	3.4	2.8
38.4	33.1	66.3	52.9	246.1	137.5	91.1	158.2
300.6	357.1	330.6	28.4	271.8	260.2	313.2	281.7
112.6	93.5	76.0	47.8	10.7	5.6	6.6	7.7
110.8	94.7	71.7	54.4	60.2	18.3	29.0	35.9
149.7	146.7	102.8	78.6	118.3	88.4	90.7	99.1
175.9	133.0	156.0	21.6	312.9	345.9	438.8	365.9
180.8	128.6	197.0	77.8	338.9	382.5	426.8	382.7
3.8	3.0	4.2	1.5	0.0	14.0	6.2	6.7
9.0	6.8	8.1	1.2	69.3	30.3	22.4	40.7
115.9	60.0	103.7	39.1	63.8	48.2	61.1	57.7
53.5	41.1	32.2	26.9	35.5	2.0	3.4	13.6
17.7	19.8	13.1	9.9	12.3	9.2	13.8	11.8
379.9	365.5	278.4	163.5	132.0	167.1	40.6	113.2
14.6	11.8	15.3	3.9	279.9	143.8	232.3	218.7
1183.6	897.6	833.2	386.6	1313.1	1154.4	1627.2	1364.9
407.7	308.4	278.0	147.3	468.0	308.7	456.3	411.0

7.4	7.1	7.7	0.8	0.0	10.2	8.9	6.4
2.9	2.4	4.1	2.5	91.3	68.8	171.1	110.4
7.8	5.2	8.1	3.0	797.8	145.0	610.2	517.6
3.4	3.8	3.3	0.7	49.3	12.8	11.0	24.4
0.5	0.8	0.7	0.2	17.5	3.8	3.6	8.3
13.2	8.9	10.3	2.5	62.1	42.2	38.1	47.4
98.7	112.6	116.7	20.3	257.3	109.3	89.5	152.0
51.5	48.6	45.8	7.5	114.6	72.7	42.5	76.6
6.0	8.2	6.0	2.2	0.0	15.3	23.5	12.9
7.5	3.8	4.9	2.3	64.6	3.3	7.2	25.0
4.8	4.5	4.0	1.1	0.0	4.3	3.4	2.6
5.9	6.8	5.7	1.2	59.1	33.4	35.1	42.5
11.4	8.7	11.0	2.1	237.6	207.8	129.3	191.6
17.9	13.9	14.1	3.8	935.0	1503.6	1113.1	1183.9
30.5	20.9	23.5	6.2	2663.9	1323.8	960.9	1649.5
14.6	20.7	22.8	9.4	8.5	106.4	45.5	53.4
319.0	333.0	498.0	297.9	93.0	30.3	35.3	52.8
5.7	4.9	5.7	0.8	0.0	82.5	28.5	37.0
1.0	2.4	1.4	0.8	0.0	26.1	7.3	11.1
59.2	48.7	52.0	6.2	71.7	73.4	48.4	64.5
26.9	14.6	23.4	7.7	510.6	352.2	301.4	388.1
3.4	3.0	3.7	1.0	157.8	58.2	43.0	86.3
14.5	21.3	24.3	11.6	0.0	20.5	13.9	11.5
0.8	0.8	4.4	6.3	62.6	31.7	14.0	36.1
1.5	1.7	1.7	0.1	438.8	71.2	84.4	198.1
23.3	16.2	18.4	4.2	150.1	136.1	130.0	138.7
7.4	7.5	8.0	1.0	140.1	70.9	60.6	90.5
3.5	3.8	3.2	0.7	37.2	25.0	15.1	25.8
4.5	6.3	6.5	2.1	46.9	5.4	5.1	19.1
17.0	28.1	25.1	7.0	0.0	9.5	9.0	6.2
17.1	21.1	19.7	2.3	0.0	14.9	16.4	10.4
29.0	34.1	28.7	5.6	58.3	12.3	10.4	27.0
177.6	142.8	145.7	30.6	250.2	198.9	161.4	203.5
15.4	15.3	16.0	1.1	0.0	41.2	31.1	24.1
5.0	4.0	5.8	2.2	122.2	65.2	31.0	72.8
571.3	357.9	355.1	217.6	212.1	193.6	178.3	194.7
64.8	60.7	48.2	25.3	85.7	38.8	33.5	52.6
64.8	49.8	42.8	26.3	107.7	53.6	69.2	76.8
167.4	108.6	104.5	64.9	1.6	96.5	95.9	64.7
60.5	56.5	54.9	6.5	163.3	87.8	77.3	109.5
14.0	8.5	10.0	3.5	0.9	22.6	15.9	13.1
8.8	14.6	10.7	3.4	112.4	49.9	45.4	69.2
64.4	67.0	62.9	5.0	691.5	305.3	439.6	478.8

61.5	81.2	58.6	24.2	63.2	36.0	26.0	41.7
14.6	25.0	20.5	5.3	0.0	27.8	16.2	14.6
9.4	19.5	15.0	5.2	13.9	26.1	17.7	19.2
0.7	0.4	0.5	0.1	97.1	5.3	2.3	34.9
4.9	4.7	4.7	0.2	0.0	34.8	18.3	17.7
11.4	9.6	11.2	1.5	111.5	25.9	23.9	53.8
2.6	2.4	3.6	1.9	28.3	10.2	11.1	16.5
10.2	7.9	9.4	1.3	174.8	82.9	125.4	127.7
17.6	17.7	20.4	4.8	0.0	28.3	14.1	14.1
169.3	155.6	130.3	56.1	90.3	49.2	45.0	61.5
11.8	8.9	9.6	2.0	10.1	19.4	19.3	16.3
59.7	35.1	41.3	16.2	21.8	5.0	4.1	10.3
7.7	2.9	5.9	2.7	147.2	82.5	111.4	113.7
108.7	133.2	107.2	26.8	129.1	60.2	42.6	77.3
97.7	96.4	88.1	15.6	142.4	34.1	27.9	68.2
89.0	72.1	79.2	8.8	122.2	61.3	39.0	74.2
2.8	3.2	3.8	1.4	0.0	2.4	2.1	1.5
17.5	17.3	21.6	7.2	12.2	22.6	22.8	19.2
29.4	18.6	24.4	5.5	51.4	56.4	76.4	61.4
9.9	10.5	11.0	1.4	14.6	45.0	35.1	31.6
104.1	104.5	98.5	10.0	127.7	84.6	81.7	98.0
216.6	162.5	191.6	27.3	89.4	364.3	287.4	247.0
90.9	94.2	86.4	10.8	1184.4	159.3	175.6	506.4
353.0	327.4	341.0	12.9	842.2	665.4	920.6	809.4
616.8	562.3	629.8	74.9	986.3	929.6	986.5	967.5
1.4	1.2	1.4	0.1	28.9	16.3	12.6	19.3
77.8	65.4	84.3	22.9	2.7	118.2	91.4	70.8
1.4	2.0	1.5	0.5	51.2	14.6	10.7	25.5
6.8	4.1	5.7	1.4	0.0	22.3	11.1	11.1
264.2	321.9	264.6	57.2	276.2	218.8	159.5	218.1
67.8	71.5	69.3	2.0	148.6	243.4	184.7	192.2
31.1	35.2	34.1	2.6	42.4	66.6	55.0	54.7
20.8	20.8	23.0	3.9	0.0	52.0	31.2	27.8
29.4	16.1	22.9	6.7	0.9	35.8	32.4	23.1
76.8	217.6	100.9	106.7	79.5	72.8	37.6	63.3
11.2	11.9	12.5	1.7	209.5	30.4	21.7	87.2
3.3	3.9	4.8	2.1	132.5	26.5	23.1	60.7
12.1	33.5	19.9	11.9	1.9	25.8	46.7	24.8
12.6	7.0	51.3	71.9	996.5	3801.6	843.3	1880.5
72.5	83.9	100.5	39.0	277.7	223.7	255.4	252.3
25.9	32.9	39.7	18.1	202.8	168.9	84.4	152.1
4.9	10.0	15.2	13.8	72.1	53.1	13.1	46.1
8.7	7.4	8.6	1.1	69.8	205.8	92.7	122.8

20.1	20.0	22.7	4.6	137.5	67.7	64.4	89.9
2.7	4.3	3.0	1.2	239.7	146.0	190.1	191.9
2.8	3.8	2.8	0.9	400.1	320.4	228.7	316.4
518.5	587.0	673.7	212.3	203.2	400.0	333.3	312.2
25.2	32.4	41.3	22.1	262.5	334.0	335.6	310.7
11.2	15.4	12.2	2.8	1011.6	238.9	313.7	521.4
11.7	15.5	13.5	1.9	970.5	145.7	231.9	449.4
16.5	18.7	16.4	2.4	368.1	177.2	260.5	268.6
10.4	12.7	11.6	1.2	178.1	98.8	131.2	136.0
27.4	35.2	29.9	4.6	843.1	144.1	196.4	394.5
5.7	10.1	8.0	2.2	53.9	14.8	13.8	27.5
30.8	29.4	28.0	3.6	71.1	24.9	18.1	38.0
37.2	44.7	38.2	6.0	71.0	23.6	19.6	38.0
228.3	151.3	157.7	67.6	154.5	130.4	124.0	136.3
25.0	22.8	22.0	3.4	391.8	53.1	22.5	155.8
5.8	10.5	12.7	8.2	0.0	50.6	13.6	21.4
5.0	7.0	9.9	6.8	0.0	43.3	12.0	18.4
220.5	229.8	176.6	84.1	4568.8	2261.1	2357.9	3062.6
511.6	355.2	353.7	158.7	18481.1	7667.7	8036.6	11395.1
11.8	6.1	8.6	2.9	266.6	204.5	235.2	235.5
174.4	214.5	255.8	108.2	102.9	149.1	126.0	126.0
231.2	264.6	329.9	143.0	169.9	495.1	401.0	355.3
2.2	3.6	3.3	1.0	36.6	14.2	15.8	22.2
10.8	12.6	14.3	4.5	53.1	16.5	12.6	27.4
1032.5	657.9	654.8	379.2	139.9	94.8	88.8	107.8
145.8	104.5	103.4	43.0	103.6	118.8	92.1	104.8
85.8	59.9	65.5	18.1	152.7	126.6	148.5	142.6
60.7	51.8	55.4	4.7	396.4	110.0	122.1	209.5
71.0	47.0	57.2	12.4	121.3	154.7	197.6	157.9
83.8	55.8	77.4	19.2	362.1	164.1	127.5	217.9
116.2	92.3	100.6	13.5	26.4	68.7	57.7	50.9
62.2	65.9	73.9	17.2	265.1	253.3	275.4	264.6
7485.2	7186.7	4983.4	4077.4	46.0	73.7	65.5	61.7
30.9	29.0	37.4	13.0	373.7	244.2	145.9	254.6
12.7	10.0	479.4	810.7	72.4	79.5	49.0	67.0
2.8	2.6	81.5	136.5	15.2	11.9	7.7	11.6
5.2	1.7	94.5	157.7	51.0	23.8	17.1	30.6
3.2	1.7	56.9	94.4	36.1	13.0	10.3	19.8
138.8	141.1	156.9	29.5	195.4	317.8	408.9	307.4
61.7	92.5	98.7	40.4	857.4	403.3	320.0	526.9
52.2	51.6	66.1	24.5	93.1	154.3	116.2	121.2
5.6	5.5	10.2	8.1	113.7	43.0	21.6	59.5
140.7	152.4	131.6	26.5	414.6	262.9	231.7	303.1

53.4	55.0	57.8	6.3	1056.7	231.2	271.0	519.6
52.3	62.8	55.0	6.8	166.3	58.0	29.9	84.7
250.4	205.2	262.0	63.5	185.8	243.4	151.1	193.4
344.8	333.3	415.7	132.8	127.5	109.8	85.1	107.5
73.2	74.4	75.0	2.1	93.8	58.3	52.5	68.2
599.9	698.2	826.5	311.3	279.3	271.8	276.6	275.9
162.7	230.4	243.0	87.3	112.4	33.3	20.8	55.5
21.8	23.1	19.9	4.5	118.4	45.7	25.9	63.3
20.5	23.2	25.8	6.9	63.0	48.0	30.6	47.2
5.1	12.5	13.7	9.3	0.0	24.9	4.9	9.9
14.5	15.7	17.2	3.6	44.5	43.9	16.1	34.8
126.0	116.9	110.0	20.3	63.0	195.7	113.6	124.1
233.7	364.6	315.0	71.0	88.6	35.7	31.9	52.1
111.4	138.7	157.6	57.9	0.0	17.9	20.9	12.9
6.5	3.9	6.7	2.9	165.6	21.5	11.7	66.3
291.8	385.7	411.4	134.3	1935.8	522.3	526.1	994.7
8116.2	6441.1	6810.4	1165.8	12143.1	18964.5	28509.2	19872.3
11367.2	12718.7	12081.8	679.1	12653.0	32710.9	42840.1	29401.4
6079.1	7102.4	5658.1	1694.5	4306.7	17086.2	23624.3	15005.7
2.0	2.0	1.7	0.6	37.4	18.0	12.7	22.7
1.7	1.0	57.6	97.4	0.0	10.6	12.3	7.6
0.5	0.5	42.9	73.5	0.0	8.6	5.2	4.6
0.3	0.9	95.7	164.8	88.5	16.5	13.4	39.5
0.4	0.5	39.9	68.4	37.4	26.7	9.6	24.6
0.5	0.0	73.4	126.7	52.4	52.1	25.9	43.5
0.4	0.2	75.3	129.9	0.0	62.5	47.7	36.7
1.1	0.7	137.2	236.0	18.7	43.4	19.1	27.1
1.6	3.9	203.1	347.1	160.7	39.0	10.3	70.0
25.8	17.9	590.1	984.2	280.3	195.0	166.7	214.0
1.6	1.7	1.9	0.5	30.5	7.0	5.3	14.2
1.6	2.2	1.8	0.4	0.0	6.2	4.6	3.6
3.8	4.5	4.2	0.4	44.3	7.5	3.8	18.6
22.0	16.6	17.3	4.3	107.2	40.1	29.5	58.9
21.2	19.6	17.5	5.1	120.9	63.3	37.3	73.8
2.3	2.6	85.6	144.0	68.8	40.2	33.2	47.4
203.1	190.6	306.2	189.5	203.9	99.6	95.2	132.9
250.2	300.3	380.5	184.1	124.4	166.3	171.2	154.0
1440.8	1347.2	1323.6	130.6	4559.5	5900.8	6753.3	5737.9
61.2	50.0	49.5	12.0	315.0	227.4	148.1	230.2
62.3	57.8	55.7	8.0	113.7	112.8	94.4	107.0
231.6	256.5	251.8	18.3	127.7	250.4	194.2	190.7
173.3	185.3	189.6	18.9	181.0	101.7	85.9	122.8
59.6	83.3	73.9	12.6	101.3	102.5	61.6	88.5

83.5	87.0	79.4	10.4	90.9	99.4	73.7	88.0
167.5	155.7	173.0	20.5	653.6	229.2	190.9	357.9
24.3	29.2	28.9	4.5	165.5	88.8	44.2	99.5
6.0	11.0	7.7	2.9	1654.5	165.3	164.1	661.3
539.9	444.3	432.2	114.1	3002.3	758.8	924.3	1561.8
1.8	3.3	2.1	1.1	0.0	57.9	44.3	34.1
26.4	31.9	22.4	11.9	216.9	72.3	34.6	107.9
6.3	3.5	3.6	2.7	52.1	32.0	12.6	32.2
54.3	38.1	39.0	14.8	609.0	94.2	48.8	250.7
32.6	27.4	27.8	4.7	206.9	45.4	36.1	96.1
6.0	10.1	8.2	2.1	15.1	3.7	3.6	7.5
42.7	39.6	34.2	12.3	21.9	30.2	36.6	29.6
25.2	21.2	21.8	3.2	88.1	30.9	22.3	47.1
7.4	10.7	15.7	11.6	116.3	35.6	22.3	58.1
2.9	3.7	4.4	2.0	0.0	39.7	25.5	21.7
7.3	11.7	9.9	2.3	86.6	4.0	4.3	31.6
13.8	15.5	14.7	0.8	0.0	13.5	11.0	8.2
10.5	6.0	9.3	2.9	0.0	21.7	21.7	14.5
15.2	11.5	12.0	3.1	868.0	95.9	153.9	372.6
6.6	6.3	6.5	0.2	195.8	67.7	94.0	119.2
12.9	14.2	14.5	1.6	51.5	30.9	28.6	37.0
4.3	11.2	8.1	3.6	0.0	55.0	24.6	26.5
2.7	3.7	3.5	0.7	12.5	13.7	8.3	11.5
8.5	6.0	12.3	8.9	0.0	14.6	8.1	7.6
9.3	8.7	9.4	0.8	54.2	8.6	6.8	23.2
2.4	3.7	3.4	1.0	39.4	38.9	27.3	35.2
190.1	231.6	256.1	81.1	241.2	422.8	422.1	362.0
10.9	8.5	12.0	4.1	39.9	19.7	13.2	24.3
20.5	19.8	23.2	5.2	15.6	39.2	46.1	33.6
16.4	22.7	23.8	8.1	97.8	93.7	98.5	96.7
5.8	3.7	6.4	3.1	90.4	52.6	51.4	64.8
12.3	13.4	23.5	18.3	63.1	40.9	39.1	47.7
64.6	75.3	81.9	21.4	74.2	258.6	239.9	190.9
562.0	682.0	744.5	220.5	920.8	669.9	759.5	783.4
236.5	237.3	297.4	104.8	357.0	229.3	240.1	275.5
6.0	2.5	3.8	1.9	605.7	195.1	224.4	341.7
233.7	228.5	228.6	5.0	456.3	208.4	213.9	292.9
16.8	21.9	18.7	2.8	0.0	52.1	43.7	31.9
1197.0	608.5	897.6	294.4	354.9	310.2	352.5	339.2
88.5	85.5	125.6	66.9	194.0	113.6	77.3	128.3
66.0	70.4	65.8	4.7	43.1	58.2	28.1	43.1
82.7	91.0	100.6	24.1	127.0	101.2	77.8	102.0
41.0	37.4	46.5	12.8	9.2	45.5	51.4	35.4

74.7	88.6	88.8	14.2	179.5	103.9	126.5	136.6
116.2	142.6	136.4	17.9	655.6	358.3	479.5	497.8
3244.2	1845.6	2039.6	1120.2	15198.1	15751.4	18382.6	16444.0
229.4	229.2	317.6	153.0	248.4	136.7	140.0	175.0
25.7	35.5	39.5	16.2	75.1	60.6	36.6	57.4
99.9	150.9	141.2	37.5	378.7	688.3	282.0	449.7
3.5	5.1	4.2	0.8	60.6	42.5	14.9	39.3
8.8	12.4	10.8	1.8	85.2	22.8	11.6	39.9
26.3	20.3	21.0	4.9	94.6	44.7	25.4	54.9
79.4	78.1	71.6	12.4	157.3	113.6	54.4	108.4
352.4	220.2	356.7	138.8	302.4	328.7	253.6	294.9
484.4	290.7	504.7	224.8	183.2	211.3	192.2	195.6
287.5	225.1	308.8	96.2	150.7	194.2	121.5	155.5
417.8	245.8	429.4	189.7	169.5	317.4	343.0	276.6
36.8	41.4	46.0	12.1	70.1	25.8	15.9	37.2
24.9	22.5	29.7	10.4	90.9	15.3	10.4	38.9
9.5	4.3	7.5	2.8	82.3	5.6	4.7	30.9
6.7	8.1	8.5	2.0	1.7	11.5	6.4	6.5
129.5	127.1	165.3	64.0	339.4	962.0	630.9	644.1
1773.4	1261.2	1147.8	689.3	3954.8	1928.2	2272.0	2718.3
32.8	46.3	53.3	24.8	145.6	130.0	89.8	121.8
56.8	70.2	67.9	10.1	162.6	147.9	149.9	153.5
41.8	62.9	61.0	18.2	300.5	114.9	102.1	172.5
5.7	11.6	11.7	6.0	103.0	48.7	18.8	56.9
85.8	88.4	90.8	6.5	205.4	265.2	264.7	245.1
37.2	39.7	46.3	13.5	347.5	95.2	63.1	168.6
35.3	38.8	42.9	10.3	216.6	257.0	221.3	231.6
45.2	51.8	59.1	18.6	173.3	211.2	241.2	208.6
104.9	83.3	149.2	95.9	80.5	183.9	136.7	133.7
72.5	51.7	47.6	27.2	37.7	701.7	319.8	353.1
14.7	20.4	19.1	4.0	67.6	27.0	23.5	39.3
0.9	1.2	1.1	0.2	24.8	23.9	16.3	21.7
79.3	72.9	71.3	8.9	200.3	306.1	219.4	242.0
79.5	83.0	68.2	22.7	752.5	222.7	180.7	385.3
202.1	201.1	166.0	61.6	481.3	438.2	339.1	419.5
23.8	18.3	20.5	2.9	508.2	161.7	164.9	278.3
10.1	14.7	13.3	2.8	344.7	116.2	55.2	172.0
5.5	6.4	5.6	0.7	169.1	115.5	96.7	127.1
6.4	8.0	6.6	1.2	265.2	144.0	161.1	190.1
2.0	2.0	2.4	0.7	91.7	12.8	23.2	42.6
530.6	400.8	360.7	193.1	94.4	223.6	134.4	150.8
3.7	6.2	4.0	2.1	0.0	16.7	10.2	9.0
7.5	9.5	9.4	1.8	22.3	9.0	6.4	12.6

35.0	43.7	40.0	4.5	196.7	114.3	48.7	119.9
6.4	7.5	8.0	2.0	31.9	32.6	41.7	35.4
4.9	3.1	3.8	1.0	111.7	22.4	24.5	52.9
71.1	64.2	63.6	7.8	445.5	181.6	218.9	282.0
2.4	3.9	3.2	0.8	297.2	164.5	175.7	212.4
12.7	18.6	16.7	3.5	4.9	49.2	39.4	31.2
7.4	7.0	7.8	1.0	166.1	28.7	19.1	71.3
126.1	128.3	120.0	12.6	117.7	174.1	151.4	147.7
14.0	11.4	13.1	1.4	81.9	29.9	19.5	43.7
24.8	24.7	23.0	3.0	16.8	26.8	27.3	23.6
15.4	17.8	14.4	3.9	0.0	42.7	31.0	24.6
19.9	21.8	18.8	3.6	116.3	41.9	28.1	62.1
31.0	33.0	32.4	1.3	93.4	37.5	46.6	59.2
35.0	40.6	37.4	2.9	280.3	47.1	54.1	127.2
24.0	22.0	28.3	9.2	442.1	229.1	247.0	306.0
89.7	94.1	93.9	4.1	6935.1	796.5	1276.8	3002.8
7.1	11.6	9.7	2.3	64.1	39.3	25.8	43.1
4.8	3.4	5.5	2.5	0.0	36.8	22.1	19.6
21.4	22.6	19.6	4.2	49.5	114.0	113.2	92.2
67.3	62.6	77.5	22.0	911.0	150.8	124.0	395.3
120.3	133.9	150.6	41.2	165.4	64.1	49.6	93.1
59.0	80.5	73.0	12.2	104.5	40.8	25.0	56.8
61.0	74.3	58.4	17.3	0.0	38.2	31.7	23.3
305.4	255.8	238.4	77.1	101.9	59.2	60.5	73.9
453.1	398.5	354.8	125.9	5.5	40.4	49.5	31.8
424.8	374.9	327.4	128.0	35.3	26.5	29.1	30.3
412.9	409.5	340.3	122.8	90.6	48.3	39.0	59.3
194.7	185.1	154.5	61.4	66.9	33.1	27.0	42.3
190.0	140.4	137.2	54.4	25.0	29.4	34.3	29.6
88.1	72.6	75.6	11.3	293.8	41.0	47.8	127.5
116.6	94.1	103.0	12.0	346.8	48.5	39.2	144.9
97.5	79.1	92.0	11.3	50.5	102.8	122.4	91.9
6.6	7.1	6.8	0.3	60.0	29.2	17.2	35.5
6.2	8.8	6.9	1.6	20.2	4.8	4.4	9.8
461.3	472.2	400.0	115.8	54.0	38.3	31.8	41.3
62.0	36.2	74.7	46.2	0.0	48.3	49.3	32.5
28.3	17.6	36.7	24.5	23.5	20.6	19.9	21.3
19.9	22.1	31.7	18.6	95.9	32.6	25.3	51.3
10.5	5.5	13.6	10.1	1.8	15.9	17.6	11.8
4.9	4.2	8.3	6.6	60.9	6.9	10.6	26.1
1.9	3.9	7.7	8.4	0.0	4.3	6.2	3.5
5.1	4.8	8.6	6.4	0.0	10.4	6.2	5.5
8.4	5.7	12.5	9.6	23.8	20.4	17.8	20.7

3.4	3.4	3.8	0.8	75.2	7.6	8.2	30.3
21.4	23.0	23.5	2.4	163.4	63.5	65.1	97.3
15.0	14.9	12.7	3.9	73.6	88.2	74.9	78.9
69.4	77.2	64.5	15.7	472.7	506.7	474.3	484.6
133.0	187.3	132.4	55.2	2339.1	733.2	536.9	1203.1
15.5	16.6	28.3	21.2	91.9	89.4	41.5	74.3
53.4	50.2	45.1	11.7	458.8	151.9	140.6	250.5
40.4	38.4	35.8	6.2	366.6	256.5	354.5	325.9
71.5	77.6	72.4	4.8	0.0	43.2	48.3	30.5
67.0	67.9	62.8	8.0	120.6	56.2	55.0	77.2
40.8	44.8	40.8	4.0	44.4	57.5	42.1	48.0
32.9	33.3	33.4	0.5	68.2	59.1	29.4	52.2
16.5	13.4	18.9	7.0	102.7	34.0	47.1	61.3
4.4	4.2	3.3	1.7	51.3	21.1	11.5	28.0
16.6	13.2	12.1	5.2	330.1	142.4	127.4	200.0
166.8	218.8	158.7	64.4	302.8	169.3	65.1	179.1
15.2	14.0	24.9	17.8	28.8	51.8	17.4	32.7
22.8	35.2	28.9	6.2	281.0	54.6	64.8	133.5
58.8	50.8	48.3	11.9	68.3	41.2	42.2	50.6
10.1	13.3	12.9	2.6	39.4	18.4	13.5	23.8
3.9	7.0	5.1	1.6	35.1	23.5	10.3	23.0
8.0	11.1	8.5	2.4	21.4	37.9	13.1	24.1
13.8	17.4	14.5	2.7	79.0	40.2	35.0	51.4
37.9	43.6	34.6	11.0	135.0	76.2	54.4	88.6
683.7	748.4	803.5	155.0	96.8	133.3	98.8	109.6
76.9	85.1	88.6	13.7	0.0	38.0	29.0	22.3
96.6	68.5	82.5	14.1	139.3	48.0	48.8	78.7
35.6	30.1	35.0	4.6	30.7	30.2	28.0	29.6
107.5	91.1	103.2	10.7	133.4	51.7	52.1	79.0
15.0	20.5	18.5	3.1	6.7	177.4	124.2	102.8
374.9	360.0	324.6	74.6	111.9	102.2	80.7	98.3
6.6	7.9	7.8	1.1	1.5	33.7	27.7	21.0
82.4	44.4	83.2	39.2	12.0	110.2	50.6	57.6
12.4	14.7	17.4	6.6	0.0	125.3	78.8	68.0
162.9	162.4	151.3	19.6	857.4	334.4	221.2	471.0
602.4	395.1	392.3	211.6	815.9	585.1	597.7	666.2
38.4	33.9	42.3	10.8	0.0	126.5	93.8	73.4
14.5	11.8	15.0	3.5	11.3	55.7	35.8	34.3
86.0	71.1	61.1	31.2	128.3	34.1	26.0	62.8
134.2	111.5	97.4	45.4	91.1	90.8	59.0	80.3
3.0	1.9	2.7	0.7	50.8	37.8	41.0	43.2
73.2	89.4	74.4	14.5	147.0	102.6	94.6	114.7
4.0	4.3	4.8	1.2	89.8	34.1	38.2	54.0

3.6	3.1	3.8	0.8	16.5	22.3	29.5	22.8
4.5	1.8	4.0	2.1	34.5	36.0	54.4	41.7
3.9	1.4	3.2	1.5	89.3	40.9	36.4	55.5
4.2	4.0	4.6	0.9	47.8	45.2	53.0	48.6
9.4	5.0	8.4	2.9	35.4	69.8	93.6	66.3
6.2	3.5	4.7	1.4	113.2	70.8	96.0	93.4
50.7	14.0	37.1	20.2	2598.3	1890.9	2719.5	2402.9
4.2	3.5	3.4	0.8	1.4	6.2	5.6	4.4
0.3	1.5	0.8	0.6	0.0	8.2	3.1	3.8
18.6	16.5	17.3	1.1	27.8	25.2	30.4	27.8
26.3	25.8	25.9	0.4	74.7	71.7	30.1	58.9
14.0	19.9	16.5	3.1	0.0	26.0	47.4	24.5
14.4	15.9	17.1	3.5	246.6	29.6	32.3	102.8
8.0	14.4	10.0	3.8	0.0	29.2	17.2	15.4
38.3	26.9	33.8	6.0	149.5	129.6	121.4	133.5
34.5	28.9	31.4	2.9	210.3	107.8	121.1	146.4
63.3	67.8	87.5	38.1	188.7	115.7	72.6	125.7
12.5	14.6	15.1	2.9	91.6	68.5	55.0	71.7
16.2	17.1	20.5	6.7	35.4	55.3	36.1	42.3
12.5	7.2	9.0	3.0	109.4	45.6	35.0	63.3
3.0	2.0	2.4	0.5	0.0	18.8	9.0	9.3
11.7	12.4	11.6	0.8	390.4	176.3	154.5	240.4
34.8	25.5	25.6	9.2	365.7	100.6	59.6	175.3
9.0	12.2	12.2	3.2	200.2	174.8	199.5	191.5
8.0	10.0	9.0	1.0	53.3	33.8	42.7	43.2
6.8	11.7	9.6	2.6	1.1	31.1	35.0	22.4
91.6	98.1	95.8	3.6	66.3	70.0	87.0	74.4
28.1	28.5	26.3	3.4	0.0	16.0	20.8	12.3
29.8	33.3	29.1	4.5	75.6	16.5	16.5	36.2
6.2	5.1	5.4	0.7	30.1	8.3	9.2	15.8
2417.7	1394.1	1995.2	534.7	90.3	43.3	40.0	57.8
8.7	8.5	10.0	2.3	165.5	102.4	130.2	132.7
150.1	151.7	136.1	25.6	382.7	405.9	499.6	429.4
3.6	6.6	7.7	4.7	21.9	30.7	26.8	26.5
21.7	25.8	24.9	2.8	101.7	52.4	48.7	67.6
27.2	21.4	24.3	2.9	238.4	94.0	82.1	138.2
72.2	68.0	64.6	9.7	0.8	23.3	26.8	17.0
10.0	10.1	10.5	0.9	31.8	29.3	20.6	27.2
203.0	232.4	222.1	16.5	246.9	66.9	34.8	116.2
83.5	118.6	98.8	17.9	60.3	55.0	23.1	46.1
101.6	97.8	92.2	13.2	71.7	74.6	50.8	65.7
16.5	23.7	18.0	5.2	54.5	9.4	6.8	23.6
6.7	7.7	6.3	1.5	38.3	8.5	5.5	17.4

64.9	190.4	96.7	82.5	153.7	268.7	81.9	168.1
43.7	98.8	53.1	41.8	69.1	132.7	42.5	81.4
8.1	11.9	11.0	2.6	179.8	33.5	19.9	77.7
14.5	15.4	14.2	1.4	17.0	7.1	5.8	10.0
5.1	6.9	5.0	1.9	102.0	27.4	36.4	55.2
1.1	2.0	1.7	0.5	0.0	13.3	35.1	16.1
24.0	29.5	21.1	10.2	207.1	65.8	70.6	114.5
8.5	8.9	7.2	2.7	170.6	69.9	67.6	102.7
29.1	27.8	27.6	1.6	41.1	11.2	10.9	21.1
2.6	2.5	2.2	0.5	24.6	4.3	3.2	10.7
6.5	5.0	7.4	3.0	113.6	28.1	19.7	53.8
19.3	15.5	15.7	3.5	340.9	624.2	364.8	443.3
58.2	33.6	53.7	18.2	200.7	172.2	299.2	224.0
91.3	44.3	93.7	50.7	418.7	338.9	362.7	373.4
1.4	1.7	1.5	0.1	42.2	9.2	8.4	19.9
54.9	49.7	49.8	5.1	135.3	52.2	56.5	81.3
29.3	30.2	29.5	0.7	0.0	45.6	31.9	25.8
24.4	30.9	28.7	3.7	0.0	37.4	31.7	23.0
1047.1	1107.5	864.1	370.5	5.0	77.0	58.4	46.8
16.9	17.3	20.8	6.4	69.3	45.1	30.3	48.2
11.6	11.0	13.9	4.5	55.3	15.9	10.1	27.1
202.8	208.1	220.7	26.6	19.6	168.8	130.9	106.5
6.3	5.9	6.2	0.3	38.5	28.9	14.3	27.2
221.7	204.6	189.8	41.4	73.6	180.0	214.3	156.0
129.4	146.0	133.7	10.7	280.3	55.0	35.1	123.4
42.3	49.2	43.8	4.8	143.3	84.1	50.4	92.6
71.5	35.5	83.1	54.3	0.0	31.8	9.3	13.7
62.2	86.2	82.3	18.5	107.2	37.9	15.0	53.4
103.5	87.1	111.7	29.6	199.2	290.6	269.5	253.1
40.8	46.0	54.7	19.7	218.0	128.3	38.6	128.3
25.5	39.8	51.2	32.9	232.6	80.2	38.6	117.1
37.1	35.9	44.8	14.4	47.7	66.3	36.4	50.1
316.9	349.7	487.0	266.7	640.9	488.7	499.9	543.2
98.3	100.5	94.0	9.3	100.1	71.4	63.9	78.5
67.6	74.2	75.2	8.2	133.7	233.6	207.4	191.5
25.0	43.7	29.6	12.5	406.5	245.3	202.9	284.9
105.3	99.3	125.2	39.8	71.9	64.2	35.9	57.3
1.7	2.0	1.8	0.2	0.6	21.9	10.4	11.0
24.2	25.9	35.4	17.8	149.7	54.4	50.2	84.8
135.7	83.8	103.4	28.2	656.0	400.0	563.5	539.8
162.8	259.1	276.8	123.8	428.0	667.0	301.0	465.3
6.9	7.9	7.0	0.9	62.2	45.3	25.7	44.4
13.4	12.0	9.8	5.0	117.3	9.1	7.6	44.7

13.2	7.8	7.7	5.5	130.8	12.6	5.8	49.8
1251.6	855.3	976.7	238.6	84.1	42.1	40.9	55.7
73.3	85.6	93.5	25.2	389.4	93.3	69.7	184.1
12.4	11.2	11.8	0.6	173.3	653.3	300.8	375.8
36.5	31.8	32.9	3.1	84.4	90.4	92.9	89.3
29.1	44.7	31.5	12.2	126.9	110.8	81.2	106.3
64.8	64.3	72.9	14.4	97.4	150.6	143.7	130.6
76.0	93.4	103.4	33.5	175.4	103.3	148.8	142.5
34.8	31.3	35.3	4.3	37.0	14.5	15.4	22.3
137.0	124.3	129.1	6.9	752.1	251.6	162.0	388.6
45.6	48.8	55.4	14.2	94.4	79.9	84.4	86.2
6177.9	7228.7	5278.7	2522.8	666.1	705.3	570.0	647.2
79.1	64.1	59.7	21.9	462.2	162.2	205.1	276.5
115.0	103.1	93.3	28.0	2306.5	2075.5	2542.8	2308.3
35.4	47.2	41.9	6.0	237.9	139.2	55.1	144.0
29.6	31.0	29.7	1.3	59.1	32.7	29.7	40.5
81.7	76.6	99.4	35.1	172.2	135.1	99.1	135.5
298.5	303.4	237.2	110.5	77.1	47.2	47.8	57.4
12.9	12.4	13.4	1.4	219.3	72.7	50.7	114.2
61.6	42.4	43.0	18.4	0.0	64.0	45.7	36.6
20.3	25.6	27.8	8.8	151.4	54.0	36.7	80.7
52.4	57.9	52.6	5.2	267.8	72.2	46.3	128.7
2.8	1.5	2.0	0.7	2748.6	1513.5	2218.6	2160.2
0.5	0.5	0.5	0.1	179.6	140.4	128.5	149.5
1.2	0.5	0.8	0.4	176.6	104.1	115.1	132.0
4.3	2.0	2.9	1.2	1650.1	212.7	285.7	716.2
414.2	438.3	426.1	12.1	629.0	1619.2	1815.9	1354.7
10.1	12.0	11.5	1.2	143.1	79.1	63.9	95.4
14.1	15.7	14.9	0.8	214.7	85.1	102.9	134.2
12.4	18.8	14.6	3.6	89.6	108.1	87.7	95.1
99.4	135.8	118.8	18.3	375.3	120.9	73.7	189.9
16.8	16.2	22.9	11.0	217.7	75.0	39.5	110.7
4.2	8.3	7.9	3.5	138.7	65.0	32.0	78.6
2.3	3.5	4.4	2.6	38.4	20.0	10.7	23.0
4.3	4.8	5.4	1.6	58.1	41.3	43.3	47.6
20.6	33.3	24.7	7.4	216.1	35.0	20.1	90.4
0.6	0.9	0.6	0.2	0.0	3.4	2.5	2.0
1.3	1.1	1.2	0.1	15.8	4.6	1.9	7.4
69.8	52.6	46.3	27.2	0.0	47.3	24.5	23.9
37.0	33.4	27.2	13.9	142.2	29.1	30.5	67.3
20.5	18.1	14.7	8.1	119.4	10.8	8.8	46.4
177.6	113.0	101.6	82.3	1.2	16.9	12.8	10.3
284.9	183.4	169.6	122.7	53.8	30.5	37.4	40.6

469.3	265.0	282.8	178.4	194.4	71.4	78.6	114.8
564.9	418.3	354.0	249.4	20.3	19.5	21.1	20.3
31.2	42.1	40.8	9.0	458.4	224.6	169.0	284.0
16.3	20.6	30.8	21.5	57.9	51.6	17.9	42.5
22.1	26.7	23.1	3.3	66.0	24.6	23.1	37.9
153.3	163.2	198.0	69.1	55.8	61.6	57.0	58.1
51.1	57.5	55.3	3.7	0.0	14.4	3.6	6.0
35.3	45.0	37.9	6.3	0.0	38.4	22.6	20.4
6.9	5.4	6.6	1.1	55.5	42.6	28.1	42.1
6.8	6.5	7.0	0.5	98.6	53.4	47.9	66.6
19.2	19.5	19.7	0.6	97.2	60.4	31.1	62.9
4.7	5.4	5.0	0.4	101.1	42.7	13.5	52.4
9.4	15.7	15.7	6.3	15.1	66.1	33.0	38.1
6.3	6.5	8.0	2.8	211.2	57.1	45.6	104.6
4.5	5.1	4.0	1.5	230.5	36.7	31.0	99.4
44.3	31.9	45.9	14.9	65.2	106.0	92.8	88.0
211.9	302.9	294.2	78.2	607.8	93.3	73.2	258.1
663.1	706.3	522.9	281.1	896.5	785.0	592.8	758.1
45.0	59.4	53.6	7.5	38.1	207.2	107.8	117.7
97.8	119.0	143.7	62.1	332.8	141.7	156.4	210.3
101.0	123.4	138.4	46.8	972.3	989.9	500.3	820.8
121.4	89.3	85.9	37.3	528.6	305.6	272.8	369.0
29.3	28.8	27.2	3.2	29.6	51.7	27.3	36.2
102.2	96.8	103.1	6.9	255.7	234.4	235.3	241.8
126.0	107.0	118.0	9.8	176.5	134.4	104.2	138.4
13.0	10.5	12.3	1.5	0.0	35.3	27.1	20.8
25.6	13.0	16.9	7.5	32.6	31.8	27.0	30.5
55.8	68.4	62.3	6.3	0.0	83.2	55.1	46.1
16.8	16.6	18.0	2.3	60.9	35.5	26.6	41.0
23.0	23.5	21.5	3.0	21.4	47.3	29.9	32.9
139.6	160.8	174.7	43.8	0.0	96.1	85.3	60.5
118.6	169.4	154.7	31.4	287.6	100.4	66.9	151.6
11.3	8.1	9.8	1.6	36.4	150.9	61.3	82.8
22.9	12.3	16.9	5.4	230.0	223.1	130.8	194.6
122.9	94.1	94.1	28.8	1399.5	945.5	534.8	959.9
90.7	71.5	68.2	24.2	599.0	1034.4	849.8	827.7
188.1	132.3	129.0	60.9	0.7	105.2	114.6	73.5
4247.9	6128.5	4085.0	2129.7	545.5	664.6	867.1	692.4
179.7	204.6	179.4	25.3	165.6	217.3	180.9	187.9
10.0	7.5	11.2	4.3	10.4	5.4	4.0	6.6
159.4	102.3	171.4	75.8	29.3	82.8	38.5	50.2
131.1	78.8	137.9	62.7	95.2	75.8	40.6	70.5
70.3	35.9	73.9	39.9	2.5	36.0	20.7	19.7

65.3	38.7	84.7	58.2	1.2	31.3	9.4	14.0
794.3	343.4	696.2	315.4	553.4	603.8	396.9	518.0
3.6	3.4	3.5	0.1	29.6	47.9	55.6	44.4
23.4	25.8	27.9	5.9	118.1	55.0	19.4	64.2
196.8	190.1	192.5	3.8	100.3	176.4	134.2	137.0
557.4	657.0	695.6	161.0	900.4	631.1	529.1	686.9
27.5	32.6	30.8	2.9	98.8	68.9	38.0	68.5
48.8	79.4	70.6	19.1	127.7	76.7	36.6	80.3
42.7	61.7	61.3	18.4	84.3	73.6	19.1	59.0
25.9	16.2	22.2	5.2	150.3	262.2	233.5	215.3
19.6	25.7	23.7	3.6	74.7	86.5	70.5	77.3
72.5	68.4	94.0	40.9	162.8	226.0	181.2	190.0
71.4	63.9	71.0	6.8	73.8	34.5	34.9	47.7
40.0	57.8	52.0	10.4	50.8	37.4	29.3	39.2
6.0	1.6	3.4	2.3	366.9	148.1	90.4	201.8
1.6	0.4	0.8	0.7	15.7	26.7	11.6	18.0
2.4	1.8	2.1	0.3	3.9	28.1	16.2	16.1
19.4	14.9	15.7	3.3	80.7	52.1	35.4	56.1
30.3	28.6	24.0	9.5	312.7	134.7	84.7	177.4
4.5	4.5	5.2	1.2	145.2	102.9	54.0	100.7
48.8	90.8	73.2	21.8	110.3	85.4	29.9	75.2
25.6	31.1	28.9	2.9	0.0	50.4	23.9	24.8
27.3	30.0	25.2	6.2	69.7	89.9	88.0	82.5
17.9	18.6	18.4	0.4	35.3	29.6	18.7	27.9
15.3	18.0	18.4	3.3	25.8	18.3	11.7	18.6
140.6	110.5	151.5	47.3	425.3	66.2	55.6	182.4
24.7	29.8	31.5	7.8	27.2	63.8	40.3	43.7
12.3	14.6	13.4	1.1	14.4	10.8	7.6	10.9
1659.7	1238.7	1011.7	786.4	1166.0	534.0	712.5	804.2
54.8	57.3	56.3	1.3	181.8	209.0	181.1	190.6
54.9	76.7	66.3	10.9	211.7	87.4	70.3	123.1
340.9	352.2	320.9	44.8	1501.6	539.9	501.3	847.6
6.2	9.9	9.4	3.0	94.1	30.1	26.3	50.2
15.5	20.7	18.5	2.7	0.0	55.2	28.0	27.7
22.3	24.6	31.1	13.3	75.6	130.6	61.9	89.4
705.0	565.8	746.8	205.0	732.3	637.5	583.3	651.0
2.1	2.3	2.8	1.0	15.1	5.8	3.9	8.3
75.8	87.9	89.4	14.5	109.0	166.3	108.1	127.8
76.6	79.4	105.9	48.3	21.8	105.6	51.6	59.7
2.3	4.1	4.2	2.0	0.0	8.7	9.4	6.0
11.7	14.2	14.9	3.6	45.6	81.8	51.7	59.7
41.4	36.0	49.5	18.9	94.4	64.5	53.7	70.9
12.7	10.6	13.9	4.1	0.0	17.9	21.2	13.0

13.5	12.6	16.4	5.8	83.7	56.0	19.1	52.9
53.3	60.2	61.1	8.4	196.9	75.5	49.1	107.1
19.0	21.5	23.7	6.1	21.6	26.4	20.0	22.7
15.0	11.5	10.8	4.5	322.8	272.0	283.6	292.8
83.4	92.3	95.0	13.1	201.0	88.8	69.2	119.7
127.1	141.1	149.5	27.5	141.5	113.7	104.1	119.8
300.1	245.6	245.1	55.2	585.6	316.8	300.2	400.9
73.0	119.8	181.5	149.2	0.0	31.7	27.7	19.8
17.2	22.7	21.3	3.7	68.7	67.9	45.3	60.6
76.0	118.3	111.5	32.7	164.1	123.2	63.2	116.8
120.4	164.5	159.7	37.2	1607.8	377.0	292.1	759.0
35.9	40.3	45.1	12.3	277.6	204.1	170.3	217.3
27.9	24.1	26.1	1.9	19.0	12.8	14.1	15.3
0.2	0.4	0.3	0.1	10.7	5.8	2.2	6.2
50.9	53.9	44.0	14.6	195.1	122.7	168.4	162.1
155.9	77.9	104.2	44.8	1667.0	240.7	369.3	759.0
0.6	0.9	0.7	0.2	16.3	9.6	6.7	10.9
2.0	3.0	2.1	0.9	39.4	11.4	7.6	19.5
188.8	157.4	187.0	28.8	104.1	164.6	104.0	124.2
34.0	42.4	33.7	8.8	48.5	58.6	48.0	51.7
19.6	17.1	18.1	1.3	0.0	81.9	67.7	49.9
24.4	21.5	27.9	8.7	71.2	80.1	85.0	78.7
3.3	0.0	2.8	2.5	0.0	39.3	17.9	19.0
4902.8	3023.9	3363.4	1400.8	291.2	394.9	481.7	389.3
163.9	169.5	182.2	26.9	89.0	134.0	159.8	127.6
20.7	19.3	20.2	0.8	0.0	81.1	57.4	46.2
21.5	17.6	18.6	2.6	67.2	38.4	35.6	47.1
32.8	38.5	39.7	7.4	29.6	26.0	17.4	24.3
61.4	78.5	70.6	8.6	32.2	32.7	27.4	30.8
209.6	241.7	216.4	22.6	38.1	136.9	137.8	104.3
37.4	58.6	48.0	10.6	56.4	33.2	31.7	40.4
46.2	57.6	45.6	12.2	20.0	34.8	32.6	29.1
102.6	135.0	102.9	32.0	38.1	160.2	173.8	124.1
50.5	70.5	71.9	22.1	212.2	143.1	137.3	164.2
13.7	20.2	16.2	3.5	70.7	22.9	12.7	35.5
22.2	25.9	25.8	3.5	0.0	26.9	18.2	15.0
10.3	16.5	13.3	3.1	248.5	15.8	13.0	92.4
38.7	46.2	36.6	10.8	106.4	50.3	38.9	65.2
2584.8	1871.5	1721.3	947.5	1604.9	466.8	491.8	854.5
3.3	3.5	3.1	0.5	119.4	10.4	8.5	46.1
8.7	9.1	10.0	1.9	7.7	25.7	20.1	17.8
141.0	120.2	110.8	35.8	80.5	62.1	42.2	61.6
76.9	84.0	80.1	3.6	43.3	34.2	28.0	35.2

10.6	10.6	13.0	4.2	104.2	21.9	14.6	46.9
14.7	16.5	15.3	1.0	29.8	40.4	31.0	33.7
66.9	68.2	75.5	13.8	76.2	47.1	41.7	55.0
479.6	381.7	499.7	129.2	720.6	315.7	337.7	458.0
56.6	64.0	80.0	34.2	49.5	67.2	55.6	57.5
121.6	103.4	156.1	76.1	0.0	186.7	152.8	113.2
37.4	32.0	26.6	14.3	801.0	568.8	682.4	684.1
82.4	76.6	71.5	14.2	72.9	90.6	74.2	79.2
47.1	47.6	54.0	11.4	78.4	53.0	39.3	56.9
52.6	62.0	60.9	7.8	239.2	123.1	52.3	138.2
78.3	92.4	96.3	20.3	132.6	123.6	98.1	118.1
55.2	59.0	63.6	11.5	61.3	70.4	54.8	62.2
495.5	494.3	532.1	64.5	202.7	363.5	341.3	302.5
92.4	93.6	89.4	6.3	127.9	186.7	175.5	163.4
150.9	161.7	178.7	39.1	153.4	128.7	134.9	139.0
189.1	179.0	200.8	29.4	211.2	246.2	238.9	232.1
53.0	62.8	61.7	8.2	27.8	27.0	25.1	26.6
733.8	893.8	942.6	236.9	366.3	423.7	512.7	434.3
25.8	31.2	29.5	3.2	0.0	30.4	21.9	17.5
129.5	162.9	148.5	17.2	397.7	121.5	92.3	203.8
94.3	115.4	98.5	15.3	0.0	113.8	82.0	65.3
163.3	173.8	156.0	22.5	196.9	114.7	100.0	137.2
277.4	258.7	288.2	36.2	186.1	157.3	114.9	152.8
290.6	171.5	204.7	75.0	106.2	95.0	59.2	86.8
18.2	16.5	23.4	10.4	54.0	28.1	22.0	34.7
88.3	82.6	98.9	23.5	273.8	153.3	137.1	188.1
26.3	22.4	24.7	2.0	118.5	72.4	85.8	92.2
61.2	53.5	54.5	6.2	259.9	123.7	124.7	169.4
72.8	92.8	84.6	10.5	0.0	106.7	109.6	72.1
106.2	106.6	112.9	11.3	319.4	120.3	112.7	184.1
25.1	26.1	29.5	6.7	103.6	45.6	42.6	63.9
56.8	47.6	57.6	10.4	138.5	69.2	54.9	87.5
43.3	45.3	44.2	1.1	42.1	141.8	103.7	95.9
10.5	12.5	11.3	1.1	6.9	30.7	16.7	18.1
1.5	2.5	1.9	0.6	70.2	30.8	31.2	44.1
24.7	20.0	22.3	2.3	24.8	25.2	17.2	22.4
19.9	19.6	20.7	1.7	28.4	26.7	11.8	22.3
21.6	28.0	25.6	3.4	0.0	14.7	11.9	8.9
5.3	5.1	4.4	1.5	58.8	33.0	11.8	34.5
6.3	8.3	8.6	2.5	60.2	37.8	32.2	43.4
13.6	21.4	20.3	6.2	25.3	51.7	21.5	32.9
509.0	530.6	401.2	205.8	24.5	16.4	11.5	17.5
16.7	18.8	16.0	3.3	1194.9	66.0	79.7	446.8

25.7	22.6	35.9	20.4	17.0	57.8	49.8	41.5
197.1	176.1	246.3	103.9	126.9	237.2	182.8	182.3
847.1	1029.8	751.6	336.4	542.3	341.9	285.6	390.0
22.1	13.7	19.5	5.1	80.9	60.7	53.2	64.9
4.0	3.1	3.6	0.5	253.7	134.3	110.7	166.2
13.2	12.9	12.6	0.7	32.0	27.5	22.5	27.3
63.5	71.2	85.4	31.4	838.4	1610.2	2107.3	1518.6
41.3	42.5	49.5	13.2	295.2	151.1	162.2	202.8
24.2	26.5	33.4	13.9	120.9	120.6	126.6	122.7
37.6	42.2	45.6	10.3	171.8	67.8	84.2	107.9
24.5	26.1	29.0	6.5	34.6	49.2	37.2	40.3
16.8	14.8	17.2	2.6	119.5	26.4	25.7	57.2
409.4	473.1	587.2	254.7	81.9	290.5	232.9	201.8
5388.9	5167.1	8151.1	4977.6	5063.7	4502.3	4121.5	4562.5
698.6	827.6	1078.7	550.5	302.3	482.2	588.2	457.6
280.5	343.1	455.8	251.4	121.3	208.4	222.7	184.1
201.9	229.4	272.1	98.7	59.9	312.3	361.3	244.5
39.3	51.5	59.2	24.7	156.2	116.4	126.7	133.1
3232.1	3400.2	2892.6	738.3	13.1	3274.4	1831.6	1706.4
2449.0	4067.5	2746.2	1200.5	1075.9	3000.2	2031.7	2035.9
7.5	15.3	13.9	5.9	75.1	22.4	15.5	37.7
124.1	137.9	139.6	16.4	346.5	278.3	215.1	279.9
353.5	356.9	412.9	99.8	131.1	151.7	170.4	151.0
13.9	13.1	21.4	13.7	36.2	97.0	38.9	57.4
45.1	29.1	35.5	8.5	24.0	78.9	70.0	57.7
110.6	129.8	119.6	9.7	500.7	303.3	279.3	361.1
129.2	137.4	158.1	43.1	923.8	613.3	621.2	719.4
55.6	65.3	54.5	11.4	110.2	58.9	46.5	71.9
135.1	157.8	200.6	94.5	176.8	113.2	101.1	130.4
71.2	51.9	70.8	18.8	132.0	55.7	61.4	83.0
47.9	49.7	43.9	8.5	78.6	92.5	77.6	82.9
228.9	276.0	234.9	38.4	109.2	255.8	122.2	162.4
6442.6	6347.4	7576.6	2047.0	9198.6	18370.8	22520.0	16696.5
9628.6	9885.0	9665.3	203.9	13753.5	16531.5	23459.7	17914.9
1304.4	1019.7	1150.1	143.8	637.7	1307.8	1309.8	1085.1
153.1	200.0	165.4	30.4	287.0	77.5	56.9	140.5
17.2	23.7	21.0	3.4	88.7	31.8	28.5	49.7
19.1	21.1	20.9	1.7	135.9	51.9	55.3	81.0
215.6	335.7	356.5	152.3	762.7	1072.0	729.1	854.6
1045.1	755.0	719.0	345.5	738.9	470.0	629.8	612.9
1116.5	991.5	922.2	236.6	1229.3	724.7	634.8	862.9
515.0	250.0	414.8	143.8	3893.2	2551.2	2013.8	2819.4
8.3	5.9	9.4	4.2	243.6	101.8	72.9	139.4

30.6	28.7	29.0	1.5	103.0	46.4	49.1	66.2
87.1	96.1	100.8	16.6	17.0	37.5	35.3	29.9
98.2	31.6	53.7	38.6	2623.2	1242.6	1841.7	1902.5
45.1	18.3	26.1	16.6	339.3	368.3	572.1	426.6
26.6	11.2	17.7	8.0	1053.1	338.1	449.8	613.7
757.7	476.4	676.2	174.0	236.9	295.6	220.3	250.9
29.0	22.0	26.9	4.3	0.0	12.8	11.1	7.9
42.5	36.8	47.8	14.4	61.6	88.2	71.0	73.6
1.2	1.4	1.3	0.1	29.8	7.0	4.7	13.8
9.1	13.0	11.8	2.4	166.8	72.7	70.0	103.2
10.4	14.0	11.3	2.4	166.6	84.2	100.8	117.2
6.1	7.3	6.1	1.2	2.0	35.9	34.3	24.1
2.4	3.2	2.4	0.7	18.8	7.6	5.2	10.5
10.7	12.3	11.8	0.9	85.2	27.7	24.5	45.8
134.8	117.5	148.8	40.1	213.2	231.4	218.8	221.1
114.8	113.7	139.3	43.3	174.1	245.6	212.7	210.8
129.1	154.8	227.1	148.1	15.5	95.8	80.4	63.9
17.1	19.9	16.1	4.5	183.6	43.8	34.6	87.3
208.2	150.2	157.3	47.7	23.5	112.3	93.2	76.3
65.3	99.3	88.4	20.1	42.8	8.5	9.3	20.2
28.5	32.4	38.7	14.4	12.2	59.7	43.2	38.4
133.0	102.2	95.6	41.1	321.9	115.4	112.4	183.2
105.4	117.5	90.9	36.1	330.8	101.6	98.3	176.9
32.6	29.7	34.5	6.0	61.5	25.5	16.6	34.5
407.3	557.0	397.1	165.3	308.8	156.7	111.1	192.2
34.2	21.5	24.2	9.0	51.2	21.5	12.3	28.3
10.0	9.6	14.3	7.9	69.2	73.9	53.0	65.4
3.6	2.2	2.6	0.9	0.0	24.3	18.0	14.1
24.0	20.2	23.1	2.5	49.4	24.2	22.3	32.0
59.5	64.4	83.9	38.2	144.0	144.0	99.9	129.3
121.8	130.8	119.2	13.0	81.6	77.8	60.2	73.2
85.2	50.8	74.8	20.8	193.3	224.4	144.7	187.4
8.2	14.3	14.9	7.0	221.7	40.1	28.2	96.7
3.0	2.1	2.3	0.6	44.1	9.3	8.3	20.5
24.0	31.0	31.3	7.5	85.6	16.7	18.9	40.4
168.7	147.1	163.7	14.7	399.5	90.7	91.3	193.8
105.6	115.1	126.2	27.8	205.5	145.3	135.8	162.2
46.0	49.0	48.7	2.5	136.5	123.3	167.2	142.3
130.0	121.5	123.8	5.4	497.4	159.7	207.9	288.4
43.5	43.5	43.5	0.0	80.3	84.9	95.9	87.0
42.8	24.9	27.1	14.7	663.5	777.7	837.6	759.6
37.1	18.5	23.2	12.2	840.1	587.8	537.3	655.1
492.5	574.2	819.5	497.3	2181.7	1674.5	2148.0	2001.4

5.4	5.7	5.4	0.3	9.5	21.7	14.2	15.1
11.1	18.1	15.9	4.2	57.3	60.7	42.9	53.7
23.7	24.7	27.9	6.4	229.1	55.0	52.3	112.1
233.9	243.4	222.3	28.7	308.3	228.4	280.8	272.5
169.1	202.7	184.8	16.9	152.1	144.2	144.4	146.9
170.7	157.2	155.9	15.5	30.5	118.7	156.8	102.0
90.4	81.2	101.8	28.0	79.5	49.5	64.4	64.5
198.0	162.6	179.6	17.8	272.2	98.1	130.3	166.8
140.2	115.3	111.4	30.9	471.1	98.0	98.1	222.4
70.2	73.5	71.0	2.2	87.8	98.6	69.8	85.4
34.6	43.9	38.0	5.2	227.9	99.1	52.9	126.6
123.9	110.6	107.8	17.7	185.9	183.2	145.8	171.6
482.2	604.5	619.9	146.0	206.2	411.4	290.5	302.7
568.4	663.7	668.7	102.8	47.6	145.0	141.6	111.4
133.8	121.8	138.5	19.4	61.4	56.1	51.2	56.2
158.1	172.7	183.5	32.2	100.7	43.2	37.1	60.3
293.9	286.1	307.7	30.9	1.0	45.9	55.3	34.1
354.3	366.6	384.7	42.3	67.0	111.9	112.4	97.1
264.3	304.1	329.0	80.0	103.2	156.7	163.1	141.0
299.9	268.0	311.2	49.8	246.1	210.1	257.5	237.9
232.3	232.9	279.7	81.7	468.6	209.4	259.7	312.6
156.6	150.8	214.6	105.5	78.0	207.6	252.8	179.5
67.3	69.8	99.7	53.9	314.5	177.5	199.5	230.5
26.3	23.9	39.5	25.0	31.0	67.5	96.2	64.9
13.0	12.6	15.7	5.1	99.2	44.8	37.1	60.4
11.6	10.9	11.6	0.8	1.0	11.2	10.3	7.5
14.3	11.4	14.8	3.7	31.5	15.8	13.5	20.3
32.1	26.0	31.3	5.0	0.0	12.2	15.7	9.3
21.2	20.7	28.4	12.9	0.0	15.7	11.1	8.9
55.2	39.7	61.4	25.5	0.0	42.6	23.3	22.0
132.8	94.7	158.7	80.1	0.0	62.2	52.5	38.2
58.5	47.0	88.5	62.2	11.9	47.2	33.9	31.0
39.5	34.3	58.0	36.5	2.3	40.4	22.9	21.9
46.6	41.2	60.9	29.6	60.0	45.0	41.6	48.9
36.9	29.4	33.0	3.7	0.0	20.8	17.6	12.8
48.0	42.1	46.6	4.0	34.8	48.9	47.8	43.8
38.7	31.3	39.3	8.2	1.4	43.0	49.4	31.3
57.6	54.0	88.3	56.3	1.1	66.4	51.1	39.5
46.0	33.8	69.1	50.9	24.6	44.3	39.8	36.2
59.0	51.0	91.2	62.9	143.7	84.1	70.7	99.5
30.4	28.5	61.1	54.7	0.0	26.0	22.6	16.2
28.3	25.9	52.4	43.9	16.9	54.4	49.0	40.1
289.2	246.0	284.8	36.8	488.6	481.0	469.7	479.8

135.1	100.0	213.2	166.6	54.6	160.6	75.8	97.0
69.2	51.4	77.1	30.3	61.6	32.9	20.5	38.3
105.0	84.5	103.2	17.9	13.1	13.0	11.3	12.5
317.3	298.6	305.5	10.3	0.0	15.7	12.0	9.2
8508.1	8115.4	7042.6	2206.9	25.3	120.2	127.9	91.1
2931.2	2401.9	2226.2	807.4	21.9	64.9	55.1	47.3
2894.1	2098.0	2236.4	600.6	249.1	57.2	61.7	122.6
170.8	151.7	141.1	36.2	0.0	27.1	25.7	17.6
1806.8	1760.9	1810.9	52.1	13.8	82.3	50.4	48.8
90.0	82.7	111.9	44.6	0.0	31.6	29.8	20.5
164.7	174.0	220.5	88.6	20.9	9.2	11.5	13.8
115.6	118.9	137.4	35.0	59.3	18.4	11.4	29.7
73.4	61.6	85.9	32.3	47.0	51.0	66.7	54.9
101.2	89.7	118.7	40.6	0.0	14.4	14.0	9.5
146.7	142.4	187.1	73.7	0.0	6.1	5.0	3.7
133.8	139.4	166.1	51.1	49.3	8.8	5.5	21.2
600.5	452.1	517.1	75.9	91.5	140.1	177.5	136.4
2061.0	2104.8	1945.1	239.7	1054.8	267.3	349.8	557.3
1844.2	2065.4	1759.4	356.0	161.3	246.1	323.4	243.6
1971.7	1989.8	1967.4	24.7	2001.4	255.0	321.3	859.2
239.9	188.1	224.3	31.5	353.4	115.6	106.0	191.6
328.2	280.6	299.3	25.4	93.7	172.0	128.3	131.3
33.1	31.8	32.4	0.6	322.6	96.7	98.1	172.4
1336.2	1023.8	1064.3	254.1	1268.3	883.6	974.7	1042.2
588.8	466.8	467.1	121.5	473.0	619.5	690.2	594.2
247.2	172.8	210.9	37.2	93.4	44.3	34.7	57.5
218.0	173.7	221.6	49.8	40.5	37.1	20.7	32.8
59.6	49.8	69.2	25.5	20.7	54.1	41.0	38.6
8.0	9.3	9.6	1.8	81.8	7.8	3.4	31.0
209.7	200.9	290.0	146.8	50.3	287.3	240.3	192.7
156.7	154.8	158.5	4.9	16.9	111.8	51.0	59.9
37.4	29.9	32.8	4.0	216.1	110.5	94.9	140.5
24.0	22.7	30.4	12.3	1.7	18.6	24.7	15.0
374.7	328.1	313.6	69.4	568.3	418.3	470.6	485.8
26.4	26.4	34.7	14.3	189.1	50.4	37.5	92.3
393.9	335.7	319.4	83.8	1045.8	1592.9	1091.4	1243.4
1238.2	1112.5	1173.0	63.0	699.5	648.4	622.8	656.9
457.1	581.5	532.7	66.4	327.5	303.4	298.6	309.8
1214.5	1258.2	1433.8	342.7	496.8	1277.4	1066.8	947.0
560.5	543.5	417.8	232.7	191.8	128.0	120.5	146.8
597.1	373.1	353.7	253.7	259.6	520.5	391.8	390.6
456.0	290.9	287.3	170.6	899.3	813.9	668.2	793.8
36.6	55.3	44.1	9.8	364.3	34.8	31.4	143.5

781.1	366.0	412.8	347.3	161.4	242.5	307.6	237.2
749.2	478.9	567.0	157.8	352.3	223.1	357.8	311.1
634.4	389.7	543.8	134.2	898.7	141.3	216.1	418.7
226.8	150.8	320.5	231.2	107.6	192.5	254.2	184.8
51.6	33.2	216.4	301.6	684.4	325.3	411.7	473.8
9.9	8.7	54.4	78.2	497.5	276.8	234.5	336.3
18.0	19.5	20.3	2.8	141.8	43.6	35.0	73.5
121.1	106.2	108.6	11.6	421.3	216.5	222.3	286.7
36.1	38.5	37.8	1.5	322.7	327.5	316.6	322.2
467.0	390.3	326.3	181.5	417.4	210.6	333.3	320.4
32.8	30.6	28.1	6.4	0.0	37.0	51.9	29.6
41.1	81.6	82.5	41.9	99.6	93.9	51.6	81.7
129.9	105.3	137.9	37.3	153.2	95.1	101.0	116.4
53.3	59.8	50.3	11.3	100.5	17.0	13.7	43.8
89.5	114.6	87.5	28.1	58.7	66.0	32.4	52.4
241.8	195.6	224.8	25.4	140.5	166.1	185.7	164.1
339.5	299.9	330.6	27.4	277.1	291.6	341.1	303.3
92.1	113.4	108.6	14.7	233.5	149.0	65.3	149.3
444.4	373.3	417.3	38.4	471.3	427.7	363.0	420.6
34.3	35.8	33.7	2.4	194.7	100.1	70.8	121.9
37.5	41.3	41.6	4.3	153.3	62.2	66.6	94.0
577.6	407.0	512.7	92.3	137.3	144.3	139.5	140.4
151.5	114.8	139.4	21.2	352.8	47.3	46.3	148.8
73.3	91.5	83.4	9.3	426.1	221.4	218.2	288.6
46.8	45.5	54.6	14.7	11.0	48.0	39.4	32.8
347.5	302.0	410.7	150.7	686.5	603.4	731.3	673.7
46.4	49.1	54.1	11.1	172.3	115.7	78.8	122.3
26.9	35.1	46.4	27.0	204.3	92.0	77.0	124.4
429.3	339.8	336.6	94.5	212.4	213.4	173.1	199.6
707.2	685.9	596.2	174.1	254.2	278.9	203.5	245.6
45.9	41.6	43.0	2.6	2455.9	2565.7	3082.6	2701.4
84.4	74.4	76.9	6.6	47.0	34.1	25.8	35.7
73.2	56.7	65.3	8.3	10.7	41.5	36.1	29.4
32.0	30.8	32.3	1.7	139.5	44.6	45.6	76.5
76.2	74.9	67.9	13.2	266.7	192.9	202.5	220.7
79.9	65.9	74.4	7.5	65.0	55.4	45.6	55.3
29.5	30.6	36.0	10.3	23.8	9.6	10.7	14.7
75.3	88.3	79.9	7.3	34.0	34.0	26.4	31.5
15.1	15.1	17.7	4.5	38.8	38.4	36.9	38.0
215.6	170.5	205.6	31.4	386.9	331.4	264.8	327.7
462.7	247.1	283.2	164.4	222.8	290.3	234.1	249.1
41.7	44.1	41.2	3.1	452.2	98.1	79.1	209.8
351.1	297.0	363.7	73.8	122.6	185.8	155.6	154.7

69.0	70.8	79.8	17.3	41.6	41.4	43.0	42.0
49.0	45.2	51.9	8.5	0.0	37.3	35.8	24.4
36.6	33.7	41.5	11.1	84.7	58.6	43.7	62.3
393.0	420.0	459.2	92.3	265.7	475.5	460.0	400.4
273.2	351.3	370.8	108.7	272.2	496.7	494.7	421.2
355.8	381.7	405.6	65.0	499.0	452.1	531.9	494.3
560.6	446.1	532.6	76.4	541.0	462.0	508.7	503.9
76.4	80.3	98.6	35.2	196.5	157.2	176.4	176.7
45.8	48.5	54.6	13.0	362.9	167.5	213.0	247.8
32.3	31.3	35.3	6.1	20.5	31.8	23.5	25.3
54.2	45.4	53.8	8.2	14.4	63.7	46.1	41.4
127.1	115.8	118.2	8.0	85.5	152.0	132.9	123.5
703.9	699.8	717.8	27.7	208.9	494.0	425.0	376.0
193.3	215.6	298.6	163.4	87.3	228.3	156.8	157.5
2074.9	3111.0	2611.9	519.1	576.4	1844.6	1464.9	1295.3
3149.1	4139.4	4010.3	804.4	2617.2	4060.6	4035.1	3571.0
272.5	339.8	309.7	34.2	140.8	306.8	213.8	220.5
29.4	25.0	30.5	6.1	23.1	8.7	8.2	13.4
83.9	95.5	85.7	9.0	459.0	91.4	79.6	210.0
158.0	212.0	238.6	96.6	142.6	146.4	173.5	154.2
145.3	156.6	186.9	62.5	0.0	110.9	130.4	80.4
625.6	623.1	628.6	7.6	36.7	431.1	415.4	294.4
143.4	221.9	189.5	41.0	434.3	174.3	172.7	260.4
59.2	57.2	73.0	25.7	115.0	65.5	57.4	79.3
1522.6	998.5	910.9	659.9	143.9	251.2	338.7	244.6
5.1	3.7	4.4	0.7	226.9	446.4	336.6	336.6
2.5	1.5	2.0	0.5	201.2	409.3	354.5	321.7
72.4	74.7	72.6	2.1	97.2	51.5	51.7	66.8
5188.9	4575.9	6350.5	2561.3	5257.2	11562.9	9129.7	8649.9
118.6	152.0	127.8	21.2	28.6	64.1	57.5	50.1
39.8	35.0	38.9	3.6	67.9	143.2	140.5	117.2
9.3	8.3	8.0	1.5	0.0	89.8	79.5	56.4
30.2	25.9	27.2	2.6	41.0	35.5	20.9	32.5
1.6	1.9	1.8	0.1	74.7	8.4	4.9	29.3
1550.7	1065.8	1195.6	311.2	2935.4	3761.2	3896.0	3530.9
153.4	126.0	119.8	37.1	285.5	139.0	131.4	185.3
71.9	88.6	74.1	13.5	138.2	104.5	83.7	108.8
14.1	16.0	15.5	1.2	19.0	37.8	28.1	28.3
9.8	11.4	11.2	1.3	23.9	28.5	22.3	24.9
14.9	17.4	15.9	1.3	39.6	47.8	40.1	42.5
37.1	32.3	33.0	3.8	94.3	87.7	86.1	89.4
74.1	57.4	63.2	9.4	4.9	164.0	155.4	108.1
72.1	83.4	84.6	13.1	170.3	47.8	36.1	84.7

114.7	94.8	162.4	100.3	83.9	136.6	99.5	106.7
86.2	60.2	101.4	50.6	281.4	129.4	88.3	166.3
73.6	59.5	56.9	18.1	188.4	86.0	69.2	114.5
125.9	111.0	137.0	33.0	50.2	181.0	269.4	166.9
1576.8	2220.3	2170.1	569.9	531.4	800.1	1244.9	858.8
46.2	31.0	38.7	7.6	100.4	76.8	119.8	99.0
525.9	518.8	553.8	54.6	588.3	469.8	507.6	521.9
73.6	72.1	69.6	5.7	0.0	54.6	45.1	33.2
112.1	75.6	135.2	73.8	26.2	23.2	15.0	21.5
65.0	48.3	68.3	21.8	398.8	295.8	453.2	382.6
21.7	27.9	31.8	12.4	183.2	87.8	52.7	107.9
21.7	21.2	24.6	5.4	79.3	62.1	47.4	63.0
317.4	325.9	329.2	13.8	339.1	275.0	255.0	289.7
38.5	27.3	27.5	10.9	10.2	239.5	142.9	130.9
5.4	5.2	4.6	1.3	21.4	4.9	6.9	11.0
21.4	16.1	18.1	2.8	0.0	7.9	7.1	5.0
13.0	10.2	10.5	2.3	23.8	4.4	4.9	11.0
9.6	4.1	7.9	3.3	0.0	2.3	4.0	2.1
5.4	5.8	4.9	1.3	0.0	1.7	2.2	1.3
5.2	4.4	4.8	0.4	0.0	1.4	1.8	1.1
2.8	2.3	2.4	0.3	71.7	2.0	1.0	24.9
1.3	1.8	1.5	0.3	67.8	2.6	2.2	24.2
13.3	9.6	10.7	2.3	83.6	33.3	35.3	50.7
9.8	10.1	9.2	1.4	0.0	18.9	19.8	12.9
3.3	4.3	3.9	0.5	41.5	4.4	5.6	17.2
1.6	1.0	1.4	0.3	45.1	1.4	0.9	15.8
2.2	2.5	2.0	0.6	80.7	4.9	5.2	30.3
9.6	6.4	7.3	2.1	67.7	5.6	9.1	27.5
10.3	8.9	9.3	0.9	45.3	10.6	8.9	21.6
14.7	17.1	16.0	1.2	26.3	7.1	9.9	14.4
2.0	1.5	1.8	0.3	18.0	2.3	2.8	7.7
99.0	41.7	64.3	30.5	200.2	27.5	20.0	82.5
1.2	1.2	1.5	0.5	0.0	8.4	2.1	3.5
1.7	2.1	1.6	0.5	29.4	8.0	9.1	15.5
356.5	286.8	312.2	38.5	53.6	149.7	157.1	120.1
313.3	285.8	287.4	25.1	373.7	240.2	204.4	272.8
159.1	173.6	177.5	20.7	301.6	89.9	62.7	151.4
199.6	164.1	178.5	18.7	0.0	105.8	113.6	73.1
23.0	29.3	26.9	3.4	3.4	19.2	10.6	11.1
30.8	20.8	20.4	10.6	57.1	21.7	15.7	31.5
24.6	13.7	18.7	5.5	0.0	12.8	15.3	9.4
4.1	3.1	3.9	0.8	0.0	2.7	2.6	1.8
6.5	5.0	6.1	1.0	1.0	2.5	2.8	2.1

4.4	5.2	4.7	0.4	32.6	4.2	2.5	13.1
7.8	6.1	7.5	1.3	22.2	3.5	4.8	10.2
8.1	6.1	8.3	2.3	17.1	4.8	8.5	10.1
14.1	13.6	15.3	2.7	16.8	7.8	6.2	10.2
2.9	1.8	2.1	0.7	0.0	5.8	2.9	2.9
95.1	69.1	64.1	33.9	0.0	12.6	11.4	8.0
12.6	12.7	11.4	2.1	27.1	3.2	5.9	12.1
46.9	39.5	30.8	21.8	30.7	16.2	15.9	20.9
30.0	30.5	33.2	5.2	0.0	46.1	45.5	30.5
1.3	1.2	1.2	0.0	28.3	5.4	5.5	13.1
0.5	0.9	0.5	0.3	0.0	5.7	1.9	2.5
113.2	87.6	141.0	71.4	154.0	217.0	174.1	181.7
3.3	4.7	3.4	1.3	51.0	31.9	30.5	37.8
12.8	8.9	9.6	2.9	3918.3	48.4	292.2	1419.6
36.7	37.3	30.9	10.6	2543.7	121.9	659.7	1108.4
7.1	12.2	12.9	6.2	263.3	25.5	28.5	105.8
1501.3	919.2	820.3	735.4	30.0	13.2	10.9	18.0
1.6	1.4	1.5	0.1	84.0	12.5	4.5	33.7
30.7	19.1	22.3	7.4	266.3	224.4	184.9	225.2
101.7	54.1	63.9	34.0	3097.3	3746.3	4966.9	3936.8
136.1	109.6	115.0	19.0	3191.3	1239.4	1593.0	2007.9
43.8	37.8	44.8	7.6	137.7	34.7	32.7	68.4
45.8	45.5	56.4	18.6	27.5	33.9	33.6	31.7
64.5	65.1	77.5	22.0	52.0	67.8	58.7	59.5
63.3	60.8	62.1	1.3	0.0	59.1	51.0	36.7
34.5	34.4	37.2	4.9	62.5	44.9	41.5	49.6
18.6	39.2	30.9	10.9	125.9	40.5	26.4	64.3
4379.8	5162.5	4294.3	914.0	798.3	1574.2	2090.9	1487.8
617.2	684.2	624.8	55.9	685.9	558.6	685.7	643.4
17.3	26.7	22.7	4.9	491.0	128.4	92.2	237.2
306.0	330.0	268.9	85.8	1.0	25.0	17.7	14.6
254.2	241.2	231.3	29.1	228.9	179.3	235.5	214.6
69.0	75.9	69.7	6.0	267.4	135.5	141.8	181.6
23.6	27.9	34.2	14.9	67.4	30.4	24.5	40.7
112.8	106.9	114.1	7.9	126.5	113.4	92.4	110.8
255.5	225.9	232.3	20.9	47.5	154.2	139.3	113.7
15.1	17.4	22.1	10.1	70.4	37.0	31.9	46.4
86.9	103.4	120.1	44.0	488.6	307.4	375.9	390.6
68.2	64.0	95.7	51.2	415.4	187.6	258.7	287.2
131.4	104.7	171.1	92.8	847.9	243.5	308.5	466.6
228.5	227.3	291.8	110.7	481.8	347.1	360.2	396.4
57.2	46.4	54.7	7.4	108.4	213.2	251.8	191.1
42.7	48.2	45.0	2.9	100.4	160.2	199.2	153.3

350.3	270.7	285.7	58.6	2381.7	1291.0	2067.1	1913.2
336.9	289.3	288.2	49.3	2567.3	801.5	1491.0	1619.9
190.5	172.3	179.0	10.0	46.8	58.1	54.2	53.0
11.3	10.7	10.1	1.5	0.0	21.6	16.3	12.6
207.3	190.2	180.8	32.1	4.3	56.9	58.8	40.0
84.5	79.8	81.5	2.6	206.2	66.4	51.6	108.0
11.8	11.8	12.5	1.2	0.0	20.5	12.4	11.0
77.7	70.6	72.1	5.0	269.3	203.8	80.2	184.4
99.6	96.2	88.0	17.3	66.8	32.6	31.4	43.6
140.1	153.6	127.6	34.0	40.2	68.7	62.3	57.1
250.9	279.9	231.7	60.1	202.6	180.9	164.2	182.6
776.3	604.4	570.1	225.4	222.9	762.7	860.5	615.3
46.9	35.8	42.8	6.1	0.0	61.2	75.0	45.4
95.6	92.9	130.0	61.9	209.9	123.8	110.9	148.2
72.6	79.2	80.3	8.4	201.4	141.1	85.0	142.5
348.4	296.9	236.7	151.1	61.5	91.4	122.9	91.9
306.8	247.3	289.8	37.1	302.1	333.6	253.3	296.3
174.4	219.3	182.0	34.1	191.1	167.3	96.0	151.5
12.7	14.1	15.2	3.2	38.3	42.0	43.1	41.1
87.7	75.8	93.4	21.0	429.7	425.3	384.3	413.1
39.9	43.1	35.0	11.2	1862.0	159.4	146.3	722.6
37.7	40.1	43.9	8.7	94.7	76.7	68.7	80.0
57.9	59.5	60.5	3.2	91.7	85.9	77.8	85.2
3231.7	3953.0	2628.2	1708.4	711.8	477.5	529.9	573.0
277.0	173.2	244.3	61.6	113.5	82.2	67.4	87.7
162.1	139.4	179.0	50.2	110.1	65.9	49.3	75.1
142.7	122.4	150.6	32.9	98.4	84.0	49.7	77.4
125.5	99.7	96.7	30.5	747.3	216.5	273.1	412.3
519.7	622.8	534.2	82.3	1482.2	588.2	653.6	908.0
222.7	186.1	195.3	24.2	321.0	116.6	82.6	173.4
106.2	93.6	86.0	24.9	70.6	61.2	55.3	62.4
2.5	4.0	3.1	0.8	0.0	11.0	7.6	6.2
125.1	121.8	121.0	4.5	28.1	51.8	35.9	38.6
259.9	245.4	201.2	89.4	32.0	54.2	47.3	44.5
140.2	68.4	101.5	36.2	529.4	296.7	376.2	400.8
140.5	182.9	191.3	55.5	38.7	140.1	87.9	88.9
6.9	10.1	11.9	6.2	50.5	19.4	8.4	26.1
38.2	34.7	35.9	2.0	0.0	29.4	31.5	20.3
45.9	50.3	61.1	22.6	105.8	61.8	34.5	67.4
7.5	5.2	8.2	3.4	233.3	74.6	73.4	127.1
13.7	8.7	12.2	3.1	445.2	161.7	125.9	244.3
132.7	175.1	168.5	33.0	963.7	1264.8	875.2	1034.6
330.2	314.4	309.0	24.3	52.8	64.3	58.3	58.5

26.2	32.4	33.4	7.6	83.6	45.0	29.4	52.7
28.7	31.2	37.2	12.7	200.0	62.8	42.2	101.7
24.1	25.6	33.2	14.6	67.0	46.6	28.3	47.3
379.4	300.9	243.2	172.4	77.0	76.8	88.0	80.6
39.2	29.9	24.3	18.4	30.7	1.2	1.7	11.2
62.3	47.8	39.0	28.8	0.0	2.3	1.9	1.4
102.3	71.4	62.3	45.2	0.0	3.4	2.7	2.0
94.0	57.4	56.2	38.5	20.3	9.3	14.1	14.5
67.9	31.2	38.7	26.4	32.0	15.6	15.9	21.2
14.3	10.4	10.8	3.2	0.0	3.0	2.1	1.7
53.1	37.5	35.6	18.5	44.1	8.5	7.8	20.1
208.5	71.4	116.6	79.6	37.7	18.9	22.2	26.3
123.8	41.0	70.7	46.1	2.4	37.9	48.2	29.5
13.8	17.0	41.1	44.5	81.2	27.3	14.9	41.1
3.8	5.0	13.5	15.8	22.0	20.6	9.4	17.3
58.6	44.7	587.5	928.2	378.1	486.3	324.4	396.3
3.1	2.8	2.6	0.5	31.0	8.2	12.5	17.2
2.8	2.8	2.5	0.5	99.2	2.9	2.7	34.9
88.4	108.8	85.7	24.6	0.0	107.3	85.2	64.2
13.6	16.2	14.1	1.9	40.1	16.6	13.0	23.2
5.6	4.2	5.1	0.8	1.8	5.3	6.5	4.5
7.7	8.4	8.2	0.5	52.5	9.2	10.2	24.0
782.7	473.6	670.5	171.1	78.1	224.3	171.4	157.9
64.9	58.3	59.1	5.6	78.0	47.1	31.4	52.2
122.5	123.5	126.3	5.7	34.4	25.0	19.3	26.3
38.6	44.9	40.1	4.2	55.3	30.0	32.0	39.1
25.0	36.0	29.9	5.6	57.7	30.2	23.2	37.0
121.2	146.4	133.5	12.6	603.3	208.1	291.5	367.6
565.9	453.8	527.7	64.0	1170.8	929.0	1106.0	1068.6
48.9	56.1	60.1	13.6	73.8	98.9	89.3	87.3
77.4	56.5	69.0	11.0	16.1	26.1	22.1	21.5
100.9	99.1	103.3	5.8	15.5	59.8	53.2	42.8
108.7	119.0	126.3	22.2	44.8	72.7	81.9	66.5
29.6	31.5	34.0	6.0	0.0	45.6	18.9	21.5
36.2	45.0	44.5	8.0	75.7	48.7	33.0	52.5
15.8	16.6	15.5	1.2	56.2	28.1	16.4	33.6
351.2	305.2	366.0	69.4	0.0	70.4	56.4	42.3
52.7	39.8	41.0	11.1	587.2	988.5	360.2	645.3
163.3	188.0	231.2	97.0	128.8	215.3	145.5	163.2
1387.5	818.5	1071.6	289.7	974.9	1353.8	1056.1	1128.3
1550.1	1593.3	1771.5	346.9	120.1	497.9	453.0	357.0
785.5	1094.2	1138.3	376.8	70.1	149.5	202.1	140.6
431.9	646.8	909.8	650.6	196.5	233.6	301.8	244.0

128.5	177.4	244.1	159.8	347.5	230.9	286.6	288.3
42.9	39.8	36.7	8.2	0.0	43.6	47.1	30.2
140.0	142.5	130.4	18.9	147.0	172.3	162.0	160.4
0.2	0.6	0.3	0.2	11.9	0.7	0.5	4.4
13.8	13.0	16.6	5.6	94.7	36.0	57.2	62.6
37.8	53.8	52.6	14.2	198.1	125.9	135.2	153.1
153.6	190.0	149.8	42.2	105.0	274.5	182.0	187.2
153.2	76.7	111.8	38.6	106.8	143.8	158.8	136.4
39.8	53.3	47.3	6.8	122.7	23.8	13.5	53.3
328.5	312.1	370.8	87.8	321.8	228.2	237.9	262.6
55.4	57.9	57.8	2.4	596.4	101.5	93.4	263.8
2178.0	2310.4	2024.5	386.3	2003.9	3957.4	4064.2	3341.8
1226.4	1109.2	1084.6	155.6	419.4	535.3	661.6	538.8
293.1	273.6	262.9	36.7	351.5	415.4	473.2	413.4
139.7	141.8	134.7	10.4	495.8	430.7	480.1	468.9
149.1	127.2	140.8	11.9	21.4	119.9	119.3	86.9
72.5	70.6	69.7	3.4	0.0	17.5	17.1	11.5
17.0	17.3	19.8	4.6	29.7	17.8	13.9	20.5
87.1	88.6	93.5	9.9	30.4	48.6	45.7	41.6
85.7	90.1	94.3	11.3	99.4	74.8	64.5	79.5
52.0	70.1	62.1	9.2	13.2	32.0	35.0	26.7
60.9	63.9	67.3	8.6	49.2	24.7	27.5	33.8
26.4	28.9	32.2	8.0	14.8	12.2	11.7	12.9
9.9	17.4	13.6	3.7	0.0	29.3	29.5	19.6
64.8	69.5	66.2	2.9	140.3	131.5	124.4	132.1
72.0	78.6	82.7	13.3	21.7	40.1	38.6	33.5
169.9	177.5	163.8	17.6	229.5	135.7	148.6	171.3
47.8	49.4	45.6	5.3	0.0	32.4	35.6	22.6
67.3	65.1	64.0	3.9	0.0	16.5	19.6	12.0
143.9	163.7	143.3	20.7	9.5	43.5	26.4	26.5
517.6	467.3	654.7	282.1	118.1	604.2	640.2	454.2
442.5	511.8	684.6	360.9	574.6	569.1	523.8	555.8
417.7	229.0	381.6	138.2	66.8	211.9	211.4	163.4
173.9	108.8	175.3	67.2	147.5	153.0	93.0	131.2
250.6	166.8	212.8	42.5	56.6	265.8	252.0	191.5
1712.2	1984.2	2846.4	1734.3	290.9	725.8	675.4	564.1
1511.0	2079.6	3244.6	2526.3	347.5	578.0	581.0	502.2
85.2	106.0	90.3	13.8	70.4	66.1	52.5	63.0
439.1	425.9	390.6	72.8	95.9	209.1	178.1	161.0
93.9	51.8	57.7	33.6	311.4	97.2	154.6	187.7
14.8	17.1	19.2	5.7	82.1	30.5	26.9	46.5
191.8	214.7	240.2	65.0	30.5	49.2	47.3	42.3
158.0	169.9	179.2	27.1	38.7	34.3	26.7	33.2

128.4	152.9	133.5	17.4	65.2	100.7	102.9	89.6
94.3	147.7	122.4	26.8	206.5	153.0	133.0	164.2
198.1	176.2	152.3	61.3	73.8	252.5	238.6	188.3
134.5	128.4	119.0	21.8	31.6	261.3	258.5	183.8
476.5	569.2	523.6	46.4	630.7	375.4	446.4	484.2
189.8	186.4	182.1	10.6	120.6	192.5	218.0	177.1
44.0	51.0	49.3	4.7	113.4	48.5	47.7	69.9
395.4	325.9	313.5	88.7	296.7	231.9	228.8	252.5
41.0	49.3	43.9	4.7	51.3	53.9	27.6	44.3
114.2	116.6	115.5	1.2	89.4	133.6	104.8	109.2
244.1	297.7	289.3	41.6	515.2	506.6	569.2	530.3
249.7	254.7	272.5	35.2	105.9	372.3	428.2	302.1
209.5	248.6	260.8	58.4	104.4	433.7	316.0	284.7
21.1	39.7	27.1	10.9	1.7	35.8	21.7	19.7
23.6	31.9	26.0	5.1	36.7	38.3	37.5	37.5
37.9	42.3	37.9	4.3	22.0	32.1	34.8	29.6
23.0	19.6	28.2	12.1	79.5	32.6	12.6	41.6
32.8	38.4	40.6	9.1	261.3	85.4	66.3	137.7
52.6	72.2	72.0	19.3	418.0	172.4	109.0	233.1
53.3	67.3	61.7	7.4	56.3	43.1	36.3	45.3
59.8	71.3	66.5	6.0	20.9	104.8	95.9	73.9
1221.7	1531.4	1637.8	478.2	295.8	3164.3	2628.7	2029.6
1590.3	1898.8	2090.2	618.2	2933.8	3766.2	3602.6	3434.2
83.0	80.0	92.9	19.7	493.1	166.5	241.0	300.2
669.8	612.7	770.7	226.1	473.5	875.7	1168.1	839.1
157.1	89.4	111.0	39.9	359.2	286.1	381.9	342.4
121.9	117.7	102.6	29.8	166.2	100.7	114.5	127.1
75.8	66.5	66.7	9.1	47.4	197.8	137.8	127.7
1600.6	1691.8	1452.1	339.2	551.4	766.3	775.5	697.7
8.2	11.7	12.9	5.4	44.0	13.7	8.3	22.0
2.0	7.2	4.6	2.6	0.0	63.7	34.1	32.6
7.3	6.7	7.7	1.3	59.7	24.8	12.9	32.5
153.7	114.1	127.2	23.0	484.6	193.0	138.5	272.0
172.3	120.6	137.1	30.5	219.4	291.5	237.3	249.4
174.3	229.0	194.7	29.9	78.6	93.3	97.5	89.8
73.3	71.3	68.9	5.9	30.0	51.6	42.7	41.4
54.0	48.2	47.3	7.2	44.5	39.7	37.9	40.7
53.3	52.8	50.3	4.7	91.3	81.9	64.8	79.3
27.0	24.8	38.4	21.6	14.0	142.4	156.8	104.4
7.6	7.3	9.3	3.2	64.1	5.5	2.9	24.2
92.5	153.3	102.0	47.2	0.0	35.7	18.3	18.0
37.8	44.8	38.3	6.3	65.0	26.3	20.0	37.1
91.0	81.5	154.1	117.6	171.6	189.7	180.0	180.4

3089.8	2824.5	3754.3	1387.0	1494.7	3116.5	3019.3	2543.5
24.2	28.7	27.5	3.0	14.7	21.7	20.7	19.0
182.1	195.1	190.9	7.6	93.4	57.1	51.3	67.3
127.9	97.9	118.7	18.0	242.9	130.1	106.4	159.8
260.6	323.6	290.5	31.6	84.7	125.0	137.0	115.6
525.5	514.9	502.4	31.2	131.8	101.6	135.6	123.0
179.4	145.5	158.2	18.5	135.6	209.0	191.0	178.5
1985.5	2373.7	2091.7	246.7	543.7	852.0	767.2	721.0
145.5	61.5	108.4	42.8	283.4	343.0	300.2	308.9
90.6	47.8	77.8	26.0	105.3	76.2	74.0	85.2
103.7	60.4	80.1	21.9	768.3	200.5	130.4	366.4
391.9	194.6	262.4	112.2	1139.5	1276.4	897.1	1104.3
11.2	6.5	12.4	6.5	89.1	6.8	5.9	33.9
290.8	312.2	320.6	34.8	61.7	241.4	175.2	159.4
164.2	125.7	142.0	20.0	47.5	134.1	104.5	95.4
348.8	285.9	310.7	33.5	180.2	258.4	209.9	216.2
32.0	35.8	39.9	10.6	149.7	60.9	43.5	84.7
89.9	99.2	110.2	27.5	221.4	83.8	75.5	126.9
148.2	134.8	181.6	69.8	171.9	97.0	90.4	119.8
256.8	269.4	341.6	136.2	216.0	332.8	298.6	282.5
9.8	10.0	8.9	1.8	48.7	10.4	10.6	23.2
5.2	6.6	5.5	0.9	28.1	3.2	2.5	11.2
3.9	6.2	4.1	2.1	118.1	2.0	3.6	41.2
2.2	4.0	2.6	1.3	17.8	1.7	3.4	7.6
4.6	7.8	5.0	2.6	0.0	11.0	6.9	6.0
97.2	104.1	116.9	28.3	66.8	95.0	92.2	84.7
28.2	33.3	35.3	8.3	71.0	20.7	15.7	35.8
546.8	344.6	420.3	110.3	332.2	184.0	193.1	236.4
64.1	57.3	51.5	16.3	0.8	19.5	18.2	12.8
5.5	6.8	8.3	3.8	67.5	45.1	35.1	49.2
40.4	39.3	37.2	4.7	90.9	40.0	37.5	56.1
48.3	36.1	41.1	6.4	53.6	17.4	18.0	29.7
12.7	10.9	10.8	1.9	1.4	11.6	10.6	7.9
6.0	6.0	6.4	0.7	69.2	15.4	14.8	33.1
79.8	71.0	80.4	9.7	3.9	16.5	15.4	12.0
142.1	173.5	166.9	22.3	75.8	68.5	65.9	70.1
33.0	26.9	28.3	4.2	114.9	97.2	75.3	95.8
4956.7	3362.2	4246.9	811.5	722.4	1347.3	1236.2	1102.0
3421.7	3660.3	3858.3	562.3	511.3	1268.4	1113.0	964.3
3988.0	4711.0	4651.5	635.9	629.6	1594.3	1449.5	1224.5
248.2	239.9	208.7	61.4	42.0	90.1	80.1	70.7
459.4	347.8	314.9	163.5	156.4	142.9	156.7	152.0
55.9	83.6	65.6	15.6	168.4	50.0	50.9	89.8

36.4	37.6	42.0	8.7	41.6	11.7	8.1	20.5
544.4	488.5	468.1	88.3	1.8	52.4	47.2	33.8
603.0	576.6	721.0	227.6	313.2	354.6	366.0	344.6
22.6	20.4	22.3	1.8	0.0	28.4	25.2	17.9
913.2	921.2	900.6	29.0	363.5	596.9	788.6	583.0
916.1	820.2	893.7	65.2	1366.4	634.7	862.3	954.5
916.8	778.2	733.0	210.1	479.6	545.7	728.3	584.5
1843.6	1465.3	1487.6	345.3	906.9	656.8	839.6	801.1
624.5	529.8	540.6	79.1	976.8	425.3	630.9	677.7
59.3	78.5	66.1	10.7	74.1	69.4	48.3	63.9
58.1	80.8	73.4	13.3	123.0	57.3	43.5	74.6
146.1	138.1	142.0	4.0	332.7	163.9	130.8	209.1
33.8	37.9	34.5	3.1	24.1	45.7	48.7	39.5
119.7	146.4	164.8	56.6	223.8	162.0	101.0	162.2
107.3	98.6	108.7	11.0	368.4	213.2	298.7	293.4
145.8	166.9	190.2	59.7	57.1	287.4	212.5	185.6
3.9	1.9	3.3	1.2	36.5	7.0	4.9	16.2
26.6	32.2	32.9	6.6	53.4	63.7	50.5	55.8
2880.0	2982.7	2013.1	1591.2	26.7	21.9	27.0	25.2
1939.4	2224.8	1435.3	1129.4	9.0	37.5	47.3	31.3
1339.9	1367.1	930.7	732.4	0.0	40.4	48.6	29.7
2270.8	2014.6	1498.5	1123.2	137.8	77.2	83.6	99.6
441.7	451.1	598.1	262.7	1338.5	1243.9	1408.8	1330.4
9.4	10.2	12.2	4.2	74.5	35.0	28.5	46.0
831.2	988.4	768.5	257.0	650.7	619.0	761.4	677.0
34.8	34.9	40.6	10.0	133.6	98.3	85.1	105.7
141.0	118.3	116.9	24.8	877.1	504.2	683.4	688.3
60.0	73.1	59.6	13.8	145.9	63.0	65.7	91.5
16.7	21.3	19.4	2.4	46.0	14.0	16.1	25.4
81.2	71.0	70.3	11.2	144.8	44.0	50.0	79.6
100.0	95.4	110.4	22.0	55.9	82.5	92.8	77.1
134.7	134.6	135.2	0.9	59.7	104.5	136.4	100.2
897.9	920.7	1020.4	192.8	76.2	451.8	422.7	316.9
168.5	210.1	224.8	64.9	357.8	231.6	157.6	249.0
42.7	67.1	56.8	12.6	46.0	65.4	46.4	52.6
92.6	92.7	87.5	8.8	463.3	210.0	270.1	314.4
7950.8	8781.3	6100.0	3946.8	347.4	511.1	520.8	459.8
697.7	588.7	477.3	292.5	19.8	89.1	96.5	68.5
657.0	357.1	399.9	238.6	942.1	1712.1	1947.5	1533.9
19.7	23.2	25.2	6.7	110.4	48.4	51.7	70.2
257.1	220.2	221.1	35.5	75.6	121.7	130.8	109.4
8.9	8.2	8.9	0.7	69.7	17.5	23.8	37.0
100.9	90.2	85.4	18.3	177.8	96.7	125.8	133.5

62.2	65.8	57.0	12.2	189.1	71.8	81.4	114.1
22.4	15.5	17.0	4.9	224.2	45.5	42.3	104.0
43.6	36.3	38.8	4.1	526.7	140.5	155.4	274.2
15.2	13.4	13.1	2.3	109.5	49.6	66.5	75.2
2.5	2.5	2.4	0.1	4.6	9.3	11.5	8.4
5.5	5.1	4.8	0.9	0.0	26.0	29.2	18.4
5.3	5.9	5.8	0.5	31.8	5.5	5.1	14.1
169.7	316.9	241.9	73.6	130.9	138.8	143.1	137.6
57.4	115.6	79.9	31.3	217.7	99.8	84.3	133.9
65.9	65.9	69.3	6.0	247.3	105.8	135.8	163.0
12.1	14.3	12.6	1.4	80.8	28.0	27.2	45.4
0.6	0.0	0.3	0.3	0.0	643.8	208.9	284.2
2.5	1.0	1.8	0.8	15.1	651.1	296.3	320.8
12.1	8.8	10.6	1.7	14.0	13.1	19.1	15.4
18.3	22.1	22.5	4.4	77.9	15.1	10.5	34.5
1.7	1.3	1.5	0.2	12.8	224.3	88.7	108.6
0.9	0.9	0.9	0.0	76.8	110.2	40.2	75.8
13.2	6.3	12.4	5.7	127.6	535.6	370.3	344.5
198.8	228.3	217.7	16.4	45.0	153.4	82.8	93.7
337.2	440.0	426.9	83.9	7.3	84.1	90.7	60.7
364.1	562.9	450.4	101.9	0.8	49.3	59.0	36.4
60.5	58.4	91.0	54.6	141.9	39.3	41.9	74.4
51.1	48.5	60.1	18.0	21.4	18.2	20.1	19.9
67.4	57.1	85.2	40.0	41.9	37.4	41.9	40.4
182.0	150.2	145.2	39.7	246.7	135.1	168.9	183.6
29.7	55.0	36.3	16.5	0.0	39.3	19.5	19.6
50.0	49.0	62.8	23.1	31.0	19.3	15.8	22.0
54.6	49.5	63.9	20.7	0.0	12.4	11.2	7.9
56.3	72.3	65.1	8.1	23.9	117.7	85.2	75.6
2555.3	2376.9	3114.6	1126.7	349.0	858.1	852.1	686.4
55.4	69.5	84.3	38.4	40.8	37.0	37.1	38.3
181.0	236.7	211.2	28.1	1339.9	329.4	314.0	661.1
79.2	67.5	62.0	20.5	57.6	30.5	28.2	38.8
45.8	33.5	34.1	11.4	90.8	161.9	239.5	164.0
580.3	556.3	559.5	19.5	398.9	371.7	349.3	373.3
82.8	68.4	68.4	14.5	65.0	82.6	61.9	69.8
1009.0	764.9	752.2	263.3	995.7	873.7	660.8	843.4
3.8	4.3	4.0	0.3	76.3	38.2	43.4	52.6
2.7	4.2	4.0	1.1	192.4	46.8	56.0	98.4
2.7	2.9	2.9	0.2	178.2	44.8	52.9	92.0
0.5	0.0	0.2	0.3	252.0	28.6	12.5	97.7
0.6	0.3	0.4	0.1	0.0	21.1	24.0	15.0
3.4	2.8	2.9	0.4	218.3	81.5	103.4	134.4

2431.4	2540.7	2527.0	89.6	723.6	777.3	1012.2	837.7
1924.2	2227.9	2347.6	494.3	359.2	518.3	650.9	509.5
4732.8	7298.9	5437.0	1628.3	543.8	4018.9	2795.6	2452.8
4805.1	6203.2	5192.0	883.7	2242.0	4151.5	3558.8	3317.4
3589.6	5170.4	4438.7	796.9	919.1	1055.4	741.3	905.2
3632.0	4282.4	4254.7	609.3	1013.9	1163.7	947.2	1041.6
1112.2	1092.7	1211.1	188.4	1217.5	1233.1	1791.1	1413.9
473.5	467.1	557.2	150.5	489.3	809.2	818.6	705.7
11558.5	13061.7	12461.1	795.8	2167.3	2542.2	2696.8	2468.8
46.1	60.3	61.6	16.3	190.5	93.9	59.3	114.6
81.8	63.0	65.1	15.7	99.6	56.7	47.1	67.8
89.9	107.4	91.4	15.3	119.6	83.7	50.9	84.7
24.2	19.7	21.0	2.7	0.0	17.2	8.7	8.6
123.8	157.5	169.7	53.0	305.7	154.1	81.7	180.5
351.3	593.2	493.5	126.4	1034.8	629.4	303.1	655.7
23.4	37.2	32.8	8.2	0.0	35.8	21.7	19.1
11.5	17.2	16.1	4.1	123.4	5.9	5.9	45.1
97.4	85.9	136.9	78.5	46.1	29.3	18.5	31.3
37.4	36.8	44.5	12.8	179.2	166.6	173.3	173.0
241.1	243.0	221.2	36.1	310.9	270.6	308.5	296.6
221.9	205.7	195.8	32.2	167.0	123.6	125.6	138.7
147.8	113.6	131.8	17.2	39.4	88.5	79.9	69.3
6.9	6.5	10.2	6.0	0.0	46.9	19.7	22.2
18.0	18.3	79.3	105.8	50.8	137.8	83.3	90.6
336.4	304.9	333.2	26.8	69.7	205.0	185.5	153.4
29.0	35.3	34.0	4.5	50.9	63.4	58.6	57.6
31.6	33.8	32.5	1.1	60.1	53.8	48.1	54.0
51.7	58.6	48.9	11.4	196.1	92.7	100.0	129.6
152.8	126.8	118.3	39.5	92.7	42.1	56.1	63.7
74.4	64.7	65.0	9.4	105.1	54.6	41.2	67.0
102.8	170.2	125.6	38.6	34.6	85.5	45.7	55.3
354.4	313.1	373.1	71.1	928.3	1262.9	1524.2	1238.5
69.2	79.2	74.1	5.0	71.7	110.3	91.4	91.1
109.3	90.3	92.3	16.1	26.8	94.7	63.3	61.6
125.2	136.1	122.6	14.9	144.8	82.2	72.4	99.8
33.6	48.1	45.8	11.3	275.1	53.1	55.2	127.8
64.5	75.2	63.7	11.8	63.0	114.3	37.5	71.6
13.9	18.5	18.3	4.3	26.4	18.3	13.9	19.6
53.8	39.8	45.3	7.4	0.0	24.4	24.6	16.3
276.7	298.7	232.9	95.5	1130.2	267.7	314.8	570.9
58.1	85.3	59.4	25.3	188.5	22.3	19.3	76.7
58.3	55.0	49.2	13.1	56.0	20.4	19.6	32.0
539.8	482.9	483.3	56.2	697.5	1299.8	1108.0	1035.1

187.1	146.2	149.3	36.4	60.2	82.2	89.6	77.3
157.0	152.0	145.4	16.0	130.0	80.4	87.0	99.1
48.1	45.5	51.6	8.5	0.0	46.1	49.3	31.8
26.1	25.4	25.6	0.5	68.4	11.4	22.6	34.1
38.8	34.9	42.3	9.7	106.4	29.9	46.7	61.0
21.4	23.2	23.8	2.6	31.4	29.0	34.6	31.7
13.9	10.3	12.3	1.9	56.0	18.9	22.1	32.3
24.7	22.1	22.1	2.6	261.0	10.0	23.3	98.1
59.2	42.5	55.3	11.4	16.9	42.8	66.3	42.0
173.9	152.2	165.7	11.8	329.1	120.2	161.4	203.6
31.4	31.0	36.3	8.8	163.3	47.1	61.2	90.5
30.2	30.1	34.9	8.3	1.5	53.9	75.2	43.5
52.4	56.7	62.6	14.2	83.2	66.7	96.8	82.2
36.7	45.9	39.8	5.3	429.2	74.2	107.3	203.6
79.1	81.1	85.1	8.8	19.5	36.1	48.2	34.6
281.7	356.9	374.0	102.0	381.3	367.6	437.1	395.4
5654.8	2959.3	3196.1	2349.3	781.9	923.9	880.3	862.0
19.0	28.1	25.2	5.3	78.4	33.6	28.8	46.9
97.3	104.5	90.7	18.1	76.4	70.8	42.3	63.2
37.5	31.5	34.5	3.0	26.6	35.2	39.8	33.9
711.8	963.9	929.7	202.9	143.3	47.8	43.5	78.2
40.4	46.1	44.6	3.7	40.6	22.6	22.0	28.4
126.8	123.1	120.0	8.8	28.3	42.5	49.5	40.1
188.5	176.0	178.2	9.4	156.4	94.9	93.6	115.0
89.3	92.6	100.7	17.0	0.0	106.8	79.3	62.1
303.2	301.9	308.7	10.6	77.4	94.5	129.1	100.3
80.2	78.0	83.8	8.2	2.7	13.6	13.9	10.0
722.3	640.5	657.1	58.6	170.3	104.3	150.8	141.8
57.0	49.9	58.5	9.5	0.0	42.0	37.8	26.6
7.1	6.5	6.6	0.5	76.3	17.4	16.7	36.8
16.4	17.4	13.2	6.5	30.8	32.8	47.0	36.9
4.5	2.7	3.0	1.4	46.1	2.4	4.5	17.7
4.3	4.0	3.5	1.0	18.2	9.7	14.5	14.1
75.0	51.3	53.8	20.1	55.0	162.2	152.8	123.3
12.0	15.4	14.9	2.7	17.8	10.9	6.8	11.8
11.9	17.8	16.6	4.2	36.1	2.8	2.3	13.7
24.1	26.1	27.0	3.4	0.0	2.6	1.9	1.5
10.5	15.9	14.9	4.1	41.4	3.6	6.0	17.0
9.8	7.7	8.2	1.4	84.3	18.9	17.1	40.1
18.9	17.6	17.6	1.3	38.4	15.2	11.5	21.7
5.0	5.4	4.7	0.9	0.0	5.2	2.4	2.5
39.9	17.2	26.1	12.1	114.3	22.7	22.5	53.2
2.8	3.2	2.2	1.5	0.0	5.6	7.7	4.4

16.1	10.2	11.9	3.7	0.0	7.6	7.2	5.0
16.0	12.8	13.6	2.1	0.0	10.9	8.9	6.6
10.0	11.3	10.2	1.1	25.6	10.9	11.7	16.1
19.5	13.9	17.7	3.3	0.0	16.0	22.7	12.9
32.4	19.7	30.4	9.9	46.9	16.3	17.5	26.9
11.8	12.4	10.3	3.1	32.6	17.2	11.6	20.5
100.5	70.8	75.5	23.0	127.3	123.9	143.4	131.5
103.8	83.9	75.5	33.3	57.5	85.9	84.9	76.1
33.7	32.0	36.5	6.4	82.8	27.1	32.6	47.5
26.0	22.2	31.2	12.5	56.3	24.2	31.8	37.4
168.4	122.5	139.4	25.2	227.6	180.3	206.9	205.0
9.9	5.6	11.0	6.1	23.8	48.0	26.8	32.9
12.7	6.4	10.8	3.8	76.8	58.4	45.0	60.1
52.7	31.7	48.8	15.5	192.6	197.7	164.1	184.8
50.2	27.4	38.5	11.4	339.5	499.5	418.7	419.2
348.8	215.5	290.0	68.0	316.0	470.3	300.6	362.3
50.8	48.8	47.3	4.4	33.4	49.4	46.8	43.2
50.6	54.8	53.2	2.3	278.8	303.8	250.3	277.6
168.7	190.3	183.7	13.1	346.3	298.8	330.8	325.3
200.4	190.0	192.2	7.4	128.1	286.4	370.9	261.8
474.7	490.2	431.5	88.6	137.9	289.4	239.5	222.3
197.1	155.4	156.3	40.4	75.5	112.8	100.8	96.4
28.8	32.5	25.6	9.0	89.9	22.2	19.0	43.7
46.5	42.0	45.9	3.7	2.1	24.8	18.8	15.2
30.4	25.1	25.6	4.6	0.0	35.0	20.2	18.4
35.8	44.9	43.4	7.0	141.2	52.8	46.6	80.2
42.6	40.4	41.0	1.4	367.6	44.3	38.4	150.1
28.5	23.0	27.5	4.1	0.0	21.4	26.3	15.9
27.6	30.3	36.4	13.0	52.4	25.6	15.8	31.3
108.7	99.7	87.1	30.0	0.0	90.9	70.9	53.9
268.2	274.2	210.8	104.7	125.3	116.6	105.1	115.7
9.6	29.5	20.5	10.1	7.1	11.0	9.2	9.1
24.8	27.9	23.9	4.6	83.7	31.0	24.6	46.4
432.5	414.4	380.1	75.6	251.3	236.0	299.4	262.3
270.5	297.0	265.9	33.7	218.8	89.8	121.1	143.2
80.4	85.2	86.3	6.5	48.1	50.0	55.2	51.1
61.2	55.6	66.5	14.4	17.9	21.2	20.1	19.8
18.3	18.1	22.6	7.6	56.6	19.2	22.5	32.8
41.9	39.8	38.9	3.6	32.9	71.8	49.2	51.3
635.2	565.5	479.9	211.4	709.0	306.1	380.2	465.1
170.1	332.3	212.0	105.7	314.2	155.6	48.0	172.6
142.3	85.4	105.5	31.9	30.0	90.0	80.4	66.8
29.0	36.2	35.4	6.0	1.1	37.3	46.6	28.3

229.6	282.5	301.3	82.8	1232.6	277.1	299.4	603.0
72.5	82.0	70.7	12.3	396.7	111.1	122.7	210.2
25.2	34.4	26.5	7.4	20.6	15.3	21.4	19.1
50.8	44.8	67.5	34.2	89.3	29.5	20.8	46.5
45.9	32.3	72.4	58.1	0.0	6.7	6.7	4.5
115.5	64.6	117.7	54.3	0.0	16.7	9.5	8.7
167.6	104.6	174.7	73.8	52.3	22.6	20.2	31.7
141.4	87.1	149.9	67.3	43.1	53.1	44.7	47.0
2059.9	1495.8	3552.8	3087.3	5621.1	2279.8	1067.9	2989.6
132.8	153.2	173.6	53.9	71.8	191.2	270.9	178.0
7186.1	7613.1	7035.3	666.2	718.2	580.7	797.1	698.7
5744.1	5741.5	5836.9	162.9	159.7	218.2	275.0	217.6
4821.8	4638.9	5002.6	480.3	85.3	168.2	210.0	154.5
4524.7	4005.7	4609.8	650.9	106.9	187.0	215.0	169.6
2873.6	3315.8	3400.1	573.3	130.2	226.1	234.0	196.8
4005.4	3832.3	4055.7	252.4	1509.1	348.8	377.0	745.0
4112.3	3029.1	3983.6	897.1	373.7	645.2	586.5	535.1
4778.1	4095.3	4542.1	387.1	379.2	895.1	808.6	694.3
2669.5	2216.6	2851.2	742.3	712.8	966.2	842.9	840.6
195.8	162.7	175.7	17.7	183.7	94.0	84.2	120.6
255.7	244.1	227.4	39.3	132.0	109.4	122.3	121.2
110.2	153.8	141.5	27.3	148.8	123.0	105.4	125.7
127.2	123.0	135.4	18.0	177.3	90.2	78.6	115.4
3.2	12.5	7.2	4.8	410.5	13.2	15.1	146.3
13.4	20.7	15.6	4.4	157.6	34.4	29.2	73.7
13.2	15.3	12.4	3.4	37.4	6.1	1.8	15.1
62.4	185.5	112.3	64.8	312.0	170.1	52.4	178.2
3.3	6.0	4.2	1.6	112.7	7.0	3.9	41.2
1.9	1.7	2.5	1.2	323.2	1.5	6.6	110.4
56.0	21.1	31.7	21.1	0.0	33.0	19.4	17.5
85.8	65.0	92.5	31.4	140.7	122.2	181.1	148.0
4.6	36.6	21.4	16.0	0.0	68.0	28.2	32.1
19.2	16.7	18.2	1.3	83.3	19.5	21.8	41.5
152.4	63.9	98.4	47.4	200.2	135.5	94.4	143.4
15.0	14.1	19.1	7.9	0.0	64.7	25.2	30.0
16.9	11.3	17.8	7.1	120.1	60.9	38.8	73.3
56.7	58.1	77.4	34.6	321.4	345.3	110.9	259.2
12.1	14.6	16.6	5.8	95.8	40.2	25.9	54.0
17.3	17.4	18.2	1.4	13.3	31.8	14.1	19.7
0.0	0.0	0.0	0.0	459.9	12.7	2.4	158.3
182.3	97.3	145.8	43.8	201.8	107.8	71.1	126.9
3.1	3.7	4.9	2.6	293.1	24.8	18.6	112.2
456.9	297.8	335.1	108.0	75.7	127.1	78.2	93.7

4.3	11.2	7.8	3.5	224.2	89.2	48.3	120.6
81.2	63.2	67.0	12.7	291.5	35.2	30.6	119.1
88.1	76.1	67.9	25.3	113.2	99.2	51.5	88.0
1327.3	824.1	814.6	517.5	91.9	164.1	250.0	168.7
4.4	8.5	8.0	3.4	83.7	27.1	12.6	41.1
1447.3	776.4	903.6	492.6	527.5	1466.2	629.2	874.3
16.2	26.8	18.1	7.9	0.0	50.8	24.6	25.1
11.3	11.7	10.7	1.4	152.2	57.0	26.7	78.6
27.4	82.2	58.0	28.0	472.4	84.0	14.4	190.3
0.0	1.8	0.8	0.9	320.3	4.7	4.4	109.8
5.2	2.9	4.2	1.2	322.7	23.7	29.9	125.5
66.2	49.4	52.7	12.1	1113.6	490.0	417.2	673.6
1.4	4.1	2.1	1.8	85.8	5.4	0.0	30.4
5.2	7.0	5.6	1.3	129.2	15.6	15.5	53.4
17.8	24.0	19.1	4.3	135.3	39.8	29.6	68.2
63.7	48.9	48.7	15.0	0.0	132.8	123.1	85.3
22103.7	9777.8	11887.0	9342.4	16102.3	138402.1	149787.0	101430.5
5.2	58.9	35.9	27.7	224.2	1433.5	98.0	585.2
8.2	0.0	2.7	4.7	0.0	41.2	45.9	29.1
47.9	32.7	45.3	11.5	32.2	68.3	69.7	56.7
38.2	38.2	35.9	4.1	912.5	79.3	27.8	339.8
73.9	52.3	49.0	26.6	1565.5	1891.5	1925.7	1794.3
23.4	16.2	19.2	3.7	0.0	47.6	48.0	31.9
7.4	8.6	11.0	5.2	0.0	40.1	16.1	18.7
414.7	347.3	377.0	34.4	310.1	180.8	93.2	194.7
52.7	85.7	72.1	17.2	151.7	87.7	24.0	87.8
3.3	5.1	4.1	0.9	202.0	20.8	10.8	77.9
200.8	87.9	117.9	72.6	0.0	217.6	286.3	168.0
6.8	5.5	9.0	5.0	101.6	15.1	12.5	43.1
3934.4	5743.2	5023.4	959.3	1501.9	1339.9	1340.4	1394.1
12.0	36.1	45.2	38.5	0.0	88.0	21.0	36.3
45.8	61.3	53.7	7.7	81.1	31.4	29.6	47.3
228.3	274.7	252.4	23.3	439.1	81.1	78.9	199.7
26.0	22.2	21.4	5.0	38.0	121.2	133.5	97.5
1895.8	646.2	1195.0	638.5	940.8	21542.1	25507.1	15996.7
36.7	56.8	60.2	25.4	186.8	40.3	42.9	90.0
146.9	150.2	160.1	20.1	458.9	273.5	135.2	289.2
24.6	27.2	29.9	7.0	0.0	46.9	36.2	27.7
2.8	2.9	2.9	0.2	6.5	7.5	4.5	6.2
1229.1	1257.9	844.1	691.9	30.4	51.1	51.1	44.2
31.6	18.5	20.9	9.7	1815.1	321.1	481.4	872.6
28.0	25.4	27.1	1.5	1540.1	279.1	186.9	668.7
5.0	4.4	4.7	0.3	0.0	14.6	15.0	9.9

30.0	31.9	24.6	11.0	96.3	69.0	48.2	71.2
816.3	466.8	521.9	271.1	242.9	280.4	324.1	282.5
56.0	58.2	48.1	15.6	22.8	28.4	26.4	25.9
16.3	9.2	12.9	3.6	14.3	46.0	63.3	41.2
14.8	8.4	11.8	3.2	498.2	354.4	502.6	451.7
13.9	13.8	13.5	0.7	38.9	33.4	17.8	30.0
5.7	6.8	6.0	0.7	49.1	17.0	6.8	24.3
10.7	7.7	8.9	1.6	3.8	29.3	43.1	25.4
163.3	198.0	181.5	17.4	129.8	204.7	198.5	177.7
61.0	48.7	56.4	6.7	352.3	99.9	119.2	190.5
76.0	69.9	70.1	5.8	0.0	159.1	126.1	95.1
67.1	44.3	38.7	31.6	33.3	5.3	6.5	15.0
5.2	4.0	4.5	0.6	0.0	2.6	3.2	1.9
6.3	7.4	7.8	1.8	0.0	9.4	7.2	5.5
8.6	7.9	12.5	7.4	73.8	18.5	10.9	34.4
12.3	8.1	11.0	2.5	0.0	22.9	11.8	11.6
15.3	14.5	15.2	0.7	19.8	21.9	27.4	23.0
7.6	6.2	6.0	1.7	57.9	22.7	17.5	32.7
23.8	31.6	25.9	5.0	195.7	81.2	75.3	117.4
13.1	13.9	13.2	0.7	56.2	45.8	43.0	48.3
6.9	8.1	8.5	1.8	64.6	13.6	7.6	28.6
13.4	29.4	16.3	12.0	102.9	46.7	50.6	66.7
98.3	130.9	121.5	20.2	0.0	115.3	86.4	67.2
28.7	29.1	27.1	3.1	27.5	20.8	29.0	25.8
9.7	11.5	9.1	2.8	6.1	8.3	10.2	8.2
19.9	14.9	19.1	3.9	128.7	4.4	7.4	46.8
24.1	29.4	27.9	3.3	42.8	25.0	28.2	32.0
16.5	22.3	18.7	3.2	109.4	32.8	24.0	55.4
4.9	5.8	5.3	0.5	0.0	4.4	4.5	3.0
3.9	4.7	4.2	0.4	43.1	2.1	2.6	15.9
28.9	21.8	21.2	8.0	0.0	19.2	14.0	11.1
27.3	17.0	15.8	12.1	21.7	7.6	5.6	11.6
61.6	54.0	54.4	6.9	247.1	40.6	40.5	109.4
13.9	16.6	19.8	8.0	54.3	1.7	1.5	19.2
9.8	10.7	12.9	4.7	10.6	4.0	3.0	5.9
20.7	29.8	25.0	4.6	28.2	16.5	13.8	19.5
17.6	26.8	24.7	6.3	0.0	32.0	23.9	18.7
17.8	32.1	27.0	8.0	82.1	48.7	35.0	55.3
4.2	4.1	4.4	0.4	9.3	11.4	10.4	10.4
23.4	20.0	23.3	3.2	155.9	65.7	69.2	96.9
29.2	19.2	22.7	5.7	540.3	908.3	1158.5	869.0
5.3	5.2	5.8	0.9	17.4	11.1	7.5	12.0
20.5	30.7	30.3	9.6	0.0	75.4	58.2	44.5

4.6	8.0	8.0	3.4	70.2	33.7	9.1	37.7
7.6	7.6	6.9	1.2	89.4	98.6	48.2	78.7
2.8	4.2	3.9	0.9	33.2	9.5	5.9	16.2
1.4	2.3	2.5	1.3	67.4	15.9	10.9	31.4
5.2	7.7	7.1	1.6	41.6	19.4	15.3	25.4
11.8	12.4	10.1	3.5	0.0	46.4	34.1	26.9
14.5	13.6	11.4	4.6	40.9	28.4	25.6	31.7
18.0	14.1	14.7	3.1	44.9	33.9	36.0	38.3
53.0	46.7	45.2	8.7	75.6	55.6	34.7	55.3
39.8	42.3	33.9	12.4	0.0	30.5	26.0	18.8
65.0	60.1	50.0	21.9	213.1	51.0	52.0	105.4
1.0	0.5	0.8	0.3	0.0	6.0	3.0	3.0
7.5	9.1	7.9	1.1	0.0	20.2	17.1	12.4
4.5	9.4	6.4	2.6	89.8	55.0	20.7	55.2
13.4	8.2	14.2	6.4	621.4	234.5	276.0	377.3
11.5	9.6	12.7	3.7	712.3	165.7	196.1	358.0
146.2	167.8	148.7	18.0	10.6	29.3	15.5	18.5
132.3	109.2	156.8	63.4	0.0	43.9	41.6	28.5
31.2	36.3	43.0	16.3	61.0	13.4	10.7	28.4
14.1	17.4	26.4	18.5	38.7	9.9	8.0	18.8
15.2	17.4	22.4	10.7	0.0	20.1	12.6	10.9
11.3	14.7	15.5	4.6	0.0	20.2	16.2	12.1
11.0	9.0	13.0	5.3	252.0	47.5	29.6	109.7
94.9	145.1	80.8	72.4	0.0	21.3	11.3	10.9
121.8	128.5	84.2	71.0	51.0	8.3	9.3	22.9
128.2	144.4	91.2	78.5	8.7	3.1	2.8	4.9
81.6	70.9	51.1	43.9	69.0	13.3	8.0	30.1
48.2	51.6	34.1	27.5	0.0	29.6	17.1	15.6
588.0	398.6	436.6	136.4	82.9	161.2	159.2	134.4
76.9	61.4	76.3	14.6	53.7	37.4	31.3	40.8
89.8	92.8	73.9	30.1	177.4	47.7	53.0	92.7
72.0	71.5	61.4	17.9	103.9	42.4	35.6	60.6
28.4	30.2	25.6	6.5	61.1	92.5	96.4	83.3
2.4	2.3	2.1	0.5	295.6	27.2	23.7	115.5
57.1	55.4	59.4	5.5	26.1	24.7	28.6	26.5
1.7	4.3	4.7	3.3	74.2	7.0	4.4	28.5
14.5	14.1	17.0	4.6	73.6	56.3	31.2	53.7
3.6	4.7	5.9	3.1	1.8	17.6	9.4	9.6
4.5	6.1	7.7	4.3	55.4	14.8	14.6	28.2
7.5	7.2	9.6	3.9	35.7	30.3	31.2	32.4
38.0	32.6	38.0	5.4	92.0	122.5	133.3	115.9
1.5	1.7	1.6	0.1	74.4	5.4	4.7	28.2
1.8	2.4	1.7	0.9	40.6	3.4	6.1	16.7

0.6	1.2	0.7	0.5	41.0	1.5	1.3	14.6
4.6	7.4	4.9	2.4	37.0	7.7	4.9	16.5
16.0	21.2	15.5	5.9	0.0	22.2	19.3	13.8
35.6	39.3	33.2	7.7	832.0	140.0	164.7	378.9
18.7	19.4	17.8	2.2	309.0	108.6	126.9	181.5
133.6	89.2	89.8	43.5	72.6	44.4	41.7	52.9
34.1	48.1	36.2	10.9	110.2	23.1	17.8	50.4
385.5	232.0	241.2	140.0	1730.7	2296.3	1022.9	1683.3
2.1	0.8	1.7	0.8	196.1	53.3	50.9	100.1
138.3	120.9	103.8	45.5	30.6	175.6	135.5	113.9
101.9	88.9	75.2	35.6	90.7	79.4	57.8	76.0
48.9	37.2	36.4	12.9	29.5	62.3	39.0	43.6
207.0	207.0	196.9	17.5	356.7	235.7	170.9	254.4
8.7	9.6	8.9	0.5	92.9	21.6	15.2	43.2
24.0	26.5	24.3	2.1	501.0	68.5	28.9	199.5
126.9	123.5	118.4	11.8	71.1	38.0	37.7	48.9
1.5	1.7	1.6	0.1	0.0	6.4	5.5	4.0
58.2	48.1	40.5	22.5	15.2	29.9	32.1	25.7
49.4	63.2	43.7	22.9	111.5	19.1	26.9	52.5
3.9	2.9	3.0	0.9	5.7	11.5	15.5	10.9
11.2	11.2	8.7	4.2	0.0	33.1	30.2	21.1
141.0	132.8	98.3	67.1	77.0	11.0	11.0	33.0
4.1	7.1	4.3	2.7	54.3	4.8	5.4	21.5
136.5	183.6	122.7	68.8	100.4	96.4	84.1	93.7
25.4	24.8	23.1	3.5	35.1	25.4	32.7	31.1
48.5	53.8	52.8	3.9	14.3	41.0	37.2	30.8
71.3	60.0	56.2	17.4	90.0	68.9	59.2	72.7
116.2	148.8	132.1	16.3	174.4	92.3	45.3	104.0
127.5	125.4	124.4	3.7	39.2	67.1	33.5	46.6
147.4	137.4	174.4	55.6	4.9	73.2	62.2	46.8
14.7	8.2	17.7	11.3	0.0	13.5	10.2	7.9
53.4	44.0	54.8	11.7	326.4	79.4	65.1	157.0
12.5	12.2	12.3	0.2	93.4	38.9	24.1	52.1
43.1	47.6	40.7	8.3	64.4	19.0	9.2	30.9
99.6	96.9	78.8	33.7	102.4	44.6	18.5	55.2
11.2	7.1	9.8	2.4	26.6	15.6	7.5	16.5
9.3	15.8	13.3	3.5	157.8	9.2	2.0	56.3
0.5	0.4	0.4	0.1	48.7	2.4	2.5	17.9
12.8	15.0	12.9	2.0	179.7	26.8	13.0	73.2
4.0	4.4	3.5	1.2	20.0	3.1	4.4	9.1
5.7	6.3	5.1	1.6	0.0	3.6	3.7	2.4
3.4	2.6	3.1	0.4	37.0	4.9	3.3	15.1
22.2	21.9	21.1	1.7	141.3	57.3	33.8	77.5

5.2	12.8	9.3	3.8	0.0	82.5	67.5	50.0
1518.4	886.1	1071.5	389.0	2851.4	8423.1	6747.9	6007.5
13.6	10.8	10.6	3.1	34.8	123.6	72.9	77.1
135.5	189.5	174.8	34.4	507.5	203.6	139.0	283.3
194.6	204.7	271.5	124.6	293.0	339.5	275.6	302.7
13.1	11.1	13.1	2.0	40.3	14.7	10.5	21.8
2.7	4.0	3.1	0.8	78.7	21.5	6.8	35.7
43.1	49.6	38.0	14.8	4.7	8.0	2.8	5.1
16.9	21.1	21.3	4.5	103.3	135.8	137.8	125.6
8.0	7.7	6.9	1.7	11.6	30.3	14.8	18.9
7.7	5.2	25.7	33.4	84.2	42.6	20.3	49.1
0.3	0.0	4.1	6.7	0.9	2.5	1.2	1.5
1.2	0.9	14.3	22.8	112.7	11.3	5.4	43.1
3.9	3.0	29.4	45.0	0.0	17.2	7.9	8.4
1.6	1.3	13.7	21.1	9.0	13.3	5.2	9.2
2.1	2.3	72.2	121.2	0.0	27.7	6.7	11.5
2.1	2.1	81.5	137.6	34.4	14.8	5.7	18.3
1.8	2.7	52.3	86.7	17.2	17.6	4.5	13.1
8.1	6.6	91.0	144.8	95.8	13.7	6.1	38.5
10.5	12.2	170.2	275.1	108.8	26.7	10.9	48.8
626.9	473.0	467.8	161.8	424.6	253.5	301.4	326.5
579.6	337.5	360.3	208.8	2.5	371.8	471.8	282.0
22.2	22.1	22.5	0.6	125.5	53.5	33.3	70.8
9.6	13.4	12.4	2.4	11.7	33.5	21.1	22.1
19.7	24.7	22.8	2.7	60.0	29.6	30.9	40.2
238.5	198.9	206.5	28.9	164.0	80.2	85.8	110.0
14.8	19.1	14.9	4.2	100.4	67.9	38.5	68.9
3.6	3.7	3.2	0.8	56.0	12.7	14.7	27.8
11.3	13.4	14.0	3.1	154.5	26.4	11.5	64.1
27.3	17.6	21.5	5.2	104.1	75.5	100.0	93.2
2.2	3.8	3.1	0.8	127.9	37.3	33.5	66.2
16.6	17.2	16.8	0.4	831.3	93.3	186.6	370.4
21.2	18.2	21.0	2.7	3178.8	43.8	230.6	1151.0
6.5	8.5	9.1	3.0	154.9	51.3	38.4	81.5
4.6	5.5	6.9	3.2	33.9	25.7	9.3	23.0
0.4	0.2	0.3	0.1	60.8	4.8	2.4	22.7
0.3	2.1	0.9	1.0	0.0	7.6	7.3	5.0
3.2	3.0	2.7	0.8	31.6	23.5	19.8	25.0
2.3	2.7	2.1	0.7	15.7	26.8	18.8	20.4
2.7	3.0	2.3	1.0	0.0	19.8	21.0	13.6
362.1	281.9	218.4	183.8	0.0	16.1	16.4	10.8
425.3	321.5	253.7	213.7	0.0	9.1	9.4	6.2
3.6	2.6	10.7	13.2	57.6	26.4	14.7	32.9

2.2	2.5	5.4	5.4	0.0	10.7	6.8	5.9
3.5	3.8	5.7	3.5	78.5	9.2	7.9	31.9
1.6	2.6	2.9	1.4	0.0	5.8	8.8	4.9
3.2	2.8	4.1	1.8	0.0	10.2	6.4	5.5
1.8	1.2	2.5	1.8	0.0	2.9	3.0	2.0
3.1	3.8	4.4	1.6	72.1	6.3	7.5	28.6
7.9	3.9	17.5	20.2	387.7	266.0	319.1	324.3
1.7	1.6	13.6	20.7	161.0	11.7	12.0	61.6
0.6	0.7	11.7	19.2	0.0	10.1	5.4	5.2
205.9	129.3	136.6	66.0	67.0	10.0	7.8	28.3
4.6	4.7	4.0	1.2	95.5	30.6	21.0	49.0
2.8	6.8	4.4	2.1	0.0	11.4	5.3	5.6
18.9	20.3	19.2	1.0	64.2	65.6	54.9	61.6
8.2	6.7	8.2	1.6	86.9	34.7	37.1	52.9
2.6	3.2	2.6	0.7	273.5	25.2	36.1	111.6
5.4	6.2	6.0	0.5	63.4	12.2	9.7	28.4
3.3	2.3	2.5	0.8	28.8	11.2	8.6	16.2
11.1	9.9	10.6	0.7	46.1	9.0	9.9	21.7
37.6	28.1	29.5	7.5	94.6	42.7	27.7	55.0
9.1	8.5	9.9	1.9	70.8	33.0	13.9	39.2
1.8	1.2	1.5	0.3	9.5	3.0	3.0	5.2
21.1	21.1	20.2	1.6	48.1	37.4	24.4	36.6
4.7	2.6	2.9	1.6	12.6	11.1	3.8	9.2
7.3	4.8	5.6	1.5	0.0	13.5	2.6	5.4
16.3	14.8	13.4	3.7	178.1	35.5	14.6	76.1
5.3	6.1	4.9	1.3	0.0	45.2	15.9	20.4
0.5	0.2	0.4	0.2	49.9	4.6	1.4	18.6
0.4	1.9	0.9	0.9	58.5	8.1	4.5	23.7
2.9	3.3	2.7	0.6	171.2	8.3	5.7	61.7
3.0	3.5	3.3	0.3	63.6	10.8	10.4	28.2
1.7	1.0	1.3	0.3	83.7	9.1	9.2	34.0
1.0	0.4	1.1	0.8	102.0	17.0	7.0	42.0
2.3	2.0	1.7	0.8	0.0	15.3	7.4	7.6
2.7	1.5	2.3	0.7	0.0	20.2	13.5	11.3
3.4	4.2	3.9	0.4	0.0	26.3	14.5	13.6
6.6	6.4	6.1	0.8	29.1	35.3	32.9	32.4
8.1	6.0	8.5	2.7	161.8	27.1	20.0	69.6
1.3	1.2	1.6	0.6	56.4	8.8	2.2	22.5
1.2	0.4	0.6	0.6	48.5	8.2	1.8	19.5
1.7	1.7	1.7	0.0	37.5	8.8	2.4	16.2
0.8	2.4	1.3	1.0	189.7	4.6	0.9	65.1
1085.9	595.0	1075.6	475.5	337.0	168.8	240.2	248.7
3803.2	1493.5	3060.7	1357.8	412.9	219.5	387.5	340.0

4.3	5.9	4.7	1.0	178.0	22.4	17.1	72.5
136.6	146.8	124.3	30.6	294.8	168.4	121.3	194.9
995.3	806.3	1562.3	1149.6	987.8	82.5	200.3	423.5
0.4	0.0	0.2	0.2	50.0	2.8	0.3	17.7
56.0	68.2	65.1	8.0	122.5	42.3	34.1	66.3
9.0	6.9	7.6	1.2	76.8	37.6	21.9	45.4
4.6	2.2	2.4	2.2	78.7	14.5	4.3	32.5
7.2	9.8	7.8	1.9	76.3	55.7	43.4	58.5
33.5	21.8	19.8	14.9	80.9	41.7	17.1	46.6
845.4	647.0	531.3	385.2	0.9	5.4	4.0	3.5
606.6	535.4	421.8	260.9	20.5	2.4	2.8	8.6
1389.9	1129.3	942.7	564.2	17.0	5.8	5.8	9.5
75.6	97.4	65.4	38.1	67.8	29.7	30.0	42.5
125.3	94.7	101.1	21.7	69.3	41.3	27.0	45.9
41.7	26.9	25.4	17.1	606.1	313.9	195.1	371.7
34.2	40.3	32.9	8.1	220.2	49.6	36.8	102.2
59.0	56.1	46.0	20.0	188.3	81.4	52.9	107.5
2.7	0.0	1.4	1.4	1007.4	2842.9	1344.1	1731.5
11.1	11.1	9.5	2.8	600.4	236.7	295.7	377.6
44.5	38.9	29.4	21.5	365.5	101.1	55.2	173.9
128.1	112.7	101.8	33.1	67.8	38.9	39.5	48.7
71.3	77.3	66.1	14.5	49.0	50.2	40.0	46.4
44.8	41.3	43.1	1.7	0.0	54.2	65.1	39.8
60.3	55.3	58.4	2.7	16.6	29.4	22.1	22.7
10.6	16.6	13.2	3.1	68.7	24.4	15.6	36.2
25.2	25.3	24.9	0.7	104.4	33.7	25.8	54.6
10.1	16.1	12.2	3.3	86.1	90.8	54.9	77.3
25.9	30.8	26.6	3.9	115.9	42.5	39.8	66.1
17.1	17.7	14.3	5.3	1557.5	286.0	388.1	743.8
28.1	24.2	27.1	2.5	379.2	167.6	123.3	223.4
23.3	15.2	16.4	6.3	158.8	166.7	187.4	171.0
44.2	52.2	53.6	10.1	228.6	57.5	46.0	110.7
14.6	16.0	16.3	1.8	141.9	45.9	28.7	72.2
40.2	43.8	42.0	1.8	94.3	81.0	62.1	79.2
15.7	14.8	16.0	1.4	1112.0	308.1	386.9	602.3
8.4	19.2	11.5	6.7	38.7	81.0	32.9	50.9
76.7	94.4	82.5	10.3	277.9	126.5	145.7	183.4
4.5	4.1	4.8	0.9	1.2	19.3	14.7	11.7
65.5	70.7	51.1	29.5	49.7	23.0	18.3	30.3
35.5	22.1	20.9	15.3	0.0	23.1	19.1	14.1
108.1	78.1	85.6	19.8	30.2	99.2	79.2	69.5
731.1	376.3	492.4	206.7	1231.0	795.8	1084.8	1037.2
5.7	5.6	5.1	1.0	214.1	168.8	167.9	183.6

2.5	3.2	2.4	0.9	60.2	9.8	4.2	24.7
30.7	38.9	49.6	25.9	2.1	7.3	3.2	4.2
80.3	97.5	69.7	34.3	61.8	42.4	24.8	43.0
13.1	13.8	15.3	3.2	109.4	18.0	14.2	47.2
23.6	28.0	28.0	4.4	86.6	43.8	32.0	54.1
13.7	12.1	12.4	1.1	27.6	34.4	31.7	31.2
17.9	21.8	20.8	2.6	9.2	28.9	21.4	19.8
54.6	56.2	57.4	3.5	60.9	91.3	56.8	69.7
142.9	141.3	150.6	14.7	0.0	226.5	166.1	130.9
114.2	128.1	116.4	10.8	287.3	179.0	127.8	198.0
12.1	8.7	11.7	2.8	173.9	44.6	30.4	83.0
44.8	30.0	33.1	10.4	589.0	852.8	425.6	622.5
146.9	102.5	108.2	36.2	387.9	631.2	610.8	543.3
161.8	120.4	133.0	25.0	465.4	768.8	995.1	743.1
3.4	2.8	2.6	0.9	28.2	17.3	10.3	18.6
52.4	43.7	48.8	4.6	155.3	93.1	67.2	105.2
2.1	1.5	1.4	0.7	62.3	11.2	9.0	27.5
8.8	7.9	8.7	0.7	132.2	30.6	17.1	59.9
49.4	42.0	46.2	3.8	63.9	59.4	61.5	61.6
43.5	45.4	45.1	1.4	53.1	48.3	79.2	60.2
19.4	23.0	26.4	9.2	164.1	60.4	79.9	101.5
16.8	16.4	20.5	6.8	79.2	63.2	51.0	64.5
24.8	24.6	26.6	3.3	88.2	83.2	77.4	83.0
5.7	9.5	9.1	3.3	49.5	33.0	29.7	37.4
240.2	259.4	195.7	94.3	860.1	1360.7	561.7	927.5
166.5	191.1	136.7	74.0	971.5	1001.6	298.1	757.1
240.4	178.7	160.8	89.8	451.9	1315.5	627.0	798.1
70.7	75.5	58.4	25.5	348.8	323.1	178.6	283.5
52.4	55.8	48.3	10.2	80.9	213.4	103.1	132.4
7.2	10.3	7.4	2.9	72.7	90.1	28.2	63.7
5.1	6.8	4.8	2.3	0.0	56.3	14.1	23.5
3.3	3.7	3.1	0.8	17.8	35.7	7.1	20.2
8.1	8.8	8.1	0.6	0.0	39.3	15.2	18.2
8.7	11.7	8.9	2.8	152.2	45.3	17.7	71.7
11.8	13.2	11.6	1.7	86.4	52.3	30.1	56.3
12.9	7.7	9.9	2.7	0.0	43.9	27.7	23.9
2.1	1.6	1.7	0.3	31.7	8.9	3.4	14.7
3.8	4.9	4.5	0.6	76.7	12.2	7.4	32.1
93.0	97.9	108.2	22.2	65.8	56.6	23.5	48.6
0.5	1.1	1.2	0.8	0.0	5.9	0.5	2.1
15.0	8.9	9.9	4.7	0.0	111.9	64.5	58.8
7.5	11.0	14.6	9.4	0.0	16.8	11.5	9.4
2.6	2.7	79.4	132.9	0.0	6.8	4.6	3.8

2.4	3.2	81.4	136.2	0.7	3.3	1.1	1.7
0.3	0.6	26.8	45.7	27.5	1.6	0.7	10.0
0.3	0.9	45.5	77.9	0.0	5.7	2.1	2.6
0.4	0.8	27.4	46.4	30.8	18.9	3.8	17.8
5.6	6.9	7.3	1.9	101.5	13.0	10.1	41.5
106.1	111.1	88.2	35.3	527.4	238.7	206.1	324.1
61.6	52.1	47.4	17.1	186.8	205.0	177.7	189.8
17.1	15.9	19.4	5.1	0.0	8.3	7.3	5.2
3.1	1.9	3.1	1.2	22.5	2.5	2.2	9.1
7.3	7.7	8.5	1.8	11.0	18.9	11.8	13.9
0.0	0.0	0.0	0.0	691.3	0.0	0.0	230.4
0.3	0.6	0.3	0.3	24.4	6.2	0.9	10.5
0.2	0.0	0.1	0.1	32.1	4.3	1.3	12.6
3.5	3.2	2.8	0.9	25.9	21.8	10.9	19.5
2.7	3.0	3.7	1.4	40.0	10.4	10.8	20.4
3.4	2.9	4.8	2.8	22.3	2.5	1.6	8.8
2.5	3.8	4.2	1.9	8.7	1.5	1.0	3.7
76.0	66.8	69.4	5.7	87.8	48.7	36.3	57.6
3.1	5.3	4.8	1.5	31.6	4.7	2.9	13.1
10.8	12.8	13.3	2.8	42.8	8.5	4.5	18.6
93.1	127.3	128.7	36.2	56.3	10.7	8.1	25.0
76.8	94.6	68.5	31.2	0.0	3.4	2.8	2.1
126.7	132.8	104.9	43.0	0.0	3.1	3.2	2.1
134.9	140.2	114.6	39.9	61.1	12.0	10.3	27.8
113.6	98.7	100.9	11.8	254.4	23.9	22.5	100.3
5.4	4.0	4.6	0.7	79.0	19.0	25.8	41.3
3.0	1.5	2.7	1.0	30.2	3.6	2.2	12.0
6.7	7.4	7.2	0.5	164.9	19.1	18.8	67.6
41.6	47.4	37.0	13.3	688.2	315.1	314.7	439.3
48.0	54.6	46.6	8.8	0.0	19.5	13.0	10.8
106.5	110.9	121.4	22.1	0.0	61.4	29.8	30.4
8.5	7.3	8.4	1.1	890.0	550.0	457.6	632.5
7.2	7.2	7.9	1.2	128.4	92.8	70.4	97.2
53.2	47.4	55.2	9.1	19.3	165.0	102.4	95.6
20.1	19.4	27.4	13.2	58.7	58.9	23.7	47.1
4.0	4.2	4.8	1.2	140.0	31.1	11.4	60.8
1.0	0.4	0.8	0.3	73.1	15.2	2.0	30.1
12.7	8.8	12.5	3.6	0.0	5.4	4.6	3.4
17.2	11.8	11.7	5.6	259.8	135.3	111.2	168.7
17.1	18.9	17.2	1.6	118.3	65.5	52.9	78.9
3.7	3.9	3.5	0.5	68.6	34.8	24.1	42.5
11.8	13.1	14.1	3.0	128.9	23.5	20.8	57.7
5.3	4.7	4.9	0.4	118.6	144.9	107.7	123.7

5.0	5.9	5.1	0.8	45.8	39.6	29.6	38.3
14.1	14.8	13.0	2.5	141.6	56.6	36.5	78.2
58.4	38.7	61.4	24.3	28.0	72.1	52.4	50.8
118.3	98.2	110.4	10.8	341.0	102.5	104.8	182.8
158.9	110.4	124.3	30.2	264.8	99.6	103.7	156.0
13.1	14.8	15.7	3.2	34.0	52.4	37.3	41.2
52.2	94.2	66.5	24.0	137.0	158.6	63.8	119.8
69.3	76.5	85.6	22.3	19.2	66.1	48.4	44.5
87.9	148.3	106.7	36.1	82.4	161.0	202.4	148.6
63.8	89.3	89.2	25.3	344.4	127.5	54.1	175.3
321.1	622.7	366.9	236.3	60.5	8.7	7.4	25.5
26.3	24.3	26.7	2.6	89.7	59.5	45.6	65.0
61.3	57.0	56.8	4.6	294.7	200.6	73.1	189.5
42.9	33.6	40.1	5.7	606.2	319.6	245.5	390.4
41.6	37.6	39.1	2.2	119.8	138.3	148.6	135.6
89.1	88.9	93.4	7.6	268.5	202.5	273.7	248.2
13.6	17.4	16.6	2.7	112.8	10.0	8.8	43.9
30.8	37.8	34.1	3.5	0.0	19.7	11.2	10.3
474.5	489.2	488.4	13.6	299.1	212.6	158.6	223.5
180.0	119.9	113.2	70.5	280.4	80.6	104.1	155.1
22.0	22.4	20.4	3.0	68.3	43.7	30.5	47.5
44.4	104.3	71.7	30.3	0.0	14.8	3.4	6.1
33.4	35.2	32.9	2.5	97.0	10.5	3.2	36.9
38.9	55.3	46.0	8.4	25.9	25.7	9.4	20.4
111.8	103.5	91.2	28.9	49.1	73.3	67.4	63.3
228.1	282.8	210.3	82.9	94.6	235.9	195.1	175.2
3284.7	2808.5	2326.9	1269.1	439.9	1213.8	962.2	871.9
55.2	58.9	49.2	13.8	1144.7	264.8	367.2	592.2
20.1	24.3	20.8	3.2	324.4	183.6	191.6	233.2
13.2	18.0	18.1	4.9	31.3	48.2	22.9	34.2
37.5	40.7	39.6	1.9	117.1	199.4	160.0	158.9
259.6	201.1	217.0	37.3	98.3	486.2	345.9	310.2
58.6	72.5	65.5	6.9	14.9	117.2	79.0	70.3
64.3	46.9	52.7	10.0	0.0	162.0	89.4	83.8
19.4	17.4	20.0	2.9	260.5	44.9	42.4	116.0
41.7	41.8	43.5	3.0	138.4	150.2	83.8	124.2
56.9	49.7	79.8	46.0	211.3	142.4	119.6	157.8
16.2	16.3	16.3	0.1	962.5	82.5	48.7	364.6
683.6	519.2	448.2	277.8	285.7	146.6	164.3	198.9
167.4	177.3	141.7	53.3	401.9	591.0	281.5	424.8
11.8	12.7	18.0	10.0	232.7	163.0	120.6	172.1
776.4	681.8	651.3	142.8	1.1	73.7	77.6	50.8
554.4	434.8	448.8	99.3	59.9	67.1	43.3	56.8

10.3	14.6	12.8	2.2	39.5	45.3	29.5	38.1
12.9	13.0	12.7	0.5	175.0	48.4	26.5	83.3
170.9	197.1	242.9	102.9	231.3	565.3	340.9	379.2
131.1	122.3	109.0	31.1	322.4	184.5	147.0	218.0
2.2	1.2	1.4	0.7	120.2	10.9	8.3	46.4
79.3	93.8	87.6	7.5	183.3	146.1	127.0	152.1
65.0	61.8	67.8	7.7	143.1	83.2	88.5	105.0
35.5	63.2	45.8	15.1	147.2	30.0	29.2	68.8
97.7	90.4	107.9	24.3	16.4	84.5	85.5	62.1
71.7	65.1	66.4	4.8	62.3	89.9	65.3	72.5
51.0	61.0	54.4	5.7	247.2	91.4	63.6	134.1
107.6	108.0	114.3	11.2	66.2	114.4	103.6	94.7
89.9	123.2	116.8	24.3	0.0	44.7	29.6	24.8
188.2	233.2	231.8	43.0	31.6	55.2	44.5	43.8
4.9	6.7	8.4	4.5	0.0	8.8	9.7	6.2
5.2	6.3	6.1	0.8	103.0	19.6	12.9	45.1
16.3	17.6	15.2	3.1	28.1	67.4	23.7	39.7
1.7	2.8	2.2	0.6	175.7	11.5	8.5	65.2
1.4	1.6	1.2	0.5	56.1	101.8	81.8	79.9
6.2	7.8	7.3	0.9	46.4	15.2	26.0	29.2
62.5	64.9	55.7	13.9	152.1	81.4	81.5	105.0
5.4	4.9	5.1	0.2	0.0	10.3	4.5	4.9
15.0	10.0	10.1	4.8	2921.4	1674.8	1664.7	2086.9
3.5	4.5	2.9	2.1	2010.3	934.5	1081.9	1342.2
2.8	2.2	1.8	1.2	1467.2	436.2	640.6	848.0
1.5	1.2	1.2	0.3	1024.7	268.7	389.9	561.1
42.6	26.9	30.1	11.3	9746.4	4886.5	5294.0	6642.3
2.8	4.2	3.3	0.8	0.0	15.4	11.3	8.9
28.9	35.8	37.4	9.5	95.7	62.5	39.5	65.9
24.1	50.8	39.9	14.0	168.6	81.8	15.3	88.6
87.6	42.9	67.0	22.6	25.6	13.8	11.7	17.0
73.2	37.9	54.5	17.8	0.0	7.6	10.5	6.0
34.9	18.9	21.7	12.1	0.0	9.2	9.7	6.3
55.3	37.5	40.0	14.3	17.4	16.8	18.1	17.4
62.6	89.1	67.2	20.0	62.3	33.1	13.6	36.3
6.9	10.7	8.5	1.9	170.2	37.4	23.9	77.2
147.6	121.1	126.2	19.3	177.4	175.8	153.5	168.9
75.4	86.1	78.0	7.1	363.1	90.8	58.9	170.9
113.2	142.9	131.3	15.9	217.7	208.1	145.8	190.5
57.9	58.8	65.9	13.2	45.1	36.3	44.1	41.8
72.5	80.1	78.2	5.0	399.2	116.9	132.0	216.1
23.8	27.0	24.9	1.8	99.2	32.2	31.3	54.2
25.1	27.7	23.8	4.8	0.0	14.7	16.7	10.5

28.2	20.7	24.7	3.8	67.5	58.6	74.0	66.7
3.1	2.0	2.4	0.6	867.7	443.2	551.7	620.9
1.0	0.7	0.7	0.2	190.6	77.1	84.0	117.2
71.6	72.5	57.0	26.1	9.0	79.6	57.4	48.6
116.6	93.3	86.8	33.5	190.7	64.3	59.1	104.7
145.2	117.3	114.6	32.0	34.0	79.2	75.6	63.0
8.7	12.8	11.8	2.7	114.5	43.3	32.0	63.3
5.4	6.1	5.9	0.4	156.3	127.2	51.7	111.7
6.0	9.0	8.1	1.8	153.9	45.8	8.9	69.5
3.0	1.5	1.6	1.2	215.6	9.7	1.9	75.7
2.0	7.3	5.0	2.7	26.5	21.6	3.4	17.2
1.5	1.5	1.9	0.8	59.0	14.7	2.1	25.2
1.7	3.4	3.9	2.5	0.0	16.9	4.4	7.1
1.5	3.5	3.0	1.3	82.8	14.8	9.4	35.7
1.8	4.4	3.9	1.9	47.2	22.1	8.4	25.9
19.0	14.5	16.9	2.3	83.2	30.0	7.8	40.3
5.0	5.3	6.1	1.7	21.1	27.4	11.4	19.9
5.4	4.8	7.7	4.5	37.8	18.6	18.4	24.9
3.8	5.5	7.2	4.5	18.1	5.2	3.7	9.0
4.3	7.2	8.3	4.6	44.8	9.9	5.0	19.9
38.7	22.4	41.5	20.6	132.4	294.5	135.3	187.4
2.1	0.4	1.1	0.9	31.5	15.9	15.3	20.9
25.4	25.1	26.5	2.1	209.9	204.5	215.2	209.9
3.1	1.8	2.9	0.9	10.8	10.3	6.3	9.1
4.3	4.6	4.4	0.1	61.9	17.1	12.7	30.6
7.0	6.4	6.0	1.4	46.8	19.5	16.1	27.5
215.9	159.8	157.5	59.6	200.0	42.6	37.4	93.4
99.4	85.2	88.3	9.9	106.9	78.8	62.2	82.6
663.1	768.8	642.9	137.2	60.5	127.9	130.7	106.4
17.3	16.1	20.2	6.1	121.8	28.8	22.1	57.6
49.6	61.9	55.5	6.2	81.2	69.9	66.2	72.4
54.3	64.8	66.2	12.6	25.7	56.5	40.6	40.9
86.4	96.3	87.1	8.9	82.2	101.1	83.5	88.9
43.2	49.6	42.3	7.8	68.9	84.4	72.7	75.3
82.3	105.3	131.2	65.8	73.8	144.6	105.5	108.0
107.2	116.4	138.3	46.1	87.0	255.4	179.1	173.8
169.0	153.2	143.9	30.9	0.0	56.6	59.8	38.8
110.8	144.0	136.3	22.6	1018.3	373.0	307.9	566.4
111.6	113.3	126.8	24.7	206.7	267.9	175.7	216.8
96.6	92.0	86.7	13.4	491.3	202.0	185.1	292.8
10.4	14.1	12.4	1.9	111.1	48.0	27.7	62.3
21.3	26.3	27.9	7.5	213.4	192.5	225.4	210.4
10.6	11.2	11.5	1.0	73.2	31.3	27.4	44.0

82.7	88.1	81.4	7.5	0.6	98.4	78.5	59.2
69.4	62.2	66.4	3.8	253.4	68.4	62.5	128.1
100.8	104.9	106.7	7.0	431.8	90.6	84.9	202.4
20.4	18.9	15.2	7.7	103.4	16.6	6.7	42.2
0.6	1.2	0.8	0.3	44.6	12.9	4.6	20.7
2.3	3.3	2.9	0.5	116.0	8.4	8.2	44.2
0.0	0.2	0.1	0.1	44.0	0.0	0.5	14.8
0.6	0.0	0.3	0.3	108.8	0.7	1.0	36.8
1.6	2.0	1.4	0.7	32.1	15.9	5.3	17.8
1.9	0.7	1.0	0.8	27.1	5.5	1.5	11.3
3.0	1.9	3.1	1.3	18.8	4.2	1.0	8.0
4.2	4.7	4.3	0.4	104.3	18.7	3.8	42.3
6.1	6.4	6.2	0.2	198.3	85.7	105.3	129.8
17.3	11.3	13.2	3.6	39.7	80.8	96.4	72.3
8.4	11.9	11.1	2.4	49.2	73.1	46.2	56.2
7.3	7.9	10.5	5.0	583.9	33.2	15.3	210.8
12.7	17.4	14.4	2.6	130.3	24.4	13.2	56.0
5.8	24.4	20.2	12.8	0.0	24.1	11.8	12.0
42.6	38.1	50.5	17.7	96.1	30.8	31.3	52.7
54.7	55.6	58.7	6.2	39.5	33.0	35.1	35.9
55.2	56.6	60.6	8.1	19.9	14.5	15.1	16.5
51.1	64.9	57.8	6.9	149.7	24.5	20.5	64.9
77.2	76.6	74.2	4.7	54.7	25.5	30.5	36.9
45.4	38.4	42.7	3.7	72.7	32.6	26.5	43.9
35.4	33.8	38.5	6.9	29.2	20.1	9.6	19.6
57.7	48.1	55.2	6.1	22.1	11.2	9.8	14.3
55.0	46.6	47.6	7.0	66.7	26.2	19.3	37.4
44.4	26.3	32.3	10.5	84.0	19.2	16.9	40.0
33.8	31.2	33.4	2.0	136.5	22.7	26.4	61.9
39.9	31.2	38.5	6.8	45.8	23.3	20.4	29.8
70.3	63.2	70.4	7.3	263.7	51.4	38.9	118.0
25.3	30.3	25.6	4.6	13.1	67.8	67.6	49.5
5.9	4.2	4.2	1.8	0.0	10.6	18.6	9.7
3.2	3.9	3.5	0.4	34.5	6.1	7.6	16.1
9.0	9.9	10.2	1.3	44.8	18.1	10.2	24.4
64.4	78.0	64.4	13.6	0.0	47.6	35.0	27.5
109.9	136.7	130.8	18.7	179.9	218.3	155.9	184.7
158.7	96.7	162.1	67.1	107.3	393.7	215.0	238.7
37.5	45.0	38.1	6.6	104.8	112.2	58.9	92.0
30.0	36.9	36.3	6.1	65.8	96.2	63.1	75.0
31.3	31.0	30.7	0.7	164.9	93.7	72.9	110.5
31.0	35.3	35.3	4.3	68.5	26.5	19.6	38.2
7.9	13.5	9.9	3.1	638.2	74.1	43.4	251.9

30.6	36.3	32.7	3.1	175.2	90.0	59.6	108.3
99.8	109.6	105.0	4.9	203.0	147.9	117.5	156.1
35.2	44.8	40.6	4.9	271.3	77.0	48.9	132.4
72.9	51.5	51.5	21.4	166.1	130.4	193.4	163.3
71.8	72.3	72.8	1.3	48.6	23.5	17.1	29.7
145.3	166.2	163.9	17.6	217.1	239.6	196.1	217.6
1.4	3.4	2.1	1.1	274.0	11.0	6.1	97.0
21.9	22.9	21.2	2.2	375.4	197.3	149.0	240.6
50.3	43.8	39.5	13.4	262.8	134.4	174.6	190.6
271.6	261.0	281.6	27.0	317.7	284.7	262.0	288.1
77.1	101.3	99.2	21.1	33.9	48.0	31.4	37.7
10.5	22.4	15.9	6.0	230.3	25.8	12.9	89.7
90.9	103.6	83.1	25.3	137.3	41.4	23.0	67.2
124.6	94.7	93.2	32.1	618.0	185.6	254.4	352.7
1.9	2.1	1.9	0.2	78.5	25.2	24.3	42.7
0.0	0.0	0.0	0.0	6.5	1.5	1.4	3.2
1.9	0.6	1.1	0.7	0.0	14.6	7.3	7.3
0.6	0.5	0.6	0.1	0.0	7.3	4.3	3.9
104.0	111.1	95.7	20.7	190.2	664.8	338.8	397.9
318.0	403.6	327.5	71.8	264.9	525.5	513.5	434.6
1.2	2.6	2.4	1.1	123.9	27.6	20.3	57.3
838.6	909.9	729.8	252.6	74.1	110.5	112.8	99.1
800.5	822.9	718.3	162.1	253.4	174.0	166.7	198.0
161.0	166.1	138.4	43.7	24.4	122.5	114.8	87.3
10.4	9.2	8.8	1.9	0.0	33.3	25.3	19.5
5.3	6.7	5.3	1.4	0.0	27.3	22.8	16.7
6.9	11.1	7.9	2.8	66.8	51.8	45.9	54.8
22.1	27.0	21.0	6.7	99.1	69.4	73.7	80.7
23.0	23.6	19.3	6.8	180.6	81.3	97.1	119.7
220.1	240.7	278.0	83.1	606.6	627.4	368.1	534.0
75.3	95.0	100.3	28.0	0.0	326.6	201.1	175.9
3516.6	2052.9	3097.5	910.5	3612.1	4709.4	3741.6	4021.0
37.7	46.8	38.8	7.5	56.5	39.2	20.6	38.8
31.7	37.9	32.8	4.6	25.2	69.8	55.4	50.1
39.6	54.8	72.6	44.5	60.2	40.8	24.3	41.7
8.7	8.9	10.9	3.7	49.0	37.6	31.7	39.4
144.9	110.7	113.6	29.9	0.0	236.8	138.9	125.2
94.7	106.7	84.4	29.0	177.0	104.2	86.9	122.7
74.4	75.7	96.8	37.7	329.2	167.4	140.4	212.3
65.9	59.2	53.9	15.4	373.7	38.2	32.2	148.0
129.3	169.2	135.0	31.7	198.8	92.8	70.5	120.7
58.3	66.8	68.7	11.5	395.0	221.5	194.7	270.4
1491.8	1540.2	1564.9	88.2	569.6	822.2	504.6	632.1

20.8	26.9	23.5	3.1	136.3	68.4	57.3	87.3
19.8	25.4	22.6	2.8	62.5	49.1	40.1	50.6
264.2	191.0	238.6	41.3	389.0	469.2	162.7	340.3
172.1	221.0	292.5	167.9	52.8	84.3	51.4	62.8
5.8	8.7	9.0	3.4	34.4	30.6	32.1	32.4
51.2	53.7	54.0	3.1	179.0	217.0	199.2	198.4
20.4	24.3	26.1	6.8	143.6	82.3	63.8	96.6
40.6	59.1	51.8	9.8	316.9	289.0	118.3	241.4
19.1	19.6	20.5	2.1	104.6	65.8	30.2	66.9
2.5	6.5	4.0	2.2	0.0	223.5	41.2	88.2
29.9	31.3	35.9	9.1	32.7	46.2	33.0	37.3
13.9	12.3	15.7	4.6	24.2	104.9	49.9	59.7
43.0	35.8	61.1	37.9	0.0	300.8	163.1	154.6
175.4	98.9	122.0	46.4	0.0	339.4	224.9	188.1
55.7	75.6	66.0	10.0	912.0	228.4	141.5	427.3
13.6	11.2	10.1	4.1	1845.0	228.3	207.5	760.3
7.7	0.0	2.6	4.5	3868.6	1577.0	179.2	1874.9
18.0	21.5	20.3	2.0	112.9	118.4	123.8	118.4
19.6	17.7	16.7	3.5	82.2	164.6	164.8	137.2
38.0	33.1	33.6	4.2	920.0	76.2	45.2	347.1
13.0	15.5	13.7	1.6	236.9	41.5	13.6	97.3
6.3	9.4	8.9	2.4	36.2	16.6	16.8	23.2
90.8	81.4	74.8	20.1	228.5	78.6	58.0	121.7
175.2	199.7	150.5	65.2	495.2	110.6	61.3	222.4
86.5	84.4	68.2	29.9	40.0	91.5	38.4	56.6
138.0	124.3	114.1	30.4	245.9	103.1	73.0	140.7
55.1	41.3	36.7	21.1	0.0	32.5	15.0	15.8
62.0	65.7	53.3	18.3	0.0	82.9	24.9	35.9
79.6	111.1	87.7	20.5	201.0	143.4	42.6	129.0
60.2	75.8	63.2	11.4	70.8	163.8	55.4	96.7
84.1	132.2	93.3	35.1	215.1	75.1	30.3	106.8
50.0	47.8	40.1	15.2	129.9	30.6	9.5	56.7
318.8	308.3	248.0	113.7	122.5	97.5	65.6	95.2
93.5	91.3	79.8	21.9	73.6	63.8	51.6	63.0
464.9	310.2	304.2	163.8	333.8	595.3	584.0	504.3
109.4	137.1	92.0	55.8	136.7	92.5	39.3	89.5
62.1	57.6	48.7	19.4	58.3	65.7	49.4	57.8
2.0	3.6	2.7	0.8	15.2	26.4	10.2	17.3
123.4	117.8	100.7	34.5	30.3	102.6	56.5	63.1
129.5	166.3	125.5	43.1	63.5	120.0	82.7	88.7
12.7	21.4	15.3	5.3	31.4	57.0	14.0	34.1
33.7	35.2	33.9	1.2	511.5	69.4	30.4	203.8
31.8	29.5	29.2	2.7	234.9	105.8	46.4	129.0

24.9	20.1	24.7	4.6	4.4	84.8	29.9	39.7
256.0	242.7	237.2	22.2	1117.2	203.6	105.1	475.3
46.7	57.2	53.2	5.7	395.5	78.3	25.8	166.5
32.1	41.0	34.6	5.6	79.2	52.4	16.0	49.2
49.3	53.9	51.4	2.3	312.1	58.9	30.4	133.8
38.3	47.8	45.3	6.1	24.0	65.8	28.9	39.5
46.6	50.5	42.5	10.7	47.0	79.2	31.9	52.7
18.5	24.0	19.8	3.7	0.0	70.2	25.9	32.1
3.3	3.1	2.5	1.2	155.4	6.0	1.2	54.2
95.2	89.7	78.7	23.9	421.4	298.5	142.8	287.6
266.3	345.8	256.9	94.0	271.2	214.2	103.5	196.3
27.6	21.8	26.3	4.0	0.0	68.5	35.6	34.7
0.4	0.4	0.8	0.7	218.7	18.9	29.3	89.0
53.7	37.0	33.9	21.5	0.0	50.3	29.6	26.6
92.3	104.9	84.9	24.6	100.6	79.0	62.3	80.6
77.4	92.9	75.2	18.8	165.8	83.3	72.2	107.1
27.8	26.9	28.6	2.2	63.6	68.1	54.3	62.0
22.5	17.9	25.7	9.9	39.0	113.3	66.7	73.0
2.1	4.4	7.8	7.9	147.5	21.2	9.4	59.4
24.0	23.7	22.9	1.7	1728.2	89.4	58.9	625.5
8.2	8.0	7.3	1.5	155.3	61.9	35.2	84.2
5.3	4.7	5.5	1.0	70.8	16.0	14.0	33.6
7.2	6.1	6.0	1.3	29.7	20.2	10.6	20.2
7.8	9.3	8.2	1.0	0.0	32.8	15.9	16.2
9.8	9.3	7.8	3.1	285.7	35.6	13.5	111.6
135.3	107.7	114.9	18.0	409.8	202.5	203.2	271.8
211.3	240.9	240.4	28.8	1.8	14.7	11.8	9.4
29.9	35.4	39.1	11.5	130.0	46.5	78.1	84.9
14.9	18.2	23.0	11.2	10.5	37.8	58.5	35.6
3.8	3.5	5.0	2.3	0.0	19.5	17.4	12.3
6.5	6.3	9.6	5.5	0.0	18.4	23.2	13.9
13.8	18.2	20.7	8.3	15.9	18.9	27.0	20.6
42.5	45.2	43.9	1.3	60.3	27.7	33.0	40.3
0.0	1.9	0.6	1.1	237.8	3.3	3.7	81.6
334.9	1842.8	760.0	944.9	1848.3	1100.0	1068.1	1338.8
257.9	2365.5	899.5	1272.9	127.7	116.8	101.9	115.5
14.6	15.0	15.4	1.1	213.2	190.9	176.3	193.5
34.0	36.1	29.3	9.9	65.9	50.8	15.8	44.2
0.2	0.6	0.4	0.2	0.0	13.3	3.6	5.6
0.9	1.2	1.1	0.2	14.5	8.0	5.0	9.2
71.0	96.0	85.0	12.8	165.5	283.0	121.4	190.0
10.7	16.6	13.9	3.0	49.3	84.6	38.1	57.3
596.8	340.6	439.7	137.6	990.8	1449.0	954.5	1131.4

12.1	12.5	12.3	0.2	108.8	117.9	94.2	107.0
112.7	138.3	138.1	25.3	3.2	81.2	55.8	46.7
33.1	31.8	41.2	15.1	26.6	96.8	34.6	52.7
43.6	37.3	48.0	13.4	128.6	177.4	104.4	136.8
79.4	68.0	73.9	5.7	48.7	137.9	114.8	100.5
535.9	396.4	380.6	163.8	760.5	1593.8	1648.0	1334.1
417.8	317.8	378.5	53.3	729.3	74.6	78.2	294.1
126.1	180.5	147.9	28.8	1003.3	41.4	29.6	358.1
1707.7	994.5	1290.9	371.5	403.1	165.4	126.1	231.5
650.1	439.4	733.5	343.5	345.9	29.0	34.0	136.3
118.6	61.0	82.0	31.9	150.9	62.6	53.0	88.8
73.2	82.5	75.2	6.5	72.7	38.0	37.9	49.5
15.9	18.5	14.0	5.7	25.4	6.7	3.7	11.9
9.7	6.3	7.4	2.0	28.2	24.9	16.9	23.4
20.9	15.9	15.2	6.0	47.0	63.1	56.9	55.7
14.2	14.3	14.3	0.1	25.9	33.0	32.7	30.5
74.7	119.5	106.8	28.0	22.5	60.1	47.1	43.2
46.3	49.7	38.7	16.2	0.0	28.8	30.7	19.8
138.7	119.4	104.8	43.1	71.0	42.9	48.4	54.1
8.2	8.0	8.0	0.1	7.1	28.5	39.6	25.1
16.9	15.5	12.0	7.4	31.4	17.3	15.5	21.4
37.0	27.2	82.5	87.5	44.9	65.9	53.9	54.9
18.6	16.8	14.8	5.0	0.0	49.4	36.9	28.8
11.9	9.3	9.8	1.9	4.7	11.7	9.2	8.5
11.5	13.7	10.8	3.3	16.4	16.9	18.3	17.2
11.9	12.2	11.2	1.6	19.2	20.1	19.1	19.5
6.9	8.2	6.4	2.0	17.5	9.4	11.3	12.7
1.9	2.8	2.2	0.6	15.2	3.0	2.8	7.0
0.4	0.6	0.5	0.1	21.1	6.2	1.8	9.7
10.8	16.4	12.8	3.2	0.0	14.5	8.8	7.8
4.0	2.7	2.9	1.0	117.4	8.2	9.0	44.9
78.8	84.1	82.2	3.0	102.0	55.7	46.7	68.1
58.5	93.1	74.9	17.4	112.7	87.2	72.1	90.7
128.8	116.8	114.2	16.1	112.5	167.3	150.5	143.4
6.9	9.2	12.1	7.0	8.6	28.1	15.9	17.5
25.3	31.4	22.7	10.2	88.4	13.2	9.8	37.1
7.9	7.1	7.5	0.4	0.0	1.9	3.2	1.7
26.6	37.7	28.1	8.9	72.5	45.8	36.8	51.7
17.9	15.5	14.6	3.8	39.4	38.1	33.5	37.0
3.1	2.6	2.3	0.9	39.9	8.8	11.6	20.1
3.7	4.0	3.1	1.3	40.7	4.8	7.6	17.7
3.6	3.3	2.8	1.2	0.0	3.8	3.1	2.3
1.8	1.5	1.5	0.3	33.2	2.3	1.6	12.4

26.0	31.0	34.1	10.0	24.9	101.7	82.4	69.7
4.7	4.2	4.1	0.7	0.0	14.7	10.9	8.5
27.7	25.4	25.5	2.3	81.4	26.6	21.0	43.0
1.2	1.7	1.0	0.7	83.0	6.9	4.1	31.4
1.2	0.7	0.8	0.3	73.5	7.9	3.0	28.1
10.3	11.5	10.6	0.9	114.9	18.6	7.6	47.0
48.8	52.0	36.0	25.0	37.9	32.7	16.7	29.1
3.1	4.1	3.3	0.8	155.5	17.7	13.0	62.0
3.3	3.5	3.1	0.4	86.6	25.2	14.8	42.2
4.0	3.1	4.4	1.5	58.6	18.5	10.6	29.3
364.8	267.9	248.5	127.2	0.0	714.9	340.8	351.9
135.1	163.0	126.2	42.0	227.0	183.6	140.4	183.7
39.2	48.5	41.3	6.3	73.1	64.7	40.1	59.3
424.3	343.8	277.1	189.6	1033.2	364.9	463.9	620.7
76.4	109.5	71.7	40.3	910.0	71.4	87.4	356.3
19.1	22.5	19.3	3.0	24.2	18.9	11.4	18.1
338.8	115.3	246.0	116.4	0.0	557.1	288.3	281.8
4.6	4.2	62.7	100.9	149.0	45.4	42.2	78.9
113.8	89.8	77.5	43.9	825.1	410.7	513.7	583.2
71.0	89.8	64.1	29.7	2704.7	273.7	322.3	1100.2
58.2	32.2	33.6	23.9	198.6	331.4	195.7	241.9
225.5	191.0	168.9	70.3	3466.5	737.7	755.0	1653.1
37.1	29.9	35.5	4.9	2792.9	171.8	160.0	1041.5
98.4	60.7	74.9	20.5	1233.2	325.0	291.6	616.6
58.8	61.6	51.2	15.7	500.7	298.1	247.9	348.9
47.7	58.7	49.4	8.5	1315.0	402.2	172.0	629.7
201.5	196.7	174.5	42.7	3308.9	908.8	945.9	1721.2
110.6	131.3	103.0	32.7	1780.4	684.7	585.2	1016.8
54.1	54.5	64.0	16.8	225.5	191.5	184.0	200.3
100.9	113.6	118.0	19.7	636.4	388.2	275.5	433.4
3.6	3.5	3.9	0.6	37.3	13.4	6.0	18.9
8.8	13.5	11.0	2.4	11.6	20.8	12.1	14.8
6.9	9.2	8.5	1.4	198.6	67.5	55.3	107.1
32.8	28.6	32.6	3.9	5260.6	1328.4	1022.6	2537.2
179.1	146.3	142.6	38.6	544.7	135.4	121.8	267.3
11.8	20.8	17.7	5.2	133.8	115.5	90.1	113.1
14.7	14.6	15.8	2.0	52.3	19.7	17.9	30.0
21.4	15.9	19.9	3.5	124.6	24.8	18.8	56.1
9.6	12.1	12.5	3.2	117.6	14.8	15.3	49.2
14.8	17.8	20.4	7.3	94.5	25.1	23.6	47.7
13.6	22.4	21.7	7.7	100.0	29.4	19.9	49.8
2.7	3.1	3.4	0.9	30.6	12.0	9.0	17.2
2.4	5.8	4.7	2.0	0.0	16.8	13.2	10.0

5.7	6.4	8.1	3.4	97.8	43.0	32.5	57.8
6.8	8.5	17.2	16.5	91.3	69.4	42.5	67.7
16.4	14.5	15.6	1.0	181.9	102.7	70.3	118.3
72.0	78.4	60.5	25.8	39.7	22.0	14.6	25.4
46.6	49.3	65.0	29.5	191.1	181.2	206.8	193.0
2.6	2.3	2.4	0.1	0.0	21.2	15.4	12.2
5.5	2.3	3.6	1.7	99.2	22.1	19.1	46.8
4.7	2.0	3.2	1.4	30.7	11.3	13.0	18.3
11.7	11.5	12.2	1.0	46.9	21.1	20.1	29.3
8.7	9.6	7.5	2.9	1.3	22.2	17.3	13.6
17.3	19.9	16.8	3.4	5.0	24.1	19.2	16.1
169.7	282.7	284.8	116.2	19.7	60.9	50.4	43.6
3.1	3.0	3.5	0.8	9.0	12.9	3.6	8.5
4.3	5.3	5.4	1.1	9.3	14.9	8.6	10.9
129.1	150.8	110.9	51.5	240.3	162.0	187.2	196.5
71.4	118.0	71.5	46.4	50.1	22.7	18.1	30.3
535.7	697.5	629.4	83.9	146.6	115.8	107.5	123.3
69.6	142.5	84.9	51.7	172.7	39.7	35.1	82.5
41.3	63.6	43.9	18.6	45.8	59.5	57.6	54.3
167.6	144.6	155.6	11.5	165.4	59.0	64.7	96.4
166.4	146.9	153.8	10.9	113.7	296.1	204.0	204.6
4.0	4.6	4.9	1.1	120.0	21.4	13.7	51.7
139.5	138.4	133.0	10.3	160.7	122.7	97.6	127.0
139.5	100.3	105.3	32.0	13.8	86.0	75.5	58.4
38.2	36.8	37.6	0.7	267.4	74.2	43.7	128.4
101.1	73.9	121.3	60.1	52.2	33.4	28.9	38.2
241.1	246.4	206.9	63.8	76.4	37.0	42.3	51.9
214.0	326.6	202.7	129.8	12.8	57.3	53.1	41.1
61.2	111.4	75.5	31.3	26.9	31.8	21.9	26.9
42.5	71.1	68.0	24.1	129.4	61.0	37.7	76.0
16.5	13.2	17.6	5.1	153.2	94.6	84.3	110.7
20.6	20.4	18.5	3.4	0.0	220.9	210.9	143.9
45.8	50.2	40.3	13.6	485.8	74.1	44.5	201.5
7.2	13.5	9.8	3.3	97.3	27.3	15.4	46.7
12.9	13.5	13.1	0.3	42.0	22.3	17.7	27.3
341.9	170.2	261.4	86.4	134.4	100.9	78.8	104.7
13.7	11.6	14.5	3.3	129.0	24.9	18.8	57.6
26.1	32.6	26.8	5.5	90.3	88.5	40.4	73.1
21.2	21.8	17.6	6.8	52.0	33.6	25.5	37.0
437.3	661.6	471.1	176.0	1034.1	763.5	456.2	751.3
5.6	3.6	7.8	5.7	18.3	20.1	13.9	17.4
1.6	2.0	4.1	3.9	92.7	11.3	5.1	36.3
0.9	0.4	1.3	1.3	0.0	4.0	1.8	1.9

1.1	0.2	1.8	2.1	32.3	9.5	3.5	15.1
2.3	3.3	10.2	12.8	7.4	32.6	13.8	17.9
148.0	107.5	126.5	20.4	37.1	364.9	237.2	213.1
31.9	22.1	50.5	40.9	89.1	140.5	128.6	119.4
47.1	34.5	55.4	26.0	58.6	75.5	86.3	73.5
57.7	35.4	62.8	30.3	70.9	113.3	94.7	93.0
17.0	21.1	18.7	2.1	176.1	126.0	59.5	120.5
72.5	73.0	123.9	88.7	72.3	84.3	67.2	74.6
4.1	6.2	5.7	1.3	0.0	6.1	4.2	3.4
66.0	61.4	69.2	9.8	52.2	15.8	12.9	27.0
20.5	23.3	23.9	3.6	57.6	56.6	28.4	47.5
28.0	27.8	27.9	0.1	87.8	28.6	22.0	46.1
36.9	39.6	38.3	1.4	123.3	285.6	391.9	267.0
28.2	27.7	27.5	0.8	224.7	334.8	478.9	346.1
7.5	10.1	10.7	3.4	38.3	5.5	3.8	15.8
207.2	160.9	146.9	68.4	329.3	239.9	163.5	244.2
5.3	4.6	4.4	1.1	38.0	15.6	14.4	22.6
2.7	5.2	3.6	1.3	41.7	38.4	26.1	35.4
14.4	16.9	19.1	6.1	52.7	35.3	23.6	37.2
158.9	92.2	107.5	45.7	371.2	240.1	166.5	259.2
0.9	0.8	14.3	23.3	112.3	49.3	19.4	60.3
33.1	26.0	30.3	3.8	1567.6	590.3	744.1	967.3
2.7	4.2	4.1	1.3	19.7	13.7	8.7	14.1
8.6	9.8	8.5	1.4	208.7	39.3	45.5	97.8
41.1	39.4	54.9	25.4	0.0	7.4	5.7	4.4
158.2	132.9	163.6	33.8	100.6	101.0	138.3	113.3
51.0	49.6	42.8	13.1	243.3	35.0	25.1	101.1
56.7	33.5	36.6	18.8	78.8	14.2	6.7	33.2
24.9	25.5	29.5	7.4	49.2	138.4	121.4	103.0
6.1	9.9	9.0	2.6	43.6	79.7	50.3	57.9
7.6	7.0	7.0	0.6	43.6	44.5	23.2	37.1
2.5	2.0	2.0	0.5	60.3	29.0	7.2	32.2
2.2	2.9	2.5	0.4	2.4	17.6	4.4	8.2
18.4	26.4	19.4	6.6	0.0	31.5	16.3	15.9
11.8	15.0	10.6	5.2	33.1	21.6	16.3	23.6
1.6	2.0	1.5	0.6	79.3	8.3	4.9	30.8
5.6	5.1	5.9	0.9	11.2	42.5	7.3	20.3
8.4	9.9	9.9	1.4	114.6	62.5	29.1	68.7
6.3	3.4	4.7	1.5	92.1	23.3	4.0	39.8
6.0	5.6	6.8	1.7	115.6	37.8	14.6	56.0
4.7	6.7	4.8	1.8	0.0	12.1	0.6	4.2
2.6	1.5	1.7	0.8	17.2	8.2	1.3	8.9
2.4	1.6	1.6	0.9	23.4	5.2	3.3	10.6

10.1	7.8	9.5	1.5	27.7	42.2	16.5	28.8
14.3	10.0	11.5	2.4	87.4	44.1	10.4	47.3
6.2	7.2	6.3	0.9	46.1	32.9	17.4	32.1
13.4	12.7	13.8	1.3	259.2	26.6	6.7	97.5
2.7	4.9	3.2	1.5	26.1	17.9	4.0	16.0
8.3	10.0	7.8	2.5	31.4	36.0	2.9	23.4
1.4	0.2	0.9	0.6	55.5	6.9	1.9	21.4
0.5	0.4	0.4	0.1	55.3	2.5	0.6	19.5
5.6	6.7	5.6	1.2	23.7	16.2	11.4	17.1
6.8	7.1	5.9	1.8	0.0	9.5	10.3	6.6
4.4	6.4	4.8	1.4	50.8	9.3	4.1	21.4
1.6	1.8	1.5	0.3	28.4	11.9	3.8	14.7
3.5	2.0	2.5	0.9	0.0	30.6	7.1	12.6
1.7	2.0	1.8	0.2	60.9	10.7	6.3	26.0
3.5	5.0	4.2	0.7	18.6	20.6	12.7	17.3
11.8	7.7	8.6	2.9	1506.0	65.5	22.9	531.5
32.0	53.4	46.0	12.1	360.4	73.9	24.5	152.9
30.3	39.3	38.1	7.4	155.7	91.7	31.8	93.1
6.8	7.7	6.7	1.0	55.6	36.8	12.7	35.1
23.7	24.9	29.8	9.5	64.3	38.5	24.4	42.4
14.7	12.7	15.2	2.7	47.7	28.9	25.7	34.1
9.7	12.5	10.3	2.1	301.9	44.3	60.6	135.6
4.2	7.3	5.6	1.6	86.5	36.8	16.7	46.7
2.7	4.5	3.2	1.2	93.4	28.8	11.6	44.6
30.0	46.7	31.9	14.0	151.8	127.7	58.5	112.7
3.6	3.1	2.9	0.8	0.0	4.4	4.5	3.0
0.5	0.2	0.3	0.1	34.7	1.1	2.2	12.7
0.2	0.2	0.2	0.1	97.5	1.1	0.8	33.1
0.5	0.5	0.7	0.3	67.0	1.6	1.8	23.5
0.8	0.7	0.9	0.4	64.8	4.8	6.1	25.2
3.6	3.0	3.3	0.3	114.2	13.3	17.3	48.2
6.6	14.0	11.4	4.1	84.3	61.4	15.4	53.7
1.3	2.4	1.4	0.9	0.0	7.4	1.2	2.8
4.2	6.9	6.9	2.7	0.0	9.8	3.3	4.4
11.0	9.2	11.5	2.6	0.0	28.1	25.1	17.7
7.8	9.8	11.2	4.4	28.2	35.3	18.5	27.4
142.2	152.5	115.0	56.2	59.4	50.6	31.9	47.3
1134.7	975.4	858.4	349.9	168.6	56.5	40.6	88.6
20.4	23.2	24.5	5.0	59.7	55.0	38.6	51.1
149.0	154.9	142.0	17.4	189.4	260.8	234.9	228.4
35.8	33.6	35.8	2.3	1420.6	376.8	398.3	731.9
53.0	41.5	43.4	8.8	5167.9	380.9	525.5	2024.8
50.5	44.0	48.5	3.9	8672.1	662.1	731.2	3355.1

74.3	58.9	68.0	8.1	7631.9	873.8	1752.2	3419.3
55.5	40.8	47.2	7.6	3353.3	1102.0	1919.3	2124.9
34.4	33.7	29.5	7.9	3225.2	480.5	636.0	1447.3
23.0	23.8	20.0	5.9	3942.1	337.7	482.8	1587.5
39.4	29.2	34.9	5.2	675.9	213.4	142.9	344.1
79.7	78.1	70.1	15.2	91.0	107.7	67.4	88.7
41.7	32.1	32.4	9.2	431.2	105.8	45.7	194.2
346.3	376.6	243.5	204.7	38.0	4.2	0.7	14.3
575.1	540.8	374.2	318.7	2.4	4.6	1.4	2.8
997.4	976.9	660.1	566.5	37.9	15.1	11.3	21.4
7.7	12.8	10.7	2.7	87.0	39.0	22.7	49.6
26.5	25.6	24.5	2.7	306.7	44.2	31.5	127.5
22.7	19.5	20.1	2.4	41.8	36.2	19.9	32.6
9.3	7.3	9.2	1.8	37.4	13.5	6.8	19.2
9.9	8.4	9.8	1.3	26.7	21.9	25.4	24.7
28.9	26.9	28.8	1.8	219.9	37.1	29.7	95.6
437.2	477.1	418.4	70.1	0.0	153.4	113.2	88.9
16.0	16.9	15.7	1.4	71.1	94.4	70.7	78.7
21.3	22.0	27.7	10.5	0.0	88.0	58.8	48.9
15.5	9.0	11.1	3.8	192.7	86.4	106.4	128.5
2.8	1.5	2.5	0.9	91.4	15.3	24.4	43.7
3.0	2.2	2.9	0.7	32.5	54.3	54.6	47.1
0.6	0.0	1.0	1.3	2.3	16.5	18.9	12.6
6.8	9.7	6.2	3.8	128.7	16.3	13.2	52.7
3.4	3.0	2.4	1.4	0.0	9.3	10.3	6.5
3.8	2.2	2.2	1.6	48.7	13.9	11.7	24.8
9.8	12.0	8.9	3.6	128.8	28.3	22.9	60.0
2.5	3.9	2.6	1.2	28.1	20.1	10.4	19.5
4.8	5.4	4.8	0.7	0.0	12.3	7.7	6.7
0.8	1.2	0.9	0.2	36.4	2.5	2.6	13.8
0.9	0.9	0.7	0.2	14.9	1.9	1.3	6.0
10.6	9.9	10.1	0.5	172.8	25.4	14.9	71.0
14.0	10.8	14.8	4.6	108.5	48.9	42.2	66.5
46.4	44.3	50.6	9.2	43.6	65.6	71.4	60.2
1108.3	632.1	998.7	325.9	181.2	39.5	47.0	89.2
1076.8	1205.5	1343.8	356.9	223.0	108.9	91.3	141.0
7.8	9.9	9.2	1.2	44.9	52.3	24.3	40.5
11.8	8.5	10.0	1.7	69.0	64.3	54.9	62.8
131.5	506.5	282.8	197.7	5.9	4.1	3.4	4.4
28.7	95.4	65.3	33.8	0.0	2.5	2.9	1.8
19.1	21.7	19.9	1.6	105.7	107.2	59.5	90.8
5.0	4.7	6.3	2.7	29.5	43.7	18.1	30.4
32.4	42.3	42.0	9.6	70.2	71.9	60.7	67.6

2.5	2.2	2.0	0.6	177.4	90.6	125.8	131.3
0.8	1.1	0.9	0.2	23.0	7.3	8.1	12.8
5.0	4.2	5.1	1.0	43.6	29.1	27.2	33.3
1.0	1.3	1.2	0.2	25.8	7.3	5.9	13.0
6.6	8.0	7.7	1.0	24.6	31.2	13.2	23.0
10.2	13.8	14.7	5.0	0.0	11.8	11.2	7.7
5.4	5.5	6.0	1.0	0.0	7.9	5.2	4.4
25.4	34.5	27.5	6.2	22.0	40.8	21.8	28.2
2.6	5.3	5.1	2.3	0.0	13.8	10.6	8.1
2.0	3.0	2.2	0.7	14.8	16.6	6.9	12.7
1.4	2.2	1.9	0.4	35.2	25.4	10.8	23.8
13.6	22.4	16.3	5.4	82.5	14.4	9.5	35.5
297.9	303.1	208.9	158.7	56.8	28.0	28.2	37.7
144.6	123.8	100.3	59.6	3141.2	204.5	194.0	1179.9
13.1	22.2	19.6	5.7	172.5	226.0	96.6	165.0
15.5	13.1	16.3	3.6	959.2	158.4	194.9	437.5
1.1	0.7	1.0	0.3	85.8	49.3	21.3	52.1
0.2	0.1	0.2	0.0	23.1	4.4	0.9	9.5
0.3	0.5	0.4	0.1	68.1	2.6	0.4	23.7
18.5	16.0	14.1	5.6	98.2	13.9	16.4	42.8
19.2	10.8	13.1	5.3	60.3	7.6	9.7	25.9
8.3	9.4	7.3	2.8	0.0	8.2	4.6	4.3
12.6	16.8	12.9	3.8	40.6	28.6	23.1	30.8
3.4	5.0	3.8	1.0	0.0	10.3	10.8	7.0
3.3	4.4	3.4	0.9	87.1	9.7	9.9	35.6
8.4	7.9	8.6	0.9	0.0	5.4	2.8	2.7
1.6	1.5	1.4	0.2	62.7	8.3	4.3	25.1
2.8	2.8	2.6	0.3	38.6	22.1	17.4	26.0
1.6	0.5	20.6	33.9	87.7	63.1	37.3	62.7
44.0	25.6	34.7	9.2	0.0	10.4	8.3	6.2
74.7	36.3	48.9	22.4	0.0	3.5	3.4	2.3
95.7	49.7	63.2	28.2	39.1	8.7	6.0	17.9
41.8	28.8	27.8	14.6	0.0	5.1	5.8	3.6
80.3	51.0	49.0	32.4	56.3	12.1	7.1	25.2
148.7	73.7	80.5	65.1	2.4	17.1	18.5	12.7
137.4	78.9	77.4	60.7	0.0	14.3	10.4	8.2
129.2	88.1	76.6	59.2	6.7	7.2	10.1	8.0
8.4	8.7	7.1	2.5	0.0	5.9	5.3	3.7
8.1	8.6	7.3	1.7	0.0	6.5	5.6	4.0
393.2	316.0	297.3	106.4	75.0	92.4	88.6	85.3
0.7	0.5	0.8	0.3	31.0	3.0	2.1	12.0
2.0	1.0	2.3	1.4	67.7	33.9	50.4	50.7
20.7	41.9	33.4	11.2	22.3	28.9	24.9	25.4

226.3	244.7	224.6	21.0	511.5	103.5	46.3	220.4
154.3	166.1	136.6	41.3	303.9	254.1	165.5	241.2
18.3	16.6	18.5	2.0	214.0	71.5	61.5	115.7
96.4	49.3	69.0	24.5	568.0	329.1	218.4	371.8
321.8	234.8	297.3	54.5	5389.7	1286.6	989.5	2555.3
14.8	7.9	12.5	4.0	412.1	96.2	66.5	191.6
16.2	7.4	13.1	4.9	316.9	99.7	56.7	157.8
14.5	13.5	12.0	3.5	0.0	45.2	36.1	27.1
4.3	5.1	4.5	0.5	47.2	21.1	16.4	28.2
4.1	2.4	3.0	1.0	0.0	13.0	11.3	8.1
3.0	1.8	2.3	0.6	2.7	7.4	7.4	5.8
3.0	2.1	2.2	0.7	0.0	5.5	6.5	4.0
1.9	1.9	2.3	0.7	69.7	3.0	6.7	26.5
6.0	10.1	8.0	2.0	101.9	17.7	24.3	48.0
37.9	44.3	34.5	11.9	199.7	81.7	53.4	111.6
86.4	64.2	62.8	24.4	306.5	108.8	183.8	199.7
6.6	3.4	5.1	1.6	95.9	23.2	32.5	50.5
0.4	0.6	0.5	0.1	50.1	2.8	1.7	18.2
0.5	0.3	0.3	0.2	0.0	2.1	2.3	1.5
0.4	0.4	0.4	0.1	27.2	4.9	2.2	11.4
1.5	1.4	1.5	0.1	13.7	7.9	5.5	9.0
1.2	1.8	1.3	0.4	0.0	6.3	2.7	3.0
0.7	0.5	0.4	0.3	38.9	1.2	2.0	14.0
1.6	1.7	1.5	0.4	36.0	8.0	6.7	16.9
1.7	1.6	1.5	0.3	31.1	9.6	8.2	16.3
3.3	2.1	2.5	0.7	0.0	17.1	13.0	10.0
26.9	25.4	24.0	3.8	116.7	52.2	44.5	71.1
21.3	29.6	24.8	4.3	55.7	48.3	47.1	50.3
14.3	13.3	13.3	0.9	0.0	25.3	25.4	16.9
32.9	23.4	27.6	4.8	117.5	125.9	46.7	96.7
18.2	14.6	15.8	2.1	101.2	39.3	29.2	56.6
30.2	21.0	23.0	6.4	18.2	117.8	62.3	66.1
33.9	33.6	31.6	3.7	0.0	86.4	92.2	59.5
40.8	53.7	52.7	11.5	0.0	73.2	68.4	47.2
42.2	52.5	52.9	10.9	49.0	83.8	74.0	68.9
68.2	57.8	59.1	8.4	93.4	93.4	102.2	96.3
7.8	8.8	7.5	1.5	44.6	12.9	9.8	22.4
2.5	2.4	2.1	0.6	172.8	74.1	13.2	86.7
4.4	2.9	3.2	1.0	435.9	91.9	28.3	185.4
28.1	24.4	22.1	7.5	163.0	94.8	131.1	129.6
5.3	5.6	4.6	1.4	12.1	25.9	29.5	22.5
34.7	32.7	31.3	4.2	182.5	200.4	225.6	202.9
230.8	182.0	167.3	71.9	122.0	276.1	142.7	180.3

2.2	2.2	2.2	0.1	7.7	16.9	13.5	12.7
7.3	8.7	10.1	3.7	304.7	17.3	11.8	111.3
3.1	3.7	3.2	0.4	49.9	12.4	14.3	25.5
47.6	27.7	42.2	12.6	2304.3	338.7	365.4	1002.8
2.8	2.7	2.7	0.1	0.0	19.2	21.2	13.5
1.8	1.9	1.8	0.1	132.3	7.1	3.5	47.6
5.3	8.3	7.4	1.9	1.2	11.0	8.1	6.8
10.5	7.7	9.7	1.7	116.1	78.8	52.2	82.3
36.5	30.8	34.8	3.5	158.5	89.8	73.5	107.2
4.3	5.1	5.0	0.7	35.5	21.7	9.5	22.2
75.1	110.7	84.4	23.1	91.4	72.9	43.0	69.1
13.3	13.3	13.0	0.5	1.2	33.9	25.0	20.1
0.4	1.7	1.3	0.8	0.0	30.8	35.9	22.2
585.8	456.7	448.4	141.7	232.4	235.8	189.5	219.2
5.6	5.3	6.2	1.3	6.3	8.8	4.1	6.4
3.0	3.1	2.9	0.3	60.0	4.1	1.1	21.7
1.8	1.6	2.0	0.6	30.8	9.2	2.6	14.2
2.5	3.7	3.9	1.6	29.9	11.8	9.7	17.1
1.1	1.3	1.5	0.6	0.0	3.5	1.0	1.5
32.3	17.3	24.3	7.5	53.4	22.5	13.0	29.6
0.7	0.7	0.7	0.0	71.6	4.4	1.0	25.7
7.8	7.7	7.3	0.8	61.4	78.1	100.0	79.8
94.5	79.9	65.9	37.6	88.6	50.6	42.9	60.7
19.4	18.1	16.8	3.4	41.2	48.5	44.4	44.7
4.1	5.5	5.0	0.8	8.8	32.7	14.3	18.6
6.3	2.6	3.4	2.6	40.1	3.9	2.0	15.3
0.7	1.2	0.9	0.3	15.5	3.7	1.4	6.9
10.4	3.3	6.1	3.8	0.0	81.0	31.7	37.6
11.7	14.0	13.1	1.2	0.0	13.0	12.6	8.5
0.5	0.2	0.4	0.2	3.2	0.9	1.1	1.8
0.7	0.0	0.3	0.4	49.5	1.0	0.6	17.0
0.2	0.0	0.1	0.1	16.4	1.1	0.1	5.9
0.1	0.0	0.0	0.0	0.0	0.4	0.6	0.3
2.1	2.4	2.0	0.5	85.7	16.0	19.3	40.3
5.8	8.5	6.2	2.1	47.1	51.3	47.6	48.7
13.6	4.5	8.8	4.6	211.0	390.8	36.0	212.6
74.0	90.2	156.4	129.0	437.7	1238.1	103.3	593.0
24.8	22.4	22.2	2.7	29.8	28.1	13.7	23.9
4.5	3.8	3.7	1.0	11.6	2.6	1.5	5.2
0.8	0.7	0.7	0.0	46.9	2.8	1.8	17.2
58.2	49.3	45.7	14.6	134.2	70.9	69.3	91.5
1.9	2.0	1.7	0.4	0.0	4.8	4.1	3.0
1.7	1.9	1.5	0.6	0.0	5.1	2.6	2.6

8.2	7.3	8.7	1.7	198.0	31.8	18.7	82.8
0.2	0.6	0.4	0.2	32.2	5.1	2.2	13.1
0.3	0.4	0.4	0.0	0.0	4.0	1.8	2.0
13.5	8.4	9.7	3.4	39.5	25.1	17.1	27.3
4.1	14.9	8.5	5.7	67.5	18.3	6.8	30.9
121.6	85.6	103.6	18.0	253.5	123.9	115.0	164.1
163.1	109.6	117.5	42.2	294.2	828.7	1213.2	778.7
6.9	6.7	7.4	1.1	101.8	14.6	17.7	44.7
1.5	3.7	2.2	1.3	76.9	43.7	24.3	48.3
22.4	35.9	30.3	7.1	289.6	94.5	85.3	156.5
2.9	3.5	4.0	1.4	0.0	31.7	26.3	19.3
21.5	17.9	28.0	14.4	358.5	27.5	25.2	137.1
6.8	7.5	7.0	0.4	0.0	66.6	11.1	25.9
15.8	15.0	15.8	0.9	0.0	10.3	5.8	5.4
22.2	24.5	20.5	5.1	26.2	22.6	13.9	20.9
53.8	51.1	37.1	26.5	0.0	26.4	12.9	13.1
130.7	120.3	91.1	59.7	0.0	45.5	17.6	21.0
54.9	39.1	44.1	9.4	86.8	39.1	25.4	50.5
0.7	0.7	1.1	0.7	0.0	3.9	2.6	2.2
1.5	2.3	1.8	0.4	74.6	3.8	1.0	26.5
8.7	10.0	7.5	3.4	67.9	6.2	5.6	26.6
10.8	5.6	8.2	2.6	0.0	10.3	6.1	5.4
11.9	11.3	11.2	0.8	40.5	12.0	10.8	21.1
41.8	26.5	30.5	9.9	24.1	23.1	25.4	24.2
14.6	15.3	12.6	4.1	0.0	13.9	10.4	8.1
10.7	4.9	6.8	3.4	68.9	3.7	8.6	27.1
7.0	8.8	6.9	1.9	32.1	5.3	2.6	13.4
0.4	0.0	0.1	0.2	60.3	1.4	0.3	20.7
13.7	8.8	11.3	2.5	0.0	4.1	4.0	2.7
6.0	9.0	7.3	1.5	0.0	15.4	9.5	8.3
0.2	1.6	1.0	0.7	0.0	8.4	2.7	3.7
18.4	23.5	31.9	19.2	56.2	75.4	67.5	66.4
38.6	39.9	39.0	0.7	56.1	44.3	31.8	44.1
4.1	5.0	4.6	0.5	35.3	10.4	6.8	17.5
60.9	67.9	69.1	8.9	94.1	85.4	66.9	82.1
18.3	25.0	22.0	3.4	131.5	52.6	57.2	80.5
2.8	2.5	2.6	0.2	9.6	9.0	8.6	9.1
1.2	1.5	1.5	0.3	0.0	5.9	4.7	3.5
14.3	13.0	13.5	0.7	45.5	21.0	11.6	26.0
157.9	132.1	140.7	14.8	577.8	525.4	464.3	522.5
11.5	18.8	16.3	4.1	86.6	18.3	23.1	42.7
22.3	22.6	23.0	0.9	42.7	29.3	19.0	30.3
353.7	344.6	322.5	46.4	131.8	145.9	143.8	140.5

39.0	82.0	53.2	25.0	83.6	116.8	78.4	92.9
15.8	16.3	16.5	0.8	61.7	52.5	47.9	54.0
96.7	70.3	81.3	13.8	93.4	117.5	111.4	107.4
26.9	22.2	26.8	4.6	177.4	54.6	54.3	95.4
527.3	341.8	362.5	155.5	515.0	345.5	287.5	382.6
617.4	350.6	416.7	177.2	484.1	332.4	407.6	408.0
41.7	32.0	39.3	6.5	111.1	60.1	46.6	72.6
52.4	38.8	43.9	7.4	83.2	92.2	62.0	79.1
53.0	44.7	45.4	7.3	277.7	87.4	94.2	153.1
45.8	44.5	44.5	1.4	212.6	104.2	80.5	132.4
13.4	16.8	17.1	3.9	108.4	26.6	20.7	51.9
88.9	113.1	119.6	34.4	176.1	156.6	78.4	137.0
143.0	140.1	151.8	17.8	169.0	137.2	93.9	133.4
85.8	99.0	106.3	24.9	126.1	134.3	84.2	114.9
59.3	29.7	30.6	28.3	0.0	8.6	0.0	2.9
25.0	58.2	28.3	28.4	189.3	11.4	0.0	66.9
39.5	78.4	60.9	19.8	0.0	49.7	16.3	22.0
17.5	39.2	24.8	12.5	0.0	81.5	9.5	30.3
52.5	157.1	99.8	53.0	136.7	712.2	254.0	367.6
6.5	13.9	7.5	5.9	0.0	30.8	27.0	19.3
64.5	107.7	75.5	28.3	0.0	193.0	118.9	104.0
38.8	22.3	25.4	12.1	36.5	55.7	70.6	54.2
29.9	27.8	28.7	1.1	52.2	375.5	283.9	237.2
18.2	24.0	22.6	3.9	22.4	18.7	4.3	15.1
86.2	80.2	70.8	21.7	316.5	64.0	21.3	133.9
0.0	1.2	0.5	0.6	80.6	2.2	0.0	27.6
6.5	5.2	5.8	0.7	94.7	67.8	42.6	68.4
331.0	484.2	345.4	132.1	412.0	760.7	378.1	516.9
0.1	0.2	0.1	0.1	43.6	0.6	0.6	15.0
2.2	2.9	2.0	1.0	0.0	31.0	6.7	12.6
431.2	1513.5	811.3	608.8	0.0	360.3	162.6	174.3
0.8	0.0	0.5	0.4	56.6	0.8	1.9	19.8
13.1	16.6	13.1	3.5	0.0	5.6	0.9	2.2
14.1	18.1	13.1	5.6	69.5	7.5	4.9	27.3
224.5	177.7	175.0	50.9	577.9	74.1	68.0	240.0
152.3	188.3	146.0	45.9	733.8	52.0	46.5	277.4
136.4	164.8	137.3	27.0	0.0	34.4	28.2	20.9
123.9	143.3	123.1	20.6	36.3	43.5	37.5	39.1
70.9	98.2	81.9	14.4	130.6	85.1	43.4	86.4
4.4	7.0	4.9	1.9	47.1	6.1	2.9	18.7
59.9	69.7	57.6	13.4	229.7	156.4	86.8	157.6
38.4	20.1	29.2	9.2	181.2	75.0	47.8	101.3
10.0	13.5	11.0	2.2	53.2	59.4	23.0	45.2

156.1	137.2	156.6	19.7	1555.0	233.0	125.1	637.7
76.6	82.6	84.7	9.4	544.9	117.7	51.5	238.1
13.8	14.6	14.1	0.4	62.3	38.7	37.3	46.1
86.3	70.5	112.2	59.1	111.6	16.4	15.5	47.9
73.2	96.8	73.5	23.1	162.5	190.1	94.8	149.1
491.9	306.2	392.7	93.5	514.7	644.8	457.4	539.0
37.6	24.2	86.1	95.9	236.7	21.1	17.4	91.7
10.4	15.8	53.3	69.7	186.8	19.1	23.0	76.3
16.1	16.3	42.6	45.7	0.0	19.4	16.7	12.0
9.2	12.1	36.5	44.7	63.0	17.3	7.6	29.3
8.2	7.5	39.4	54.7	6.3	7.0	4.9	6.1
9.7	6.7	36.0	48.2	0.0	4.3	5.3	3.2
7.9	6.3	33.8	46.1	44.4	4.5	6.8	18.5
7.0	6.7	32.2	43.9	25.9	3.2	3.8	11.0
9.6	9.2	31.7	38.7	0.0	2.6	1.9	1.5
8.2	7.9	27.6	33.8	10.8	1.5	1.4	4.6
16.4	12.5	36.8	38.9	82.7	5.7	6.4	31.6
38.4	27.2	60.3	47.9	70.2	12.0	10.8	31.0
15.0	17.4	30.9	25.6	72.4	7.6	5.6	28.5
49.5	35.2	70.0	48.5	155.8	9.7	13.8	59.8
100.7	86.4	127.0	58.3	161.7	63.2	85.4	103.4
433.6	291.9	304.0	124.0	89.1	28.3	34.2	50.5
387.1	273.7	298.1	79.6	75.8	20.7	25.7	40.8
1.9	2.7	4.5	3.8	74.4	2.6	0.6	25.9
4.6	1.2	16.2	23.0	123.3	3.7	2.4	43.2
9.5	8.2	16.2	12.9	63.0	4.8	7.2	25.0
7.6	7.0	10.9	6.4	0.0	2.7	3.0	1.9
5.7	4.4	9.5	7.8	32.1	0.0	0.5	10.9
5.2	4.9	9.6	7.8	21.6	1.9	1.9	8.5
4.7	6.6	9.1	6.1	0.0	1.0	1.8	0.9
6.0	6.0	9.7	6.4	7.4	3.3	3.3	4.7
16.3	17.8	24.1	12.3	0.0	8.0	8.4	5.5
6.5	7.0	12.2	9.3	25.3	1.4	0.9	9.2
9.9	8.6	16.8	13.1	0.0	2.1	0.8	1.0
7.8	6.5	11.8	8.1	0.0	0.4	0.4	0.2
7.8	7.3	9.6	3.6	29.9	2.1	2.8	11.6
8.4	11.0	12.7	5.3	32.6	5.1	5.5	14.4
9.6	11.1	12.4	3.7	43.3	8.3	4.3	18.6
9.0	11.1	13.4	5.9	71.9	7.1	7.5	28.8
3.7	3.3	6.4	5.1	25.7	1.8	1.0	9.5
8.2	8.2	11.4	5.5	83.4	15.9	18.1	39.1

fischeri(SWT).

Vnt_rpkm_	**Plk-vs-SWT**	**Plk-vs-SWT**	**Vnt-vs-Plk_**	**Vnt-vs-Plk_**	**Vnt-vs-SWT**	**Vnt-vs-SWT**
13.3	-2.1	0.0	-0.5	0.6	-2.6	0.0
29.3	0.0	0.9	-1.2	0.1	-1.2	0.0
84.1	-0.9	0.1	-0.8	0.2	-1.7	0.0
71.2	-0.6	0.4	0.0	1.0	-0.7	0.3
2643.1	-0.1	0.9	-1.0	0.3	-1.1	0.2
23.2	3.4	0.0	-0.7	0.3	2.7	0.0
38.4	3.9	0.0	0.4	0.7	4.2	0.0
817.3	4.6	0.0	1.1	0.2	5.7	0.0
39.7	-1.9	0.0	1.0	0.2	-0.9	0.2
38.5	-1.5	0.0	0.6	0.4	-0.9	0.1
69.2	-1.3	0.0	0.4	0.2	-0.9	0.0
32.0	-2.0	0.0	-1.2	0.1	-3.1	0.0
113.3	0.5	0.5	-1.4	0.1	-0.8	0.3
19.5	-1.0	0.0	0.3	0.6	-0.8	0.1
23.7	-2.6	0.0	-0.3	0.7	-2.9	0.0
19.8	-2.2	0.0	-1.0	0.1	-3.2	0.0
8.2	-0.2	0.6	0.0	1.0	-0.3	0.5
440.6	0.5	0.6	-1.9	0.0	-1.4	0.1
12.6	1.8	0.0	-0.7	0.3	1.1	0.1
562.1	2.9	0.0	-0.8	0.4	2.1	0.0
38.7	0.5	0.4	0.0	1.0	0.5	0.3
10.1	0.2	0.8	0.0	1.0	0.2	0.7
110.2	1.4	0.0	-1.1	0.1	0.3	0.7
619.6	6.4	0.0	0.2	0.8	6.6	0.0
529.1	6.3	0.0	0.8	0.2	7.1	0.0
28.3	-1.0	0.3	-0.5	0.7	-1.5	0.1
16.8	-0.7	0.1	0.4	0.4	-0.3	0.5
22.6	-1.3	0.1	0.0	1.0	-1.3	0.1
30.4	-1.2	0.1	0.1	1.0	-1.2	0.1
39.0	-0.6	0.7	-0.7	0.6	-1.3	0.2
55.7	2.3	0.0	0.3	0.6	2.6	0.0
13.2	-0.7	0.1	3.3	0.0	2.7	0.0
40.9	-0.5	0.5	2.8	0.0	2.3	0.0
12.7	-0.5	0.7	1.3	0.2	0.8	0.4
17.4	-0.8	0.5	1.6	0.2	0.7	0.5
11.5	0.1	0.9	1.2	0.0	1.3	0.0
8.7	0.5	0.3	-0.1	0.9	0.4	0.3
21.0	-1.4	0.0	0.0	1.0	-1.4	0.0
59.6	0.1	0.9	0.8	0.5	0.9	0.3
88.7	-1.1	0.1	1.3	0.1	0.2	0.8

133.2	0.2	0.6	0.4	0.3	0.5	0.1
2.6	1.5	0.0	-1.4	0.0	0.1	0.8
4.4	-1.3	0.0	0.0	1.0	-1.3	0.0
25.7	-1.9	0.0	1.0	0.0	-0.9	0.1
18.5	-1.6	0.1	-0.1	1.0	-1.6	0.1
49.5	0.8	0.1	-0.3	0.6	0.5	0.2
786.2	0.5	0.5	-0.7	0.3	-0.3	0.7
207.1	0.6	0.2	-1.0	0.0	-0.4	0.4
34.0	1.1	0.0	-1.5	0.0	-0.5	0.3
16.9	-0.8	0.4	-0.3	0.8	-1.1	0.2
144.6	-1.7	0.0	-0.4	0.6	-2.0	0.0
43.6	-1.2	0.0	-1.7	0.0	-2.8	0.0
61.1	-1.8	0.0	-1.2	0.0	-3.0	0.0
118.5	0.3	0.6	-0.4	0.4	-0.2	0.7
35.6	0.4	0.5	-1.0	0.1	-0.6	0.2
10.5	3.2	0.0	-0.6	0.2	2.6	0.0
12.3	0.4	0.3	-1.3	0.0	-0.9	0.0
105.9	-0.1	0.9	-0.4	0.6	-0.5	0.4
35.5	-1.1	0.1	-0.8	0.3	-1.9	0.0
12.3	-1.5	0.0	0.0	1.0	-1.5	0.0
22.0	-1.9	0.0	-0.1	0.8	-2.0	0.0
14.3	-0.6	0.3	-0.6	0.3	-1.2	0.0
11.7	-2.0	0.0	-0.6	0.3	-2.6	0.0
17.2	0.9	0.0	-1.1	0.0	-0.3	0.4
5.4	-0.4	0.5	-1.5	0.0	-1.9	0.0
6.2	0.5	0.5	-0.5	0.6	0.1	0.9
1.9	-0.4	0.6	-0.3	0.7	-0.7	0.3
5.7	0.2	0.9	-1.8	0.1	-1.6	0.1
7.0	-6.4	0.0	0.6	0.3	-5.8	0.0
31.1	0.0	1.0	0.4	0.7	0.3	0.7
25.7	-1.5	0.0	0.1	0.9	-1.5	0.0
23.0	-0.4	0.3	-0.4	0.4	-0.8	0.0
162.3	-0.5	0.3	0.5	0.4	0.0	0.9
166.7	1.0	0.1	0.0	1.0	1.1	0.0
47.2	1.2	0.0	-0.9	0.1	0.3	0.6
30.1	0.7	0.3	-0.9	0.2	-0.2	0.8
7.7	0.0	1.0	-1.1	0.0	-1.1	0.0
44.3	-0.5	0.3	-0.4	0.5	-0.9	0.1
23.0	-0.9	0.0	0.6	0.1	-0.2	0.6
553.8	-2.4	0.0	-0.3	0.8	-2.7	0.0
780.1	0.1	0.9	-0.2	0.8	-0.1	0.9
184.2	2.0	0.0	0.0	1.0	2.0	0.0
95.2	2.1	0.0	0.7	0.2	2.8	0.0

9.1	2.5	0.0	0.0	1.0	2.5	0.0
24.6	1.1	0.3	-0.7	0.6	0.3	0.8
35.8	1.3	0.0	-0.1	0.8	1.2	0.0
32.4	0.1	0.9	-0.8	0.5	-0.7	0.5
2.7	-0.9	0.4	1.2	0.3	0.2	0.8
30.4	-0.1	0.9	-0.1	0.8	-0.2	0.7
2.6	-0.3	0.6	-1.7	0.0	-2.0	0.0
3.5	-2.1	0.0	-0.4	0.4	-2.5	0.0
20.6	-1.6	0.0	0.9	0.2	-0.7	0.3
53.0	-0.8	0.5	1.0	0.4	0.2	0.8
54.9	-1.4	0.0	-0.8	0.1	-2.2	0.0
152.0	1.5	0.0	-1.4	0.0	0.2	0.8
28.0	-0.5	0.1	0.4	0.4	-0.2	0.7
27.5	-0.6	0.5	-1.2	0.2	-1.8	0.0
69.9	-0.7	0.2	-0.4	0.6	-1.1	0.0
8.2	-0.6	0.6	-0.9	0.4	-1.4	0.1
37.9	0.3	0.4	-1.2	0.0	-1.0	0.0
391.7	0.6	0.0	-0.4	0.2	0.2	0.6
124.3	0.5	0.6	-0.6	0.5	-0.1	0.9
20.3	3.4	0.0	-1.1	0.0	2.4	0.0
27.4	-0.1	0.9	0.7	0.6	0.6	0.5
24.6	1.9	0.0	1.7	0.0	3.6	0.0
27.9	-0.3	0.6	-0.5	0.5	-0.8	0.1
143.3	0.7	0.5	-0.5	0.7	0.3	0.8
37.7	0.1	0.9	-0.5	0.7	-0.4	0.6
8.3	0.4	0.5	-0.1	0.9	0.3	0.7
72.8	-0.6	0.3	-1.0	0.1	-1.6	0.0
27.4	-1.3	0.0	0.4	0.6	-0.9	0.1
14.2	-0.3	0.8	1.4	0.1	1.2	0.1
4.7	0.9	0.3	0.2	0.9	1.1	0.2
28.5	-0.6	0.2	0.2	0.7	-0.4	0.4
146.2	-0.6	0.3	0.0	1.0	-0.5	0.3
4.3	-3.7	0.0	-0.9	0.0	-4.7	0.0
12.3	-1.5	0.1	-1.0	0.3	-2.5	0.0
29.7	-0.1	0.8	-0.6	0.4	-0.7	0.2
16.7	-0.3	0.8	-1.1	0.3	-1.4	0.1
12.1	-1.4	0.0	-0.5	0.5	-1.9	0.0
37.2	-0.1	1.0	-1.3	0.3	-1.4	0.2
1324.2	0.5	0.5	-1.1	0.2	-0.6	0.5
272.6	0.4	0.6	-0.8	0.3	-0.4	0.6
18.7	-0.3	0.7	-1.3	0.1	-1.6	0.0
10.1	-0.4	0.7	-1.2	0.2	-1.6	0.1
19.0	0.2	0.7	-1.2	0.0	-1.1	0.0

38.8	0.2	0.7	-0.3	0.6	-0.1	0.8
8.7	-0.2	0.7	-1.1	0.0	-1.3	0.0
15.0	-0.2	0.9	-1.5	0.1	-1.7	0.0
27.5	0.3	0.8	-1.5	0.2	-1.2	0.3
12.3	-0.7	0.1	-1.1	0.0	-1.8	0.0
58.4	-0.2	0.7	-0.5	0.3	-0.7	0.1
8.4	-0.4	0.5	-0.6	0.3	-1.0	0.0
40.5	-0.3	0.8	-1.0	0.5	-1.2	0.2
424.7	-1.1	0.0	0.3	0.6	-0.7	0.1
296.1	-0.8	0.1	-0.2	0.8	-0.9	0.1
70.3	-0.3	0.6	-1.0	0.2	-1.3	0.0
17.9	-0.7	0.2	-1.1	0.0	-1.7	0.0
41.5	-0.5	0.5	-1.0	0.2	-1.5	0.0
4.3	-0.8	0.0	-0.8	0.0	-1.6	0.0
16.2	-0.7	0.0	-0.5	0.1	-1.3	0.0
23.4	-0.9	0.0	-0.4	0.3	-1.3	0.0
330.0	-1.5	0.0	0.4	0.6	-1.1	0.1
39.6	-1.1	0.0	0.3	0.6	-0.8	0.0
44.0	-0.1	0.9	-0.9	0.4	-1.0	0.2
30.1	1.1	0.0	-1.3	0.0	-0.2	0.8
82.3	-0.1	0.9	-1.1	0.2	-1.2	0.1
10.5	2.5	0.0	-1.6	0.1	0.9	0.3
131.4	1.0	0.3	1.2	0.3	2.2	0.0
169.5	0.1	0.9	0.2	0.8	0.3	0.6
5.9	-1.7	0.0	0.1	0.9	-1.6	0.0
0.6	-2.7	0.0	-0.3	0.9	-3.0	0.0
1.3	-3.0	0.0	1.0	0.4	-2.0	0.0
1916.6	-2.7	0.0	1.3	0.1	-1.4	0.1
19.9	-2.8	0.0	1.2	0.0	-1.6	0.0
51.1	-2.2	0.0	1.0	0.1	-1.2	0.0
7.8	-2.9	0.0	-0.4	0.7	-3.4	0.0
19.4	-3.0	0.0	0.1	0.9	-2.9	0.0
2.5	-2.7	0.0	-0.4	0.5	-3.1	0.0
15.2	-2.6	0.0	-0.1	0.9	-2.6	0.0
12.9	-2.1	0.0	-0.4	0.8	-2.5	0.0
30.2	-1.8	0.0	0.4	0.7	-1.4	0.0
27.8	-0.9	0.4	0.5	0.7	-0.4	0.7
36.2	-0.7	0.6	0.4	0.8	-0.3	0.8
184.5	-1.2	0.3	0.4	0.8	-0.9	0.5
53.6	-0.7	0.6	1.5	0.3	0.8	0.5
83.8	-1.4	0.2	0.4	0.8	-1.1	0.4
20.3	-1.9	0.0	-0.7	0.6	-2.6	0.0
30.7	-2.6	0.0	-0.9	0.5	-3.4	0.0

44.1	-2.2	0.0	0.1	0.9	-2.1	0.0
51.6	-2.2	0.0	0.0	1.0	-2.2	0.0
16.9	-2.6	0.0	-0.3	0.8	-2.9	0.0
59.1	-2.0	0.0	0.5	0.3	-1.5	0.0
79.7	0.9	0.1	-0.9	0.1	-0.1	0.9
16.8	0.4	0.5	-1.3	0.0	-0.9	0.0
107.0	0.5	0.2	-1.7	0.0	-1.2	0.0
56.1	-0.1	0.8	-1.2	0.0	-1.3	0.0
20.7	0.8	0.0	-1.3	0.0	-0.6	0.1
148.3	1.3	0.0	-1.4	0.0	-0.1	0.9
255.3	0.6	0.4	-0.8	0.3	-0.2	0.8
67.3	0.7	0.1	-1.0	0.0	-0.3	0.5
41.6	2.1	0.0	-1.1	0.1	1.0	0.1
281.5	0.7	0.5	0.4	0.8	1.1	0.2
72.4	-0.4	0.2	-0.7	0.0	-1.1	0.0
118.6	0.1	0.8	-1.3	0.0	-1.1	0.0
12.9	-0.3	0.3	-1.6	0.0	-1.9	0.0
48.1	0.6	0.1	-1.4	0.0	-0.8	0.0
23.1	0.4	0.5	-1.4	0.0	-1.0	0.0
200.7	1.0	0.1	-0.7	0.3	0.3	0.6
22.9	1.0	0.0	-1.1	0.0	-0.1	0.8
7.9	0.3	0.5	-0.5	0.3	-0.2	0.7
27.8	-0.1	0.9	-1.0	0.0	-1.1	0.0
123.2	-1.2	0.1	-0.8	0.3	-2.0	0.0
3.7	0.7	0.4	-1.3	0.1	-0.6	0.4
54.2	-1.2	0.0	-0.1	0.9	-1.3	0.0
90.2	-1.7	0.0	-0.4	0.6	-2.1	0.0
548.1	-0.5	0.6	-0.2	0.8	-0.7	0.3
18.6	-0.2	0.8	-0.1	0.8	-0.3	0.5
43.8	5.8	0.0	-0.7	0.6	5.1	0.0
29.2	-1.8	0.0	0.5	0.6	-1.2	0.1
172.5	-1.7	0.0	0.5	0.3	-1.2	0.0
36.8	-0.6	0.3	-1.2	0.0	-1.8	0.0
50.8	1.9	0.0	-1.3	0.0	0.5	0.2
19.7	-0.4	0.5	-0.3	0.7	-0.8	0.2
25.1	0.1	0.9	-0.4	0.7	-0.3	0.7
36.6	0.8	0.1	-0.4	0.5	0.3	0.5
4.7	-0.4	0.7	0.6	0.6	0.2	0.9
10.9	-0.6	0.2	-0.2	0.7	-0.8	0.0
124.8	0.6	0.4	0.2	0.8	0.8	0.2
3.8	0.7	0.1	-0.8	0.1	-0.1	0.9
161.9	0.3	0.5	-0.6	0.1	-0.3	0.4
142.0	-0.2	0.7	-0.8	0.2	-1.0	0.1

27.2	-0.5	0.6	-1.3	0.2	-1.9	0.0
25.6	0.0	1.0	-0.5	0.5	-0.5	0.4
54.4	-1.4	0.0	0.5	0.4	-0.9	0.0
21.9	-1.0	0.0	0.8	0.1	-0.2	0.7
264.6	-1.2	0.1	1.9	0.0	0.7	0.3
14.1	-1.2	0.0	1.0	0.1	-0.2	0.8
362.3	-0.9	0.1	-0.8	0.2	-1.7	0.0
852.2	-0.7	0.4	-1.2	0.1	-1.9	0.0
100.7	-0.6	0.3	-0.6	0.3	-1.2	0.0
304.7	-1.9	0.0	-1.0	0.0	-2.9	0.0
246.2	-1.4	0.0	-0.8	0.1	-2.1	0.0
211.7	-1.4	0.0	-1.1	0.0	-2.5	0.0
246.2	-1.5	0.0	-1.8	0.0	-3.3	0.0
765.5	-1.5	0.0	-1.2	0.1	-2.7	0.0
112.2	-1.4	0.0	-2.4	0.0	-3.8	0.0
189.3	-1.3	0.0	-2.6	0.0	-3.9	0.0
44.4	-1.5	0.0	-2.2	0.0	-3.7	0.0
85.5	-1.3	0.0	-2.0	0.0	-3.3	0.0
170.1	-1.2	0.0	-1.6	0.0	-2.8	0.0
1897.9	-1.3	0.0	-0.7	0.3	-2.0	0.0
1837.5	-0.8	0.4	-1.3	0.1	-2.0	0.0
644.7	-0.4	0.6	-1.7	0.0	-2.1	0.0
464.3	-0.2	0.9	-2.1	0.0	-2.3	0.0
242.3	-0.2	0.8	-2.4	0.0	-2.7	0.0
267.7	-0.2	0.8	-2.6	0.0	-2.8	0.0
37.7	-0.4	0.5	-2.7	0.0	-3.1	0.0
153.2	-0.5	0.5	-3.0	0.0	-3.5	0.0
133.8	-0.5	0.5	-3.2	0.0	-3.7	0.0
126.4	-0.4	0.6	-3.5	0.0	-4.0	0.0
290.2	-0.3	0.8	-3.1	0.0	-3.4	0.0
345.9	-0.4	0.6	-2.9	0.0	-3.3	0.0
189.8	-0.3	0.6	-2.6	0.0	-2.9	0.0
578.6	0.0	1.0	-2.1	0.0	-2.0	0.0
318.4	-0.1	0.9	-2.3	0.0	-2.4	0.0
216.5	-0.2	0.8	-3.3	0.0	-3.5	0.0
63.0	-0.2	0.6	-3.4	0.0	-3.7	0.0
218.2	-0.2	0.8	-3.1	0.0	-3.3	0.0
439.7	0.2	0.8	-2.7	0.0	-2.5	0.0
275.3	-0.4	0.5	-0.1	0.9	-0.5	0.4
56.5	-0.4	0.3	0.1	0.9	-0.4	0.3
182.6	1.6	0.0	-0.4	0.5	1.2	0.0
7.7	0.0	1.0	0.9	0.0	0.9	0.0
11.9	0.8	0.1	1.2	0.0	2.0	0.0

6.6	-0.3	0.5	1.1	0.0	0.8	0.1
52.8	2.5	0.0	-0.4	0.4	2.1	0.0
104.0	2.5	0.0	0.0	1.0	2.5	0.0
122.7	-1.1	0.0	0.1	0.9	-1.0	0.0
46.4	0.1	0.9	-0.5	0.3	-0.5	0.3
57.5	0.4	0.5	-0.5	0.5	-0.1	0.9
52.8	0.3	0.8	-1.4	0.1	-1.1	0.2
57.0	-2.5	0.0	-0.3	0.7	-2.7	0.0
22.3	-0.5	0.3	-0.5	0.3	-1.0	0.0
1277.6	0.4	0.4	-1.3	0.0	-0.9	0.0
1516.9	0.9	0.2	-1.8	0.0	-0.9	0.2
31.1	1.3	0.0	-0.8	0.1	0.5	0.4
2.9	-1.1	0.1	-1.6	0.1	-2.7	0.0
3.6	-0.9	0.2	-0.8	0.4	-1.7	0.0
17.1	-1.3	0.0	0.3	0.5	-1.0	0.0
6.3	-0.1	0.8	-0.7	0.2	-0.8	0.1
63.4	0.5	0.4	-1.1	0.1	-0.5	0.3
16.5	-0.9	0.0	-1.0	0.0	-1.9	0.0
4.8	-1.0	0.0	-0.7	0.1	-1.7	0.0
20.6	-0.5	0.1	-0.4	0.3	-0.9	0.0
194.2	0.6	0.3	0.3	0.7	0.9	0.1
155.0	2.9	0.0	-0.4	0.7	2.6	0.0
8.7	-0.9	0.3	-3.2	0.0	-4.1	0.0
6.0	-1.3	0.0	-2.4	0.0	-3.7	0.0
19.9	-1.3	0.2	-1.7	0.1	-3.0	0.0
13.5	-0.9	0.2	-1.3	0.0	-2.2	0.0
21.8	0.3	0.8	-0.3	0.8	0.0	1.0
6.2	0.0	0.9	-0.6	0.3	-0.7	0.2
78.4	0.6	0.5	-0.1	0.9	0.5	0.6
44.9	-1.4	0.0	1.6	0.0	0.2	0.8
8.7	-0.2	0.8	-0.6	0.3	-0.7	0.1
7.7	0.7	0.2	-1.2	0.0	-0.6	0.2
4.1	2.5	0.0	-0.7	0.2	1.8	0.0
88.4	1.3	0.0	-0.1	0.9	1.2	0.0
47.1	-0.6	0.5	-0.5	0.7	-1.1	0.2
227.3	-0.7	0.3	1.3	0.1	0.6	0.4
56.3	1.5	0.0	-1.4	0.0	0.1	0.9
18.8	0.8	0.1	-1.9	0.0	-1.1	0.0
130.9	3.0	0.0	-0.1	0.9	2.9	0.0
15.1	3.1	0.0	0.7	0.3	3.8	0.0
72.1	1.1	0.1	0.7	0.3	1.8	0.0
10.3	1.9	0.0	-0.3	0.7	1.6	0.0
99.1	3.3	0.0	-0.7	0.4	2.5	0.0

35.2	-2.2	0.0	-0.1	0.9	-2.3	0.0
38.6	0.2	0.7	-0.8	0.1	-0.6	0.2
1.9	2.0	0.0	-2.7	0.0	-0.7	0.5
6.0	1.8	0.1	-3.1	0.0	-1.2	0.2
30.0	0.2	0.8	1.5	0.1	1.7	0.0
21.0	-2.8	0.0	-0.1	0.9	-2.9	0.0
54.3	3.9	0.0	1.5	0.1	5.3	0.0
18.7	3.8	0.0	0.7	0.5	4.5	0.0
63.8	4.0	0.0	1.3	0.1	5.3	0.0
104.5	2.3	0.0	1.4	0.1	3.7	0.0
21.8	-2.1	0.0	-0.7	0.3	-2.7	0.0
18.9	0.5	0.5	-1.0	0.2	-0.5	0.5
5.2	1.3	0.0	-1.0	0.0	0.3	0.6
14.9	2.6	0.0	-1.2	0.1	1.4	0.0
46.2	1.9	0.0	0.1	0.9	2.0	0.0
47.2	-2.3	0.0	-0.7	0.1	-3.0	0.0
5010.5	3.0	0.0	0.4	0.8	3.4	0.0
137.7	2.0	0.0	-0.4	0.6	1.6	0.0
92.6	-0.3	0.7	1.0	0.1	0.7	0.2
51.5	-0.1	0.9	0.4	0.6	0.4	0.6
108.9	1.4	0.0	-0.3	0.6	1.1	0.0
137.7	-0.4	0.3	1.2	0.0	0.7	0.1
54.8	-0.6	0.1	1.1	0.0	0.6	0.1
17.8	0.2	0.7	0.8	0.1	1.1	0.0
13.8	-0.5	0.5	-0.1	0.9	-0.6	0.3
7.0	-0.9	0.0	-1.1	0.0	-2.1	0.0
79.4	-1.3	0.0	0.3	0.7	-1.0	0.1
22.8	0.1	0.9	0.5	0.4	0.5	0.2
30.3	-0.2	0.7	0.0	1.0	-0.3	0.6
21.6	-0.3	0.6	-0.4	0.6	-0.6	0.2
7.7	-0.4	0.4	-0.5	0.4	-1.0	0.0
5.6	0.8	0.4	-1.6	0.1	-0.8	0.4
32.4	1.3	0.1	0.1	1.0	1.4	0.1
41.3	0.7	0.3	-0.3	0.7	0.4	0.5
150.0	0.5	0.5	0.4	0.6	1.0	0.1
100.7	0.5	0.5	0.1	1.0	0.6	0.4
40.6	1.2	0.0	-0.5	0.5	0.6	0.3
21.7	-0.8	0.1	-1.8	0.0	-2.6	0.0
36.8	1.5	0.0	0.3	0.7	1.9	0.0
13.0	0.4	0.1	-0.1	0.7	0.3	0.3
20.9	-1.2	0.0	0.6	0.3	-0.6	0.2
18.7	-1.6	0.0	0.7	0.3	-1.0	0.1
10.2	-1.5	0.0	-0.3	0.8	-1.8	0.0

28.0	-1.4	0.0	0.0	1.0	-1.4	0.0
8.4	-1.5	0.0	0.1	0.9	-1.4	0.0
17.6	-1.8	0.0	0.3	0.6	-1.5	0.0
32.8	-1.8	0.0	0.3	0.6	-1.5	0.0
33.5	-1.5	0.0	0.4	0.4	-1.1	0.0
81.0	-1.5	0.0	1.2	0.2	-0.4	0.6
37.2	-2.1	0.0	-0.2	0.9	-2.3	0.0
36.9	-3.5	0.0	0.1	0.9	-3.5	0.0
8.4	-0.5	0.6	-0.6	0.6	-1.1	0.1
7.8	-0.8	0.4	-0.3	0.8	-1.1	0.2
3.2	0.3	0.8	-1.2	0.2	-0.9	0.3
13.1	0.1	0.9	-0.3	0.8	-0.1	0.9
55.6	0.6	0.3	0.3	0.7	0.9	0.1
80.4	-1.1	0.0	0.3	0.5	-0.8	0.0
13.8	-1.9	0.0	0.3	0.6	-1.6	0.0
13.7	-1.3	0.1	-1.1	0.3	-2.4	0.0
4.4	-0.9	0.0	-0.6	0.2	-1.5	0.0
22.2	-1.2	0.0	-0.4	0.5	-1.5	0.0
44.4	0.2	0.7	-0.5	0.3	-0.3	0.4
75.6	1.4	0.0	-1.0	0.0	0.4	0.3
54.7	-0.1	0.9	-0.8	0.4	-0.9	0.2
141.8	1.4	0.0	-1.3	0.0	0.1	0.8
7.8	-1.0	0.0	-0.1	0.8	-1.2	0.0
2.4	1.9	0.0	-1.4	0.0	0.4	0.3
9.2	-1.9	0.0	0.0	1.0	-1.8	0.0
16.0	-2.1	0.0	0.3	0.8	-1.8	0.0
45.9	-1.4	0.0	1.3	0.0	-0.1	0.8
76.4	-0.1	0.9	0.0	1.0	-0.1	0.8
124.9	0.3	0.7	-0.5	0.4	-0.2	0.7
30.7	0.6	0.3	-0.2	0.8	0.4	0.5
45.3	0.9	0.1	-0.4	0.6	0.6	0.3
164.4	1.4	0.0	0.0	1.0	1.4	0.0
50.5	1.1	0.0	-0.4	0.5	0.7	0.1
37.3	-0.2	0.7	-0.1	0.8	-0.4	0.5
7.9	0.0	1.0	-0.2	0.8	-0.2	0.7
21.0	0.8	0.1	-0.6	0.2	0.2	0.7
56.5	1.2	0.1	-0.5	0.5	0.6	0.3
27.1	0.6	0.2	-0.4	0.5	0.2	0.7
375.9	0.2	0.9	1.2	0.2	1.3	0.1
61.9	0.0	1.0	0.6	0.3	0.6	0.2
892.7	0.8	0.1	0.5	0.4	1.3	0.0
70.9	-0.1	0.8	0.1	0.9	-0.1	0.9
74.0	-0.3	0.6	0.4	0.5	0.1	0.9

22.6	-0.2	0.7	0.7	0.3	0.5	0.4
116.4	-1.2	0.1	-0.3	0.7	-1.5	0.0
8.3	0.7	0.2	-0.1	0.9	0.7	0.2
40.3	0.5	0.3	0.6	0.2	1.1	0.0
4.0	0.9	0.2	-3.0	0.0	-2.2	0.0
16.2	-1.0	0.2	-0.8	0.3	-1.8	0.0
87.9	1.1	0.0	-0.8	0.0	0.3	0.4
21.2	1.4	0.0	-0.4	0.5	0.9	0.1
29.6	-1.2	0.0	-0.9	0.1	-2.1	0.0
21.0	-1.5	0.0	-0.3	0.6	-1.9	0.0
90.4	-1.3	0.0	-0.8	0.3	-2.1	0.0
164.9	0.2	0.7	0.0	1.0	0.2	0.7
16.7	0.3	0.3	-1.3	0.0	-0.9	0.0
35.2	-0.5	0.6	-0.2	0.9	-0.8	0.4
80.6	-0.2	0.9	0.4	0.8	0.2	0.9
13.8	0.4	0.6	0.5	0.5	0.9	0.1
22.1	-1.7	0.0	0.2	0.8	-1.5	0.0
479.5	-0.7	0.2	0.7	0.2	0.0	0.9
50.4	-0.8	0.3	0.4	0.7	-0.3	0.7
14.0	-0.3	0.6	0.3	0.7	0.0	1.0
51.9	0.2	0.8	-0.2	0.8	0.0	1.0
21.1	-0.5	0.5	-0.6	0.5	-1.0	0.1
55.8	-0.3	0.7	0.8	0.2	0.5	0.4
124.9	0.6	0.3	-0.5	0.5	0.1	0.9
6.4	0.0	1.0	-0.7	0.1	-0.7	0.1
22.2	-0.2	0.7	-0.2	0.7	-0.4	0.4
36.7	-0.5	0.3	-0.4	0.5	-0.8	0.1
5.8	-0.6	0.2	0.3	0.6	-0.3	0.5
98.6	-0.3	0.5	0.2	0.7	-0.1	0.8
34.2	0.5	0.4	-0.1	0.9	0.4	0.5
37.6	0.3	0.5	-0.1	0.9	0.3	0.6
44.8	-0.3	0.7	-0.7	0.2	-0.9	0.0
30.9	0.1	0.9	-1.0	0.1	-1.0	0.1
6.4	1.6	0.1	-1.7	0.1	-0.1	0.9
35.3	-2.6	0.0	2.4	0.0	-0.2	0.9
103.9	-2.2	0.0	2.6	0.0	0.4	0.6
39.8	-2.5	0.0	0.3	0.8	-2.2	0.0
42.6	0.5	0.3	-0.5	0.4	0.1	0.9
272.9	-0.6	0.3	0.0	1.0	-0.6	0.2
480.9	-1.7	0.0	0.1	1.0	-1.7	0.0
49.8	0.0	1.0	-0.3	0.8	-0.3	0.7
4.6	-1.5	0.0	1.1	0.0	-0.4	0.4
30.2	1.5	0.0	0.0	1.0	1.5	0.0

28.6	-1.1	0.0	0.0	1.0	-1.1	0.0
37.5	-0.7	0.2	0.8	0.1	0.1	0.8
44.0	1.7	0.0	-0.7	0.1	1.0	0.0
37.3	0.4	0.4	0.7	0.1	1.1	0.0
342.9	-0.4	0.6	-0.4	0.6	-0.8	0.2
25.1	-0.4	0.6	-0.4	0.6	-0.8	0.2
33.1	-1.1	0.0	-1.2	0.0	-2.3	0.0
144.8	0.1	0.9	0.4	0.7	0.4	0.5
80.4	-0.1	0.9	0.4	0.6	0.3	0.6
136.8	-1.3	0.0	0.5	0.6	-0.8	0.2
18.2	-0.5	0.0	0.2	0.6	-0.3	0.2
1.0	1.1	0.0	0.2	0.7	1.3	0.0
9.5	0.6	0.2	-0.3	0.6	0.4	0.4
60.7	0.2	0.6	-0.3	0.5	-0.1	0.8
238.1	5.7	0.0	0.2	0.8	6.0	0.0
26.4	-1.4	0.0	1.3	0.0	-0.1	0.8
106.4	-0.9	0.0	1.3	0.0	0.4	0.4
1086.5	1.0	0.1	-0.8	0.2	0.1	0.9
13.1	0.8	0.1	-0.1	0.8	0.6	0.1
14.0	-0.2	0.7	0.5	0.3	0.3	0.5
9.2	-1.3	0.0	-0.4	0.5	-1.7	0.0
37.5	-0.2	0.6	-0.2	0.8	-0.4	0.3
36.2	0.5	0.2	-0.5	0.2	0.0	0.9
11.3	0.0	0.9	-1.0	0.0	-0.9	0.0
120.1	0.2	0.8	-0.6	0.3	-0.4	0.4
31.5	-1.4	0.2	-0.5	0.7	-1.9	0.1
3.4	-1.6	0.0	-0.7	0.2	-2.4	0.0
9.4	-0.9	0.0	0.5	0.4	-0.5	0.3
1694.9	-2.5	0.0	1.6	0.0	-0.9	0.1
774.3	-0.7	0.1	0.5	0.3	-0.2	0.5
71.1	1.8	0.0	-0.5	0.3	1.3	0.0
1477.4	0.7	0.3	0.7	0.3	1.4	0.0
111.0	-0.3	0.6	-0.2	0.8	-0.5	0.3
14.3	-0.8	0.2	-0.4	0.6	-1.3	0.1
2.8	-1.7	0.0	-0.5	0.3	-2.2	0.0
97.3	-1.2	0.0	0.1	0.9	-1.1	0.0
19.1	-0.8	0.1	-0.8	0.1	-1.6	0.0
21.9	-1.1	0.0	-1.1	0.0	-2.2	0.0
23.4	-1.0	0.0	-1.9	0.0	-3.0	0.0
60.3	0.6	0.3	-0.7	0.2	-0.2	0.8
49.7	0.8	0.1	-0.8	0.1	0.0	1.0
1525.6	0.2	0.8	-0.6	0.4	-0.4	0.5
105.6	-1.0	0.1	-0.9	0.2	-1.9	0.0

72.8	-0.8	0.0	-0.2	0.7	-1.0	0.0
7.7	0.0	1.0	-0.2	0.9	-0.1	0.9
13.0	0.1	0.9	-1.1	0.1	-1.0	0.1
13.7	-0.7	0.2	0.0	1.0	-0.7	0.1
157.9	-1.8	0.0	0.8	0.3	-1.0	0.1
23.4	-1.0	0.1	-0.1	0.9	-1.2	0.1
43.8	0.7	0.7	2.7	0.0	3.5	0.0
183.9	-0.5	0.4	1.6	0.0	1.1	0.0
19.7	-0.4	0.5	0.8	0.2	0.4	0.4
38.0	-0.6	0.4	-0.1	1.0	-0.6	0.3
23.5	1.2	0.0	0.3	0.6	1.5	0.0
319.1	-2.3	0.0	-0.2	0.9	-2.5	0.0
512.3	1.9	0.0	-2.0	0.0	-0.1	0.9
123.8	0.7	0.2	-2.0	0.0	-1.2	0.0
38.4	-1.2	0.1	-1.7	0.0	-2.9	0.0
11.4	-1.1	0.0	-2.9	0.0	-4.0	0.0
24.5	0.0	1.0	-2.1	0.0	-2.0	0.0
54.4	2.1	0.0	-0.8	0.1	1.3	0.0
44.5	0.3	0.5	-0.7	0.1	-0.4	0.3
11.9	0.6	0.7	3.1	0.0	3.8	0.0
2.3	1.1	0.2	0.3	0.8	1.4	0.1
5.0	1.0	0.1	1.0	0.1	2.0	0.0
31.9	1.1	0.1	1.3	0.1	2.4	0.0
29.2	0.9	0.4	0.9	0.4	1.7	0.0
19.2	0.7	0.4	0.9	0.3	1.6	0.0
40.2	1.1	0.2	1.8	0.1	2.9	0.0
4.4	0.5	0.6	0.1	0.9	0.6	0.5
37.2	1.0	0.3	1.2	0.2	2.2	0.0
5.7	1.4	0.1	0.0	1.0	1.4	0.1
30.7	0.8	0.3	0.8	0.3	1.6	0.0
19.0	1.0	0.1	-0.6	0.3	0.4	0.5
15.7	0.3	0.7	0.3	0.7	0.6	0.4
49.5	-0.2	0.8	1.3	0.1	1.1	0.1
105.4	-0.3	0.7	1.0	0.2	0.7	0.3
35.5	-0.7	0.1	0.1	0.8	-0.6	0.1
17.4	-1.2	0.0	0.2	0.9	-1.1	0.1
1410.5	0.0	1.0	-0.4	0.6	-0.5	0.5
77.1	2.0	0.0	-1.0	0.4	1.0	0.3
13.7	-0.6	0.1	0.5	0.2	-0.1	0.7
43.6	0.2	0.9	1.8	0.0	2.0	0.0
57.4	3.8	0.0	-1.7	0.0	2.1	0.0
10.0	-1.1	0.0	-0.6	0.2	-1.7	0.0
32.5	-2.8	0.0	0.1	0.9	-2.7	0.0

19.3	-0.9	0.0	-0.5	0.4	-1.4	0.0
247.4	-0.5	0.2	0.1	0.8	-0.4	0.3
228.8	-0.8	0.1	-0.2	0.7	-1.0	0.0
11.0	0.1	0.9	-0.9	0.1	-0.8	0.1
47.5	1.5	0.0	-0.6	0.2	1.0	0.0
5.3	0.3	0.7	-1.2	0.1	-0.9	0.1
526.0	0.5	0.5	0.2	0.8	0.7	0.3
46.0	0.0	1.0	-0.4	0.2	-0.4	0.2
32.5	-1.0	0.0	0.0	1.0	-1.0	0.0
139.6	-0.2	0.7	-0.3	0.5	-0.5	0.2
16.6	0.0	0.9	-0.6	0.1	-0.7	0.0
22.4	0.5	0.3	-0.7	0.2	-0.2	0.8
70.3	0.5	0.1	-1.0	0.0	-0.5	0.2
439.7	-0.8	0.1	-1.2	0.0	-2.0	0.0
236.4	-0.8	0.1	-0.9	0.1	-1.6	0.0
485.3	-0.8	0.3	-1.4	0.1	-2.3	0.0
340.8	-0.9	0.1	-1.5	0.0	-2.4	0.0
50.9	-1.6	0.0	1.9	0.0	0.3	0.5
55.3	-0.9	0.0	1.1	0.0	0.2	0.5
3.9	-0.8	0.1	0.0	1.0	-0.8	0.1
185.7	-0.8	0.2	1.2	0.1	0.4	0.5
38.8	-0.1	0.9	-1.9	0.0	-2.1	0.0
65.2	-0.4	0.4	0.1	0.8	-0.2	0.6
36.3	0.0	1.0	0.5	0.5	0.6	0.4
85.4	-0.6	0.3	0.8	0.2	0.3	0.7
51.0	-1.0	0.0	0.9	0.0	-0.1	0.7
301.7	-1.5	0.0	-1.8	0.0	-3.3	0.0
144.5	-0.3	0.4	0.6	0.1	0.3	0.4
44.1	-0.8	0.1	0.1	0.9	-0.7	0.1
13.4	-1.4	0.0	0.2	0.7	-1.2	0.0
24.3	-1.3	0.0	-0.1	0.9	-1.4	0.0
138.9	2.6	0.0	1.0	0.4	3.6	0.0
80.1	0.6	0.6	2.8	0.0	3.4	0.0
17.7	-0.9	0.4	2.3	0.0	1.4	0.2
10.6	-1.4	0.1	0.7	0.6	-0.7	0.4
2.6	0.1	0.9	0.6	0.4	0.7	0.2
91.9	-1.0	0.2	2.0	0.0	1.0	0.2
11.5	-2.2	0.0	0.3	0.7	-1.9	0.0
83.9	-0.9	0.4	-0.7	0.6	-1.7	0.1
88.6	-0.5	0.5	1.9	0.0	1.3	0.1
8.1	-0.1	0.9	0.6	0.4	0.5	0.5
32.7	-0.8	0.1	1.4	0.0	0.6	0.3
6.5	-1.6	0.0	-0.6	0.1	-2.2	0.0

17.9	-1.0	0.0	-0.5	0.3	-1.5	0.0
4.8	-0.7	0.2	-1.0	0.1	-1.7	0.0
33.1	1.1	0.0	1.2	0.0	2.2	0.0
3.0	3.2	0.0	-3.3	0.0	-0.2	0.9
30.1	-0.7	0.5	-0.4	0.7	-1.1	0.2
18.0	-0.6	0.2	1.2	0.0	0.5	0.3
6.4	-2.0	0.0	1.8	0.0	-0.1	0.8
26.3	-0.3	0.8	0.0	1.0	-0.3	0.8
2.3	-0.1	0.9	0.1	0.9	0.0	1.0
47.3	-0.2	0.9	0.6	0.7	0.3	0.8
31.2	-0.4	0.4	1.4	0.0	1.0	0.0
13.0	0.2	0.8	0.3	0.6	0.5	0.3
10.9	0.2	0.7	-0.8	0.0	-0.7	0.0
9.9	-1.6	0.0	-1.9	0.0	-3.5	0.0
26.1	-1.9	0.0	0.9	0.0	-1.0	0.0
53.2	-0.1	0.9	0.2	0.8	0.1	0.9
8.6	-0.5	0.2	-0.3	0.6	-0.8	0.0
14.3	0.0	1.0	-0.1	0.9	0.0	0.9
13.8	-0.9	0.1	0.6	0.3	-0.3	0.6
28.9	0.9	0.0	-0.8	0.1	0.1	0.9
40.4	0.4	0.7	-0.7	0.5	-0.4	0.7
38.9	-0.6	0.5	1.4	0.1	0.8	0.3
32.5	-2.1	0.0	0.9	0.4	-1.2	0.2
5.2	-1.0	0.1	-0.6	0.4	-1.6	0.0
40.4	-0.8	0.2	1.0	0.1	0.2	0.8
63.5	-1.3	0.1	0.7	0.4	-0.6	0.5
9.3	-0.3	0.5	0.6	0.1	0.3	0.3
35.5	-0.7	0.3	1.4	0.1	0.6	0.4
18.6	-0.3	0.6	-0.5	0.5	-0.7	0.1
16.2	-0.7	0.0	0.2	0.7	-0.5	0.1
126.4	0.4	0.6	1.0	0.1	1.4	0.0
55.1	0.2	0.7	0.2	0.7	0.4	0.3
140.5	0.0	1.0	1.7	0.0	1.7	0.0
64.7	-1.6	0.0	1.0	0.2	-0.6	0.4
242.0	1.3	0.0	0.4	0.5	1.7	0.0
228.0	1.8	0.0	-0.6	0.4	1.2	0.0
718.2	2.7	0.0	-1.1	0.1	1.6	0.0
64.5	3.2	0.0	-1.8	0.0	1.4	0.0
51.4	1.4	0.1	-1.5	0.1	0.0	1.0
64.1	1.5	0.0	-1.7	0.0	-0.2	0.8
520.9	1.4	0.0	-1.1	0.1	0.3	0.6
105.2	2.7	0.0	-2.3	0.0	0.5	0.6
18.4	-0.3	0.5	-1.8	0.0	-2.1	0.0

74.2	-2.4	0.0	0.0	1.0	-2.5	0.0
16.7	-1.1	0.1	1.2	0.1	0.1	0.9
31.2	-0.5	0.6	-0.3	0.7	-0.8	0.3
127.1	-0.9	0.0	0.5	0.3	-0.4	0.4
14.4	-0.5	0.3	-1.0	0.1	-1.6	0.0
34.1	-0.4	0.5	-0.4	0.5	-0.8	0.1
64.5	-0.4	0.5	-0.3	0.7	-0.6	0.2
113.3	0.0	1.0	-0.6	0.4	-0.6	0.3
25.5	0.4	0.5	-0.1	0.9	0.3	0.6
30.6	0.1	0.9	0.3	0.6	0.3	0.5
99.1	-1.2	0.1	0.2	0.8	-1.0	0.1
27.2	1.5	0.0	-0.5	0.6	0.9	0.2
50.3	-0.5	0.5	-0.1	0.9	-0.6	0.4
52.5	-0.5	0.4	-0.1	0.9	-0.7	0.3
27.7	-0.7	0.3	0.4	0.7	-0.4	0.6
50.5	-0.4	0.5	0.3	0.6	-0.1	0.9
5.8	-2.8	0.0	0.9	0.0	-1.9	0.0
5.0	-4.4	0.0	0.5	0.6	-3.9	0.0
15.8	-1.3	0.0	1.0	0.1	-0.3	0.6
76.3	2.3	0.0	0.0	1.0	2.3	0.0
185.9	3.1	0.0	-1.0	0.3	2.1	0.0
136.0	-0.3	0.6	0.8	0.2	0.5	0.4
12.2	2.7	0.0	-0.6	0.2	2.2	0.0
193.9	3.4	0.0	-1.0	0.2	2.4	0.0
21.9	-1.4	0.0	0.8	0.1	-0.6	0.1
51.9	0.7	0.1	-0.2	0.8	0.6	0.2
7.3	-1.5	0.0	0.3	0.7	-1.2	0.0
11.1	-2.7	0.0	1.1	0.0	-1.6	0.0
19.7	0.3	0.5	0.6	0.2	0.9	0.0
63.2	1.0	0.0	-0.2	0.8	0.8	0.1
29.4	3.3	0.0	-0.7	0.2	2.6	0.0
2.7	-0.4	0.5	0.9	0.2	0.5	0.4
34.7	1.1	0.0	-0.3	0.5	0.8	0.1
61.3	2.1	0.0	-0.3	0.5	1.7	0.0
54.4	2.3	0.0	-0.4	0.5	1.9	0.0
44.0	1.1	0.0	1.5	0.0	2.6	0.0
39.5	0.1	0.9	-0.4	0.7	-0.3	0.7
13.2	-0.6	0.5	-0.8	0.4	-1.4	0.1
27.1	-4.3	0.0	0.3	0.8	-4.0	0.0
20.1	-1.2	0.0	0.0	1.0	-1.2	0.0
44.4	-3.5	0.0	0.9	0.1	-2.6	0.0
25.7	-6.2	0.0	1.8	0.0	-4.4	0.0
14.0	-5.5	0.0	1.2	0.2	-4.3	0.0

12.7	-5.5	0.0	1.4	0.0	-4.1	0.0
18.9	-3.6	0.0	0.4	0.5	-3.2	0.0
3.9	-2.6	0.0	-0.7	0.3	-3.3	0.0
2.7	-2.3	0.0	-0.3	0.8	-2.6	0.0
3.4	-2.5	0.0	-0.3	0.7	-2.8	0.0
2.4	-2.4	0.0	-0.9	0.2	-3.3	0.0
1.7	-1.9	0.0	-0.5	0.7	-2.4	0.0
4.4	-2.2	0.0	0.2	0.9	-2.0	0.0
16.6	-3.8	0.0	3.9	0.0	0.0	1.0
49.2	-0.8	0.5	2.2	0.0	1.4	0.1
17.0	-0.4	0.7	3.0	0.0	2.6	0.0
9.1	-1.2	0.0	3.1	0.0	1.9	0.0
60.7	-0.1	0.9	-0.8	0.2	-0.9	0.1
8.4	-0.8	0.4	-0.4	0.8	-1.1	0.2
125.5	-0.4	0.2	-0.3	0.5	-0.7	0.0
51.0	0.7	0.5	0.0	1.0	0.7	0.4
24.1	0.6	0.3	1.2	0.0	1.7	0.0
43.1	0.7	0.3	-0.5	0.6	0.2	0.8
20.5	0.9	0.4	-0.1	1.0	0.9	0.4
78.2	0.6	0.5	1.0	0.3	1.6	0.0
15.7	-0.4	0.3	-0.6	0.2	-1.0	0.0
24.3	-0.5	0.4	-0.3	0.6	-0.8	0.1
10.0	-0.7	0.5	-0.6	0.6	-1.2	0.2
25.8	2.2	0.0	-1.1	0.0	1.0	0.0
45.2	0.3	0.7	0.5	0.7	0.8	0.3
62.2	-0.9	0.1	-0.9	0.1	-1.8	0.0
5.8	-2.1	0.0	0.5	0.2	-1.5	0.0
213.7	0.5	0.4	-0.5	0.4	0.0	0.9
41.7	-0.1	0.9	0.1	1.0	0.0	1.0
89.4	0.0	1.0	-0.3	0.8	-0.4	0.7
19.2	0.4	0.5	-1.1	0.1	-0.7	0.2
72.9	0.5	0.3	-0.7	0.1	-0.3	0.5
17.0	-0.4	0.3	-0.4	0.4	-0.8	0.0
109.9	-0.3	0.7	-0.3	0.8	-0.5	0.4
24.2	-0.2	0.8	-0.3	0.7	-0.4	0.4
65.4	-0.8	0.3	1.4	0.1	0.6	0.4
79.0	-0.6	0.6	0.4	0.8	-0.2	0.9
23.8	-0.2	0.8	0.9	0.2	0.7	0.3
22.1	0.2	0.8	1.4	0.1	1.6	0.0
250.7	1.1	0.3	1.8	0.1	2.9	0.0
60.3	0.2	0.8	0.5	0.6	0.7	0.3
5.1	0.2	0.8	-0.7	0.2	-0.5	0.3
39.6	-1.3	0.0	1.7	0.0	0.4	0.4

79.8	-0.1	0.9	0.8	0.6	0.6	0.6
16.1	0.2	0.8	-2.2	0.0	-2.0	0.0
6.4	0.6	0.3	-2.8	0.0	-2.2	0.0
49.5	0.6	0.4	0.1	0.9	0.8	0.3
22.1	0.8	0.2	-0.7	0.3	0.1	0.9
1.5	-0.2	0.7	0.2	0.8	0.0	1.0
164.5	-3.9	0.0	1.1	0.0	-2.9	0.0
10.6	0.1	0.8	-0.3	0.6	-0.2	0.7
140.8	0.2	0.8	-0.6	0.5	-0.4	0.5
67.3	-1.7	0.0	0.6	0.4	-1.1	0.1
12.9	-1.2	0.0	0.0	1.0	-1.2	0.0
116.6	-0.6	0.1	0.5	0.2	-0.1	0.8
246.3	-0.8	0.2	-0.5	0.6	-1.3	0.0
12.3	-0.8	0.2	-1.2	0.0	-2.0	0.0
96.6	-0.6	0.3	-1.4	0.0	-2.0	0.0
106.1	-0.6	0.4	-1.7	0.0	-2.3	0.0
39.8	-0.7	0.1	-1.7	0.0	-2.5	0.0
113.3	-0.5	0.4	-2.0	0.0	-2.5	0.0
42.4	1.1	0.0	-1.0	0.1	0.1	0.8
150.3	3.1	0.0	-0.8	0.2	2.3	0.0
3.3	-0.8	0.0	0.2	0.8	-0.6	0.1
32.4	-0.6	0.1	0.2	0.7	-0.4	0.3
33.1	-2.6	0.0	-0.3	0.5	-2.9	0.0
18.2	-1.8	0.0	0.8	0.3	-1.1	0.1
187.1	0.2	0.8	0.0	1.0	0.2	0.8
12.2	-1.2	0.0	-0.2	0.8	-1.4	0.0
73.8	-1.4	0.0	0.1	0.9	-1.3	0.0
35.5	-1.4	0.0	0.1	0.9	-1.4	0.0
34.8	0.1	1.0	-1.9	0.1	-1.8	0.0
107.4	-0.2	0.7	0.7	0.2	0.5	0.3
202.3	1.5	0.0	-1.3	0.1	0.2	0.8
51.3	0.1	0.9	-0.1	0.9	0.0	1.0
19.7	-1.5	0.0	0.5	0.4	-0.9	0.0
13.8	-1.0	0.0	0.6	0.4	-0.5	0.4
4.2	-0.5	0.4	-0.7	0.3	-1.2	0.0
9.2	-0.8	0.1	0.0	1.0	-0.9	0.1
39.0	-0.8	0.3	-0.1	0.9	-0.9	0.2
124.5	-1.5	0.0	2.1	0.0	0.6	0.3
292.2	-0.5	0.5	1.4	0.0	0.9	0.2
19.3	-1.0	0.0	-0.3	0.7	-1.4	0.0
136.9	-0.3	0.6	0.4	0.6	0.1	0.9
1.6	0.2	0.7	-0.7	0.1	-0.5	0.2
157.8	0.5	0.4	-0.6	0.4	-0.1	0.9

18.3	-0.2	0.8	-0.2	0.8	-0.3	0.5
37.5	-1.1	0.0	-0.2	0.8	-1.3	0.0
26.6	-1.1	0.1	0.2	0.8	-1.0	0.1
23.9	0.2	0.7	-0.5	0.3	-0.3	0.4
82.5	-0.3	0.7	-0.5	0.6	-0.9	0.2
39.0	0.1	0.8	-0.2	0.8	-0.1	0.9
82.4	-0.4	0.5	-0.4	0.6	-0.8	0.2
24.8	0.0	1.0	-0.9	0.1	-0.9	0.1
151.9	0.5	0.6	1.4	0.1	1.8	0.0
67.5	-0.4	0.4	1.6	0.0	1.2	0.0
28.1	-1.4	0.0	0.2	0.8	-1.2	0.0
44.3	-1.1	0.0	0.6	0.2	-0.4	0.3
81.4	-1.1	0.1	1.0	0.2	-0.1	0.9
54.9	-0.5	0.1	0.4	0.3	-0.1	0.9
19.8	-1.3	0.0	0.3	0.6	-1.0	0.0
22.5	0.4	0.5	-0.3	0.7	0.1	0.9
11.7	-1.3	0.0	0.8	0.3	-0.6	0.4
12.7	-2.5	0.0	-0.4	0.7	-2.9	0.0
5.2	-1.7	0.1	-1.1	0.4	-2.8	0.0
15.3	-3.0	0.0	-1.7	0.0	-4.7	0.0
247.1	-2.1	0.0	0.1	0.9	-2.0	0.0
104.1	1.2	0.2	-0.7	0.6	0.6	0.5
463.6	3.6	0.0	-1.3	0.4	2.3	0.0
260.4	2.7	0.0	-0.2	0.9	2.5	0.0
101.6	-0.3	0.7	1.3	0.1	1.0	0.1
17.0	0.2	0.8	-1.0	0.1	-0.7	0.2
57.6	-0.1	0.9	1.4	0.1	1.2	0.1
32.1	0.3	0.7	-0.2	0.9	0.2	0.8
37.3	0.5	0.7	0.6	0.7	1.1	0.3
24.2	-0.2	0.9	1.5	0.1	1.4	0.1
42.7	2.3	0.0	-0.9	0.1	1.4	0.0
36.0	1.0	0.1	-0.5	0.5	0.5	0.4
70.0	-0.2	0.8	-0.9	0.2	-1.1	0.1
319.0	-0.5	0.3	0.5	0.3	0.0	0.9
28.2	-2.3	0.0	0.3	0.7	-2.0	0.0
179.6	-0.4	0.6	-0.6	0.5	-1.0	0.1
51.1	-1.6	0.0	0.8	0.1	-0.8	0.1
219.1	-1.5	0.0	0.0	1.0	-1.6	0.0
121.0	-2.0	0.0	0.1	0.9	-1.9	0.0
195.1	0.5	0.3	-0.5	0.3	0.0	0.9
107.6	-1.5	0.0	0.3	0.6	-1.2	0.0
315.9	-1.7	0.0	0.7	0.2	-1.0	0.0
18.6	-0.5	0.3	0.1	0.9	-0.5	0.3

8.5	2.2	0.0	-1.3	0.3	0.9	0.4
13.2	0.4	0.5	-1.2	0.0	-0.8	0.1
58.7	0.5	0.5	-0.8	0.3	-0.3	0.7
20.9	-2.1	0.0	1.1	0.0	-0.9	0.0
13.4	0.1	0.9	-0.7	0.0	-0.7	0.0
92.0	-0.6	0.4	-0.1	0.9	-0.7	0.3
273.2	-0.8	0.2	1.7	0.0	0.9	0.1
151.9	-2.3	0.0	1.1	0.1	-1.2	0.0
76.5	-1.6	0.0	0.3	0.6	-1.3	0.0
148.1	0.9	0.1	-0.1	0.9	0.8	0.2
610.8	2.4	0.0	2.4	0.0	4.8	0.0
250.2	0.1	0.9	-0.3	0.8	-0.2	0.9
178.5	1.2	0.0	0.3	0.5	1.5	0.0
41.8	2.0	0.0	-0.3	0.7	1.8	0.0
71.6	-0.4	0.6	0.0	1.0	-0.4	0.5
44.4	-1.5	0.0	-0.7	0.2	-2.2	0.0
17.4	-0.8	0.0	-0.7	0.1	-1.6	0.0
127.6	-0.7	0.4	-1.1	0.2	-1.8	0.0
113.4	-2.4	0.0	0.6	0.5	-1.9	0.0
106.7	-2.4	0.0	1.0	0.0	-1.4	0.0
16.3	-2.5	0.0	-0.5	0.5	-3.0	0.0
37.1	-2.1	0.0	-0.9	0.2	-3.0	0.0
4.9	-2.9	0.0	-1.5	0.0	-4.5	0.0
26.1	-2.9	0.0	-2.3	0.0	-5.2	0.0
11.8	-2.7	0.0	-3.5	0.0	-6.3	0.0
34.3	-2.6	0.0	-2.2	0.0	-4.8	0.0
23.3	-0.3	0.7	0.8	0.2	0.6	0.3
70.3	0.9	0.3	1.0	0.3	2.0	0.0
14.5	0.5	0.6	-0.3	0.8	0.2	0.8
82.0	-0.1	0.9	1.5	0.0	1.4	0.0
26.5	-0.3	0.6	0.9	0.1	0.6	0.2
55.9	0.7	0.2	0.6	0.3	1.3	0.0
45.7	1.6	0.1	-2.3	0.0	-0.6	0.6
50.9	1.7	0.1	-1.9	0.1	-0.2	0.9
23.1	3.0	0.0	-1.6	0.1	1.4	0.1
12.8	-1.8	0.0	-0.7	0.5	-2.5	0.0
282.5	0.7	0.4	-0.9	0.3	-0.2	0.8
2586.4	1.8	0.0	-0.1	0.9	1.6	0.0
59.4	0.0	1.0	-1.0	0.3	-1.0	0.2
9.3	0.7	0.1	-0.6	0.2	0.1	0.8
5.9	-1.8	0.0	0.3	0.6	-1.6	0.0
26.9	-2.4	0.0	0.7	0.0	-1.7	0.0
79.4	-1.6	0.0	1.0	0.1	-0.6	0.3

31.6	-1.0	0.1	0.6	0.4	-0.4	0.5
27.7	0.7	0.3	-0.1	0.9	0.6	0.4
76.1	-0.5	0.2	0.3	0.5	-0.1	0.8
84.5	-0.5	0.3	0.2	0.8	-0.3	0.5
10.6	-1.1	0.0	0.9	0.1	-0.2	0.7
2.5	-1.0	0.0	0.0	1.0	-0.9	0.1
64.6	0.3	0.7	0.8	0.3	1.1	0.1
6.0	-0.4	0.4	-0.6	0.2	-1.0	0.0
32.9	-1.3	0.1	-0.6	0.5	-1.9	0.0
14.9	-1.0	0.0	0.0	1.0	-1.0	0.0
17.2	-0.7	0.1	-0.1	0.9	-0.7	0.1
6.1	0.2	0.9	-1.7	0.1	-1.5	0.1
53.6	0.0	1.0	0.1	0.9	0.1	0.9
15.4	-0.9	0.0	-1.0	0.0	-1.9	0.0
9.7	-1.1	0.1	-1.6	0.0	-2.7	0.0
38.7	-1.2	0.0	-0.4	0.4	-1.6	0.0
4.6	-1.5	0.0	-1.1	0.0	-2.6	0.0
398.7	1.3	0.0	-0.2	0.7	1.1	0.0
1148.3	0.2	0.8	-0.5	0.4	-0.3	0.6
161.3	1.3	0.0	-0.4	0.3	0.8	0.0
6.9	-0.8	0.2	0.2	0.8	-0.6	0.3
8.3	1.3	0.0	-0.4	0.5	0.8	0.1
16.2	0.6	0.6	1.9	0.1	2.5	0.0
6.6	0.9	0.4	0.1	0.9	1.0	0.3
29.9	0.0	1.0	-0.4	0.8	-0.4	0.7
7.0	-0.3	0.7	-0.2	0.9	-0.5	0.6
2.2	-2.2	0.0	0.7	0.6	-1.5	0.1
13.7	-1.2	0.2	0.2	0.9	-1.1	0.2
22.5	0.4	0.6	0.9	0.2	1.3	0.0
26.1	-2.6	0.0	1.1	0.2	-1.5	0.0
5.1	0.0	1.0	-0.2	0.9	-0.2	0.9
12.0	-1.1	0.2	1.8	0.0	0.7	0.4
107.3	-0.6	0.5	1.9	0.0	1.4	0.0
16.3	3.7	0.0	-1.2	0.1	2.5	0.0
5.8	-2.0	0.0	0.9	0.0	-1.1	0.0
3.2	-2.1	0.0	0.4	0.7	-1.6	0.0
31.1	0.4	0.6	0.1	0.9	0.5	0.4
6.3	-0.2	0.9	-1.4	0.2	-1.5	0.1
109.7	-0.4	0.6	0.8	0.2	0.4	0.5
51.5	2.5	0.0	-1.2	0.0	1.2	0.0
22.9	0.1	0.9	0.4	0.7	0.5	0.5
4.3	0.7	0.1	-0.8	0.1	-0.1	0.8
25.5	1.0	0.0	-0.2	0.8	0.8	0.1

45.9	0.0	1.0	0.0	1.0	0.0	1.0
179.1	-1.1	0.0	-0.1	0.9	-1.2	0.0
8.2	2.1	0.0	-1.7	0.0	0.4	0.4
77.3	-0.6	0.2	0.5	0.4	-0.1	0.9
51.9	0.3	0.7	0.8	0.2	1.1	0.0
24.1	0.5	0.5	-0.6	0.5	-0.1	0.9
31.4	-1.1	0.0	0.8	0.2	-0.4	0.5
19.1	0.0	1.0	0.9	0.4	0.9	0.3
63.8	-1.0	0.0	0.7	0.2	-0.2	0.6
982.8	0.0	1.0	1.8	0.0	1.9	0.0
208.4	-0.1	0.9	-0.6	0.6	-0.7	0.4
63.0	-1.4	0.0	0.6	0.1	-0.7	0.0
40.3	0.1	0.9	-0.4	0.6	-0.4	0.5
5.3	-0.9	0.1	-1.2	0.0	-2.1	0.0
10.9	-0.5	0.3	-0.8	0.1	-1.3	0.0
30.0	-0.8	0.0	-0.4	0.3	-1.2	0.0
9.3	-3.5	0.0	-2.0	0.0	-5.5	0.0
56.7	-1.4	0.0	-0.4	0.4	-1.8	0.0
24.4	-0.1	0.7	-0.1	0.9	-0.2	0.5
34.2	0.5	0.1	-1.0	0.0	-0.5	0.1
20.1	0.0	0.9	0.4	0.3	0.4	0.3
142.5	-1.5	0.0	-0.3	0.8	-1.8	0.0
154.8	-0.6	0.2	0.5	0.5	-0.2	0.7
152.6	2.0	0.0	-0.5	0.6	1.4	0.0
7.0	1.0	0.0	0.1	0.8	1.1	0.0
30.8	-0.5	0.3	0.1	0.9	-0.4	0.4
509.7	-2.3	0.0	-0.2	0.8	-2.5	0.0
238.0	0.7	0.1	0.2	0.8	0.8	0.0
103.4	-1.2	0.2	0.4	0.7	-0.8	0.4
1631.6	0.1	0.9	3.0	0.0	3.2	0.0
12.7	1.1	0.0	0.0	0.9	1.1	0.0
246.6	-2.0	0.0	0.6	0.6	-1.4	0.1
200.1	1.9	0.0	-0.3	0.8	1.6	0.0
40.3	-1.5	0.1	-1.4	0.1	-2.9	0.0
23.6	-1.9	0.0	-0.3	0.6	-2.2	0.0
163.8	0.2	0.8	-1.0	0.1	-0.9	0.1
5.2	-0.6	0.3	-0.1	0.9	-0.8	0.2
6.9	-0.1	0.8	-0.6	0.2	-0.8	0.1
6.8	0.4	0.4	0.1	0.8	0.5	0.2
14.2	1.9	0.0	-2.1	0.0	-0.2	0.8
250.4	0.9	0.5	0.1	0.9	1.0	0.4
267.1	-0.9	0.1	0.1	0.8	-0.8	0.1
189.2	0.0	1.0	0.2	0.8	0.2	0.8

23.9	0.6	0.1	-0.7	0.1	-0.2	0.6
11.2	-0.1	0.9	-0.8	0.1	-0.8	0.0
52.5	-0.4	0.6	0.1	0.9	-0.3	0.7
1.5	-0.4	0.5	-0.9	0.2	-1.4	0.0
10.7	-0.2	0.8	-0.2	0.8	-0.4	0.5
24.9	0.1	0.9	0.7	0.3	0.8	0.2
68.8	-0.4	0.4	0.4	0.5	-0.1	0.9
41.5	-0.7	0.1	1.3	0.0	0.6	0.1
306.1	0.2	0.8	1.6	0.1	1.8	0.0
18.9	-0.9	0.1	-0.3	0.7	-1.2	0.0
46.6	1.5	0.0	0.6	0.3	2.2	0.0
88.5	-0.6	0.5	1.2	0.3	0.5	0.6
3.4	-0.2	0.8	1.5	0.0	1.3	0.0
16.5	0.1	0.8	0.9	0.1	1.1	0.0
89.1	0.5	0.3	-0.5	0.4	0.0	1.0
108.4	0.2	0.8	-0.9	0.2	-0.7	0.3
9.3	-1.6	0.0	0.5	0.4	-1.1	0.0
77.5	-0.6	0.1	0.7	0.1	0.1	0.8
32.2	0.0	1.0	0.4	0.6	0.4	0.6
71.4	0.0	1.0	-0.8	0.2	-0.8	0.1
2.3	0.8	0.4	-1.5	0.2	-0.7	0.5
88.1	-0.5	0.3	0.5	0.4	0.0	1.0
47.9	0.5	0.3	-0.1	0.9	0.4	0.4
131.2	-0.6	0.3	-1.0	0.1	-1.6	0.0
80.7	-0.9	0.0	-1.2	0.0	-2.1	0.0
49.8	-0.7	0.4	-1.8	0.0	-2.5	0.0
359.5	0.3	0.7	-1.4	0.0	-1.1	0.0
29.4	-0.4	0.3	0.5	0.2	0.2	0.7
11.2	-0.1	0.8	0.3	0.5	0.2	0.7
96.9	0.1	0.9	0.6	0.3	0.6	0.1
29.6	2.1	0.0	-0.5	0.3	1.6	0.0
118.5	0.4	0.4	-0.3	0.5	0.1	0.8
1553.6	-0.7	0.3	-0.3	0.8	-1.0	0.1
60.0	0.6	0.3	-1.0	0.1	-0.4	0.4
29.3	0.1	0.9	-0.5	0.5	-0.4	0.6
25.5	-1.3	0.0	-0.1	0.9	-1.4	0.0
37.7	-5.5	0.0	2.9	0.0	-2.6	0.0
9.2	1.2	0.0	0.2	0.7	1.5	0.0
311.4	2.6	0.0	0.0	1.0	2.6	0.0
424.0	2.1	0.0	1.1	0.2	3.2	0.0
24.4	0.5	0.4	0.4	0.5	0.9	0.1
60.1	0.2	0.6	0.1	0.8	0.4	0.4
8.1	4.1	0.0	-1.6	0.0	2.5	0.0

17.7	3.1	0.0	-0.8	0.0	2.3	0.0
19.6	2.2	0.0	-0.6	0.3	1.7	0.0
21.2	0.4	0.2	0.2	0.7	0.5	0.0
23.5	0.7	0.1	-0.1	0.8	0.6	0.1
10.1	-0.6	0.3	0.0	1.0	-0.7	0.3
59.7	1.5	0.1	-0.4	0.8	1.1	0.3
26.7	-1.0	0.3	2.5	0.0	1.4	0.1
7.0	2.9	0.0	-0.2	0.8	2.7	0.0
21.3	-0.2	0.8	0.5	0.5	0.4	0.6
365.7	1.2	0.0	-0.1	0.9	1.1	0.0
14.5	0.9	0.1	-0.8	0.2	0.1	0.9
48.0	2.4	0.0	0.8	0.1	3.2	0.0
4.1	2.1	0.0	-0.5	0.6	1.6	0.0
222.1	2.8	0.0	1.2	0.1	4.0	0.0
55.8	1.0	0.1	0.6	0.3	1.6	0.0
84.7	-0.1	0.9	1.1	0.2	1.0	0.1
16.1	0.6	0.5	1.0	0.2	1.6	0.0
3.2	0.2	0.8	0.5	0.5	0.7	0.2
24.5	0.4	0.7	1.4	0.2	1.7	0.0
29.1	-0.3	0.8	1.4	0.2	1.1	0.3
37.0	-0.6	0.6	1.9	0.1	1.3	0.2
21.9	-0.8	0.5	1.2	0.3	0.4	0.7
17.3	-1.0	0.4	2.0	0.1	1.0	0.4
7.6	-1.2	0.1	0.9	0.4	-0.3	0.7
9.9	-0.2	0.9	1.9	0.2	1.7	0.1
6.0	-1.3	0.1	0.9	0.3	-0.4	0.6
69.9	-0.7	0.6	4.0	0.0	3.3	0.0
115.7	-1.4	0.2	2.6	0.0	1.2	0.3
9.0	-0.7	0.5	0.1	0.9	-0.6	0.5
5.4	0.3	0.7	-0.3	0.7	-0.1	0.9
13.8	0.5	0.3	-0.3	0.7	0.2	0.6
1213.3	0.4	0.7	0.6	0.5	0.9	0.2
169.0	-4.6	0.0	-0.6	0.3	-5.2	0.0
90.1	-0.3	0.7	0.5	0.4	0.2	0.7
9.8	0.1	0.9	-0.8	0.2	-0.8	0.2
10.9	-0.1	0.9	-1.6	0.0	-1.7	0.0
6.6	0.1	0.8	-1.4	0.0	-1.2	0.0
13.8	0.7	0.3	-1.6	0.0	-0.9	0.1
15.5	0.3	0.6	-1.6	0.0	-1.3	0.0
22.0	0.4	0.5	-1.0	0.1	-0.6	0.2
42.7	-0.1	0.9	-0.6	0.3	-0.6	0.2
2.1	-0.1	0.9	1.4	0.0	1.3	0.0
12.9	0.5	0.4	0.2	0.7	0.7	0.2

58.7	-0.4	0.6	-0.3	0.8	-0.7	0.4
78.2	-0.7	0.0	0.9	0.0	0.1	0.8
63.7	1.9	0.1	-0.6	0.7	1.4	0.2
29.4	1.6	0.0	0.5	0.5	2.1	0.0
38.3	0.5	0.5	1.2	0.1	1.7	0.0
15.4	-0.5	0.4	-1.6	0.0	-2.1	0.0
35.0	-1.1	0.0	-0.8	0.1	-1.9	0.0
8.3	-0.6	0.2	-0.4	0.6	-1.0	0.0
12.0	-0.6	0.5	-1.1	0.3	-1.7	0.0
27.3	-0.7	0.3	-0.6	0.5	-1.3	0.0
2.6	-0.6	0.1	-1.0	0.0	-1.6	0.0
46.2	-0.5	0.3	-0.3	0.5	-0.8	0.0
46.5	-1.4	0.0	-0.7	0.3	-2.1	0.0
87.5	2.5	0.0	0.2	0.8	2.7	0.0
49.3	2.0	0.0	0.4	0.7	2.4	0.0
103.6	0.6	0.4	-0.2	0.8	0.4	0.6
18.2	-0.9	0.1	0.6	0.3	-0.2	0.7
104.7	-0.9	0.2	1.0	0.1	0.1	0.9
31.4	0.2	0.9	1.3	0.3	1.5	0.1
243.4	0.3	0.8	1.8	0.0	2.1	0.0
166.6	-1.5	0.0	1.1	0.2	-0.4	0.7
11.8	-1.4	0.0	1.3	0.0	0.0	0.9
10.5	-0.3	0.7	1.4	0.1	1.1	0.2
19.3	-1.5	0.0	1.4	0.0	-0.2	0.8
33.2	-2.4	0.0	1.0	0.4	-1.4	0.1
54.4	0.6	0.5	1.0	0.2	1.6	0.0
2.6	0.2	0.8	0.6	0.6	0.9	0.4
79.5	0.8	0.3	-0.3	0.8	0.5	0.5
27.8	-0.4	0.4	-0.4	0.5	-0.8	0.1
2.7	-2.9	0.0	-0.9	0.3	-3.8	0.0
21.7	-1.7	0.0	0.1	1.0	-1.6	0.0
16.6	-0.8	0.4	0.1	0.9	-0.6	0.5
65.3	0.4	0.5	0.3	0.7	0.7	0.1
43.9	1.9	0.0	-1.5	0.0	0.4	0.4
7.0	0.8	0.4	-0.5	0.7	0.3	0.7
25.1	2.0	0.0	-0.5	0.5	1.5	0.0
8.4	0.6	0.4	-2.0	0.0	-1.4	0.0
19.0	-1.4	0.2	-0.5	0.8	-1.9	0.1
2.4	-1.0	0.2	0.4	0.8	-0.7	0.4
65.3	-3.5	0.0	1.6	0.0	-1.9	0.0
69.1	3.7	0.0	-0.6	0.4	3.1	0.0
240.7	0.0	1.0	0.1	0.9	0.1	0.8
88.8	0.1	0.9	-0.2	0.9	0.0	1.0

5.6	0.1	1.0	-0.6	0.6	-0.5	0.5
53.8	1.2	0.1	2.8	0.0	4.0	0.0
336.1	1.6	0.0	3.5	0.0	5.1	0.0
21.6	2.4	0.0	-0.4	0.7	1.9	0.0
8.0	2.0	0.0	0.5	0.6	2.5	0.0
12.8	1.2	0.0	0.3	0.5	1.5	0.0
91.7	-0.8	0.1	0.5	0.4	-0.4	0.4
36.2	-1.1	0.0	1.1	0.0	0.0	1.0
11.9	1.2	0.2	-0.5	0.7	0.7	0.5
34.3	-0.5	0.6	1.7	0.1	1.2	0.2
2.3	-1.0	0.3	0.2	0.9	-0.8	0.4
14.4	1.2	0.0	1.1	0.0	2.2	0.0
56.0	-0.3	0.6	3.7	0.0	3.4	0.0
290.8	0.1	0.9	5.6	0.0	5.6	0.0
897.0	0.4	0.4	4.9	0.0	5.3	0.0
49.4	-0.4	0.7	1.2	0.2	0.8	0.4
34.8	-1.1	0.0	-2.7	0.0	-3.8	0.0
41.9	0.9	0.5	1.1	0.4	2.0	0.0
13.5	1.4	0.2	0.9	0.5	2.3	0.0
14.0	-0.5	0.1	0.2	0.6	-0.3	0.4
109.1	3.0	0.0	0.3	0.6	3.3	0.0
62.4	3.6	0.0	0.0	1.0	3.6	0.0
10.5	-1.5	0.1	0.2	0.9	-1.3	0.2
24.6	1.5	0.1	0.6	0.6	2.1	0.0
208.6	5.8	0.0	-0.2	0.9	5.7	0.0
10.3	2.4	0.0	-0.2	0.8	2.2	0.0
43.3	0.8	0.0	1.9	0.0	2.7	0.0
11.1	1.4	0.0	0.8	0.1	2.2	0.0
24.0	-0.2	0.8	0.7	0.5	0.5	0.5
5.3	-2.0	0.0	-0.1	1.0	-2.1	0.0
9.1	-1.5	0.1	0.4	0.7	-1.1	0.2
27.1	-2.0	0.0	1.0	0.2	-1.0	0.1
44.6	-0.3	0.5	0.2	0.8	-0.2	0.7
21.5	-0.7	0.5	1.0	0.4	0.2	0.8
46.0	2.7	0.0	0.0	1.0	2.7	0.0
16.9	-0.8	0.2	-0.6	0.5	-1.4	0.0
28.7	0.3	0.7	-0.9	0.2	-0.6	0.3
27.8	0.7	0.3	-0.5	0.5	0.2	0.8
54.6	0.2	0.9	-1.1	0.4	-0.9	0.4
46.9	0.7	0.0	-0.5	0.3	0.3	0.4
11.1	0.6	0.6	-0.6	0.6	0.0	1.0
37.5	0.6	0.1	1.3	0.0	1.9	0.0
196.1	2.5	0.0	-0.3	0.7	2.2	0.0

19.2	-1.5	0.0	0.3	0.7	-1.2	0.1
13.9	-0.5	0.7	-0.3	0.9	-0.7	0.5
6.2	0.2	0.8	-0.3	0.8	-0.1	0.9
53.9	2.8	0.0	1.5	0.2	4.3	0.0
17.4	1.5	0.2	-0.1	0.9	1.3	0.2
50.0	-1.0	0.1	2.3	0.0	1.3	0.0
10.2	0.4	0.6	1.0	0.2	1.3	0.0
46.0	3.6	0.0	-0.5	0.3	3.1	0.0
14.1	-2.1	0.0	1.3	0.3	-0.8	0.4
25.0	-1.1	0.0	-0.6	0.3	-1.7	0.0
5.3	1.3	0.0	-1.1	0.1	0.3	0.7
10.0	-5.4	0.0	2.6	0.0	-2.8	0.0
32.4	2.8	0.0	0.6	0.5	3.4	0.0
45.7	-3.2	0.0	1.9	0.0	-1.2	0.0
64.4	-2.7	0.0	1.5	0.0	-1.2	0.0
43.0	-1.8	0.0	1.0	0.0	-0.8	0.1
1.3	0.1	0.9	-1.4	0.1	-1.3	0.1
6.1	-0.3	0.7	-0.2	0.8	-0.6	0.4
13.2	0.6	0.3	0.2	0.8	0.8	0.1
15.5	0.6	0.4	0.4	0.6	1.0	0.1
25.8	0.2	0.8	-0.8	0.3	-0.6	0.4
141.8	0.4	0.6	-0.5	0.6	-0.1	0.9
587.2	1.0	0.1	0.5	0.5	1.6	0.0
130.7	1.3	0.0	-0.7	0.3	0.7	0.2
32.8	0.6	0.2	-0.6	0.3	0.1	0.9
8.5	2.4	0.0	0.6	0.2	3.0	0.0
60.5	0.0	1.0	-0.5	0.7	-0.5	0.6
22.3	0.8	0.3	2.3	0.0	3.1	0.0
11.1	0.2	0.9	0.3	0.8	0.5	0.6
58.4	-1.6	0.0	0.7	0.1	-0.9	0.0
47.8	0.0	1.0	0.9	0.1	0.9	0.0
12.1	-0.4	0.6	0.5	0.5	0.2	0.8
26.2	0.3	0.8	-0.4	0.8	-0.1	0.9
19.2	0.0	1.0	-0.3	0.8	-0.3	0.8
22.5	1.7	0.1	-2.9	0.0	-1.2	0.2
106.0	0.5	0.6	1.2	0.1	1.7	0.0
62.2	3.1	0.0	-0.4	0.6	2.7	0.0
22.4	-1.3	0.2	1.3	0.2	0.0	1.0
1665.5	4.1	0.0	0.0	1.0	4.1	0.0
27.1	2.0	0.0	-1.2	0.0	0.7	0.1
61.0	1.0	0.0	0.2	0.7	1.2	0.0
30.1	0.3	0.7	0.5	0.7	0.8	0.3
72.8	4.0	0.0	-1.0	0.4	3.0	0.0

41.3	0.2	0.8	1.1	0.0	1.3	0.0
46.9	6.6	0.0	-1.5	0.0	5.2	0.0
85.8	5.4	0.0	0.6	0.4	6.0	0.0
100.1	-2.1	0.0	0.5	0.5	-1.5	0.0
41.8	2.3	0.0	0.0	1.0	2.3	0.0
426.2	-0.1	0.9	4.6	0.0	4.5	0.0
453.4	0.3	0.7	3.7	0.0	4.0	0.0
95.7	1.4	0.0	2.0	0.0	3.3	0.0
39.9	1.4	0.0	1.5	0.0	2.9	0.0
389.3	0.0	1.0	2.8	0.0	2.8	0.0
22.8	0.4	0.6	0.5	0.6	0.9	0.2
28.9	-1.2	0.0	0.8	0.1	-0.4	0.4
28.6	-0.9	0.0	0.1	0.9	-0.8	0.1
16.1	-0.5	0.4	-0.3	0.6	-0.8	0.1
205.0	-0.2	0.9	1.8	0.0	1.7	0.0
26.2	-0.3	0.8	0.6	0.7	0.3	0.8
22.3	0.1	1.0	0.4	0.8	0.4	0.7
1305.3	3.3	0.0	0.0	1.0	3.3	0.0
6139.4	3.7	0.0	0.4	0.6	4.1	0.0
31.1	4.5	0.0	-0.5	0.4	4.1	0.0
23.1	-1.4	0.0	0.0	1.0	-1.4	0.0
167.3	-1.1	0.2	0.8	0.5	-0.3	0.7
12.5	1.7	0.0	0.2	0.8	1.9	0.0
22.4	-0.4	0.6	0.5	0.5	0.1	0.9
28.0	-3.1	0.0	-0.1	0.9	-3.1	0.0
13.4	0.0	1.0	-0.6	0.4	-0.5	0.3
14.0	1.7	0.0	-1.2	0.0	0.5	0.3
162.0	1.7	0.0	-0.6	0.3	1.1	0.0
38.3	1.6	0.0	-0.7	0.3	0.9	0.1
126.2	0.7	0.1	0.1	0.9	0.7	0.1
22.0	-0.6	0.4	-0.8	0.2	-1.4	0.0
11.0	1.4	0.0	-0.1	0.9	1.3	0.0
14.2	-6.0	0.0	-0.2	0.9	-6.2	0.0
114.2	2.3	0.0	-0.3	0.7	2.0	0.0
15.9	-1.0	0.5	-1.7	0.2	-2.7	0.0
3.8	-2.2	0.1	-0.7	0.7	-2.8	0.0
18.0	-1.4	0.3	-0.5	0.8	-1.9	0.1
14.2	-0.7	0.6	-1.1	0.4	-1.9	0.1
107.2	1.2	0.0	-0.7	0.3	0.5	0.4
289.2	1.4	0.0	0.3	0.6	1.7	0.0
30.9	-0.1	0.9	0.5	0.5	0.4	0.5
48.2	1.2	0.2	0.5	0.7	1.6	0.0
97.8	1.2	0.0	-0.6	0.1	0.5	0.1

465.5	2.1	0.0	0.2	0.8	2.2	0.0
72.0	-0.4	0.6	0.2	0.8	-0.2	0.8
46.6	-1.0	0.0	0.0	1.0	-1.0	0.0
21.3	-1.8	0.0	-0.7	0.1	-2.5	0.0
22.4	-1.4	0.0	0.6	0.1	-0.8	0.0
3.8	-1.8	0.0	-0.3	0.7	-2.1	0.0
49.7	-1.4	0.0	-1.4	0.0	-2.8	0.0
48.7	-0.7	0.2	1.5	0.0	0.8	0.1
16.2	-1.0	0.0	1.2	0.0	0.2	0.7
13.2	-1.6	0.1	0.9	0.5	-0.7	0.5
16.2	-0.2	0.7	0.6	0.3	0.3	0.5
66.9	-0.2	0.8	-0.1	0.9	-0.3	0.6
31.7	1.2	0.4	-3.8	0.0	-2.7	0.0
11.3	1.3	0.4	-3.6	0.0	-2.3	0.1
86.2	0.3	0.8	1.8	0.0	2.1	0.0
815.0	0.7	0.2	-0.2	0.8	0.5	0.4
8220.8	1.2	0.0	-0.2	0.8	1.0	0.1
15363.3	0.1	0.9	0.7	0.3	0.8	0.2
9825.4	0.3	0.7	0.6	0.5	0.9	0.2
13.0	3.3	0.0	-0.4	0.7	2.9	0.0
6.6	0.4	0.8	-2.3	0.2	-2.0	0.2
4.3	-0.2	0.9	-1.9	0.3	-2.1	0.2
42.5	-1.0	0.6	-0.4	0.8	-1.4	0.3
14.0	-0.3	0.9	-0.8	0.7	-1.1	0.4
15.2	-0.2	0.9	-0.7	0.8	-0.8	0.6
32.7	0.2	0.9	-0.9	0.7	-0.7	0.7
14.1	-0.3	0.9	-1.5	0.4	-1.9	0.2
79.9	-1.2	0.5	-0.5	0.8	-1.7	0.2
59.1	-0.7	0.6	-1.0	0.5	-1.7	0.1
14.1	0.1	0.9	1.8	0.0	1.9	0.0
3.2	-0.2	0.8	0.9	0.4	0.7	0.5
22.4	-0.1	0.9	1.2	0.2	1.1	0.1
42.1	0.1	0.9	0.9	0.1	0.9	0.0
42.8	0.7	0.2	0.6	0.3	1.3	0.0
18.9	0.0	1.0	-1.2	0.4	-1.2	0.3
61.5	-1.5	0.0	-0.3	0.7	-1.8	0.0
25.7	-1.1	0.1	-0.6	0.4	-1.7	0.0
1105.9	1.3	0.0	0.2	0.8	1.5	0.0
83.5	0.6	0.2	0.9	0.0	1.5	0.0
10.9	0.0	1.0	0.3	0.5	0.3	0.4
61.4	0.0	1.0	-0.9	0.2	-0.9	0.1
51.0	-0.6	0.1	-0.7	0.1	-1.3	0.0
23.3	-1.1	0.0	0.7	0.1	-0.3	0.3

13.1	-0.3	0.6	-0.1	0.8	-0.4	0.3
256.8	0.4	0.4	-0.2	0.8	0.3	0.6
61.4	0.9	0.0	0.1	0.9	1.0	0.0
860.1	2.5	0.0	2.6	0.0	5.1	0.0
1250.3	-0.8	0.1	1.8	0.0	1.0	0.0
30.3	3.8	0.0	-0.4	0.7	3.4	0.0
96.2	1.2	0.1	0.2	0.9	1.3	0.0
19.8	2.8	0.0	-0.6	0.5	2.2	0.0
311.2	1.1	0.2	0.5	0.6	1.6	0.0
96.1	1.6	0.0	-0.7	0.3	0.9	0.1
6.6	-0.5	0.4	-0.5	0.4	-1.0	0.1
7.4	0.4	0.6	-1.1	0.1	-0.7	0.3
35.7	1.7	0.0	-1.4	0.0	0.3	0.6
50.9	-0.1	0.9	1.1	0.1	1.0	0.1
20.1	2.9	0.0	-1.1	0.3	1.8	0.0
47.6	-1.4	0.2	1.9	0.1	0.5	0.6
7.2	0.1	1.0	-1.1	0.2	-1.0	0.1
12.5	0.2	0.8	0.1	0.9	0.3	0.7
430.0	2.8	0.0	1.0	0.2	3.8	0.0
67.7	3.5	0.0	-0.1	0.9	3.4	0.0
12.6	-0.1	0.9	0.8	0.1	0.7	0.1
27.5	1.0	0.4	0.3	0.9	1.2	0.2
2.8	1.0	0.1	0.1	1.0	1.1	0.0
7.3	-0.6	0.5	-0.3	0.8	-0.9	0.3
26.9	-0.4	0.7	0.7	0.5	0.3	0.7
6.9	1.5	0.0	1.2	0.0	2.7	0.0
104.6	0.1	0.9	-0.1	0.9	0.0	1.0
13.9	1.6	0.0	-1.4	0.0	0.2	0.6
16.0	1.0	0.1	-0.9	0.3	0.1	0.9
2.6	2.3	0.0	-0.9	0.1	1.4	0.0
22.2	2.8	0.0	-0.2	0.7	2.6	0.0
13.4	0.8	0.2	-0.4	0.7	0.4	0.5
101.5	0.8	0.3	0.0	1.0	0.8	0.2
127.1	0.2	0.7	-0.7	0.1	-0.5	0.2
70.8	0.1	0.9	-0.8	0.1	-0.7	0.0
229.1	5.5	0.0	0.0	1.0	5.4	0.0
141.6	-0.5	0.2	0.1	0.8	-0.3	0.4
28.0	0.6	0.6	-0.1	0.9	0.4	0.7
25.2	-1.3	0.0	-0.7	0.2	-1.9	0.0
59.7	-1.4	0.0	0.8	0.2	-0.6	0.2
15.0	0.2	0.7	-1.3	0.0	-1.2	0.0
24.6	0.1	0.9	-0.7	0.3	-0.6	0.3
22.8	0.4	0.7	-1.0	0.3	-0.7	0.4

38.8	0.5	0.2	-0.5	0.2	0.0	1.0
149.5	1.5	0.0	-0.3	0.5	1.2	0.0
1701.5	3.4	0.0	-1.0	0.1	2.4	0.0
63.6	0.1	0.9	-1.5	0.0	-1.5	0.0
19.5	-0.4	0.4	0.3	0.6	-0.1	0.8
212.3	-0.1	0.9	1.2	0.0	1.1	0.0
23.0	-0.6	0.4	3.0	0.0	2.4	0.0
39.7	-0.4	0.5	1.4	0.0	1.0	0.1
35.7	-0.9	0.1	1.5	0.0	0.6	0.2
51.7	-1.4	0.0	1.2	0.0	-0.1	0.8
38.1	-0.5	0.3	-0.3	0.6	-0.8	0.1
14.4	-0.6	0.2	-1.2	0.0	-1.9	0.0
36.6	-0.3	0.5	-1.2	0.0	-1.5	0.0
93.6	0.3	0.7	-1.4	0.0	-1.1	0.1
28.9	-1.1	0.1	-0.1	1.0	-1.1	0.0
45.2	-1.5	0.0	1.0	0.2	-0.5	0.5
44.6	-1.2	0.3	1.9	0.1	0.7	0.5
4.9	-0.8	0.2	0.2	0.9	-0.7	0.3
311.5	1.9	0.0	-0.5	0.5	1.4	0.0
1084.5	0.5	0.4	0.0	1.0	0.5	0.4
28.8	-0.1	0.9	0.6	0.3	0.6	0.3
8.0	1.1	0.0	-0.5	0.3	0.6	0.1
111.0	0.7	0.1	0.0	1.0	0.7	0.1
42.7	0.4	0.5	1.0	0.2	1.4	0.0
34.4	-0.3	0.6	1.2	0.0	0.9	0.0
155.8	-0.5	0.5	1.5	0.0	1.0	0.1
22.1	2.0	0.0	-0.2	0.8	1.8	0.0
34.0	1.5	0.0	-0.2	0.8	1.3	0.0
51.8	0.6	0.5	-1.2	0.2	-0.6	0.4
333.3	1.9	0.1	0.2	0.9	2.1	0.0
24.5	-0.4	0.4	0.6	0.2	0.3	0.5
4.7	2.3	0.0	1.4	0.0	3.7	0.0
56.4	1.3	0.0	-0.1	0.9	1.2	0.0
318.7	0.9	0.1	0.7	0.3	1.6	0.0
72.9	0.9	0.1	-0.2	0.8	0.7	0.2
199.1	2.6	0.0	0.4	0.6	2.9	0.0
152.6	1.7	0.0	1.0	0.1	2.7	0.0
37.6	3.4	0.0	0.4	0.3	3.8	0.0
65.6	4.4	0.0	-0.4	0.6	4.1	0.0
42.9	3.5	0.0	-0.4	0.7	3.1	0.0
66.1	-2.0	0.0	0.3	0.8	-1.7	0.0
8.4	-0.8	0.5	1.5	0.2	0.7	0.5
8.5	-1.2	0.0	0.8	0.2	-0.4	0.5

74.1	0.0	1.0	0.8	0.1	0.8	0.1
5.5	1.3	0.0	0.3	0.7	1.6	0.0
51.0	1.6	0.0	1.1	0.1	2.8	0.0
142.8	2.5	0.0	-1.1	0.0	1.4	0.0
73.6	6.2	0.0	-0.8	0.0	5.4	0.0
23.3	0.6	0.5	-0.1	0.9	0.5	0.5
82.2	0.2	0.8	1.9	0.0	2.1	0.0
28.4	-0.6	0.2	0.4	0.5	-0.2	0.7
33.4	0.2	0.8	0.7	0.3	0.8	0.1
5.9	-0.3	0.7	-0.1	0.9	-0.4	0.5
22.0	0.4	0.7	0.0	1.0	0.4	0.7
47.4	0.6	0.3	0.3	0.6	0.9	0.1
30.0	0.5	0.3	-0.4	0.6	0.1	0.8
132.6	0.4	0.6	0.5	0.5	0.8	0.2
118.2	0.5	0.3	2.2	0.0	2.7	0.0
3413.9	0.4	0.7	3.6	0.0	3.9	0.0
19.4	0.4	0.4	1.0	0.1	1.4	0.0
18.5	0.7	0.5	0.6	0.6	1.3	0.2
37.0	1.6	0.0	0.1	0.9	1.7	0.0
446.9	0.1	0.9	1.3	0.1	1.4	0.0
63.1	-2.2	0.0	0.7	0.1	-1.4	0.0
42.1	-1.6	0.0	0.4	0.5	-1.1	0.0
20.4	-1.8	0.0	0.3	0.8	-1.5	0.1
24.3	-0.2	0.7	-2.1	0.0	-2.3	0.0
23.2	-0.9	0.3	-2.7	0.0	-3.5	0.0
4.5	-1.0	0.1	-2.9	0.0	-3.9	0.0
27.5	-1.1	0.0	-2.1	0.0	-3.2	0.0
21.5	-0.6	0.3	-1.9	0.0	-2.5	0.0
4.6	-0.5	0.5	-2.1	0.0	-2.6	0.0
144.0	-0.3	0.7	0.1	0.9	-0.2	0.8
175.0	-0.9	0.2	0.5	0.6	-0.4	0.5
37.2	0.2	0.7	-0.7	0.3	-0.4	0.5
22.0	-0.4	0.5	1.9	0.0	1.6	0.0
9.0	-2.6	0.0	2.2	0.0	-0.4	0.6
11.4	-4.5	0.0	0.7	0.2	-3.9	0.0
28.2	-0.1	1.0	-1.3	0.3	-1.3	0.2
1.9	-0.4	0.6	-0.9	0.2	-1.3	0.0
38.8	-0.2	0.8	0.1	0.9	-0.1	0.9
8.7	0.8	0.4	-1.2	0.2	-0.5	0.6
30.2	1.3	0.1	-0.6	0.5	0.7	0.4
3.2	0.2	0.9	-1.3	0.3	-1.2	0.2
5.2	0.1	0.9	-0.9	0.4	-0.8	0.4
3.0	0.1	0.9	0.0	1.0	0.1	0.9

38.9	0.1	0.9	1.7	0.0	1.8	0.0
57.2	1.3	0.0	0.0	1.0	1.3	0.0
8.1	2.0	0.0	-0.1	1.0	2.0	0.0
19.2	1.8	0.0	0.5	0.5	2.3	0.0
988.7	1.9	0.0	0.3	0.8	2.2	0.0
28.4	0.8	0.3	-0.1	0.9	0.7	0.3
180.6	-0.3	0.6	1.9	0.0	1.6	0.0
60.4	3.0	0.0	-0.5	0.5	2.5	0.0
26.5	-1.2	0.2	-0.2	0.9	-1.4	0.1
37.5	-1.0	0.0	0.6	0.1	-0.4	0.2
8.3	-0.9	0.0	0.6	0.2	-0.3	0.5
20.3	-1.5	0.0	1.5	0.0	0.0	1.0
36.5	0.1	0.9	0.9	0.1	1.0	0.0
20.8	1.6	0.0	0.5	0.6	2.1	0.0
113.0	0.2	0.7	3.0	0.0	3.2	0.0
119.2	-2.0	0.0	1.4	0.0	-0.6	0.3
17.5	0.0	1.0	-0.2	0.9	-0.2	0.9
127.9	0.7	0.3	0.6	0.4	1.3	0.0
15.3	0.0	0.9	-0.5	0.3	-0.6	0.2
13.8	1.1	0.0	-0.9	0.1	0.1	0.8
12.4	0.5	0.4	0.9	0.2	1.4	0.0
12.6	0.4	0.6	0.5	0.5	0.9	0.1
24.1	0.7	0.1	0.4	0.5	1.1	0.0
41.7	0.2	0.7	0.4	0.6	0.6	0.3
20.5	-2.7	0.0	-0.5	0.5	-3.3	0.0
19.9	-1.5	0.1	-0.6	0.6	-2.1	0.0
52.5	-0.9	0.0	0.0	0.9	-0.8	0.0
1.4	0.0	0.9	-0.8	0.1	-0.8	0.1
47.1	-0.2	0.6	-0.9	0.0	-1.1	0.0
87.3	1.9	0.0	0.0	1.0	1.9	0.0
16.0	-2.4	0.0	0.1	0.9	-2.3	0.0
17.1	-0.1	0.9	1.1	0.3	1.0	0.3
49.5	-0.7	0.4	-0.2	0.9	-0.9	0.3
63.3	1.3	0.2	0.1	1.0	1.4	0.2
339.4	0.3	0.6	0.5	0.5	0.8	0.1
129.8	1.2	0.0	-1.1	0.1	0.1	0.9
65.7	-0.2	0.9	0.6	0.7	0.4	0.7
22.2	0.7	0.5	0.0	1.0	0.7	0.4
56.9	-1.6	0.0	0.8	0.3	-0.8	0.2
18.4	-1.9	0.0	1.0	0.1	-0.9	0.1
6.8	2.5	0.0	0.7	0.3	3.3	0.0
28.2	-0.2	0.7	0.1	0.8	0.0	1.0
31.0	2.1	0.0	0.6	0.4	2.7	0.0

6.5	2.4	0.0	-0.4	0.6	2.0	0.0
11.0	2.8	0.0	-0.1	0.9	2.7	0.0
29.3	2.9	0.0	0.3	0.8	3.2	0.0
4.0	3.2	0.0	-0.5	0.6	2.7	0.0
29.3	3.1	0.0	-0.7	0.4	2.4	0.0
21.3	4.0	0.0	-0.4	0.6	3.6	0.0
447.5	5.5	0.0	-0.3	0.7	5.2	0.0
2.6	0.9	0.2	-0.9	0.2	0.0	1.0
4.1	0.7	0.6	1.1	0.4	1.8	0.1
2.6	-0.5	0.3	0.6	0.2	0.1	0.8
25.0	0.1	0.8	0.4	0.6	0.5	0.3
23.7	-0.5	0.7	0.8	0.5	0.3	0.8
124.5	-0.5	0.6	2.0	0.0	1.5	0.0
14.7	0.3	0.8	0.1	1.0	0.4	0.7
14.4	1.4	0.0	-0.1	0.9	1.4	0.0
55.8	1.6	0.0	-0.1	0.9	1.5	0.0
58.7	-0.5	0.3	0.4	0.6	-0.2	0.7
18.5	2.3	0.0	-0.7	0.2	1.6	0.0
11.2	0.7	0.2	-0.2	0.8	0.5	0.3
40.3	0.7	0.2	1.2	0.0	1.9	0.0
9.4	1.7	0.1	-0.3	0.8	1.4	0.1
130.3	4.0	0.0	-0.4	0.4	3.6	0.0
166.2	1.5	0.0	0.3	0.7	1.8	0.0
14.5	1.3	0.0	2.0	0.0	3.3	0.0
9.8	1.0	0.1	0.6	0.5	1.6	0.0
18.5	1.4	0.2	-0.6	0.7	0.8	0.4
11.0	0.5	0.4	-1.4	0.0	-0.9	0.1
10.9	-0.1	1.0	-1.2	0.3	-1.3	0.2
34.1	-0.2	0.8	-0.3	0.8	-0.5	0.5
12.3	1.1	0.0	-0.5	0.4	0.7	0.2
28.1	-2.8	0.0	-2.9	0.0	-5.6	0.0
31.6	4.2	0.0	-1.1	0.0	3.1	0.0
61.9	0.8	0.1	0.3	0.7	1.1	0.0
4.4	3.4	0.0	-2.2	0.0	1.2	0.1
29.6	1.4	0.0	-0.6	0.1	0.7	0.0
87.0	1.3	0.0	0.5	0.4	1.7	0.0
14.1	-0.2	0.9	-1.9	0.0	-2.1	0.0
5.9	-1.0	0.0	1.8	0.0	0.8	0.0
114.3	-2.9	0.0	1.1	0.1	-1.7	0.0
20.1	-3.7	0.0	1.9	0.0	-1.7	0.0
13.0	-2.9	0.0	1.9	0.0	-1.1	0.0
26.8	-1.5	0.0	0.9	0.3	-0.5	0.5
18.2	-1.7	0.0	2.2	0.0	0.5	0.5

94.2	-0.7	0.5	0.8	0.4	0.2	0.9
46.3	0.5	0.7	-0.5	0.7	0.0	1.0
88.6	0.5	0.6	1.3	0.1	1.8	0.0
6.1	-1.2	0.0	0.0	1.0	-1.3	0.0
40.7	2.9	0.0	-0.3	0.7	2.6	0.0
17.7	3.6	0.0	-1.0	0.4	2.7	0.0
80.3	2.2	0.0	-0.6	0.5	1.6	0.0
58.8	3.1	0.0	-0.1	0.9	3.0	0.0
17.4	-2.9	0.0	1.7	0.0	-1.2	0.0
12.0	-0.4	0.7	1.6	0.0	1.2	0.1
51.9	-0.1	0.9	1.9	0.0	1.9	0.0
157.1	4.1	0.0	0.0	1.0	4.1	0.0
66.6	2.3	0.0	-0.8	0.3	1.5	0.0
41.0	0.2	0.9	1.1	0.2	1.3	0.1
19.3	1.5	0.0	1.2	0.1	2.7	0.0
46.8	0.6	0.2	-0.7	0.2	0.0	1.0
23.4	0.0	1.0	-0.4	0.7	-0.5	0.6
20.2	-0.4	0.7	-0.2	0.9	-0.6	0.6
37.3	-3.5	0.0	-0.7	0.5	-4.2	0.0
19.7	-0.7	0.3	1.2	0.1	0.5	0.4
24.6	-1.6	0.0	1.7	0.0	0.1	0.9
77.6	-2.1	0.0	0.7	0.5	-1.4	0.1
12.2	0.2	0.7	1.2	0.0	1.4	0.0
73.4	-0.4	0.6	-0.3	0.7	-0.7	0.3
136.2	-1.3	0.0	0.3	0.7	-1.0	0.1
47.0	0.4	0.3	-0.1	0.9	0.3	0.4
16.3	-2.4	0.0	-0.3	0.8	-2.7	0.0
48.0	-2.7	0.0	1.2	0.1	-1.5	0.0
47.9	1.1	0.0	-0.5	0.5	0.6	0.2
89.7	-0.6	0.4	1.0	0.1	0.4	0.5
102.1	-1.0	0.1	1.4	0.0	0.4	0.6
15.1	-2.1	0.0	1.7	0.0	-0.4	0.5
84.8	0.2	0.7	-0.6	0.3	-0.4	0.4
19.1	-0.1	0.9	-0.8	0.0	-0.9	0.0
51.8	1.2	0.0	-0.4	0.6	0.8	0.1
107.4	2.7	0.0	-0.3	0.8	2.5	0.0
19.0	-2.1	0.0	0.4	0.6	-1.7	0.0
10.7	2.4	0.0	-0.4	0.8	2.0	0.0
56.2	0.8	0.2	-0.3	0.7	0.5	0.4
129.6	2.4	0.0	-0.6	0.2	1.7	0.0
185.8	1.1	0.1	-1.0	0.2	0.2	0.8
18.2	1.5	0.0	0.4	0.6	1.9	0.0
62.9	-1.0	0.3	2.0	0.0	1.0	0.3

70.3	0.4	0.7	1.0	0.4	1.4	0.1
24.6	-4.3	0.0	-0.5	0.4	-4.8	0.0
178.2	-1.0	0.1	1.1	0.1	0.1	0.9
248.6	3.2	0.0	1.1	0.1	4.3	0.0
4.4	0.6	0.2	0.3	0.7	0.9	0.0
23.2	1.0	0.1	0.1	0.9	1.1	0.0
28.9	0.6	0.3	-0.2	0.8	0.3	0.5
36.5	0.4	0.5	-0.5	0.4	-0.1	0.8
12.7	-0.8	0.0	-0.6	0.1	-1.4	0.0
318.0	0.5	0.4	0.3	0.6	0.7	0.1
7.4	0.6	0.2	-0.5	0.3	0.1	0.9
69.6	-3.0	0.0	-0.4	0.7	-3.5	0.0
162.3	0.8	0.3	0.6	0.5	1.4	0.0
233.7	4.5	0.0	-0.7	0.4	3.9	0.0
91.5	0.2	0.8	0.8	0.1	1.0	0.0
16.2	-0.2	0.6	-0.1	0.9	-0.2	0.4
36.6	-0.2	0.7	0.0	1.0	-0.2	0.7
17.0	-2.6	0.0	0.0	1.0	-2.6	0.0
91.7	0.2	0.8	2.0	0.0	2.2	0.0
33.0	1.4	0.1	-1.9	0.1	-0.5	0.6
61.8	0.1	0.8	0.6	0.4	0.7	0.2
121.1	-1.0	0.1	1.4	0.0	0.4	0.5
619.6	8.8	0.0	0.4	0.5	9.2	0.0
26.8	8.7	0.0	-1.2	0.0	7.5	0.0
39.1	7.9	0.0	-1.4	0.0	6.5	0.0
809.7	6.4	0.0	0.2	0.8	6.6	0.0
636.1	2.2	0.0	-1.0	0.2	1.2	0.1
42.0	1.4	0.0	0.9	0.0	2.3	0.0
70.2	4.0	0.0	-1.6	0.0	2.4	0.0
11.3	3.5	0.0	-1.5	0.0	2.1	0.0
162.2	-0.6	0.3	0.4	0.5	-0.2	0.8
94.3	0.7	0.3	0.7	0.3	1.4	0.0
54.6	0.8	0.3	1.7	0.0	2.4	0.0
14.1	1.0	0.1	0.5	0.5	1.6	0.0
9.2	2.5	0.0	-0.1	0.9	2.5	0.0
109.1	-1.6	0.0	2.4	0.0	0.9	0.2
1.8	1.8	0.0	-0.5	0.7	1.3	0.2
7.3	1.4	0.1	0.1	0.9	1.5	0.1
23.7	-1.1	0.3	-0.1	1.0	-1.2	0.2
65.0	-0.2	0.8	0.6	0.5	0.4	0.6
63.3	-0.8	0.4	1.4	0.2	0.6	0.5
8.2	-2.6	0.0	-0.7	0.6	-3.3	0.0
12.0	-2.5	0.0	-0.1	1.0	-2.6	0.0

69.0	-2.2	0.0	0.3	0.8	-2.0	0.0
0.8	-2.9	0.0	-1.5	0.1	-4.4	0.0
153.6	1.5	0.0	0.4	0.6	2.0	0.0
21.5	1.6	0.0	-1.8	0.0	-0.2	0.8
24.4	-0.7	0.1	0.6	0.2	-0.1	0.9
3.1	-0.3	0.7	-2.0	0.0	-2.2	0.0
7.5	-2.7	0.0	-0.5	0.6	-3.2	0.0
19.3	-1.2	0.2	0.1	1.0	-1.1	0.2
13.7	1.8	0.0	0.2	0.7	2.0	0.0
27.8	2.8	0.0	-0.3	0.6	2.5	0.0
33.1	0.8	0.2	0.1	0.9	0.9	0.1
44.6	0.3	0.6	2.1	0.0	2.4	0.0
25.9	-0.4	0.6	1.2	0.1	0.8	0.3
92.5	0.5	0.6	2.3	0.0	2.7	0.0
113.6	2.5	0.0	1.0	0.3	3.5	0.0
20.8	0.4	0.6	0.0	1.0	0.4	0.6
303.0	-1.3	0.0	0.3	0.8	-1.1	0.1
153.6	-0.3	0.6	0.2	0.8	-0.1	0.9
85.0	0.2	0.8	0.4	0.7	0.7	0.4
106.3	-0.8	0.1	0.7	0.2	-0.1	0.8
277.7	1.8	0.0	0.1	0.9	1.9	0.0
139.2	1.5	0.0	-0.1	0.8	1.4	0.0
13.5	-0.4	0.5	0.3	0.7	-0.1	0.9
12.0	-0.2	0.7	0.8	0.0	0.7	0.1
36.3	-0.4	0.1	0.0	1.0	-0.4	0.1
18.5	0.2	0.9	0.2	0.9	0.4	0.7
3.0	-1.2	0.0	1.5	0.0	0.2	0.7
42.3	-0.3	0.8	-0.4	0.8	-0.7	0.5
17.8	0.6	0.1	-0.1	0.8	0.5	0.1
13.2	-0.1	0.9	0.2	0.8	0.1	0.9
52.6	-1.5	0.2	-0.2	0.9	-1.6	0.1
118.9	-0.6	0.3	-0.2	0.8	-0.8	0.1
60.2	3.4	0.0	-0.9	0.2	2.5	0.0
55.4	3.2	0.0	-0.4	0.4	2.8	0.0
432.5	2.2	0.0	0.4	0.4	2.6	0.0
218.5	2.3	0.0	0.6	0.3	3.0	0.0
63.2	0.0	1.0	-1.0	0.5	-1.0	0.4
162.6	-2.4	0.0	-0.6	0.5	-3.0	0.0
26.6	0.1	0.9	-0.6	0.3	-0.5	0.3
3.4	-1.4	0.0	0.0	1.0	-1.5	0.0
28.6	-1.2	0.1	-0.9	0.2	-2.2	0.0
27.7	-1.3	0.0	-0.2	0.8	-1.6	0.0
16.8	-1.2	0.2	-0.9	0.4	-2.1	0.0

15.6	-1.7	0.1	-1.0	0.3	-2.7	0.0
107.9	-1.1	0.0	0.1	0.9	-1.0	0.1
13.4	4.4	0.0	-1.4	0.1	3.0	0.0
50.0	-0.6	0.3	1.0	0.1	0.4	0.5
38.1	-1.0	0.0	0.0	1.0	-1.0	0.0
191.8	-0.1	0.8	-0.5	0.2	-0.6	0.1
30.4	-1.1	0.0	1.6	0.0	0.4	0.3
45.6	-0.3	0.7	-0.3	0.7	-0.5	0.3
35.0	0.1	0.9	-0.8	0.2	-0.8	0.2
58.2	1.8	0.0	0.9	0.2	2.7	0.0
8.3	3.1	0.0	-1.9	0.0	1.1	0.0
32.5	1.0	0.1	-0.5	0.4	0.5	0.4
22.6	0.0	0.9	-1.2	0.0	-1.3	0.0
10.9	0.6	0.1	-1.6	0.0	-1.0	0.0
145.8	10.5	0.0	-5.7	0.0	4.8	0.0
7.8	9.4	0.0	-5.9	0.0	3.5	0.0
12.1	7.7	0.0	-5.3	0.0	2.4	0.0
22.9	6.6	0.0	-5.5	0.0	1.1	0.0
119.9	1.1	0.1	0.9	0.2	2.0	0.0
45.7	2.3	0.0	1.2	0.0	3.4	0.0
41.2	-1.4	0.0	0.7	0.2	-0.7	0.2
25.2	-1.4	0.1	0.8	0.5	-0.5	0.6
11.1	1.2	0.0	0.0	1.0	1.2	0.0
8.4	0.5	0.2	-0.5	0.2	0.0	0.9
7.1	-0.4	0.4	-0.3	0.7	-0.7	0.1
210.4	-0.5	0.6	-0.1	0.9	-0.6	0.4
18.6	0.3	0.7	-0.3	0.7	0.0	1.0
3.4	-1.3	0.0	0.4	0.3	-0.9	0.0
325.8	-0.5	0.6	-0.4	0.7	-1.0	0.3
15.9	1.4	0.0	-0.2	0.7	1.2	0.0
77.2	-0.5	0.2	0.7	0.1	0.1	0.7
566.7	-0.7	0.1	1.3	0.0	0.6	0.2
38.1	0.2	0.7	1.3	0.0	1.6	0.0
27.6	-0.6	0.6	0.8	0.5	0.2	0.9
36.3	0.2	0.8	0.7	0.4	0.9	0.2
75.4	-0.3	0.5	-0.5	0.3	-0.8	0.0
6.0	0.2	0.8	0.4	0.6	0.7	0.3
33.4	-0.3	0.6	0.3	0.7	0.0	1.0
42.5	-1.9	0.0	0.7	0.5	-1.2	0.1
5.2	1.0	0.3	-0.7	0.5	0.3	0.8
19.4	1.8	0.0	-0.4	0.6	1.5	0.0
21.1	-0.1	0.9	0.0	0.9	-0.1	0.8
11.4	-0.7	0.5	0.3	0.8	-0.4	0.7

32.4	-0.6	0.3	1.5	0.0	0.9	0.1
78.8	-2.0	0.0	2.0	0.0	0.0	1.0
3.3	-1.4	0.0	0.8	0.1	-0.6	0.2
26.6	3.3	0.0	0.8	0.2	4.0	0.0
71.1	-0.6	0.1	0.1	0.8	-0.4	0.2
19.4	-0.7	0.3	-0.2	0.8	-0.9	0.1
160.2	0.2	0.7	-0.2	0.8	0.0	1.0
17.3	-3.8	0.0	0.8	0.6	-3.1	0.0
13.3	0.2	0.7	0.7	0.1	0.9	0.0
50.7	-1.3	0.0	0.7	0.1	-0.6	0.1
736.3	0.3	0.6	1.0	0.1	1.3	0.0
54.9	2.0	0.0	-0.4	0.4	1.6	0.0
3.3	-0.9	0.0	-0.4	0.4	-1.3	0.0
4.2	2.2	0.0	1.3	0.1	3.5	0.0
36.6	0.0	1.0	1.2	0.0	1.2	0.0
788.9	0.7	0.3	1.1	0.1	1.9	0.0
4.9	1.5	0.0	1.8	0.0	3.3	0.0
17.4	1.0	0.1	1.2	0.1	2.3	0.0
34.9	-1.0	0.0	-0.1	0.8	-1.1	0.0
6.0	-1.0	0.0	1.1	0.0	0.1	0.9
43.8	0.1	0.9	0.9	0.5	1.0	0.4
7.0	-0.4	0.6	1.4	0.1	0.9	0.2
19.7	0.9	0.5	1.1	0.4	2.0	0.1
95.4	-2.6	0.0	-0.9	0.2	-3.5	0.0
35.8	0.9	0.1	-1.8	0.0	-1.0	0.1
41.7	0.1	0.9	0.6	0.7	0.7	0.5
17.5	1.6	0.0	-0.9	0.0	0.6	0.1
6.3	-1.4	0.0	0.1	0.9	-1.3	0.0
2.9	-2.0	0.0	0.3	0.7	-1.7	0.0
57.3	-1.1	0.2	-0.3	0.8	-1.4	0.1
13.9	-1.0	0.0	0.1	0.9	-0.9	0.0
8.0	-0.2	0.8	-0.9	0.1	-1.1	0.0
74.7	-0.1	1.0	-0.1	0.9	-0.1	0.9
41.7	0.4	0.4	0.2	0.8	0.6	0.2
31.0	-0.8	0.1	1.1	0.1	0.3	0.7
13.7	-1.5	0.1	0.5	0.6	-1.0	0.2
135.1	-1.0	0.3	2.6	0.0	1.6	0.1
36.1	-0.3	0.6	0.3	0.6	0.1	0.9
650.0	-2.4	0.0	0.7	0.4	-1.7	0.0
63.5	1.9	0.0	0.8	0.5	2.6	0.0
9.2	1.2	0.1	-0.8	0.4	0.4	0.6
19.1	-1.5	0.0	0.0	1.0	-1.5	0.0
7.7	-1.2	0.0	-0.6	0.1	-1.8	0.0

49.8	-1.0	0.2	1.8	0.0	0.9	0.2
5.8	0.1	0.8	0.5	0.4	0.6	0.2
18.6	-1.6	0.0	0.5	0.2	-1.1	0.0
227.7	-0.8	0.0	0.0	1.0	-0.8	0.0
9.0	-0.9	0.1	-0.1	0.9	-1.0	0.1
99.5	-0.2	0.9	-0.5	0.8	-0.7	0.6
116.1	4.3	0.0	-0.4	0.6	3.9	0.0
9.9	-0.3	0.6	-0.1	0.9	-0.4	0.4
19.9	-1.7	0.0	1.2	0.0	-0.6	0.0
94.4	-0.3	0.5	0.7	0.2	0.4	0.4
17.9	-0.5	0.1	0.2	0.6	-0.3	0.4
7.9	-0.6	0.1	0.0	1.0	-0.6	0.1
87.2	-0.7	0.2	-0.6	0.3	-1.3	0.0
31.2	0.9	0.1	-0.5	0.3	0.3	0.5
12.9	-0.6	0.1	-0.3	0.5	-0.9	0.0
18.5	0.2	0.8	-0.5	0.4	-0.3	0.5
1.4	0.0	0.9	-1.7	0.0	-1.7	0.0
73.8	-0.6	0.2	-1.0	0.1	-1.6	0.0
15.7	-0.1	0.9	-0.9	0.5	-1.0	0.3
168.5	-1.1	0.0	0.8	0.1	-0.4	0.5
58.7	-0.7	0.5	-0.2	0.9	-0.9	0.4
52.2	-1.5	0.0	0.6	0.1	-0.9	0.0
35.8	-2.1	0.0	0.5	0.1	-1.5	0.0
24.6	-1.5	0.0	-0.3	0.6	-1.8	0.0
17.0	0.2	0.7	-0.4	0.5	-0.1	0.8
74.7	-0.6	0.0	0.9	0.0	0.3	0.4
23.7	1.1	0.0	0.2	0.8	1.3	0.0
78.4	1.2	0.0	-0.3	0.4	0.9	0.0
62.5	0.5	0.7	-1.0	0.4	-0.5	0.6
117.2	0.2	0.8	-0.2	0.8	0.0	0.9
34.4	1.3	0.0	-0.9	0.1	0.4	0.4
44.7	-0.8	0.0	0.7	0.1	-0.1	0.8
50.3	1.4	0.0	-0.8	0.3	0.6	0.3
12.0	-0.3	0.7	0.5	0.5	0.3	0.7
22.6	3.4	0.0	0.3	0.7	3.7	0.0
4.5	-1.3	0.0	0.8	0.1	-0.6	0.1
9.1	-1.6	0.0	1.0	0.1	-0.5	0.4
7.8	-1.6	0.1	-0.1	0.9	-1.7	0.0
23.6	3.3	0.0	-1.2	0.1	2.1	0.0
14.8	1.0	0.0	0.6	0.2	1.6	0.0
16.4	-0.1	0.8	0.3	0.7	0.2	0.8
6.6	-5.6	0.0	0.6	0.4	-5.0	0.0
647.8	-0.3	0.8	3.7	0.0	3.5	0.0

21.6	-0.4	0.6	0.2	0.8	-0.2	0.8
55.2	-1.8	0.0	0.9	0.2	-0.9	0.2
134.9	-0.9	0.1	-0.6	0.3	-1.6	0.0
14.3	1.2	0.0	-0.1	0.8	1.1	0.0
76.7	3.6	0.0	1.1	0.0	4.7	0.0
4.8	0.2	0.6	0.3	0.6	0.5	0.2
639.4	2.7	0.0	0.8	0.3	3.6	0.0
80.2	1.2	0.0	0.2	0.8	1.3	0.0
3.4	1.1	0.0	0.2	0.8	1.3	0.0
55.9	1.0	0.0	-0.5	0.3	0.5	0.2
7.7	0.3	0.6	-0.3	0.6	0.0	0.9
53.9	1.0	0.1	-0.1	0.9	0.8	0.1
107.7	-1.7	0.0	-0.1	0.9	-1.9	0.0
474.0	-0.8	0.1	-0.6	0.4	-1.4	0.0
144.6	-0.9	0.1	-0.7	0.3	-1.6	0.0
54.9	-0.5	0.5	-1.2	0.1	-1.7	0.0
161.7	0.4	0.7	-0.9	0.4	-0.5	0.5
20.7	1.3	0.0	-0.7	0.2	0.6	0.3
1634.3	-0.3	0.9	-0.7	0.6	-1.0	0.4
962.2	-0.5	0.5	-0.4	0.7	-0.9	0.2
32.6	-0.6	0.4	1.2	0.1	0.6	0.4
65.7	0.2	0.6	0.2	0.7	0.4	0.2
19.7	-0.3	0.6	-1.6	0.0	-1.9	0.0
34.3	1.5	0.0	-0.6	0.5	0.9	0.3
29.5	0.6	0.4	-0.4	0.7	0.3	0.7
121.5	1.3	0.0	-0.4	0.4	0.9	0.0
177.0	1.9	0.0	-0.3	0.5	1.5	0.0
33.8	0.0	1.0	-0.3	0.6	-0.3	0.4
40.7	-1.4	0.0	0.2	0.8	-1.2	0.0
42.5	-0.2	0.7	-0.2	0.8	-0.5	0.5
8.3	1.1	0.0	-0.8	0.1	0.3	0.4
81.2	-0.6	0.4	-0.4	0.6	-1.0	0.1
6816.7	1.1	0.1	-0.5	0.6	0.7	0.3
4998.8	0.1	0.9	0.3	0.7	0.4	0.5
387.5	-0.2	0.7	-0.3	0.7	-0.5	0.4
127.3	-2.1	0.0	1.1	0.1	-1.1	0.0
33.9	-0.1	0.9	0.5	0.3	0.4	0.3
47.5	0.9	0.0	0.3	0.5	1.2	0.0
189.0	1.2	0.0	-0.5	0.4	0.7	0.2
135.2	0.4	0.6	-1.2	0.1	-0.8	0.2
320.4	0.3	0.7	-1.1	0.2	-0.7	0.3
968.0	2.9	0.0	-0.9	0.2	2.0	0.0
91.4	2.0	0.0	1.0	0.1	3.0	0.0

31.9	0.9	0.0	-0.4	0.4	0.5	0.2
11.3	-0.9	0.1	-1.2	0.1	-2.1	0.0
692.3	4.0	0.0	0.2	0.8	4.2	0.0
126.9	4.1	0.0	-0.8	0.4	3.3	0.0
384.6	4.7	0.0	-0.5	0.6	4.1	0.0
39.6	-2.0	0.0	0.0	1.0	-1.9	0.0
6.9	0.1	0.9	-2.0	0.0	-1.9	0.0
13.5	0.9	0.1	-0.7	0.2	0.1	0.8
13.9	0.2	0.8	2.1	0.0	2.3	0.0
55.1	2.2	0.0	0.1	0.9	2.3	0.0
43.6	2.5	0.0	0.1	0.9	2.6	0.0
19.2	2.0	0.0	-0.6	0.6	1.5	0.1
7.3	0.6	0.3	0.7	0.3	1.3	0.0
34.2	-0.1	0.9	1.2	0.0	1.1	0.0
9.3	0.6	0.4	-0.6	0.4	0.0	1.0
35.8	1.1	0.0	-1.1	0.1	0.1	0.9
42.6	-1.8	0.0	-0.3	0.8	-2.1	0.0
83.5	0.5	0.5	1.0	0.1	1.5	0.0
46.7	-0.9	0.2	-0.5	0.6	-1.4	0.1
19.6	-2.5	0.0	-0.4	0.6	-2.9	0.0
24.1	0.3	0.7	-0.7	0.4	-0.4	0.6
120.1	0.0	1.0	0.2	0.8	0.2	0.8
133.3	-0.2	0.8	0.3	0.7	0.1	0.8
23.8	-1.0	0.0	0.3	0.7	-0.8	0.1
103.5	-1.5	0.0	-0.3	0.7	-1.7	0.0
20.4	-1.7	0.0	1.1	0.1	-0.6	0.3
11.0	0.8	0.1	0.8	0.2	1.6	0.0
12.6	3.0	0.0	-1.2	0.3	1.8	0.1
15.1	-0.2	0.6	0.0	1.0	-0.2	0.6
25.5	0.6	0.3	-0.5	0.4	0.0	1.0
11.4	-0.6	0.2	-0.7	0.1	-1.3	0.0
40.2	1.2	0.0	-0.5	0.3	0.7	0.1
108.4	0.5	0.6	1.2	0.1	1.7	0.0
20.4	-0.2	0.9	2.2	0.0	2.0	0.0
39.1	-2.3	0.0	1.8	0.0	-0.5	0.4
178.1	-0.4	0.6	-0.2	0.8	-0.6	0.3
37.8	-0.6	0.2	0.3	0.5	-0.3	0.6
22.6	1.9	0.0	-0.9	0.1	1.0	0.0
182.7	1.0	0.0	-0.5	0.3	0.5	0.3
8.0	0.8	0.1	-0.4	0.5	0.4	0.4
88.4	4.3	0.0	-0.2	0.8	4.1	0.0
162.2	4.0	0.0	0.0	1.0	4.0	0.0
283.6	-0.1	0.9	0.8	0.2	0.7	0.2

6.2	0.6	0.3	0.4	0.6	1.0	0.1
9.5	1.0	0.1	0.1	0.9	1.1	0.1
101.3	0.4	0.5	0.7	0.3	1.1	0.1
40.6	0.6	0.2	-0.9	0.0	-0.3	0.5
4.5	0.3	0.6	-1.1	0.0	-0.9	0.0
64.8	0.4	0.7	-1.3	0.1	-0.9	0.2
15.0	0.4	0.3	-1.7	0.0	-1.2	0.0
92.6	-0.2	0.7	-0.6	0.2	-0.8	0.0
215.4	-0.2	0.8	0.3	0.7	0.1	0.9
14.6	-0.4	0.4	0.1	0.9	-0.3	0.4
90.7	-0.1	0.9	1.0	0.0	0.9	0.0
22.4	-0.5	0.4	0.5	0.4	0.1	0.9
103.1	-0.9	0.1	-0.6	0.3	-1.5	0.0
55.3	-1.8	0.0	-1.1	0.1	-2.9	0.0
5.1	-0.1	0.8	-1.7	0.0	-1.8	0.0
35.1	-0.2	0.7	-2.1	0.0	-2.3	0.0
29.0	-0.3	0.8	-2.8	0.0	-3.1	0.0
26.1	0.1	0.9	-2.5	0.0	-2.4	0.0
32.9	0.2	0.7	-1.9	0.0	-1.6	0.0
24.7	0.8	0.1	-1.7	0.0	-0.9	0.1
137.5	1.1	0.0	-1.6	0.0	-0.5	0.3
90.7	1.5	0.0	-2.1	0.0	-0.6	0.4
73.6	2.3	0.0	-1.7	0.0	0.6	0.4
32.7	2.5	0.0	-2.2	0.0	0.3	0.7
33.8	0.8	0.1	0.3	0.6	1.2	0.0
5.7	2.1	0.0	-3.0	0.0	-0.9	0.3
9.8	2.3	0.0	-2.6	0.0	-0.3	0.7
8.2	1.2	0.1	-3.0	0.0	-1.8	0.0
8.1	1.4	0.1	-3.2	0.0	-1.8	0.0
21.3	1.4	0.1	-3.1	0.0	-1.6	0.1
33.5	0.8	0.5	-2.9	0.0	-2.1	0.0
17.8	0.9	0.3	-2.7	0.0	-1.8	0.0
19.1	1.2	0.2	-2.8	0.0	-1.6	0.1
9.8	1.7	0.0	-2.6	0.0	-0.9	0.1
11.2	1.0	0.2	-2.5	0.0	-1.5	0.0
7.8	1.1	0.0	-1.7	0.0	-0.6	0.3
26.1	1.5	0.1	-2.1	0.0	-0.6	0.6
34.2	2.1	0.0	-3.4	0.0	-1.3	0.2
10.4	2.3	0.0	-3.6	0.0	-1.3	0.1
38.9	2.1	0.0	-2.6	0.0	-0.5	0.4
14.1	1.6	0.1	-3.5	0.0	-1.9	0.1
20.3	2.1	0.0	-2.8	0.0	-0.7	0.4
9.5	0.5	0.2	-0.3	0.5	0.2	0.7

56.1	0.5	0.6	-2.0	0.0	-1.5	0.1
21.1	0.2	0.8	-1.9	0.0	-1.7	0.0
1.0	-0.5	0.4	-3.0	0.0	-3.5	0.0
8.2	-1.1	0.1	-3.9	0.0	-5.0	0.0
57.1	-3.8	0.0	-2.4	0.0	-6.2	0.0
22.6	-2.6	0.0	-3.1	0.0	-5.6	0.0
109.5	-4.2	0.0	-0.6	0.3	-4.9	0.0
15.2	-0.9	0.4	-2.1	0.1	-3.0	0.0
34.3	-3.1	0.0	-2.2	0.0	-5.3	0.0
17.8	-1.8	0.1	-0.7	0.6	-2.5	0.0
6.2	-3.3	0.0	-1.3	0.0	-4.6	0.0
25.9	-1.0	0.2	-1.9	0.0	-2.9	0.0
10.4	1.2	0.1	-2.3	0.0	-1.1	0.1
8.2	-2.0	0.0	-1.6	0.1	-3.6	0.0
3.2	-2.8	0.0	-2.7	0.0	-5.5	0.0
24.4	-3.0	0.0	-0.7	0.4	-3.7	0.0
43.1	-0.9	0.1	-1.4	0.0	-2.3	0.0
432.8	-1.7	0.0	-0.8	0.2	-2.5	0.0
81.1	-1.9	0.0	-1.3	0.0	-3.2	0.0
989.7	-1.8	0.0	-0.2	0.8	-2.0	0.0
140.1	-0.6	0.3	-0.3	0.6	-1.0	0.1
39.2	-0.8	0.3	-0.9	0.3	-1.6	0.0
130.0	1.5	0.0	0.1	0.9	1.6	0.0
201.1	0.8	0.1	-1.4	0.0	-0.6	0.2
110.8	1.9	0.0	-2.0	0.0	-0.2	0.8
31.5	-0.7	0.4	-1.8	0.0	-2.5	0.0
10.6	-1.3	0.0	-1.9	0.0	-3.3	0.0
16.8	0.3	0.7	-1.5	0.0	-1.2	0.0
44.1	-1.9	0.0	2.5	0.0	0.6	0.5
125.5	-0.4	0.7	-0.5	0.7	-0.9	0.3
48.1	-0.8	0.3	-0.9	0.3	-1.7	0.0
65.9	0.8	0.0	0.6	0.1	1.4	0.0
11.9	0.7	0.5	-1.9	0.0	-1.2	0.1
76.1	0.4	0.4	-0.3	0.5	0.0	1.0
84.0	0.6	0.3	-0.1	0.9	0.5	0.4
303.5	1.0	0.1	0.3	0.8	1.3	0.0
39.1	-1.7	0.0	0.3	0.5	-1.4	0.0
15.5	-1.4	0.0	0.1	0.9	-1.3	0.0
403.9	-0.9	0.1	-0.1	0.9	-1.0	0.1
39.2	-2.4	0.0	0.4	0.7	-2.1	0.0
130.5	-1.3	0.1	0.9	0.4	-0.4	0.7
116.8	-0.6	0.5	1.4	0.1	0.8	0.3
191.2	-0.3	0.8	0.9	0.3	0.7	0.4

73.3	-0.5	0.6	-0.7	0.5	-1.2	0.1
76.2	-0.1	0.9	-1.3	0.0	-1.4	0.0
417.4	-0.1	0.9	-1.1	0.1	-1.2	0.1
73.6	0.6	0.4	-1.8	0.0	-1.2	0.1
187.4	1.2	0.2	-0.7	0.5	0.5	0.6
141.2	2.6	0.0	-0.8	0.5	1.8	0.0
59.3	1.1	0.1	-0.1	0.9	1.0	0.1
116.6	0.7	0.0	0.0	1.0	0.7	0.0
5.5	3.5	0.0	-1.0	0.0	2.5	0.0
104.0	-0.2	0.8	-0.5	0.6	-0.6	0.3
26.7	0.0	1.0	-0.1	0.9	-0.2	0.9
26.3	-0.5	0.4	-0.1	0.9	-0.6	0.3
32.0	-0.7	0.0	-0.1	0.8	-0.9	0.0
49.2	-1.1	0.1	0.0	1.0	-1.1	0.1
17.7	0.3	0.7	-1.6	0.1	-1.3	0.1
22.6	0.1	0.8	-1.1	0.0	-1.0	0.0
33.6	-0.3	0.5	-0.3	0.5	-0.6	0.1
84.1	-0.4	0.4	0.1	0.9	-0.3	0.5
54.5	0.0	1.0	-0.6	0.1	-0.6	0.1
64.8	0.4	0.2	0.7	0.1	1.1	0.0
51.4	-0.3	0.5	0.7	0.1	0.5	0.2
3.6	-2.2	0.0	-0.1	0.9	-2.3	0.0
176.7	-1.5	0.0	0.7	0.4	-0.8	0.3
119.1	0.7	0.0	0.4	0.2	1.1	0.0
19.3	0.1	0.9	-1.2	0.1	-1.1	0.1
64.9	0.7	0.1	-0.5	0.3	0.2	0.7
47.1	-2.0	0.0	2.4	0.0	0.5	0.3
69.6	0.0	1.0	0.7	0.3	0.7	0.2
23.0	-1.3	0.0	0.0	1.0	-1.3	0.0
38.5	-2.0	0.0	0.2	0.8	-1.8	0.0
334.7	4.8	0.0	0.5	0.3	5.3	0.0
10.7	-0.1	0.9	-1.7	0.0	-1.7	0.0
16.4	0.3	0.7	-1.8	0.0	-1.5	0.0
54.6	0.3	0.5	0.1	0.9	0.4	0.4
40.1	0.8	0.0	0.3	0.5	1.1	0.0
9.7	-0.7	0.0	-0.3	0.4	-1.0	0.0
7.9	-1.3	0.0	-0.6	0.2	-2.0	0.0
4.4	-1.4	0.0	-0.5	0.3	-1.9	0.0
1.0	0.8	0.1	-0.2	0.7	0.5	0.2
61.1	0.5	0.3	-0.4	0.5	0.1	0.9
36.2	0.7	0.3	-1.4	0.0	-0.7	0.2
210.1	1.9	0.0	-0.5	0.5	1.4	0.0
31.6	-0.6	0.3	-1.1	0.1	-1.7	0.0

0.9	-0.2	0.7	-1.2	0.0	-1.4	0.0
21.1	-0.1	0.9	-1.1	0.3	-1.3	0.2
20.7	0.1	0.8	-0.2	0.7	-0.1	0.9
116.9	-0.3	0.6	-0.3	0.7	-0.7	0.2
129.0	-0.3	0.7	0.0	1.0	-0.3	0.6
40.1	0.3	0.6	-0.5	0.3	-0.3	0.5
39.7	-0.1	0.9	-0.6	0.2	-0.6	0.1
19.6	0.1	0.9	0.2	0.7	0.3	0.5
102.3	0.7	0.1	0.8	0.1	1.5	0.0
5.9	-1.4	0.0	0.5	0.5	-1.0	0.0
25.0	0.1	0.9	-0.9	0.3	-0.8	0.3
34.3	-0.4	0.5	0.0	1.0	-0.4	0.5
148.7	-1.6	0.0	0.3	0.8	-1.4	0.0
70.5	-1.9	0.0	0.6	0.5	-1.3	0.0
650.9	-1.2	0.1	-0.2	0.8	-1.4	0.0
826.1	-0.2	0.8	-0.5	0.5	-0.6	0.2
83.2	-0.7	0.2	-0.2	0.8	-1.0	0.1
8.4	-0.8	0.1	-1.1	0.1	-1.9	0.0
215.7	-0.1	0.9	0.5	0.6	0.4	0.6
16.8	-1.0	0.0	-0.1	0.8	-1.1	0.0
70.3	-1.5	0.2	0.2	0.9	-1.3	0.3
223.3	-0.9	0.4	-0.5	0.7	-1.4	0.1
150.6	-0.8	0.1	0.5	0.3	-0.3	0.6
31.2	-1.7	0.0	1.2	0.0	-0.5	0.2
97.6	-1.3	0.1	-0.9	0.4	-2.2	0.0
109.7	7.7	0.0	-2.2	0.0	5.5	0.0
107.9	8.0	0.0	-1.5	0.0	6.5	0.0
26.3	-1.6	0.0	0.8	0.0	-0.8	0.0
3180.1	-1.4	0.0	1.3	0.0	0.0	1.0
18.9	-0.8	0.1	-0.9	0.1	-1.7	0.0
42.7	1.2	0.0	-0.1	0.9	1.1	0.0
49.1	1.0	0.4	1.1	0.4	2.1	0.0
10.4	-1.1	0.0	0.7	0.2	-0.4	0.5
39.4	1.1	0.3	1.6	0.1	2.7	0.0
520.1	1.0	0.1	0.0	1.0	1.0	0.1
86.8	0.1	0.9	-0.1	0.8	-0.1	0.9
27.5	0.3	0.6	-0.3	0.5	-0.1	0.9
9.4	1.6	0.0	-1.2	0.0	0.4	0.5
3.2	1.8	0.0	-1.2	0.0	0.6	0.2
4.6	-0.9	0.0	1.8	0.0	0.9	0.0
4.3	-1.3	0.0	2.1	0.0	0.8	0.0
89.5	-2.1	0.0	2.5	0.0	0.4	0.7
74.3	-1.2	0.0	0.4	0.6	-0.8	0.1

27.1	-0.6	0.5	-0.4	0.7	-1.0	0.2
101.7	1.4	0.1	-1.4	0.1	0.0	1.0
64.5	0.1	0.9	0.1	0.9	0.3	0.7
110.3	0.0	1.0	-0.1	0.9	-0.1	0.9
360.4	-1.3	0.0	-0.4	0.6	-1.7	0.0
21.5	1.8	0.0	-1.0	0.1	0.8	0.1
60.5	-0.4	0.4	-0.3	0.5	-0.7	0.1
29.2	-0.7	0.5	-0.5	0.7	-1.3	0.2
5.8	-3.0	0.0	-0.2	0.8	-3.2	0.0
80.0	1.9	0.0	0.0	1.0	1.9	0.0
67.6	0.3	0.6	0.6	0.3	1.0	0.0
16.0	0.0	1.0	0.7	0.1	0.7	0.0
43.9	0.1	0.8	-0.9	0.0	-0.8	0.0
115.1	0.9	0.4	0.7	0.5	1.7	0.1
9.0	1.1	0.1	-0.7	0.3	0.4	0.5
4.4	-0.6	0.4	-1.2	0.1	-1.8	0.0
11.0	-0.3	0.7	-0.6	0.5	-0.9	0.2
2.0	-0.4	0.7	-1.3	0.2	-1.8	0.1
1.2	-0.8	0.3	-1.1	0.2	-1.8	0.0
0.9	-1.3	0.1	-0.8	0.4	-2.1	0.0
40.5	-0.9	0.5	2.8	0.0	1.9	0.1
37.8	0.4	0.7	2.1	0.1	2.6	0.0
28.5	1.1	0.0	0.3	0.7	1.4	0.0
11.2	0.4	0.7	-0.2	0.9	0.1	0.9
21.1	0.1	0.9	1.0	0.3	1.1	0.2
25.4	-0.5	0.7	2.6	0.0	2.0	0.1
43.7	-0.2	0.8	2.8	0.0	2.6	0.0
34.9	0.6	0.6	0.2	0.8	0.8	0.4
20.5	0.0	1.0	0.3	0.7	0.3	0.7
10.3	-0.4	0.7	-0.5	0.6	-0.9	0.2
8.9	0.7	0.4	0.4	0.7	1.0	0.2
101.9	-1.6	0.0	1.0	0.3	-0.6	0.5
4.4	0.5	0.7	0.3	0.9	0.7	0.5
12.0	-0.4	0.7	2.7	0.0	2.3	0.0
57.7	0.4	0.7	-2.1	0.0	-1.7	0.0
89.2	0.1	0.8	-0.9	0.1	-0.7	0.1
130.8	-0.9	0.1	-0.1	0.8	-1.0	0.0
63.4	-0.4	0.7	-1.0	0.4	-1.4	0.1
7.9	-1.3	0.0	-0.3	0.8	-1.6	0.0
22.4	2.0	0.0	-2.1	0.0	-0.2	0.9
8.2	-1.5	0.1	0.4	0.8	-1.2	0.2
1.5	-1.4	0.0	0.1	0.9	-1.2	0.1
1.0	-1.0	0.1	-0.7	0.3	-1.7	0.0

16.9	-1.3	0.1	1.6	0.1	0.3	0.7
10.4	-1.3	0.1	0.8	0.3	-0.5	0.5
6.3	-0.7	0.2	0.3	0.7	-0.4	0.5
5.7	-2.4	0.0	1.1	0.0	-1.3	0.0
2.9	0.3	0.8	-0.1	0.9	0.2	0.9
6.9	-2.3	0.0	-0.7	0.6	-3.0	0.0
13.1	-1.1	0.2	0.2	0.8	-0.8	0.3
8.5	-1.4	0.1	0.2	0.8	-1.2	0.1
26.4	0.1	1.0	-0.5	0.7	-0.4	0.7
13.2	-0.1	0.9	2.5	0.0	2.4	0.0
2.9	0.2	0.9	1.4	0.2	1.7	0.1
32.2	-0.6	0.4	0.4	0.6	-0.2	0.8
11.5	2.4	0.0	0.4	0.6	2.8	0.0
2167.3	0.8	0.5	4.6	0.0	5.4	0.0
1271.7	-0.6	0.6	4.5	0.0	4.0	0.0
136.5	-0.7	0.4	2.7	0.0	1.9	0.0
10.4	-5.9	0.0	0.2	0.9	-5.7	0.0
43.7	1.2	0.2	2.0	0.0	3.2	0.0
40.7	3.1	0.0	-0.4	0.5	2.6	0.0
949.3	5.5	0.0	-0.3	0.8	5.2	0.0
1040.0	3.8	0.0	-0.5	0.4	3.3	0.0
60.0	-0.9	0.1	0.7	0.3	-0.2	0.7
3.6	-1.0	0.0	-0.3	0.7	-1.3	0.0
7.9	-0.7	0.1	-0.1	0.8	-0.9	0.0
32.1	-0.8	0.5	-0.2	0.9	-1.0	0.3
11.3	-0.8	0.0	0.6	0.2	-0.2	0.6
53.8	-0.9	0.1	1.1	0.1	0.2	0.8
650.7	-1.3	0.0	-0.6	0.5	-1.9	0.0
73.4	-0.2	0.6	-0.3	0.6	-0.5	0.2
220.5	1.9	0.0	0.5	0.6	2.4	0.0
12.3	-0.8	0.5	-3.4	0.0	-4.1	0.0
30.7	0.3	0.5	-1.0	0.0	-0.7	0.1
74.4	1.1	0.0	-0.4	0.3	0.7	0.0
23.2	0.3	0.6	-0.8	0.2	-0.5	0.4
17.2	-0.7	0.0	0.1	0.8	-0.6	0.1
57.8	-1.2	0.1	-0.2	0.9	-1.4	0.0
20.9	0.6	0.2	-0.2	0.7	0.4	0.4
91.5	1.3	0.0	-0.3	0.7	1.1	0.0
116.6	1.3	0.0	-0.4	0.5	0.9	0.0
331.8	0.6	0.4	0.1	0.9	0.7	0.2
74.2	-0.5	0.2	0.4	0.5	-0.2	0.8
74.2	1.8	0.0	-0.5	0.5	1.3	0.0
49.8	1.8	0.0	-0.5	0.4	1.3	0.0

561.4	1.9	0.0	0.2	0.8	2.1	0.0
889.9	1.8	0.0	-0.1	0.9	1.8	0.0
5.7	0.2	0.7	-2.5	0.0	-2.2	0.0
11.2	-0.7	0.5	0.7	0.6	0.0	1.0
30.9	-1.7	0.0	-0.6	0.6	-2.3	0.0
85.3	-1.0	0.0	0.6	0.3	-0.4	0.4
10.3	-1.5	0.1	1.1	0.3	-0.5	0.6
96.0	3.1	0.0	-2.5	0.0	0.6	0.4
20.1	-1.2	0.0	-0.5	0.3	-1.7	0.0
15.0	-1.5	0.0	-0.2	0.8	-1.6	0.0
19.2	-1.2	0.0	0.3	0.7	-0.9	0.0
343.4	-0.5	0.5	0.2	0.8	-0.3	0.7
39.9	-0.8	0.5	0.6	0.7	-0.2	0.9
53.8	-0.1	0.9	-0.3	0.6	-0.5	0.4
58.2	-0.7	0.1	0.8	0.1	0.1	0.8
30.7	-0.4	0.6	-1.3	0.1	-1.7	0.0
40.4	-0.2	0.6	-0.3	0.5	-0.5	0.1
49.5	-1.4	0.0	0.5	0.3	-0.9	0.0
2.5	0.4	0.4	0.5	0.4	0.9	0.0
25.0	4.6	0.0	-3.2	0.0	1.4	0.1
986.8	2.7	0.0	0.4	0.7	3.1	0.0
13.3	0.5	0.1	-0.3	0.5	0.3	0.4
7.0	0.0	0.9	0.0	0.9	-0.1	0.8
123.0	0.2	0.8	-2.9	0.0	-2.7	0.0
23.5	-1.7	0.0	-0.4	0.4	-2.1	0.0
31.5	-1.5	0.0	-0.4	0.3	-1.9	0.0
25.0	-1.7	0.0	0.1	0.8	-1.6	0.0
291.5	1.6	0.0	-0.3	0.7	1.3	0.0
498.4	0.2	0.7	-0.2	0.8	0.0	0.9
128.9	-1.2	0.0	0.2	0.8	-1.0	0.0
7.7	-1.0	0.0	0.0	1.0	-1.1	0.0
5.6	0.5	0.6	0.1	1.0	0.6	0.5
12.1	-0.5	0.5	-1.6	0.0	-2.1	0.0
11.4	-0.6	0.4	-2.0	0.0	-2.6	0.0
118.2	2.3	0.0	-1.0	0.1	1.3	0.0
50.7	-1.3	0.0	-0.2	0.8	-1.5	0.0
21.9	-0.4	0.6	0.7	0.4	0.3	0.7
17.6	-0.9	0.4	-0.1	0.9	-1.0	0.3
36.0	-0.6	0.1	0.1	0.9	-0.6	0.2
92.0	4.7	0.0	-1.6	0.0	3.1	0.0
174.9	4.2	0.0	-0.7	0.2	3.4	0.0
204.2	2.3	0.0	-0.3	0.7	2.0	0.0
5.8	-0.9	0.0	-1.9	0.0	-2.9	0.0

27.9	0.4	0.4	-0.5	0.4	-0.1	0.9
85.8	-0.8	0.2	1.4	0.0	0.6	0.3
19.4	-0.8	0.1	0.6	0.2	-0.2	0.7
6.4	-0.9	0.3	-1.1	0.3	-2.0	0.0
16.9	-2.1	0.1	0.2	0.9	-1.9	0.1
1.2	-2.3	0.0	-2.2	0.0	-4.5	0.0
1.8	-2.5	0.0	-2.2	0.0	-4.7	0.0
5.5	-1.7	0.0	-0.8	0.4	-2.5	0.0
9.4	-1.0	0.1	-0.5	0.6	-1.5	0.0
1.5	-0.8	0.2	-1.8	0.0	-2.6	0.0
20.7	-1.6	0.0	-0.1	0.9	-1.7	0.0
10.1	-2.5	0.0	-0.3	0.7	-2.7	0.0
24.0	-0.2	0.9	-1.3	0.2	-1.5	0.1
35.3	0.4	0.7	-1.2	0.2	-0.7	0.4
6.9	1.2	0.2	-1.5	0.1	-0.2	0.8
82.5	0.4	0.7	-1.4	0.3	-0.9	0.4
12.1	2.4	0.0	-0.6	0.4	1.9	0.0
55.7	0.9	0.5	1.4	0.3	2.3	0.0
56.6	0.4	0.8	-1.0	0.4	-0.7	0.5
14.7	-1.3	0.0	1.3	0.0	-0.1	0.9
2.5	3.6	0.0	-4.1	0.0	-0.5	0.6
24.7	2.4	0.0	-1.8	0.0	0.6	0.5
74.0	-0.7	0.3	-1.7	0.0	-2.4	0.0
23.7	-0.7	0.0	-0.2	0.7	-0.9	0.0
7.6	-1.5	0.0	-1.3	0.0	-2.8	0.0
14.1	-0.7	0.0	0.0	1.0	-0.7	0.0
18.3	-0.9	0.0	0.5	0.2	-0.4	0.2
208.3	1.6	0.0	-0.9	0.1	0.7	0.1
125.2	1.3	0.0	-0.8	0.1	0.4	0.3
12.7	-0.2	0.8	0.2	0.8	0.0	1.0
5.0	-1.3	0.0	-0.8	0.2	-2.1	0.0
23.9	-1.6	0.0	0.0	1.0	-1.6	0.0
19.3	-0.7	0.2	-0.6	0.4	-1.3	0.0
22.9	-0.6	0.6	-0.3	0.8	-0.9	0.3
21.6	-1.3	0.0	0.8	0.0	-0.4	0.3
20.4	0.2	0.8	0.2	0.8	0.3	0.5
37.3	-1.9	0.0	-1.2	0.3	-3.1	0.0
318.2	3.0	0.0	0.3	0.8	3.2	0.0
45.9	-0.7	0.2	-0.3	0.7	-1.0	0.1
199.5	-0.2	0.8	-0.3	0.7	-0.5	0.4
206.4	-2.1	0.0	-0.5	0.6	-2.6	0.0
66.4	-1.3	0.0	-1.9	0.0	-3.3	0.0
53.4	-1.0	0.1	-1.3	0.1	-2.3	0.0

58.3	0.0	1.0	-0.3	0.7	-0.3	0.6
26.3	-0.1	0.9	-0.5	0.7	-0.5	0.6
12.7	0.0	1.0	-0.3	0.7	-0.2	0.6
6.5	-0.1	0.9	2.5	0.0	2.4	0.0
29.7	1.3	0.0	0.0	1.0	1.2	0.0
39.2	1.1	0.0	-0.2	0.8	0.9	0.0
84.9	-0.1	0.8	0.0	1.0	-0.2	0.8
26.8	0.6	0.3	-0.8	0.2	-0.2	0.7
60.3	-1.5	0.0	0.7	0.4	-0.7	0.3
51.5	-1.0	0.0	-0.1	0.8	-1.1	0.0
288.1	0.6	0.4	0.6	0.4	1.2	0.0
1159.9	0.7	0.3	-0.5	0.5	0.2	0.7
121.2	-0.1	0.9	-1.4	0.0	-1.5	0.0
60.9	0.4	0.5	-0.3	0.7	0.1	0.8
34.0	1.1	0.0	0.1	0.9	1.2	0.0
56.7	-1.0	0.2	-0.1	1.0	-1.0	0.2
10.0	-1.7	0.0	-1.0	0.3	-2.7	0.0
8.3	0.0	1.0	-0.6	0.1	-0.6	0.1
9.7	-0.5	0.3	-1.1	0.0	-1.6	0.0
17.9	-0.2	0.7	-0.7	0.1	-0.9	0.0
11.8	-0.1	0.9	-1.5	0.0	-1.6	0.0
13.4	-0.5	0.2	-1.2	0.0	-1.6	0.0
1.7	-0.2	0.7	-1.7	0.0	-1.8	0.0
17.0	0.9	0.3	-0.7	0.5	0.2	0.8
7.9	0.2	0.8	0.2	0.7	0.4	0.4
10.2	-0.1	0.9	-1.6	0.0	-1.7	0.0
50.9	0.0	1.0	-0.6	0.1	-0.6	0.1
19.7	-0.5	0.6	-0.7	0.5	-1.2	0.1
10.5	-0.8	0.3	-1.7	0.0	-2.5	0.0
17.0	-1.7	0.0	-1.0	0.1	-2.7	0.0
291.6	0.8	0.4	-1.6	0.1	-0.8	0.3
27.9	-0.1	0.8	-0.7	0.2	-0.8	0.1
83.6	-0.4	0.6	-1.2	0.1	-1.6	0.0
33.2	-0.3	0.6	-0.7	0.2	-1.0	0.0
117.0	-0.6	0.5	0.1	1.0	-0.5	0.5
237.9	-1.1	0.1	-1.5	0.0	-2.6	0.0
133.9	-1.6	0.0	-1.4	0.0	-3.0	0.0
9.3	-1.3	0.0	0.2	0.8	-1.1	0.0
58.5	-1.5	0.0	-0.2	0.8	-1.7	0.0
110.9	2.0	0.0	-1.1	0.2	0.9	0.2
30.9	1.0	0.0	-0.5	0.3	0.5	0.3
10.3	-1.9	0.0	-1.0	0.1	-2.9	0.0
6.1	-2.3	0.0	-0.6	0.2	-3.0	0.0

21.2	-0.7	0.2	-0.3	0.7	-1.0	0.0
38.0	-0.5	0.1	0.3	0.4	-0.2	0.6
99.4	-0.3	0.7	0.2	0.8	-0.1	0.9
131.8	0.2	0.8	0.0	1.0	0.2	0.8
131.8	-0.4	0.2	-0.3	0.5	-0.7	0.0
50.5	-0.3	0.7	-0.3	0.7	-0.5	0.3
37.7	-0.4	0.2	0.2	0.6	-0.2	0.5
38.3	-1.5	0.0	0.5	0.3	-0.9	0.0
14.5	-0.6	0.3	0.0	1.0	-0.6	0.3
22.4	-0.4	0.4	-0.2	0.8	-0.6	0.2
33.9	0.6	0.1	-0.3	0.6	0.3	0.4
172.2	0.7	0.4	-0.9	0.3	-0.2	0.7
166.9	-0.3	0.7	0.0	1.0	-0.3	0.7
17.1	-0.3	0.8	-0.5	0.7	-0.8	0.4
0.8	-0.1	0.8	0.1	0.9	0.0	1.0
6.8	-0.1	0.9	-0.8	0.2	-0.8	0.1
34.3	-2.2	0.0	1.9	0.0	-0.3	0.7
107.5	-0.8	0.2	1.7	0.0	0.9	0.1
163.2	-0.6	0.3	1.5	0.0	0.9	0.1
10.2	-1.5	0.0	0.4	0.3	-1.0	0.0
46.1	0.6	0.5	-0.8	0.4	-0.2	0.8
1525.2	0.2	0.9	-0.2	0.9	-0.1	0.9
441.0	0.7	0.3	-0.6	0.5	0.2	0.8
171.2	0.9	0.0	0.1	0.9	1.0	0.0
348.7	0.0	1.0	-0.3	0.7	-0.3	0.6
50.0	1.0	0.1	0.1	1.0	1.0	0.0
34.5	-0.2	0.7	-0.1	0.9	-0.3	0.5
75.7	1.8	0.0	-1.4	0.1	0.5	0.5
126.8	-1.0	0.1	-0.6	0.4	-1.5	0.0
19.2	-0.7	0.3	0.6	0.5	-0.1	0.9
31.9	4.3	0.0	-2.2	0.1	2.1	0.1
24.3	0.8	0.1	0.4	0.5	1.2	0.0
186.1	1.1	0.0	-0.8	0.1	0.3	0.5
37.6	1.0	0.0	-0.7	0.2	0.3	0.6
9.9	-0.9	0.1	-0.7	0.3	-1.6	0.0
10.9	-0.3	0.6	-0.9	0.2	-1.2	0.0
3.4	-0.7	0.1	-0.1	0.8	-0.8	0.0
13.4	-1.0	0.0	1.0	0.0	0.0	0.9
78.6	0.0	1.0	1.0	0.3	1.0	0.2
34.6	-0.5	0.7	0.8	0.5	0.3	0.8
17.8	-0.8	0.6	-1.5	0.3	-2.3	0.0
24.4	-0.5	0.3	-0.4	0.5	-0.8	0.0
9.1	0.5	0.5	-0.7	0.3	-0.3	0.7

909.6	-0.4	0.6	-0.6	0.5	-1.0	0.1
3.8	-0.7	0.2	-0.3	0.6	-1.0	0.0
22.8	-3.2	0.0	1.0	0.0	-2.1	0.0
72.9	-0.7	0.2	0.5	0.5	-0.3	0.6
27.4	-1.3	0.0	-0.5	0.5	-1.8	0.0
18.6	-1.5	0.0	-1.0	0.0	-2.6	0.0
38.2	0.8	0.1	-1.1	0.0	-0.3	0.5
159.3	-2.2	0.0	0.2	0.8	-2.0	0.0
30.7	3.1	0.0	-2.2	0.0	0.9	0.2
17.5	1.9	0.0	-2.3	0.0	-0.5	0.4
349.8	0.7	0.3	0.6	0.4	1.3	0.0
192.1	0.9	0.1	0.5	0.4	1.4	0.0
47.8	-2.6	0.0	2.9	0.0	0.4	0.7
90.9	-1.5	0.0	0.1	0.9	-1.4	0.0
44.0	-1.7	0.0	0.7	0.5	-1.0	0.2
39.5	-2.0	0.0	1.0	0.2	-1.0	0.1
57.0	-0.9	0.0	1.2	0.0	0.3	0.5
81.9	-0.4	0.3	-0.1	0.8	-0.5	0.2
45.3	-0.7	0.1	-0.6	0.2	-1.2	0.0
60.1	0.1	0.8	-0.9	0.2	-0.7	0.2
22.1	-0.6	0.3	1.1	0.1	0.5	0.4
14.6	-0.1	0.9	0.0	1.0	-0.1	0.9
66.6	-0.8	0.5	2.7	0.0	1.9	0.1
8.8	-0.3	0.8	0.8	0.5	0.5	0.6
5.6	-0.5	0.6	0.4	0.7	-0.1	1.0
15.5	-0.2	0.8	-0.8	0.1	-0.9	0.0
30.6	-1.1	0.0	0.3	0.6	-0.8	0.1
83.0	-2.4	0.0	1.0	0.0	-1.5	0.0
10.5	-1.3	0.2	-0.9	0.4	-2.2	0.0
16.6	1.5	0.0	0.3	0.7	1.8	0.0
30.1	1.3	0.1	-1.4	0.1	-0.1	0.9
20.8	2.2	0.0	-3.4	0.0	-1.2	0.1
5.6	3.2	0.0	-3.9	0.0	-0.7	0.5
31.2	4.2	0.0	-2.8	0.0	1.3	0.2
7.0	-1.5	0.0	-1.5	0.1	-2.9	0.0
5.2	-0.7	0.2	-1.1	0.1	-1.8	0.0
19.8	2.0	0.0	-0.9	0.1	1.1	0.0
333.4	-0.4	0.6	-2.0	0.0	-2.4	0.0
399.9	-0.4	0.5	-1.9	0.0	-2.4	0.0
520.2	-0.7	0.3	-1.6	0.0	-2.3	0.0
25.4	-0.5	0.4	-1.4	0.0	-2.0	0.0
7.9	-0.7	0.3	-0.9	0.2	-1.6	0.0
68.1	-0.5	0.4	0.1	0.9	-0.4	0.5

18.4	-1.4	0.0	-0.5	0.5	-1.9	0.0
27.8	-0.6	0.6	-3.1	0.0	-3.7	0.0
27.8	-1.1	0.0	-0.4	0.5	-1.6	0.0
15.5	-0.3	0.8	-0.2	0.8	-0.5	0.6
212.9	-1.2	0.1	0.2	0.9	-1.0	0.1
374.4	-1.1	0.0	0.6	0.2	-0.5	0.2
128.8	-1.0	0.1	0.2	0.8	-0.8	0.1
129.4	-0.9	0.1	-0.5	0.4	-1.4	0.0
278.7	-0.2	0.8	-0.2	0.8	-0.3	0.5
13.7	0.0	1.0	-0.6	0.2	-0.7	0.2
42.5	-0.8	0.0	0.1	0.8	-0.7	0.0
108.3	-0.6	0.0	0.4	0.2	-0.2	0.6
13.4	0.3	0.6	-0.6	0.4	-0.2	0.7
61.4	-0.5	0.2	-0.2	0.8	-0.7	0.1
77.8	0.7	0.1	0.1	0.8	0.8	0.0
117.5	-0.2	0.9	-0.3	0.8	-0.4	0.6
17.6	-0.5	0.6	1.7	0.0	1.2	0.1
6.9	-0.4	0.3	0.6	0.2	0.2	0.6
2.8	-5.2	0.0	-1.2	0.2	-6.3	0.0
19.9	-4.4	0.0	-0.9	0.5	-5.3	0.0
26.0	-4.0	0.0	-0.6	0.7	-4.6	0.0
33.3	-3.5	0.0	-0.8	0.4	-4.3	0.0
82.7	0.4	0.5	0.2	0.7	0.6	0.2
24.9	0.2	0.8	1.0	0.0	1.2	0.0
74.8	-0.4	0.5	-0.3	0.6	-0.7	0.1
25.1	0.8	0.0	0.0	0.9	0.7	0.0
186.5	2.2	0.0	-0.3	0.7	1.9	0.0
47.1	0.3	0.6	-0.4	0.5	-0.1	0.9
17.9	0.5	0.4	-0.9	0.2	-0.4	0.5
56.6	-0.6	0.2	0.0	1.0	-0.6	0.2
19.0	0.2	0.8	-1.1	0.0	-1.0	0.1
38.5	-0.5	0.4	-0.3	0.7	-0.9	0.1
209.0	-2.7	0.0	0.8	0.4	-2.0	0.0
101.2	-1.7	0.0	1.2	0.0	-0.5	0.3
11.1	-0.7	0.1	0.1	0.9	-0.6	0.2
132.3	1.2	0.0	-0.1	0.9	1.2	0.0
97.4	-2.8	0.0	-1.2	0.2	-4.0	0.0
42.3	-0.9	0.4	-2.0	0.0	-2.9	0.0
525.9	1.7	0.0	-0.3	0.8	1.4	0.0
34.9	1.6	0.0	-0.9	0.0	0.8	0.0
29.6	-0.6	0.3	-0.9	0.1	-1.5	0.0
28.5	1.8	0.0	-0.6	0.5	1.2	0.1
41.1	1.0	0.2	-1.0	0.2	0.0	1.0

65.1	0.4	0.7	-0.2	0.9	0.2	0.8
104.1	1.3	0.2	0.3	0.8	1.6	0.1
218.8	1.6	0.0	0.4	0.6	2.0	0.0
30.9	2.1	0.0	-0.3	0.7	1.8	0.0
3.5	1.4	0.0	-0.1	0.9	1.3	0.0
16.0	1.9	0.1	-0.5	0.7	1.4	0.1
15.3	0.3	0.7	0.0	1.0	0.3	0.7
6.2	-0.2	0.8	-1.2	0.0	-1.3	0.0
73.0	-0.2	0.8	0.2	0.8	0.0	1.0
74.6	0.3	0.4	0.2	0.7	0.5	0.2
30.7	0.8	0.1	0.2	0.8	1.0	0.0
328.5	4.6	0.0	-0.1	1.0	4.4	0.0
318.7	6.9	0.0	-1.0	0.5	5.9	0.0
3.2	1.0	0.0	-1.0	0.1	0.0	1.0
37.7	-3.1	0.0	2.8	0.0	-0.3	0.7
107.1	4.0	0.0	0.9	0.5	4.9	0.0
35.0	3.7	0.0	1.5	0.1	5.2	0.0
205.2	5.1	0.0	-1.0	0.3	4.1	0.0
55.0	-1.8	0.0	0.2	0.8	-1.6	0.0
46.3	-2.4	0.0	-0.5	0.6	-2.9	0.0
31.2	-2.4	0.0	-1.2	0.3	-3.5	0.0
58.5	-1.8	0.0	0.8	0.3	-1.0	0.1
1.6	-0.5	0.5	-1.5	0.0	-2.0	0.0
2.6	0.3	0.7	-1.8	0.0	-1.5	0.0
57.2	0.8	0.1	-1.1	0.1	-0.3	0.6
19.6	-0.7	0.5	-0.4	0.8	-1.1	0.2
7.9	-2.0	0.0	-0.2	0.8	-2.1	0.0
6.8	-1.7	0.0	-1.3	0.2	-3.1	0.0
47.7	0.8	0.3	-0.9	0.3	-0.2	0.8
292.2	-1.8	0.0	-0.8	0.3	-2.5	0.0
2.2	-0.8	0.1	-0.9	0.1	-1.6	0.0
587.9	0.6	0.3	0.2	0.7	0.8	0.1
16.3	-1.1	0.0	-0.3	0.7	-1.4	0.0
74.4	2.3	0.0	-0.6	0.5	1.7	0.0
24.8	-0.9	0.0	-0.3	0.6	-1.1	0.0
11.2	-0.3	0.5	-0.2	0.8	-0.5	0.3
169.5	-0.5	0.3	0.0	1.0	-0.5	0.3
20.7	4.7	0.0	-1.7	0.0	3.0	0.0
81.5	4.8	0.0	-1.1	0.1	3.7	0.0
74.8	5.7	0.0	-1.7	0.0	4.0	0.0
133.9	6.9	0.0	-0.4	0.8	6.5	0.0
13.1	3.8	0.0	0.3	0.8	4.2	0.0
73.4	3.7	0.0	1.1	0.0	4.7	0.0

153.5	-0.6	0.3	-1.5	0.0	-2.1	0.0
146.0	-0.4	0.6	-2.2	0.0	-2.6	0.0
1762.7	-0.2	0.8	-1.2	0.2	-1.4	0.1
977.3	-0.2	0.8	-0.9	0.3	-1.1	0.1
157.5	-1.1	0.1	-1.7	0.0	-2.8	0.0
110.8	-1.2	0.1	-1.3	0.1	-2.5	0.0
326.7	0.3	0.6	-0.6	0.3	-0.3	0.6
187.4	0.3	0.6	-0.4	0.5	-0.1	0.8
272.3	-1.9	0.0	-0.9	0.0	-2.8	0.0
68.0	-1.4	0.0	1.6	0.0	0.1	0.8
27.9	-0.9	0.0	0.2	0.7	-0.6	0.1
34.3	-0.9	0.0	0.1	0.8	-0.8	0.0
8.6	-2.3	0.0	0.9	0.3	-1.5	0.0
114.3	-1.2	0.0	0.5	0.3	-0.6	0.2
366.5	-1.6	0.0	1.3	0.0	-0.3	0.5
18.0	-0.9	0.4	-0.2	0.9	-1.0	0.3
67.9	-1.7	0.1	2.1	0.0	0.4	0.7
13.9	-2.9	0.0	0.2	0.8	-2.7	0.0
6.3	2.2	0.0	-0.8	0.1	1.4	0.0
22.6	0.3	0.6	-0.4	0.5	-0.1	0.8
24.5	-1.0	0.0	-0.1	0.8	-1.1	0.0
26.2	-1.8	0.0	0.4	0.6	-1.3	0.0
23.6	1.2	0.3	-0.5	0.7	0.6	0.6
44.0	0.4	0.8	-0.6	0.7	-0.2	0.8
73.1	-1.0	0.1	-0.5	0.5	-1.5	0.0
6.3	0.8	0.1	-0.6	0.2	0.2	0.6
6.0	1.0	0.0	-0.8	0.0	0.2	0.7
57.7	0.2	0.7	0.5	0.3	0.7	0.1
26.1	-0.4	0.5	-1.2	0.0	-1.5	0.0
33.7	-0.9	0.0	0.2	0.7	-0.7	0.1
26.8	-1.7	0.0	0.1	0.9	-1.6	0.0
298.7	2.1	0.0	-0.9	0.1	1.2	0.0
19.3	0.5	0.3	-0.7	0.2	-0.2	0.7
34.0	-0.3	0.7	-0.7	0.4	-1.0	0.1
39.3	-0.7	0.0	-0.3	0.6	-1.0	0.0
127.6	0.3	0.7	0.3	0.7	0.6	0.3
39.1	-0.2	0.8	-0.2	0.8	-0.4	0.5
6.3	-0.5	0.3	-0.1	0.9	-0.5	0.2
14.2	-0.2	0.8	-1.4	0.1	-1.6	0.0
484.9	0.5	0.5	0.0	1.0	0.4	0.5
96.8	-1.8	0.0	1.2	0.2	-0.6	0.5
20.8	-1.1	0.0	-0.2	0.7	-1.4	0.0
307.7	0.3	0.6	0.2	0.8	0.6	0.3

15.3	-1.3	0.0	-0.1	0.9	-1.4	0.0
26.9	-1.3	0.0	0.1	0.8	-1.2	0.0
27.6	-0.7	0.6	-0.2	0.9	-0.9	0.4
30.2	-0.6	0.3	0.2	0.8	-0.4	0.5
40.2	-0.9	0.1	0.7	0.2	-0.2	0.7
2.8	0.3	0.6	-0.4	0.5	-0.1	0.8
20.5	0.7	0.1	-0.1	0.8	0.6	0.2
141.2	-0.2	0.9	1.2	0.3	1.0	0.3
24.7	-0.2	0.8	-0.5	0.6	-0.7	0.3
110.7	-0.3	0.7	-0.1	0.9	-0.4	0.5
63.4	1.0	0.1	-0.4	0.5	0.5	0.3
37.9	0.4	0.7	-0.4	0.8	0.0	1.0
15.1	0.4	0.5	-0.5	0.4	-0.1	0.8
196.1	1.2	0.1	0.2	0.8	1.4	0.0
14.4	-0.2	0.8	-1.4	0.0	-1.6	0.0
36.8	0.5	0.4	-1.0	0.1	-0.4	0.4
72.7	-1.3	0.1	-1.1	0.2	-2.3	0.0
27.3	0.3	0.6	-0.1	0.8	0.2	0.7
18.3	-0.8	0.1	-0.3	0.7	-1.1	0.0
6.7	-0.4	0.4	-0.1	0.9	-0.5	0.3
56.4	-5.9	0.0	1.6	0.0	-4.3	0.0
10.6	-1.7	0.0	0.3	0.5	-1.3	0.0
10.8	-2.0	0.0	0.0	1.0	-2.0	0.0
35.9	-1.5	0.0	0.3	0.5	-1.3	0.0
55.5	-0.8	0.4	-0.1	0.9	-0.9	0.3
26.4	-1.3	0.0	-0.8	0.2	-2.0	0.0
6.4	-1.3	0.0	-2.0	0.0	-3.2	0.0
33.9	-1.1	0.0	-1.7	0.0	-2.8	0.0
23.2	-1.6	0.1	0.3	0.8	-1.3	0.1
34.2	0.5	0.4	1.1	0.1	1.6	0.0
8.9	2.1	0.0	-1.2	0.2	0.9	0.3
24.7	1.7	0.2	-0.4	0.8	1.2	0.3
4.3	1.5	0.1	-0.2	0.8	1.3	0.1
59.4	1.8	0.0	-1.1	0.2	0.7	0.3
5.5	-3.0	0.0	2.0	0.0	-1.0	0.0
19.4	-3.6	0.0	2.4	0.0	-1.2	0.1
1.4	-4.5	0.0	0.4	0.6	-4.0	0.0
21.2	-1.7	0.0	1.0	0.3	-0.7	0.4
38.3	0.8	0.2	0.5	0.5	1.3	0.0
14.6	-1.6	0.0	1.1	0.0	-0.5	0.2
2.6	0.6	0.6	-1.5	0.2	-0.9	0.4
52.9	0.6	0.5	-0.5	0.6	0.1	0.9
4.0	2.7	0.0	-2.0	0.1	0.7	0.5

4.3	0.6	0.6	-1.9	0.1	-1.4	0.1
5.8	0.5	0.6	-1.7	0.1	-1.2	0.2
8.3	1.0	0.0	-1.1	0.0	-0.1	0.9
11.7	1.0	0.3	-1.7	0.1	-0.7	0.5
17.3	0.6	0.2	-1.6	0.0	-0.9	0.0
10.9	0.8	0.2	-0.6	0.5	0.2	0.7
10.4	0.9	0.1	-0.6	0.3	0.2	0.7
16.1	0.3	0.7	-0.8	0.3	-0.5	0.5
30.7	0.7	0.3	-1.1	0.1	-0.3	0.6
16.8	1.4	0.0	-1.8	0.0	-0.4	0.5
23.7	0.9	0.0	-0.9	0.0	0.0	0.9
13.2	3.7	0.0	-2.7	0.0	1.0	0.1
16.0	3.8	0.0	-2.0	0.0	1.8	0.0
18.1	3.2	0.0	-1.9	0.0	1.3	0.0
80.0	2.9	0.0	-0.1	0.9	2.8	0.0
93.8	-0.5	0.4	0.2	0.7	-0.2	0.7
8.6	-0.4	0.5	-0.2	0.8	-0.6	0.2
26.7	2.5	0.0	-0.7	0.3	1.8	0.0
24.2	0.7	0.1	-0.4	0.4	0.2	0.6
123.2	0.3	0.7	-0.2	0.8	0.0	1.0
77.2	-0.1	0.9	-1.2	0.1	-1.4	0.0
19.0	-1.0	0.0	-0.2	0.8	-1.2	0.0
40.1	-0.3	0.6	0.2	0.8	-0.1	0.9
11.8	-2.4	0.0	0.6	0.6	-1.8	0.0
17.6	-0.8	0.4	0.0	1.0	-0.7	0.4
52.9	-0.9	0.0	1.0	0.0	0.1	0.8
188.4	-0.9	0.2	1.7	0.0	0.9	0.2
14.0	-2.2	0.0	1.2	0.2	-1.0	0.3
18.9	-1.8	0.0	0.8	0.1	-1.0	0.0
47.8	-1.0	0.4	0.0	1.0	-0.9	0.4
10.2	-1.7	0.0	0.3	0.7	-1.4	0.0
2.0	-1.3	0.0	-0.2	0.8	-1.6	0.0
32.5	-1.2	0.0	1.3	0.0	0.2	0.8
33.1	-0.4	0.4	-0.6	0.3	-1.1	0.0
67.3	-0.5	0.2	-1.1	0.0	-1.6	0.0
3.6	-0.7	0.1	-0.6	0.2	-1.3	0.0
1.7	-0.4	0.3	-1.8	0.0	-2.2	0.0
20.7	0.3	0.6	-0.5	0.3	-0.2	0.7
19.5	-0.1	0.9	0.0	1.0	-0.1	0.9
214.4	-0.7	0.2	0.0	1.0	-0.7	0.2
133.9	-0.2	0.9	-0.9	0.4	-1.0	0.2
32.2	-0.1	0.9	-1.0	0.2	-1.1	0.1
24.0	0.5	0.6	-1.1	0.3	-0.6	0.6

545.3	0.2	0.8	0.0	1.0	0.2	0.8
161.6	0.5	0.3	0.2	0.8	0.8	0.1
3.3	-0.5	0.4	-0.5	0.4	-1.0	0.0
37.3	-2.0	0.0	0.7	0.4	-1.3	0.0
3.9	-2.1	0.0	-1.7	0.1	-3.8	0.0
8.4	-2.1	0.0	-1.7	0.1	-3.8	0.0
17.9	-1.8	0.0	-1.2	0.0	-3.1	0.0
5.3	-1.7	0.0	-0.5	0.5	-2.1	0.0
2358.1	-1.0	0.2	0.0	1.0	-1.0	0.2
100.2	0.2	0.8	-0.5	0.5	-0.3	0.6
109.5	-2.6	0.0	-1.1	0.1	-3.8	0.0
57.6	-2.7	0.0	-2.3	0.0	-5.0	0.0
63.5	-2.4	0.0	-2.8	0.0	-5.2	0.0
56.1	-2.5	0.0	-2.6	0.0	-5.1	0.0
57.8	-2.2	0.0	-2.3	0.0	-4.4	0.0
662.0	-2.2	0.0	-0.9	0.1	-3.2	0.0
142.9	-1.7	0.0	-1.5	0.0	-3.3	0.0
276.3	-2.0	0.0	-1.1	0.1	-3.1	0.0
126.7	-1.2	0.0	-1.0	0.1	-2.2	0.0
54.8	-0.1	0.9	-1.1	0.0	-1.2	0.0
11.4	-0.1	0.8	-1.3	0.0	-1.4	0.0
21.8	0.6	0.2	-1.4	0.0	-0.8	0.1
54.0	0.8	0.2	-1.7	0.0	-0.9	0.1
228.9	-0.8	0.5	3.7	0.0	2.9	0.0
72.7	0.6	0.4	0.7	0.4	1.3	0.1
19.4	-0.2	0.9	-0.4	0.8	-0.6	0.6
130.0	-1.1	0.2	1.0	0.3	-0.1	0.9
61.9	-1.9	0.1	3.8	0.0	1.9	0.1
184.3	0.0	1.0	3.4	0.0	3.4	0.0
16.6	2.1	0.0	-3.0	0.0	-1.0	0.3
30.1	1.1	0.0	-1.0	0.1	0.2	0.8
34.2	0.9	0.5	-0.7	0.7	0.2	0.9
36.2	-0.2	0.8	0.5	0.5	0.3	0.6
53.3	0.0	0.9	-0.2	0.8	-0.2	0.8
32.6	-0.2	0.9	0.5	0.7	0.2	0.8
42.0	0.7	0.2	0.4	0.6	1.2	0.0
129.0	-0.7	0.2	1.8	0.0	1.0	0.1
36.9	0.6	0.3	0.2	0.8	0.8	0.1
10.4	-0.7	0.2	0.4	0.6	-0.4	0.5
261.2	0.2	0.9	5.7	0.0	5.9	0.0
67.4	0.5	0.3	-1.4	0.0	-0.9	0.0
156.7	0.8	0.5	2.3	0.0	3.1	0.0
28.9	-0.7	0.4	-1.6	0.0	-2.3	0.0

92.0	2.7	0.0	0.4	0.7	3.0	0.0
149.3	-1.4	0.1	1.2	0.2	-0.2	0.8
32.3	-1.3	0.0	1.0	0.1	-0.3	0.6
79.2	-0.7	0.5	-1.7	0.1	-2.4	0.0
37.6	2.3	0.0	-0.9	0.3	1.4	0.0
515.1	0.0	1.0	-0.6	0.6	-0.6	0.5
25.4	0.2	0.9	-0.1	1.0	0.1	0.9
65.5	1.7	0.0	0.2	0.8	1.9	0.0
246.8	0.1	0.9	0.5	0.8	0.6	0.6
182.3	1.0	0.5	3.7	0.0	4.7	0.0
170.9	3.0	0.0	0.4	0.8	3.4	0.0
382.8	2.3	0.0	0.6	0.2	2.9	0.0
48.0	0.3	0.9	1.6	0.3	2.0	0.2
65.6	-0.2	0.8	2.3	0.0	2.1	0.0
58.3	1.3	0.0	-0.4	0.6	0.9	0.1
74.0	1.1	0.3	-0.7	0.6	0.4	0.7
74115.3	4.1	0.0	-1.7	0.1	2.4	0.0
737.3	2.3	0.0	0.6	0.7	2.9	0.0
25.3	2.3	0.1	-0.1	1.0	2.2	0.1
21.2	0.8	0.2	-0.9	0.3	-0.1	0.9
496.6	0.3	0.8	1.7	0.1	2.0	0.0
198.8	6.0	0.0	-1.6	0.0	4.4	0.0
27.6	0.7	0.5	-0.3	0.8	0.4	0.7
20.2	2.1	0.0	-1.6	0.1	0.4	0.6
109.1	-0.3	0.6	-1.4	0.0	-1.7	0.0
63.9	-0.2	0.8	-0.3	0.7	-0.5	0.4
107.6	0.2	0.9	2.6	0.0	2.8	0.0
149.5	1.7	0.1	-1.5	0.2	0.2	0.9
50.7	0.1	0.9	1.1	0.2	1.2	0.1
93.4	-0.7	0.2	-1.7	0.0	-2.4	0.0
46.0	-1.3	0.2	0.7	0.6	-0.6	0.6
29.2	-1.5	0.0	0.6	0.2	-0.9	0.0
207.3	-1.8	0.0	0.6	0.4	-1.2	0.0
52.0	1.5	0.0	0.1	0.9	1.7	0.0
13188.6	3.3	0.0	-0.3	0.8	3.0	0.0
83.9	-0.8	0.2	0.5	0.6	-0.3	0.7
162.4	-0.4	0.5	0.5	0.4	0.1	0.8
24.6	-0.4	0.7	0.0	1.0	-0.4	0.7
1.5	-0.9	0.1	1.4	0.0	0.5	0.4
12.0	-4.4	0.0	0.1	0.9	-4.3	0.0
820.2	4.0	0.0	0.3	0.8	4.3	0.0
756.1	2.6	0.0	0.9	0.3	3.5	0.0
8.6	1.2	0.2	-0.4	0.7	0.7	0.4

24.1	0.7	0.2	0.1	0.9	0.8	0.1
40.6	-1.2	0.0	-0.2	0.8	-1.4	0.0
2.8	-1.4	0.0	0.0	1.0	-1.4	0.0
24.9	3.3	0.0	-2.1	0.0	1.2	0.2
84.3	6.1	0.0	-1.5	0.0	4.5	0.0
10.9	-0.7	0.1	1.2	0.0	0.5	0.3
22.1	-0.7	0.4	1.7	0.0	1.1	0.1
19.9	2.8	0.0	-1.8	0.0	1.1	0.2
41.6	0.1	0.8	-0.7	0.3	-0.5	0.3
140.5	0.5	0.5	0.5	0.5	0.9	0.1
84.0	-0.1	0.9	0.2	0.9	0.1	0.9
15.8	-3.0	0.0	0.9	0.4	-2.1	0.0
1.7	-1.1	0.2	-0.2	0.9	-1.2	0.1
4.9	-0.4	0.6	-0.3	0.8	-0.7	0.4
34.3	-2.4	0.0	2.9	0.0	0.5	0.5
11.4	-0.2	0.8	0.1	1.0	-0.2	0.8
3.9	1.7	0.0	-1.6	0.0	0.1	0.8
22.0	0.4	0.5	1.2	0.0	1.6	0.0
67.9	0.0	0.9	1.4	0.0	1.4	0.0
6.9	1.6	0.0	-0.3	0.5	1.3	0.0
31.3	-1.2	0.1	1.9	0.0	0.8	0.3
31.4	0.4	0.6	0.9	0.3	1.3	0.0
60.0	-0.6	0.6	-0.5	0.7	-1.1	0.3
4.4	0.1	0.9	-0.7	0.2	-0.6	0.2
2.1	-0.6	0.3	0.1	1.0	-0.6	0.3
70.9	-0.3	0.8	0.5	0.7	0.2	0.9
9.5	-0.6	0.1	0.2	0.7	-0.4	0.3
47.0	-0.8	0.1	1.5	0.0	0.7	0.2
2.6	-0.1	0.9	-0.9	0.3	-1.0	0.2
23.5	-0.4	0.7	1.2	0.3	0.8	0.4
9.9	-0.5	0.6	-0.6	0.6	-1.1	0.2
8.8	-2.8	0.0	1.6	0.1	-1.2	0.1
119.3	-1.1	0.1	1.2	0.1	0.1	0.9
30.4	-4.8	0.0	3.8	0.0	-1.0	0.4
4.1	-3.2	0.0	1.2	0.0	-1.9	0.0
7.6	-2.0	0.0	1.0	0.0	-1.0	0.0
16.7	-0.1	0.9	-0.5	0.6	-0.6	0.5
24.2	-0.3	0.5	0.7	0.2	0.3	0.5
1.1	0.0	1.0	0.7	0.2	0.7	0.1
51.1	0.9	0.0	0.4	0.4	1.3	0.0
311.0	4.3	0.0	0.3	0.7	4.6	0.0
5.0	-0.7	0.2	1.0	0.1	0.3	0.5
39.5	-0.1	0.9	0.3	0.8	0.2	0.8

30.7	-0.5	0.5	1.9	0.0	1.3	0.1
26.8	3.1	0.0	-0.4	0.7	2.7	0.0
14.8	0.2	0.8	0.9	0.2	1.1	0.1
31.3	1.4	0.1	1.1	0.2	2.5	0.0
14.1	-0.6	0.2	1.7	0.0	1.1	0.0
24.1	1.5	0.1	-0.6	0.7	0.9	0.4
8.1	1.4	0.0	-0.6	0.4	0.8	0.2
5.9	1.4	0.0	-0.6	0.3	0.8	0.1
20.5	-1.1	0.0	0.7	0.2	-0.4	0.5
16.5	-0.1	0.9	-1.0	0.4	-1.1	0.3
93.3	0.2	0.8	0.1	1.0	0.2	0.8
3.0	0.1	0.9	1.4	0.2	1.5	0.1
10.9	0.6	0.6	-0.3	0.8	0.3	0.7
34.5	1.5	0.0	0.7	0.3	2.3	0.0
212.4	3.7	0.0	0.1	0.9	3.9	0.0
307.2	3.7	0.0	0.1	0.9	3.8	0.0
9.7	-1.8	0.0	-1.5	0.0	-3.4	0.0
24.7	-1.2	0.3	-1.3	0.3	-2.5	0.0
28.3	-0.6	0.4	-0.8	0.3	-1.4	0.0
17.2	-1.1	0.2	-0.2	0.8	-1.3	0.1
10.2	-0.5	0.6	-0.7	0.6	-1.2	0.2
10.7	-0.4	0.7	-0.2	0.9	-0.6	0.5
123.6	0.0	1.0	2.0	0.0	2.0	0.0
10.6	-2.3	0.1	-0.5	0.8	-2.8	0.0
24.4	-2.8	0.0	0.3	0.8	-2.5	0.0
3.3	-3.9	0.0	-0.5	0.8	-4.4	0.0
33.8	-2.0	0.1	0.6	0.7	-1.5	0.2
14.8	-1.4	0.2	0.1	1.0	-1.3	0.3
44.6	-1.8	0.0	-0.4	0.7	-2.1	0.0
11.6	-0.7	0.1	-0.9	0.0	-1.5	0.0
73.4	0.0	1.0	-0.4	0.6	-0.5	0.5
37.6	-1.9	0.0	1.1	0.0	-0.8	0.1
19.3	0.7	0.2	0.5	0.5	1.2	0.0
156.0	1.3	0.1	3.1	0.0	4.4	0.0
2.0	0.3	0.6	-1.9	0.0	-1.7	0.0
39.5	-1.1	0.2	2.6	0.0	1.5	0.1
21.3	-0.4	0.5	1.4	0.0	1.0	0.1
7.9	1.7	0.0	-1.3	0.1	0.3	0.7
23.5	1.2	0.1	-0.2	0.8	1.0	0.1
2.9	1.9	0.0	-0.7	0.3	1.2	0.0
21.5	1.4	0.0	-0.3	0.7	1.1	0.0
40.0	0.7	0.5	2.1	0.0	2.8	0.0
20.7	0.3	0.8	1.9	0.1	2.1	0.0

22.9	0.1	0.9	2.7	0.0	2.8	0.0
17.8	-1.5	0.0	2.3	0.0	0.8	0.3
12.1	-1.5	0.1	1.1	0.3	-0.4	0.7
392.6	2.6	0.0	-0.1	0.9	2.5	0.0
110.8	3.6	0.0	-1.0	0.0	2.6	0.0
17.1	-1.7	0.0	0.3	0.7	-1.4	0.0
51.9	-1.3	0.0	0.9	0.2	-0.4	0.5
638.1	1.0	0.1	1.1	0.1	2.1	0.0
83.1	4.3	0.0	0.4	0.7	4.7	0.0
74.8	-0.9	0.3	0.6	0.5	-0.3	0.7
16.7	-0.9	0.1	0.3	0.7	-0.6	0.3
16.9	-0.3	0.7	0.0	1.0	-0.3	0.7
94.3	1.2	0.0	-1.5	0.0	-0.3	0.6
43.2	-0.2	0.8	1.5	0.0	1.3	0.0
261.9	-0.1	0.9	2.0	0.0	1.9	0.0
19.2	-2.5	0.0	0.5	0.2	-1.9	0.0
3.5	1.5	0.1	-0.6	0.6	1.0	0.3
9.2	-0.5	0.6	-0.6	0.5	-1.1	0.1
51.2	-0.9	0.2	0.3	0.7	-0.6	0.4
4.9	2.2	0.0	-0.8	0.3	1.4	0.0
18.3	1.5	0.1	-0.7	0.6	0.8	0.4
38.1	-2.2	0.0	-0.1	0.9	-2.3	0.0
28.4	1.6	0.1	-0.4	0.8	1.1	0.3
8.5	-1.5	0.0	0.6	0.6	-0.9	0.2
5.1	-0.2	0.7	0.1	0.9	-0.1	0.8
14.5	-1.0	0.1	-0.2	0.8	-1.1	0.0
15.7	-0.7	0.2	0.5	0.5	-0.3	0.7
65.4	-2.1	0.0	1.1	0.2	-1.1	0.1
17.9	-2.2	0.0	0.3	0.7	-1.9	0.0
36.7	-1.9	0.0	-0.2	0.9	-2.1	0.0
7.1	-1.6	0.1	0.2	0.9	-1.3	0.1
146.9	1.4	0.0	-0.8	0.4	0.6	0.4
36.5	0.3	0.7	1.0	0.1	1.2	0.0
29.4	-2.8	0.0	1.6	0.0	-1.2	0.0
42.9	-2.1	0.0	0.8	0.3	-1.3	0.0
9.6	-1.4	0.0	1.3	0.0	0.0	0.9
87.9	-2.7	0.0	3.5	0.0	0.9	0.4
26.7	2.1	0.0	1.6	0.2	3.7	0.0
92.5	0.1	0.9	1.3	0.1	1.4	0.1
9.4	-0.5	0.5	1.0	0.2	0.5	0.5
2.1	-1.3	0.1	0.1	0.9	-1.2	0.1
19.0	0.3	0.8	0.8	0.5	1.1	0.2
56.5	-0.3	0.6	1.3	0.0	1.0	0.0

43.9	1.1	0.3	0.8	0.5	1.9	0.1
2858.7	2.3	0.0	-0.4	0.6	1.9	0.0
44.6	1.8	0.0	0.4	0.7	2.2	0.0
196.8	-0.3	0.6	0.3	0.7	-0.1	0.9
33.0	-0.1	0.9	-0.3	0.8	-0.4	0.6
16.1	-1.7	0.0	1.6	0.0	-0.1	0.9
38.0	0.4	0.6	2.0	0.0	2.5	0.0
2.6	-4.1	0.0	0.8	0.3	-3.3	0.0
19.3	2.1	0.0	-0.1	0.9	2.0	0.0
10.0	-0.7	0.3	1.6	0.0	0.9	0.2
32.4	0.1	0.9	0.0	1.0	0.2	0.9
0.8	0.4	0.8	-1.8	0.2	-1.4	0.3
60.3	-0.8	0.6	1.3	0.4	0.5	0.7
8.6	-1.5	0.2	-0.2	0.9	-1.8	0.1
4.1	-0.9	0.4	0.0	1.0	-1.0	0.4
14.4	-1.0	0.6	-0.9	0.7	-1.9	0.2
14.7	-1.7	0.2	-0.6	0.7	-2.3	0.1
7.4	-1.3	0.3	-0.8	0.6	-2.1	0.1
49.7	-1.7	0.2	0.0	1.0	-1.8	0.1
52.5	-2.4	0.0	0.1	0.9	-2.2	0.0
88.3	-1.5	0.0	0.4	0.5	-1.1	0.0
247.2	-0.1	0.9	-0.5	0.8	-0.6	0.6
48.4	0.1	0.9	0.8	0.1	0.8	0.0
10.9	1.0	0.1	-0.7	0.3	0.4	0.6
17.2	-0.8	0.0	0.9	0.0	0.1	0.7
46.8	-0.8	0.0	-0.8	0.0	-1.6	0.0
30.9	1.8	0.0	-0.3	0.7	1.4	0.0
24.4	0.9	0.1	1.2	0.1	2.2	0.0
78.6	-0.1	0.9	1.2	0.2	1.1	0.2
15.4	1.5	0.0	0.0	1.0	1.5	0.0
53.4	3.5	0.0	-0.2	0.9	3.3	0.0
401.9	2.4	0.0	1.0	0.3	3.4	0.0
1758.6	0.0	1.0	4.2	0.0	4.2	0.0
63.9	0.8	0.2	1.5	0.0	2.3	0.0
12.5	-0.1	0.9	1.1	0.1	1.0	0.1
33.1	2.0	0.1	2.5	0.0	4.5	0.0
4.3	1.7	0.1	0.3	0.9	1.9	0.1
6.0	2.3	0.0	0.2	0.8	2.5	0.0
5.7	2.7	0.0	-0.1	1.0	2.7	0.0
11.8	2.6	0.0	-0.5	0.7	2.0	0.0
9.4	-2.0	0.1	-1.8	0.2	-3.8	0.0
5.3	-3.2	0.0	-1.7	0.2	-4.9	0.0
22.1	1.3	0.2	-0.4	0.7	0.8	0.4

5.4	0.7	0.5	-0.9	0.5	-0.2	0.9
40.4	0.7	0.5	0.8	0.5	1.4	0.1
4.5	1.5	0.1	-1.0	0.4	0.6	0.6
5.1	1.2	0.2	-1.0	0.3	0.2	0.8
1.7	1.4	0.1	-1.8	0.1	-0.5	0.6
37.7	0.7	0.5	0.9	0.3	1.6	0.0
61.0	4.0	0.0	-0.6	0.6	3.4	0.0
86.1	0.9	0.5	0.1	0.9	1.0	0.4
5.0	0.7	0.7	-1.8	0.2	-1.1	0.4
33.6	-3.1	0.0	0.0	1.0	-3.1	0.0
40.6	4.7	0.0	-2.1	0.0	2.7	0.0
5.7	-0.3	0.8	0.4	0.8	0.1	1.0
5.8	0.6	0.2	0.4	0.5	1.1	0.0
29.5	2.2	0.0	-0.2	0.7	1.9	0.0
140.3	4.3	0.0	-0.1	0.9	4.1	0.0
30.3	-0.2	0.8	1.5	0.0	1.3	0.0
11.0	1.1	0.1	0.7	0.3	1.8	0.0
21.2	-0.4	0.6	0.5	0.5	0.1	0.8
35.1	0.3	0.6	-0.2	0.7	0.1	0.9
29.0	1.1	0.0	0.0	1.0	1.1	0.0
3.7	1.4	0.0	-0.5	0.5	0.9	0.1
11.9	-0.3	0.6	0.4	0.3	0.2	0.6
4.7	-0.4	0.7	1.2	0.1	0.9	0.2
7.2	-0.4	0.7	0.0	1.0	-0.4	0.7
89.0	1.0	0.2	0.4	0.7	1.4	0.1
22.9	1.6	0.1	-0.1	1.0	1.5	0.1
27.1	0.0	1.0	3.7	0.0	3.7	0.0
30.2	1.0	0.3	2.5	0.0	3.5	0.0
94.8	0.6	0.6	2.4	0.0	3.1	0.0
30.6	0.9	0.2	1.2	0.1	2.1	0.0
43.0	2.5	0.0	0.9	0.3	3.4	0.0
52.2	2.5	0.0	1.3	0.2	3.8	0.0
7.7	1.6	0.1	0.0	1.0	1.6	0.1
10.3	1.9	0.0	-0.2	0.9	1.7	0.1
13.2	2.0	0.0	-0.6	0.6	1.3	0.1
3.1	2.2	0.0	-0.3	0.6	1.8	0.0
79.9	1.1	0.1	0.9	0.3	2.0	0.0
29.6	-0.3	0.8	2.7	0.0	2.4	0.0
25.3	0.6	0.7	2.5	0.1	3.2	0.0
18.7	0.6	0.5	1.5	0.1	2.1	0.0
107.9	-1.1	0.5	4.8	0.0	3.8	0.0
84.4	-4.0	0.0	1.4	0.0	-2.6	0.0
105.1	-3.8	0.0	0.2	0.8	-3.6	0.0

91.4	1.6	0.0	1.2	0.2	2.8	0.0
89.7	-2.1	0.0	2.0	0.0	-0.1	0.9
492.2	-5.7	0.0	3.1	0.0	-2.6	0.0
28.0	-0.3	0.9	4.1	0.0	3.9	0.0
48.9	-0.5	0.3	-0.2	0.7	-0.8	0.1
28.3	2.3	0.0	-0.6	0.3	1.8	0.0
40.3	0.1	0.9	2.1	0.1	2.2	0.0
16.6	1.9	0.0	0.3	0.7	2.2	0.0
32.2	-0.4	0.7	0.8	0.4	0.4	0.6
2.3	-7.5	0.0	0.5	0.7	-7.0	0.0
10.3	-8.5	0.0	2.3	0.0	-6.2	0.0
6.4	-8.8	0.0	1.7	0.0	-7.1	0.0
21.9	0.4	0.6	-1.7	0.0	-1.3	0.1
21.5	-2.1	0.0	0.3	0.6	-1.8	0.0
211.5	-0.7	0.4	3.6	0.0	2.9	0.0
102.4	-1.0	0.1	1.7	0.0	0.7	0.3
71.4	-1.2	0.0	1.6	0.0	0.4	0.5
977.1	9.8	0.0	-1.1	0.3	8.7	0.0
195.2	3.0	0.0	1.5	0.0	4.5	0.0
167.5	-0.4	0.7	1.9	0.0	1.5	0.1
16.5	-0.5	0.3	-1.2	0.0	-1.7	0.0
5.6	-0.3	0.6	-0.7	0.2	-1.1	0.0
34.9	0.4	0.7	-0.8	0.5	-0.4	0.7
6.4	-0.7	0.2	-1.1	0.0	-1.8	0.0
28.4	1.1	0.0	-0.5	0.4	0.6	0.2
43.3	0.2	0.7	0.0	1.0	0.3	0.6
19.5	0.9	0.0	1.1	0.0	2.0	0.0
43.2	0.8	0.1	-0.3	0.7	0.5	0.3
706.5	4.0	0.0	0.6	0.5	4.6	0.0
136.8	2.3	0.0	-0.1	0.9	2.2	0.0
14.8	3.1	0.0	-0.4	0.6	2.7	0.0
102.3	0.0	1.0	0.2	0.8	0.2	0.8
61.0	1.1	0.1	0.1	0.9	1.2	0.1
16.2	-0.6	0.2	0.8	0.1	0.3	0.5
443.2	4.3	0.0	0.1	0.9	4.3	0.0
26.3	0.9	0.2	0.7	0.4	1.5	0.0
82.4	0.7	0.1	-0.3	0.6	0.5	0.3
9.4	0.7	0.5	0.2	0.9	0.9	0.3
16.9	-2.6	0.0	1.2	0.1	-1.5	0.0
12.4	-1.8	0.1	0.9	0.5	-0.8	0.4
35.5	-0.9	0.2	0.2	0.9	-0.7	0.3
221.5	0.8	0.2	-0.3	0.6	0.5	0.4
26.4	5.9	0.0	-1.4	0.0	4.5	0.0

30.9	0.2	0.8	2.0	0.0	2.2	0.0
2.8	-0.9	0.2	-2.7	0.0	-3.7	0.0
18.5	-0.5	0.5	-0.9	0.2	-1.4	0.0
53.9	-0.3	0.7	1.0	0.2	0.7	0.3
28.7	-0.1	0.7	0.3	0.4	0.2	0.6
3.4	0.5	0.3	0.3	0.7	0.8	0.1
9.9	-0.2	0.7	-0.2	0.8	-0.5	0.4
18.9	0.4	0.3	-0.7	0.1	-0.3	0.6
117.3	0.6	0.6	-1.1	0.3	-0.5	0.6
81.4	0.2	0.6	-0.2	0.8	0.1	0.9
79.1	0.3	0.7	1.5	0.0	1.8	0.0
215.6	3.1	0.0	0.4	0.5	3.5	0.0
135.0	2.1	0.0	-0.4	0.6	1.8	0.0
265.8	2.3	0.0	-0.4	0.6	1.9	0.0
9.0	3.3	0.0	-1.2	0.0	2.1	0.0
45.3	0.3	0.4	0.1	0.9	0.4	0.2
30.1	2.0	0.0	1.1	0.2	3.1	0.0
62.9	2.4	0.0	-0.7	0.4	1.8	0.0
2.2	1.1	0.0	-1.2	0.0	-0.1	0.7
16.6	1.2	0.0	-1.3	0.0	-0.1	0.9
55.1	1.7	0.0	-0.5	0.4	1.2	0.0
14.2	2.3	0.0	-1.3	0.0	1.0	0.0
5.4	2.2	0.0	-1.2	0.0	1.1	0.0
10.6	1.5	0.0	-0.1	0.9	1.4	0.0
403.7	1.5	0.0	0.1	0.9	1.6	0.0
397.8	1.1	0.1	0.6	0.5	1.7	0.0
456.6	1.5	0.0	0.2	0.9	1.7	0.0
91.8	0.8	0.2	0.8	0.3	1.6	0.0
71.0	1.0	0.1	-0.2	0.9	0.9	0.1
31.9	-1.2	0.1	3.5	0.0	2.4	0.0
29.3	-1.4	0.2	3.1	0.0	1.6	0.1
14.4	-0.3	0.8	2.3	0.0	2.0	0.0
19.8	-0.3	0.8	1.0	0.4	0.7	0.5
71.0	0.1	0.9	1.9	0.0	2.0	0.0
28.4	0.5	0.3	1.0	0.0	1.5	0.0
22.2	1.1	0.3	-0.3	0.8	0.8	0.4
15.0	0.5	0.6	1.5	0.1	1.9	0.0
38.7	0.8	0.3	1.0	0.2	1.8	0.0
22.2	-0.5	0.5	-1.3	0.0	-1.8	0.0
3.3	-0.3	0.9	0.7	0.7	0.4	0.8
56.2	2.2	0.0	-0.3	0.8	1.9	0.0
8.6	-0.8	0.5	0.0	1.0	-0.8	0.4
3.5	-3.2	0.0	-0.5	0.8	-3.7	0.0

1.4	-4.2	0.0	-0.7	0.7	-4.8	0.0
15.2	-2.6	0.1	0.9	0.6	-1.7	0.3
2.9	-3.2	0.0	0.2	0.9	-3.0	0.0
13.5	-2.1	0.1	1.0	0.5	-1.1	0.4
52.0	-0.6	0.5	2.0	0.0	1.4	0.1
176.8	0.1	0.9	1.0	0.1	1.1	0.0
13.9	0.8	0.1	0.6	0.3	1.4	0.0
4.5	-2.1	0.0	0.0	1.0	-2.0	0.0
11.6	-0.9	0.3	1.3	0.2	0.4	0.7
4.3	0.1	0.9	0.1	0.9	0.2	0.7
399.1	0.0	1.0	2.1	0.2	2.1	0.1
12.3	0.5	0.7	3.1	0.0	3.7	0.0
16.9	1.4	0.2	3.1	0.0	4.5	0.0
7.7	1.2	0.0	0.9	0.1	2.1	0.0
17.0	1.6	0.0	0.0	1.0	1.6	0.0
11.7	-1.9	0.0	1.7	0.1	-0.3	0.8
4.3	-2.2	0.0	1.1	0.2	-1.1	0.1
26.9	-1.4	0.0	0.4	0.3	-1.0	0.0
16.1	-1.6	0.1	2.0	0.0	0.4	0.7
21.0	-2.0	0.0	1.5	0.0	-0.5	0.5
27.1	-3.5	0.0	0.4	0.7	-3.1	0.0
1.8	-4.0	0.0	-0.9	0.3	-4.9	0.0
1.8	-5.6	0.0	0.1	0.9	-5.5	0.0
28.9	-4.5	0.0	1.7	0.0	-2.9	0.0
133.5	-2.7	0.0	1.8	0.0	-0.9	0.2
32.8	1.6	0.0	0.7	0.2	2.3	0.0
15.8	-1.4	0.1	2.4	0.0	1.0	0.3
84.2	-0.2	0.8	2.3	0.0	2.1	0.0
215.5	2.5	0.0	0.2	0.8	2.7	0.0
9.9	-2.6	0.0	0.4	0.8	-2.2	0.0
30.7	-3.6	0.0	1.5	0.1	-2.2	0.0
227.7	4.6	0.0	0.8	0.1	5.4	0.0
29.2	0.9	0.0	2.0	0.0	2.9	0.0
73.1	0.2	0.8	0.1	0.9	0.4	0.7
20.3	-1.0	0.1	1.1	0.1	0.1	0.9
69.3	-0.1	0.9	2.7	0.0	2.6	0.0
37.9	1.4	0.2	2.4	0.0	3.8	0.0
2.9	-1.4	0.1	-0.6	0.6	-2.0	0.0
79.7	3.1	0.0	-0.1	0.9	3.0	0.0
34.7	1.2	0.0	0.2	0.8	1.5	0.0
23.2	0.7	0.1	2.1	0.0	2.8	0.0
61.6	-0.7	0.3	1.8	0.0	1.1	0.1
19.1	2.7	0.0	1.3	0.0	4.0	0.0

8.2	0.9	0.1	1.3	0.0	2.2	0.0
55.8	0.5	0.3	1.2	0.0	1.7	0.0
22.1	0.4	0.7	-1.1	0.2	-0.7	0.3
137.0	0.1	0.8	-0.2	0.8	-0.1	0.9
94.2	-0.3	0.7	-0.2	0.8	-0.4	0.4
9.8	0.4	0.5	0.5	0.4	0.9	0.1
49.7	0.0	1.0	0.2	0.8	0.2	0.8
23.7	-0.2	0.8	-1.1	0.1	-1.3	0.0
61.0	0.9	0.2	-0.9	0.2	0.0	1.0
151.0	-0.4	0.6	0.5	0.5	0.1	0.8
30.3	-6.5	0.0	2.0	0.0	-4.5	0.0
22.5	-0.6	0.1	1.2	0.0	0.6	0.1
111.2	0.5	0.4	0.5	0.4	1.0	0.0
190.5	1.4	0.0	1.0	0.1	2.5	0.0
14.6	1.1	0.0	0.1	0.9	1.2	0.0
39.7	0.6	0.1	0.2	0.6	0.8	0.0
59.7	-1.1	0.2	1.5	0.1	0.4	0.7
9.9	-2.7	0.0	0.8	0.4	-1.9	0.0
70.9	-1.8	0.0	0.0	0.9	-1.8	0.0
109.2	-0.1	0.9	-0.2	0.8	-0.3	0.7
19.2	0.2	0.7	0.3	0.5	0.5	0.2
7.8	-3.1	0.0	-0.4	0.7	-3.5	0.0
52.1	-3.1	0.0	2.3	0.0	-0.8	0.4
9.5	-3.5	0.0	1.7	0.0	-1.8	0.0
12.6	-1.2	0.0	0.2	0.8	-1.0	0.0
72.7	-1.2	0.1	0.4	0.6	-0.7	0.3
394.8	-2.1	0.0	0.3	0.8	-1.8	0.0
481.2	2.3	0.0	0.4	0.6	2.7	0.0
79.1	2.5	0.0	0.3	0.6	2.8	0.0
12.9	0.8	0.1	-0.5	0.4	0.4	0.5
41.2	1.4	0.0	0.1	0.9	1.5	0.0
196.4	1.2	0.1	-1.1	0.2	0.1	0.9
51.7	0.2	0.9	-0.4	0.7	-0.3	0.7
81.1	0.3	0.8	-0.1	1.0	0.3	0.8
125.2	-0.1	0.9	1.6	0.0	1.5	0.0
35.4	1.0	0.1	-0.1	0.9	0.9	0.1
47.8	-1.5	0.0	1.8	0.0	0.3	0.5
518.1	0.6	0.5	2.6	0.0	3.2	0.0
75.7	-1.6	0.0	-0.1	0.9	-1.8	0.0
156.0	0.1	0.9	0.8	0.2	0.9	0.1
56.6	3.3	0.0	-0.8	0.2	2.5	0.0
43.1	-3.2	0.0	-0.4	0.8	-3.6	0.0
12.2	-2.9	0.0	-0.5	0.5	-3.5	0.0

8.0	0.2	0.7	0.7	0.2	1.0	0.0
80.1	0.7	0.3	1.0	0.1	1.7	0.0
170.3	0.0	1.0	0.1	0.9	0.1	0.8
92.4	-0.4	0.5	0.6	0.2	0.3	0.6
63.9	1.3	0.1	2.4	0.0	3.6	0.0
28.6	1.1	0.0	-0.9	0.0	0.2	0.6
33.1	0.6	0.1	-0.6	0.2	0.0	1.0
67.9	-0.6	0.4	0.3	0.8	-0.3	0.7
39.6	0.6	0.5	-1.7	0.0	-1.1	0.1
15.2	1.2	0.1	-1.6	0.0	-0.4	0.6
99.0	-0.7	0.2	1.2	0.0	0.5	0.3
25.3	-1.6	0.0	0.9	0.2	-0.7	0.2
22.7	-2.2	0.0	-0.1	0.9	-2.3	0.0
11.8	-1.6	0.0	-1.2	0.1	-2.8	0.0
5.3	1.8	0.0	-2.4	0.0	-0.6	0.5
50.2	1.3	0.0	0.6	0.5	1.9	0.0
24.1	-0.1	0.9	0.9	0.2	0.8	0.2
95.7	0.2	0.9	3.2	0.0	3.4	0.0
22.9	2.4	0.0	2.8	0.0	5.2	0.0
15.8	3.3	0.0	-2.0	0.0	1.3	0.0
40.8	0.1	0.8	0.1	0.8	0.2	0.6
5.2	-0.6	0.6	0.2	0.9	-0.3	0.7
722.7	3.4	0.0	0.9	0.6	4.3	0.0
583.2	3.1	0.0	0.7	0.7	3.7	0.0
545.9	3.5	0.0	0.0	1.0	3.6	0.0
406.1	4.3	0.0	-0.6	0.8	3.8	0.0
2695.9	3.7	0.0	1.0	0.6	4.6	0.0
8.0	1.8	0.0	-0.8	0.5	1.0	0.3
28.2	0.7	0.1	-0.5	0.2	0.1	0.7
76.9	-1.2	0.2	1.5	0.1	0.3	0.8
7.5	-1.7	0.0	-1.0	0.1	-2.6	0.0
5.4	-1.4	0.1	-1.8	0.1	-3.2	0.0
5.5	-0.5	0.7	-1.4	0.2	-1.9	0.0
0.7	-0.1	0.9	-1.6	0.0	-1.7	0.0
24.5	-2.8	0.0	1.1	0.1	-1.6	0.0
80.8	1.4	0.0	0.7	0.3	2.2	0.0
13.3	0.2	0.6	-0.4	0.4	-0.2	0.7
167.2	-1.2	0.0	1.5	0.0	0.2	0.7
39.0	0.5	0.2	-0.5	0.2	-0.1	0.9
4.8	0.1	0.8	-1.3	0.0	-1.2	0.0
158.8	0.4	0.4	0.2	0.7	0.7	0.1
38.9	0.1	0.8	0.2	0.8	0.3	0.5
9.1	0.2	0.8	-1.6	0.1	-1.4	0.1

7.8	1.0	0.0	-0.1	0.8	0.9	0.0
220.5	8.0	0.0	-0.9	0.1	7.1	0.0
63.6	5.4	0.0	1.0	0.1	6.3	0.0
36.1	-0.9	0.3	0.3	0.8	-0.6	0.5
74.5	-1.0	0.1	0.5	0.5	-0.5	0.3
25.1	-0.8	0.2	-0.4	0.6	-1.3	0.0
44.7	1.1	0.0	0.5	0.3	1.6	0.0
54.0	2.7	0.0	0.7	0.3	3.4	0.0
75.4	-1.3	0.1	3.3	0.0	2.0	0.0
121.2	-1.2	0.4	4.9	0.0	3.7	0.0
12.2	-2.0	0.0	3.0	0.0	1.0	0.2
29.9	-1.5	0.1	4.1	0.0	2.5	0.0
8.8	-1.4	0.2	1.8	0.1	0.4	0.7
40.9	0.0	1.0	2.5	0.0	2.5	0.0
19.7	-0.4	0.6	2.2	0.0	1.8	0.0
38.8	-1.4	0.0	1.7	0.0	0.3	0.6
8.0	1.2	0.0	-0.1	0.9	1.1	0.0
11.1	0.0	1.0	1.0	0.1	1.0	0.1
7.9	-0.9	0.2	0.4	0.6	-0.5	0.5
21.7	-0.9	0.2	1.2	0.1	0.3	0.7
92.7	3.3	0.0	-1.7	0.0	1.6	0.0
9.2	10.0	0.0	-6.7	0.0	3.3	0.0
5.3	3.3	0.0	-0.9	0.1	2.4	0.0
2.5	0.0	1.0	1.0	0.2	1.0	0.1
27.2	0.9	0.2	1.0	0.1	1.9	0.0
16.9	1.6	0.0	-0.2	0.8	1.4	0.0
92.4	-1.5	0.0	-0.1	0.9	-1.6	0.0
22.6	-1.6	0.0	0.8	0.0	-0.7	0.0
39.8	-1.9	0.0	-1.0	0.1	-3.0	0.0
55.7	-0.6	0.4	1.2	0.1	0.6	0.4
7.8	-0.9	0.0	0.7	0.1	-0.2	0.6
15.4	-0.5	0.4	-0.6	0.3	-1.1	0.0
10.6	-0.4	0.4	-0.1	0.9	-0.5	0.3
8.1	0.3	0.6	0.0	1.0	0.3	0.6
35.5	-0.6	0.3	-0.1	0.9	-0.7	0.2
84.3	0.2	0.8	-0.4	0.7	-0.1	0.9
33.6	-0.8	0.5	-1.2	0.3	-2.0	0.1
392.7	1.6	0.0	-0.4	0.6	1.2	0.0
46.9	0.7	0.1	-0.5	0.3	0.2	0.7
172.1	0.3	0.6	0.7	0.1	1.0	0.0
43.5	0.7	0.1	0.8	0.1	1.5	0.0
16.7	2.5	0.0	-0.2	0.7	2.3	0.0
25.4	0.1	0.9	1.0	0.1	1.2	0.0

51.7	-0.7	0.5	0.0	1.0	-0.7	0.5
108.5	-0.4	0.4	0.6	0.3	0.1	0.8
198.7	-0.2	0.8	0.2	0.8	0.1	0.9
53.2	-1.2	0.2	1.6	0.1	0.4	0.7
21.1	1.8	0.0	1.8	0.0	3.6	0.0
62.2	0.5	0.6	2.2	0.0	2.7	0.0
25.2	0.1	1.0	1.7	0.3	1.8	0.2
62.3	0.5	0.8	3.8	0.0	4.4	0.0
13.5	0.7	0.4	2.0	0.0	2.7	0.0
13.8	-0.3	0.8	2.5	0.0	2.1	0.0
9.5	-2.3	0.0	2.7	0.0	0.3	0.7
54.3	-0.4	0.7	2.5	0.0	2.1	0.0
60.1	0.9	0.0	2.7	0.0	3.6	0.0
29.3	1.8	0.0	0.2	0.9	1.9	0.0
14.7	1.1	0.0	0.6	0.3	1.8	0.0
323.2	0.1	0.9	2.7	0.0	2.9	0.0
64.6	0.3	0.7	0.7	0.4	1.0	0.2
12.1	-0.7	0.7	-0.2	0.9	-0.8	0.5
37.5	-1.2	0.1	0.6	0.5	-0.7	0.3
3.3	-1.2	0.0	-0.1	0.9	-1.3	0.0
2.9	-1.0	0.0	-1.5	0.0	-2.4	0.0
73.4	-0.5	0.5	-0.3	0.8	-0.7	0.3
15.6	-0.4	0.3	-1.3	0.0	-1.7	0.0
25.1	-0.5	0.3	-0.2	0.8	-0.7	0.1
9.8	-2.2	0.0	0.5	0.3	-1.7	0.0
6.7	-2.0	0.0	-0.6	0.2	-2.6	0.0
25.6	-1.5	0.0	0.3	0.6	-1.2	0.0
38.1	-1.4	0.0	0.8	0.3	-0.6	0.3
64.7	-0.9	0.2	0.9	0.2	0.0	1.0
13.9	-0.5	0.2	-0.6	0.2	-1.1	0.0
126.3	-0.1	0.9	-0.1	1.0	-0.2	0.8
31.5	0.6	0.4	-0.1	0.9	0.5	0.5
9.3	2.7	0.0	-1.8	0.1	0.9	0.3
16.0	2.4	0.0	-1.2	0.1	1.2	0.0
18.1	0.4	0.6	0.0	1.0	0.4	0.5
24.7	-1.5	0.1	0.1	1.0	-1.4	0.1
31.5	-0.2	0.8	0.1	0.9	-0.1	0.9
144.7	1.3	0.1	-1.2	0.1	0.1	0.9
28.9	2.3	0.0	-1.7	0.0	0.6	0.2
18.4	-1.0	0.0	1.5	0.0	0.5	0.3
48.3	0.6	0.1	0.6	0.1	1.1	0.0
26.5	-0.8	0.1	0.1	0.9	-0.7	0.2
334.9	0.6	0.5	2.8	0.0	3.4	0.0

59.9	0.3	0.5	0.7	0.1	1.0	0.0
43.4	-0.6	0.0	0.5	0.1	-0.1	0.8
121.1	0.0	0.9	0.9	0.1	0.8	0.1
31.6	2.1	0.0	-1.0	0.1	1.1	0.1
16.6	0.0	1.0	-2.0	0.0	-1.9	0.0
21.8	0.3	0.5	-0.4	0.3	-0.2	0.7
153.3	1.4	0.3	2.4	0.1	3.7	0.0
119.2	1.9	0.0	0.8	0.1	2.7	0.0
65.7	1.4	0.0	0.2	0.8	1.6	0.0
28.0	-0.1	0.9	-0.5	0.3	-0.5	0.1
9.0	-2.1	0.0	0.2	0.8	-1.9	0.0
122.0	-0.9	0.3	2.3	0.0	1.4	0.1
61.4	-2.4	0.0	1.2	0.1	-1.2	0.0
232.3	0.8	0.2	0.3	0.7	1.1	0.0
31.0	3.6	0.0	0.0	1.0	3.6	0.0
2.9	3.7	0.0	1.0	0.4	4.8	0.0
7.3	2.0	0.1	0.1	1.0	2.1	0.0
3.7	1.1	0.3	1.1	0.3	2.2	0.0
242.8	0.9	0.2	0.5	0.6	1.5	0.0
147.1	0.1	0.9	-0.2	0.8	-0.1	0.9
57.8	3.2	0.0	0.3	0.7	3.5	0.0
21.7	-1.9	0.0	-1.4	0.0	-3.3	0.0
48.1	-1.9	0.0	-0.5	0.3	-2.5	0.0
54.6	-0.9	0.3	-0.1	0.9	-1.0	0.2
17.4	1.9	0.0	-1.1	0.3	0.7	0.4
14.6	2.6	0.0	-1.4	0.2	1.2	0.2
10.8	2.5	0.0	-0.4	0.5	2.1	0.0
16.1	2.3	0.0	-1.0	0.0	1.3	0.0
53.4	2.4	0.0	-0.5	0.4	1.9	0.0
144.1	-0.3	0.4	0.7	0.1	0.3	0.4
164.8	1.3	0.3	-0.9	0.5	0.4	0.7
599.6	1.9	0.0	-2.0	0.0	-0.2	0.7
17.9	-0.5	0.4	-0.2	0.7	-0.7	0.1
22.8	0.1	0.9	0.0	1.0	0.2	0.8
18.0	-2.2	0.0	0.8	0.3	-1.4	0.0
8.8	-0.6	0.2	1.8	0.0	1.2	0.0
119.0	0.1	0.9	-0.4	0.8	-0.2	0.9
47.8	-0.5	0.4	0.3	0.6	-0.1	0.8
102.1	-0.2	0.8	0.6	0.2	0.4	0.3
195.4	-1.0	0.2	1.4	0.1	0.4	0.6
68.6	-1.6	0.0	0.7	0.1	-0.9	0.0
108.7	0.5	0.2	0.8	0.1	1.3	0.0
167.8	-1.9	0.0	0.1	0.9	-1.8	0.0

42.8	1.5	0.0	-0.4	0.5	1.2	0.0
11.2	0.4	0.4	0.2	0.8	0.5	0.2
159.0	-0.1	0.9	0.0	1.0	-0.1	0.8
18.6	-4.3	0.0	1.7	0.0	-2.6	0.0
1.9	0.9	0.1	0.3	0.7	1.2	0.0
19.0	1.7	0.0	-0.4	0.5	1.3	0.0
41.7	-0.2	0.6	1.4	0.0	1.2	0.0
107.5	1.2	0.0	0.3	0.5	1.5	0.0
37.2	-0.3	0.6	1.2	0.0	0.9	0.1
118.9	3.0	0.0	0.3	0.8	3.3	0.0
7.7	0.9	0.1	-1.3	0.0	-0.5	0.3
41.2	3.2	0.0	-1.9	0.1	1.3	0.2
150.6	0.4	0.8	0.5	0.8	0.8	0.5
172.6	1.0	0.4	-0.8	0.6	0.2	0.9
422.0	-1.4	0.0	3.2	0.0	1.8	0.0
939.5	0.3	0.7	4.6	0.0	5.0	0.0
1862.6	0.4	0.8	6.7	0.0	7.1	0.0
5.5	1.2	0.0	0.8	0.2	1.9	0.0
47.6	1.8	0.0	0.7	0.4	2.4	0.0
496.4	0.1	1.0	2.0	0.0	2.1	0.0
121.7	-1.1	0.2	2.9	0.0	1.7	0.0
11.3	-0.3	0.6	1.0	0.1	0.7	0.2
93.1	-1.7	0.0	1.6	0.0	-0.1	0.8
237.6	-1.7	0.0	1.3	0.1	-0.3	0.7
30.2	-0.9	0.2	0.2	0.9	-0.8	0.2
92.4	-2.2	0.0	1.7	0.0	-0.5	0.3
16.3	-2.6	0.0	1.2	0.3	-1.4	0.1
42.5	-0.9	0.4	0.0	1.0	-0.9	0.4
80.2	-2.6	0.0	2.4	0.0	-0.2	0.8
58.6	-1.7	0.0	1.7	0.0	0.1	0.9
96.4	-2.1	0.0	1.4	0.1	-0.6	0.4
64.3	-3.4	0.0	2.9	0.0	-0.4	0.6
28.5	-3.4	0.0	1.4	0.0	-2.0	0.0
11.0	-1.4	0.0	0.5	0.5	-0.9	0.1
147.8	-0.3	0.7	0.5	0.6	0.2	0.8
48.8	-0.5	0.6	-0.3	0.8	-0.8	0.3
8.2	-1.3	0.0	1.0	0.1	-0.3	0.6
8.3	0.7	0.4	1.4	0.1	2.0	0.0
36.6	-2.9	0.0	1.8	0.0	-1.1	0.1
28.8	-2.2	0.0	1.2	0.1	-1.0	0.1
21.6	-1.2	0.1	1.7	0.0	0.5	0.5
267.2	-1.4	0.1	2.8	0.0	1.5	0.1
96.4	-1.0	0.1	2.2	0.0	1.3	0.0

41.1	-0.7	0.5	1.0	0.3	0.3	0.8
558.0	-1.2	0.1	1.3	0.1	0.1	0.9
200.0	-0.4	0.6	1.1	0.2	0.6	0.4
31.7	-3.0	0.0	2.8	0.0	-0.3	0.7
155.1	-2.7	0.0	3.1	0.0	0.4	0.6
22.8	-2.6	0.0	2.0	0.0	-0.7	0.3
24.2	-1.5	0.0	1.2	0.0	-0.3	0.7
35.5	-1.7	0.1	1.9	0.1	0.3	0.8
87.7	-0.4	0.8	3.2	0.0	2.7	0.0
139.7	0.6	0.3	0.5	0.5	1.1	0.0
85.3	-2.1	0.0	1.1	0.0	-1.1	0.0
34.3	-0.3	0.8	0.4	0.8	0.0	1.0
112.5	3.8	0.0	1.3	0.2	5.2	0.0
25.3	-0.3	0.8	-0.3	0.8	-0.6	0.6
19.2	-0.8	0.1	0.1	0.9	-0.7	0.1
51.1	-0.7	0.1	0.5	0.4	-0.2	0.7
7.0	-0.5	0.3	1.0	0.0	0.5	0.2
37.5	0.9	0.2	0.1	0.9	1.0	0.1
76.5	-0.2	0.9	1.9	0.1	1.7	0.1
955.1	0.9	0.4	2.4	0.0	3.3	0.0
63.0	1.4	0.0	1.2	0.0	2.6	0.0
32.2	-0.4	0.5	2.1	0.0	1.7	0.0
9.5	-0.8	0.1	1.8	0.0	1.0	0.0
16.4	-1.4	0.1	2.0	0.0	0.6	0.6
151.2	-0.5	0.7	2.9	0.0	2.5	0.0
119.5	0.4	0.3	0.1	0.8	0.5	0.1
6.8	-2.4	0.0	-2.3	0.0	-4.7	0.0
42.2	1.4	0.0	-1.0	0.1	0.4	0.4
24.1	1.4	0.1	-1.2	0.2	0.3	0.8
10.7	1.9	0.0	-1.0	0.3	0.9	0.3
12.3	1.8	0.1	-1.6	0.2	0.2	0.8
5.7	1.2	0.1	-1.6	0.0	-0.4	0.6
17.5	0.8	0.3	-1.6	0.0	-0.8	0.3
135.3	0.2	0.9	4.3	0.0	4.5	0.0
441.5	-0.4	0.7	0.5	0.7	0.1	0.9
13.0	-2.2	0.0	-1.0	0.4	-3.2	0.0
18.6	3.9	0.0	-0.9	0.0	3.0	0.0
25.7	-0.8	0.2	0.6	0.4	-0.2	0.8
6.9	1.3	0.3	1.5	0.2	2.9	0.0
4.9	1.9	0.0	0.4	0.4	2.3	0.0
83.5	-0.3	0.6	0.9	0.1	0.6	0.2
24.3	0.9	0.1	0.6	0.4	1.4	0.0
275.6	1.2	0.0	-0.5	0.5	0.8	0.1

11.9	3.1	0.0	-0.5	0.2	2.5	0.0
39.8	-1.9	0.0	0.2	0.9	-1.8	0.0
38.4	-0.4	0.6	0.3	0.8	-0.1	0.9
37.2	1.7	0.0	-0.7	0.1	0.9	0.0
46.3	1.5	0.0	-1.5	0.0	0.0	1.0
497.5	1.7	0.0	-0.4	0.6	1.3	0.0
376.9	-3.8	0.0	2.6	0.0	-1.2	0.1
558.8	-5.4	0.0	5.5	0.0	0.2	0.9
149.9	-6.7	0.0	3.5	0.0	-3.2	0.0
181.6	-5.8	0.0	2.7	0.0	-3.2	0.0
54.0	-0.8	0.1	0.2	0.8	-0.6	0.2
20.1	-0.9	0.0	-0.4	0.2	-1.3	0.0
11.8	-2.8	0.0	1.7	0.0	-1.1	0.1
5.8	0.2	0.7	0.8	0.1	1.0	0.0
8.1	0.7	0.4	0.6	0.6	1.2	0.1
4.0	0.4	0.5	0.1	0.9	0.6	0.3
19.1	-1.2	0.1	-0.5	0.6	-1.7	0.0
17.2	-2.4	0.0	1.2	0.3	-1.2	0.2
14.9	-2.6	0.0	1.0	0.1	-1.5	0.0
16.5	1.3	0.1	-0.1	0.9	1.2	0.1
8.7	-0.4	0.6	0.5	0.5	0.1	0.9
10.5	-0.6	0.5	-0.4	0.7	-1.0	0.2
25.7	1.1	0.3	-0.5	0.7	0.6	0.5
3.5	0.3	0.7	-0.9	0.2	-0.6	0.3
0.9	0.1	0.9	0.0	1.0	0.1	0.8
0.5	0.8	0.1	-0.6	0.3	0.2	0.7
4.2	-0.2	0.8	0.5	0.5	0.3	0.6
7.1	-0.9	0.2	1.6	0.0	0.7	0.3
10.1	4.7	0.0	-1.8	0.1	2.9	0.0
7.3	-1.5	0.1	0.5	0.7	-1.0	0.3
62.8	1.1	0.3	1.6	0.1	2.7	0.0
29.7	-0.7	0.0	-0.3	0.5	-1.0	0.0
20.6	0.0	1.0	-0.3	0.5	-0.3	0.4
28.1	0.4	0.5	-0.5	0.3	-0.2	0.7
9.9	0.8	0.3	-0.7	0.4	0.1	0.9
44.4	-2.0	0.0	1.7	0.0	-0.3	0.8
1.6	-1.8	0.0	-0.3	0.8	-2.1	0.0
18.6	0.1	0.9	0.1	0.9	0.2	0.7
3.1	1.0	0.0	-0.2	0.7	0.7	0.1
17.2	1.8	0.0	0.3	0.7	2.2	0.0
20.0	0.9	0.3	0.6	0.6	1.5	0.1
2.0	0.9	0.3	-1.4	0.1	-0.4	0.6
18.0	1.1	0.3	0.5	0.7	1.7	0.1

39.9	0.3	0.7	0.3	0.8	0.6	0.4
7.6	0.4	0.7	0.4	0.8	0.8	0.4
33.4	-0.9	0.1	0.8	0.1	-0.1	0.9
44.8	0.7	0.6	2.7	0.0	3.4	0.0
39.4	0.6	0.6	3.0	0.0	3.6	0.0
59.0	-0.9	0.3	2.0	0.0	1.1	0.2
11.0	1.5	0.0	-2.4	0.0	-0.9	0.2
81.0	3.4	0.0	-0.3	0.8	3.0	0.0
38.8	3.8	0.0	-1.1	0.2	2.7	0.0
25.7	3.8	0.0	-2.0	0.0	1.8	0.0
357.6	0.8	0.5	-0.8	0.6	0.1	1.0
43.3	-1.1	0.0	1.0	0.0	-0.1	0.8
17.2	-1.0	0.0	0.9	0.1	-0.1	0.8
360.7	1.8	0.0	-1.4	0.1	0.4	0.6
479.6	2.1	0.0	-0.9	0.4	1.2	0.2
6.4	-0.1	0.7	-0.6	0.1	-0.8	0.0
278.6	2.4	0.0	-2.6	0.0	-0.2	0.9
60.8	0.8	0.5	-1.1	0.4	-0.3	0.8
215.8	3.9	0.0	-1.7	0.0	2.1	0.0
1389.7	3.7	0.0	-0.8	0.4	2.9	0.0
77.5	3.3	0.0	-1.1	0.2	2.1	0.0
1570.5	2.9	0.0	-0.6	0.5	2.3	0.0
1516.7	3.0	0.0	0.6	0.6	3.5	0.0
534.2	3.0	0.0	-0.8	0.2	2.1	0.0
133.9	3.5	0.0	-1.5	0.0	2.0	0.0
604.5	3.4	0.0	-0.8	0.3	2.7	0.0
1375.1	3.3	0.0	-0.9	0.1	2.4	0.0
663.2	3.0	0.0	-0.6	0.3	2.5	0.0
22.1	2.2	0.0	-1.2	0.0	1.0	0.0
184.7	1.8	0.0	-0.7	0.3	1.2	0.0
16.4	0.8	0.2	0.6	0.4	1.3	0.0
5.2	-0.8	0.1	0.7	0.2	0.0	0.9
79.4	1.4	0.0	1.3	0.1	2.7	0.0
2363.5	4.0	0.0	1.2	0.0	5.2	0.0
240.4	0.2	0.8	-0.1	0.9	0.1	0.9
22.0	1.8	0.0	0.3	0.6	2.0	0.0
19.4	0.9	0.0	-0.8	0.1	0.1	0.8
59.4	0.8	0.2	-0.3	0.8	0.5	0.4
59.2	1.1	0.1	-0.2	0.9	0.9	0.2
40.5	0.9	0.1	-0.5	0.5	0.4	0.5
43.8	0.7	0.3	-0.3	0.7	0.3	0.6
11.7	2.9	0.0	-1.4	0.0	1.5	0.0
8.8	2.4	0.0	-1.7	0.1	0.7	0.5

35.1	2.5	0.0	-0.5	0.6	2.0	0.0
24.4	2.5	0.0	-1.2	0.2	1.3	0.1
57.4	1.6	0.0	0.5	0.4	2.1	0.0
12.9	-2.6	0.0	0.7	0.3	-1.9	0.0
12.9	2.4	0.0	-1.4	0.0	1.0	0.1
11.0	3.2	0.0	-1.4	0.2	1.8	0.1
45.4	1.4	0.0	1.2	0.1	2.6	0.0
10.7	1.5	0.0	0.1	0.9	1.6	0.0
15.2	0.8	0.3	-0.3	0.8	0.5	0.5
10.9	0.9	0.3	-0.4	0.7	0.5	0.6
10.0	-0.4	0.6	0.0	1.0	-0.4	0.6
21.4	-2.4	0.0	-0.6	0.5	-3.0	0.0
4.7	0.1	0.9	0.5	0.6	0.6	0.4
3.5	0.0	1.0	0.5	0.6	0.5	0.5
40.0	0.3	0.7	-0.1	0.9	0.2	0.7
17.3	-2.1	0.0	0.2	0.8	-1.9	0.0
20.6	-3.3	0.0	0.4	0.5	-2.9	0.0
78.2	-1.4	0.0	0.5	0.5	-0.9	0.2
7.4	-0.1	0.9	-0.1	0.9	-0.2	0.7
59.9	-0.7	0.1	-0.7	0.2	-1.4	0.0
91.2	0.7	0.3	-0.7	0.3	-0.1	0.9
59.3	2.1	0.0	0.2	0.9	2.3	0.0
31.8	1.1	0.1	-1.8	0.0	-0.7	0.2
39.0	0.7	0.5	-1.8	0.0	-1.2	0.1
121.3	0.9	0.2	0.0	1.0	0.9	0.2
12.4	-1.9	0.0	-0.4	0.6	-2.3	0.0
21.4	-2.8	0.0	0.1	0.8	-2.6	0.0
24.6	-3.2	0.0	0.6	0.6	-2.5	0.0
4.9	-2.1	0.0	0.1	0.9	-2.0	0.0
47.7	-1.0	0.0	0.4	0.5	-0.6	0.2
37.1	0.0	1.0	1.9	0.0	1.9	0.0
124.7	3.3	0.0	-1.0	0.4	2.3	0.0
246.7	-0.4	0.7	1.6	0.0	1.3	0.1
44.2	0.3	0.7	1.0	0.1	1.3	0.0
12.9	-0.2	0.7	0.5	0.3	0.3	0.4
28.0	-1.2	0.1	-0.7	0.4	-1.9	0.0
61.9	1.0	0.1	0.0	1.0	1.0	0.1
28.3	1.7	0.0	-0.9	0.2	0.8	0.2
13.6	1.2	0.0	-0.8	0.1	0.4	0.5
289.2	1.0	0.1	-1.0	0.2	0.0	1.0
3.2	1.0	0.1	-0.4	0.6	0.6	0.4
48.9	1.0	0.3	0.9	0.5	1.9	0.0
2.0	1.4	0.2	-1.2	0.3	0.2	0.9

15.2	1.4	0.2	0.5	0.7	1.9	0.0
13.1	1.7	0.1	-1.3	0.2	0.3	0.7
165.3	0.9	0.3	-0.6	0.5	0.3	0.7
26.9	2.4	0.0	-1.6	0.0	0.7	0.3
14.0	2.3	0.0	-2.4	0.0	-0.1	0.9
21.2	1.6	0.0	-1.6	0.0	0.1	0.9
58.5	1.8	0.0	0.1	0.9	1.9	0.0
8.8	1.0	0.1	-2.3	0.0	-1.2	0.1
3.1	0.2	0.8	-1.0	0.2	-0.8	0.2
21.9	-1.9	0.0	-0.3	0.6	-2.2	0.0
16.6	0.5	0.3	-0.1	0.8	0.3	0.5
36.3	-1.2	0.0	1.1	0.0	-0.1	0.8
135.2	2.9	0.0	-0.6	0.5	2.3	0.0
127.5	3.3	0.0	-0.2	0.8	3.1	0.0
19.4	0.0	1.0	-0.4	0.7	-0.4	0.6
83.0	0.0	1.0	0.0	1.0	0.0	0.9
13.3	0.6	0.3	1.0	0.0	1.6	0.0
8.2	2.6	0.0	0.1	0.9	2.7	0.0
14.6	-0.5	0.3	0.7	0.1	0.3	0.5
103.7	0.3	0.6	0.2	0.8	0.5	0.3
47.4	1.6	0.2	-0.5	0.8	1.1	0.4
525.5	5.1	0.0	-0.9	0.1	4.2	0.0
5.5	0.8	0.1	0.3	0.7	1.1	0.0
96.1	3.1	0.0	-0.5	0.5	2.5	0.0
3.9	-3.0	0.0	-0.6	0.5	-3.6	0.0
21.7	0.7	0.1	-1.7	0.0	-1.0	0.0
123.2	-0.5	0.5	0.8	0.4	0.3	0.8
39.7	-1.4	0.1	0.3	0.8	-1.1	0.2
47.4	0.7	0.4	0.6	0.5	1.3	0.1
19.2	1.4	0.0	0.6	0.5	2.1	0.0
12.0	3.4	0.0	-1.6	0.0	1.7	0.0
26.7	5.5	0.0	-2.7	0.0	2.9	0.0
8.3	4.3	0.0	-3.1	0.0	1.2	0.1
15.7	0.6	0.6	-1.2	0.3	-0.6	0.6
8.6	1.2	0.0	-0.7	0.3	0.5	0.5
42.0	0.5	0.7	2.6	0.0	3.1	0.0
19.3	0.3	0.8	0.9	0.3	1.2	0.1
43.1	0.8	0.1	1.1	0.0	2.0	0.0
46.3	0.2	0.9	1.8	0.1	1.9	0.0
52.9	-0.4	0.6	2.5	0.0	2.1	0.0
6.8	-1.2	0.3	0.7	0.6	-0.5	0.7
8.0	-0.8	0.4	2.2	0.0	1.3	0.2
11.1	-0.7	0.6	2.2	0.0	1.6	0.1

12.9	-0.5	0.4	1.5	0.0	1.0	0.1
38.6	-0.7	0.4	1.8	0.0	1.1	0.1
14.4	0.2	0.7	1.4	0.0	1.6	0.0
140.4	-1.0	0.3	2.6	0.0	1.6	0.1
11.1	0.2	0.8	1.3	0.1	1.5	0.0
18.0	-1.2	0.2	2.0	0.0	0.8	0.4
29.7	0.0	1.0	3.1	0.0	3.1	0.0
31.0	0.9	0.6	2.6	0.1	3.5	0.0
6.2	-0.1	0.8	1.1	0.0	0.9	0.0
5.7	0.0	1.0	-0.1	0.9	-0.1	0.9
25.6	-0.3	0.7	1.4	0.1	1.1	0.1
12.6	0.3	0.7	2.0	0.0	2.3	0.0
16.0	-0.8	0.5	2.5	0.0	1.7	0.1
30.4	1.1	0.2	1.6	0.1	2.7	0.0
4.1	0.5	0.2	0.9	0.0	1.4	0.0
844.2	1.5	0.2	2.7	0.0	4.2	0.0
181.4	-0.7	0.4	1.4	0.1	0.7	0.4
61.9	0.3	0.6	0.2	0.8	0.5	0.4
21.5	0.4	0.5	1.2	0.1	1.6	0.0
20.2	-0.6	0.3	0.4	0.6	-0.2	0.7
11.9	0.7	0.1	-0.2	0.8	0.5	0.2
144.3	0.8	0.2	1.9	0.0	2.7	0.0
35.9	0.3	0.7	1.8	0.0	2.1	0.0
43.1	0.8	0.3	1.9	0.0	2.8	0.0
48.4	-0.3	0.6	1.4	0.0	1.1	0.0
2.6	-0.1	0.9	-0.1	1.0	-0.2	0.8
19.1	1.7	0.1	2.0	0.1	3.6	0.0
55.7	0.9	0.5	3.8	0.0	4.8	0.0
37.7	0.4	0.8	3.0	0.0	3.4	0.0
34.3	1.3	0.1	2.2	0.0	3.5	0.0
57.1	1.7	0.0	1.1	0.2	2.7	0.0
35.1	0.9	0.2	0.6	0.5	1.4	0.0
4.0	-0.2	0.9	0.8	0.6	0.6	0.6
5.0	-0.2	0.9	-0.7	0.5	-0.9	0.3
15.4	0.5	0.7	-0.2	0.9	0.3	0.8
8.4	1.2	0.1	-0.5	0.5	0.7	0.3
14.1	-2.9	0.0	1.0	0.1	-1.9	0.0
69.7	-4.8	0.0	0.8	0.2	-4.0	0.0
11.1	-1.5	0.0	2.0	0.0	0.4	0.4
36.2	0.5	0.4	-0.3	0.7	0.2	0.8
596.5	-0.9	0.2	4.3	0.0	3.4	0.0
2723.0	-0.7	0.5	4.9	0.0	4.2	0.0
4604.8	-0.8	0.4	5.5	0.0	4.7	0.0

3674.5	-1.0	0.3	5.4	0.0	4.5	0.0
1139.7	-0.4	0.6	5.0	0.0	4.5	0.0
1541.7	-0.4	0.7	4.8	0.0	4.5	0.0
2040.4	0.4	0.7	4.5	0.0	5.0	0.0
289.5	0.1	0.9	2.3	0.0	2.4	0.0
20.2	-0.9	0.1	0.6	0.3	-0.3	0.6
207.4	1.2	0.1	0.3	0.8	1.5	0.0
20.6	-5.1	0.0	0.7	0.7	-4.4	0.0
1.6	-5.7	0.0	-0.9	0.5	-6.6	0.0
14.4	-5.5	0.0	0.5	0.8	-5.0	0.0
33.4	2.0	0.0	-0.6	0.3	1.4	0.0
155.4	2.0	0.0	-0.6	0.5	1.3	0.0
11.3	-0.4	0.7	0.4	0.7	0.0	1.0
16.0	1.5	0.0	-1.4	0.0	0.1	0.9
2.5	2.0	0.0	-1.2	0.0	0.8	0.1
107.7	1.2	0.1	-0.4	0.7	0.8	0.3
79.5	-2.2	0.0	-0.1	1.0	-2.3	0.0
13.6	0.6	0.2	1.1	0.0	1.7	0.0
44.8	0.0	1.0	0.4	0.8	0.4	0.7
56.5	2.3	0.0	0.5	0.4	2.8	0.0
41.6	3.3	0.0	-0.2	0.8	3.1	0.0
12.7	3.2	0.0	0.2	0.9	3.4	0.0
9.0	2.3	0.0	0.5	0.7	2.8	0.0
65.8	-0.1	1.0	2.0	0.0	1.9	0.0
5.7	0.6	0.6	0.4	0.8	1.0	0.3
20.8	1.1	0.3	1.3	0.2	2.4	0.0
59.6	0.7	0.4	1.0	0.2	1.8	0.0
8.9	1.3	0.1	0.9	0.3	2.1	0.0
6.2	0.0	1.0	0.2	0.9	0.2	0.8
19.5	-0.7	0.6	3.2	0.0	2.5	0.0
7.7	-0.4	0.7	2.2	0.0	1.8	0.1
88.3	-0.1	1.0	1.8	0.0	1.7	0.0
36.5	0.4	0.3	0.9	0.0	1.4	0.0
14.7	0.5	0.4	-0.7	0.2	-0.2	0.7
79.8	-5.7	0.0	1.6	0.0	-4.2	0.0
71.5	-7.1	0.0	3.2	0.0	-3.9	0.0
14.5	2.4	0.0	-0.9	0.1	1.5	0.0
7.2	2.6	0.0	-0.6	0.4	2.0	0.0
1.3	-3.1	0.0	-3.1	0.0	-6.2	0.0
1.6	-2.2	0.0	-2.7	0.0	-4.9	0.0
27.1	2.1	0.0	-0.6	0.2	1.5	0.0
12.9	0.4	0.6	1.2	0.1	1.6	0.0
6.1	-0.5	0.4	0.6	0.3	0.1	0.9

43.7	6.2	0.0	-0.9	0.0	5.3	0.0
8.8	2.9	0.0	0.1	1.0	3.0	0.0
9.0	2.1	0.0	0.0	0.9	2.0	0.0
11.1	2.1	0.0	0.4	0.5	2.5	0.0
9.1	0.4	0.5	0.6	0.4	1.0	0.1
6.7	-1.5	0.1	0.4	0.7	-1.1	0.2
4.0	-1.2	0.1	0.5	0.6	-0.7	0.4
10.9	-1.4	0.0	0.9	0.1	-0.5	0.4
7.2	-0.1	0.9	0.5	0.7	0.4	0.7
5.2	0.5	0.4	1.3	0.0	1.8	0.0
12.3	2.9	0.0	-0.1	0.9	2.8	0.0
40.8	-2.3	0.0	2.4	0.0	0.2	0.8
16.5	-2.3	0.0	-0.6	0.6	-2.9	0.0
1698.5	1.0	0.4	1.2	0.3	2.2	0.0
65.0	1.7	0.0	0.6	0.6	2.3	0.0
452.2	1.3	0.1	2.4	0.0	3.7	0.0
32.3	1.9	0.0	2.6	0.0	4.6	0.0
11.9	0.6	0.7	3.7	0.0	4.2	0.0
38.5	1.0	0.5	2.9	0.0	3.9	0.0
48.0	0.5	0.6	0.2	0.9	0.6	0.4
29.8	0.1	0.9	-0.1	0.9	0.0	1.0
4.1	0.0	1.0	-1.0	0.3	-1.0	0.2
9.0	0.3	0.7	0.3	0.7	0.6	0.3
6.1	0.7	0.5	-0.2	0.9	0.5	0.6
44.7	0.6	0.5	1.7	0.0	2.3	0.0
2.7	-0.4	0.7	-1.5	0.1	-1.8	0.0
32.6	1.1	0.2	1.7	0.1	2.8	0.0
11.2	2.1	0.0	0.5	0.3	2.6	0.0
25.2	2.6	0.0	-1.8	0.2	0.8	0.5
5.5	-0.8	0.3	-1.8	0.0	-2.6	0.0
2.0	-2.5	0.0	-1.8	0.0	-4.3	0.0
18.4	-2.7	0.0	0.0	1.0	-2.7	0.0
3.2	-1.7	0.0	-1.2	0.2	-2.9	0.0
27.1	-2.1	0.0	0.3	0.8	-1.8	0.0
8.9	-1.6	0.1	-1.1	0.3	-2.8	0.0
7.4	-2.1	0.0	-1.1	0.4	-3.2	0.0
1.8	-2.1	0.0	-1.3	0.2	-3.4	0.0
3.2	-0.6	0.5	-0.5	0.7	-1.1	0.2
3.5	-1.7	0.0	0.6	0.6	-1.1	0.2
9.1	-3.0	0.0	0.8	0.2	-2.3	0.0
16.4	1.6	0.1	0.9	0.5	2.5	0.0
16.9	3.8	0.0	-0.2	0.8	3.6	0.0
3.3	-2.0	0.0	1.1	0.0	-0.9	0.1

253.7	-2.7	0.0	1.7	0.0	-0.9	0.2
70.1	-0.5	0.4	0.6	0.2	0.2	0.8
85.3	2.2	0.0	-0.5	0.7	1.7	0.0
178.7	2.5	0.0	-0.8	0.2	1.7	0.0
2459.2	2.0	0.0	0.1	0.9	2.1	0.0
191.6	3.4	0.0	-0.6	0.6	2.8	0.0
139.5	2.9	0.0	-0.4	0.8	2.5	0.0
23.9	1.7	0.1	-0.9	0.4	0.7	0.4
16.6	1.5	0.0	0.4	0.5	1.9	0.0
7.0	2.4	0.0	-1.2	0.2	1.1	0.2
2.7	2.5	0.0	-1.6	0.0	1.0	0.1
3.5	1.9	0.0	-1.4	0.2	0.5	0.6
37.4	1.1	0.3	1.1	0.3	2.2	0.0
46.8	1.6	0.0	0.0	1.0	1.7	0.0
77.6	0.4	0.5	0.5	0.5	0.9	0.1
99.8	2.0	0.0	-1.1	0.1	0.9	0.1
39.6	2.6	0.0	-0.2	0.8	2.4	0.0
27.6	2.9	0.0	0.8	0.6	3.6	0.0
1.3	3.3	0.0	-1.3	0.2	1.9	0.1
13.7	2.3	0.0	1.1	0.3	3.4	0.0
4.2	1.6	0.0	0.2	0.7	1.8	0.0
3.2	1.6	0.1	-0.7	0.5	0.9	0.3
21.5	2.0	0.1	1.3	0.3	3.3	0.0
16.6	2.0	0.0	0.5	0.5	2.5	0.0
12.9	2.0	0.0	0.5	0.5	2.5	0.0
8.9	1.6	0.1	-0.1	0.9	1.5	0.1
39.6	0.5	0.3	0.3	0.7	0.8	0.1
4.6	0.4	0.4	0.1	0.9	0.5	0.3
14.6	1.0	0.2	-0.8	0.4	0.1	0.9
43.5	1.0	0.1	0.0	1.0	1.1	0.1
38.9	1.6	0.0	-0.5	0.3	1.0	0.0
49.9	1.4	0.1	-0.4	0.7	1.0	0.2
51.6	1.2	0.3	-0.7	0.6	0.5	0.7
40.9	-1.3	0.2	0.9	0.5	-0.4	0.7
18.0	0.2	0.8	-0.3	0.7	-0.1	0.9
5.1	-0.2	0.7	0.4	0.5	0.1	0.8
19.3	-0.2	0.8	0.9	0.3	0.7	0.3
80.6	-0.4	0.7	4.6	0.0	4.2	0.0
219.3	2.4	0.0	2.1	0.0	4.5	0.0
34.1	2.1	0.0	-0.2	0.7	1.9	0.0
9.2	2.2	0.0	-0.5	0.6	1.7	0.0
21.7	2.6	0.0	-0.5	0.5	2.1	0.0
83.7	-0.2	0.8	-0.2	0.8	-0.4	0.5

4.7	2.1	0.0	-0.1	0.9	2.0	0.0
167.5	0.7	0.5	1.5	0.2	2.2	0.0
21.1	7.8	0.0	-5.7	0.0	2.1	0.0
1127.2	-0.5	0.5	4.0	0.0	3.5	0.0
11.7	2.5	0.0	-0.7	0.6	1.8	0.1
73.3	0.7	0.6	2.6	0.0	3.3	0.0
5.0	-0.2	0.8	-0.2	0.9	-0.4	0.6
32.1	2.4	0.0	-0.1	0.9	2.3	0.0
45.1	0.1	0.8	0.8	0.1	0.9	0.0
13.0	1.1	0.0	0.2	0.8	1.4	0.0
24.4	-2.4	0.0	1.4	0.0	-0.9	0.0
16.9	-0.1	0.9	0.4	0.8	0.2	0.8
19.4	0.2	0.9	3.1	0.0	3.3	0.0
25.8	-1.3	0.0	-0.3	0.8	-1.6	0.0
2.3	-1.5	0.0	1.0	0.1	-0.5	0.4
33.2	-1.2	0.3	2.6	0.0	1.4	0.2
14.7	-0.5	0.6	2.3	0.0	1.7	0.0
11.1	-0.2	0.7	1.6	0.0	1.3	0.0
1.8	-0.3	0.8	0.0	1.0	-0.3	0.8
21.1	-0.2	0.8	-0.3	0.7	-0.5	0.4
39.8	-0.1	0.9	3.6	0.0	3.5	0.0
19.4	2.9	0.0	0.0	1.0	2.9	0.0
24.5	-1.4	0.0	0.6	0.5	-0.8	0.2
3.7	1.5	0.0	-0.7	0.4	0.8	0.2
12.5	0.7	0.3	0.6	0.4	1.4	0.0
21.5	0.2	0.9	0.8	0.6	0.9	0.4
7.6	1.2	0.2	0.6	0.6	1.8	0.0
40.8	1.1	0.3	0.9	0.5	1.9	0.1
7.4	-0.6	0.5	-0.2	0.9	-0.8	0.3
1.2	9.8	0.0	-8.7	0.0	1.1	0.2
28.1	6.9	0.0	-3.5	0.0	3.4	0.0
9.1	7.6	0.0	-4.6	0.0	3.0	0.0
0.3	10.0	0.0	-7.7	0.0	2.3	0.0
39.3	6.2	0.0	-2.9	0.0	3.3	0.0
2.3	4.5	0.0	-2.2	0.0	2.3	0.0
177.4	1.4	0.2	2.1	0.1	3.5	0.0
583.1	-3.8	0.0	5.0	0.0	1.2	0.2
8.8	-1.0	0.1	0.5	0.5	-0.5	0.4
5.6	-2.1	0.0	1.6	0.0	-0.5	0.5
25.7	-0.2	0.9	3.3	0.0	3.1	0.0
37.0	-0.4	0.5	0.7	0.2	0.3	0.5
2.6	0.2	0.9	0.3	0.8	0.4	0.7
2.5	0.0	1.0	0.5	0.7	0.5	0.7

99.9	0.3	0.7	1.8	0.0	2.2	0.0
16.5	0.8	0.5	2.7	0.0	3.5	0.0
2.0	0.9	0.4	1.1	0.4	1.9	0.0
11.3	0.6	0.2	0.1	0.8	0.8	0.1
32.2	1.6	0.1	-0.8	0.5	0.8	0.4
77.6	-0.5	0.1	0.5	0.2	0.0	0.9
461.5	2.0	0.0	0.2	0.9	2.2	0.0
49.5	-0.4	0.6	2.0	0.0	1.6	0.0
26.6	0.4	0.8	3.1	0.0	3.5	0.0
115.4	0.9	0.1	0.6	0.3	1.5	0.0
17.0	1.9	0.0	-0.2	0.9	1.7	0.1
191.8	-1.2	0.2	2.4	0.0	1.2	0.2
35.7	-0.7	0.6	1.9	0.1	1.3	0.2
5.1	-0.8	0.4	-0.9	0.3	-1.7	0.0
6.3	-0.5	0.4	-0.1	0.9	-0.6	0.2
13.2	0.0	1.0	-1.6	0.2	-1.7	0.1
22.9	-0.8	0.5	-1.4	0.2	-2.2	0.0
32.2	-1.2	0.0	0.6	0.3	-0.6	0.2
2.0	0.7	0.5	-0.1	1.0	0.6	0.5
41.7	-0.4	0.8	2.8	0.0	2.4	0.0
35.8	0.1	0.9	0.5	0.7	0.6	0.5
5.2	0.8	0.4	-1.5	0.1	-0.7	0.5
16.8	-0.1	0.8	0.2	0.8	0.1	0.9
1.1	-0.4	0.5	-0.4	0.6	-0.8	0.1
7.2	-0.7	0.5	-0.1	0.9	-0.8	0.3
36.3	-0.8	0.5	1.6	0.1	0.8	0.4
16.3	-0.9	0.4	0.7	0.6	-0.2	0.9
34.3	0.3	0.9	3.7	0.0	4.1	0.0
2.3	0.8	0.4	-2.7	0.0	-1.9	0.0
7.8	-0.5	0.6	0.4	0.7	-0.1	0.9
4.3	0.4	0.8	0.9	0.5	1.4	0.2
9.7	1.0	0.1	-0.4	0.6	0.5	0.4
12.1	-0.6	0.2	0.1	0.9	-0.5	0.3
15.5	-1.0	0.2	1.9	0.0	1.0	0.1
13.9	-0.8	0.0	0.4	0.2	-0.3	0.3
44.3	0.7	0.1	0.5	0.3	1.1	0.0
0.5	1.8	0.0	-0.7	0.3	1.2	0.0
3.1	2.5	0.0	-1.6	0.1	0.9	0.3
17.5	-0.9	0.0	1.0	0.0	0.1	0.8
56.8	2.0	0.0	-0.7	0.1	1.3	0.0
38.1	0.0	1.0	0.5	0.5	0.5	0.5
11.9	-0.5	0.1	0.2	0.6	-0.3	0.4
7.6	-2.0	0.0	0.3	0.7	-1.7	0.0

20.8	-2.2	0.0	2.4	0.0	0.2	0.7
7.0	0.6	0.1	0.5	0.2	1.1	0.0
12.5	0.7	0.1	-0.8	0.1	-0.1	0.8
71.0	0.6	0.3	0.4	0.6	1.0	0.1
118.2	-0.7	0.3	0.2	0.9	-0.6	0.4
75.9	-0.4	0.6	-0.3	0.8	-0.6	0.4
34.0	0.4	0.3	-0.3	0.6	0.2	0.7
15.5	0.2	0.8	0.1	0.9	0.2	0.6
108.0	0.8	0.2	0.2	0.8	0.9	0.1
70.4	0.8	0.2	0.0	1.0	0.8	0.2
49.0	0.0	0.9	0.8	0.2	0.7	0.2
51.7	0.3	0.5	-0.8	0.2	-0.4	0.4
37.7	-0.4	0.5	-0.4	0.5	-0.8	0.1
26.8	-0.6	0.3	0.1	0.9	-0.5	0.4
5.0	-2.8	0.0	-0.2	0.9	-3.0	0.0
106.1	-2.7	0.0	2.8	0.1	0.1	1.0
25.3	-1.8	0.0	0.2	0.9	-1.6	0.0
44.6	-2.2	0.0	2.2	0.1	-0.1	1.0
304.1	0.3	0.8	1.0	0.3	1.3	0.1
16.8	1.2	0.4	-0.2	0.9	0.9	0.4
97.4	0.9	0.4	-0.8	0.5	0.1	0.9
17.1	0.5	0.5	0.1	0.9	0.6	0.4
166.6	3.0	0.0	-0.6	0.6	2.4	0.0
9.6	-0.2	0.9	-1.0	0.5	-1.2	0.3
159.6	-1.2	0.2	1.1	0.3	-0.1	1.0
45.9	-0.8	0.7	3.8	0.0	3.0	0.0
26.1	3.8	0.0	-1.1	0.1	2.7	0.0
211.8	2.4	0.0	-2.3	0.0	0.0	1.0
24.8	1.8	0.2	2.7	0.0	4.5	0.0
16.3	0.8	0.5	1.2	0.4	2.0	0.1
180.4	-3.0	0.0	0.7	0.6	-2.3	0.0
31.9	-0.6	0.7	3.5	0.0	2.9	0.0
3.0	-1.4	0.2	-1.0	0.5	-2.4	0.0
36.5	-0.3	0.8	0.4	0.8	0.0	1.0
292.7	-0.9	0.2	0.5	0.6	-0.5	0.5
395.2	-1.4	0.1	1.3	0.2	-0.1	0.9
18.3	-1.5	0.0	-1.3	0.1	-2.8	0.0
3.9	-1.6	0.0	-0.6	0.3	-2.1	0.0
43.6	-0.6	0.2	-0.1	0.9	-0.6	0.1
24.6	-0.4	0.7	1.2	0.3	0.7	0.4
71.4	2.7	0.0	-2.0	0.0	0.7	0.3
70.5	2.5	0.0	-1.6	0.0	0.9	0.1
19.5	1.8	0.0	-0.4	0.5	1.4	0.0

796.2	0.7	0.4	0.3	0.8	1.0	0.2
267.8	-0.1	0.9	0.6	0.4	0.5	0.4
14.0	1.5	0.0	-0.4	0.4	1.0	0.0
55.2	-0.9	0.2	-1.1	0.2	-2.1	0.0
49.0	-1.3	0.0	1.7	0.0	0.4	0.5
96.0	1.5	0.0	-1.7	0.0	-0.1	0.8
125.6	0.4	0.8	-1.2	0.3	-0.8	0.4
95.7	-0.1	0.9	-0.2	0.9	-0.4	0.7
10.5	0.4	0.8	-2.2	0.0	-1.8	0.0
29.6	0.2	0.9	-1.3	0.3	-1.1	0.3
1.1	-0.8	0.5	-1.9	0.1	-2.8	0.0
2.8	-1.2	0.3	-1.9	0.1	-3.2	0.0
22.4	-1.2	0.2	-0.3	0.8	-1.5	0.1
12.9	-1.3	0.2	-0.9	0.5	-2.2	0.0
1.3	-1.7	0.1	-2.3	0.0	-4.0	0.0
5.4	-1.5	0.1	-1.7	0.1	-3.2	0.0
44.2	-1.0	0.4	-0.1	0.9	-1.1	0.3
34.0	-1.3	0.1	-0.5	0.7	-1.7	0.0
38.0	-1.0	0.3	0.0	1.0	-1.0	0.2
83.2	-0.7	0.5	-0.4	0.8	-1.1	0.2
51.7	-0.3	0.6	-0.6	0.4	-0.9	0.1
33.5	-0.9	0.2	-2.4	0.0	-3.2	0.0
30.5	-0.4	0.6	-3.0	0.0	-3.4	0.0
42.0	-0.1	1.0	1.2	0.4	1.2	0.3
69.5	-0.7	0.6	1.0	0.5	0.3	0.8
32.9	-0.1	0.9	-0.2	0.9	-0.3	0.8
1.6	-0.5	0.6	-2.0	0.0	-2.4	0.0
18.4	-0.4	0.8	-0.3	0.9	-0.7	0.6
11.4	-0.2	0.9	-0.9	0.4	-1.1	0.2
0.9	-0.2	0.9	-2.8	0.0	-3.0	0.0
2.3	0.3	0.8	-1.9	0.0	-1.7	0.0
4.7	0.9	0.4	-3.0	0.0	-2.1	0.0
13.9	-1.5	0.2	0.2	0.9	-1.3	0.2
1.1	-1.7	0.1	-2.0	0.1	-3.7	0.0
0.2	-1.8	0.0	-2.7	0.0	-4.5	0.0
15.9	-0.6	0.6	-0.1	1.0	-0.7	0.5
15.7	-0.2	0.9	-0.5	0.7	-0.7	0.4
21.5	-0.4	0.7	0.1	1.0	-0.4	0.7
37.3	0.0	1.0	0.1	0.9	0.1	0.9
14.1	-1.0	0.4	0.5	0.8	-0.5	0.7
38.3	1.4	0.0	-0.5	0.5	0.9	0.2

Description	**KO_number**
flavodoxin	K06205
tRNA modification GTPase TrmE	K03650
inner membrane protein translocase component YidC	K03217
ribonuclease P	K03536
50S ribosomal protein L34	K02914
cystine transport ATP-binding protein	K02028
cystine transport system permease	K02029
cystine-binding protein	K02030
chromosome replication initiator DnaA	K02313
DNA polymerase III subunit beta	K02338
recombination protein F	K03629
DNA gyrase subunit B	K02470
heat shock chaperone	K04080
valine--pyruvate transaminase	K00835
glycyl-tRNA synthetase subunit alpha	K01878
glycyl-tRNA synthetase subunit beta	K01879
alpha-amylase	K01176
NADH dehydrogenase subunit II-like protein	
sulfur transfer protein SirA	K04085
hypothetical protein	
LysR family transcriptional regulator	
hypothetical protein	
oxidoreductase%2C Zn-dependent and NAD%28P%29-binding	
3-ketoacyl-CoA thiolase	K00632
multifunctional fatty acid oxidation complex subunit alpha	K01825
elongation factor	
potassium transporter	K03498
protoporphyrinogen oxidase	K00230
zinc protease	K07263
hypothetical protein	
chloride channel protein	
thiamine biosynthesis protein ThiC	K03147
thiamin phosphate synthase	K00788
thiamin %28thiazole moiety%29 biosynthesis protein	K03148
thiazole synthase	K03149
thiamine biosynthesis protein ThiH	K03150
beta-N-acetylhexosaminidase	K12373
Xaa-Pro aminopeptidase	K01262
LysR family transcriptional regulator	
multidrug efflux system protein	K07552

hypothetical protein	
drug%2Fmetabolite exporter family protein	
recombination limiting protein	K09760
ubiquinone%2Fmenaquinone biosynthesis methyltransferase	K03183
hypothetical protein	K03690
ubiquinone biosynthesis protein UbiB	K03688
twin-arginine translocation protein TatA	K03116
sec-independent translocase	K03117
TatABCE protein translocation system subunit	K03118
TatD family Dnase	K03424
delta-aminolevulinic acid dehydratase	K01698
guanosine pentaphosphate phosphohydrolase	K01524
ATP-dependent RNA helicase RhlB	K03732
thioredoxin	K03671
transcription termination factor Rho	K03628
hypothetical protein	
3-octaprenyl-4-hydroxybenzoate carboxy-lyase	K03182
phenol hydroxylase P5 protein	K03380
FMN reductase	K05368
protoheme IX synthesis protein	K02498
uroporphyrinogen III methylase	K02496
uroporphyrinogen III synthase	K01719
porphobilinogen deaminase	K01749
adenylate cyclase	K05851
DNA-dependent helicase II	K03657
chloramphenical resistance permease	K05786
ATP-dependent DNA helicase RecQ	K03654
hypothetical protein	
sn-glycerol-3-phosphate transporter	K02445
hypothetical protein	K09125
DNA polymerase I	K02335
ribosome biogenesis GTP-binding protein YsxC	K03978
cytochrome c4	
2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1%2C4-benzoquinol methylase	
hypothetical protein	K09894
coproporphyrinogen III oxidase	
coproporphyrinogen III oxidase	K02495
DNA-binding transcriptional regulator AsnC	K03718
SAM-dependent methyltransferase	
universal stress global response regulator	K06149
ferritin iron storage protein	K02217
universal stress protein UspB	K06144
oxidoreductase	K07007

sensory transduction protein kinase	K00936
cytoplasmic protein	
hypothetical protein	K08985
multifunctional 2-keto-3-deoxygluconate 6-phosphate aldolase a	K01625
diguanylate cyclase	
adenosine deaminase	K01488
diguanylate cyclase	
bifunctional DNA-binding response regulator in two-component	K07712
nitrogen regulation protein NR%28II%29	K07708
hypothetical protein	
glutamine synthetase	K01915
GTP-binding protein	K06207
ribonuclease BN	K07058
D-tyrosyl-tRNA%28Tyr%29 deacylase	K07560
acetyltransferase	K00680
tRNA guanosine-2%27-O-methyltransferase	K00556
bifunctional %28p%29ppGpp synthetase II%2F guanosine-3%27%	K01139
DNA-directed RNA polymerase subunit omega	K03060
guanylate kinase	K00942
hypothetical protein	K13256
hypothetical protein	
hypothetical protein	
hypothetical protein	
ribonuclease PH	K00989
orotate phosphoribosyltransferase	K00762
chromosome partitioning protein ParA	K03496
osmolarity response regulator	K07659
osmolarity sensor protein	K07638
transporter	K03458
gluconate periplasmic binding protein	
carboxylesterase of pimeloyl-CoA synthesis	K02170
hypothetical protein	
transcriptional accessory protein	K06959
transcription elongation factor GreB	K04760
lipid A biosynthesis lauroyl acyltransferase	K02517
nucleoid occlusion protein	K05501
bifunctional phosphopantothenoylcysteine decarboxylase%2Fph	K13038
DNA repair protein RadC	K03630
50S ribosomal protein L28	K02902
50S ribosomal protein L33	K02913
hypothetical protein	
formamidopyrimidine-DNA glycosylase	K10563
phosphoglycerol transferase	

phosphopantetheine adenylyltransferase	K00954
glycosyltransferase	
alpha-L-glycero-D-manno-heptose beta-1%2C4-glucosyltransfera	K12984
ADP-heptose--LPS heptosyltransferase III	K12982
3-deoxy-D-manno-octulosonic-acid kinase	K11211
choline-sulfatase	K07014
3-deoxy-D-manno-octulosonic-acid transferase	K02527
ADP-heptose--LPS heptosyltransferase	K02843
UDP-N-acetylglucosamine 4%2C6-dehydratase	K01726
UDP-bacillosamine synthetase	K00837
UDP-N-acetylglucosamine 2-epimerase	
N-acetylneuraminate synthase	K01654
sialic acid synthase	
mannose-1-phosphate guanylyltransferase	K00966
oxidoreductase	K00100
acylneuraminate cytidylyltransferase	K00983
flagellin modification protein A	
glycosyltransferase	
hypothetical protein	
O-antigen ligase	
ADP-L-glycero-D-manno-heptose-6-epimerase	K03274
right junction gene%2C LPS locus	K07576
hypothetical protein	
TetR family transcriptional regulator	
WbfB protein	
hypothetical protein	
WbfD protein	
hypothetical protein	
exopolysaccharide export protein	K01991
hypothetical protein	
phosphotyrosine-protein phosphatase	K01104
protein-tyrosine kinase%2C chain length regulator in capsular po	K00903
dTDP-glucose 4%2C6-dehydratase	K01710
glucose-1-phosphate thymidylyltransferase	K00973
dTDP-4-deoxyrhamnose-3%2C5-epimerase	K01790
dTDP-glucose-4%2C6-dehydratase	
polisoprenol-linked O-antigen transporter	K03328
hypothetical protein	
O-acetyltransferase	
hypothetical protein	
beta-D-GlcNAc beta-1%2C3-galactosyltransferase	K00754
glycosyltransferase	K00754
2-dehydro-3-deoxyphosphooctonate aldolase	K01627

3-deoxy-manno-octulosonate-8-phosphatase	K03270
3-deoxy-manno-octulosonate cytidylyltransferase	K00979
arabinose-5-phosphate isomerase	K06041
UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate trans	K02851
CDP-6-deoxy-delta-3%2C4-glucoseen reductase	K00523
glucose-1-phosphate cytidylyltransferase	K00978
CDP-glucose 4%2C6-dehydratase	K01709
CDP-4-dehydro-6-deoxy-D-glucose 3-dehydratase	K12452
acetolactate synthase%2C large subunit	K01652
dTDP-glucose 4%2C6-dehydratase	K01710
glycosyltransferase	
glycosyltransferase	
hypothetical protein	
hypothetical protein	
UDP-N-acetylglucosamine 4%2C6-dehydratase	K01795
UDP-2-acetamido-2%2C6-dideoxy-beta-L-talose 4-dehydrogenas	K00100
UDP-N-acetyl glucosamine-2-epimerase	
group 1 glycosyl transferase	
UDP-N-acetyl-D-quinovosamine 4-epimerase	K01795
undecaprenyl-phosphate beta-N-acetyl-D-fucosaminephosphotr	K01005
UDP-D-quinovosamine 4-dehydrogenase	
acetyltransferase	K00680
UDP-glucose 4-epimerase	K01784
phosphoglyceromutase	K01834
Na%28%2B%29 driven multidrug efflux pump	
co-chaperonin GroES	K04078
molecular chaperone GroEL	K04077
triosephosphate isomerase	K01803
5-carboxymethyl-2-hydroxymuconate delta-isomerase	K01826
hypothetical protein	
fructose 1%2C6-bisphosphatase II	K02446
transcriptional regulator	K09892
ribonuclease activity regulator protein RraA	K02553
1%2C4-dihydroxy-2-naphthoate octaprenyltransferase	K02548
phosphoribulokinase	K00855
hypothetical protein	K09898
hydrolase	K07019
hypothetical protein	
ABC transporter ATP-binding protein	K06158
glutathione-regulated potassium-efflux system ancillary protein	K11748
glutathione-regulated potassium-efflux system protein KefB	K11747
hypothetical protein	K07070
FKBP-type peptidylprolyl isomerase	K03775

hypothetical protein	K03745
vegetatible incompatibility protein HET-E-1	
FKBP-type peptidylprolyl isomerase	K03772
DNA-binding transcriptional regulator	
sulfur transfer complex subunit TusD	K07235
sulfur transfer protein complex subunit TusC	K07236
30S ribosomal protein S12	K02950
30S ribosomal protein S7	K02992
elongation factor G	K02355
elongation factor Tu	K02358
30S ribosomal protein S10	K02946
50S ribosomal protein L3	K02906
50S ribosomal protein L4	K02926
50S ribosomal protein L23	K02892
50S ribosomal protein L2	K02886
30S ribosomal protein S19	K02965
50S ribosomal protein L22	K02890
30S ribosomal protein S3	K02982
50S ribosomal protein L16	K02878
50S ribosomal protein L29	K02904
30S ribosomal protein S17	K02961
50S ribosomal protein L14	K02874
50S ribosomal protein L24	K02895
50S ribosomal protein L5	K02931
30S ribosomal protein S14	K02954
30S ribosomal protein S8	K02994
50S ribosomal protein L6	K02933
50S ribosomal protein L18	K02881
30S ribosomal protein S5	K02988
50S ribosomal protein L30	K02907
50S ribosomal protein L15	K02876
preprotein translocase subunit SecY	K03076
50S ribosomal protein L36	K02919
30S ribosomal protein S13	K02952
30S ribosomal protein S11	K02948
30S ribosomal protein S4	K02986
DNA-directed RNA polymerase subunit alpha	K03040
50S ribosomal protein L17	K02879
fructose-1%2C6-bisphosphatase	K03841
UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diami	K02558
aromatic acid decarboxylase	K03186
thiamine transporter substrate binding subunit	K02064
thiamine transporter membrane protein	K02063

thiamine ABC transporter ATP-binding protein ThiQ%2FSfuC	K02062
ATP-dependent helicase HepA	K03580
pseudouridine synthase	K06177
universal stress protein	
transporter	
hypothetical protein	K07080
arginine repressor ArgR	K03402
malate dehydrogenase	K00024
octaprenyl diphosphate synthase	K02523
50S ribosomal protein L21	K02888
50S ribosomal protein L27	K02899
GTPase ObgE	K03979
hypothetical protein	
hypothetical protein	
dihydrofolate reductase	K00287
diadenosine tetraphosphatase	K01525
dimethyladenosine transferase	K02528
4-hydroxythreonine-4-phosphate dehydrogenase	K00097
peptidyl-prolyl cis-trans isomerase	K03771
organic solvent tolerance protein	K04744
Dna-J like membrane chaperone protein	K05801
hypothetical protein	
isopropylmalate isomerase small subunit	K01704
isopropylmalate isomerase large subunit	K01703
3-isopropylmalate dehydrogenase	K00052
2-isopropylmalate synthase	K01649
TetR family transcriptional regulator	
acriflavin resistance periplasmic protein	
acriflavin resistance plasma membrane protein	
salt-induced outer membrane protein	K07283
replicative DNA helicase	K02314
alanine racemase	K01775
hypothetical protein	
glucose-6-phosphate isomerase	K01810
chemotaxis CheY-phosphatase CheX	K03409
DNA-binding transcriptional repressor%2C Zn%28II%29-binding	K09823
tRNA-dihydrouridine synthase A	K05539
hypothetical protein	
hypothetical protein	
sulfite reductase subunit alpha	K00380
sulfite reductase subunit beta	K00381
phosphoadenosine phosphosulfate reductase	K00390
hypothetical protein	

FKBP-type peptidylprolyl isomerase	K03773
opacity associated protein OapA	K07269
drug%2Fmetabolite exporter family protein	
acyltransferase	K02348
Crp%2FFnr family transcriptional regulator	
bifunctional 2%27%2C3%27-cyclic nucleotide 2%27-phosphodies	K01119
sulfate adenylyltransferase subunit 2	K00957
sulfate adenylyltransferase subunit 1	K00956
divalent anion:sodium symporter family protein	
adenylylsulfate kinase	K00860
hypothetical protein	
hypothetical protein	K09950
permease	K02004
ABC transporter ATP-binding protein	K02003
hypothetical protein	
transcriptional regulator	K07109
hypothetical protein	
peptide-methionine %28S%29-S-oxide reductase	K07304
hypothetical protein	K07278
hypothetical protein	K09800
cation%2Fproton antiporter	K03316
B12-dependent methionine synthase	K00548
aspartate kinase	K00928
serine--pyruvate aminotransferase	K00830
Lipid A core -- O-antigen ligase Wzy-like protein	K13009
excinuclease ABC subunit A	K03701
glucose-1-phosphate uridylyltransferase	K00963
hypothetical protein	
glycosyltransferase	K00754
lipopolysaccharide N-acetylglucosaminyltransferase	
hypothetical protein	
hypothetical protein	
sensor protein UhpB	K00936
chain length regulator%2C exopolysaccharide biosynthesis protein	
polysaccharide export periplasmic protein	K01991
TetR family transcriptional regulator	
UDP-glucose lipid carrier transferase	K03606
single-stranded DNA-binding protein	K03111
hypothetical protein	
regulatory protein CsrD	
MSHA biogenesis protein MshI	K12279
MSHA biogenesis protein MshJ	K12280
hypothetical protein	K12281

MSHA biogenesis protein MshL	K12282
MSHA biogenesis protein MshM	K12283
MSHA biogenesis protein MshN	K12284
MSHA biogenesis protein MshE	K12276
MSHA biogenesis protein MshG	K12278
hypothetical protein	K12277
MSHA pilin protein MshB	K10925
MSHA pilin protein MshA	K10924
MSHA pilin protein MshC	K10926
MshD protein	K10927
MSHA pilus assembly protein MshO	K12285
MSHA biogenesis protein MshP	K12286
MshQ protein	K12287
rod shape-determining protein MreB	K03569
rod shape-determining protein MreC	K03570
rod shape-determining protein MreD	K03571
Maf-like protein	K06287
ribonuclease G	K08301
membrane protein%2C transporter	
beta-ureidopropionase	K01431
peptidase	K03568
hypothetical protein	K09889
peptidase PmbA	K03592
magnesium transporter	K06213
phosphocarrier protein HPr	K08485
hypothetical protein	K06958
sugar-specific enzyme IIA component of PTS	K02806
ribosome-associated%2C sigma 54 modulation protein	K05808
RNA polymerase factor sigma-54	K03092
ABC transporter ATP-binding protein	K06861
ABC transporter substrate-binding protein	K09774
hypothetical protein	K11719
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	K03270
D-arabinose 5-phosphate isomerase	K06041
calcium%2Fsodium:proton antiporter	K07301
toluene ABC transporter ATP-binding protein	K02065
toluene ABC transporter membrane protein	K02066
organic solvent ABC transporter	K02067
organic solvent ABC transporter	K07323
NTP-binding protein	K07122
DNA-binding transcriptional regulator	
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	K00790
1-acyl-sn-glycerol-3-phosphate acyltransferase	K00655

isopentenyl-diphosphate delta-isomerase	K01823
ketoacid-binding protein	K09022
aspartate carbamoyltransferase	K00610
aspartate carbamoyltransferase	K00609
ornithine carbamoyltransferase	K00611
arginine deiminase	K01478
hypothetical protein	K09893
hypothetical protein	
valyl-tRNA synthetase	K01873
DNA polymerase III subunit chi	K02339
leucyl aminopeptidase	K01255
hypothetical protein	K07091
hypothetical protein	K11720
hypothetical protein	
hypothetical protein	
diacylglycerol kinase	K00901
membrane-bound lytic murein transglycosylase C	K08306
hypothetical protein	
adenine DNA glycosylase	K03575
glutaminase	K01425
coproporphyrinogen III oxidase	K02495
deoxyribonucleotide triphosphate pyrophosphatase	K01516
hypothetical protein	
hypothetical protein	K09131
hypothetical protein	K02221
pyrroline-5-carboxylate reductase	K00286
hypothetical protein	K06997
transporter	K02669
pili retraction protein PilU	K02670
Holliday junction resolvase-like protein	K07447
hypothetical protein	K07735
glutathione synthetase	K01920
16S ribosomal RNA methyltransferase RsmE	K09761
DNA-specific endonuclease I	K01150
hypothetical protein	K02742
S-adenosylmethionine synthetase	K00789
transketolase	K00615
erythrose 4-phosphate dehydrogenase	K03472
phosphoglycerate kinase	K00927
fructose-bisphosphate aldolase	K01624
ATP-dependent RNA helicase SrmB	K05590
S-adenosyl-L-methionine-dependent methyltransferase	K00599
branched chain amino acid ABC transporter	K03311

flavodoxin FldB	K03840
site-specific tyrosine recombinase XerD	K04763
protein disulfide isomerase	K03981
ssDNA exonuclease RecJ	K07462
peptide chain release factor 2	K02836
peptide chain release factor 2	K02836
lysyl-tRNA synthetase	K04567
Fis family transcriptional regulator	
DNA mismatch repair protein	K03573
dinucleoside polyphosphate hydrolase	K08311
fused phosphoenolpyruvate-protein phosphotransferase PtsP%2	K08484
hypothetical protein	K07090
prolipoprotein diacylglyceryl transferase	K13292
thymidylate synthase	K00560
sodium-dependent phosphate transporter	K14683
transcriptional activator NhaR	K03717
transcriptional activator HlyU	
30S ribosomal protein S20	K02968
hypothetical protein	K03980
bifunctional riboflavin kinase%2FFMN adenylyltransferase	K11753
isoleucyl-tRNA synthetase	K01870
lipoprotein signal peptidase	K03101
FKBP-type peptidylprolyl isomerase	K03774
4-hydroxy-3-methylbut-2-enyl diphosphate reductase	K03527
dihydrodipicolinate reductase	K00215
carbamoyl phosphate synthase small subunit	K01956
carbamoyl phosphate synthase large subunit	K01955
D-alanyl-D-alanine carboxypeptidase	K07259
outer membrane protein U porin OmpU	K08720
transcription elongation factor GreA	K03624
RNA-binding protein	K07574
23S rRNA methyltransferase	K02427
ATP-dependent zinc-metalloprotease	K03798
7%2C8-dihydropteroate synthase	K00796
phosphoglucosamine mutase	K03431
preprotein translocase subunit SecG	K03075
hypothetical protein	K09748
transcription elongation factor NusA	K02600
translation initiation factor IF-2	K02519
ribosome-binding factor A	K02834
tRNA pseudouridine synthase B	K03177
30S ribosomal protein S15	K02956
polynucleotide phosphorylase	K00962

lipoprotein NlpI	K05803
collagenase-like protease YhbV	K01423
collagenase-like protease YhbU	K08303
modulator of RNase II stability	K00936
lipid carrier protein	
acyltransferase	K03824
hypothetical protein	
DNA polymerase III subunit psi	K02344
acetylase for 30S ribosomal subunit protein S18	K03789
peptide chain release factor 3	K02837
Dnase	K03424
nucleoside transporter	K03317
hypothetical protein	
deoxyribose-phosphate aldolase	K01619
thymidine phosphorylase	K00758
phosphopentomutase	K01839
purine nucleoside phosphorylase	K03784
SMP protein	K07186
phosphoserine phosphatase	K01079
hypothetical protein	K02278
CpaB family Flp pilus assembly protein	K02279
general secretion pathway protein D	K02280
chromosome partitioning ATPase	K02282
type IV secretion NTPase	K02283
TadB-like protein involved in pilus formation and%2For protein s	K12510
bipartite nuclear localization signal containing protein	K12511
hypothetical protein	K12512
TadE-like protein	
ATP%2FGTP-binding motif-containing protein	K12514
TadG-like protein	K12515
hypothetical protein	
sensory histidine kinase in two-component regulatory system wi	K07637
sensory histidine kinase in two-component regulatory system wi	K07637
two component system DNA-binding response regulator	K07660
hypothetical protein	
DNA repair protein RadA	K04485
elongation factor G	K02355
hypothetical protein	
cytosine deaminase	K01485
cytosine permease	K10974
long-chain-fatty-acid--CoA ligase	K01897
DNA mismatch repair protein MutS	K03555
recombinase A	K03553

alanyl-tRNA synthetase	K01872
aspartate kinase	K00928
carbon storage regulator	K03563
oxaloacetate decarboxylase	K01571
oxaloacetate decarboxylase subunit beta	K01572
hypothetical protein	
M16 family peptidase	K07263
glutamate--cysteine ligase	K01919
lipoprotein	
S-ribosylhomocysteinase	K07173
magnesium and cobalt efflux protein CorB	
CcsA-like protein	
Signal recognition particle %28SRP%29 component with 4.5S RN	K03106
30S ribosomal protein S16	K02959
16S rRNA-processing protein RimM	K02860
tRNA %28guanine-N%281%29-%29-methyltransferase	K00554
50S ribosomal protein L19	K02884
phospho-2-dehydro-3-deoxyheptonate aldolase	K01626
bifunctional chorismate mutase%2Fprephenate dehydrogenase	K14187
TagE-like protein	
hypothetical protein	
ABC transporter ATP-binding protein	
lytic murein transglycosylase%2C soluble	K08309
Trp operon repressor	K03720
NTPase	
bifunctional chorismate mutase P%2Fprephenate dehydratase	K14170
stationary phase translation inhibitor and ribosome stability fact	K05809
lipoprotein component of outer membrane protein assembly cor	K05807
23S rRNA pseudouridine synthase D	K06180
hypothetical protein	K05810
protein disaggregation chaperone	K03695
hypothetical protein	K02671
hypothetical protein	
type IV pilin	K08084
pili subunit PilA1	K02655
chromate transport protein	K07240
LysR family transcriptional regulator	
2%2C3%2C4%2C5-tetrahydropyridine-2%2C6-carboxylate N-succ	K00674
hypothetical protein	K09918
alternative oxidase 1	K00540
DNA-binding transcriptional regulator	
hypothetical protein	
exonuclease V subunit gamma	K03583

exonuclease V subunit beta	K03582
exonuclease V subunit alpha	K03581
DLP12 prophage%3B multidrug resistance protein	K03297
N-acetylglutamate synthase	K14682
hypothetical protein	
murein transglycosylase A	K08304
hypothetical protein	
Fe-S metabolism protein	K02426
cysteine sulfinate desulfinase	K01766
DNA-binding transcriptional activator GcvA	K03566
hypothetical protein	
RNA 2%27-O-ribose methyltransferase	K06968
exonuclease IX	K01146
hypothetical protein	K06966
diguanylate cyclase%2Fphosphodiesterase	
hypothetical protein	
7-cyano-7-deazaguanine reductase	K06879
SecY interacting protein Syd	
hypothetical protein	
hypothetical protein	K09768
hypothetical protein	
PTS system%2C cellobiose-utilization IIC component	K02761
PTS system%2C cellobiose-utilization IIB component	K02760
6-phospho-beta-glucosidase	
glucokinase	
PTS system cellobiose-specific transporter subunit IIA	K02759
LacI family DNA-binding transcriptional repressor	
outer membrane protein S	K02024
hypothetical protein	
hypothetical protein	
hypothetical protein	
tRNA pseudouridine synthase C	K06175
inositol monophosphatase	K01092
methyltransferase	K02533
Fe-S cluster synthesis regulatory protein IscR%2C DNA-binding tr	K13643
cysteine desulfurase	K04487
scaffold protein	K04488
Fe-S cluster assembly protein IscA	K13628
co-chaperone HscB	K04082
chaperone protein HscA	K04044
%282Fe-2S%29 ferredoxin	K04755
hypothetical protein	
aminopeptidase	K07751

nucleoside diphosphate kinase	K00940
ribosomal RNA large subunit methyltransferase N	K06941
type IV pilus biogenesis%2Fstability protein	K02656
hypothetical protein	
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	K03526
histidyl-tRNA synthetase	K01892
hypothetical protein	
outer membrane protein assembly complex subunit YfgL	
GTP-binding protein EngA	K03977
metal-dependent hydrolase	K07050
hypothetical protein	
exodeoxyribonuclease VII large subunit	K03601
inosine 5%27-monophosphate dehydrogenase	K00088
GMP synthase	K01951
aminobenzoyl-glutamate transport protein	
hypothetical protein	
hypothetical protein	
endoribonuclease L-PSP	
serine transporter	
esterase	K01070
alcohol dehydrogenase	K00121
periplasmic protein disulfide isomerase%2C DsbA-like protein	K03673
proton%2Fsodium-glutamate symport protein	
glutathione-dependent formaldehyde dehydrogenase	K00121
LysR family transcriptional regulator	
tRNA-specific adenosine deaminase	K11991
transglycosylase	
phosphoribosylformylglycinamidine synthase	K01952
23S rRNA methyltransferase	K00599
hypothetical protein	
endochitinase	K01183
transcription elongation factor	
succinylglutamate desuccinylase%2Faspartoacylase family protei	K06987
ribosomal protein S6 modification protein	K05844
ribosomal protein S6 modification protein	
sodium-dependent transporter	K03308
hypothetical protein	
hypothetical protein	
N-acetylneuraminate lyase	K01639
DNA-binding transcriptional repressor	
N-acetylglucosamine-6-phosphate deacetylase	K01443
N-acetylmannosamine-6-phosphate 2-epimerase	K01788
N-acetylmannosamine kinase	K00885

N-acetylneuraminate transporter%2C sodium-glucose%2Fgalacto	K03307
hypothetical protein	
urease accessory protein UreG	K03189
urease accessory protein UreF	K03188
urease accessory protein UreE	K03187
urease subunit alpha	K01428
urea amidohydrolase%2C beta subunit	K01429
urease subunit gamma	K01430
urease accessory protein UreD	K03190
oligopeptide transport ATP-binding protein OppD	
oligopeptide transport system permease OppB	K02033
oligopeptide-binding protein OppA	K02035
prolyl-tRNA synthetase	K01881
hypothetical protein	
DL-methionine transporter substrate-binding subunit	K02073
DL-methionine transporter subunit	K02072
DL-methionine transporter ATP-binding subunit	K02071
D%2CD-heptose 1%2C7-bisphosphate phosphatase	K03273
oligopeptide transporter subunit	K13894
oligopeptide transporter subunit	K13895
oligopeptide-binding protein OppA	K02035
oligopeptide transport ATP-binding protein OppD	K02031
oligopeptide transport ATP-binding protein OppF	K02032
lipoprotein	
hypothetical protein	
serine hydroxymethyltransferase	K00600
accessory colonization factor AcfD-like protein	K10939
lipoprotein	
methyl-accepting chemotaxis protein	
transcriptional regulator NrdR	K07738
bifunctional diaminohydroxyphosphoribosylaminopyrimidine dea	K11752
riboflavin synthase subunit alpha	K00793
3%2C4-dihydroxy-2-butanone-4-phosphate synthase	K14652
6%2C7-dimethyl-8-ribityllumazine synthase	K00794
transcription antitermination protein NusB	K03625
thiamin-monophosphate kinase	K00946
phosphatidylglycerophosphatase A	K01095
periplasmic AI-2 binding protein LuxP	K10910
membrane-bound sensor histidine kinase LuxQ	K10909
hypothetical protein	
antibiotic biosynthesis monooxygenase domain-containing protein	
1-deoxy-D-xylulose-5-phosphate synthase	K01662
geranyltranstransferase	K00795

exodeoxyribonuclease VII small subunit	K03602
flagellar motor protein PomA	K02556
flagellar motor protein MotB	K02557
thiamine biosynthesis protein ThiI	K03151
hypothetical protein	K03152
2-dehydropantoate 2-reductase	K00077
hypothetical protein	
muropeptide transporter AmpG	K08218
peptidyl-prolyl cis-trans isomerase	K03767
lipoprotein	K07286
methyltransferase small subunit	K11391
regulator of penicillin binding proteins and beta lactamase transc	K05527
Na%28%2B%29-translocating NADH-quinone reductase subunit	K00346
Na%28%2B%29-translocating NADH-quinone reductase subunit	K00347
Na%28%2B%29-translocating NADH-quinone reductase subunit	K00348
Na%28%2B%29-translocating NADH-quinone reductase subunit	K00349
Na%28%2B%29-translocating NADH-quinone reductase subunit	K00350
Na%28%2B%29-translocating NADH-quinone reductase subunit	K00351
thiamine biosynthesis lipoprotein	K03734
hypothetical protein	K05952
DNA polymerase IV	K02346
alanine racemase	K01775
aminoacyl-histidine dipeptidase	K01270
hypothetical protein	K06901
xanthine-guanine phosphoribosyltransferase	K00769
fermentation%2Frespiration switch protein	K11750
gamma-glutamyl kinase	K00931
gamma-glutamyl phosphate reductase	K00147
lipoyl synthase	K03644
lipoate-protein ligase B	K03801
hypothetical protein	K09158
D-alanyl-D-alanine carboxypeptidase	K07258
minor lipoprotein	K03642
cell wall shape-determining protein	K05837
transpeptidase	K05515
rRNA large subunit methyltransferase	K00783
hypothetical protein	K09710
DNA polymerase III subunit delta	K02340
lipoprotein component of outer membrane LPS assembly comple	K03643
leucyl-tRNA synthetase	K01869
hypothetical protein	
apolipoprotein N-acyltransferase	K03820
ion transport protein	K06189

metalloprotease	K07042
PhoH-like protein	K06217
%28dimethylallyl%29adenosine tRNA methylthiotransferase	K06168
2-octaprenyl-3-methyl-6-methoxy-1%2C4-benzoquinol hydroxyla	K03184
GTP-dependent nucleic acid-binding protein EngD	K06942
peptidyl-tRNA hydrolase	K01056
ribose-phosphate pyrophosphokinase	K00948
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	K00919
molecular chaperone LolB	K02494
glutamyl-tRNA reductase	K02492
peptide chain release factor 1	K02835
N5-glutamine methyltransferase%2C modifies release factors RF	K02493
transcriptional regulator	
transcriptional regulator	
2-dehydro-3-deoxyphosphooctonate aldolase	K01627
uroporphyrin-III C-methyltransferase	K02303
nitrite transporter	
nitrite reductase small subunit	K00363
nitrite reductase%2C large subunit%2C NAD%28P%29H-binding	K00362
methyl-accepting chemotaxis protein	K03406
bifunctional UDP-sugar hydrolase%2F5%27-nucleotidase peripla	K11751
hypothetical protein	
copper amine oxidase N-terminal protein	
copper transporter	K01533
DNA-binding transcriptional activator of copper-responsive regul	K11923
thioredoxin	K05838
short chain dehydrogenase	
glycine betaine transporter periplasmic subunit	K02002
glycine betaine transporter subunit	K02001
glycine betaine transporter subunit	K02000
hypothetical protein	K07071
phosphodiesterase	K07095
regulatory protein ToxS	K10922
transcriptional activator ToxR	K10921
heat shock protein 90	K04079
adenylate kinase	K00939
ferrochelatase	K01772
trigger factor	K03545
ATP-dependent Clp protease proteolytic subunit	K01358
ATP-dependent protease ATP-binding subunit ClpX	K03544
DNA-binding ATP-dependent protease Lon %28La%29	K01338
HU%2C DNA-binding transcriptional regulator subunit beta	K03530
peptidyl-prolyl cis-trans isomerase	K03770

competence protein ComE	K02237
di-%2Ftripeptide transporter	K03305
transcriptional activator RfaH	K05785
asparagine synthetase B	K01953
glutathione-regulated potassium-efflux system protein KefC	
DNA-binding transcriptional dual regulator	K02565
N-acetylglucosamine-6-phosphate deacetylase	K01443
PTS system N-acetyl glucosamine specific transporter subunit IIC	K02804
glutaminyl-tRNA synthetase	K01886
ferric uptake regulator	K03711
hypothetical protein	
flavodoxin FldA	K03839
hypothetical protein	
esterase%2Flipase YbfF	K01175
replication initiation regulator SeqA	K03645
phosphoglucomutase	K01835
metal-binding protein	
type II citrate synthase	K01647
succinate dehydrogenase cytochrome b556 large membrane sub	K00241
succinate dehydrogenase%2C membrane subunit%2C binds cyto	K00242
succinate dehydrogenase flavoprotein subunit	K00239
succinate dehydrogenase iron-sulfur subunit	K00240
2-oxoglutarate dehydrogenase E1	K00164
dihydrolipoamide succinyltransferase	K00658
succinyl-CoA synthetase subunit beta	K01903
succinyl-CoA synthetase subunit alpha	K01902
methyl-accepting chemotaxis protein	
zinc ABC transporter membrane protein	K09816
zinc ABC transporter ATP-binding protein	K09817
zinc ABC transporter periplasmic substrate-binding protein	K09815
peptidase	
hypothetical protein	
ferrous ion transport protein A	K04758
bifunctional ferrous iron transporter%2C protein B%2F GTP-bind	K04759
hypothetical protein	K10123
phosphate acetyltransferase	K13788
acetate kinase	K00925
hypothetical protein	K09899
arginyl-tRNA synthetase	K01887
hypothetical protein	K09907
dehydrogenase	
O-methyltransferase	
lipoprotein	

hypothetical protein	
1-acyl-sn-glycerol-3-phosphate acyltransferase	K00655
acyl carrier protein	K02078
acyl carrier protein	K02078
DNA gyrase subunit B	
AMP-%28fatty%29acid ligase	
AMP-%28fatty%29acid ligase	
acyltransferase	
phenylalanine and histidine ammonia-lyase	K01745
esterase	K07107
hypothetical protein	
transporter	
phospho-N-acetylmuramoyl-pentapeptide-transferase	K01000
3-oxoacyl-ACP synthase	K00647
3-hydroxylacyl-ACP dehydratase	
3-ketoacyl-ACP reductase	K00059
3-oxoacyl-ACP synthase	K09458
heat shock protein HslJ	K03668
50S ribosomal protein L25	K02897
hypothetical protein	
ATP-dependet helicase	
hydrolase	K01005
hypothetical protein	
lipoprotein	
hypothetical protein	
hypothetical protein	K09982
acetyltransferase	
TetR family transcriptional regulator	
methyl-accepting chemotaxis protein	
hypothetical protein	
preprotein translocase subunit SecF	K03074
preprotein translocase subunit SecD	K03072
hypothetical protein	
LysR family transcriptional regulator	
EmrKY-TolC multidrug resistance efflux pump%2C membrane fus	K03543
multidrug efflux system protein	K03446
16S rRNA pseudouridylate 516 synthase	K06183
bicyclomycin%2Fmultidrug efflux system protein	K07552
hypothetical protein	
hypothetical protein	
ABC transporter ATP-binding protein	K02003
ABC transporter permease	K02004
hypothetical protein	

pH-dependent sodium%2Fproton antiporter	K03313
trans-2-enoyl-CoA reductase	K00540
hypothetical protein	K07085
glutaredoxin	K03674
DNA-binding transcriptional regulator HexR	
glutamate decarboxylase	K01580
hypothetical protein	
transporter	
hypothetical protein	
DNA transformation protein TfoX1 %28Sxy%29	K07343
hypothetical protein	
lipoprotein	
phosphoserine aminotransferase	K00831
cysteine%2Fglutathione ABC transporter membrane%2FATP-bin	K06147
cysteine%2Fglutathione ABC transporter membrane%2FATP-bin	K06147
thioredoxin reductase	K00384
alanine dehydrogenase	K00259
leucine-responsive transcriptional regulator	K03719
DNA-binding membrane protein	K03466
outer-membrane lipoprotein carrier protein	K03634
recombination factor protein RarA	K07478
seryl-tRNA synthetase	K01875
thioredoxin	K03672
dsDNA-mimic protein	K09901
inosine%2Fguanosine kinase	K00892
hypothetical protein	K01792
glyceraldehyde-3-phosphate dehydrogenase	K00134
methionine sulfoxide reductase B	K07305
hypothetical protein	
general negative regulator of transcription subunit 1	K09916
cation transporter%2C voltage-gated ion channel cation transporter	
bifunctional acetaldehyde-CoA dehydrogenase%2Firon-depende	K04072
short chain dehydrogenase	
hypothetical protein	
superoxide dismutase%2C Fe	K04564
glutaredoxin	K07390
response regulator receiver domain-containing protein	
transporter	K07084
ribonuclease T	K03683
flagellar motor protein MotY	
hypothetical protein	
glyoxalase I%2C Ni-dependent	K01759
DNA glycosylase and apyrimidinic %28AP%29 lyase	K10773

electron transport complex protein RsxE	K03613
electron transport complex protein RnfG	K03612
inner membrane oxidoreductase %28Rnf%2FRsx reducing systen	K03614
electron transport complex protein RnfC	K03615
electron transport complex protein RnfB	K03616
Na%28%2B%29-translocating NADH-quinone reductase subunit I	K03617
excinuclease ABC subunit B	K03702
autoinducer repressor protein LuxO	K10912
autoinducer phosphorelay protein LuxU	K10911
transferase	
molybdenum cofactor biosynthesis protein A	K03639
molybdenum cofactor biosynthesis protein MoaC	K03637
molybdopterin synthase small subunit	K03636
molybdopterin synthase%2C large subunit	K03635
glutathione synthase%2Fribosomal protein S6 modification glutaminyl transferase	
hypothetical protein	
ATP-dependent Zn protease	
S-adenosyl-L-methionine-dependent methyltransferase	
methyltransferase	
aspartyl-tRNA synthetase	K01876
Holliday junction resolvase	K01159
Holliday junction DNA helicase RuvA	K03550
Holliday junction DNA helicase RuvB	K03551
cytochrome d terminal oxidase%2C subunit I	K00425
cytochrome d terminal oxidase%2C subunit II	K00426
cyd operon protein YbgT	
hypothetical protein	
acyl-CoA thioesterase	K07107
membrane spanning protein in TolA-TolQ-TolR complex	K03562
membrane spanning protein in TolA-TolQ-TolR complex	K03560
membrane anchored protein in TolA-TolQ-TolR complex	K03646
translocation protein TolB	K03641
peptidoglycan-associated outer membrane lipoprotein	K03640
hypothetical protein	
quinolinate synthetase	K03517
hypothetical protein	K07039
hypothetical protein	
beta-lactamase family protein	
potential redox protein	
C factor cell-cell signaling protein	
GTP-binding protein HflX	K03665
RNA polymerase sigma factor SigZ	K03088
glutamate--cysteine ligase	K01919

multidrug ABC transporter ATP-binding protein	K06147
multidrug ABC transporter ATP-binding protein	K06147
glutathione synthetase	K01920
acetyltransferase	K00680
quinone oxidoreductase	K00344
hypothetical protein	
transporter	
hypothetical protein	
hypothetical protein	
lipoprotein	K09712
lipoprotein	
diguanylate cyclase	
ClC family chloride transporter	K01183
methyl-accepting chemotaxis protein	K03406
hypothetical protein	
diguanylate cyclase %28GGDEF%29%2C inhibitor of flagellar motility	
serine%2Fthreonine protein kinase	K08282
protein phosphatase 2C	K01090
secretion protein IcmF	K11891
OmpA family protein	K11892
hypothetical protein	K11893
phospho-specific protein-protein interaction motif-containing pr	K11894
transcriptional regulator	
ATP-dependent protease subunit	K11907
hypothetical protein	K11896
hypothetical protein	K11900
hypothetical protein	K11910
hypothetical protein	
primosomal replication protein N%27	K04067
hypothetical protein	K07090
ATP-dependent DNA helicase DinG	K03722
hypothetical protein	
hypothetical protein	
ATP phosphoribosyltransferase	K00765
histidinol dehydrogenase	K00013
histidinol-phosphate aminotransferase	K00817
imidazole glycerol-phosphate dehydratase%2Fhistidinol phospha	K01089
imidazole glycerol phosphate synthase subunit HisH	K02501
1-%285-phosphoribosyl%29-5-%5B%285-phosphoribosylamino%	K01814
imidazole glycerol phosphate synthase subunit HisF	K02500
bifunctional phosphoribosyl-AMP cyclohydrolase%2Fphosphorib	K11755
23S rRNA and tRNA pseudouridine synthase	K06177
methyltransferase	K06969

hypothetical protein	
hypothetical protein	K09780
hydrolase	K10806
intracellular septation protein A	K06190
glutamate%2Faspartate:proton symporter	
tryptophan synthase subunit alpha	K01695
tryptophan synthase subunit beta	K01696
bifunctional indole-3-glycerol phosphate synthase%2Fphosphoril	K13498
anthranilate phosphoribosyltransferase	K00766
anthranilate synthase component II	K01658
component I of anthranilate synthase	K01657
hypothetical protein	K07053
hypothetical protein	K07566
autoinducer regulatory protein AinR	
C8-HSL autoinducer synthesis protein AinS	K13062
23S rRNA pseudouridylate synthase	K06178
short chain dehydrogenase	
periplasmic protease	K04774
hypothetical protein	
hypothetical protein	
hypothetical protein	
reverse transcriptase	K00986
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
DNA methylase	K07319
hypothetical protein	
DNA topoisomerase I	K03168
divalent anion:sodium symporter family protein	K14445
sensory transduction protein kinase	K00936
ScrF protein	K03413
fermentative D-lactate dehydrogenase%2C NAD-dependent	K03778
phosphoglucomutase	K01840
lysine exporter protein	
isomerase%2Fhydrolase	
basic endochitinase	
peptidase T	K01258
anaerobic C4-dicarboxylate transporter	K03326
adenylosuccinate synthetase	K01939
transcriptional regulator	
glutamate decarboxylase	K01580
hypothetical protein	K07085

LysR family transcriptional regulator	
quinol oxidase subunit	
pirin	K06911
CDP-4-dehydro-6-deoxy-D-glucose 3-dehydratase	K01726
CDP-4-dehydro-6-deoxy-D-glucose 3-dehydratase	
LysR family transcriptional regulator	
hypothetical protein	
AraC family transcriptional regulator	
amino acid transporter LysE	
sulfite-dehydrogenase	K07147
protein NirV	
hypothetical protein	
TetR family transcriptional regulator	
glutathione S-transferase	K00799
glutathione S-transferase YghU	K11209
branched-chain amino acid transport system II carrier protein	
hypothetical protein	
transcriptional regulatory protein	
hypothetical protein	
anaerobic C4-dicarboxylate transporter	K07792
hypothetical protein	K07080
transporter	
methyl-accepting chemotaxis protein	K03406
methyl-accepting chemotaxis protein	
glutamate-gated potassium channel	K02030
SAM-dependent methyltransferase	
LysR family transcriptional regulator	
nucleoside permease NupC	K03317
BAX protein	
peptidyl-prolyl cis-trans isomerase	K03768
beta-lactamase	K01467
D-cysteine desulfhydrase	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
transporter	
ABC transporter permease	
ABC transporter ATP-binding protein	K09810
molecular chaperone DnaJ	K03686
hypothetical protein	
LysR family transcriptional regulator	
nonspecific acid phosphatase	

DNA-binding transcriptional regulator	
N-acetylmuramic acid 6-phosphate etherase	K07106
PTS system N-acetylmuramic acid transporter subunit IIBC	K11192
transcriptional regulatory protein	
methyl-accepting chemotaxis protein	
hypothetical protein	
permease	K07090
acetyltransferase	K03824
transporter	K03451
prolyl endopeptidase	K01322
lipoprotein	
transporter	K03305
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
23S rRNA methyltransferase	K00599
hypothetical protein	
alpha-amylase	K01176
methyl-accepting chemotaxis protein	K03406
purine nucleoside phosphoramidase	
hypothetical protein	K09859
hypothetical protein	
lipoprotein	K07337
methyl-accepting chemotaxis protein%2C TcpI-related	K10961
hypothetical protein	K09923
methyltransferase	K00599
thiamine kinase	
hypothetical protein	K07000
respiratory NADH dehydrogenase 2%2Fcupric reductase	K03885
DNA and RNA helicase	
hypothetical protein	
chitodextrinase	
peptide transporter induced by carbon starvation	
two-component response-regulatory protein YehT	K02477
sensory kinase in two-component system with YehT	K02478
inner membrane protein associated with acetate transport	K07034
hypothetical protein	
heat shock protein HtpX	K03799
hypothetical protein	
hypothetical protein	
proton glutamate symport protein	

chlorohydrolase%2Fdeaminase family protein	
carboxypeptidase	
hypothetical protein	
asparaginyl-tRNA synthetase	K01893
6-pyruvoyl tetrahydrobiopterin synthase	K01737
periplasmic protein of efflux system	K02005
outer membrane protein TolC	
export ABC transporter permease	K02004
export ABC transporter permease	K02004
macrolide ABC transporter ATP-binding%2Fmembrane protein	K02003
hypothetical protein	
exonuclease SbcD	K03547
exonuclease%2C dsDNA%2C ATP-dependent	K03546
acyl-CoA hydrolase	
hypothetical protein	
tyrosine-specific transport protein	K03834
tyrosine-specific transport protein	
lipoprotein	
lipoprotein	
hypothetical protein	
L-serine deaminase I	K01752
serine transporter	K03837
NUDIX hydrolase	K01529
aminodeoxychorismate synthase subunit I	K01665
anaerobic class I fumarate hydratase	K01676
lipoprotein	
acriflavin resistance periplasmic protein	
acriflavin resistance periplasmic protein	
acriflavin resistance plasma membrane protein	
hypothetical protein	
cystathionine beta-lyase	K01760
hypothetical protein	
Fe-containing alcohol dehydrogenase	K13954
GTP cyclohydrolase II	K01497
hypothetical protein	K07231
thiol oxidoreductase	
lipoprotein	K07338
hypothetical protein	K09947
metal-binding protein	
hypothetical protein	
hypothetical protein	
tyrosine transporter	K03834
competence-damage protein	K03742

%28Fe-S%29-binding protein	K11107
diguanylate cyclase	
ribonucleotide-diphosphate reductase subunit beta	K00526
ribonucleotide-diphosphate reductase subunit alpha	K00525
3-demethylubiquinone-9 3-methyltransferase	K00568
DNA gyrase subunit A	K02469
hypothetical protein	
PAP2 family phosphoesterase	
chaperone	K04046
hypothetical protein	K09900
membrane metalloprotease	
Gram-positive sporulation control protein Spo0M	K06377
hypothetical protein	
lactoylglutathione lyase	K01759
hypothetical protein	
threonyl-tRNA synthetase	K01868
protein chain initiation factor IF-3	K02520
50S ribosomal protein L35	K02916
50S ribosomal protein L20	K02887
oxidoreductase NAD-binding domain-containing protein	
hemin importer ATP-binding subunit	K02013
hemin transport system permease HmuU	K02015
hemin-binding periplasmic protein HmuT precursor	K02016
TonB system transport protein ExbD1	
TonB system transport protein ExbB1	K03561
TonB1 protein	K03832
coproporphyrinogen III oxidase	K02495
HuvX protein	K07227
HutZ protein	K07226
VgrG protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
heme transport protein HutA	K02014
phenylalanyl-tRNA synthetase subunit alpha	K01889
phenylalanyl-tRNA synthetase subunit beta	K01890
integration host factor subunit alpha	K04764
succinylglutamate desuccinylase	K05526
oligoendopeptidase F	K08602
nucleotide-binding protein	K09767
phospho-2-dehydro-3-deoxyheptonate aldolase	K01626
phosphoenolpyruvate synthase	K01007

hypothetical protein	
hypothetical protein	K00243
diguanylate cyclase	
outer membrane protease	
lipoprotein precursor	
cystathionine beta-lyase	
phosphoenolpyruvate phosphomutase	K01841
C4-dicarboxylate anaerobic carrier	
hypothetical protein	
ureidoglycolate dehydrogenase	
cystathionine beta-lyase	K14155
transcriptional repressor	K02529
3%27%2C5%27-cyclic-nucleotide phosphodiesterase	K01120
hypothetical protein	
acyl-CoA hydrolase	K10806
hypothetical protein	
TetR family transcriptional regulator	
lactoylglutathione lyase family protein	
glutaredoxin	
mercuric reductase	
chlorohydrolase%2Faminohydrolase	
hypothetical protein	
multidrug efflux system	
DNA polymerase V%2C subunit D	K03503
cyclohexadienyl dehydratase	K01713
hypothetical protein	
elongation factor P	K02356
hypothetical protein	
rRNA %28cytosine-C%285%29-%29-methyltransferase RsmF	K11392
paraquat-inducible protein B	
paraquat-inducible protein A	K03808
transporter	K06147
hypothetical protein	K07170
solute%2FDNA competence effector	K03607
carboxy-terminal protease	K03797
hypothetical protein	
aminopeptidase	K01256
hypothetical protein	
NAD-specific glutamate dehydrogenase	K00260
dihydroorotate dehydrogenase 2	K00226
hypothetical protein	
23S rRNA m%282%29G2445 methyltransferase	K12297
glutaredoxin-like domain-containing protein	

ABC transporter ATPase	
hypothetical protein	
ribosome modulation factor	K03812
3-hydroxydecanoyl-ACP dehydratase	K01716
ATP-dependent protease %28Lon-like%29	K04770
hypothetical protein	K09911
hypothetical protein	
hybrid sensory histidine kinase	K00936
hypothetical protein	
hypothetical protein	
cbb3-type cytochrome c oxidase subunit I	K00404
cbb3-type cytochrome c oxidase subunit II	K00405
cytochrome oxidase component FixQ	K00407
cytochrome c oxidase%2C cbb3-type subunit III	K00406
hypothetical protein	K09926
copper-exporting ATPase	K01533
cbb3-type cytochrome oxidase maturation protein	
hypothetical protein	K09792
fumarate%2Fnitrate reduction transcriptional regulator	K01420
universal stress protein UspE	K14055
C32 tRNA thiolase	K14058
hypothetical protein	
hypothetical protein	K03796
hypothetical protein	
putrescine%2Fspermidine ABC transporter ATPase	K11072
spermidine%2Fputrescine ABC transporter membrane protein	K11071
spermidine%2Fputrescine ABC transporter membrane protein	K11070
polyamine transporter binding protein	K11069
polyamine transporter binding protein	K11069
NAD-dependent deacetylase	K12410
LysR family transcriptional regulator	
nucleoside permease NupC	K03317
lipoprotein	
pentapeptide repeat-containing protein	
hypothetical protein	
acetyltransferase	K00680
transporter	
ferrichrome-binding protein	
soluble lytic murein transglycosylase	K08309
carbohydrate binding domain-containing protein	
hypothetical protein	
sodium-driven multidrug efflux pump	
LysR family transcriptional regulator	

oxalate%2Fformate antiporter	
phosphohydrolase	K06950
hypothetical protein	
maltose O-acetyltransferase	K00661
neutral amino-acid efflux system	
hypothetical protein	
hypothetical protein	
hypothetical protein	K03478
phosphoribosylaminoimidazole carboxylase ATPase subunit	K11312
hypothetical protein	
acetyltransferase	K03830
ribosomal-protein-L7%2FL12-serine acetyltransferase	K03817
hypothetical protein	
alkylphosphonate utilization operon protein	K06193
cytoplasmic protein	
subtilisin-like serine protease	
diguanylate cyclase	
hypothetical protein	
MutT%2Fnudix family protein	K08310
virulence gene repressor RsaL	K07726
DNA-binding protein	K03655
hypothetical protein	
hypothetical protein	
formate dehydrogenase N subunit gamma	K00127
formate dehydrogenase N subunit beta	K00124
formate dehydrogenase N subunit alpha	K00123
Tat pathway signal sequence domain-containing protein	
TorD family cytoplasmic chaperone	
formate hydrogenlyase subunit 6	
hypothetical protein	
hypothetical protein	
formate dehydrogenase subunit delta	K02379
two-component response regulator	
membrane-bound lytic murein transglycosylase C	K08306
methyl-accepting chemotaxis protein	K03406
pyrrolidone-carboxylate peptidase	K01304
permease	
permease	
transporter	
allophanate hydrolase subunit 2	
allophanate hydrolase subunit 1	
LamB%2FYcsF family protein	K07160
hypothetical protein	

LysR family transcriptional regulator	
hypothetical protein	
penicillin-binding protein	
hypothetical protein	
ribosomal-protein-alanine acetyltransferase	K00676
U32 family peptidase	K08303
glutathione S-transferase	
histone acetyltransferase HPA2	
acetyltransferase	
3-mercaptopyruvate sulfurtransferase	K01011
epimerase	
ribosomal-protein-alanine acetyltransferase	K00676
carbohydrate binding domain-containing protein	
lipoprotein	
hypothetical protein	
hypothetical protein	
glycine betaine transporter	
hypothetical protein	
DNA-binding response regulator	
sensor histidine kinase	
hypothetical protein	
cell wall biosynthesis glycosyltransferase	K00786
sensor histidine kinase	K02482
Fis family transcriptional regulator	
molybdate ABC transporter periplasmic binding protein ModA	K05772
molybdate ABC transporter permease ModB	K05773
molybdate ABC transporter ATP-binding component ModC	K06857
molybdopterin-guanine dinucleotide biosynthesis protein MobA	K03752
bifunctional molybdopterin-guanine dinucleotide biosynthesis pr	K03750
preprotein translocase subunit-like protein	
N-acetyl-D-glucosamine kinase	K00884
hypothetical protein	K05812
aminobenzoyl-glutamate transporter	K12942
lipoprotein NlpC	
Type IIA topoisomerase%2C B subunit	
phosphotransferase%2Fkinase	
riboflavin synthase subunit alpha	K00793
multidrug efflux protein	K03327
hypothetical protein	
arylsulfatase	K06871
hypothetical protein	
LysR family transcriptional regulator	
hypothetical protein	

transporter	K07114
von Willebrand factor A	K07114
hypothetical protein	
MoxR protein	
MoxR protein	K03924
hypothetical protein	
acrylsulfatase-like protein	K01130
sulfatase family protein	K01130
hypothetical protein	
sulfatase family protein	K01130
hypothetical protein	
DNA-binding protein	
hypothetical protein	
hypothetical protein	K05952
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
DEAD%2FDEAH box helicase	
hypothetical protein	
lipoprotein	
hypothetical protein	
transcriptional regulatory protein	
D-ribose pyranase	K06726
D-ribose transporter ATP-binding protein	K10441
ribose ABC transporter permease	K10440
D-ribose transporter subunit RbsB	K10439
ribokinase	K00852
transcriptional repressor RbsR	K02529
DNA ligase	K01971
nuclease	K07004
sodium-driven multidrug efflux pump	
hypothetical protein	
sodium-linked D-alanine glycine permease	K03310
mechanosensitive ion channel MscS	K03442
homoserine%2Fhomoserine lactone efflux protein	
thermostable carboxypeptidase 1	K01299
LysR family transcriptional regulator	
hypothetical protein	
hypothetical protein	
hypothetical protein	
superfamily I DNA%2FRNA helicase	
superfamily I DNA%2FRNA helicase	K03658

small heat shock protein	K04080
molecular chaperone DnaK	K04043
hypothetical protein	
serine kinase HipA	K07154
hypothetical protein	K06876
zinc finger protein	
hypothetical protein	
exonuclease	
LysR family transcriptional regulator	
exoenzyme regulatory protein AepA precursor	K07047
hypothetical protein	K07126
hypothetical protein	
aquaporin Z	K06188
hypothetical protein	
penicillin binding protein transpeptidase	K05515
exonuclease I	K01141
murein hydrolase exporter	K06518
hypothetical protein	
cytidine deaminase	K01489
glutamyl-tRNA%28Gln%29 amidotransferase%2C subunit A	
phosphoribosylglycinamide formyltransferase 2	K08289
aromatic amino acid aminotransferase	K00832
hypothetical protein	
transcriptional regulator CysB	K13634
DNA repair ATPase	
tRNA-%28MS%282%29IO%286%29A%29-hydroxylase	K06169
hypothetical protein	
transporter	
cytoplasmic protein	K09749
glutaredoxin	K03676
hypothetical protein	
phosphoribosylaminoimidazole-succinocarboxamide synthase	K01923
hypothetical protein	
ATP-dependent RNA helicase HrpA	K03578
sulfur transfer protein TusE	K11179
acylphosphatase	K01512
methyl-accepting chemotaxis protein	K03406
methyl-accepting chemotaxis protein	
methyltransferase	K06969
RTX repeat-containing calcium-binding cytotoxin RtxA1	
hypothetical protein	
transporter	K03326
isoaspartyl dipeptidase	K01305

transcriptional regulator	
2%27%2C3%27-cyclic-nucleotide 2%27-phosphodiesterase	K01119
thiopurine S-methyltransferase	K00569
transporter	K06956
exonuclease KapD	
diguanylate cyclase	
hypothetical protein	
DnaK-like molecular chaperone	
DnaK-like molecular chaperone	
hypothetical protein	
hypothetical protein	
uridine phosphorylase	K00757
zinc%2Fcadmium%2Fmercury%2Flead-transporting ATPase	K01534
hypothetical protein	
hypothetical protein	
FAD-linked oxidoreductase	K06911
hypothetical protein	
L-asparaginase II	K01424
transcriptional regulator SyrB	
hypothetical protein	
GntR family transcriptional regulator	
ferrochelatase	K02304
general L-amino acid-binding protein	K09969
amino-acid transporter permease	K09970
amino-acid transporter permease	K09971
amino-acid transporter ATPase	K09972
hypothetical protein	K06890
hypothetical protein	
hypothetical protein	
transporter	
suppressor%2Fenhancer of lin-12	K07126
phosphohydrolase	
acetyltransferase	K00680
long-chain fatty acid transport protein	K06076
phosphatidylglycerophosphatase B	K01096
DNA-binding transcriptional regulator	
anaerobic C4-dicarboxylate transporter	K07791
aspartate racemase	K01779
heme lyase %28NrfEFG%29 for insertion of heme into c552%2C s	K02200
thiol:disulfide interchange protein TlpA	K02199
heme lyase %28NrfEFG%29 for insertion of heme into c552%2C s	K02198
formate-dependent nitrite reductase%2C membrane subunit	K04015
formate-dependent nitrite reductase%2C 4Fe4S subunit	K04014

cytochrome c nitrite reductase pentaheme subunit	K04013
cytochrome c552	K03385
heme lyase %28NrfEFG%29 for insertion of heme into c552%2C subunit NrfG	
outer membrane phospholipase A	K01058
ATP-dependent helicase HrpA	
malate dehydrogenase	K00027
hypothetical protein	
SanA protein	K03748
diguanylate cyclase	
hypothetical protein	K07274
hypothetical protein	
hypothetical protein	K02008
cobalt transport ATP-binding protein CbiO	K02006
hypothetical protein	
hypothetical protein	
23S rRNA pseudouridine synthase	K06182
hypothetical protein	
DNA-binding transcriptional regulator TorR	K07772
chaperone protein TorD	K03533
DNA-binding transcriptional repressor%2C hypoxanthine-binding	K03604
DNA transformation protein TfoX2 %28Sxy%29	K07343
hypothetical protein	
O6-methylguanine-DNA methyltransferase	K07443
outer membrane lipoprotein	K09914
acyl-CoA thioesterase	K10805
DNA-binding transcriptional regulator	K05800
cysteine synthase	K01738
queuosine biosynthesis protein QueC	K06920
acriflavin resistance plasma membrane protein	K03296
periplasmic protein of efflux system	
exonuclease III	K01142
glutaredoxin	K03675
histidine%2Flysine%2Farginine%2Fornithine transporter subunit	K10015
histidine%2Flysine%2Farginine%2Fornithine transporter subunit	K10016
lysine%2Farginine%2Fornithine transporter subunit	K02030
histidine%2Flysine%2Farginine%2Fornithine transporter subunit	K10017
hypothetical protein	
pyruvate formate lyase I	K00656
pyruvate formate lyase-activating enzyme 1	K04069
hypothetical protein	
oligopeptide transporter ATP-binding protein OppF	K02032
oligopeptide ABC transporter ATP-binding protein	K02031
oligopeptide transport system permease OppC	K02034

oligopeptide transporter permease	K02033
oligopeptide-binding protein OppA	K02035
exochitinase	K01183
thymidine kinase	K00857
cysteinyl-tRNA synthetase	K01883
peptidyl-prolyl cis-trans isomerase B	K03768
UDP-2%2C3-diacylglucosamine hydrolase	K03269
diguanylate cyclase	K07181
hypothetical protein	K09858
hypothetical protein	K03308
cardiolipin synthetase	K06131
GTP cyclohydrolase I	K01495
molybdopterin biosynthesis protein	K03750
molybdopterin biosynthesis protein MoeB	K11996
phosphate-binding protein	K02040
phosphate ABC transporter%2C permease protein PstC	K02037
phosphate ABC transporter%2C permease protein PstA	K02038
phosphate ABC transporter ATP-binding protein	K02036
hypothetical protein	
hypothetical protein	
hypothetical protein	K09909
hypothetical protein	
methyl-accepting chemotaxis protein	K03406
hybrid sensory histidine kinase in two-component regulatory sys	K07647
TMAO reductase system periplasmic protein TorT	K11930
methylglyoxal synthase	K01734
DNA helicase IV	K03658
hypothetical protein	
hypothetical protein	
phosphatidylglycerophosphate synthetase	K00995
excinuclease ABC subunit C	K03703
response regulator	K07689
DNA polymerase II	K02336
hypothetical protein	
sodium:proton antiporter	
global DNA-binding transcriptional dual regulator H-NS	K03746
scaffolding protein for murein synthesizing machinery	K07274
fatty acid metabolism regulator	K03603
sodium%2Fproton antiporter	K03314
disulfide bond formation protein B	K03611
preprotein translocase subunit-like protein	K07039
MshA-like protein	
tRNA-dihydrouridine synthase C	K05541

diguanylate cyclase	
hypothetical protein	
DNA topoisomerase III	K03169
2%2C4-dienoyl-CoA reductase	K00219
endopeptidase IV	K04773
asparaginase	K01424
aspartate-semialdehyde dehydrogenase	K00133
malate-2-proton%2Flactate-sodium antiporter	K03315
hypothetical protein	
nucleoid-associated protein NdpA	K06899
hypothetical protein	K09904
hydrolase%2C inner membrane	K07014
A-type carbonic anhydrase	K01674
methyl-accepting chemotaxis protein	
hypothetical protein	K01243
acetyltransferase	K03828
hypothetical protein	
hypothetical protein	
oxidoreductase	K04126
short chain dehydrogenase	
hypothetical protein	
hypothetical protein	K09160
hypothetical protein	K06940
DNA-binding protein	
Tim44-like domain-contain protein	
TetR family transcriptional regulator	
1-acyl-sn-glycerol-3-phosphate acyltransferase	
O-succinylbenzoic acid--CoA ligase	K01911
O-succinylbenzoate synthase	K02549
naphthoate synthase	K01661
acyl-CoA thioester hydrolase	K08680
2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate	K02551
isochorismate synthase 2	K02552
aminotransferase	K14260
oligopeptide-binding protein OppA	
pyrimidine reductase	
hypothetical protein	
DNA-binding transcriptional regulator	
alcohol dehydrogenase	K08325
hypothetical protein	
drug%2Fmetabolite exporter family protein	
coniferyl aldehyde dehydrogenase	K00154
deoxyguanosinetriphosphate triphosphohydrolase-like protein	K01129

cytoplasmic protein	
rhomboid family integral membrane protein	
recombination protein RecR	K06187
hypothetical protein	K09747
DNA polymerase III subunits gamma and tau	K02343
adenine phosphoribosyltransferase	K00759
proteolytic adapter for RpoS degradation by ClpXP %28RssB%2C ExpM%29	
LysR family transcriptional regulator	K10918
amidophosphoribosyltransferase	K00764
membrane protein required for colicin V production	K03558
DedD protein	K03749
bifunctional folylpolyglutamate synthase%2F dihydrofolate synth	K11754
acetyl-CoA carboxylase subunit beta	K01963
tRNA pseudouridine synthase A	K06173
latent nuclear antigen	K07288
aspartate-semialdehyde dehydrogenase	K00133
erythronate-4-phosphate dehydrogenase	K03473
3-oxoacyl-ACP synthase	K00647
5-methylaminomethyl-2-thiouridine methyltransferase	K00599
membrane-bound lytic murein transglycosylase B	K08305
hypothetical protein	K09902
septum formation inhibitor	K03610
membrane ATPase of the MinC-MinD-MinE system	K03609
cell division topological specificity factor MinE	K03608
ribonuclease D	K03684
long-chain-fatty-acid--CoA ligase	K01897
hydrolase	K01567
outer membrane protein Slp	K07285
hypothetical protein	
peptidase	K14742
hypothetical protein	K03722
formyltetrahydrofolate deformylase	K01433
tetranactin resistance protein	
AraC family transcriptional regulator	
drug%2Fmetabolite exporter family protein	
bifunctional beta-cystathionase%2C PLP-dependent%2F regulato	K14155
bifunctional PTS system maltose and glucose-specific transporter	K02791
DNA-binding transcriptional repressor MalI	
5-methyltetrahydropteroyltriglutamate--homocysteine S-methyl	K00549
DNA-binding transcriptional activator%2C homocysteine-binding	K03576
hypothetical protein	
C4-dicarboxylate transporter DcuC	K03326
secretory tripeptidyl aminopeptidase	K01269

hypothetical protein	K03423
tyrosyl-tRNA synthetase	K01866
hypothetical protein	
hypothetical protein	
sodium%2Fproline symporter	K03308
stringent starvation protein A	
PTS system glucose-specific transporter subunit IIBC	K02779
metallodependent hydrolase	K03424
DNA polymerase III%2C delta prime subunit	K02341
thymidylate kinase	K00943
aminodeoxychorismate lyase	K07082
4-amino-4-deoxychorismate lyase	K02619
3-oxoacyl-ACP synthase	K09458
acyl carrier protein	K02078
3-ketoacyl-ACP reductase	K00059
malonyl-CoA:%28acyl carrier protein%29 S-malonyltransferase	K00645
3-oxoacyl-ACP synthase	K00648
glycerol-3-phosphate acyltransferase PlsX	K03621
50S ribosomal protein L32	K02911
hypothetical protein	K07040
hypothetical protein	
23S rRNA pseudouridylate synthase	K06179
hypothetical protein	K08300
sulfate transporter	
cob%28I%29yrinic acid a%2Cc-diamide adenosyltransferase	K00798
assembly protein	K07289
uridine kinase	K00876
antiporter inner membrane protein	K03593
methionyl-tRNA synthetase	K01874
orotidine 5%27-phosphate decarboxylase	K01591
tetratricopeptide repeat protein	
hypothetical protein	K08992
integration host factor subunit beta	K05788
30S ribosomal protein S1	K02945
cytidylate kinase	K00945
3-phosphoshikimate 1-carboxyvinyltransferase	K00800
leucyl%2Fphenylalanyl-tRNA--protein transferase	K00684
arginyl-tRNA-protein transferase	K00685
translation initiation factor IF-1	K02518
ATP-dependent Clp protease ATP-binding subunit	K03694
ATP-dependent Clp protease adaptor protein ClpS	K06891
DNA replication inhibitor	K03704
hypothetical protein	

hypothetical protein	
bifunctional 5%2C10-methylene-tetrahydrofolate dehydrogenas	K01491
serine kinase PrkA	K07180
hypothetical protein	K09786
SpoVR family protein	
isocitrate dehydrogenase	K00031
23S rRNA pseudouridine synthase	K06181
hypothetical protein	
methyl-accepting chemotaxis protein	K03406
tellurite resistance protein B	
ferredoxin-NADP reductase	K00528
nitric oxide reductase	K12265
anaerobic nitric oxide reductase flavorubredoxin	K12264
anaerobic nitric oxide reductase transcriptional regulator	K12266
tRNA-specific 2-thiouridylase MnmA	K00566
hypothetical protein	K07153
adenylosuccinate lyase	K01756
AraC family transcriptional regulator	
hypothetical protein	
methyl-accepting chemotaxis protein	K03406
ATP-dependent RNA helicase	
serine protease	K07001
hypothetical protein	
formate--tetrahydrofolate ligase	K01938
hypothetical protein	K09161
outer membrane protein OmpC	
23S rRNA methyltransferase	K00563
hypothetical protein	
chloride channel protein	K03281
lipid A biosynthesis %28KDO%292-%28lauroyl%29-lipid IVA acylt	K02560
HIT family hydrolase	
hypothetical protein	
hypothetical protein	K09906
magnesium transport ATPase protein C	K07507
hypothetical protein	
chorismate synthase	K01736
N5-glutamine S-adenosyl-L-methionine-dependent methyltransf	K07320
hypothetical protein	
phosphohistidine phosphatase	K08296
protease III	
multifunctional fatty acid oxidation complex subunit alpha	K01782
3-ketoacyl-CoA thiolase	K00632
long-chain fatty acid transport protein	K06076

long-chain fatty acid transport protein	K06076
hypothetical protein	K08984
VacJ lipoprotein	K04754
cytochrome c-type biogenesis protein CcmI	
cytochrome c-type biogenesis protein CcmH	K02200
periplasmic thioredoxin of cytochrome c-type biogenesis	K02199
heme lyase%2C CcmF subunit	K02198
cytochrome c-type biogenesis protein CcmE	K02197
heme exporter protein D	K02196
heme exporter subunit C	K02195
heme exporter subunit B	K02194
cytochrome c biogenesis protein CcmA	K02193
hypothetical protein	
chemotaxis coupling protein CheW	K03408
chemotaxis coupling protein	K03408
chromosome partitioning protein ParA	K03496
chemotaxis-specific methylesterase	K03412
chemotactic sensory histidine kinase CheA%2C in two-componer	K03407
chemotaxis regulator CheZ%2C protein phosphatase for CheY	K03414
chemotaxis regulator CheY%2C transmits signal to flagellar moto	K03413
flagellar biosynthesis sigma factor	K02405
flagellar synthesis regulator FlhG	K04562
flagellar biosynthesis regulator FlhF	K02404
flagellar biosynthesis protein FlhA	K02400
hypothetical protein	
flagellar biosynthesis protein FlhB	K02401
flagellar biosynthesis protein FliR	K02421
flagellar biosynthesis protein FliQ	K02420
flagellar biosynthesis protein FliP	K02419
flagellar biosynthesis protein FliO	K02418
flagellar motor switch protein	K02417
flagellar motor switch protein FliM	K02416
flagellar basal body protein FliL	K02415
flagellar hook length control protein FliK	K02414
flagellar biosynthesis chaperone	K02413
flagellum-specific ATP synthase	K02412
flagellar assembly protein H	K02411
flagellar motor switch protein G	K02410
flagellar MS-ring protein	K02409
flagellar hook-basal body protein FliE	K02408
two-component response regulator FlrC	K10943
sensory histidine kinase FlrB	K10942
sigma-54-dependent transcriptional activator FlrA	K10941

flagellar protein FliS	K02422
flagellar protein FlaI	K06604
flagellar capping protein	K02407
flagellar protein FlaG	K06603
flagellin	K02406
flagellin	K02406
flagellin	K02406
flagellin	K02406
flagellin	K02406
flagellar hook-associated protein FlgL	K02397
flagellar hook-associated protein FlgK	K02396
flagellar rod assembly protein%2Fmuramidase FlgJ	K02395
flagellar basal body P-ring biosynthesis protein FlgA	K02394
flagellar basal body L-ring protein	K02393
flagellar basal body rod protein FlgG	K02392
flagellar basal body rod protein FlgF	K02391
flagellar hook protein FlgE	K02390
flagellar basal body rod modification protein	K02389
flagellar basal body rod protein FlgC	K02388
flagellar basal-body rod protein FlgB	K02387
chemotaxis regulator%2C protein-glutamate methyltransferase%	K00575
chemotaxis protein CheW	K03415
flagellar basal body P-ring biosynthesis protein FlgA	K02386
flagellar anti-sigma-28 factor FlgM	K02398
chaperone FlgN	K02399
hypothetical protein	K09860
hypothetical protein	
hypothetical protein	
hypothetical protein	
glutamyl-tRNA synthetase	K01885
lipoprotein	
chitoporin ChiP	
NAD-dependent DNA ligase LigA	K01972
cell division protein ZipA	K03528
sulfate transport protein CysZ	K06203
cysteine synthase A	K01738
phosphohistidinoprotein-hexose phosphotransferase componen	K02784
phosphoenolpyruvate-protein phosphotransferase	K08483
PTS system glucose-specific transporter	K02777
hypothetical protein	K07223
hypothetical protein	
competence protein ComE	
hypothetical protein	

hypothetical protein	
nitrate reductase%2C cytochrome c-type%2C periplasmic	K02569
nitrate reductase%2C small%2C cytochrome C550 subunit%2C pe	K02568
nitrate reductase catalytic subunit	K02567
protein required for assembly of periplasmic nitrate reductase %	K02570
ferredoxin-type protein	K02572
nitrate%2Fnitrite sensor protein NarQ	K07674
DNA-binding response regulator in two-component regulatory sy	K07685
ubiquinone biosynthesis protein AarF	
hypothetical protein	
hypothetical protein	
arsenate reductase	
succinyl-diaminopimelate desuccinylase	K01439
D-alanyl-D-alanine carboxypeptidase	
hypothetical protein	
lipoprotein	K07287
dihydrodipicolinate synthase	K01714
DNA-binding transcriptional repressor	K03567
thioredoxin-dependent thiol peroxidase	K03564
hypothetical protein	K03548
peptidase	
oxidoreductase	K00537
hypothetical protein	
hypothetical protein	K09938
uracil transporter	K02824
uracil phosphoribosyltransferase	K00761
phosphoribosylaminoimidazole synthetase	K01933
phosphoribosylglycinamide formyltransferase 1	K11175
amidotransferase	K07008
phosphoheptose isomerase	K03271
acyl-CoA dehydrogenase	K06445
ferredoxin-dependent glutamate synthase	
DNA polymerase III subunit epsilon	K02342
ribonuclease H	K03469
S-adenosyl-L-methionine-dependent methyltransferase	K00599
hydroxyacylglutathione hydrolase	K01069
membrane-bound lytic murein transglycosylase D	K08307
hypothetical protein	
hypothetical protein	
regulatory protein P-II for glutamine synthetase	K04751
cytochrome c-554%28548%29	
tRNA%28Ile%29-lysidine synthetase	K04075
acetyl-CoA carboxylase carboxyltransferase subunit alpha	K01962

DNA polymerase III subunit alpha	K02337
ribonuclease HII	K03470
lipid-A-disaccharide synthase	K00748
UDP-N-acetylglucosamine acyltransferase	K00677
%283R%29-hydroxymyristoyl-ACP dehydratase	K02372
UDP-3-O-%5B3-hydroxymyristoyl%5D glucosamine N-acyltransfe	K02536
periplasmic chaperone	K06142
outer membrane protein assembly factor YaeT	K07277
membrane-associated zinc protease	K11749
1-deoxy-D-xylulose 5-phosphate reductoisomerase	K00099
CDP-diglyceride synthase	K00981
undecaprenyl pyrophosphate synthase	K00806
ribosome recycling factor	K02838
uridylate kinase	K09903
elongation factor Ts	K02357
30S ribosomal protein S2	K02967
methionine aminopeptidase	K01265
PII uridylyl-transferase	K00990
hypothetical protein	
preprotein translocase subunit SecF	K03074
preprotein translocase subunit SecD	K03072
preprotein translocase subunit YajC	K03210
queuine tRNA-ribosyltransferase	K00773
S-adenosylmethionine--tRNA ribosyltransferase-isomerase	K07568
acetoin utilization AcuB protein	
isocitrate lyase	K01637
malate synthase	K01638
LysR family transcriptional regulator	K04761
alkyl hydroperoxide reductase	K03386
copper homeostasis protein	K06201
hypothetical protein	
accessory colonization factor AcfA-like protein	K10936
LysR family transcriptional regulator	
hypothetical protein	
hypothetical protein	
transcriptional regulator PhoU	K02039
phosphate transporter ATP-binding protein	K02036
phosphate transport system permease protein PstA	K02038
phosphate transport system permease protein PstC	K02037
phosphate-binding protein	K02040
phosphate regulon sensor protein	K07636
DNA-binding response regulator in two-component regulatory sy	K07657
recombination associated protein	K03554

peptidase	K08303
%284Fe-4S%29-binding protein	
hypothetical protein	
molecular chaperone DnaJ	K03686
molecular chaperone DnaK	K04043
hypothetical protein	
heat shock protein	K03687
inorganic polyphosphate%2FATP-NAD kinase	K00858
recombination and repair protein	K03631
small protein A	K06186
hypothetical protein	K09801
hypothetical protein	
SsrA-binding protein	K03664
hypothetical protein	
hypothetical protein	
phage tail protein	
phage R protein	
hypothetical protein	
tail sheath protein	
major capsid protein	
capsid scaffolding protein	
capsid portal protein	
hypothetical protein	
phage tail protein	
phage protein	
phage tail protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
exodeoxyribonuclease VIII	
hypothetical protein	
hypothetical protein	
hypothetical protein	
phage regulatory protein %28CII%29	
Cro%2FCI family transcriptional regulator	
hypothetical protein	
hypothetical protein	
hypothetical protein	
DNA integration%2Frecombination%2Finvertion protein	
methyl-accepting chemotaxis protein	K03406
maltose%2Fmaltodextrin-binding protein	K10108
maltose ABC transporter permease	K10109
maltose ABC transporter ATP-binding protein	K10112

hypothetical protein	
amylo-1%2C6-glucosidase	
maltodextrin glucosidase	K05992
LysR family transcriptional regulator	
magnesium transporter MgtE	K06213
hypothetical protein	
hypothetical protein	
cytochrome C peroxidase	K00428
pyridoxal kinase 2%2Fpyridoxine kinase	K00868
lysine decarboxylase 1	K01582
lysine%2Fcadaverine antiporter	K03757
sodium-linked D-alanine glycine permease	K03310
DNA-binding transcriptional activator CadC	K03765
hypothetical protein	K07112
hypothetical protein	K07112
homoserine O-succinyltransferase	K00651
anaerobic C4-dicarboxylate transporter	K07792
nucleoside permease NupC	K03317
hypothetical protein	
RNA polymerase%2C sigma-S %28sigma-38%29 factor	K03087
lipoprotein NlpD	K06194
protein-L-isoaspartate O-methyltransferase	K00573
stationary phase survival protein SurE	K03787
tRNA pseudouridine synthase D	K06176
2-C-methyl-D-erythritol 2%2C4-cyclodiphosphate synthase	K01770
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	K00991
cell division protein	K05589
phosphopyruvate hydratase	K01689
CTP synthetase	K01937
nucleoside triphosphate pyrophosphohydrolase	K02428
flagellin	K02406
%28p%29ppGpp synthetase I	K00951
23S rRNA 5-methyluridine methyltransferase	K03215
hybrid sensory histidine kinase BarA	K07678
4%27-phosphopantetheinyl transferase	K00997
pyridoxine 5%27-phosphate synthase	K03474
DNA repair protein RecO	K03584
GTP-binding protein Era	K03595
ribonuclease III	K03685
leader peptidase %28signal peptidase I%29	K03100
GTP-binding protein LepA	K03596
sigma-E factor regulatory protein RseC	K03803
periplasmic negative regulator of sigmaE	K03598

anti-sigmaE factor%2C inner membrane	K03597
RNA polymerase sigma factor RpoE	K03088
L-aspartate oxidase	K00278
hypothetical protein	
hypothetical protein	K09159
folate-dependent regulatory protein	K06980
regulatory protein	
hypothetical protein	
2-octaprenyl-6-methoxyphenol hydroxylase	
2-octaprenyl-6-methoxyphenyl hydroxylase	K03185
hypothetical protein	K09895
hypothetical protein	K09888
ligase	K01934
ribose-5-phosphate isomerase A	K01807
D-3-phosphoglycerate dehydrogenase	K00058
hypothetical protein	K09807
mechanosensitive ion channel MscS	K03442
hypothetical protein	K09861
transporter	K03310
hypothetical protein	
hypothetical protein	
uracil-DNA glycosylase	K03648
endonuclease IV	K01151
autonomous glycyl radical cofactor GrcA	K06866
threonine synthase	K01733
homoserine kinase	K00872
bifunctional aspartokinase I%2Fhomoserine dehydrogenase I	K12524
ribonuclease activity regulator protein RraA	K02553
two-component response regulator	K07773
lipoprotein	
aerobic respiration control sensor protein ArcB	K07648
Fe-S oxidoreductase	K07139
glutamate synthase%2C large subunit	K00265
glutamate synthase subunit beta	K00266
hypothetical protein	
5%27-methylthioadenosine%2FS-adenosylhomocysteine nucleos	K01243
adenosylcobinamide-phosphate synthase	K02227
hypothetical protein	
cell wall endopeptidase	
acriflavin resistance plasma membrane protein	
periplasmic protein of efflux system	
iron-sulfur cluster insertion protein ErpA	
glutamate-1-semialdehyde aminotransferase	K01845

permease	
16S rRNA m2G1207 methylase	K00564
chitin sensor histidine kinase ChiS	K00936
chitooligosaccharide-binding protein	K02035
chitooligosaccharide transport system permease	K02033
chitooligosaccharide transport system permease	K02034
chitooligosaccharide transport ATP-binding protein	K02031
chitooligosaccharide transport ATP-binding protein	K02032
endochitinase	
N-acetylglucosamine kinase	
beta-hexosaminidase	K12373
N%2CN%27-diacetylchitobiose phosphorylase	
phosphoglucomutase	K01840
iron%28III%29-transport system ATP-binding protein	K02010
iron%28III%29-transport system permease SfuB	K02011
iron%28III%29 ABC transporter periplasmic binding protein	K02012
ammonium transporter	
nitrogen regulatory protein GlnK	K04752
hypothetical protein	K09910
DNA-binding transcriptional activator	K02647
fructuronate transporter	
glycerate kinase	K00865
bifunctional aconitate hydratase 2%2F2-methylisocitrate dehydr	K01682
serine protease	K07001
methyl-accepting chemotaxis protein	K03406
bifunctional glycosyl transferase and transpeptidase	K05365
ATP-dependent RNA helicase HrpB	K03579
sugar fermentation stimulation protein A%2C DNA-binding trans	K06206
DNA-binding transcriptional regulator of rRNA transcription%2C	K06204
poly%28A%29 polymerase	K00970
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosp	K00950
3-methyl-2-oxobutanoate hydroxymethyltransferase	K00606
pantoate--beta-alanine ligase	K01918
ABC transporter membrane protein	K09686
ABC transporter ATP-binding protein	K09687
transporter	K03321
carbonic anhydrase	K01673
hypothetical protein	
hypoxanthine phosphoribosyltransferase	K00760
quorum sensing transcriptional regulator LitR	K10913
dihydrolipoamide dehydrogenase	K00382
dihydrolipoamide acetyltransferase	K00627
pyruvate dehydrogenase%2C decarboxylase component E1%2C t	K00163

transcriptional regulator PdhR	K05799
N-acetyl-anhydromuranmyl-L-alanine amidase	K03806
quinolinate phosphoribosyltransferase	K00767
pilus assembly protein PilB	K02652
type 4 prepilin peptidase PilD	K02654
dephospho-CoA kinase	K00859
hypothetical protein	
zinc-binding protein	K09862
nucleoside triphosphate pyrophosphohydrolase	K03574
preprotein translocase subunit SecA	K03070
hypothetical protein	
UDP-3-O-%5B3-hydroxymyristoyl%5D N-acetylglucosamine deac	K02535
cell division protein FtsZ	K03531
cell division protein FtsA	K03590
cell division protein FtsQ	K03589
UDP-N-acetylmuramate--L-alanine ligase	K01924
undecaprenyldiphospho-muramoylpentapeptide beta-N- acetylg	K02563
integral membrane protein involved in stabilizing FtsZ ring durin	K03588
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	K01925
phospho-N-acetylmuramoyl-pentapeptide-transferase	K01000
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	K01929
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso-diaminopim	K01928
transpeptidase	K03587
membrane bound cell division protein	K03586
S-adenosyl-methyltransferase MraW	K03438
methyltransferase	K07056
hypothetical protein	K07121
hypothetical protein	K07460
DnaA initiator-associating factor for replication initiation	K12961
hypothetical protein	
ClpXP protease specificity-enhancing factor	K03600
stringent starvation protein A	K03599
cytochrome c1	K00413
cytochrome b	K00412
ubiquinol-cytochrome c reductase iron-sulfur subunit	K00411
30S ribosomal protein S9	K02996
50S ribosomal protein L13	K02871
hypothetical protein	K06916
cytochrome d ubiquinol oxidase subunit III	K09908
serine endoprotease DegP %28protease Do%29%2C periplasmic	K04771
serine endoprotease DegS%2C periplasmic	K04691
DNA topoisomerase IV subunit A	K02621
DNA topoisomerase IV subunit B	K02622

esterase	K07000
cyclic 3%27%2C5%27-adenosine monophosphate phosphodieste	K03651
hypothetical protein	K09920
ADP-ribose pyrophosphatase	K01515
outer membrane channel protein	K12340
bifunctional heptose 7-phosphate kinase%2Fheptose 1-phosphat	K03272
bifunctional glutamine-synthetase adenylyltransferase%2Fdeade	K00982
methyl-accepting chemotaxis protein	K03406
potassium channel protein	
adenylate cyclase	
hypothetical protein	K07220
phosphate transporter%2C low-affinity	K03306
signal transduction protein	K07184
general secretion pathway protein B	K02451
general secretion pathway protein A	K02450
multifunctional tRNA nucleotidyl transferase%2F2%273%27-cycli	K00974
undecaprenyl pyrophosphate phosphatase	K06153
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosp	K00950
bifunctional dihydroneopterin aldolase%2Fdihydroneopterin trip	K01633
glycerol-3-phosphate acyltransferase PlsY	K08591
DNA-binding%2Firon metalloprotein%2FAP endonuclease	K01409
30S ribosomal protein S21	K02970
GatB%2FYqeY domain-containing protein	K09117
DNA primase	K02316
RNA polymerase sigma factor RpoD	K03086
hypothetical protein	
long-chain-fatty-acid--CoA ligase	K01897
hypothetical protein	
pyruvate kinase	K00873
DNA-binding transcriptional regulator	
hypothetical protein	
diguanylate cyclase	
acetolactate synthase 3 regulatory subunit	K01653
acetolactate synthase 3 catalytic subunit	K01652
long-chain-fatty-acid--CoA ligase	K01897
leucine transcriptional activator	K05798
bifunctional aspartate kinase II%2Fhomoserine dehydrogenase II	K12525
cystathionine gamma-synthase	K01739
transcriptional repressor protein MetJ	K03764
glycosidase	
hypothetical protein	
maltose operon periplasmic protein	K05775
bifunctional malic enzyme oxidoreductase%2F phosphotransacet	K00029

50S ribosomal protein L31	K02909
primosome assembly protein PriA	K04066
DNA-binding transcriptional regulator CytR	K05499
cell division protein FtsN	
ATP-dependent protease peptidase subunit	K01419
ATP-dependent protease ATP-binding subunit HslU	K03667
hypothetical protein	K07397
cAMP-regulatory protein	K10914
hypothetical protein	
succinylglutamic semialdehyde dehydrogenase	K06447
arginine succinyltransferase	K00673
bifunctional N-succinyldiaminopimelate-aminotransferase%2Fac	K00821
para-aminobenzoate synthase component II	K01664
tryptophanyl-tRNA synthetase	K01867
phosphoglycolate phosphatase	K01091
ribulose-phosphate 3-epimerase	K01783
DNA adenine methylase	K06223
hypothetical protein	K03112
3-dehydroquinate synthase	K01735
shikimate kinase I	K00891
pili ecretion protein PilQ	K02666
pili assembly protein PilP	K02665
pili assembly protein PilO	K02664
pili assembly protein PilN	K02663
pili assembly protein PilM	K02662
bifunctional penicillin-binding protein 1a%2F murein transglycos	K05366
DNA-binding transcriptional regulator OxyR	K04761
glutaredoxin	K00435
dihydrolipoamide dehydrogenase	K00382
hypothetical protein	
bifunctional argininosuccinate lyase%2FN-acetylglutamate synth	K14681
argininosuccinate synthase	K01940
acetylglutamate kinase	K00930
N-acetyl-gamma-glutamyl-phosphate reductase	K00145
acetylornithine deacetylase	K01438
phosphoenolpyruvate carboxylase	K01595
5%2C10-methylenetetrahydrofolate reductase	K00297
50S ribosomal protein L9	K02939
30S ribosomal protein S18	K02963
30S ribosomal protein S6	K02990
23S rRNA %28guanosine-2%27-O-%29-methyltransferase	K03218
exoribonuclease R	K12573
transcriptional repressor NsrR	K13771

nitric oxide dioxygenase	K05916
flagellar motor protein MotX	
adenylosuccinate synthetase	K01939
hypothetical protein	K09937
modulator for HflB protease specific for phage lambda cII repres	K04087
modulator for HflB protease specific for phage lambda cII repres	K04088
GTPase HflX	K03665
RNA-binding protein Hfq	K03666
tRNA delta%282%29-isopentenylpyrophosphate transferase	K00791
DNA mismatch repair protein	K03572
N-acetylmuramoyl-L-alanine amidase	K01448
ATPase	K06925
Fe-S electron transport protein	
oligoribonuclease	K13288
ribosome-associated GTPase	K06949
phosphatidylserine decarboxylase	K01613
drug%2Fmetabolite exporter family protein	
lysyl-tRNA synthetase	K04568
fumarate reductase flavoprotein subunit	K00244
fumarate reductase iron-sulfur subunit	K00245
fumarate reductase subunit C	K00246
fumarate reductase subunit D	K00247
elongation factor P	K02356
lysine aminomutase	K01843
6-phosphofructokinase	K00850
ferrous iron efflux protein F	K13283
periplasmic protein CpxP%2C modulator of CpxAR signaling	K06006
DNA-binding response regulator in two-component regulatory sy	K07662
two-component sensor protein	K07640
rRNA methylase	K03216
serine acetyltransferase	K00640
NAD%28P%29H-dependent glycerol-3-phosphate dehydrogenas	K00057
preprotein translocase subunit SecB	K03071
rhodanese-related sulfurtransferase	
protease with a role in cell division	
FxsA protein	K07113
aspartate ammonia-lyase	K01744
anaerobic C4-dicarboxylate transporter	K07791
universal stress protein A	
thiol:disulfide interchange protein	K04084
glucosamine-6-phosphate deaminase	K02564
major facilitator transporter	
protein tyrosine phosphatase	

glyceraldehyde-3-phosphate dehydrogenase	K00134
DNA-binding transcriptional repressor	K03892
diguanylate cyclase	
hypothetical protein	
NADH dehydrogenase	K03885
high-affinity zinc uptake system protein ZnuA2	K09815
hypothetical protein	
glucosamine--fructose-6-phosphate aminotransferase	K00820
DNA-binding transcriptional repressor	
two-component response regulator	
hypothetical protein	K05595
hypothetical protein	
hypothetical protein	K14393
sensory transduction protein kinase	K00936
3-phenylpropionic acid transporter	K05820
cyclic nucleotide binding protein%2FCBS domain-containing prot	K07182
DNA polymerase III subunit epsilon	K02342
acetyl-CoA synthetase	K01895
3-dehydroquinate dehydratase	K03786
acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	K02160
acetyl-CoA carboxylase biotin carboxylase subunit	K01961
50S ribosomal protein L11 methyltransferase	K02687
tRNA-dihydrouridine synthase B	K05540
Fis family transcriptional regulator	K03557
hypothetical protein	
zinc-responsive transcriptional regulator	K13638
bifunctional phosphoribosylaminoimidazolecarboxamide formylt	K00602
phosphoribosylamine--glycine ligase	K01945
hypothetical protein	
HU%2C DNA-binding transcriptional regulator subunit alpha	K05787
hypothetical protein	
hypothetical protein	K09891
2-ketoacid reductase	
protein YhgI	
uroporphyrinogen decarboxylase	K01599
NADH pyrophosphatase	K03426
anti-RNA polymerase sigma 70 factor	K07740
curli production assembly%2Ftransport outer membrane lipopro	K06214
curli assembly protein CsgF	K04338
curli production assembly%2Ftransport component CsgE	K04337
DNA-binding transcriptional activator VpsT %28CsgD-like%29	K04333
minor curlin subunit%2C nucleator CsgB	K04335
major curlin subunit CsgA	

DNA-directed RNA polymerase subunit beta%27	K03046
DNA-directed RNA polymerase subunit beta	K03043
50S ribosomal protein L7%2FL12	K02935
50S ribosomal protein L10	K02864
50S ribosomal protein L1	K02863
50S ribosomal protein L11	K02867
transcription antitermination protein NusG	K02601
preprotein translocase subunit SecE	K03073
elongation factor Tu	K02358
pantothenate kinase	K00867
biotin--protein ligase	K03524
UDP-N-acetylenolpyruvoylglucosamine reductase	K00075
hypothetical protein	
phosphatidylserine synthase	K00998
RNA-binding protein	
glutamate racemase	K01776
hypothetical protein	K06927
vitamin B12%2Fcobalamin outer membrane transporter	K02014
tRNA %28uracil-5-%29-methyltransferase	K00557
hypothetical protein	
DNA-binding transcriptional repressor FabR	
soluble pyridine nucleotide transhydrogenase	K00322
DNA-damage-inducible SOS response protein	K03327
hypothetical protein	
LexA repressor	K01356
glycerol-3-phosphate acyltransferase	K00631
4-hydroxybenzoate octaprenyltransferase	K03179
chorismate--pyruvate lyase	K03181
flagellar basal body protein FliL	K02415
intramembrane serine protease	K02441
thiosulfate sulfurtransferase	K02439
RNA polymerase factor sigma-32	K03089
ABC transporter membrane protein	K09811
ABC transporter ATP-binding protein	K09812
bifunctional Signal recognition particle %28SRP%29 receptor%2F	K03110
methyltransferase	K08316
hypothetical protein	K08993
multiple antibiotic resistance protein MarC	K05595
hypothetical protein	
hypothetical protein	
hypothetical protein	
ATP-dependent DNA helicase RecG	K03655
DNA uptake protein	K07400

adenosine 3%27-phosphate 5%27-phosphosulfate 3%27%282%2	K03677
ADP-ribose diphosphatase	K08312
general secretion pathway protein N	K02463
cholera toxin secretion protein EpsM	K02462
general secretion pathway protein L	K02461
general secretion pathway protein K	K02460
general secretion pathway protein J	K02459
general secretion pathway protein I	K02458
general secretion pathway protein H	K02457
general secretion pathway protein G	K02456
general secretion pathway protein F	K02455
general secretion pathway protein E	K02454
general secretion pathway protein D	K02453
general secretion pathway protein C	K02452
ribosome-associated heat shock protein Hsp15	K04762
heat shock protein 33	K04083
phosphoenolpyruvate carboxykinase	K01610
hypothetical protein	
diguanylate cyclase	K07181
lysophospholipase L%282%29	K01048
hydrolase	K07024
site-specific tyrosine recombinase XerC	K03733
diaminopimelate epimerase	K01778
diaminopimelate decarboxylase%2C PLP-binding	K01586
frataxin-like protein	K06202
oligopeptidase A	K01414
DNA %28exogenous%29 processing protein	K07115
glutathione reductase	K00383
hypothetical protein	
hypothetical protein	
copper sensitivity protein ScsC	
thiol:disulfide interchange protein TlpA	
thiol:disulfide interchange protein DsbD	
hypothetical protein	
serine%2Fthreonine protein kinase	K08884
hypothetical protein	
RNA polymerase ECF-type sigma factor	
hypothetical protein	
hypothetical protein	
lipoprotein	
transcriptional regulator	
transcriptional regulator	
cytoplasmic protein	

permease	
hypothetical protein	
dihydroorotase	K01465
L-seryl-tRNA selenium transferase family protein	K01042
2-dehydro-3-deoxyphosphooctonate aldolase	
PTS system mannitol %28cryptic%29-specific transporter subunit IIA	
hypothetical protein	
hypothetical protein	
cyclic nucleotide binding protein%2FCBS domain-containing prot	K07182
DNA polymerase III subunit epsilon	K02342
choline transporter of high affinity	K03451
dipeptide transport system permease DppC	K02034
dipeptide transport system permease DppB	K02033
dipeptide-binding protein DppA	K02035
dipeptide transport ATP-binding protein DppD	K02032
cytochrome c5	
DNA helicase and single-stranded DNA-dependent ATPase	K03656
TetR family transcriptional regulator	
periplasmic protein of efflux system	
acriflavin resistance plasma membrane protein	
hypothetical protein	K09806
ketol-acid reductoisomerase	K00053
DNA-binding transcriptional regulator IlvY	K02521
hypothetical protein	
hypothetical protein	
shikimate 5-dehydrogenase	K00014
ribosome maturation factor	K07566
N5-carboxyaminoimidazole ribonucleotide mutase	K01588
phosphoribosylaminoimidazole carboxylase ATPase subunit	K01589
DNA topoisomerase	K07479
hypothetical protein	K03747
DNA processing protein DprA	K04096
peptidoglycan binding domain-containing protein	
peptide deformylase	K01462
methionyl-tRNA formyltransferase	K00604
16S rRNA m5C967 methyltransferase%2C S-adenosyl-L-methioni	K03500
potassium transporter peripheral membrane protein	K03499
Trk system potassium uptake protein TrkH	K03498
oxidoreductase%2C inner membrane subunit	K11068
Gram-positive sporulation control protein Spo0M	K06377
hypothetical protein	K09896
hypothetical protein	
serine%2Fthreonine protein kinase	K01362

protein disulfide isomerase	K03673
acyltransferase	
magnesium chelatase	K07391
acetolactate synthase 2 catalytic subunit	K01652
acetolactate synthase 2 regulatory subunit	K11258
branched-chain amino acid aminotransferase	K00826
dihydroxy-acid dehydratase	K01687
threonine dehydratase	K01754
cold shock protein	K03704
bifunctional N-acetylglucosamine-1-phosphate uridyltransferase	K04042
ATP synthase F0F1 subunit epsilon	K02114
ATP synthase F0F1 subunit beta	K02112
ATP synthase F0F1 subunit gamma	K02115
ATP synthase F0F1 subunit alpha	K02111
ATP synthase F0F1 subunit delta	K02113
ATP synthase F0F1 subunit B	K02109
ATP synthase F0F1 subunit C	K02110
ATP synthase F0F1 subunit A	K02108
F0F1 ATP synthase subunit I	K02116
chromosome partitioning protein ParB	K03497
chromosome partitioning protein ParA	K03496
16S rRNA methyltransferase GidB	K03501
tRNA uridine 5-carboxymethylaminomethyl modification protein	K03495
sulfur carrier protein ThiS	K03154
hypothetical protein	
hypothetical protein	
sulfur transfer protein complex subunit TusB	K07237
hypothetical protein	
hypothetical protein	
pyr operon leader peptide	
tRNA %28guanine-N%287%29-%29-methyltransferase	K03439
hypothetical protein	
CinA-like protein	K03743
oxaloacetate decarboxylase subunit gamma	K01573
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
component I of anthranilate synthase	K01657
trp operon leader peptide	
hypothetical protein	
hypothetical protein	
hypothetical protein	

hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
sterol desaturate	
hypothetical protein	
hypothetical protein	
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hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
lipoprotein	
hypothetical protein	
hypothetical protein	
SirA-like redox protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
thr operon leader peptide	
glutamyl-Q tRNA%28Asp%29 synthetase	K01894
primosomal replication protein N	K02686
hypothetical protein	K03043
hypothetical protein	K09921
lipoprotein	
hypothetical protein	
hypothetical protein	
ilvB operon leader peptide	
hypothetical protein	
hypothetical protein	
hypothetical protein	
peptidase T-like protein	K01258
peptide-methionine %28S%29-S-oxide reductase	K12267
hypothetical protein	
glutathione-dependent formaldehyde-activating enzyme	K03396

phospholipase	K01175
hydroperoxidase HPII%28III%29 %28catalase%29 KatA	K03781
hypothetical protein	
chitin-binding protein	
hypothetical protein	
ABC transporter ATP-binding protein	
DNA polymerase III%2C epsilon-subunit paralog %283%27 to 5%	K02342
lipoprotein	
ribosome-associated GTPase	K06949
hypoxanthine-guanine phosphoribosyltransferase	K00760
hypothetical protein	
di-%2Ftripeptide transporter	
enoyl-CoA hydratase	K01692
LysR family transcriptional regulator	
MarR family transcriptional regulator	
hypothetical protein	
NADH oxidase	K00540
sugar efflux system	K03291
AraC family transcriptional regulator	
drug%2Fmetabolite exporter family protein	
LysR family transcriptional regulator	
thioredoxin peroxidase	
hypothetical protein	
LysR family transcriptional regulator	
alkyl sulfatase	K01138
hypothetical protein	
hypothetical protein	
LysR family transcriptional regulator	
regulatory protein UhpC	K07783
sensory histidine kinase UhpB	K07675
DNA-binding response regulator in two-component regulatory sy	K07686
sugar phosphate antiporter	K07784
TetR family transcriptional regulator	
acriflavin resistance periplasmic protein	
hypothetical protein	
acriflavin resistance plasma membrane protein	
pentapeptide repeat-containing protein	
ArsR family transcriptional regulator	
transporter	K07089
cytoplasmic protein	
L-allo-threonine dehydrogenase%2C NAD%28P%29-binding	
LysR family transcriptional regulator	
Cro%2FCl family transcriptional regulator	K07727

hypothetical protein	
GGDEF domain-containing protein	
GGDEF domain-containing protein	K00936
hypothetical protein	
TonB-dependent outer membrane receptor	K02014
mannitol-specific enzyme IIA component of PTS	K02798
fused mannitol-specific PTS enzymes: IIB component%2FIIC com	K02800
dehydrogenase	K00100
DNA-binding transcriptional regulator	
fructose transport system kinase	K02173
hydrolase	K04477
oxalate%2Fformate antiporter	
hypothetical protein	
lipoprotein	
heme nitric oxide and%2For oxygen binding protein HNOX	
hybrid two component sensor histidine kinase	K00936
di-%2Ftripeptide transporter	
hypothetical protein	
MshQ protein	K12287
MshP protein	K12286
MshO protein	K12285
MshD protein	K10927
MSHA pilin protein MshC	K10926
dimethyl sulfoxide reductase%2C anaerobic%2C subunit C	K07308
oxidoreductase%2C Fe-S subunit	K07311
dimethyl sulfoxide reductase%2C anaerobic%2C subunit A	K07306
twin-argninine leader-binding protein for DmsA and TorA	K00397
ferredoxin-type protein NapF	
transporter	
gamma-glutamyltranspeptidase	K00681
outer membrane protein RomA	
transcriptional regulator	
hydrolase%2Flipase	
astacin-like metalloendopeptidase	
M3 family peptidase	
methyl-accepting chemotaxis protein%2C aerotaxis receptor	K03406
transporter	K06901
phosphatidyl transferase%2C inner membrane protein	K00995
ABC transporter ATP-binding protein	K05779
ABC transporter permease protein	K05778
ABC transporter solute-binding protein	K05777
hypothetical protein	
glutamate synthase	

thiosulfate sulfurtransferase	K01011
two component sensor histidine kinase	K13040
two component response regulator	
nucleoside-diphosphate-sugar epimerase	
transcriptional regulator	
beta-mannosidase	K01192
methyl-accepting chemotaxis protein	K03406
hypothetical protein	
hypothetical protein	
membrane fusion protein %28MFP%29 component of efflux pum	K01993
ABC transporter ATP-binding protein	K09687
ABC transporter membrane protein	K09686
NAD%28P%29H-dependent flavin reductase	
methyltransferase	K00599
acetyltransferase	K00680
oxidoreductase	K03810
drug%2Fmetabolite exporter family protein	
morphinone reductase	K10680
lactoylglutathione lyase	K01759
cytoplasmic protein	
hypothetical protein	
hypothetical protein	
transporter	K03305
tripeptide transporter permease	K03305
rhodanese-related sulfurtransferase	K03972
DNA-3-methyladenine glycosylase	
hypothetical protein	
PTS system%2C IIB component	K02822
PTS system ascorbate-specific transporter subunit IIC	K03475
PTS system%2C 3-keto-L-gulonate specific IIA component	K02821
CAAX amino protease	K07052
hypothetical protein	
hypothetical protein	
DNA helicase II	K01529
hypothetical protein	
Type II restriction-modification system methylation subunit	
hypothetical protein	
hypothetical protein	
hypothetical protein	
formate acetyltransferase	K00656
N-acetylglucosamine-binding protein A	K03933
halovibrin HvnB	
metal dependent hydrolase	K07043

hypothetical protein	
hypothetical protein	
PilA-like type-IV pilus protein	
hypothetical protein	
hypothetical protein	
RNA helicase	K11927
GGDEF domain-containing protein	
multidrug resistance protein D	K08154
ATP-dependent RNA helicase DbpA	K05591
GGDEF domain-containing protein	
hypothetical protein	
permease	
iron-hydroxamate transporter subunit	K02013
iron-hydroxamate transporter subunit	K02016
iron-hydroxamate transporter permease subunit	K02015
aerobactin siderophore biosynthesis protein IucA	K03894
aerobactin siderophore synthesis protein IucB	K03896
aerobactin siderophore biosynthesis protein IucC	K03895
aerobactin siderophore biosynthesis protein IucD	K03897
ferric aerobactin receptor precursor IutA	
protease%2C membrane anchored	
hypothetical protein	K07340
methyl-accepting chemotaxis protein	
methyl-accepting chemotaxis protein	K03406
methyl-accepting chemotaxis protein	K03406
3-hydroxyisobutyrate dehydrogenase	K00020
hypothetical protein	
hypothetical protein	K07089
ArsR family transcriptional regulator	
O-6-alkylguanine-DNA:cysteine-protein methyltransferase	K00567
sensory histidine kinase in two-component regulatory system wi	K07644
DNA-binding response regulator in two-component regulatory sy	K07665
hypothetical protein	
transcriptional regulator SyrB	
two component sensor histidine kinase	
hypothetical protein	
hypothetical protein	
hypothetical protein	
flagellar motor protein MotA2	K02556
flagellar motor protein MotB2	K02557
TMAO reductase III %28TorYZ%29%2C TorZ subunit	K07812
TMAO reductase III %28TorYZ%29%2C cytochrome c-type subun	K07821
FhuE receptor precursor	K02014

hypothetical protein	
TolQ protein	K03561
TolQ protein	K03561
TolR protein	K03559
TonB protein	K03832
TPR domain-containing protein	
transcriptional repressor	
chitooligosaccharide transport ATP-binding protein oppD	K02032
chitooligosaccharide transport ATP-binding protein oppF	K02031
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
transporter	
hypothetical protein	
arylsulfatase	K06871
phosphatidylserine decarboxylase	
metal dependent hydrolase	K03760
transcriptional regulator	
two component sensor histidine kinase	
sulfatase family protein	
transcriptional regulator SyrB	
hypothetical protein	
two component response regulator	
hypothetical protein	
fimbrial protein precursor Flp1	
tungstate-binding protein precursor	K02279
general secretion pathway protein D	K02280
chromosome partitioning ATPase	K02282
type IV secretion NTPase	K02283
TadB-like protein involved in pilus formation and%2For protein s	K12510
bipartite nuclear localization signal containing protein	K12511
TPR repeat-containing protein	K12512
TadE-like protein	K12513
ATP%2FGTP-binding motif-containing protein	K12514
TadG-like protein	K12515
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
glycerol uptake facilitator protein GlpF	K02440
glycerol kinase	K00864

hybrid sensor kinase RscS	
glycerol-3-phosphate regulon repressor protein GlpR	K02444
glycerol-3-phosphate dehydrogenase	K00111
SUA5 protein	
choloylglycine hydrolase	K01442
GGDEF%2FEAL domain-containing protein	
hypothetical protein	
methyl-accepting chemotaxis protein	
SUA5 protein	
sn-glycerol-3-phosphate dehydrogenase subunit C	K00113
anaerobic glycerol-3-phosphate dehydrogenase subunit B	K00112
sn-glycerol-3-phosphate dehydrogenase subunit A	K00111
formate dehydrogenase-H	K00123
peptidase T	K01258
lipoprotein	
DNA-binding transcriptional regulator	
hypothetical protein	
malate synthase	K01638
MerR family transcriptional regulator	
transcriptional regulator	
glutathione-regulated potassium-efflux system protein KefC	K03455
modulator of glutathione-dependent potassium efflux system	K00358
hypothetical protein	K14761
2Fe-2S cluster-containing protein	K07140
two component sensor histidine kinase	K00936
transcriptional regulator	
hypothetical protein	
hypothetical protein	K09781
lipoprotein	
hypothetical protein	
elastase 2 precursor	K01346
acyl-CoA desaturase	K00507
hypothetical protein	
GGDEF domain-containing protein	
hypothetical protein	
membrane-bound redox modulator that IS induced by high pH	K05794
hypothetical protein	
hypothetical protein	
anaerobic ribonucleoside triphosphate reductase	K00527
anaerobic ribonucleotide reductase-activating protein	K04068
aromatic amino acid aminotransferase	K00813
ATP-dependent Zn protease	
amino-acid ABC transporter binding protein	

amino-acid ABC transporter binding protein	
hypothetical protein	
protein YgiW precursor	
cobyric acid synthase	K02232
molybdate ABC transporter%2C periplasmic molybdate-binding	K02020
molybdate ABC transporter permease protein	K02018
molybdate transporter ATP-binding protein	K02017
nucleotidase	K07025
hypothetical protein	
nucleoprotein%2Fpolynucleotide-associated enzyme	K09912
hypothetical protein	
TorE protein	K02571
trimethylamine N-oxide reductase%2C cytochrome c-type subun	K03532
trimethylamine N-oxide %28TMAO%29 reductase I%2C catalytic	K07811
methyl-accepting chemotaxis protein	
alpha-galactosidase	K07407
methyl-accepting chemotaxis protein	
hypothetical protein	
peptide transport system ATP-binding protein SapF	K02032
peptide transport system ATP-binding protein SapD	K02031
peptide transport system permease protein SapC	K02034
peptide transport system permease protein SapB	K02033
peptide transport protein SapA	K02035
DNA-binding transcriptional activator	K03974
regulatory protein for phage-shock-protein operon	K03969
phage shock protein B	K03970
PspC transcriptional regulator%2C toxin of PspCB toxin-antitoxin	K03973
hypothetical protein	K06918
hypothetical protein	K08990
phosphomethylpyrimidine kinase	K00941
hydroxymethylpyrimidine transport ATP-binding protein	K02049
taurine transporter permease subunit	K02050
hydroxymethylpyrimidine-binding protein	K02051
transcriptional activator TenA	K03707
hydroxyethylthiazole kinase	K00878
thiamine-phosphate pyrophosphorylase	K00788
GGDEF domain-containing protein	
thiol:disulfide interchange protein DsbD	
methyl-accepting chemotaxis protein	K03406
hypothetical protein	
hypothetical protein	
outer membrane lipoprotein	
hypothetical protein	

hypothetical protein	
hypothetical protein	
TonB system receptor	K02014
oligopeptidase B	K01354
MarR family transcriptional regulator	
osmotically inducible protein C	
hypothetical protein	
glucosyl hydrolase precursor	K03931
hypothetical protein	
amino acid permease	
hypothetical protein	
GGDEF domain-containing protein	
GGDEF domain-containing protein	K00936
diguanylate phosphodiesterase	
transporter	
cryptic beta-D-galactosidase subunit beta	K12112
cryptic beta-D-galactosidase subunit alpha	K12111
DNA-binding transcriptional repressor EbgR	K12113
DNA polymerase III%2C epsilon-subunit paralog %283%27 to 5%	K02342
cyclic nucleotide binding protein%2FCBS domain-containing prot	K07182
transporter	K03307
UDP-galactose-4-epimerase	K01784
galactose-1-phosphate uridylyltransferase	K00965
galactokinase	K00849
aldose 1-epimerase	K01785
acriflavin resistance plasma membrane protein	
acriflavin resistance periplasmic protein	
TetR family transcriptional regulator	
sensor histidine kinase	K00936
DNA-binding transcriptional repressor	K02529
hypothetical protein	K06878
sodium%2Fproton-dependent alanine carrier protein	K03310
transporter	K09964
translation initiation inhibitor	
branched-chain amino acid transport system II carrier protein	
deacetylase	
hypothetical protein	
PTS system%2C fructose-like enzyme IIC component	K02770
hypothetical protein	
mechanosensitive ion channel MscS	
mechanosensitive ion channel MscS	
ATP-dependent RNA helicase	K11927
hypothetical protein	

hypothetical protein	
hypothetical protein	
glycine betaine transporter	
membrane fusion protein %28MFP%29 component of efflux pump%2C signal anchor	
hypothetical protein	
GGDEF domain-containing protein	K00936
hypothetical protein	
exoribonuclease II	K01147
ATP-dependent RNA helicase	K05592
spermidine N1-acetyltransferase	K00657
formate%2Fnitrite transporter family protein	
LysR family transcriptional regulator	
hypothetical protein	
methyl-accepting chemotaxis protein	K03406
amino acid ABC transporter permease	K02029
ABC transporter amino acid-binding protein	K02030
amino acid ABC transporter permease	K02029
amino acid transport ATP-binding protein	K02028
phospho-2-dehydro-3-deoxyheptonate aldolase	K01626
hypothetical protein	K07459
5%27-nucleotidase	K01081
hypothetical protein	
GGDEF domain-containing protein	
hypothetical protein	
transcriptional repressor	
hypothetical protein	
purine nucleoside phosphorylase	K03784
potassium uptake protein KtrA	K03499
potassium uptake protein KtrB	K03498
hypothetical protein	
hydrogenase cytochrome b-type	
cytochrome c%27	
phosphohydrolase %28MutT%2Fnudix family protein%29	
hypothetical protein	K09954
hypothetical protein	
oxidoreductase	K00100
dihydroorotase	K01465
hypothetical protein	K09890
ATP-dependent protease %28Lon-like%29	
hypothetical protein	
DOPA 4%2C5-dioxygenase	K10253
L-threonine 3-dehydrogenase	K00060
2-amino-3-ketobutyrate CoA ligase	K00639

LysR family transcriptional regulator	
hypothetical protein	
manganese-dependent inorganic pyrophosphatase	K01507
hypothetical protein	K09928
recombination protein	K02238
lipid transporter ATP-binding%2Fpermease protein	K11085
tetraacyldisaccharide 4%27-kinase	K00912
cytosolic protein	K09791
3-deoxy-manno-octulosonate cytidylyltransferase	K00979
hypothetical protein	
metallothionein SmtA	K06219
condesin subunit F	K03633
condesin subunit E	K03804
fused chromosome partitioning protein: nucleotide hydrolase	K03632
DnaJ-related protein	
two component sensor histidine kinase	K00936
transcriptional regulatory protein	K02483
hypothetical protein	
fused N-acetyl glucosamine specific PTS enzyme: IIC and IIB com	K02804
nitrite and%2For nitric oxide reductase	K07234
esterase	K01175
hypothetical protein	
hypothetical protein	
copper%2Fsilver resistance outer membrane protein	
copper%2Fsilver efflux system%2C membrane fusion protein	K07798
copper%2Fsilver efflux system%2C membrane component	K07787
copper-binding protein	
methyl-accepting chemotaxis protein	K03406
methyl-accepting chemotaxis protein	K03406
hypothetical protein	
histidine ammonia-lyase	K01745
urocanate hydratase	K01712
formimidoylglutamase	K01479
imidazolonepropionase	K01468
histidine utilization repressor	K05836
hypothetical protein	
peptidyl-prolyl cis-trans isomerase	K01802
lipoprotein	
hypothetical protein	
transcription-repair coupling factor	K03723
hypothetical protein	
outer membrane-specific lipoprotein transporter subunit	K09808
outer membrane-specific lipoprotein transporter subunit	K09810

outer membrane-specific lipoprotein transporter subunit LolE	K09808
hypothetical protein	
permease	
glucose-6-phosphate 1-dehydrogenase	K00036
6-phosphogluconolactonase	K01057
6-phosphogluconate dehydrogenase	K00033
hypothetical protein	
transporter	
transcriptional regulatory protein TcpP	K10920
TcpH protein	
GGDEF domain-containing protein	
GGDEF domain-containing protein	
hypothetical protein	
N-acetylglucosaminyltransferase	K00754
hypothetical protein	
methyl-accepting chemotaxis protein	
sodium%2Fglutamate symporter	K03312
rod shape-determining protein RodA	
ribosomal large subunit pseudouridine synthase A	K06177
ribosomal large subunit pseudouridine synthase A	K06177
hypothetical protein	
outer membrane protein U paralog%2C OmpU2	
hypothetical protein	
LysR family transcriptional regulator	
soluble lytic murein transglycosylase	
soluble lytic murein transglycosylase	
anhydro-N-acetylmuramic acid kinase	K09001
beta-hexosaminidase	K01207
pyruvate kinase II	K00873
hypothetical protein	K10026
DNA-binding transcriptional repressor	
L-allo-threonine aldolase	K01620
MoxR-like ATPase%2C regulatory ATPase variant A%2C RavA	K03924
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
CreA family protein	K05805
hypothetical protein	
hypothetical protein	
two component response regulator	
glutamate transporter	K03312
hypothetical protein	

multidrug resistance ABC transporter ATP-binding and permease	K06147
low-affinity zinc transport protein	
ribosomal biogenesis GTPase	K14540
hypothetical protein	
prophage protein	
lipoprotein	
hypothetical protein	
DNA repair protein RadC	K03630
AraC family transcriptional regulator	
GGDEF domain-containing protein	
methyl-accepting chemotaxis protein	
methyl-accepting chemotaxis protein	K03406
nicotinamide mononucleotide transporter	K03811
uridine phosphorylase	K00757
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
DNA methylase M	K03427
hypothetical protein	
type I restriction-modification system methylation subunit	K03427
type I restriction-modification system specificity subunit	K01154
type I restriction-modification system restriction subunit	K01153
hypothetical protein	
hypothetical protein	
superfamily I DNA helicase	
hypothetical protein	
hypothetical protein	
cytoplasmic protein	
hypothetical protein	
hypothetical protein	
phage family integrase	
lipoprotein	
cytoplasmic protein	
diguanylate phosphodiesterase	
cytoplasmic protein	
ATP-dependent RNA helicase	
cytoplasmic protein	K09913
phosphate-binding protein	K02040
hypothetical protein	
DNA-binding transcriptional regulator	K11925
coproporphyrinogen III oxidase	K00228
hypothetical protein	

two component sensor histidine kinase	K00936
two component response regulator	
hypothetical protein	
hypothetical protein	K09917
TraF protein	
molybdenum cofactor biosynthesis protein MogA	K03831
hypothetical protein	
GGDEF domain-containing protein	
fused acyl-CoA synthetase: NAD%28P%29-binding subunit%2FAT	K09181
hypothetical protein	
D-alanyl-alanine synthetase A	K01921
DNA integration%2Frecombination%2Finvertion protein	
minor tail protein	
translation initiation factor Sui1	K03113
zona occludens toxin	K10954
OrfU	
RstB2 protein	
RstA2 protein	K07467
transcriptional repressor rstR	
hypothetical protein	K06193
hypothetical protein	
pyridine nucleotide transhydrogenase	K00325
NAD%28P%29 transhydrogenase subunit alpha	K00324
transcriptional activator HlyU	
OmpA family domain-containing protein	
hypothetical protein	K09686
daunorubicin resistance transmembrane protein	K09686
multidrug resistance protein A	K01993
type I secretion outer membrane protein	
LuxT transcriptional regulator	
hypothetical protein	
cold shock protein	K03704
hypothetical protein	
LysR family transcriptional regulator	
hypothetical protein	
hypothetical protein	
hypothetical protein	
nicotinic acid mononucleotide adenylyltransferase	K00969
NAD synthetase	K01916
endonuclease	K07461
hypothetical protein	K09915
hypothetical protein	
hypothetical protein	K09802

hypothetical protein	
two component response regulator	
hypothetical protein	
hypothetical protein	
transporter	
9-hexadecenoic acid cis-trans isomerase	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
lipoprotein	
hypothetical protein	
racemase	K01779
hypothetical protein	
acetyltransferase	K00680
hypothetical protein	
3-methyl-2-oxobutanoate hydroxymethyltransferase	K00606
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
glyoxylase	K01759
hypothetical protein	
hypothetical protein	
phosphotransferase family protein	
hypothetical protein	
acetyltransferase	
hypothetical protein	
hypothetical protein	
hypothetical protein	
toxin of toxin-antitoxin %28TA%29 stability system	

antitoxin of toxin-antitoxin %28TA%29 stability system	
hypothetical protein	
hypothetical protein	
IAA acetyltransferase	K00680
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
prolyl endopeptidase	K01322
hypothetical protein	
acetyltransferase	
XerC%2FCodV family integrase%2Frecombinase	
hypothetical protein	
cytoplasmic protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
outer membrane heme receptor	
transporter	
hypothetical protein	
hypothetical protein	
hypothetical protein	
methyl-accepting chemotaxis protein	K03406
MoxR protein	K03924
cytoplasmic protein	
hypothetical protein	
hypothetical protein	K07114
transporter	K07114
hypothetical protein	
hypothetical protein	
transaldolase B	K00616
transketolase	K00615
lipid A biosynthesis lauroyl acyltransferase	K02517
hypothetical protein	
hypothetical protein	
hypothetical protein	
dihydropteridine reductase%2C NAD%28P%29H-dependent%2C	K10679
GGDEF domain-containing protein	
hypothetical protein	

hexapeptide repeat-containing transferase	
guanosine 5%27-monophosphate oxidoreductase	K00364
inosine-guanosine kinase	K00892
peptidyl-prolyl cis-trans isomerase C %28rotamase C%29	K03769
chemotaxis protein CheW	K03415
nodulation protein N	
glycine cleavage system protein T	K00605
transcriptional regulator	
glycine cleavage system protein H	K02437
glycine dehydrogenase	K00281
hypothetical protein	
hypothetical protein	
diguanylate phosphodiesterase	
drug%2Fmetabolite exporter family protein	
DNA-binding transcriptional regulator	
PTS system%2C mannose-specific IIAB component	K02770
mannose-6-phosphate isomerase	K01809
PTS system%2C IIA component	K02806
hypothetical protein	K02769
enzyme IIC component of PTS	K11203
serine protease	K01362
chitodextrinase precursor	
hypothetical protein	
lipoprotein	
hypothetical protein	
hypothetical protein	
lipoprotein	
hypothetical protein	
sodium%2Fproton antiporter	
LysR family transcriptional regulator	
choloylglycine hydrolase family protein	
NAD-dependent oxidoreductase	K00100
cytoplasmic protein	
acetyltransferase	K06975
major facilitator transporter	
DNA-binding transcriptional regulator	
trehalose-6-P hydrolase	K01215
transcriptional regulator	
two component sensor histidine kinase	K00936
hypothetical protein	
hypothetical protein	
ABC transporter permease protein	K02004
hypothetical protein	

acetyltransferase	K03825
hypothetical protein	
hypothetical protein	
hypothetical protein	
multidrug resistance protein A	
LysR family transcriptional regulator	
dithiobiotin synthetase	K01935
biotin biosynthesis protein BioC	K02169
8-amino-7-oxononanoate synthase	K00652
adenosylmethionine-8-amino-7-oxononanoate aminotransferase	K00833
hypothetical protein	
ribosomal-protein-S5-alanine N-acetyltransferase	K03790
DNA-binding transcriptional regulator%2C tyrosine-binding	K03721
hypothetical protein	
deoxyribodipyrimidine photolyase Phr%2C FAD-binding	K01669
peptide-methionine %28S%29-S-oxide reductase	
hypothetical protein	
lipoprotein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
cyclopropane fatty acyl phospholipid synthase	K00574
plasmid partition ParA protein	K09701
dehydrogenase	
short chain dehydrogenase	
transcriptional regulator	
zinc-binding anti-sigmaE4 factor ChrR	K07167
RNA polymerase sigma factor	K03088
cysteine desulfhydrase	
agglutination protein	
bicyclomycin resistance protein	
LysR family transcriptional regulator	
homogentisate export protein	
hypothetical protein	
hydrolase	K04477
short chain dehydrogenase	
TonB protein	K03832
TonB system transport protein ExbD2	K03559
TolQ protein	K03561
TolQ protein	K03561
hypothetical protein	
iron-hydroxamate transporter permease subunit	K02015
ferrichrome-binding protein	K02016

ferrichrome ABC transporter ATP-binding protein	K02013
ferrichrome outer membrane transporter	K02014
AraC family transcriptional regulator	K13653
PTS system%2C glucose-specific II BC component	K02791
ABC transporter ATP-binding protein	
hypothetical protein	
lactoylglutathione lyase	
chloramphenicol acetyltransferase	K00638
LysR family transcriptional regulator	
proline iminopeptidase	K01259
LysR family transcriptional regulator	
acetate kinase	K00925
two component response regulator	
GGDEF domain-containing protein	K00936
maltose ABC transporter permease	K10110
maltose transporter membrane protein	K10109
maltose ABC transporter substrate-binding protein	K10108
maltose ABC transporter ATP-binding protein	K10111
glycogen debranching enzyme	K02438
chemotaxis protein CheW	K03415
serine%2Fthreonine transporter SstT	K07862
permease	
glycogen synthase	K00703
glucose-1-phosphate adenylyltransferase	K00975
hypothetical protein	
glycogen branching enzyme	K00700
4-alpha-glucanotransferase	K00705
maltodextrin phosphorylase	K00688
transcriptional regulator MalT	K03556
hypothetical protein	K08974
formate transporter	K06212
hypothetical protein	
3-methyl-adenine DNA glycosylase I	K01246
hypothetical protein	
Sco1-related protein	K07152
hypothetical protein	K09796
drug%2Fmetabolite exporter family protein	
RNA polymerase sigma factor SigZ	K03088
glutathione S-transferase	K00799
hypothetical protein	K09794
vulnibactin utilization protein ViuB	K07229
ferric anguibactin transport ATP-binding protein	K02013
ferric anguibactin transport system permease protein FatC	K02015

ferric anguibactin transport system permease protein FatD	K02015
ferric anguibactin-binding protein	K02016
glutaredoxin 2	
proline:sodium symporter	K11928
delta-1-pyrroline-5-carboxylate dehydrogenase	
bifunctional proline dehydrogenase%2Fpyrroline-5-carboxylate c	K13821
AraC family transcriptional regulator	
NirV precursor	
hypothetical protein	K02069
oxidoreductase%2C NADP%28H%29-dependent aldo-keto reductase	
ATPase involved in pili biogenesis	
hypothetical protein	
agmatinase	K01480
arginine decarboxylase	K01585
3-hydroxy-3-methylglutaryl-CoA reductase	K00021
outer membrane lipoprotein %28lipocalin%29	K03098
outer membrane protein P1 precursor	
hypothetical protein	
hypothetical protein	
succinylarginine dihydrolase	K01484
hypothetical protein	
glutathione S-transferase YghU	K11209
chloramphenicol-sensitive protein RarD	
transcriptional regulatory protein	K13652
fused DNA-binding transcriptional regulator%2F amino transferase	
zinc-carboxypeptidase precursor	
hypothetical protein	
hypothetical protein	
transcriptional repressor SmtB	
arsenical-resistance protein ACR3	K03325
methyl-accepting chemotaxis protein	
hypothetical protein	
hypothetical protein	
anaerobic nitric oxide reductase transcription regulator	K12266
hydroxylamine reductase	K00378
HCP oxidoreductase%2C NADH-dependent	K11933
methyl-accepting chemotaxis protein	
toxin coregulated pilus biosynthesis protein TcpF	
toxin coregulated pilus biosynthesis protein TcpE	K10934
toxin coregulated pilus biosynthesis protein TcpT	K10965
toxin coregulated pilus biosynthesis protein TcpS	K10964
toxin coregulated pilus biosynthesis protein TcpD	K10933
hypothetical protein	

toxin coregulated pilus outer membrane protein TcpC	K10932
toxin coregulated pilus biosynthesis protein TcpY%2FTcpQ	K10962
toxin coregulated pilus biosynthesis protein TcpB	K10931
toxin coregulated pilin subunit precursor TcpA	K10930
hypothetical protein	
chromosome partitioning protein ParA	K03496
diguanylate phosphodiesterase	
AraC family transcriptional regulator	
cellulose synthase operon C protein	
endo-1%2C4-D-glucanase	K01179
cellulose synthase regulator protein	
cellulose synthase catalytic subunit	K00694
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
lipid hydroperoxide peroxidase	K11065
thioredoxin peroxidase	K11065
methyl-accepting chemotaxis protein	
hypothetical protein	
AraC family transcriptional regulator	
surface protein	
hypothetical protein	
multidrug resistance protein A	
LysR family transcriptional regulator	
arylsulfatase	K01130
transporter	
hypothetical protein	
acriflavin resistance periplasmic protein	
acriflavin resistance plasma membrane protein	
lipoprotein	
hypothetical protein	K03565
hypothetical protein	K00358
LysR family transcriptional regulator	
ABC transporter ATP-binding protein	K01990
hypothetical protein	K01992
hypothetical protein	K03699
acetyltransferase	K00661
multidrug efflux pump VmrA	
deoxycytidylate deaminase	K01493
FMN reductase	K00299
long-chain-fatty-acid ligase LuxE	K06046
luciferase beta chain LuxB	K00494

luciferase alpha chain LuxA	K00494
acyl transferase	K00680
acyl-CoA reductase	K03400
3-oxo-C6-HSL autoinducer synthesis protein LuxI	K13060
LuxR family transcriptional regulator	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
carboxypeptidase G2 precursor	K01295
transcriptional regulatory protein%2C AraC-like protein	
kinase inhibitor	K06910
hypothetical protein	
hypothetical protein	
LysR family transcriptional regulator	
lipase%2Facylhydrolase family protein	
phosphoglycolate phosphatase	
threonine efflux protein	
hypothetical protein	
fused fructose-specific PTS enzymes: iibcomponent%2FIIC comp	K02770
fructose-1-phosphate kinase	K00882
bifunctional PTS system fructose-specific transporter subunit IIA	K11183
DNA-binding transcriptional regulator FruR	K03435
lipoprotein	
hypothetical protein	
hypothetical protein	
lipoprotein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
VgrG protein	K11904
hemolysin co-regulated protein	K11903
SAM-dependent methyltransferase	K06967
hydrolase	K07024
transporter	
glycerophosphoryl diester phosphodiesterase GlpQ %28UgpQ%2	K01126
diguanylate cyclase %28GGDEF%29%2C inhibitor of flagellar motility	
periplasmic protein that regulates MifA%2FB activity	
hypothetical protein	
pyruvate formate lyase activating enzyme	K04069
LysR family transcriptional regulator	
hypothetical protein	
nitroreductase A	K10678

L-serine ammonia-lyase	K01752
nucleoside permease NupC	K03317
purine nucleoside phosphorylase	K03784
guanine deaminase	K01487
hypothetical protein	
vitamin B12 transport ATP-binding protein BtuD	K02013
KpLE2 phage-like element%3B iron-dicitrate transporter subunit	K02015
ABC transporter%2C periplasmic component	K02016
adenosyltransferase	
GGDEF domain-containing protein	
transporter	
LysR family transcriptional regulator	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
transglycosylase	
lipoprotein	
4-methyl-5%28B-hydroxyethyl%29-thiazole monophosphate biosynthesis enzyme	
keto-hydroxyglutarate-aldolase%2Fketo-deoxy-phosphogluconat	K01625
ketodeoxygluconokinase	K00874
tagatose-bisphosphate aldolase	K08302
trimethylamine-N-oxide reductase	K07812
hypothetical protein	
hypothetical protein	K01138
arylsulfatase	K06871
hyaluronate lyase precursor	K01727
high-affinity iron permease	K07243
hypothetical protein	
2-deoxy-D-gluconate 3-dehydrogenase	K00065
5-keto-4-deoxyuronate isomerase	K01815
N-acetylglucosamine-6-phosphate deacetylase	K02079
PTS system%2C N-acetylgalactosamine-specific IIA component	K02744
N-acetylgalactosamine-specific enzyme IID component of PTS	K02747
PTS system%2C N-acetylgalactosamine-specific IIC component	K02746
N-acetylgalactosamine-specific enzyme IIB component of PTS	K02745
tagatose-6-phosphate ketose%2Faldose isomerase	K02082
tagatose 6-phosphate aldolase 1 subunit KbaZ	K00917
DNA-binding transcriptional dual regulator	K02081
sulfatase%2Fphosphatase	K01137
hypothetical protein	
beta-hexosaminidase	K12373

hypothetical protein	
two component response regulator protein	K02488
hypothetical protein	
diguanylate phosphodiesterase	
sigma-Q factor RpoQ%2C quorum-sensing regulated RpoS-like si	K03087
two component sensory histidine kinase	K00936
two component response regulator	
lipoprotein	
cytoplasmic protein	
sulphate transporter%2C anti-sigma factor antagonist	
hypothetical protein	
polysaccharide export periplasmic protein	
chromosome partitioning ATPase	
two-component response regulator%2C sigma factor PP2C-like phosphatase	
two-component hybrid sensor histidine kinase	
Fis family transcriptional regulator	
glycosyl transferases group 1	K00754
glycosyl transferases group 1	K00754
glycosyl transferases group 1	
oligosaccharide translocase	
polysaccharide ligase	
acetyltransferase	
chain length regulator %28capsular polysaccharide biosynthesis%29	
glycosyltransferase	
glycosyltransferase	
sugar transferase	
diguanylate phosphodiesterase	
hypothetical protein	K09941
glutaredoxin	K00435
protein YgiW precursor	
hypothetical protein	K02004
ABC transporter ATP-binding protein	K02003
multifunctional acyl-CoA thioesterase I and protease I and lysop	K10804
hypothetical protein	K09897
DNA-binding transcriptional regulator	
magnesium transporter MgtE	K06213
LysR family transcriptional regulator	
N-ethylmaleimide reductase%2C FMN-linked	K10680
glycine betaine-binding protein	K02002
universal stress protein	
sulfate transporter	
MerR family transcriptional regulator	
acetyltransferase	K03827

drug%2Fmetabolite exporter family protein	
lipoprotein	
phosphatase	K07093
LuxR family transcriptional regulator	
hypothetical protein	
hypothetical protein	
LysR family transcriptional regulator	
transporter	
MarR family transcriptional regulator	
transporter	K07088
hypothetical protein	
LysR family transcriptional regulator	K03566
hypothetical protein	
peptidase E	K05995
methyl-accepting chemotaxis protein	K03406
hypothetical protein	K09897
methyl-accepting chemotaxis protein%2C aerotaxis receptor	K03406
methyl-accepting chemotaxis protein	K03406
methyl-accepting chemotaxis protein	
accessory colonization factor AcfC	K10938
heptosyltransferase	
RIO1 protein	K07178
acetyltransferase%2Fhydrolase family protein	
hypothetical protein	
hypothetical protein	
AraC family transcriptional regulator	
methyl-accepting chemotaxis protein	K03406
hypothetical protein	
LysR family transcriptional regulator	
ABC transporter substrate-binding protein	K02055
hypothetical protein	
ABC transporter permease protein	K02054
ABC transporter permease protein	K02053
CP4-6 prophage%3B ferric transporter subunit	K02052
hypothetical protein	
hypothetical protein	
DNA-binding transcriptional regulator	K03704
halovibrin HvnA	
hypothetical protein	
hypothetical protein	
hypothetical protein	
lipoprotein	
outer membrane protein OmpA	K03286

phage integrase family site specific recombinase	
multidrug resistance protein A	K03543
multidrug resistance protein B	K03446
halovibrin HvnC	
hypothetical protein	
mechanosensitive ion channel MscS	K03442
hypothetical protein	
LysR family transcriptional regulator	
hypothetical protein	
hypothetical protein	
amino acid transporter LysE	
AsnC family transcriptional regulator	
cobalt-zinc-cadmium resistance protein CzcD	
LysR family transcriptional regulator	
homoserine%2Fhomoserine lactone efflux protein	
hypothetical protein	
hypothetical protein	
MarR family transcriptional regulator	
diaminobutyrate--2-oxoglutarate aminotransferase	K00836
aspartate kinase	K00928
hypothetical protein	
hypothetical protein	
hypothetical protein	
anaerobic glycerol-3-phosphate dehydrogenase subunit C	
anaerobic glycerol-3-phosphate dehydrogenase subunit C	
anaerobic glycerol-3-phosphate dehydrogenase subunit C	
anaerobic glycerol-3-phosphate dehydrogenase subunit C	
structural protein P5	
hypothetical protein	
LysR family transcriptional regulator	
hypothetical protein	
cytoplasmic protein	
hypothetical protein	
carbamate kinase	K00926
hydrolase	K07024
LysR family transcriptional regulator	
multidrug efflux system protein	K03296
multidrug efflux system	K03585
SAM-dependent methyltransferase	K06970
hypothetical protein	
peptidyl-tRNA hydrolase domain protein	K15034
ATP-dependent DNA helicase RecQ	K03654
cytoplasmic protein	K09749

inner membrane transport protein YdhC	
DNA-binding transcriptional regulator	
pyridoxamine 5%27-phosphate oxidase	K00275
RTX repeat-containing calcium-binding cytotoxin RtxA2	
hypothetical protein	
porin	
ATP-binding protein%2C RTX transport secretion component Rtx	K06148
GGDEF%2FEAL domain-containing protein	
hypothetical protein	
RTX transport membrane fusion protein RtxD	K02022
hydrolase	K06957
hypothetical protein	
ParB family protein	K03497
ParA family protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
Cep	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
biotin synthase	K01012
hypothetical protein	
hypothetical protein	K07114
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
DNA primase TraC	K00992
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
DNA repair protein RadC	K03630
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	

hypothetical protein	
hypothetical protein	K03496
resolvease%2Frecombinase	
hypothetical protein	
hypothetical protein	
DNA-binding protein RDGA	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
hypothetical protein	
exonuclease sbcC	
hypothetical protein	
hypothetical protein	
transporter	
hypothetical protein	
hypothetical protein	
trypsin protease precursor	
hypothetical protein	
hypothetical protein	
attachment mediating protein VirB2-like protein	K03197
VirB4 ATPase	K03199
channel protein VirB8	K03203
channel protein VirB9	K03204
channel protein VirB10	K03195
VirB11 ATPase	K03196
protein VirD4	K03205
single-strand DNA binding protein	K03111
DNA topoisomerase III	K03169
outer membrane protein	
hypothetical protein	
relaxase	
hypothetical protein	
hypothetical protein	
hypothetical protein	
attachment mediating protein VirB5-like protein	K03200
channel protein VirB6	K03201

Reaction Abbreviation	**Reaction Name**
12PPDStex	(S)-Propane-1,2-diol transport via diffusion (extr
14GLUCANabcpp	1,4-alpha-D-glucan transport via ABC system (p
14GLUCANtexi	1,4-alpha-D-glucan transport via diffusion (extra
23CAMPtex	23cAMP transport via diffusion (extracellular to
23CCMPtex	23cCMP transport via diffusion (extracellular to
23CGMPtex	23cGMP transport via diffusion (extracellular to
23CUMPtex	23cUMP transport via diffusion (extracellular to
23DAPPAtex	2,3-diaminopropionate transport via diffusion
23PDE2pp	2',3'-cyclic-nucleotide phosphodiesterase (UMP
23PDE4pp	2',3'-cyclic-nucleotide phosphodiesterase (CMP
23PDE7pp	2',3'-cyclic-nucleotide phosphodiesterase (AMP
23PDE9pp	2',3'-cyclic-nucleotide phosphodiesterase (GMP
26DAHtex	meso-2,6-Diaminoheptanedioate transport via d
34dhpactex	dihydroxyphenylacetaldehyde transport via diffu
3AMPtex	3AMP transport via diffusion (extracellular to pe
3CMPtex	3CMP transport via diffusion (extracellular to pe
3GMPtex	3GMP transport via diffusion (extracellular to pe
3HAD100	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD120	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD121	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD140	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD141	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD160	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD161	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD180	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD181	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD40	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD60	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HAD80	3-hydroxyacyl-[acyl-carrier-protein] dehydratase
3HPPtex	3-hydroxypropionate transport via diffusion (extr
3NTD2pp	3'-nucleotidase (UMP) (periplasm)
3NTD4pp	3'-nucleotidase (CMP) (periplasm)
3NTD7pp	3'-nucleotidase (AMP) (periplasm)
3NTD9pp	3'-nucleotidase (GMP) (periplasm)
3OAR100	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR120	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR121	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR140	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR141	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR160	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR161	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR180	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR181	3-oxoacyl-[acyl-carrier-protein] reductase (n-C1
3OAR40	3-oxoacyl-[acyl-carrier-protein] reductase (n-C4:
3OAR60	3-oxoacyl-[acyl-carrier-protein] reductase (n-C6:
3OAR80	3-oxoacyl-[acyl-carrier-protein] reductase (n-C8:
3OAS100	3-oxoacyl-[acyl-carrier-protein] synthase (n-C10

3OAS120	3-oxoacyl-[acyl-carrier-protein] synthase (n-C12
3OAS121	3-oxoacyl-[acyl-carrier-protein] synthase (n-C12
3OAS140	3-oxoacyl-[acyl-carrier-protein] synthase (n-C14
3OAS141	3-oxoacyl-[acyl-carrier-protein] synthase (n-C14
3OAS160	3-oxoacyl-[acyl-carrier-protein] synthase (n-C16
3OAS161	3-oxoacyl-[acyl-carrier-protein] synthase (n-C16
3OAS180	3-oxoacyl-[acyl-carrier-protein] synthase (n-C18
3OAS181	3-oxoacyl-[acyl-carrier-protein] synthase (n-C18
3OAS60	3-oxoacyl-[acyl-carrier-protein] synthase (n-C6:
3OAS80	3-oxoacyl-[acyl-carrier-protein] synthase (n-C8:
3PEPTtex	LalaDgluMdap (tripeptide) transport via diffusion
3UMPtex	3UMP transport via diffusion (extracellular to pe
4HOXPACDtex	4-hydroxyphenylacetaldehyde transport via diffu
4HTHRS	4-Hydroxy-L-threonine synthase
4PEPTabcpp	tetrapeptide (LalaDgluMdapDala) transport via
4PEPTtex	LalaDgluMdapDala (pentapeptide) transport via
5CMHMISO	5-carboxymethyl-2-hydroxymuconate Delta-iso
5DGLCNtex	5-Dehydro-D-gluconate transport via diffusion (
5DOAN	5'-deoxyadenosine nuclosidase
5MTRtex	5-Methylthio-D-ribose transport via proton diffus
A5PISO	arabinose-5-phosphate isomerase
AAMYLpp	alpha-amylase (periplasm)
AB6PGH	Arbutin 6-phosphate glucohydrolase
ABTA	4-aminobutyrate transaminase
ABUTtex	4-aminobutyrate transport via diffusion (extracel
ACACT1r	acetyl-CoA C-acetyltransferase
ACACT2r	acetyl-CoA C-acyltransferase (butanoyl-CoA) (r)
ACACT3r	acetyl-CoA C-acyltransferase (hexanoyl-CoA) (r
ACACT4r	acetyl-CoA C-acyltransferase (octanoyl-CoA) (r)
ACACT5r	acetyl-CoA C-acyltransferase (decanoyl-CoA) (r
ACACT6r	acetyl-CoA C-acyltransferase (dodecanoyl-CoA)
ACACT7r	acetyl-CoA C-acyltransferase (tetradecanoyl-Co
ACACT8r	acetyl-CoA acyltransferase (hexadecanoyl-CoA)
ACACtex	acetoacetate transport via diffusion (extracellula
ACALD	acetaldehyde dehydrogenase (acetylating)
ACALDtex	acetaldehyde transport via diffusion (extracellula
ACCOAC	acetyl-CoA carboxylase
ACCOAL	acetate-CoA ligase (ADP-forming)
ACGAL1Ptex	N-acetyl-D-galactosamine 1-phosphate transpor
ACGALDA	N-Acetyl-D-galactosamine-6-phosphate deactyl
ACGALPTspp	N-Acetyl-D-galactosamine transport via PEP:Py
ACGALtex	N-acetyl-D-galactosamine transport via diffusion
ACGAM1Ptex	N-acetyl-D-glucosamine 1-phosphate transport
ACGAM2abcpp	chitobiose transport via ABC system (periplasm)
ACGAM2P	N,N'-diacetylchitobiose phosphorylase
ACGAM2tex	chitobiose transport via diffusion (extracellular t
ACGAMK	N-acetylglucosamine kinase
ACGAMPM	phosphoacetylglucosamine mutase

ACGAMT	UDP-N-acetylglucosamine:undecaprenylphosph
ACGAptspp	N-Acetyl-D-glucosamine transport via PEP:Pyr P
ACGAtex	N-Acetyl-D-glucosamine transport via diffusion (
ACGK	acetylglutamate kinase
ACGS	N-acetylglutamate synthase
ACHBS	2-aceto-2-hydroxybutanoate synthase
ACKr	acetate kinase
ACLS	acetolactate synthase
ACM6PH	N-acetylmuramate 6-phosphate hydrolase
ACMANAptspp	N-acetyl-D-mannosamine transport via PTS (pe
ACMANAtex	N-acetyl-D-mannosamine transport via diffusion
ACMUMptspp	N-acetylmuramate transport via PEP:Pyr PTS (p
ACMUMtex	N-acetylmuramate transport via diffusion (extrac
ACNAMt4pp	N-Acetylneuraminate transport via sodium symp
ACNAMtex	N-acetylneuraminate transport via diffusion (extr
ACNML	N-Acetylneuraminate lyase
ACOAD1f	acyl-CoA dehydrogenase (butanoyl-CoA)
ACOAD2f	acyl-CoA dehydrogenase (hexanoyl-CoA)
ACOAD3f	acyl-CoA dehydrogenase (octanoyl-CoA)
ACOAD4f	acyl-CoA dehydrogenase (decanoyl-CoA)
ACOAD5f	acyl-CoA dehydrogenase (dodecanoyl-CoA)
ACOAD6f	acyl-CoA dehydrogenase (tetradecanoyl-CoA)
ACOAD7f	acyl-CoA dehydrogenase (hexadecanoyl-CoA)
ACOAD8f	acyl-CoA dehydrogenase (octadecanoyl-CoA)
ACOATA	Acetyl-CoA ACP transacylase
ACODA	acetylornithine deacetylase
ACONTa	aconitase (half-reaction A, Citrate hydro-lyase)
ACONTb	aconitase (half-reaction B, Isocitrate hydro-lyase
ACOTA	acetylornithine transaminase
ACPPAT120	acyl-(acyl carrier protein):phosphate acyltransfer
ACPPAT140	acyl-(acyl carrier protein):phosphate acyltransfer
ACPPAT141	acyl-(acyl carrier protein):phosphate acyltransfer
ACPPAT160	acyl-(acyl carrier protein):phosphate acyltransfer
ACPPAT161	acyl-(acyl carrier protein):phosphate acyltransfer
ACPPAT180	acyl-(acyl carrier protein):phosphate acyltransfer
ACPPAT181	acyl-(acyl carrier protein):phosphate acyltransfer
ACPS1	acyl-carrier protein synthase
ACS	acetyl-CoA synthetase
ACSERtex	O-Acetyl-L-serine transport via diffusion (extrace
ACt2rpp	acetate reversible transport via proton symport (
ACtex	Acetate transport via diffusion (extracellular to p
ADA	Adenosine deaminase
ADCL	4-aminobenzoate synthase
ADCS	4-amino-4-deoxychorismate synthase
ADEt2rpp	adenine transport via proton symport (reversible
ADEtex	adenine transport via diffusion (extracellular to p
ADK1	adenylate kinase
ADK3	adentylate kinase (GTP)

ADK4	adentylate kinase (ITP)
ADNCYC	adenylate cyclase
ADNK1	adenosine kinase
ADNt2pp	adenosine transport in via proton symport (perip
ADNt2rpp	adenosine transport in via proton symport, rever
ADNtex	adenosine transport via diffusion (extracellular t
ADOCBLtonex	Adenosylcobalimin transport via ton system (ext
ADPRDP	ADPribose diphosphatase
ADPT	adenine phosphoribosyltransferase
ADSK	adenylyl-sulfate kinase
ADSL1r	adenylsuccinate lyase
ADSL2r	adenylosuccinate lyase
ADSS	adenylosuccinate synthase
AGDC	N-acetylglucosamine-6-phosphate deacetylase
AGM3PA	N-Acetyl-D-glucosamine(anhydrous)N-Acetylmu
AGM3PApp	N-Acetyl-D-glucosamine(anhydrous)N-Acetylmu
AGM3PH	N-Acetyl-D-glucosamine(anhydrous)N-Acetylmu
AGM3Pt2pp	GlcNAc-anhMurNAc tripeptide transport in via p
AGM4PA	N-Acetyl-D-glucosamine(anhydrous)N-Acetylmu
AGM4PApp	N-Acetyl-D-glucosamine(anhydrous)N-Acetylmu
AGM4PH	N-Acetyl-D-glucosamine(anhydrous)N-Acetylmu
AGM4Pt2pp	GlcNAc-anhMurNAc tetrapeptide transport in vi
AGMH	N-Acetyl-D-glucosamine(anhydrous)N-Acetylmu
AGMHE	ADP-D-glycero-D-manno-heptose epimerase
AGMT	agmatinase
AGMt2pp	GlcNAc-anhMurNAc transport in via proton sym
AGMtex	agmatine transport via diffusion (extracellular to
AGPAT120	1-tetradecanoyl-sn-glycerol 3-phosphate O-acyl
AGPAT140	1-tetradecanoyl-sn-glycerol 3-phosphate O-acyl
AGPAT141	1-tetradec-7-enoyl-sn-glycerol 3-phosphate O-a
AGPAT160	1-hexadecanoyl-sn-glycerol 3-phosphate O-acyl
AGPAT161	1-hexadec-7-enoyl-sn-glycerol 3-phosphate O-a
AGPAT180	1-octadecanoyl-sn-glycerol 3-phosphate O-acylt
AGPAT181	1-octadec-7-enoyl-sn-glycerol 3-phosphate O-a
AGPR	N-acetyl-g-glutamyl-phosphate reductase
AHCYSNS	S-adenosylhomocysteine nucleosidase
AICART	phosphoribosylaminoimidazolecarboxamide for
AIRC2	phosphoribosylaminoimidazole carboxylase
AIRC3	phosphoribosylaminoimidazole carboxylase (mu
AKGDH	2-Oxogluterate dehydrogenase
AKGtex	alpha-ketoglutarate transport via diffusion (extra
ALAabcpp	L-alanine transport via ABC system (periplasm)
ALAALAabcpp	D-alanyl-D-alanine (DalaDala) transport via AB
ALAALAr	D-alanine-D-alanine ligase (reversible)
ALAALAtex	D-alanyl-D-alanine (DalaDala) transport via diffu
ALAD_L	L-alanine dehydrogenase
ALAR	alanine racemase
ALAt4pp	L-alanine transport in via sodium symport (perip

ALATA_D2	D-alanine transaminase
ALATA_L2	alanine transaminase
ALAtex	L-alanine transport via diffusion (extracellular to
ALATRS	Alanyl-tRNA synthetase
ALCD19	alcohol dehydrogenase (glycerol)
ALCD2x	alcohol dehydrogenase (ethanol)
ALLtex	Allose transport via diffusion (extracellular to pe
ALLTNtex	allantoin transport via diffusion (extracellular to
AM3PA	anhydrous-N-Acetylmuramyl-tripeptide amidase
AM4PA	anhydrous-N-Acetylmuramyl-tetrapeptide amida
AMALT1	Amylomaltase (maltotriose)
AMALT2	Amylomaltase (maltotetraose)
AMALT3	Amylomaltase (maltopentaose)
AMALT4	Amylomaltase (maltohexaose)
AMANAPEr	N-acetylmannosamine 6-phosphate epimerase
AMANK	N-acetyl-D-mannosamine kinase
AMAOTr	adenosylmethionine-8-amino-7-oxononanoate t
AMMQLT8	S-adenosylmethione:2-demthylmenaquinole me
AMPMS2	4-amino-2-methyl-5-phosphomethylpyrimidine s
AMPTASECG	alanyl aminopeptidase (cys-gly)
AMPTASEPG	aminopeptidase (pro-gly)
AMPtex	AMP transport via diffusion (extracellular to peri
ANHGMtex	GlcNAc-anhMurNAc transport via diffusion (extr
ANHMK	1,6-anhydrous-N-Acetylmuramate kinase
ANPRT	anthranilate phosphoribosyltransferase
ANS	anthranilate synthase
AOXSr2	8-amino-7-oxononanoate synthase
AP4AH	Ap4A hydrolase
AP4AS	Ap4A synthetase
AP5AH	Ap5A hydrolase
APG3PAT120	acyl-phosphate:glycerol-3-phosphate acyltransf
APG3PAT140	acyl-phosphate:glycerol-3-phosphate acyltransf
APG3PAT141	acyl-phosphate:glycerol-3-phosphate acyltransf
APG3PAT160	acyl-phosphate:glycerol-3-phosphate acyltransf
APG3PAT161	acyl-phosphate:glycerol-3-phosphate acyltransf
APG3PAT180	acyl-phosphate:glycerol-3-phosphate acyltransf
APG3PAT181	acyl-phosphate:glycerol-3-phosphate acyltransf
APH120	acylphosphatase (C12:0)
APH140	acylphosphatase (C14:0)
APH141	acylphosphatase (C14:1)
APH160	acylphosphatase (C16:0)
APH161	acylphosphatase (C16:1)
APH180	acylphosphatase (C18:0)
APH181	acylphosphatase (C18:1)
APRAUR	5-amino-6-(5-phosphoribosylamino)uracil reduc
ARBtex	L-arabinose transport via diffusion (extracellular
ARBTNabcpp	aerobactin transport via ABC system (periplasm
ARBTtex	arbutin transport via diffusion (extracellular to pe

ARGabcpp	L-arginine transport via ABC system (periplasm)
ARGD	L-arginine deiminase
ARGDCpp	arginine decarboxylase
ARGSL	argininosuccinate lyase
ARGSS	argininosuccinate synthase
ARGtex	L-arginine transport via diffusion (extracellular t
ARGTRS	Arginyl-tRNA synthetase
ASAD	aspartate-semialdehyde dehydrogenase
ASCBptspp	L-ascorbate transport via PEP:Pyr PTS (periplas
ASCBtex	L-ascorbate transport via diffusion (extracellular
ASNabcpp	L-asparagine transport via ABC system (periplas
ASNN	L-asparaginase
ASNNpp	L-asparaginase
ASNS1	asparagine synthase (glutamine-hydrolysing)
ASNtex	L-asparagine transport via diffusion (extracellula
ASNTRS	Asparaginyl-tRNA synthetase
ASO3tex	arsenite transport via diffusion (extracellular to
ASP1DC	aspartate 1-decarboxylase
ASPCT	aspartate carbamoyltransferase
ASPK	aspartate kinase
ASPO3	L-aspartate oxidase
ASPO4	L-aspartate oxidase
ASPO5	L-aspartate oxidase
ASPO6	L-aspartate oxidase
ASPT	L-aspartase
ASPt2_3pp	L-asparate transport via proton symport (3 H) (p
ASPt2pp	L-aspartate transport in via proton symport (peri
ASPTA	aspartate transaminase
ASPtex	L-aspartate transport via diffusion (extracellular
ASPTRS	Aspartyl-tRNA synthetase
AST	Arginine succinyltransferase
ATPM	ATP maintenance requirement
ATPPRT	ATP phosphoribosyltransferase
ATPS4rpp	ATP synthase (four protons for one ATP) (peripl
BALAtex	beta-alanine transport via diffusion (extracellular
BMOCOS	bis-molybdenum cofactor synthase
BMOGDS1	bis-molybdopterin guanine dinucleotide synthas
BMOGDS2	bis-molybdopterin guanine dinucleotide synthas
BPNT	3',5'-bisphosphate nucleotidase
BTNt2ipp	Biotin transport via proton symport (periplasm)
BTNtex	Biotin transport via diffusion (extracellular to per
BTS5	Biotin synthase
BUTCT	Acetyl-CoA:butyrate-CoA transferase
BUTSO3tex	butanesulfonate transport via diffusion (extracell
BUTt2rpp	Butyrate transport via proton symport, reversible
BUTtex	Butyrate transport via diffusion (extracellular to
BWCOGDS1	tungsten bispterin guanine dinucleotide synthas
BWCOGDS2	tungsten bispterin guanine dinucleotide synthas

BWCOS	tungsten bispterin cofactor synthase
CA2tex	calcium (Ca+2) transport via diffusion (extracell
CADVtpp	Lysine/Cadaverine antiporter (periplasm)
CAt6pp	calcium / sodium antiporter (1:1)
CBIAT	Cobinamide adenyltransferase
CBItonex	Cobinamide transport via ton system (extermal)
CBL1tonex	Cob(1)alamin transport via ton system (exterma
CBLAT	cob(I)alamin adenosyltransferase
CBMKr	Carbamate kinase
CBPS	carbamoyl-phosphate synthase (glutamine-hydr
CCGS	7-cyano-7-carbaguanine synthase
CD2abcpp	Cadmium (Cd+2) ABC transporter (periplasm)
CD2t3pp	cadmium (Cd+2) transport out via proton antipo
CD2tex	cadmium (Cd+2) transport via diffusion (extrace
CDGR	7-cyano-7-deazaguanine reductase
CDPGDH	CDP-glucose 4,6-dehydratase
CDPMEK	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythrito
CELLOBG	cellobiose glucosidase
CELLOBptspp	cellobiose transport via PTS (periplasm)
CELLOBtex	cellobiose transport via diffusion (extracellular t
CFAS160E	cyclopropane fatty acid synthase (Phosphatidyl
CFAS160G	cyclopropane fatty acid synthase (Phosphatidyl
CFAS180E	cyclopropane fatty acid synthase (Phosphatidyl
CFAS180G	cyclopropane fatty acid synthase (Phosphatidyl
CGLYabcpp	L-Cysteinylglycine (Cys-Gly) transport via ABC
CGLYtex	L-Cysteinylglycine transport via diffusion (extrac
CHLt2pp	choline transport via proton symport (periplasm)
CHLtex	choline transport via diffusion (extracellular to p
CHOLSH	choline sulfatase
CHORM	chorismate mutase
CHORS	chorismate synthase
CHRPL	Chorismate pyruvate lyase
CHTBSptspp	chitobiose transport via PEP:Pyr PTS (periplas
CHTBStex	chitobiose transport via diffusion (extracellular t
CITtex	citrate transport via diffusion (extracellular to pe
CLPNS120pp	cardiolipin synthase (periplasmic, n-C12:0)
CLPNS140pp	cardiolipin synthase (periplasmic, n-C14:0)
CLPNS141pp	cardiolipin synthase (periplasmic, n-C14:1)
CLPNS160pp	cardiolipin synthase (periplasmic, n-C16:0)
CLPNS161pp	cardiolipin synthase (periplasmic, n-C16:1)
CLPNS180pp	cardiolipin synthase (periplasmic, n-C18:0)
CLPNS181pp	cardiolipin synthase (periplasmic, n-C18:1)
CLt3_2pp	chloride transport out via proton antiport (2:1) (p
CLtex	chloride (Cl-1) transport via diffusion (extracellu
CMPtex	CMP transport via diffusion (extracellular to peri
CMtex	Chloramphenicol transport via diffusion (extrace
CO2tex	CO2 transport via diffusion (extracellular to peri
COBALT2abcpp	Cobalt (Co+2) ABC transporter (periplasm)

COBALT2t3pp	cobalt (Co+2) transport out via proton antiport (p
COBALT2tex	cobalt (Co+2) transport via diffusion (extracellula
COBALT2tpp	cobalt transport in via permease (no H+)
COMD	chito-oligosaccharide mono-deacetylase
CPGNabcpp	coprogen transport via ABC system (periplasm)
CPH4S	6-carboxy-5,6,7,8-tetrahydropterin synthase
CPMPS	cyclic pyranopterin monophosphate synthase
CPPPGO	coproporphyrinogen oxidase (O2 required)
CPPPGO2	Oxygen Independent coproporphyrinogen-III oxi
CRNabcpp	L-carnitine transport via ABC system (periplasm
CRNDabcpp	D-carnitine transport via ABC system (periplasm
CRNDtex	D-carnitine transport via diffusion (extracellular t
CRNtex	L-carnitine transport via diffusion (extracellular t
CS	citrate synthase
CSND	Cytosine deaminase
CSNt2pp	cytosine transport in via proton symport (periplas
CSNtex	cytosine transport via diffusion (extracellular to p
CTBTabcpp	crotonobetaine transport via ABC system (peripl
CTECOAI6	3-cis-2-trans-enoyl-CoA isomerase
CTECOAI7	3-cis-2-trans-enoyl-CoA isomerase
CTECOAI8	3-cis-2-trans-enoyl-CoA isomerase
CTPS2	CTP synthase (glutamine)
CU1abcpp	Copper (Cu +1) ABC transporter (periplasm)
CU2abcpp	Copper (Cu+2) ABC transporter (periplasm)
CU2tex	copper (Cu+2) transport via diffusion (extracellul
CU2tpp	copper transport in via permease (no H+)
CUtex	copper (Cu+1) transport via diffusion (extracellul
CYANST	Cyanide sulfurtransferase
CYANSTpp	Cyanide sulfurtransferase (periplasmic)
CYANtex	Cyanide transport via diffusion (extracellular to p
CYNTtex	Cyanate transport via diffusion (extracellular to p
CYO1a	ubiquinol---cytochrome-c reductase (3 protons)
CYO1b	cytochrome-c oxidase (2 protons)
CYSabc2pp	L-cysteine export via ABC system (cytoplasm to
CYSabcpp	L-cysteine uptake via ABC system (periplasm)
CYSDabcpp	D-cysteine uptake via ABC system (periplasm)
CYSDS	Cysteine Desulfhydrase
CYSDtex	D-cysteine transport via diffusion (extracellular t
CYSS	cysteine synthase
CYSSADS	L-cysteine sulfinic acid desulfurase
CYStex	L-cysteine transport via diffusion (extracellular t
CYSTL	cystathionine b-lyase
CYSTRS	Cysteinyl-tRNA synthetase
CYTBDpp	cytochrome oxidase bd (ubiquinol-8: 2 protons)
CYTD	cytidine deaminase
CYTDK2	cytidine kinase (GTP)
CYTDt2pp	cytidine transport in via proton symport (periplas
CYTDt2rpp	cytidine transport in via proton symport, reversib

CYTDtex	cytidine transport via diffusion (extracellular to p
CYTK1	cytidylate kinase (CMP)
CYTK2	cytidylate kinase (dCMP)
DADA	Deoxyadenosine deaminase
DADK	deoxyadenylate kinase
DADNt2pp	deoxyadenosine transport in via proton symport
DADNtex	deoxyadenosine transport via diffusion (extracel
DAGK120	diacylglycerol kinase (n-C12:0)
DAGK140	diacylglycerol kinase (n-C14:0)
DAGK141	diacylglycerol kinase (n-C14:1)
DAGK160	diacylglycerol kinase (n-C16:0)
DAGK161	diacylglycerol kinase (n-C16:1)
DAGK180	diacylglycerol kinase (n-C18:0)
DAGK181	diacylglycerol kinase (n-C18:1)
DALAtex	D-Alanine transport via diffusion (extracellular to
DAMPtex	dAMP transport via diffusion (extracellular to pe
DAPabcpp	M-diaminopimelic acid ABC transport (periplasm
DAPDC	diaminopimelate decarboxylase
DAPE	diaminopimelate epimerase
DAPtex	1,5-Diaminopentane transport via diffusion (extra
DASYN120	CDP-diacylglycerol synthetase (n-C12:0)
DASYN140	CDP-diacylglycerol synthetase (n-C14:0)
DASYN141	CDP-diacylglycerol synthetase (n-C14:1)
DASYN160	CDP-diacylglycerol synthetase (n-C16:0)
DASYN161	CDP-diacylglycerol synthetase (n-C16:1)
DASYN180	CDP-diacylglycerol synthetase (n-C18:0)
DASYN181	CDP-diacylglycerol synthetase (n-C18:1)
DB4PS	3,4-Dihydroxy-2-butanone-4-phosphate synthas
DBTS	dethiobiotin synthase
DCAtex	Decanoate transport via diffusion (extracellular t
DCMPDA	dCMP deaminase
DCMPtex	dCMP transport via diffusion (extracellular to pe
DCYTD	deoxycytidine deaminase
DCYTt2pp	deoxycytidine transport in via proton symport (p
DCYTtex	deoxycytidine transport via diffusion (extracellula
DDCAtexi	Fatty acid (dodecanoate) transport via facilitate
DDGLCNtex	2-dehydro-3-deoxy-D-gluconate transport via dif
DDGLK	2-dehydro-3-deoxygluconokinase
DDPA	3-deoxy-D-arabino-heptulosonate 7-phosphate
DGK1	deoxyguanylate kinase (dGMP:ATP)
DGMPtex	dGMP transport via diffusion (extracellular to pe
DGSNtex	deoxyguanosine transport via diffusion (extracel
DHAD1	dihydroxy-acid dehydratase (2,3-dihydroxy-3-me
DHAD2	Dihydroxy-acid dehydratase (2,3-dihydroxy-3-m
DHAtex	Dihydroxyacetone transport via diffusion (extrac
DHDPRy	dihydrodipicolinate reductase (NADPH)
DHDPS	dihydrodipicolinate synthase
DHFR	dihydrofolate reductase

DHFR2	dihydrofolate reductase (folate to dhf)
DHFR3	dihydrofolate reductase (folate to thf)
DHFS	dihydrofolate synthase
DHNAOT4	1,4-dihydroxy-2-naphthoate octaprenyltransfera
DHNCOAS	1,4-dihydroxy-2-napthoyl-CoA synthase
DHNCOAT	1,4-dihydroxy-2-napthoyl-CoA thioesterase
DHNPA2r	dihydroneopterin aldolase reversible
DHNPTE	Dihydroneopterin epimerase
DHORD2	dihydoorotic acid dehydrogenase (quinone8)
DHORD5	dihydroorotic acid (menaquinone-8)
DHORTS	dihydroorotase
DHPPDA2	diaminohydroxyphosphoribosylaminopryrimidin
DHPS2	dihydropteroate synthase
DHPTDCs2	4,5-dihydroxy-2,3-pentanedione cyclization (spo
DHQS	3-dehydroquinate synthase
DHQTi	3-dehydroquinate dehydratase, irreversible
DIMPtex	dIMP transport via diffusion (extracellular to peri
DINStex	deoxyinosine transport via diffusion (extracellula
D-LACt2pp	D-lactate transport via proton symport (periplasr
D-LACtex	D-lactate transport via diffusion (extracellular to
DM_4CRSOL	Sink needed to allow p-Cresol to leave system
DM_5DRIB	Sink needed to allow 5'-deoxyribose to leave sy
DM_AMOB	Sink needed to allow S-Adenosyl-4-methylthio-2
DM_MTHTHF	Sink needed to allow (2R,4S)-2-methyl-2,3,3,4-t
DMATT	dimethylallyltranstransferase
DMPPS	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
DMQMT	3-Dimethylubiquinonol 3-methyltransferase
DMSOR1	Dimethyl sulfoxide reductase (Menaquinol 8)
DMSOR1pp	Dimethyl sulfoxide reductase (Menaquinol 8) (p
DMSOR2	Dimethyl sulfoxide reductase (Demethylmenaqu
DMSOR2pp	Dimethyl sulfoxide reductase (Demethylmenaqu
DMSOtex	Dimethyl sulfoxide transport via diffusion (extrac
DMStex	Dimethyl sulfide transport via diffusion (extracell
DNMPPA	Dihydroneopterin monophosphate dephosphory
DNTPPA	Dihydroneopterin triphosphate pyrophosphatas
DOPAtex	dopamine transport via diffusion (extracellular to
DOXRBCNtex	Doxorubicin transport via diffusion (extracellular
DPCOAK	dephospho-CoA kinase
DPR	2-dehydropantoate 2-reductase
DRPA	deoxyribose-phosphate aldolase
DSBAO1	DsbA protein reoxidation reaction (aerobic)
DSBAO2	DsbA protein reoxidation reaction (anaerobic)
DSBCGT	DsbC:glutathione thiotransferase
DSBDR	DsbD reductase
DSERtex	D-serine transport via diffusion (extracellular to
DTMPK	dTMP kinase
DTMPtex	dTMP transport via diffusion (extracellular to per
DUMPtex	dUMP transport via diffusion (extracellular to pe

DURIK1	deoxyuridine kinase (ATP:Deoxyuridine)
DURIPP	deoxyuridine phosphorylase
DURIt2pp	deoxyuridine transport in via proton symport (pe
DURItex	deoxyuridine transport via diffusion (extracellula
DXPRIi	1-deoxy-D-xylulose reductoisomerase
DXPS	1-deoxy-D-xylulose 5-phosphate synthase
E4PD	Erythrose 4-phosphate dehydrogenase
EAR100x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR100y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR120x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR120y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR121x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR121y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR140x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR140y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR141x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR141y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR160x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR160y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR161x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR161y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR180x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR180y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR181x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR181y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR40x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR40y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR60x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR60y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
EAR80x	enoyl-[acyl-carrier-protein] reductase (NADH) (n
EAR80y	enoyl-[acyl-carrier-protein] reductase (NADPH) (
ECOAH1	3-hydroxyacyl-CoA dehydratase (3-hydroxybuta
ECOAH2	3-hydroxyacyl-CoA dehydratase (3-hydroxyhexa
ECOAH3	3-hydroxyacyl-CoA dehydratase (3-hydroxyocta
ECOAH4	3-hydroxyacyl-CoA dehydratase (3-hydroxydeca
ECOAH5	3-hydroxyacyl-CoA dehydratase (3-hydroxydode
ECOAH6	3-hydroxyacyl-CoA dehydratase (3-hydroxytetra
ECOAH7	3-hydroxyacyl-CoA dehydratase (3-hydroxyhexa
ECOAH8	3-hydroxyacyl-CoA dehydratase (3-hydroxyocta
EDA	2-dehydro-3-deoxy-phosphogluconate aldolase
EDA2	4-hydroxy-2-oxoglutarate aldolase
EDTXSVF	V. fischeri endotoxin synthesis
EGMEACPR	Enoylglutaryl-[ACP] methyl ester reductase
ENO	enolase
EPMEACPR	Enoylpimeloyl-[ACP] methyl ester reductase
ETHAtex	ethanolamine transport via diffusion (extracellula
ETHSO3tex	ethanesulfonate transport via diffusion (extracell
ETOHtex	ethanol transport via diffusion (extracellular to pe

EX_12ppd-R(e)	(R)-Propane-1,2-diol exchange
EX_12ppd-S(e)	(S)-Propane-1,2-diol exchange
EX_14glucan(e)	1,4-alpha-D-glucan exchange
EX_15dap(e)	1,5-Diaminopentane exchange
EX_23camp(e)	2',3'-Cyclic AMP exchange
EX_23ccmp(e)	2',3'-Cyclic CMP exchange
EX_23cgmp(e)	2',3'-Cyclic GMP exchange
EX_23cump(e)	2',3'-Cyclic UMP exchange
EX_23dappa(e)	2,3-diaminopropionate exchange
EX_26dap-M(e)	meso-2,6-Diaminoheptanedioate exchange
EX_2ddglcn(e)	2-Dehydro-3-deoxy-D-gluconate exchange
EX_34dhpac(e)	3,4-Dihydroxyphenylacetaldehyde exchange
EX_3amp(e)	3'-AMP exchange
EX_3cmp(e)	3'-cmp exchange
EX_3gmp(e)	3'-GMP exchange
EX_3hcinnm(e)	3-hydroxycinnamic acid exchange
EX_3hpp(e)	3-Hydroxypropanoate exchange
EX_3hpppn(e)	3-(3-hydroxy-phenyl)propionate exchange
EX_3ump(e)	3'-UMP exchange
EX_4abut(e)	4-Aminobutanoate exchange
EX_4hoxpacd(e)	4-Hydroxyphenylacetaldehyde exchange
EX_5dglcn(e)	5-Dehydro-D-gluconate exchange
EX_5mtr(e)	5-Methylthio-D-ribose exchange
EX_ac(e)	Acetate exchange
EX_acac(e)	Acetoacetate exchange
EX_acald(e)	Acetaldehyde exchange
EX_acgal(e)	N-Acetyl-D-galactosamine exchange
EX_acgal1p(e)	N-Acetyl-D-galactosamine 1-phosphate exchang
EX_acgam(e)	N-Acetyl-D-glucosamine exchange
EX_acgam1p(e)	N-Acetyl-D-glucosamine 1-phosphate exchange
EX_acgam2(e)	chitobiose exchange
EX_acmana(e)	N-Acetyl-D-mannosamine exchange
EX_acmum(e)	N-Acetylmuramate exchange
EX_acnam(e)	N-Acetylneuraminate exchange
EX_acser(e)	O-Acetyl-L-serine exchange
EX_ade(e)	Adenine exchange
EX_adn(e)	Adenosine exchange
EX_adocbl(e)	Adenosylcobalamin exchange
EX_ag(e)	silver exchange
EX_agm(e)	Agmatine exchange
EX_akg(e)	2-Oxoglutarate exchange
EX_alaala(e)	D-Alanyl-D-alanine exchange
EX_ala-B(e)	beta-Alanine exchange
EX_ala-D(e)	D-Alanine exchange
EX_ala-L(e)	L-Alanine exchange
EX_all-D(e)	D-Allose exchange
EX_alltn(e)	Allantoin exchange
EX_amp(e)	AMP exchange

EX_anhgm(e)	N-Acetyl-D-glucosamine(anhydrous)N-Acetylmu
EX_arab-L(e)	L-Arabinose exchange
EX_arbt(e)	Arbutin exchange
EX_arbtn(e)	aerobactin minus Fe3 exchange
EX_arbtn-fe3(e)	Aerobactin exchange
EX_arg-L(e)	L-Arginine exchange
EX_ascb-L(e)	L-Ascorbate exchange
EX_asn-L(e)	L-Asparagine exchange
EX_aso3(e)	arsenite exchange
EX_asp-L(e)	L-Aspartate exchange
EX_btn(e)	Biotin exchange
EX_but(e)	Butyrate (n-C4:0) exchange
EX_butso3(e)	butanesulfonate exchange
EX_ca2(e)	Calcium exchange
EX_cAMP(e)	cAMP exchange
EX_cbi(e)	Cobinamide exchange
EX_cbl1(e)	Cob(I)alamin exchange
EX_cd2(e)	Cadmium exchange
EX_cellob(e)	cellobiose exchange
EX_cgly(e)	Cys-Gly exchange
EX_chol(e)	Choline exchange
EX_chtbs(e)	chitobiose exchange
EX_cit(e)	Citrate exchange
EX_cl(e)	Chloride exchange
EX_cm(e)	Chloramphenicol exchange
EX_cmp(e)	CMP exchange
EX_co2(e)	CO2 exchange
EX_cobalt2(e)	Co2+ exchange
EX_cpgn(e)	coprogen exchange
EX_cpgn-un(e)	coprogen unloaded (no Fe(III)) exchange
EX_crn(e)	L-Carnitine exchange
EX_crn-D(e)	D-carnitine exchange
EX_csn(e)	Cytosine exchange
EX_cu(e)	Cu+ exchange
EX_cu2(e)	Cu2+ exchange
EX_cyan(e)	Hydrogen cyanide exchange
EX_cynt(e)	Cyanate exchange
EX_cys-D(e)	D-Cysteine exchange
EX_cys-L(e)	L-Cysteine exchange
EX_cytd(e)	Cytidine exchange
EX_dad-2(e)	Deoxyadenosine exchange
EX_damp(e)	dAMP exchange
EX_dca(e)	Decanoate (n-C10:0) exchange
EX_dcmp(e)	dCMP exchange
EX_dcyt(e)	Deoxycytidine exchange
EX_ddca(e)	Dodecanoate (n-C12:0) exchange
EX_dgmp(e)	dGMP exchange
EX_dgsn(e)	Deoxyguanosine exchange

EX_dha(e)	Dihydroxyacetone exchange
EX_dimp(e)	dIMP exchange
EX_din(e)	Deoxyinosine exchange
EX_dms(e)	Dimethyl sulfide exchange
EX_dmso(e)	Dimethyl sulfoxide exchange
EX_dopa(e)	Dopamine exchange
EX_doxrbcn(e)	doxorubicin exchange
EX_dtmp(e)	dTMP exchange
EX_dump(e)	dUMP exchange
EX_duri(e)	Deoxyuridine exchange
EX_enter(e)	Enterochelin exchange
EX_etha(e)	Ethanolamine exchange
EX_ethso3(e)	ethanesulfonate exchange
EX_etoh€	Ethanol exchange
EX_f6p(e)	D-fructose 6-phosphate exchange
EX_fald(e)	Formaldehyde exchange
EX_fe2(e)	Fe2+ exchange
EX_fe3(e)	Fe3+ exchange
EX_fe3dcit(e)	Fe(III)dicitrate exchange
EX_fe3dhbzs(e)	ferric 2,3-dihydroxybenzoylserine exchange
EX_fe3hox(e)	Fe(III)hydroxamate exchange
EX_fe3hox-un(e)	Fe(III)hydoxamate, unloaded exchange
EX_fecrm(e)	Ferrichrome exchange
EX_fecrm-un(e)	Ferrichrome minus Fe(III) exchange
EX_feenter(e)	Fe-enterobactin exchange
EX_feoxam(e)	ferroxamine exchange
EX_feoxam-un(e)	ferroxamine minus Fe(3) exchange
EX_fol(e)	folate exchange
EX_for(e)	Formate exchange
EX_fru(e)	D-Fructose exchange
EX_frulys(e)	fructoselysine exchange
EX_fruur(e)	D-Fructuronate exchange
EX_fuc-L(e)	L-Fucose exchange
EX_fum(e)	Fumarate exchange
EX_fusa(e)	fusidic acid exchange
EX_g1p(e)	D-Glucose 1-phosphate exchange
EX_g3pc(e)	sn-Glycero-3-phosphocholine exchange
EX_g3pe(e)	sn-Glycero-3-phosphoethanolamine exchange
EX_g3pg(e)	Glycerophosphoglycerol exchange
EX_g3pi(e)	sn-Glycero-3-phospho-1-inositol exchange
EX_g3ps(e)	Glycerophosphoserine exchange
EX_g6p(e)	D-Glucose 6-phosphate exchange
EX_gal(e)	D-Galactose exchange
EX_gal1p(e)	alpha-D-Galactose 1-phosphate exchange
EX_gal-bD(e)	beta D-Galactose exchange
EX_galct-D(e)	D-Galactarate exchange
EX_galctn-D(e)	D-Galactonate exchange
EX_galctn-L(e)	L-Galactonate exchange

EX_galt(e)	Galactitol exchange
EX_galur(e)	D-Galacturonate exchange
EX_gam(e)	D-Glucosamine exchange
EX_gam6p(e)	D-Glucosamine 6-phosphate exchange
EX_gbbtn(e)	gamma-butyrobetaine exchange
EX_gdp(e)	GDP exchange
EX_glc(e)	D-Glucose exchange
EX_glcn(e)	D-Gluconate exchange
EX_glcr(e)	D-Glucarate exchange
EX_glcur(e)	D-Glucuronate exchange
EX_glcur1p(e)	D-Glucuronate 1-phosphate exchange
EX_gln-L(e)	L-Glutamine exchange
EX_glu-L(e)	L-Glutamate exchange
EX_gly(e)	Glycine exchange
EX_glyald(e)	D-Glyceraldehyde exchange
EX_glyb(e)	Glycine betaine exchange
EX_glyc(e)	Glycerol exchange
EX_glyc2p(e)	Glycerol 2-phosphate exchange
EX_glyc3p(e)	Glycerol 3-phosphate exchange
EX_glyclt(e)	Glycolate exchange
EX_glyc-R(e)	(R)-Glycerate exchange
EX_gmp(e)	GMP exchange
EX_gsn(e)	Guanosine exchange
EX_gthox(e)	Oxidized glutathione exchange
EX_gthrd(e)	Reduced glutathione exchange
EX_gtp(e)	GTP exchange
EX_gua(e)	Guanine exchange
EX_h(e)	H+ exchange
EX_h2(e)	H2 exchange
EX_h2o(e)	H2O exchange
EX_h2o2(e)	Hydrogen peroxide exchange
EX_h2s(e)	Hydrogen sulfide exchange
EX_hdca(e)	Hexadecanoate (n-C16:0) exchange
EX_hdcea(e)	hexadecenoate (n-C16:1) exchange
EX_hg2(e)	Hg2+ exchange
EX_his-L(e)	L-Histidine exchange
EX_hom-L(e)	L-Homoserine exchange
EX_hv(e)	luciferase exchange flux
EX_hxa(e)	Hexanoate (n-C6:0) exchange
EX_hxan(e)	Hypoxanthine exchange
EX_idon-L(e)	L-Idonate exchange
EX_ile-L(e)	L-Isoleucine exchange
EX_imp(e)	IMP exchange
EX_indole(e)	Indole exchange
EX_inost(e)	myo-Inositol exchange
EX_ins(e)	Inosine exchange
EX_isetac(e)	Isethionic acid exchange
EX_k(e)	K+ exchange

EX_kdo2lipid4(e)	KDO(2)-lipid IV(A) exchange
EX_lac-D(e)	D-lactate exchange
EX_lac-L(e)	L-Lactate exchange
EX_LalaDglu(e)	L-alanine-D-glutamate exchange
EX_LalaDgluMdap(e)	L-alanine-D-glutamate-meso-2,6-diaminoheptan
EX_LalaDgluMdapDala(e)	L-alanine-D-glutamate-meso-2,6-diaminoheptan
EX_LalaLglu(e)	L-alanine-L-glutamate exchange
EX_lcts(e)	Lactose exchange
EX_leu-L(e)	L-Leucine exchange
EX_lipavf(e)	V. fischeri lipid A exchange
EX_lipoate(e)	Lipoate exchange
EX_lys-L(e)	L-Lysine exchange
EX_lyx-L(e)	L-Lyxose exchange
EX_mal-D(e)	D-Malate exchange
EX_mal-L(e)	L-Malate exchange
EX_malt(e)	Maltose exchange
EX_malthx(e)	Maltohexaose exchange
EX_maltpt(e)	Maltopentaose exchange
EX_malttr(e)	Maltotriose exchange
EX_maltttr(e)	Maltotetraose exchange
EX_man(e)	D-Mannose exchange
EX_man6p(e)	D-Mannose 6-phosphate exchange
EX_manglyc(e)	2(alpha-D-Mannosyl)-D-glycerate exchange
EX_melib(e)	Melibiose exchange
EX_meoh(e)	methanol exchange
EX_met-D(e)	D-Methionine exchange
EX_met-L(e)	L-Methionine exchange
EX_metsox-R-L(e)	L-methionine-R-sulfoxide exchange
EX_metsox-S-L(e)	L-Methionine S-oxide exchange
EX_mg2(e)	Mg exchange
EX_mincyc(e)	minocycline exchange
EX_minohp(e)	myo-Inositol hexakisphosphate exchange
EX_mmet(e)	S-Methyl-L-methionine exchange
EX_mn2(e)	Mn2+ exchange
EX_mnl(e)	D-Mannitol exchange
EX_mobd(e)	Molybdate exchange
EX_mso3(e)	methanesulfonate exchange
EX_n2o(e)	Nitrous oxide exchange
EX_na1(e)	Sodium exchange
EX_nac(e)	Nicotinate exchange
EX_nh4(e)	Ammonia exchange
EX_ni2(e)	Ni2+ exchange
EX_nmn(e)	NMN exchange
EX_no(e)	Nitric oxide exchange
EX_no2(e)	Nitrite exchange
EX_no3(e)	Nitrate exchange
EX_novbcn(e)	novobiocin exchange
EX_o2(e)	O2 exchange

EX_o2s(e)	Superoxide anion exchange
EX_ocdca(e)	octadecanoate (n-C18:0) exchange
EX_ocdcea(e)	octadecenoate (n-C18:1) exchange
EX_octa(e)	octanoate (n-C8:0) exchange
EX_orn(e)	Ornithine exchange
EX_orot(e)	Orotate exchange
EX_pacald(e)	Phenylacetaldehyde exchange
EX_peamn(e)	Phenethylamine exchange
EX_phe-L(e)	L-Phenylalanine exchange
EX_pheme(e)	Protoheme exchange
EX_pi(e)	Phosphate exchange
EX_pnto-R(e)	(R)-Pantothenate exchange
EX_ppa(e)	Propionate exchange
EX_ppal(e)	Propanal exchange
EX_pppn(e)	Phenylpropanoate exchange
EX_ppt(e)	Phosphonate exchange
EX_progly(e)	L-Prolinylglycine exchange
EX_pro-L(e)	L-Proline exchange
EX_psclys(e)	psicoselysine exchange
EX_pser-L(e)	O-Phospho-L-serine exchange
EX_ptrc(e)	Putrescine exchange
EX_pydam(e)	Pyridoxamine exchange
EX_pydx(e)	Pyridoxal exchange
EX_pydxn(e)	Pyridoxine exchange
EX_pyr(e)	Pyruvate exchange
EX_quin(e)	Quinate exchange
EX_r5p(e)	alpha-D-Ribose 5-phosphate exchange
EX_rfamp(e)	rifampin exchange
EX_rib-D(e)	D-Ribose exchange
EX_ribflv(e)	riboflavin exchange
EX_rmn(e)	L-Rhamnose exchange
EX_sbt-D(e)	D-Sorbitol exchange
EX_sel(e)	Selenate exchange
EX_ser-D(e)	D-Serine exchange
EX_ser-L(e)	L-Serine exchange
EX_skm(e)	Shikimate exchange
EX_slnt(e)	selenite exchange
EX_so2(e)	sulfur dioxide exchange
EX_so3(e)	Sulfite exchange
EX_so4(e)	Sulfate exchange
EX_spmd(e)	Spermidine exchange
EX_succ(e)	Succinate exchange
EX_sucr(e)	Sucrose exchange
EX_sulfac(e)	sulfoacetate exchange
EX_tartr-D(e)	D-tartrate exchange
EX_tartr-L(e)	L-tartrate exchange
EX_taur(e)	Taurine exchange
EX_tcynt(e)	Thiocyanate exchange

EX_thm(e)	Thiamin exchange
EX_thr-L(e)	L-Threonine exchange
EX_thrp(e)	L-Threonine O-3-phosphate exchange
EX_thym(e)	Thymine exchange
EX_thymd(e)	Thymidine exchange
EX_tma(e)	Trimethylamine exchange
EX_tmao(e)	Trimethylamine N-oxide exchange
EX_tre(e)	Trehalose exchange
EX_trp-L(e)	L-Tryptophan exchange
EX_tsul(e)	Thiosulfate exchange
EX_ttdca(e)	tetradecanoate (n-C14:0) exchange
EX_ttdcea(e)	tetradecenoate (n-C14:1) exchange
EX_ttrcyc(e)	tetracycline exchange
EX_tungs(e)	tungstate exchange
EX_tym(e)	Tyramine exchange
EX_tyr-L(e)	L-Tyrosine exchange
EX_tyrp(e)	Phosphotyrosine exchange
EX_uacgam(e)	UDP-N-acetyl-D-glucosamine exchange
EX_udpacgal(e)	UDP-N-acetyl-D-galactosamine exchange
EX_udpg(e)	UDPglucose exchange
EX_udpgal(e)	UDPgalactose exchange
EX_udpglcur(e)	UDP-D-glucuronate exchange
EX_ump(e)	UMP exchange
EX_ura(e)	Uracil exchange
EX_urea(e)	Urea exchange
EX_uri(e)	Uridine exchange
EX_val-L(e)	L-Valine exchange
EX_xan(e)	Xanthine exchange
EX_xmp(e)	Xanthosine 5'-phosphate exchange
EX_xtsn(e)	Xanthosine exchange
EX_xyl-D(e)	D-Xylose exchange
EX_xylu-L(e)	L-Xylulose exchange
EX_zn2(e)	Zinc exchange
F6Pt6_2pp	Fructose-6-phosphate transport via phosphate
F6Ptex	fructose 6-phosphate transport via diffusion (ext
FACOAE100	fatty-acid-CoA thioesterase (decanoate)
FACOAE120	fatty-acid-CoA thioesterase (dodecanoate)
FACOAE140	fatty-acid-CoA thioesterase (tetradecanoate)
FACOAE141	fatty-acid-CoA thioesterase (tetradecenoate)
FACOAE160	fatty-acid-CoA thioesterase (hexadecanoate)
FACOAE161	fatty-acid-CoA thioesterase (hexadecenoate)
FACOAE180	fatty-acid-CoA thioesterase (octadecanoate)
FACOAE181	fatty-acid-CoA thioesterase (octadecenoate)
FACOAE60	fatty-acid-CoA thioesterase (hexanoate)
FACOAE80	fatty-acid-CoA thioesterase (octanoate)
FACOAL100t2pp	fatty-acid-CoA ligase (decanoate transport via
FACOAL120t2pp	fatty-acid-CoA ligase (dodecanoate transport vi
FACOAL140t2pp	fatty-acid-CoA ligase (tetradecanoate transport

FACOAL141t2pp	fatty-acid-CoA ligase (tetradecenoate transport v
FACOAL160t2pp	fatty-acid-CoA ligase (hexadecanoate transport
FACOAL161t2pp	fatty-acid-CoA ligase (hexadecenoate transport
FACOAL180t2pp	fatty-acid-CoA ligase (octadecanoate transport v
FACOAL181t2pp	fatty-acid-CoA ligase (octadecenoate transport v
FACOAL60t2pp	fatty-acid-CoA ligase (hexanoate transport via ve
FACOAL80t2pp	fatty-acid-CoA ligase (octanoate transport via ve
FADRx	FAD reductase
FADRx2	FAD reductase
FALDH2	formaldehyde dehydrogenase
FALDtex	formaldehyde transport via diffusion (extracellula
FAR	fatty acid reductase
FBA	fructose-bisphosphate aldolase
FBA3	Sedoheptulose 1,7-bisphosphate D-glyceraldeh
FBP	fructose-bisphosphatase
FCLT	Ferrochelatase
FDH	formate dehydrogenase
FDH4pp	formate dehydrogenase (quinone-8) (periplasm)
FDH5pp	Formate Dehydrogenase (menaquinone-8) (peri
FE2abcpp	iron (II) transport via ABC system (periplasm)
FE2t3pp	iron (Fe+2) transport out via proton antiport (per
FE2tex	iron (II) transport via diffusion (extracellular to pe
FE2tpp	iron (+2) transport in via permease (no H+)
FE3abcpp	iron (III) transport via ABC system (periplasm to
FE3HOXabcpp	ferric-dicitrate transport via ABC system (peripla
FE3HOXtonex	Fe(III)hydroxamine transport via ton system (ext
FE3Ri	Fe(III) reduction
FE3tex	iron (III) transport via diffusion (extracellular to p
FECRMabcpp	ferrichrome transport via ABC system (periplasm
FECRMtonex	ferrichrome transport via ton system (extracellula
FEENTERtex	enterochelin transport (secretion periplasm)
FEOXAMabcpp	ferroxamine transport via ABC system (periplasm
FEOXAMtonex	ferroxamine transport via ton system (extracellul
FGLU	formimidoylglutamase
FLDR2	flavodoxin reductase (NADPH)
FLVR	flavin reductase
FLVRx	flavin reductase (NAD)
FMETTRS	Methionyl-tRNA formyltransferase
FMNAT	FMN adenylyltransferase
FMNRx	FMN reductase
FMNRx2	FMN reductase
FOMETRi	Aminomethyltransferase
FORO	formate:NADP+ oxidoreductase
FORt2pp	formate transport via proton symport (uptake on
FORtex	formate transport via diffusion (extracellular to p
FORtppi	formate transport via diffusion (cytoplasm to per
FRD2	fumarate reductase
FRD3	fumarate reductase

FRTT	farnesyltransferase
FRUK	fructose-1-phosphate kinase
FRULYStex	fructoselysine transporter via diffusion (extracell
FRUpts2pp	Fructose transport via PEP:Pyr PTS (f6p genera
FRUptspp	D-fructose transport via PEP:Pyr PTS (periplas
FRUtex	D-fructose transport via diffusion (extracellular t
FRUURtex	D-fructuronate transport via diffusion (extracellul
FTHFD	formyltetrahydrofolate deformylase
FTHFL	formate-tetrahydrofolate ligase
FUCtex	L-fucose transport via diffusion (extracellular to
FUM	fumarase
FUMt2_3pp	Fumarate transport via proton symport (3 H) (pe
FUMtex	Fumarate transport via diffusion (extracellular to
FUSAtex	Fusidic acid transport via diffusion (extracellular
G1PACT	glucosamine-1-phosphate N-acetyltransferase
G1PCT	glucose-1-phosphate cytidylyltransferase
G1Ptex	D-glucose 1-phosphate transport via diffusion
G1PTT	glucose-1-phosphate thymidylyltransferase
G1SAT	glutamate-1-semialdehyde aminotransferase
G2PP	glycerol-2-phosphate phosphatase
G3PAT120	glycerol-3-phosphate acyltransferase (C12:0)
G3PAT140	glycerol-3-phosphate acyltransferase (C14:0)
G3PAT141	glycerol-3-phosphate acyltransferase (C14:1)
G3PAT160	glycerol-3-phosphate acyltransferase (C16:0)
G3PAT161	glycerol-3-phosphate acyltransferase (C16:1)
G3PAT180	glycerol-3-phosphate acyltransferase (C18:0)
G3PAT181	glycerol-3-phosphate acyltransferase (C18:1)
G3PCtex	glycero-3-phosphocholine transport via diffusion
G3PD2	glycerol-3-phosphate dehydrogenase (NADP)
G3PD5	glycerol-3-phosphate dehydrogenase (ubiquino
G3PD6	glycerol-3-phosphate dehydrogenase (menaqui
G3PD7	glycerol-3-phosphate dehydrogenase (demethyl
G3PEtex	glycero-3-phosphoethanolamine transport via di
G3PGtex	glycerophoglycerol transport via diffusion (extra
G3PItex	glycero-3-phospho-1-inositol transport via diffusi
G3PStex	glycerophosphserine transport via diffusion (extr
G5SADs	L-glutamate 5-semialdehyde dehydratase (spon
G5SD	glutamate-5-semialdehyde dehydrogenase
G6PDA	glucosamine-6-phosphate deaminase
G6PDH2r	glucose 6-phosphate dehydrogenase
G6Pt6_2pp	Glucose-6-phosphate transport via phosphate a
G6Ptex	glucose 6-phosphate transport via diffusion (extr
GAL1Ptex	D-galactose 1-phosphate transport via diffusion
GALAM6PISO	D-Galactosamine-6-phosphate isomerase
GALBDtex	beta D-galactose transport via diffusion (extrace
GALCTNLtex	L-galactonate transport via diffusion (extracellul
GALCTNtex	D-galactonate transport via diffusion (extracellul
GALCTtex	D-galactarte transport via diffusion (extracellular

GALKr	galactokinase
GALM2pp	aldose-1-epimerase
GALt2pp	D-galactose transport in via proton symport (per
GALtex	D-galactose transport via diffusion (extracellular
GALTtex	Galactitol transport via diffusion (extracellular to
GALUi	UTP-glucose-1-phosphate uridylyltransferase (ir
GALURtex	D-galacturonate transport via diffusion (extracell
GAM6Pt6_2pp	D-Glucosamine 6-phosphate transport via phos
GAMAN6Ptex	D-glucosamine 6-phosphate transport via diffusi
GAMK	N-Acetylglucosamine kinase
GAMptspp	D-glucosamine transport via PEP:Pyr PTS (peri
GAMtex	D-glucosamine transport via diffusion (extracellu
GAPD	glyceraldehyde-3-phosphate dehydrogenase
GARFT	phosphoribosylglycinamide formyltransferase
GART	GAR transformylase-T
GBBTNtex	gamma-butyrobetaine transport via diffusion (ex
GCALDD	Glycolaldehyde dehydrogenase
GDPDPK	GDP diphosphokinase
GDPtex	GDP transport via diffusion (extracellular to peri
GDPTPDP	guanosine 3'-diphosphate 5'-triphosphate 3'-dipl
GF6PTA	glutamine-fructose-6-phosphate transaminase
GHMT2r	glycine hydroxymethyltransferase, reversible
GK1	guanylate kinase (GMP:ATP)
GLBRAN2	1,4-alpha-glucan branching enzyme (glycogen -
GLCATr	D-glucose O-acetyltransferase
GLCNAC2ptspp	chitobiose transport via PTS (periplasm)
GLCNtex	D-gluconate transport via diffusion (extracellular
GLCP	glycogen phosphorylase
GLCP2	glycogen phosphorylase
GLCptspp	D-glucose transport via PEP:Pyr PTS (periplasn
GLCRtex	D-glucarate transport via diffusion (extracellular
GLCS1	glycogen synthase (ADPGlc)
GLCt2pp	D-glucose transport in via proton symport (perip
GLCtex	glucose transport via diffusion (extracellular to p
GLCtexi	D-glucose transport via diffusion (extracellular tc
GLCUR1Ptex	D-glucuronate 1-phosphate transport via diffusic
GLCURt2rpp	D-glucuronate transport via proton symport, reve
GLCURtex	D-glucuronat transport via diffusion (extracellula
GLDBRAN2	glycogen debranching enzyme (bglycogen -> gl
GLGC	glucose-1-phosphate adenylyltransferase
GLNS	glutamine synthetase
GLNt2rpp	L-glutamine transport via proton symport (peripl
GLNtex	L-glutamine transport via diffusion (extracellular
GLNTRS	Glutaminyl-tRNA synthetase
GLU5K	glutamate 5-kinase
GLUCYS	gamma-glutamylcysteine synthetase
GLUDC	Glutamate Decarboxylase
GLUDx	glutamate dehydrogenase (NAD)

GLUN	glutaminase
GLUNpp	glutaminase
GLUPRT	glutamine phosphoribosyldiphosphate amidotra
GLUR	glutamate racemase
GLUSy	glutamate synthase (NADPH)
GLUt2rpp	L-glutamate transport via proton symport, revers
GLUt4pp	Na+/glutamate symport (periplasm)
GLUtex	L-glutamate transport via diffusion (extracellular
GLUTRR	glutamyl-tRNA reductase
GLUTRS	Glutamyl-tRNA synthetase
GLYALDtex	Glyceraldehyde transport via diffusion (extracell
GLYALDtpp	Glyceraldehyde facilitated diffusion (periplasm)
GLYAT	glycine C-acetyltransferase
GLYBt2pp	Glycine betaine transport via proton symport (p
GLYBtex	Glycine betaine transport via diffusion (extracell
GLYC2Ptex	Glycerol-2-phosphate transport via diffusion (ex
GLYC3Pt6pp	Glycerol-3-phosphate : phosphate antiporter (p
GLYC3Ptex	Glycerol-3-phosphate transport via diffusion (ex
GLYCAtex	D-glycerate transport via diffusion (extracellular
GLYCK	glycerate kinase
GLYCL	Glycine Cleavage System
GLYCLTt2rpp	glycolate transport via proton symport, reversibl
GLYCLTtex	glycolate transport via diffusion (extracellular to
GLYCtex	glycerol transport via diffusion (extracellular to p
GLYCtpp	glycerol transport via channel (periplasm)
GLYK	glycerol kinase
GLYOX	hydroxyacylglutathione hydrolase
GLYt2pp	glycine transport in via proton symport (periplas
GLYt4pp	glycine transport in via sodium symport (periplas
GLYtex	Glycine transport via diffusion (extracellular to p
GLYTRS	Glycyl-tRNA synthetase
GMHEPAT	D-glycero-D-manno-hepose 1-phosphate adeny
GMHEPK	D-glycero-D-manno-heptose 7-phosphate kinas
GMHEPPA	D-glycero-D-manno-heptose 1,7-bisphosphate
GMPR	GMP reductase
GMPS2	GMP synthase
GMPtex	GMP transport via diffusion (extracellular to peri
GND	phosphogluconate dehydrogenase
GP4GH	Gp4G hydrolase
GPDDA1	Glycerophosphodiester phosphodiesterase (Gly
GPDDA1pp	Glycerophosphodiester phosphodiesterase (Gly
GPDDA2	Glycerophosphodiester phosphodiesterase (Gly
GPDDA2pp	Glycerophosphodiester phosphodiesterase (Gly
GPDDA3	Glycerophosphodiester phosphodiesterase (Gly
GPDDA3pp	Glycerophosphodiester phosphodiesterase (Gly
GPDDA4	Glycerophosphodiester phosphodiesterase (Gly
GPDDA4pp	Glycerophosphodiester phosphodiesterase (Gly
GPDDA5	Glycerophosphodiester phosphodiesterase (Gly

GPDDA5pp	Glycerophosphodiester phosphodiesterase (Gly
GRTT	geranyltranstransferase
GRXR	glutaredoxin reductase
GSNK	guanosine kinase
GSNt2pp	guanosine transport in via proton symport (perip
GSNtex	guanosine transport via diffusion (extracellular t
GTHOr	glutathione oxidoreductase
GTHOXtex	glutathione (ox) transport via diffusion (extracell
GTHRDabc2pp	glutathione export via ABC system (cytoplasm t
GTHRDHpp	glutathione hydralase (periplasmic)
GTHRDtex	glutathione transport via diffusion (extracellular t
GTHS	glutathione synthetase
GTPCI	GTP cyclohydrolase I
GTPCII2	GTP cyclohydrolase II (25drapp)
GTPDPDP	guanosine-5'-triphosphate,3'-diphosphate dipho
GTPDPK	GTP diphosphokinase
GTPtex	GTP transport via diffusion (extracellular to peri
GUAD	guanine deaminase
GUAPRT	guanine phosphoribosyltransferase
GUAt2pp	guanine transport in via proton symport (periplas
GUAtex	Guanine transport via diffusion (extracellular to
H2O2tex	hydrogen peroxide transport via diffusion (exter
H2Otex	H2O transport via diffusion (extracellular to peri
H2Otpp	H2O transport via diffusion (periplasm)
H2Stex	h2s transport via diffusion (extracellular to peripl
H2tex	hydrogen transport via diffusion (extracellular to
HACD1	3-hydroxyacyl-CoA dehydrogenase (acetoacetyl
HACD2	3-hydroxyacyl-CoA dehydrogenase (3-oxohexa
HACD3	3-hydroxyacyl-CoA dehydrogenase (3-oxoocta
HACD4	3-hydroxyacyl-CoA dehydrogenase (3-oxodeca
HACD5	3-hydroxyacyl-CoA dehydrogenase (3-oxodode
HACD6	3-hydroxyacyl-CoA dehydrogenase (3-oxotetrad
HACD7	3-hydroxyacyl-CoA dehydrogenase (3-oxohexa
HACD8	3-hydroxyacyl-CoA dehydrogenase (3-oxooctad
HBZOPT	Hydroxybenzoate octaprenyltransferase
HCINNMtex	3-hydroxycinnamic acid transport via diffusion (
HCO3E	HCO3 equilibration reaction
HDCAtexi	Hexadecanoate transport via facilitated irreversi
HDCEAtexi	Hexadecenoate transport via facilitated irreversi
HETZK	hydroxyethylthiazole kinase
HEX1	hexokinase (D-glucose:ATP)
HEXt2rpp	hexanoate transport via proton symport, reversi
HG2abcpp	Mercury (Hg+2) ABC transporter (periplasm)
HG2t3pp	mercury (Hg+2) transport out via proton antiport
HG2tex	mercury (Hg+2) transport via diffusion (extracell
HIBDkt	3-hydroxyisobutyrate dehydrogenase
HISabcpp	L-histidine transport via ABC system (periplasm
HISD	histidase

HISTD	histidinol dehydrogenase
HIStex	L-histidine transport via diffusion (extracellular to
HISTP	histidinol-phosphatase
HISTRS	Histidyl-tRNA synthetase
HMBS	hydroxymethylbilane synthase
HMPK1	hydroxymethylpyrimidine kinase (ATP)
HOMtex	L-homoserine transport via diffusion (extracellula
HPPK2	6-hydroxymethyl-dihydropterin pyrophosphokina
HPPPNtex	3-(3-hydroxyphenyl)propionate transport via diffu
HSDy	homoserine dehydrogenase (NADPH)
HSK	homoserine kinase
HSST	homoserine O-succinyltransferase
HSTPT	histidinol-phosphate transaminase
Htex	proton transport via diffusion (extracellular to pe
HXAD	beta-hexoamindase
HXAtex	Hexanoate transport via diffusion (extracellular t
HXCT	Acetyl-CoA:hexanoate-CoA transferase
HXPRT	hypoxanthine phosphoribosyltransferase (Hypox
HYXNtex	Hypoxanthine transport via diffusion (extracellula
HYXNtpp	Hypoxanthine transport (periplasm)
I2FE2SR	ISC [2Fe-2S] regeneration
I2FE2SS	ISC [2Fe-2S] Synthesis
I2FE2SS2	ISC [2Fe-2S] Synthesis II
I2FE2ST	ISC [2Fe-2S] Transfer
I4FE4SR	ISC [4Fe-4S] Reduction
I4FE4ST	ISC [4Fe-4S] Transfer
ICDHyr	isocitrate dehydrogenase (NADP)
ICHORS	isochorismate synthase
ICL	Isocitrate lyase
ICYSDS	ISC Cysteine desulfuration
IDONtex	L-idonate transport via diffusion (extracellular to
IG3PS	Imidazole-glycerol-3-phosphate synthase
IGPDH	imidazoleglycerol-phosphate dehydratase
IGPS	indole-3-glycerol-phosphate synthase
ILEabcpp	L-isoleucine transport via ABC system (periplasm
ILEt2rpp	L-isoleucine reversible transport via proton symp
ILETA	isoleucine transaminase
ILEtex	L-isoleucine transport via diffusion (extracellular
ILETRS	Isoleucyl-tRNA synthetase
IMPC	IMP cyclohydrolase
IMPD	IMP dehydrogenase
IMPtex	IMP transport via diffusion (extracellular to perip
INDOLEtex	Indole transport via diffusion (extracellular to per
INOSTt4pp	Na+/myo-inositol symporter (periplasm)
INSK	insosine kinase
INSt2rpp	inosine transport in via proton symport, reversibl
INStex	inosine transport via diffusion (extracellular to pe
INSTtex	inositol transport via diffusion (extracellular to pe

IPDDI	isopentenyl-diphosphate D-isomerase
IPDPS	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
IPMD	3-isopropylmalate dehydrogenase
IPPMIa	3-isopropylmalate dehydratase
IPPMIb	2-isopropylmalate hydratase
IPPS	2-isopropylmalate synthase
ISETACtex	isethionate transport via diffusion (extracellular t
IZPN	imidazolonepropionase
KARA1	ketol-acid reductoisomerase (2,3-dihydroxy-3-m
KARA2	ketol-acid reductoisomerase (2-Acetolactate)
KAS14	beta-ketoacyl-ACP synthase
KAS15	beta-ketoacyl-ACP synthase (2)
KDOCT2	3-deoxy-manno-octulosonate cytidylyltransferas
KDOPP	3-deoxy-manno-octulosonate-8-phosphatase
KDOPS	3-deoxy -D-manno-octulosonic -acid 8-phospha
Kt2pp	potassium transport in via proton symport (perip
Kt3pp	potassium transport out via proton antiport (peri
Ktex	potassium transport via diffusion (extracellular t
LALADGLUtex	L-alanyl-D-glutamate transport via diffusion (ext
LALADGLUtpp	L-alanyl-D-glutamate transport in via proton syr
LALALGLUtex	L-alanyl-L-glutamate transport via diffusion (extr
LALALGLUtpp	L-alanyl-L-glutamate transport in via proton sym
LALGP	L-alanyl-gamma-L-glutamate peptidase
LCADi	lactaldehyde dehydrogenase
LCTStex	Lactose transport via diffusion (extracellular to p
LDH_D	D-lactate dehydrogenase
LEUabcpp	L-leucine transport via ABC system (periplasm)
LEUt2rpp	L-leucine reversible transport via proton sympor
LEUTAi	leucine transaminase (irreversible)
LEUtex	L-leucine transport via diffusion (extracellular to
LEUTRS	Leucyl-tRNA synthetase
LGTHL	lactoylglutathione lyase
LIPAVFabcpp	V. fischeri lipid A transport via ABC system (peri
LIPAVFabctex	V. fischeri lipid A transport via ABC system (peri
LIPOCT	Lipoyl(octanoyl) transferase
LIPOS	Lipoate synthase
LIPOtex	lipoate transport via diffusion (extracellular to pe
L-LACt2rpp	L-lactate reversible transport via proton symport
L-LACtex	L-lactate transport via diffusion (extracellular to
LPADSSVF	V. fischeri lipid A disaccaride synthase
LPLIPAL1A120pp	Lysophospholipase L1 (2-acylglycerophosphoti
LPLIPAL1A140pp	Lysophospholipase L1 (2-acylglycerophosphoti
LPLIPAL1A141pp	Lysophospholipase L1 (2-acylglycerophosphoti
LPLIPAL1A160pp	Lysophospholipase L1 (2-acylglycerophosphoti
LPLIPAL1A161pp	Lysophospholipase L1 (2-acylglycerophosphoti
LPLIPAL1A180pp	Lysophospholipase L1 (2-acylglycerophosphoti
LPLIPAL1A181pp	Lysophospholipase L1 (2-acylglycerophosphoti
LPLIPAL1E120pp	Lysophospholipase L1 (2-acylglycerophosphoet

LPLIPAL1E140pp	Lysophospholipase L1 (2-acylglycerophosphoet
LPLIPAL1E141pp	Lysophospholipase L1 (2-acylglycerophosphoet
LPLIPAL1E160pp	Lysophospholipase L1 (2-acylglycerophosphoet
LPLIPAL1E161pp	Lysophospholipase L1 (2-acylglycerophosphoet
LPLIPAL1E180pp	Lysophospholipase L1 (2-acylglycerophosphoet
LPLIPAL1E181pp	Lysophospholipase L1 (2-acylglycerophosphoet
LPLIPAL1G120pp	Lysophospholipase L1 (2-acylglycerophosphogl
LPLIPAL1G140pp	Lysophospholipase L1 (2-acylglycerophosphogl
LPLIPAL1G141pp	Lysophospholipase L1 (2-acylglycerophosphogl
LPLIPAL1G160pp	Lysophospholipase L1 (2-acylglycerophosphogl
LPLIPAL1G161pp	Lysophospholipase L1 (2-acylglycerophosphogl
LPLIPAL1G180pp	Lysophospholipase L1 (2-acylglycerophosphogl
LPLIPAL1G181pp	Lysophospholipase L1 (2-acylglycerophosphogl
LPLIPAL2A120	Lysophospholipase L2 (2-acylglycerophosphoti
LPLIPAL2A140	Lysophospholipase L2 (2-acylglycerophosphoti
LPLIPAL2A141	Lysophospholipase L2 (2-acylglycerophosphoti
LPLIPAL2A160	Lysophospholipase L2 (2-acylglycerophosphoti
LPLIPAL2A161	Lysophospholipase L2 (2-acylglycerophosphoti
LPLIPAL2A180	Lysophospholipase L2 (2-acylglycerophosphoti
LPLIPAL2A181	Lysophospholipase L2 (2-acylglycerophosphoti
LPLIPAL2ATE120	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATE140	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATE141	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATE160	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATE161	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATE180	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATE181	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATG120	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATG140	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATG141	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATG160	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATG161	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATG180	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2ATG181	Lysophospholipase L2 (acyltransferase, 2-acyl-g
LPLIPAL2E120	Lysophospholipase L2 (2-acylglycerophosphoet
LPLIPAL2E140	Lysophospholipase L2 (2-acylglycerophosphoet
LPLIPAL2E141	Lysophospholipase L2 (2-acylglycerophosphoet
LPLIPAL2E160	Lysophospholipase L2 (2-acylglycerophosphoet
LPLIPAL2E161	Lysophospholipase L2 (2-acylglycerophosphoet
LPLIPAL2E180	Lysophospholipase L2 (2-acylglycerophosphoet
LPLIPAL2E181	Lysophospholipase L2 (2-acylglycerophosphoet
LPLIPAL2G120	Lysophospholipase L2 (2-acylglycerophosphogl
LPLIPAL2G140	Lysophospholipase L2 (2-acylglycerophosphogl
LPLIPAL2G141	Lysophospholipase L2 (2-acylglycerophosphogl
LPLIPAL2G160	Lysophospholipase L2 (2-acylglycerophosphogl
LPLIPAL2G161	Lysophospholipase L2 (2-acylglycerophosphogl
LPLIPAL2G180	Lysophospholipase L2 (2-acylglycerophosphogl
LPLIPAL2G181	Lysophospholipase L2 (2-acylglycerophosphogl

LPSVF	V. fischeri LPS synthesis
LPSVFabcpp	V. fischeri LPS transport via ABC system (peripl
LPSVFabctex	V. fischeri LPS transport via ABC system (peripl
LUC	luciferase
LYSabcpp	L-lysine transport via ABC system (periplasm)
LYSAM	lysine 2,3-aminomutase
LYSDC	lysine decarboxylase
LYStex	L-lysine transport via diffusion (extracellular to p
LYSTRS	Lysyl-tRNA synthetase
LYXtex	L-Lyxose transport via diffusion (extracellular to
M1PD	mannitol-1-phosphate 5-dehydrogenase
MACGAM26PH	6-phospho-beta-glucosidase
MACPD	Malonyl-ACP decarboxylase
MALCOAMT	Malonyl-CoA methyltransferase
MALDtex	D-Malate transport via diffusion (extracellular to
MALS	malate synthase
MALt2_3pp	Malate transport via proton symport (3 H) (peripl
MALTabcpp	maltose transport via ABC system (periplasm)
MALTATr	maltose O-acetyltransferase
MALtex	Malate transport via diffusion (extracellular to pe
MALTHXabcpp	maltohexaose transport via ABC system (peripl
MALTHXtexi	maltohexaose transport via diffusion (extracellul
MALTPTabcpp	maltopentaose transport via ABC system (peripl
MALTptspp	maltose transport via PEP:Pyr PTS (periplasm)
MALTPTtexi	maltopentaoseMaltotriose transport via diffusion
MALTtexi	maltoseMaltotriose transport via diffusion (extra
MALTTRabcpp	Maltotriose transport via ABC system (periplasm
MALTTRtexi	Maltotriose transport via diffusion (extracellular t
MALTTTRabcpp	maltotetraose transport via ABC system (peripl
MALTTTRtexi	maltotetraoseMaltotriose transport via diffusion
MAN6PI	mannose-6-phosphate isomerase
MAN6Pt6_2pp	Mannose-6-phosphate transport via phosphate
MAN6Ptex	Mannose 6-phosphate transport via diffusion (e
MANGLYCtex	2-O-alpha-mannosyl-D-glycerate transport via d
MANptspp	D-mannose transport via PEP:Pyr PTS (periplas
MANtex	D-mannose transport via diffusion (extracellular
MCITD	2-methylcitrate dehydratase
MCITL2	methylisocitrate lyase
MCITS	2-methylcitrate synthase
MCOATA	Malonyl-CoA-ACP transacylase
MCPST	3-mercaptopyruvate sulfurtransferase
MCTP1App	murein crosslinking transpeptidase 1A:(A2pm->
MCTP1Bpp	murein crosslinking transpeptidase 1B:(A2pm->
MCTP2App	murein crosslinking transpeptidase 1A:(A2pm->
MDDCP1pp	murein D,D-carboxypeptidase (murein5px4p) (p
MDDCP2pp	murein D,D-carboxypeptidase (murein5px4px4p
MDDCP3pp	murein D,D-carboxypeptidase (murein5p5p) (pe
MDDCP4pp	murein D,D-carboxypeptidase (murein5p4p) (pe

MDDCP5pp	murein D,D-carboxypeptidase (murein5p3p) (pe
MDDEP1pp	murein D,D-endopeptidase (murein4px4p) (peri
MDDEP2pp	murein D,D-endopeptidase (murein3px4p) (peri
MDDEP3pp	murein D,D-endopeptidase (murein5px4p) (peri
MDDEP4pp	murein D,D-endopeptidase (murein4px4px4p) (
MDH	malate dehydrogenase
MDHy	malate dehydrogenase (NADP+)
ME1	malic enzyme (NAD)
ME2	malic enzyme (NADP)
MECDPDH5	2C-methyl-D-erythritol 2,4 cyclodiphosphate deh
MECDPS	2-C-methyl-D-erythritol 2,4-cyclodiphosphate sy
MELIBtex	melibiose transport via diffusion (extracellular to
MEOHtex	Methanol transport via diffusion (extracellular to
MEOHtrpp	Methanol reversible transport via diffusion (perip
MEPCT	2-C-methyl-D-erythritol 4-phosphate cytidylyltrar
METabcpp	L-methionine transport via ABC system (periplas
METAT	methionine adenosyltransferase
METDabcpp	D-methionine transport via ABC system (periplas
METDtex	D-methionine transport via diffusion (extracellula
METS	methionine synthase
METSOX1tex	L-methionine S-oxide diffusion (extracellular)
METSOX2tex	L-methionine R-oxide diffusion (extracellular)
METSOXR1	L-methionine-S-oxide reductase
METSOXR2	L-methionine-R-sulfoxide reductase
METtex	L-methionine transport via diffusion (extracellula
METTRS	Methionyl-tRNA synthetase
MG2t3_2pp	magnesium (Mg+2) transport in/out via proton a
MG2tex	magnesium (Mg+2) transport via diffusion (extra
MG2tpp	magnesium (+2) transport in via diffusion
MG2uabcpp	Magnesium (Mg+2) ABC transporter (ubtake, pe
MGSA	methylglyoxal synthase
MI1PP	myo-inositol 1-phosphatase
MICITDr	2-methylisocitrate dehydratase
MINCYCtex	Minocycline transport via diffusion (extracellular
MLTG1	Maltodextrin glucosidase (maltotriose)
MLTG2	Maltodextrin glucosidase (maltotetraose)
MLTG3	Maltodextrin glucosidase (maltopentaose)
MLTG4	Maltodextrin glucosidase (maltohexaose)
MLTG5	Maltodextrin glucosidase (maltoheptaose)
MLTGY1pp	murein lytic transglycosylase (murein4p4p) (peri
MLTGY2pp	murein lytic transglycosylase (murein4p3p) (peri
MLTGY3pp	murein lytic transglycosylase (murein3p3p) (peri
MLTGY4pp	murein lytic transglycosylase (murein4px4p4p) (
MLTP1	Maltodextrin phosphorylase (maltopentaose)
MLTP2	Maltodextrin phosphorylase (maltohexaose)
MLTP3	Maltodextrin phosphorylase (maltoheptaose)
MMETtex	S-methyl-L-methionine transport via diffusion (e
MN2t3pp	manganese (Mn+2) transport out via proton anti

MN2tpp	manganese transport in via permease (no H+)
MNLptspp	mannitol transport via PEP:Pyr PTS (periplasm)
MNLtex	mannitol transport via diffusion (extracellular to
MNtex	Manganese (Mn+2) transport via diffusion (extra
MOADSUx	MoaD sulfuration (nadh, assumed)
MOBDabcpp	molybdate transport via ABC system (periplasm
MOBDtex	molybdate transport via diffusion (extracellular t
MOCOS	molybdenum cofactor synthase
MOGDS	molybdopterin guanine dinucleotide synthase
MOHMT	3-methyl-2-oxobutanoate hydroxymethyltransfer
MOX	malate oxidase
MPTAT	molybdopterin adenylyltransferase
MPTG	murein polymerizing transglycosylase
MPTG2	murein polymerizing transglycosylase 2 (three li
MPTS	molybdopterin synthase
MPTSS	molybdopterin synthase sulfurylase
MSO3tex	methanesulfonate transport via diffusion (extrac
MTAN	methylthioadenosine nucleosidase
MTHFC	methenyltetrahydrofolate cyclohydrolase
MTHFD	methylenetetrahydrofolate dehydrogenase (NAD
MTHFR2	5,10-methylenetetrahydrofolate reductase (NAD
MTHTHFSs	(2R,4S)-2-methyl-2,3,3,4-tetrahydroxytetrahydro
N2Otex	nitrious oxide transport via diffusion (extracellula
NACODA	N-acetylornithine deacetylase
NACtex	Nicotinic acid transport via diffusion (extracellula
NADDP	NAD diphosphatase
NADH10	NADH dehydrogenase (menaquinone-8 & 0 pro
NADH5	NADH dehydrogenase (ubiquinone-8)
NADH9	NADH dehydrogenase (demethylmenaquinone-
NADK	NAD kinase
NADS1	NAD synthase (nh3)
NADTRHD	NAD transhydrogenase
NAt3_1p5pp	sodium proton antiporter (H:NA is 1.5) (periplas
NAt3_2pp	sodium proton antiporter (H:NA is 2) (periplasm)
NAtex	sodium transport via diffusion (extracellular to pe
NDPK1	nucleoside-diphosphate kinase (ATP:GDP)
NDPK2	nucleoside-diphosphate kinase (ATP:UDP)
NDPK3	nucleoside-diphosphate kinase (ATP:CDP)
NDPK4	nucleoside-diphosphate kinase (ATP:dTDP)
NDPK5	nucleoside-diphosphate kinase (ATP:dGDP)
NDPK6	nucleoside-diphosphate kinase (ATP:dUDP)
NDPK7	nucleoside-diphosphate kinase (ATP:dCDP)
NDPK8	nucleoside-diphosphate kinase (ATP:dADP)
NH4tex	ammonia transport via diffusion (extracellular to
NH4tpp	ammonia reversible transport (periplasm)
NHFRBO	NADH:flavorubredoxin oxidoreductase
NI2abcpp	Nickle (Ni+2) ABC transporter (periplasm)
NI2t3pp	nickle (Ni+2) transport out via proton antiport (pe

NI2tex	nickel transport via diffusion (extracellular to per
NI2tpp	nickel (+2) transport in via permease (no H+)
NI2uabcpp	nickel transport via ABC system (uptake, peripla
NMNAT	nicotinamide-nucleotide adenylyltransferase
NMNPtpp	NMN permease (periplasm)
NMNtex	NMN transport via diffusion (extracellular to peri
NNATr	nicotinate-nucleotide adenylyltransferase
NNDPR	nicotinate-nucleotide diphosphorylase (carboxyla
NO2tex	nitrite transport via diffusion (extracellular to peri
NO3R2bpp	Nitrate reductase (Menaquinol-8) (periplasm)
NO3tex	nitrate transport via diffusion (extracellular to per
NODOx	nitric oxide dioxygenase
NODOy	nitric oxide dioxygenase
NOtex	nitric oxide transport via diffusion (extracellular t
NTD1	5'-nucleotidase (dUMP)
NTD10	5'-nucleotidase (XMP)
NTD10pp	5'-nucleotidase (XMP)
NTD11	5'-nucleotidase (IMP)
NTD11pp	5'-nucleotidase (IMP)
NTD12	5'-nucleotidase (dIMP)
NTD12pp	5'-nucleotidase (dIMP) (periplasm)
NTD1pp	5'-nucleotidase (dUMP)
NTD2	5'-nucleotidase (UMP)
NTD2pp	5'-nucleotidase (UMP)
NTD3	5'-nucleotidase (dCMP)
NTD3pp	5'-nucleotidase (dCMP)
NTD4	5'-nucleotidase (CMP)
NTD4pp	5'-nucleotidase (CMP)
NTD5	5'-nucleotidase (dTMP)
NTD5pp	5'-nucleotidase (dTMP)
NTD6	5'-nucleotidase (dAMP)
NTD6pp	5'-nucleotidase (dAMP)
NTD7	5'-nucleotidase (AMP)
NTD7pp	5'-nucleotidase (AMP)
NTD8	5'-nucleotidase (dGMP)
NTD8pp	5'-nucleotidase (dGMP)
NTD9	5'-nucleotidase (GMP)
NTD9pp	5'-nucleotidase (GMP)
NTP10	nucleoside-triphosphatase (ITP)
NTP11	nucleoside-triphosphatase (dITP)
NTP12	nucleoside-triphosphatase (XTP)
NTPP1	Nucleoside triphosphate pyrophosphorylase (dg
NTPP10	Nucleoside triphosphate pyrophosphorylase (dit
NTPP11	Nucleoside triphosphate pyrophosphorylase (xtp
NTPP2	Nucleoside triphosphate pyrophosphorylase (gtp
NTPP3	Nucleoside triphosphate pyrophosphorylase (dc
NTPP4	Nucleoside triphosphate pyrophosphorylase (ctp
NTPP5	Nucleoside triphosphate pyrophosphorylase (da

NTPP6	Nucleoside triphosphate pyrophosphorylase (at
NTPP7	Nucleoside triphosphate pyrophosphorylase (dtt
NTPP8	Nucleoside triphosphate pyrophosphorylase (ut
NTPP9	Nucleoside triphosphate pyrophosphorylase (itp
NTPTP1	Nucleoside triphosphate tripolyhydrolase
NTPTP2	Nucleoside triphosphate tripolyhydrolase
NTRIR2x	nitrite Reductase (NADH)
NTRIR3pp	nitrite Reductase (Ubiquinole-8, periplasm)
NTRIR4pp	nitrite Reductase (Menaquinole-8, periplasm)
O2Stex	superoxide anion transport via diffusion (extrace
O2tex	oxygen transport via diffusion (extracellular to p
O2tpp	o2 transport via diffusion (periplasm)
OAADC	oxaloacetate decarboxylase
OBTFL	2-Oxobutanoate formate lyase
OCBT	ornithine carbamoyltransferase
OCDCAtexi	Octadecanoate transport via facilitated irreversi
OCDCEAtexi	Octadecenoate (n-C18:1) transport via facilitate
OCTAtex	Octanoate transport via diffusion (extracellular t
OCTDPS	Octaprenyl pyrophosphate synthase
OGMEACPD	3-Oxo-glutaryl-[ACP] methyl ester dehydratase
OGMEACPR	3-Oxo-glutaryl-[ACP] methyl ester reductase
OGMEACPS	3-Oxo-glutaryl-[ACP] methyl ester synthase
OHPBAT	O-Phospho-4-hydroxy-L-threonine:2-oxoglutara
OHPHM	2-octaprenyl-6-hydroxyphenol methylase
OMBZLM	2-Octaprenyl-6-methoxy-benzoquinol methylase
OMCDC	2-Oxo-4-methyl-3-carboxypentanoate decarbox
OMMBLHX	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoqui
OMPDC	orotidine-5'-phosphate decarboxylase
OMPHHX	2-octaprenyl-6-methoxyphenol hydroxylase
OPHBDC	Octaprenyl-hydroxybenzoate decarboxylase
OPHHX	2-Octaprenylphenol hydroxylase
OPHHX3	2-Octaprenylphenol hydroxylase (anaerobic)
OPMEACPD	3-Oxo-pimeloyl-[ACP] methyl ester dehydratase
OPMEACPR	3-Oxo-pimeloyl-[ACP] methyl ester reductase
OPMEACPS	3-Oxo-pimeloyl-[ACP] methyl ester synthase
ORNabcpp	ornithine transport via ABC system (periplasm)
ORNtex	ornithine transport via diffusion (extracellular to
OROTtex	Orotate transport via diffusion (extracellular to p
ORPT	orotate phosphoribosyltransferase
P5CD	1-pyrroline-5-carboxylate dehydrogenase
P5CR	pyrroline-5-carboxylate reductase
PA120abcpp	phosphatidate transport via ABC system (n-C12
PA140abcpp	phosphatidate transport via ABC system (n-C14
PA141abcpp	phosphatidate transport via ABC system (n-C14
PA160abcpp	phosphatidate transport via ABC system (n-C16
PA161abcpp	phosphatidate transport via ABC system (n-C16
PA180abcpp	phosphatidate transport via ABC system (n-C18
PA181abcpp	phosphatidate transport via ABC system (n-C18

PACALDtex	phenethylacetaldehyde transport via diffusion (e
PANTS	pantothenate synthase
PAPA120	Phosphatidate phosphatase (n-C12:0)
PAPA120pp	Phosphatidate phosphatase (periplasmic, n-C12
PAPA140	Phosphatidate phosphatase (n-C14:0)
PAPA140pp	Phosphatidate phosphatase (periplasmic, n-C14
PAPA141	Phosphatidate phosphatase (n-C14:1)
PAPA141pp	Phosphatidate phosphatase (periplasmic, n-C14
PAPA160	Phosphatidate phosphatase (n-C16:0)
PAPA160pp	Phosphatidate phosphatase (periplasmic, n-C1
PAPA161	Phosphatidate phosphatase (n-C16:1)
PAPA161pp	Phosphatidate phosphatase (periplasmic, n-C1
PAPA180	Phosphatidate phosphatase (n-C18:0)
PAPA180pp	Phosphatidate phosphatase (periplasmic, n-C1
PAPA181	Phosphatidate phosphatase (n-C18:1)
PAPA181pp	Phosphatidate phosphatase (periplasmic, n-C1
PAPPT3	phospho-N-acetylmuramoyl-pentapeptide-transf
PAPSR	phosphoadenylyl-sulfate reductase (thioredoxin
PAPSR2	phosphoadenylyl-sulfate reductase (glutaredoxi
PDH	pyruvate dehydrogenase
PDHcr	pyruvate dehydrogenase (dihydrolipoamide deh
PDX5POi	pyridoxine 5'-phosphate oxidase
PDX5PS	Pyridoxine 5'-phosphate synthase
PE120abcpp	phosphatidylethanolamine transport via ABC sy
PE140abcpp	phosphatidylethanolamine transport via ABC sy
PE141abcpp	phosphatidylethanolamine transport via ABC sy
PE160abcpp	phosphatidylethanolamine transport via ABC sy
PE161abcpp	phosphatidylethanolamine transport via ABC sy
PE180abcpp	phosphatidylethanolamine transport via ABC sy
PE181abcpp	phosphatidylethanolamine transport via ABC sy
PEAMNtex	phenethylamine transport via diffusion (extracell
PERD	Erythronate 4-phosphate (4per) dehydrogenase
PFK	phosphofructokinase
PFK_2	Phosphofructokinase
PFK_3	phosphofructokinase (s7p)
PFL	pyruvate formate lyase
PG120abcpp	phosphatidylglycerol transport via ABC system (
PG140abcpp	phosphatidylglycerol transport via ABC system (
PG141abcpp	phosphatidylglycerol transport via ABC system (
PG160abcpp	phosphatidylglycerol transport via ABC system (
PG161abcpp	phosphatidylglycerol transport via ABC system (
PG180abcpp	phosphatidylglycerol transport via ABC system (
PG181abcpp	phosphatidylglycerol transport via ABC system (
PGAMT	phosphoglucosamine mutase
PGCD	phosphoglycerate dehydrogenase
PGI	glucose-6-phosphate isomerase
PGK	phosphoglycerate kinase
PGL	6-phosphogluconolactonase

PGLYCP	Phosphoglycolate phosphatase
PGM	phosphoglycerate mutase
PGMT	phosphoglucomutase
PGP120abcpp	phosphatidylglycerophosphate transport via AB
PGP140abcpp	phosphatidylglycerophosphate transport via AB
PGP141abcpp	phosphatidylglycerophosphate transport via AB
PGP160abcpp	phosphatidylglycerophosphate transport via AB
PGP161abcpp	phosphatidylglycerophosphate transport via AB
PGP180abcpp	phosphatidylglycerophosphate transport via AB
PGP181abcpp	phosphatidylglycerophosphate transport via AB
PGPP120	phosphatidylglycerol phosphate phosphatase (n
PGPP120pp	phosphatidylglycerol phosphate phosphatase (p
PGPP140	phosphatidylglycerol phosphate phosphatase (n
PGPP140pp	phosphatidylglycerol phosphate phosphatase (p
PGPP141	phosphatidylglycerol phosphate phosphatase (n
PGPP141pp	phosphatidylglycerol phosphate phosphatase (p
PGPP160	phosphatidylglycerol phosphate phosphatase (n
PGPP160pp	phosphatidylglycerol phosphate phosphatase (p
PGPP161	phosphatidylglycerol phosphate phosphatase (n
PGPP161pp	phosphatidylglycerol phosphate phosphatase (p
PGPP180	phosphatidylglycerol phosphate phosphatase (n
PGPP180pp	phosphatidylglycerol phosphate phosphatase (p
PGPP181	phosphatidylglycerol phosphate phosphatase (n
PGPP181pp	phosphatidylglycerol phosphate phosphatase (p
PGSA120	Phosphatidylglycerol synthase (n-C12:0)
PGSA140	Phosphatidylglycerol synthase (n-C14:0)
PGSA141	Phosphatidylglycerol synthase (n-C14:1)
PGSA160	Phosphatidylglycerol synthase (n-C16:0)
PGSA161	Phosphatidylglycerol synthase (n-C16:1)
PGSA180	Phosphatidylglycerol synthase (n-C18:0)
PGSA181	Phosphatidylglycerol synthase (n-C18:1)
PHEMEabcpp	protoheme transport via ABC system (periplasm
PHEt2rpp	L-phenylalanine reversible transport via proton
PHETA1	phenylalanine transaminase
PHEtex	L-phenylalanine transport via diffusion (extracell
PHETRS	Phenylalanyl-tRNA synthetase
PIt2rpp	phosphate reversible transport via symport (peri
PItex	phosphate transport via diffusion (extracellular
PIuabcpp	phosphate transport via ABC system (uptake, pe
PLIPA1A120pp	Phospholipase A1 (phosphatidate, n-C12:0) (pe
PLIPA1A140pp	Phospholipase A1 (phosphatidate, n-C14:0) (pe
PLIPA1A141pp	Phospholipase A1 (phosphatidate, n-C14:1) (pe
PLIPA1A160pp	Phospholipase A1 (phosphatidate, n-C16:0) (pe
PLIPA1A161pp	Phospholipase A1 (phosphatidate, n-C16:1) (pe
PLIPA1A180pp	Phospholipase A1 (phosphatidate, n-C18:0) (pe
PLIPA1A181pp	Phospholipase A1 (phosphatidate, n-C18:1) (pe
PLIPA1E120pp	Phospholipase A1 (phosphatidylethanolamine,
PLIPA1E140pp	Phospholipase A1 (phosphatidylethanolamine,

PLIPA1E141pp	Phospholipase A1 (phosphatidylethanolamine, n
PLIPA1E160pp	Phospholipase A1 (phosphatidylethanolamine, n
PLIPA1E161pp	Phospholipase A1 (phosphatidylethanolamine, n
PLIPA1E180pp	Phospholipase A1 (phosphatidylethanolamine, n
PLIPA1E181pp	Phospholipase A1 (phosphatidylethanolamine, n
PLIPA1G120pp	Phospholipase A1 (phosphatidylglycerol, n-C12:
PLIPA1G140pp	Phospholipase A1 (phosphatidylglycerol, n-C14:
PLIPA1G141pp	Phospholipase A1 (phosphatidylglycerol, n-C14:
PLIPA1G160pp	Phospholipase A1 (phosphatidylglycerol, n-C16:
PLIPA1G161pp	Phospholipase A1 (phosphatidylglycerol, n-C16:
PLIPA1G180pp	Phospholipase A1 (phosphatidylglycerol, n-C18:
PLIPA1G181pp	Phospholipase A1 (phosphatidylglycerol, n-C18:
PLIPA2A120pp	Phospholipase A2 (phosphatidate, n-C12:0) (per
PLIPA2A140pp	Phospholipase A2 (phosphatidate, n-C14:0) (per
PLIPA2A141pp	Phospholipase A2 (phosphatidate, n-C14:1) (per
PLIPA2A160pp	Phospholipase A2 (phosphatidate, n-C16:0) (per
PLIPA2A161pp	Phospholipase A2 (phosphatidate, n-C16:1) (per
PLIPA2A180pp	Phospholipase A2 (phosphatidate, n-C18:0) (per
PLIPA2A181pp	Phospholipase A2 (phosphatidate, n-C18:1) (per
PLIPA2E120pp	Phospholipase A2 (phosphatidylethanolamine, n
PLIPA2E140pp	Phospholipase A2 (phosphatidylethanolamine, n
PLIPA2E141pp	Phospholipase A2 (phosphatidylethanolamine, n
PLIPA2E160pp	Phospholipase A2 (phosphatidylethanolamine, n
PLIPA2E161pp	Phospholipase A2 (phosphatidylethanolamine, n
PLIPA2E180pp	Phospholipase A2 (phosphatidylethanolamine, n
PLIPA2E181pp	Phospholipase A2 (phosphatidylethanolamine, n
PLIPA2G120pp	Phospholipase A2 (phosphatidylglycerol, n-C12:
PLIPA2G140pp	Phospholipase A2 (phosphatidylglycerol, n-C14:
PLIPA2G141pp	Phospholipase A2 (phosphatidylglycerol, n-C14:
PLIPA2G160pp	Phospholipase A2 (phosphatidylglycerol, n-C16:
PLIPA2G161pp	Phospholipase A2 (phosphatidylglycerol, n-C16:
PLIPA2G180pp	Phospholipase A2 (phosphatidylglycerol, n-C18:
PLIPA2G181pp	Phospholipase A2 (phosphatidylglycerol, n-C18:
PMANM	phosphomannomutase
PMDPHT	pyrimidine phosphatase
PMEACPE	Pimeloyl-[ACP] methyl ester esterase
PMPK	phosphomethylpyrimidine kinase
PNTK	pantothenate kinase
PNTOtex	Pantothenate transport via diffusion (extracellula
PPA	inorganic diphosphatase
PPA2	inorganic triphosphatase
PPALtex	propanal transport via diffusion (extracellular to
PPAt4pp	Na+/Propionate symporter (periplasm)
PPAtex	propionate transport via diffusion
PPBNGS	porphobilinogen synthase
PPC	phosphoenolpyruvate carboxylase
PPCDC	phosphopantothenoylcysteine decarboxylase
PPCK	phosphoenolpyruvate carboxykinase

PPGPPDP	guanosine-3',5'-bis(diphosphate) 3'-diphosphata
PPM	phosphopentomutase
PPM2	phosphopentomutase 2 (deoxyribose)
PPNCL2	phosphopantothenate-cysteine ligase
PPND	prephenate dehydrogenase
PPNDH	prephenate dehydratase
PPPGO	protoporphyrinogen oxidase (aerobic)
PPPGO3	protoporphyrinogen oxidase (anaerobic)
PPPNt2rpp	3-phenylpropionate transport via proton symport
PPPNtex	3-phenylpropionate transport via diffusion (extra
PPS	phosphoenolpyruvate synthase
PPTtex	Phosphonate transport via diffusion (extracellula
PRAGSr	phosphoribosylglycinamide synthase
PRAIi	phosphoribosylanthranilate isomerase (irreversi
PRAIS	phosphoribosylaminoimidazole synthase
PRAMPC	phosphoribosyl-AMP cyclohydrolase
PRASCSi	phosphoribosylaminoimidazolesuccinocarboxa
PRATPP	phosphoribosyl-ATP pyrophosphatase
PRFGS	phosphoribosylformylglycinamidine synthase
PRMICI	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino
PROabcpp	L-proline transport via ABC system (periplasm)
PROD2	Proline dehydrogenase
PROGLYabcpp	L-Prolinylglycine (Pro-Gly) transport via ABC sys
PROGLYtex	L-Prolinylglycine transport via diffusion (extracel
PROt4pp	Na+/Proline-L symporter (periplasm)
PROtex	L-proline transport via diffusion (extracellular to
PROTRS	Prolyl-tRNA synthetase
PRPPS	phosphoribosylpyrophosphate synthetase
PSCLYStex	psicoselysine transporter via diffusion (extracellu
PSCVT	3-phosphoshikimate 1-carboxyvinyltransferase
PSD120	Phosphatidylserine decarboxylase (n-C12:0)
PSD140	Phosphatidylserine decarboxylase (n-C14:0)
PSD141	Phosphatidylserine decarboxylase (n-C14:1)
PSD160	Phosphatidylserine decarboxylase (n-C16:0)
PSD161	Phosphatidylserine decarboxylase (n-C16:1)
PSD180	Phosphatidylserine decarboxylase (n-C18:0)
PSD181	Phosphatidylserine decarboxylase (n-C18:1)
PSERT	phosphoserine transaminase
PSERtex	phospho-L-serine transport via diffusion (extrace
PSP_L	phosphoserine phosphatase (L-serine)
PSSA120	Phosphatidylserine syntase (n-C12:0)
PSSA140	Phosphatidylserine syntase (n-C14:0)
PSSA141	Phosphatidylserine syntase (n-C14:1)
PSSA160	Phosphatidylserine syntase (n-C16:0)
PSSA161	Phosphatidylserine syntase (n-C16:1)
PSSA180	Phosphatidylserine syntase (n-C18:0)
PSSA181	Phosphatidylserine syntase (n-C18:1)
PTA2	Phosphate acetyltransferase

PTAr	phosphotransacetylase
PTPATi	pantetheine-phosphate adenylyltransferase
PTRCabcpp	putrescine transport via ABC system (periplasm
PTRCtex	putrescine transport via diffusion (extracellular t
PUNP1	purine-nucleoside phosphorylase (Adenosine)
PUNP2	purine-nucleoside phosphorylase (Deoxyadenos
PUNP3	purine-nucleoside phosphorylase (Guanosine)
PUNP4	purine-nucleoside phosphorylase (Deoxyguanos
PUNP5	purine-nucleoside phosphorylase (Inosine)
PUNP6	purine-nucleoside phosphorylase (Deoxyinosine
PYAM5PO	pyridoxamine 5'-phosphate oxidase
PYDAMtex	pyridoxamine transport via diffusion (extracellula
PYDXK	pyridoxal kinase
PYDXNtex	pyridoxine transport via diffusion (extracellular)
PYDXPP	Pyridoxal 5-phosphate phosphatase
PYDXtex	pyridoxal transport via diffusion (extracellular)
PYDXtpp	pyridoxal import
PYK	pyruvate kinase
PYNP2r	pyrimidine-nucleoside phosphorylase (uracil)
PYRt2rpp	pyruvate reversible transport via proton symport
PYRtex	pyruvate transport via diffusion (extracellular to
QUIN2tex	Quinate transport via diffusion (extracellular to p
QULNS	quinolinate synthase
R5Ptex	Ribose 5-phosphate transport via diffusion (extr
RBFK	riboflavin kinase
RBFSa	riboflavin synthase
RBFSb	riboflavin synthase
RBK	ribokinase
RHCCE	S-ribosylhomocysteine cleavage enzyme
RIBabcpp	D-ribose transport via ABC system (periplasm)
RIBtex	ribose transport via diffusion (extracellular to pe
RMNtex	L-rhamnose transport via diffusion (extracellular
RNDR1	ribonucleoside-diphosphate reductase (ADP)
RNDR2	ribonucleoside-diphosphate reductase (GDP)
RNDR3	ribonucleoside-diphosphate reductase (CDP)
RNDR4	ribonucleoside-diphosphate reductase (UDP)
RNTR1c2	ribonucleoside-triphosphate reductase (ATP) (fl
RNTR2c2	ribonucleoside-triphosphate reductase (GTP) (fl
RNTR3c2	ribonucleoside-triphosphate reductase (CTP) (fl
RNTR4c2	ribonucleoside-triphosphate reductase (UTP) (fl
RPE	ribulose 5-phosphate 3-epimerase
RPI	ribose-5-phosphate isomerase
S7PI	sedoheptulose 7-phosphate isomerase
SADH	Succinylarginine dihydrolase
SADT2	Sulfate adenyltransferase
SBTtex	D-sorbitol transport via diffusion (extracellular to
SDPDS	succinyl-diaminopimelate desuccinylase
SDPTA	succinyldiaminopimelate transaminase

SELCYSS	selenocysteine synthase
SELtex	selenate transport via diffusion (extracellular to p
SEPHCHCS	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexe
SERAT	serine O-acetyltransferase
SERD_L	L-serine deaminase
SERt2rpp	L-serine reversible transport via proton symport
SERt4pp	L-serine via sodium symport (periplasm)
SERtex	L-serine transport via diffusion (extracellular to p
SERTRS	Seryl-tRNA synthetase
SERTRS2	Seryl-tRNA synthetase (selenocystein)
SFGTHi	S-Formylglutathione hydralase
SGDS	Succinylglutamate desuccinylase
SGSAD	Succinylglutamic semialdehyde dehydrogenase
SHCHCS3	2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-carb
SHCHD2	sirohydrochlorin dehydrogenase (NAD)
SHCHF	sirohydrochlorin ferrochelatase
SHK3Dr	shikimate dehydrogenase
SHKK	shikimate kinase
SHSL1	O-succinylhomoserine lyase (L-cysteine)
SKMtex	shikimate transport via diffusion (extracellular to
SLNTtex	selenite transport via diffusion (extracellular to p
SO2tex	SO2 transport via diffusion (extracellular to perip
SO3tex	sulfite transport via diffusion (extracellular to per
SO4t2pp	sulfate transport in via proton symport (periplasr
SO4tex	sulfate transport via diffusion (extracellular to pe
SOTA	Succinylornithine transaminase
SPA	serine--pyruvate aminotransferase
SPMDabcpp	spermidine transport via ABC system (periplasm
SPMDAT1	Spermidine acetyltransferase
SPMDAT2	Spermidine acetyltransferase (N8)
SPMDtex	spermidine transport via diffusion (extracellular t
SUCBZL	o-succinylbenzoate-CoA ligase
SUCBZS	O-succinylbenzoate-CoA synthase
SUCCt2_3pp	Succintate transport via proton symport (3 H) (p
SUCCt3pp	succinate transport out via proton antiport (perip
SUCCtex	succinate transport via diffusion (extracellular to
SUCDi	succinate dehydrogenase (irreversible)
SUCOAS	succinyl-CoA synthetase (ADP-forming)
SUCptspp	sucrose transport via PEP:Pyr (periplasm)
SUCRtex	sucrose transport transport via diffusion (extrace
SULabcpp	sulfate transport via ABC system (periplasm)
SULFACtex	sulfoaceate transport via diffusion (extracellular
SULRi	sulfite reductase (NADPH2)
T2DECAI	trans-2-decenoyl-ACP isomerase
TAG6PK	D-Tagatose 6-phosphate kinase
TALA	transaldolase
TARTRDtex	D-tartrate transport via diffusion (extracellular to
TARTRtex	Tartrate transport via diffusion (extracellular to p

TARTt2_3pp	D-tartrate transport via proton symport (3 H) (pe
TAURtex	taurine transport via diffusion (extracellular to pe
TCYNTtex	Thiocyanate transport via diffusion (extracellular
TDPDRE	dTDP-4-dehydrorhamnose 3,5-epimerase
TDPGDH	dTDPglucose 4,6-dehydratase
TDSKVF	V. fischeri Tetraacyldisaccharide 4'kinase
TDSR1	thiol:disulfide reductase (DsbC)
TGBPA	Tagatose-bisphosphate aldolase
THD2pp	NAD(P) transhydrogenase (periplasm)
THDPS	tetrahydrodipicolinate succinylase
THFAT	Tetrahydrofolate aminomethyltransferase
THIORDXi	hydrogen peroxide reductase (thioredoxin)
THMabcpp	thiamine transport via ABC system (periplasm)
THMDt2pp	thymidine transport in via proton symport (peripl
THMDt2rpp	thymidine transport in via proton symport, revers
THMDtex	thymidine transport via diffusion (extracellular to
THMtex	Thiamine transport via diffusion (extracellular to
THRA2i	L-allo-Threonine Aldolase
THRabcpp	L-threonine transport via ABC system (periplasn
THRAi	Threonine aldolase
THRD	L-threonine dehydrogenase
THRD_L	L-threonine deaminase
THRPtex	phospho-L-threonine transport via diffusion (extr
THRS	threonine synthase
THRt4pp	L-threonine via sodium symport (periplasm)
THRtex	L-threonine transport via diffusion (extracellular
THRTRS	Threonyl-tRNA synthetase
THYMt3pp	thymine transport out via proton antiport (peripla
THYMtex	thymine transport via diffusion (extracellular to p
THZPSN3	thiazole phosphate synthesis
TKT1	transketolase
TKT2	transketolase
TMAOR1	Trimethylamine N-oxide reductase (menaquinol
TMAOR1pp	Trimethylamine N-oxide reductase (menaquinol
TMAOR2	Trimethylamine N-oxide reductase (demethylme
TMAOR2pp	Trimethylamine N-oxide reductase (demethylme
TMAOtex	Trimethylamine N-oxide transport via diffusion (
TMAtex	Trimethylamine transport via diffusion (extracellu
TMDK1	thymidine kinase (ATP:thymidine)
TMDPP	thymidine phosphorylase
TMDS	thymidylate synthase
TMK	thiamine kinase
TMPK	thiamine-phosphate kinase
TMPPP	thiamine-phosphate diphosphorylase
TPI	triose-phosphate isomerase
TRDR	thioredoxin reductase (NADPH)
TREtex	trehalose transport via diffusion (extracellular to
TRPS1	tryptophan synthase (indoleglycerol phosphate)

TRPS2	tryptophan synthase (indole)
TRPS3	tryptophan synthase (indoleglycerol phosphate)
TRPt2rpp	L-tryptophan reversible transport via proton sym
TRPtex	L-tryptophan transport via diffusion (extracellular
TRPTRS	Tryptophanyl-tRNA synthetase
TSULtex	thiosulfate transport via diffusion (extracellular to
TTDCAtexi	Tetradecanoate transport via facilitated irreversib
TTDCEAtexi	Tetradecenoate transport via facilitated irreversib
TTRCYCtex	Tetracycline transport via diffusion (extracellular
TUNGSabcpp	tungstate transport via ABC system (periplasm)
TUNGStex	tungstate transport via diffusion (extracellular to
TYMtex	tyramine transport via diffusion (extracellular to p
TYRL	tyrosine lyase
TYRPtex	phopho-L-tyrosine transport via diffusion (extrac
TYRt2rpp	L-tyrosine reversible transport via proton sympo
TYRTA	tyrosine transaminase
TYRtex	L-tyrosine transport via diffusion (extracellular to
TYRTRS	tyrosyl-tRNA synthetase
U23GAATVF	V. fischeri UDP-3-O-(3-hydroxydodecanoyl)gluc
UAAGDS	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-me
UACGALPpp	UDP-N-acetyl-D-galactosamine pyrophosphohy
UACGAMPpp	UDP-N-acetyl-D-glucosamine pyrophosphohydr
UACGAMtex	UDP-N-acetyl-D-glucosamine transport via diffus
UAG2E	UDP-N-acetylglucosamine 2-epimerase
UAGAAT	UDP-N-acetylglucosamine acyltransferase
UAGCVT	UDP-N-acetylglucosamine 1-carboxyvinyltransfe
UAGDP	UDP-N-acetylglucosamine diphosphorylase
UAGPT3	UDP-N-acetylglucosamine-N-acetylmuramyl-(pe
UAMAGS	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate sy
UAMAS	UDP-N-acetylmuramoyl-L-alanine synthetase
UAPGR	UDP-N-acetylenolpyruvoylglucosamine reductas
UDCPDP	undecaprenyl-diphosphatase
UDCPDPpp	undecaprenyl-diphosphatase (periplasm)
UDCPDPS	Undecaprenyl diphosphate synthase
UDPACGALtex	UDP-N-acetyl-D-galactosamine transport via diff
UDPG4E	UDPglucose 4-epimerase
UDPGALPpp	UDPgalactose pyrophosphohydrolase
UDPGALtex	UDPgalactose transport via diffusion (extracellul
UDPGLCURtex	UDP-D-glucuronate transport via diffusion (extra
UDPGPpp	UDPglucose pyrophosphohydrolase
UDPGtex	UDPglucose transport via diffusion (extracellular
UGLCURPpp	UDP-D-glucuronate pyrophosphohydrolase (per
UGLT	UDPglucose--hexose-1-phosphate uridylyltransf
UGMDDS	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-me
UHGADA	UDP-3-O-acetylglucosamine deacetylase
UM3PL	UDP-N-acetylmuramate:L-alanyl-gamma-D-glut
UM4PL	UDP-N-acetylmuramate:L-alanyl-gamma-D-glut
UMPK	UMP kinase

UMPtex	UMP transport via diffusion (extracellular to peri
UPP3MT	uroporphyrinogen methyltransferase
UPP3S	uroporphyrinogen-III synthase
UPPDC1	uroporphyrinogen decarboxylase (uroporphyrin
UPPRT	uracil phosphoribosyltransferase
URAt2pp	uracil transport in via proton symport (periplasm
URAt2rpp	uracil transport in via proton symport, reversible
URAtex	uracil transport via diffusion (extracellular to peri
URCN	urocanase
UREAtex	Urea transport via diffusion (extracellular to peri
UREAtpp	Urea transport via facilitate diffusion (periplasm)
URIK2	uridine kinase (GTP:Uridine)
URIt2pp	uridine transport in via proton symport (periplas
URIt2rpp	uridine transport in via proton symport, reversibl
URItex	uridine transport via diffusion (extracellular to pe
USHDVF	V. fischeri UDP-sugar hydrolase
VALabcpp	L-valine transport via ABC system (periplasm)
VALt2rpp	L-valine reversible transport via proton symport
VALTA	valine transaminase
VALtex	L-valine transport via diffusion (extracellular to p
VALTRS	Valyl-tRNA synthetase
VF_biomass	V. fischeri biomass objective function
VPAMTr	Valine-pyruvate aminotransferase
WCOS	tungsten pterin cofactor synthase
XANt2pp	xanthine transport in via proton symport (peripla
XANtex	xanthine transport via diffusion (extracellular to
XMPtex	XMP transport via diffusion (extracellular to peri
XPPT	xanthine phosphoribosyltransferase
XTSNt2rpp	Xanthosine transport via proton symport (peripla
XTSNtex	xanthosine transport via diffusion (extracellular t
XYLtex	D-xylose transport via diffusion (extracellular to
XYLUtex	L-xylulose transport via diffusion (extracellular t
ZN2abcpp	Zinc (Zn+2) ABC transporter, efflux (periplasm)
ZN2t3pp	zinc (Zn+2) transport out via proton antiport (per
Zn2tex	zinc (Zn+2) transport via diffusion (extracellular
ZN2tpp	zinc transport in via permease (no H+)
ZNabcpp	zinc (Zn+2) transport via ABC system (periplas

Formula	Subsystem	Gene-Protei
12ppd-S[e] <=> 12ppd-S[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + 14glucan[p] -> 14glucan[c] + a	Transport, Inner Membrane	(VF_A0797
14glucan[e] -> 14glucan[p]	Transport, Outer Membrane	
23camp[e] <=> 23camp[p]	Transport, Outer Membrane Porin	
23ccmp[e] <=> 23ccmp[p]	Transport, Outer Membrane Porin	
23cgmp[e] <=> 23cgmp[p]	Transport, Outer Membrane Porin	
23cump[e] <=> 23cump[p]	Transport, Outer Membrane Porin	
23dappa[e] <=> 23dappa[p]	Transport, Outer Membrane Porin	
23cump[p] + h2o[p] -> 3ump[p] + h[p]	Nucleotide Salvage Pathway	(VF_0319)
23ccmp[p] + h2o[p] -> 3cmp[p] + h[p]	Nucleotide Salvage Pathway	(VF_0319)
23camp[p] + h2o[p] -> 3amp[p] + h[p]	Nucleotide Salvage Pathway	(VF_0319)
23cgmp[p] + h2o[p] -> 3gmp[p] + h[p]	Nucleotide Salvage Pathway	(VF_0319)
26dap-M[e] <=> 26dap-M[p]	Transport, Outer Membrane Porin	
34dhpac[e] <=> 34dhpac[p]	Transport, Outer Membrane Porin	
3amp[e] <=> 3amp[p]	Transport, Outer Membrane Porin	
3cmp[e] <=> 3cmp[p]	Transport, Outer Membrane Porin	
3gmp[e] <=> 3gmp[p]	Transport, Outer Membrane Porin	
3hdecACP[c] -> h2o[c] + tdec2eACP[c]	Cell Envelope Biosynthesis	(VF_1292)
3hddecACP[c] -> h2o[c] + tddec2eACP[c]	Cell Envelope Biosynthesis	(VF_1951)
3hcddec5eACP[c] -> h2o[c] + t3c5ddeceACP[c	Cell Envelope Biosynthesis	(VF_1951)
3hmrsACP[c] -> h2o[c] + tmrs2eACP[c]	Cell Envelope Biosynthesis	(VF_1292)
3hcmrs7eACP[c] -> h2o[c] + t3c7mrseACP[c]	Cell Envelope Biosynthesis	(VF_1292)
3hpalmACP[c] -> h2o[c] + tpalm2eACP[c]	Cell Envelope Biosynthesis	(VF_1292)
3hcpalm9eACP[c] -> h2o[c] + t3c9palmeACP[c	Cell Envelope Biosynthesis	(VF_1951)
3hoctaACP[c] -> h2o[c] + toctd2eACP[c]	Cell Envelope Biosynthesis	(VF_1292)
3hcvac11eACP[c] -> h2o[c] + t3c11vaceACP[c]	Cell Envelope Biosynthesis	(VF_1292)
3haACP[c] -> but2eACP[c] + h2o[c]	Cell Envelope Biosynthesis	(VF_1292)
3hhexACP[c] -> h2o[c] + thex2eACP[c]	Cell Envelope Biosynthesis	(VF_1292)
3hoctACP[c] -> h2o[c] + toct2eACP[c]	Cell Envelope Biosynthesis	(VF_1292)
3hpp[e] <=> 3hpp[p]	Transport, Outer Membrane Porin	
3ump[p] + h2o[p] -> pi[p] + uri[p]	Nucleotide Salvage Pathway	(VF_0319)
3cmp[p] + h2o[p] -> cytd[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0319)
3amp[p] + h2o[p] -> adn[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0319)
3gmp[p] + h2o[p] -> gsn[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0319)
3odecACP[c] + h[c] + nadph[c] <=> 3hdecACP[	Cell Envelope Biosynthesis	(VF_1740)
3oddecACP[c] + h[c] + nadph[c] <=> 3hddecAC	Cell Envelope Biosynthesis	(VF_1740)
3ocddec5eACP[c] + h[c] + nadph[c] -> 3hcddec	Cell Envelope Biosynthesis	(VF_1740)
3omrsACP[c] + h[c] + nadph[c] <=> 3hmrsACP[	Cell Envelope Biosynthesis	(VF_1740)
3ocmrs7eACP[c] + h[c] + nadph[c] -> 3hcmrs7	Cell Envelope Biosynthesis	(VF_1740)
3opalmACP[c] + h[c] + nadph[c] <=> 3hpalmAC	Cell Envelope Biosynthesis	(VF_1740)
3ocpalm9eACP[c] + h[c] + nadph[c] -> 3hcpalm	Cell Envelope Biosynthesis	(VF_1740)
3ooctdACP[c] + h[c] + nadph[c] <=> 3hoctaAC	Cell Envelope Biosynthesis	(VF_1740)
3ocvac11eACP[c] + h[c] + nadph[c] -> 3hcvac1	Cell Envelope Biosynthesis	(VF_1740)
actACP[c] + h[c] + nadph[c] <=> 3haACP[c] + n	Cell Envelope Biosynthesis	(VF_1740)
3ohexACP[c] + h[c] + nadph[c] <=> 3hhexACP[	Cell Envelope Biosynthesis	(VF_1740)
3ooctACP[c] + h[c] + nadph[c] <=> 3hoctACP[c	Cell Envelope Biosynthesis	(VF_1740)
h[c] + malACP[c] + ocACP[c] -> 3odecACP[c] +	Cell Envelope Biosynthesis	(VF_1700)

dcaACP[c] + h[c] + malACP[c] -> 3oddecACP[c	Cell Envelope Biosynthesis	(VF_1738)
cdec3eACP[c] + h[c] + malACP[c] -> 3ocddec5	Cell Envelope Biosynthesis	(VF_1700)
ddcaACP[c] + h[c] + malACP[c] -> 3omrsACP[c	Cell Envelope Biosynthesis	(VF_1700)
cddec5eACP[c] + h[c] + malACP[c] -> 3ocmrs7	Cell Envelope Biosynthesis	(VF_1700)
h[c] + malACP[c] + myrsACP[c] -> 3opalmACP[	Cell Envelope Biosynthesis	(VF_1700)
h[c] + malACP[c] + tdeACP[c] -> 3ocpalm9eAC	Cell Envelope Biosynthesis	(VF_1700)
h[c] + malACP[c] + palmACP[c] -> 3ooctdACP[	Cell Envelope Biosynthesis	(VF_1738)
h[c] + hdeACP[c] + malACP[c] -> 3ocvac11eAC	Cell Envelope Biosynthesis	(VF_1738)
butACP[c] + h[c] + malACP[c] -> 3ohexACP[c]	Cell Envelope Biosynthesis	(VF_1738)
h[c] + hexACP[c] + malACP[c] -> 3ooctACP[c]	Cell Envelope Biosynthesis	(VF_1700)
LalaDgluMdap[e] <=> LalaDgluMdap[p]	Transport, Outer Membrane Porin	
3ump[e] <=> 3ump[p]	Transport, Outer Membrane Porin	
4hoxpacd[e] <=> 4hoxpacd[p]	Transport, Outer Membrane Porin	
h2o[c] + phthr[c] -> 4hthr[c] + pi[c]	Cofactor and Prosthetic Group	(VF_2116)
atp[c] + h2o[c] + LalaDgluMdapDala[p] -> LalaD	Murein Recycling	(VF_1593 ar
LalaDgluMdapDala[e] <=> LalaDgluMdapDala[	Transport, Outer Membrane Porin	
5cmhm[c] <=> 5cohe[c]	Tyrosine, Tryptophan, and Phe	(VF_0207)
5dglcn[e] <=> 5dglcn[p]	Transport, Outer Membrane Porin	
dad-5[c] + h2o[c] -> 5drib[c] + ade[c]	Cofactor and Prosthetic Group	(VF_2128)
5mtr[e] <=> 5mtr[p]	Transport, Outer Membrane Porin	
ru5p-D[c] <=> ara5p[c]	Alternate Carbon Metabolism	(VF_0392)
14glucan[p] -> malthx[p]	Alternate Carbon Metabolism	(VF_0017)
arbt6p[c] + h2o[c] -> g6p[c] + hqn[c]	Alternate Carbon Metabolism	(VF_0605)
4abut[c] + akg[c] -> glu-L[c] + sucsal[c]	Arginine and Proline Metabolis	(VF_A1123
4abut[e] <=> 4abut[p]	Transport, Outer Membrane Porin	
2 accoa[c] <=> aacoa[c] + coa[c]	Membrane Lipid Metabolism	(VF_1811)
accoa[c] + btcoa[c] <=> 3ohcoa[c] + coa[c]	Membrane Lipid Metabolism	(VF_1811)
accoa[c] + hxcoa[c] <=> 3oocoa[c] + coa[c]	Membrane Lipid Metabolism	(VF_1811)
accoa[c] + occoa[c] <=> 3odcoa[c] + coa[c]	Membrane Lipid Metabolism	(VF_1811)
accoa[c] + dcacoa[c] <=> 3oddcoa[c] + coa[c]	Membrane Lipid Metabolism	(VF_1811)
accoa[c] + ddcacoa[c] <=> 3otdcoa[c] + coa[c]	Membrane Lipid Metabolism	(VF_1811)
accoa[c] + tdcoa[c] <=> 3ohdcoa[c] + coa[c]	Membrane Lipid Metabolism	(VF_1811)
3oodcoa[c] + coa[c] <=> accoa[c] + pmtcoa[c]	Membrane Lipid Metabolism	(VF_1811)
acac[e] <=> acac[p]	Transport, Outer Membrane Porin	
acald[c] + coa[c] + nad[c] <=> accoa[c] + h[c] +	Pyruvate Metabolism	(VF_0918)
acald[e] <=> acald[p]	Transport, Outer Membrane Porin	
accoa[c] + atp[c] + hco3[c] -> adp[c] + h[c] + ma	Membrane Lipid Metabolism	(VF_1695 ar
atp[c] + coa[c] + ppa[c] -> adp[c] + pi[c] + ppco	Alternate Carbon Metabolism	(VF_2383)
acgal1p[e] <=> acgal1p[p]	Transport, Outer Membrane Porin	
acgal6p[c] + h2o[c] -> ac[c] + galam6p[c]	Alternate Carbon Metabolism	(VF_A0999
pep[c] + acgal[p] -> pyr[c] + acgal6p[c]	Transport, Inner Membrane	(VF_A1000
acgal[e] <=> acgal[p]	Transport, Outer Membrane Porin	
acgam1p[e] <=> acgam1p[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + acgam2[p] -> acgam2[c] + adp	Transport, Inner Membrane	(VF_2139 ar
acgam2[c] + pi [c] -> acgam1p[c] + acgam[c]	Alternate Carbon Metabolism	(VF_2147)
acgam2[e] -> acgam2[p]	Transport, Outer Membrane	
acgam[c] + atp[c] -> acgam6p[c] + adp[c] + h[c]	Murein Recycling	(VF_2145)
acgam1p [c] <=> acgam6p[c]	Alternate Carbon Metabolism	(VF_2148)

uacgam[c] + udcpp[c] -> ump[c] + unaga[c]	Cell Envelope Biosynthesis	(VF_0180)
pep[c] + acgam[p] -> acgam6p[c] + pyr[c]	Transport, Inner Membrane	(VF_0808 a
acgam[e] <=> acgam[p]	Transport, Outer Membrane Porin	
acglu[c] + atp[c] -> acg5p[c] + adp[c]	Arginine and Proline Metabolis	(VF_2305)
accoa[c] + glu-L[c] -> acglu[c] + coa[c] + h[c]	Arginine and Proline Metabolis	(VF_0585)
2obut[c] + h[c] + pyr[c] -> 2ahbut[c] + co2[c]	Valine, Leucine, and Isoleucin	(VF_0185)
ac[c] + atp[c] <=> actp[c] + adp[c]	Pyruvate Metabolism	(VF_0837)
h[c] + 2 pyr[c] -> alac-S[c] + co2[c]	Valine, Leucine, and Isoleucin	(VF_0185)
acmum6p[c] + h2o[c] -> acgam6p[c] + lac-D[c]	Alternate Carbon Metabolism	(VF_1114)
pep[c] + acmana[p] -> acmanap[c] + pyr[c]	Transport, Inner Membrane	(VF_1894 a
acmana[e] <=> acmana[p]	Transport, Outer Membrane Porin	
pep[c] + acmum[p] -> acmum6p[c] + pyr[c]	Transport, Inner Membrane	(VF_1115 ar
acmum[e] -> acmum[p]	Transport, Outer Membrane Porin	
acnam[p] + na1[p] -> acnam[c] + na1[c]	Transport, Inner Membrane	(VF_0668)
acnam[e] <=> acnam[p]	Transport, Outer Membrane	(VF_A1008
acnam[c] -> acmana[c] + pyr[c]	Alternate Carbon Metabolism	(VF_0663)
btcoa[c] + fad[c] <=> b2coa[c] + fadh2[c]	Membrane Lipid Metabolism	(VF_1932)
fad[c] + hxcoa[c] <=> fadh2[c] + hx2coa[c]	Membrane Lipid Metabolism	(VF_1932)
fad[c] + occoa[c] <=> fadh2[c] + oc2coa[c]	Membrane Lipid Metabolism	(VF_1932)
dcacoa[c] + fad[c] <=> dc2coa[c] + fadh2[c]	Membrane Lipid Metabolism	(VF_1932)
ddcacoa[c] + fad[c] <=> dd2coa[c] + fadh2[c]	Membrane Lipid Metabolism	(VF_1932)
fad[c] + tdcoa[c] <=> fadh2[c] + td2coa[c]	Membrane Lipid Metabolism	(VF_1932)
fad[c] + pmtcoa[c] <=> fadh2[c] + hdd2coa[c]	Membrane Lipid Metabolism	(VF_1932)
fad[c] + stcoa[c] <=> fadh2[c] + od2coa[c]	Membrane Lipid Metabolism	(VF_1932)
ACP[c] + accoa[c] <=> acACP[c] + coa[c]	Membrane Lipid Metabolism	(VF_1739 a
acorn[c] + h2o[c] -> ac[c] + orn[c]	Arginine and Proline Metabolis	(VF_2307)
cit[c] <=> acon-C[c] + h2o[c]	Citric Acid Cycle	(VF_2158)
acon-C[c] + h2o[c] <=> icit[c]	Citric Acid Cycle	(VF_2158)
acorn[c] + akg[c] <=> acg5sa[c] + glu-L[c]	Arginine and Proline Metabolis	(VF_2284)
ddcaACP[c] + h[c] + pi[c] -> ACP[c] + ddcap[c]	Glycerophospholipid Metabolis	(VF_1739 a
h[c] + myrsACP[c] + pi[c] -> ACP[c] + ttdcap[c]	Glycerophospholipid Metabolis	(VF_1739 a
h[c] + pi[c] + tdeACP[c] -> ACP[c] + ttdceap[c]	Glycerophospholipid Metabolis	(VF_1739 a
h[c] + palmACP[c] + pi[c] -> ACP[c] + hdcap[c]	Glycerophospholipid Metabolis	(VF_1739 a
h[c] + hdeACP[c] + pi[c] -> ACP[c] + hdceap[c]	Glycerophospholipid Metabolis	(VF_1739 a
h[c] + ocdcaACP[c] + pi[c] -> ACP[c] + ocdcap[	Glycerophospholipid Metabolis	(VF_1739 a
h[c] + octeACP[c] + pi[c] -> ACP[c] + ocdceap[c	Glycerophospholipid Metabolis	(VF_1739 a
apoACP[c] + coa[c] -> ACP[c] + h[c] + pap[c]	Cofactor and Prosthetic Group	(VF_2083)
ac[c] + atp[c] + coa[c] -> accoa[c] + amp[c] + p	Pyruvate Metabolism	(VF_2383)
acser[e] <=> acser[p]	Transport, Outer Membrane Porin	
ac[p] + h[p] <=> ac[c] + h[c]	Transport, Inner Membrane	
ac[e] <=> ac[p]	Transport, Outer Membrane Porin	
adn[c] + h[c] + h2o[c] -> ins[c] + nh4[c]	Nucleotide Salvage Pathway	(VF_0093)
4adcho[c] -> 4abz[c] + h[c] + pyr[c]	Cofactor and Prosthetic Group	(VF_1737)
chor[c] + gln-L[c] -> 4adcho[c] + glu-L[c]	Cofactor and Prosthetic Group	(VF_1179 a
ade[p] + h[p] <=> ade[c] + h[c]	Transport, Inner Membrane	(VF_0116)
ade[e] <=> ade[p]	Transport, Outer Membrane Porin	
amp[c] + atp[c] <=> 2 adp[c]	Nucleotide Salvage Pathway	(VF_0793)
amp[c] + gtp[c] <=> adp[c] + gdp[c]	Nucleotide Salvage Pathway	(VF_0793)

amp[c] + itp[c] <=> adp[c] + idp[c]	Nucleotide Salvage Pathway	(VF_0793)
atp[c] -> camp[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_0067)
adn[c] + atp[c] -> adp[c] + amp[c] + h[c]	Nucleotide Salvage Pathway	(VF_0793)
adn[p] + h[p] -> adn[c] + h[c]	Transport, Inner Membrane	(VF_2065)
adn[p] + h[p] <=> adn[c] + h[c]	Transport, Inner Membrane	
adn[e] <=> adn[p]	Transport, Outer Membrane	
adocbl[e] + h[p] -> h[c] + adocbl[p]	Transport, Outer Membrane	(VF_1223 a
adprib[c] + h2o[c] -> amp[c] + 2 h[c] + r5p[c]	Nucleotide Salvage Pathway	(VF_2463)
ade[c] + prpp[c] -> amp[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_1688)
aps[c] + atp[c] -> adp[c] + h[c] + paps[c]	Cysteine Metabolism	(VF_0323)
dcamp[c] <=> amp[c] + fum[c]	Purine and Pyrimidine Biosynt	(VF_1786)
25aics[c] <=> aicar[c] + fum[c]	Purine and Pyrimidine Biosynt	(VF_1786)
asp-L[c] + gtp[c] + imp[c] -> dcamp[c] + gdp[c]	Purine and Pyrimidine Biosynt	(VF_2318)
acgam6p[c] + h2o[c] -> ac[c] + gam6p[c]	Alternate Carbon Metabolism	(VF_0807)
anhgm3p[c] + h2o[c] -> LalaDgluMdap[c] + anh	Murein Recycling	(VF_2183)
anhgm3p[p] + h2o[p] -> LalaDgluMdap[p] + an	Murein Recycling	(VF_2326)
anhgm3p[c] + h2o[c] -> acgam[c] + anhm3p[c]	Murein Recycling	(VF_A0493
anhgm3p[p] + h[p] -> anhgm3p[c] + h[c]	Murein Recycling	(VF_0720)
anhgm4p[c] + h2o[c] -> LalaDgluMdapDala[c] +	Murein Recycling	(VF_2183)
anhgm4p[p] + h2o[p] -> LalaDgluMdapDala[p]	Murein Recycling	(VF_2326)
anhgm4p[c] + h2o[c] -> acgam[c] + anhm4p[c]	Murein Recycling	(VF_A0493
anhgm4p[p] + h[p] -> anhgm4p[c] + h[c]	Murein Recycling	(VF_0720)
anhgm[c] + h2o[c] -> acgam[c] + anhm[c]	Murein Recycling	(VF_A0493
adphep-DD[c] -> adphep-LD[c]	Lipopolysaccharide Biosynthes	(VF_0152)
agm[c] + h2o[c] -> ptrc[c] + urea[c]	Arginine and Proline Metabolis	(VF_A0839
anhgm[p] + h[p] -> anhgm[c] + h[c]	Murein Recycling	(VF_0720)
agm[e] <=> agm[p]	Transport, Outer Membrane Porin	
1ddecg3p[c] + ddcaACP[c] -> ACP[c] + pa120[	Glycerophospholipid Metabolis	(VF_0402)
1tdecg3p[c] + myrsACP[c] -> ACP[c] + pa140[c	Glycerophospholipid Metabolis	(VF_0402)
1tdec7eg3p[c] + tdeACP[c] -> ACP[c] + pa141[	Glycerophospholipid Metabolis	(VF_0402)
1hdecg3p[c] + palmACP[c] -> ACP[c] + pa160[	Glycerophospholipid Metabolis	(VF_0402)
1hdec9eg3p[c] + hdeACP[c] -> ACP[c] + pa161	Glycerophospholipid Metabolis	(VF_0402)
1odecg3p[c] + ocdcaACP[c] -> ACP[c] + pa180	Glycerophospholipid Metabolis	(VF_0402)
1odec11eg3p[c] + octeACP[c] -> ACP[c] + pa1	Glycerophospholipid Metabolis	(VF_0402)
acg5sa[c] + nadp[c] + pi[c] <=> acg5p[c] + h[c]	Arginine and Proline Metabolis	(VF_2306)
ahcys[c] + h2o[c] -> ade[c] + rhcys[c]	Methionine Metabolism	(VF_2128)
10fthf[c] + aicar[c] <=> fprica[c] + thf[c]	Purine and Pyrimidine Biosynt	(VF_2394)
air[c] + atp[c] + hco3[c] -> 5caiz[c] + adp[c] + h	Purine and Pyrimidine Biosynt	(VF_2538)
5aizc[c] <=> 5caiz[c]	Purine and Pyrimidine Biosynt	(VF_2537)
akg[c] + coa[c] + nad[c] -> co2[c] + nadh[c] + s	Citric Acid Cycle	(VF_0823 a
akg[e] <=> akg[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + ala-L[p] -> adp[c] + ala-L[c] +	Transport, Inner Membrane	(VF_1084)
atp[c] + h2o[c] + alaala[p] -> adp[c] + alaala[c]	Transport, Inner Membrane	(VF_2516 a
2 ala-D[c] + atp[c] <=> adp[c] + alaala[c] + h[c]	Cell Envelope Biosynthesis	(VF_A0570
alaala[e] <=> alaala[p]	Transport, Outer Membrane Porin	
ala-L[c] + h2o[c] + nad[c] -> h[c] + nadh[c] + nh	Alanine and Aspartate Metabol	(VF_0903)
ala-L[c] <=> ala-D[c]	Alanine and Aspartate Metabol	(VF_0302)
ala-L[p] + na1[p] -> ala-L[c] + na1[c]	Transport, Inner Membrane	(VF_2110)

ala-D[c] + pydx5p[c] -> pyam5p[c] + pyr[c]	Cofactor and Prosthetic Group	(VF_0695)
ala-L[c] + pydx5p[c] -> pyam5p[c] + pyr[c]	Cofactor and Prosthetic Group	(VF_A0497
ala-L[e] <=> ala-L[p]	Transport, Outer Membrane Porin	
ala-L[c] + atp[c] + trnaala[c] -> alatrna[c] + amp	tRNA Charging	(VF_0536)
glyald[c] + h[c] + nadh[c] <=> glyc[c] + nad[c]	Alternate Carbon Metabolism	(VF_0023)
etoh[c] + nad[c] <=> acald[c] + h[c] + nadh[c]	Pyruvate Metabolism	(VF_1188)
all-D[e] <=> all-D[p]	Transport, Outer Membrane Porin	
alltn[e] <=> alltn[p]	Transport, Outer Membrane Porin	
anhm3p[c] + h2o[c] -> LalaDgluMdap[c] + anhm	Murein Recycling	(VF_2183)
anhm4p[c] + h2o[c] -> LalaDgluMdapDala[c] +	Murein Recycling	(VF_2183)
malt[c] + malttr[c] -> glc-D[c] + maltttr[c]	Alternate Carbon Metabolism	(VF_A0809
malt[c] + maltttr[c] -> glc-D[c] + maltpt[c]	Alternate Carbon Metabolism	(VF_A0809
malt[c] + maltpt[c] -> glc-D[c] + malthx[c]	Alternate Carbon Metabolism	(VF_A0809
malt[c] + malthx[c] -> glc-D[c] + malthp[c]	Alternate Carbon Metabolism	(VF_A0809
acmanap[c] <=> acgam6p[c]	Alternate Carbon Metabolism	(VF_0666)
acmana[c] + atp[c] -> acmanap[c] + adp[c] + h[	Alternate Carbon Metabolism	(VF_0667)
8aonn[c] + amet[c] <=> amob[c] + dann[c]	Cofactor and Prosthetic Group	(VF_A0748
2dmmql8[c] + amet[c] -> ahcys[c] + h[c] + mql8	Cofactor and Prosthetic Group	(VF_0046)
air[c] + h2o[c] + nad[c] -> 4ampm[c] + 2 format	Cofactor and Prosthetic Group	(VF_0032)
cgly[c] + h2o[c] -> cys-L[c] + gly[c]	Cysteine Metabolism	(VF_0736)
h2o[c] + progly[c] -> gly[c] + pro-L[c]	Arginine and Proline Metabolis	(VF_0413)
amp[e] <=> amp[p]	Transport, Outer Membrane Porin	
anhgm[e] <=> anhgm[p]	Transport, Outer Membrane Porin	
anhm[c] + atp[c] + h2o[c] -> acmum6p[c] + adp	Murein Recycling	(VF_A0492
anth[c] + prpp[c] -> ppi[c] + pran[c]	Tyrosine, Tryptophan, and Phe	(VF_1031)
chor[c] + gln-L[c] -> anth[c] + glu-L[c] + h[c] + p	Tyrosine, Tryptophan, and Phe	(VF_1032 a
ala-L[c] + pimACP[c] -> 8aonn[c] + ACP[c] + co	Cofactor and Prosthetic Group	(VF_A0747
ap4a[c] + h2o[c] -> 2 adp[c] + 2 h[c]	Nucleotide Salvage Pathway	(VF_0285)
2 atp[c] + h[c] -> ap4a[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_0453)
ap5a[c] + h2o[c] -> adp[c] + atp[c] + 2 h[c]	Nucleotide Salvage Pathway	(VF_0285)
ddcap[c] + glyc3p[c] -> 1ddecg3p[c] + h[c] + pi[	Glycerophospholipid Metabolis	(VF_2248)
glyc3p[c] + ttdcap[c] -> 1tdecg3p[c] + h[c] + pi[c	Glycerophospholipid Metabolis	(VF_2248)
glyc3p[c] + ttdceap[c] -> 1tdec7eg3p[c] + h[c] +	Glycerophospholipid Metabolis	(VF_2248)
glyc3p[c] + hdcap[c] -> 1hdecg3p[c] + h[c] + pi[	Glycerophospholipid Metabolis	(VF_2248)
glyc3p[c] + hdceap[c] -> 1hdec9eg3p[c] + h[c] +	Glycerophospholipid Metabolis	(VF_2248)
glyc3p[c] + ocdcap[c] -> 1odecg3p[c] + h[c] + pi	Glycerophospholipid Metabolis	(VF_2248)
glyc3p[c] + ocdceap[c] -> 1odec11eg3p[c] + h[c	Glycerophospholipid Metabolis	(VF_2248)
ddcap[c] + h2o[c] -> ddca[c] + 2 h[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1502)
h2o[c] + ttdcap[c] -> 2 h[c] + pi[c] + ttdca[c]	Glycerophospholipid Metabolis	(VF_1502)
h2o[c] + ttdceap[c] -> 2 h[c] + pi[c] + ttdcea[c]	Glycerophospholipid Metabolis	(VF_1502)
h2o[c] + hdcap[c] -> 2 h[c] + hdca[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1502)
h2o[c] + hdceap[c] -> 2 h[c] + hdcea[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1502)
h2o[c] + ocdcap[c] -> 2 h[c] + ocdca[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1502)
h2o[c] + ocdceap[c] -> 2 h[c] + ocdcea[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1502)
5apru[c] + h[c] + nadph[c] -> 5aprbu[c] + nadp[	Cofactor and Prosthetic Group	(VF_0700)
arab-L[e] <=> arab-L[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + arbtn-fe3[p] -> adp[c] + arbtn-f	Transport, Inner Membrane	(VF_A0158
arbt[e] -> arbt[p]	Transport, Outer Membrane Porin	

atp[c] + h2o[c] + arg-L[p] -> adp[c] + arg-L[c] +	Transport, Inner Membrane	(VF_1585 a
arg-L[c] + h2o[c] -> citr-L[c] + nh4[c]	Arginine and Proline Metabolis	(VF_0408)
arg-L[p] + h[p] -> agm[p] + co2[p]	Arginine and Proline Metabolis	(VF_A0840
argsuc[c] <=> arg-L[c] + fum[c]	Arginine and Proline Metabolis	(VF_2303)
asp-L[c] + atp[c] + citr-L[c] -> amp[c] + argsuc[c	Arginine and Proline Metabolis	(VF_2304)
arg-L[e] <=> arg-L[p]	Transport, Outer Membrane Porin	
arg-L[c] + atp[c] + trnaarg[c] -> amp[c] + argtrn	tRNA Charging	(VF_0839)
aspsa[c] + nadp[c] + pi[c] <=> 4pasp[c] + h[c] +	Threonine and Lysine Metaboli	(VF_1645)
pep[c] + ascb-L[p] -> ascb6p[c] + pyr[c]	Transport, Inner Membrane	(VF_1894 a
ascb-L[e] <=> ascb-L[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + asn-L[p] -> adp[c] + asn-L[c] +	Transport, Inner Membrane	
asn-L[c] + h2o[c] -> asp-L[c] + nh4[c]	Alanine and Aspartate Metabol	(VF_1644)
asn-L[p] + h2o[p] -> asp-L[p] + nh4[p]	Alanine and Aspartate Metabol	(VF_1527)
asp-L[c] + atp[c] + gln-L[c] + h2o[c] -> amp[c] +	Alanine and Aspartate Metabol	(VF_0804)
asn-L[e] <=> asn-L[p]	Transport, Outer Membrane Porin	
asn-L[c] + atp[c] + trnaasn[c] -> amp[c] + asntr	tRNA Charging	(VF_1159)
aso3[e] <=> aso3[p]	Transport, Outer Membrane Porin	
asp-L[c] + h[c] -> ala-B[c] + co2[c]	Cofactor and Prosthetic Group	(VF_0892)
asp-L[c] + cbp[c] -> cbasp[c] + h[c] + pi[c]	Purine and Pyrimidine Biosynt	(VF_0405 a
asp-L[c] + atp[c] <=> 4pasp[c] + adp[c]	Threonine and Lysine Metaboli	(VF_2118)
asp-L[c] + q8[c] -> h[c] + iasp[c] + q8h2[c]	Cofactor and Prosthetic Group	(VF_2094)
asp-L[c] + mqn8[c] -> h[c] + iasp[c] + mql8[c]	Cofactor and Prosthetic Group	(VF_2094)
asp-L[c] + fum[c] -> h[c] + iasp[c] + succ[c]	Cofactor and Prosthetic Group	(VF_2094)
asp-L[c] + o2[c] -> h[c] + h2o2[c] + iasp[c]	Cofactor and Prosthetic Group	(VF_2094)
asp-L[c] -> fum[c] + nh4[c]	Alanine and Aspartate Metabol	(VF_2353)
asp-L[p] + 3 h[p] -> asp-L[c] + 3 h[c]	Transport, Inner Membrane	(VF_2354)
asp-L[p] + h[p] -> asp-L[c] + h[c]	Transport, Inner Membrane	(VF_1026)
akg[c] + asp-L[c] <=> glu-L[c] + oaa[c]	Alanine and Aspartate Metabol	(VF_1673)
asp-L[e] <=> asp-L[p]	Transport, Outer Membrane Porin	
asp-L[c] + atp[c] + trnaasp[c] -> amp[c] + asptr	tRNA Charging	(VF_0949)
arg-L[c] + succoa[c] -> coa[c] + h[c] + sucarg[c]	Arginine and Proline Metabolis	(VF_2283)
atp[c] + h2o[c] -> adp[c] + h[c] + pi[c]	Unassigned	
atp[c] + prpp[c] -> ppi[c] + prbatp[c]	Histidine Metabolism	(VF_1012)
adp[c] + pi[c] + 4 h[p] <=> atp[c] + 3 h[c] + h2o[	Oxidative Phosphorylation	(VF_2563 a
ala-B[e] <=> ala-B[p]	Transport, Outer Membrane Porin	
moco[c] + mptamp[c] -> amp[c] + bmoco[c] + c	Cofactor and Prosthetic Group	(VF_1608)
bmoco[c] + gtp[c] + h[c] -> bmoco1gdp[c] + ppi[	Cofactor and Prosthetic Group	(VF_1405)
bmoco1gdp[c] + gtp[c] + h[c] -> bmocogdp[c] +	Cofactor and Prosthetic Group	(VF_1405)
h2o[c] + pap[c] -> amp[c] + pi[c]	Cysteine Metabolism	(VF_2462)
btn[p] + h[p] -> btn[c] + h[c]	Transport, Inner Membrane	
btn[e] <=> btn[p]	Transport, Outer Membrane Porin	
2fe2s[c] + amet[c] + dtbt[c] -> 2fe1s[c] + btn[c]	Cofactor and Prosthetic Group	(VF_A1189
accoa[c] + but[c] -> ac[c] + btcoa[c]	Alternate Carbon Metabolism	
butso3[e] <=> butso3[p]	Transport, Outer Membrane Porin	
but[p] + h[p] <=> but[c] + h[c]	Transport, Inner Membrane	
but[e] <=> but[p]	Transport, Outer Membrane Porin	
bwco[c] + gtp[c] + h[c] -> bwco1gdp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_1405)
bwco1gdp[c] + gtp[c] + h[c] -> bwcogdp[c] + ppi	Cofactor and Prosthetic Group	(VF_1405)

mptamp[c] + wco[c] -> amp[c] + bwco[c] + cu2[	Cofactor and Prosthetic Group	(VF_1608)
ca2[e] <=> ca2[p]	Transport, Outer Membrane Porin	
15dap[c] + h[p] + lys-L[p] -> h[c] + lys-L[c] + 15	Transport, Inner Membrane	(VF_2058)
ca2[c] + na1[p] <=> na1[c] + ca2[p]	Inorganic Ion Transport and M	(VF_0393)
atp[c] + cbi[c] + h[c] <=> adocbi[c] + pppi[c]	Cofactor and Prosthetic Group	(VF_1750)
cbi[e] + h[p] -> h[c] + cbi[p]	Transport, Outer Membrane	(VF_1223 a
cbl1[e] + h[p] -> h[c] + cbl1[p]	Transport, Outer Membrane	(VF_1223 a
atp[c] + cbl1[c] + h[c] <=> adocbl[c] + pppi[c]	Cofactor and Prosthetic Group	(VF_1750)
atp[c] + co2[c] + nh4[c] <=> adp[c] + cbp[c] + 2	Unassigned	(VF_A1146
2 atp[c] + gln-L[c] + h2o[c] + hco3[c] -> 2 adp[c]	Arginine and Proline Metabolis	(VF_0472 a
atp[c] + cdg[c] + nh4[c] -> adp[c] + h[c] + h2o[c]	Cofactor and Prosthetic Group	(VF_1580)
atp[c] + cd2[c] + h2o[c] -> adp[c] + h[c] + pi[c] +	Inorganic Ion Transport and M	(VF_1522)
cd2[c] + h[p] -> h[c] + cd2[p]	Inorganic Ion Transport and M	(VF_2341)
cd2[e] <=> cd2[p]	Transport, Outer Membrane Porin	
3 h[c] + 2 nadph[c] + preq0[c] -> 2 nadp[c] + pre	Cofactor and Prosthetic Group	(VF_0598)
cdpglu[c] -> cdpddglu[c] + h2o[c]	Alternate Carbon Metabolism	(VF_0183)
4c2me[c] + atp[c] -> 2p4c2me[c] + adp[c] + h[c]	Cofactor and Prosthetic Group	(VF_0765)
6pgg[c] + h2o[c] -> g6p[c] + glc-D[c]	Alternate Carbon Metabolism	(VF_0605)
pep[c] + cellob[p] -> pyr[c] + 6pgg[c]	Transport, Outer Membrane	(VF_0603 a
cellob[e] -> cellob[p]	Transport, Inner Membrane	
2 amet[c] + pe161[c] -> 2 ahcys[c] + cpe160[c]	Glycerophospholipid Metabolis	(VF_A0760
2 amet[c] + pg161[c] -> 2 ahcys[c] + cpg160[c]	Glycerophospholipid Metabolis	(VF_A0760
2 amet[c] + pe181[c] -> 2 ahcys[c] + cpe180[c]	Glycerophospholipid Metabolis	(VF_A0760
2 amet[c] + pg181[c] -> 2 ahcys[c] + cpg180[c]	Glycerophospholipid Metabolis	(VF_A0760
atp[c] + h2o[c] + cgly[p] -> adp[c] + cgly[c] + h[c	Transport, Inner Membrane	(VF_2516 a
cgly[e] <=> cgly[p]	Transport, Outer Membrane Porin	
chol[p] + h[p] -> chol[c] + h[c]	Transport, Inner Membrane	(VF_2515)
chol[e] <=> chol[p]	Transport, Outer Membrane Porin	
chols[c] + h2o[c] <=> chol[c] + h[c] + so4[c]	Unassigned	(VF_0137)
chor[c] -> pphn[c]	Tyrosine, Tryptophan, and Phe	(VF_0561)
3psme[c] -> chor[c] + pi[c]	Tyrosine, Tryptophan, and Phe	(VF_1805)
chor[c] -> 4hbz[c] + pyr[c]	Cofactor and Prosthetic Group	(VF_2445)
pep[c] + chtbs[p] -> chtbs6p[c] + pyr[c]	Transport, Inner Membrane	(VF_1895)
chtbs[e] <=> chtbs[p]	Transport, Outer Membrane Porin	
cit[e] <=> cit[p]	Transport, Outer Membrane Porin	
2 pg120[p] <=> clpn120[p] + glyc[p]	Glycerophospholipid Metabolis	(VF_1606)
2 pg140[p] <=> clpn140[p] + glyc[p]	Glycerophospholipid Metabolis	(VF_1606)
2 pg141[p] <=> clpn141[p] + glyc[p]	Glycerophospholipid Metabolis	(VF_1606)
2 pg160[p] <=> clpn160[p] + glyc[p]	Glycerophospholipid Metabolis	(VF_1606)
2 pg161[p] <=> clpn161[p] + glyc[p]	Glycerophospholipid Metabolis	(VF_1606)
2 pg180[p] <=> clpn180[p] + glyc[p]	Glycerophospholipid Metabolis	(VF_1606)
2 pg181[p] <=> clpn181[p] + glyc[p]	Glycerophospholipid Metabolis	(VF_1606)
h[c] + 2 cl[p] -> 2 cl[c] + h[p]	Inorganic Ion Transport and M	(VF_1798)
cl[e] <=> cl[p]	Transport, Outer Membrane Porin	
cmp[e] <=> cmp[p]	Transport, Outer Membrane Porin	
cm[e] <=> cm[p]	Transport, Outer Membrane Porin	
co2[e] <=> co2[p]	Transport, Outer Membrane Porin	
atp[c] + cobalt2[c] + h2o[c] -> adp[c] + h[c] + pi[	Inorganic Ion Transport and M	(VF_1522)

cobalt2[c] + h[p] -> h[c] + cobalt2[p]	Inorganic Ion Transport and Me	(VF_2341)
cobalt2[e] <=> cobalt2[p]	Transport, Outer Membrane Porin	
cobalt2[p] -> cobalt2[c]	Inorganic Ion Transport and Metabolism	
acgam26p[c] + h2o[c] -> macgam26p[c] + ac[c]	Alternate Carbon Metabolism	(VF_1341)
atp[c] + h2o[c] + cpgn[p] -> adp[c] + cpgn[c] + h	Transport, Inner Membrane	(VF_A0158
ahdt[c] + h2o[c] -> acald[c] + cph4[c] + h[c] + p	Cofactor and Prosthetic Group	(VF_1160)
gtp[c] + h2o[c] -> cpmp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0940 a
cpppg3[c] + 2 h[c] + o2[c] -> 2 co2[c] + 2 h2o[c]	Cofactor and Prosthetic Group	(VF_A0558
2 amet[c] + cpppg3[c] -> 2 co2[c] + 2 dad-5[c] +	Cofactor and Prosthetic Group	(VF_0080)
atp[c] + h2o[c] + crn[p] -> adp[c] + crn[c] + h[c]	Transport, Inner Membrane	(VF_0785 a
atp[c] + h2o[c] + crn-D[p] -> adp[c] + crn-D[c] +	Transport, Inner Membrane	(VF_0785 a
crn-D[e] <=> crn-D[p]	Transport, Outer Membrane Porin	
crn[e] <=> crn[p]	Transport, Outer Membrane Porin	
accoa[c] + h2o[c] + oaa[c] -> cit[c] + coa[c] + h[	Citric Acid Cycle	(VF_0818)
csn[c] + h[c] + h2o[c] -> nh4[c] + ura[c]	Nucleotide Salvage Pathway	(VF_0531)
csn[p] + h[p] -> csn[c] + h[c]	Transport, Inner Membrane	(VF_0532)
csn[e] <=> csn[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + ctbt[p] -> adp[c] + ctbt[c] + h[c]	Transport, Inner Membrane	(VF_0785 a
tdecoa[c] <=> td2coa[c]	Membrane Lipid Metabolism	(VF_0025)
hdcoa[c] <=> hdd2coa[c]	Membrane Lipid Metabolism	(VF_0025)
odecoa[c] <=> od2coa[c]	Membrane Lipid Metabolism	(VF_0025)
atp[c] + gln-L[c] + h2o[c] + utp[c] -> adp[c] + ctp	Purine and Pyrimidine Biosynt	(VF_2076)
atp[c] + cu[c] + h2o[c] -> adp[c] + h[c] + pi[c] +	Inorganic Ion Transport and Me	(VF_0781)
atp[c] + cu2[c] + h2o[c] -> adp[c] + h[c] + pi[c] +	Inorganic Ion Transport and Me	(VF_1522)
cu2[e] <=> cu2[p]	Transport, Outer Membrane Porin	
cu2[p] -> cu2[c]	Inorganic Ion Transport and Metabolism	
cu[e] <=> cu[p]	Transport, Outer Membrane Porin	
cyan[c] + tsul[c] -> h[c] + so3[c] + tcynt[c]	Unassigned	(VF_2448)
cyan[p] + tsul[p] -> h[p] + so3[p] + tcynt[p]	Inorganic Ion Transport and Me	(VF_A0125
cyan[e] <=> cyan[p]	Transport, Outer Membrane Porin	
cynt[e] <=> cynt[p]	Transport, Outer Membrane Porin	
2 ficytc[c] + 3 h[c] + q8h2[c] -> 2 focytc[c] + 3 h[	Oxidative Phosphorylation	(VF_2218 a
2 focytc[c] + 0.5 o2 -> 2 ficytc[c] + h2o[c]	Oxidative Phosphorylation	(VF_1299 a
atp[c] + cys-L[c] + h2o[c] -> adp[c] + h[c] + pi[c]	Transport, Inner Membrane	(VF_0900 a
atp[c] + h2o[c] + cys-L[p] -> adp[c] + cys-L[c] +	Transport, Inner Membrane	
atp[c] + h2o[c] + cys-D[p] -> adp[c] + cys-D[c] +	Transport, Inner Membrane	
cys-L[c] + h2o[c] -> h2s[c] + nh4[c] + pyr[c]	Cysteine Metabolism	(VF_1186)
cys-D[e] <=> cys-D[p]	Transport, Outer Membrane Porin	
acser[c] + h2s[c] -> ac[c] + cys-L[c] + h[c]	Cysteine Metabolism	(VF_1893)
3sala[c] + 2 h[c] -> ala-L[c] + so2[c]	Cysteine Metabolism	(VF_0590)
cys-L[e] <=> cys-L[p]	Transport, Outer Membrane Porin	
cyst-L[c] + h2o[c] -> hcys-L[c] + nh4[c] + pyr[c]	Methionine Metabolism	(VF_1718)
atp[c] + cys-L[c] + trnacys[c] -> amp[c] + cystrn	tRNA Charging	(VF_1600)
2 h[c] + 0.5 o2[c] + q8h2[c] -> h2o[c] + q8[c] + 2	Oxidative Phosphorylation	(VF_0953 a
cytd[c] + h[c] + h2o[c] -> nh4[c] + uri[c]	Nucleotide Salvage Pathway	(VF_1485)
cytd[c] + gtp[c] -> cmp[c] + gdp[c] + h[c]	Nucleotide Salvage Pathway	(VF_1752)
cytd[p] + h[p] -> cytd[c] + h[c]	Transport, Inner Membrane	(VF_2065)
cytd[p] + h[p] <=> cytd[c] + h[c]	Transport, Inner Membrane	

cytd[e] <=> cytd[p]	Transport, Outer Membrane Porin	
atp[c] + cmp[c] <=> adp[c] + cdp[c]	Nucleotide Salvage Pathway	(VF_1760)
atp[c] + dcmp[c] <=> adp[c] + dcdp[c]	Nucleotide Salvage Pathway	(VF_1760)
dad-2[c] + h[c] + h2o[c] -> din[c] + nh4[c]	Nucleotide Salvage Pathway	(VF_0093)
atp[c] + damp[c] <=> adp[c] + dadp[c]	Nucleotide Salvage Pathway	(VF_0793)
dad-2[p] + h[p] -> dad-2[c] + h[c]	Transport, Inner Membrane	(VF_2065)
dad-2[e] <=> dad-2[p]	Transport, Outer Membrane	
12dgr120[c] + atp[c] -> adp[c] + h[c] + pa120[c]	Glycerophospholipid Metabolis	(VF_0418)
12dgr140[c] + atp[c] -> adp[c] + h[c] + pa140[c]	Glycerophospholipid Metabolis	(VF_0418)
12dgr141[c] + atp[c] -> adp[c] + h[c] + pa141[c]	Glycerophospholipid Metabolis	(VF_0418)
12dgr160[c] + atp[c] -> adp[c] + h[c] + pa160[c]	Glycerophospholipid Metabolis	(VF_0418)
12dgr161[c] + atp[c] -> adp[c] + h[c] + pa161[c]	Glycerophospholipid Metabolis	(VF_0418)
12dgr180[c] + atp[c] -> adp[c] + h[c] + pa180[c]	Glycerophospholipid Metabolis	(VF_0418)
12dgr181[c] + atp[c] -> adp[c] + h[c] + pa181[c]	Glycerophospholipid Metabolis	(VF_0418)
ala-D[e] <=> ala-D[p]	Transport, Outer Membrane Porin	
damp[e] <=> damp[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + 26dap-M[p] -> 26dap-M[c] + a	Transport, Inner Membrane	
26dap-M[c] + h[c] -> co2[c] + lys-L[c]	Threonine and Lysine Metaboli	(VF_2485)
26dap-LL[c] <=> 26dap-M[c]	Threonine and Lysine Metaboli	(VF_2484)
15dap[e] <=> 15dap[p]	Transport, Outer Membrane Porin	
ctp[c] + h[c] + pa120[c] -> cdpdddecg[c] + ppi[c	Glycerophospholipid Metabolis	(VF_1957)
ctp[c] + h[c] + pa140[c] -> cdpdtdecg[c] + ppi[c]	Glycerophospholipid Metabolis	(VF_1957)
ctp[c] + h[c] + pa141[c] -> cdpdtdec7eg[c] + ppi	Glycerophospholipid Metabolis	(VF_1957)
ctp[c] + h[c] + pa160[c] -> cdpdhdecg[c] + ppi[c	Glycerophospholipid Metabolis	(VF_1957)
ctp[c] + h[c] + pa161[c] -> cdpdhdec9eg[c] + pp	Glycerophospholipid Metabolis	(VF_1957)
ctp[c] + h[c] + pa180[c] -> cdpdodecg[c] + ppi[c	Glycerophospholipid Metabolis	(VF_1957)
ctp[c] + h[c] + pa181[c] -> cdpdodec11eg[c] + p	Glycerophospholipid Metabolis	(VF_1957)
ru5p-D[c] -> db4p[c] + formate[c] + h[c]	Cofactor and Prosthetic Group	(VF_0702)
atp[c] + co2[c] + dann[c] -> adp[c] + dtbt[c] + 3	Cofactor and Prosthetic Group	(VF_A0745
dca[e] <=> dca[p]	Transport, Outer Membrane Porin	
dcmp[c] + h[c] + h2o[c] <=> dump[c] + nh4[c]	Nucleotide Salvage Pathway	(VF_A0917
dcmp[e] <=> dcmp[p]	Transport, Outer Membrane Porin	
dcyt[c] + h[c] + h2o[c] -> duri[c] + nh4[c]	Nucleotide Salvage Pathway	(VF_1485)
dcyt[p] + h[p] -> dcyt[c] + h[c]	Transport, Inner Membrane	(VF_2065)
dcyt[e] <=> dcyt[p]	Transport, Outer Membrane	
ddca[e] -> ddca[p]	Transport, Outer Membrane	(VF_1543)
2ddglcn[e] <=> 2ddglcn[p]	Transport, Outer Membrane Porin	
2ddglcn[c] + atp[c] -> 2ddg6p[c] + adp[c] + h[c]	Alternate Carbon Metabolism	(VF_A0988
e4p[c] + h2o[c] + pep[c] -> 2dda7p[c] + pi[c]	Tyrosine, Tryptophan, and Phe	(VF_0553)
atp[c] + dgmp[c] <=> adp[c] + dgdp[c]	Nucleotide Salvage Pathway	(VF_0106)
dgmp[e] <=> dgmp[p]	Transport, Outer Membrane Porin	
dgsn[e] <=> dgsn[p]	Transport, Outer Membrane Porin	
23dhmb[c] -> 3mob[c] + h2o[c]	Valine, Leucine, and Isoleucine	(VF_2559)
23dhmp[c] -> 3mop[c] + h2o[c]	Valine, Leucine, and Isoleucine	(VF_2559)
dha[e] <=> dha[p]	Transport, Outer Membrane Porin	
23dhdp[c] + h[c] + nadph[c] -> nadp[c] + thdp[c]	Threonine and Lysine Metaboli	(VF_0471)
aspsa[c] + pyr[c] -> 23dhdp[c] + h[c] + 2 h2o[c]	Threonine and Lysine Metaboli	(VF_1918)
dhf[c] + h[c] + nadph[c] <=> nadp[c] + thf[c]	Cofactor and Prosthetic Group	(VF_0284)

fol[c] + h[c] + nadph[c] -> nadp[c] + dhf[c]	Cofactor and Prosthetic Group	(VF_0284)
fol[c] + 2 h[c] + 2 nadph[c] -> 2 nadp[c] + thf[c]	Cofactor and Prosthetic Group	(VF_0284)
atp[c] + dhpt[c] + glu-L[c] -> adp[c] + dhf[c] + h[	Cofactor and Prosthetic Group	(VF_1694)
dhna[c] + h[c] + octdp[c] -> 2dmmql8[c] + co2[c	Cofactor and Prosthetic Group	(VF_0212)
h[c] + sbzcoa[c] -> 14dhncoa[c] + h2o[c]	Cofactor and Prosthetic Group	(VF_1669)
14dhncoa[c] + h2o[c] -> coa[c] + dhna[c] + h[c]	Cofactor and Prosthetic Group	(VF_0957)
dhnpt[c] <=> 6hmhpt[c] + gcald[c]	Cofactor and Prosthetic Group	(VF_2247)
dhnpt[c] <=> dhmpt[c]	Cofactor and Prosthetic Group	(VF_2247)
dhor-S[c] + q8[c] -> orot[c] + q8h2[c]	Purine and Pyrimidine Biosynt	(VF_1285)
dhor-S[c] + mqn8[c] -> mql8[c] + orot[c]	Purine and Pyrimidine Biosynt	(VF_1285)
dhor-S[c] + h2o[c] <=> cbasp[c] + h[c]	Purine and Pyrimidine Biosynt	(VF_A0412
25drapp[c] + h[c] + h2o[c] -> 5apru[c] + nh4[c]	Cofactor and Prosthetic Group	(VF_0700)
4abz[c] + 6hmhptpp[c] -> dhpt[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0480)
dhptd[c] -> mdhdhf[c]	Methionine Metabolism	
2dda7p[c] -> 3dhq[c] + pi[c]	Tyrosine, Tryptophan, and Phe	(VF_2291)
3dhq[c] -> 3dhsk[c] + h2o[c]	Tyrosine, Tryptophan, and Phe	(VF_2385)
dimp[e] <=> dimp[p]	Transport, Outer Membrane Porin	
din[e] <=> din[p]	Transport, Outer Membrane Porin	
h[p] + lac-D[p] <=> h[c] + lac-D[c]	Transport, Inner Membrane	
lac-D[e] <=> lac-D[p]	Transport, Outer Membrane Porin	
4crsol[c] ->	Exchange	
5drib[c] ->	Exchange	
amob[c] ->	Exchange	
mththf[c] ->	Exchange	
dmpp[c] + ipdp[c] -> grdp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0712)
h[c] + h2mb4p[c] + nadh[c] -> dmpp[c] + h2o[c]	Cofactor and Prosthetic Group	(VF_0470)
2omhmbl[c] + amet[c] -> ahcys[c] + h[c] + q8h2	Cofactor and Prosthetic Group	(VF_1203)
dmso[c] + mql8[c] -> dms[c] + h2o[c] + mqn8[c]	Oxidative Phosphorylation	(VF_A0080
mql8[c] + dmso[p] -> mqn8[c] + dms[p] + h2o[p]	Oxidative Phosphorylation	(VF_A0188
2dmmql8[c] + dmso[c] -> 2dmmq8[c] + dms[c]	Oxidative Phosphorylation	(VF_A0080
2dmmql8[c] + dmso[p] -> 2dmmq8[c] + dms[p]	Oxidative Phosphorylation	(VF_A0188
dmso[e] <=> dmso[p]	Transport, Outer Membrane Porin	
dms[e] <=> dms[p]	Transport, Outer Membrane Porin	
dhpmp[c] + h2o[c] -> dhnpt[c] + pi[c]	Cofactor and Prosthetic Group Biosynthesis	
ahdt[c] + h2o[c] -> dhpmp[c] + h[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_2192)
dopa[e] <=> dopa[p]	Transport, Outer Membrane Porin	
doxrbcn[e] <=> doxrbcn[p]	Transport, Outer Membrane Porin	
atp[c] + dpcoa[c] -> adp[c] + coa[c] + h[c]	Cofactor and Prosthetic Group	(VF_2189)
2dhp[c] + h[c] + nadph[c] -> nadp[c] + pant-R[c]	Cofactor and Prosthetic Group	(VF_0718)
2dr5p[c] -> acald[c] + g3p[c]	Alternate Carbon Metabolism	(VF_0504)
q8[c] + dsbard[p] -> q8h2[c] + dsbaox[p]	Unassigned	(VF_1635 a
mqn8[c] + dsbard[p] -> mql8[c] + dsbaox[p]	Unassigned	(VF_1635 a
dsbcox[p] + 2 gthrd[p] -> dsbcrd[p] + gthox[p]	Unassigned	(VF_0449)
dsbdox[c] + trdrd[c] -> dsbdrd[c] + trdox[c]	Unassigned	(VF_0909 a
ser-D[e] <=> ser-D[p]	Transport, Outer Membrane Porin	
atp[c] + dtmp[c] <=> adp[c] + dtdp[c]	Nucleotide Salvage Pathway	(VF_1735)
dtmp[e] <=> dtmp[p]	Transport, Outer Membrane Porin	
dump[e] <=> dump[p]	Transport, Outer Membrane Porin	

atp[c] + duri[c] -> adp[c] + dump[c] + h[c]	Nucleotide Salvage Pathway	(VF_1599)
duri[c] + pi[c] <=> 2dr1p[c] + ura[c]	Nucleotide Salvage Pathway	(VF_0505)
duri[p] + h[p] -> duri[c] + h[c]	Transport, Inner Membrane	(VF_2065)
duri[e] <=> duri[p]	Transport, Outer Membrane	
dxyl5p[c] + h[c] + nadph[c] -> 2me4p[c] + nadp[	Cofactor and Prosthetic Group	(VF_1956)
g3p[c] + h[c] + pyr[c] -> co2[c] + dxyl5p[c]	Cofactor and Prosthetic Group	(VF_0711)
e4p[c] + h2o[c] + nad[c] <=> 4per[c] + 2 h[c] + r	Cofactor and Prosthetic Group	(VF_0441)
h[c] + nadh[c] + tdec2eACP[c] -> dcaACP[c] + r	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + tdec2eACP[c] -> dcaACP[c] +	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + tddec2eACP[c] -> ddcaACP[c]	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + tddec2eACP[c] -> ddcaACP[c	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + t3c5ddeceACP[c] -> cddec5eA	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + t3c5ddeceACP[c] -> cddec5e	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + tmrs2eACP[c] -> myrsACP[c] +	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + tmrs2eACP[c] -> myrsACP[c]	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + t3c7mrseACP[c] -> nad[c] + tde	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + t3c7mrseACP[c] -> nadp[c] +	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + tpalm2eACP[c] -> nad[c] + palr	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + tpalm2eACP[c] -> nadp[c] + p	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + t3c9palmeACP[c] -> hdeACP[c	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + t3c9palmeACP[c] -> hdeACP[	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + toctd2eACP[c] -> nad[c] + ocdc	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + toctd2eACP[c] -> nadp[c] + oc	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + t3c11vaceACP[c] -> nad[c] + oc	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + t3c11vaceACP[c] -> nadp[c] +	Cell Envelope Biosynthesis	(VF_0888)
but2eACP[c] + h[c] + nadh[c] -> butACP[c] + na	Cell Envelope Biosynthesis	(VF_0888)
but2eACP[c] + h[c] + nadph[c] -> butACP[c] + n	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + thex2eACP[c] -> hexACP[c] + r	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + thex2eACP[c] -> hexACP[c] +	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadh[c] + toct2eACP[c] -> nad[c] + ocACI	Cell Envelope Biosynthesis	(VF_0888)
h[c] + nadph[c] + toct2eACP[c] -> nadp[c] + oc	Cell Envelope Biosynthesis	(VF_0888)
3hbcoa[c] <=> b2coa[c] + h2o[c]	Membrane Lipid Metabolism	(VF_0025)
3hhcoa[c] <=> h2o[c] + hx2coa[c]	Membrane Lipid Metabolism	(VF_0025)
3hocoa[c] <=> h2o[c] + oc2coa[c]	Membrane Lipid Metabolism	(VF_0025)
3hdcoa[c] <=> dc2coa[c] + h2o[c]	Membrane Lipid Metabolism	(VF_0025)
3hddcoa[c] <=> dd2coa[c] + h2o[c]	Membrane Lipid Metabolism	(VF_0025)
3htdcoa[c] <=> h2o[c] + td2coa[c]	Membrane Lipid Metabolism	(VF_0025)
3hhdcoa[c] <=> h2o[c] + hdd2coa[c]	Membrane Lipid Metabolism	(VF_0025)
3hodcoa[c] <=> h2o[c] + od2coa[c]	Membrane Lipid Metabolism	(VF_0025)
2ddg6p[c] -> g3p[c] + pyr[c]	Pentose Phosphate Pathway	(VF_0090)
4h2oglt[c] <=> glx[c] + pyr[c]	Arginine and Proline Metabolis	(VF_A0987
lipidAvf[c] + myrsACP[c] -> ACP[c] + lipavf[c]	Lipopolysaccharide Biosynthes	(VF_1799)
egmeACP[c] + h[c] + nadph[c] -> gmeACP[c] +	Cofactor and Prosthetic Group	(VF_0888)
2pg[c] <=> h2o[c] + pep[c]	Glycolysis/Gluconeogenesis	(VF_2075)
epmeACP[c] + h[c] + nadph[c] -> nadp[c] + pme	Cofactor and Prosthetic Group	(VF_0888)
etha[e] <=> etha[p]	Transport, Outer Membrane Porin	
ethso3[e] <=> ethso3[p]	Transport, Outer Membrane Porin	
etoh[e] <=> etoh[p]	Transport, Outer Membrane Porin	

12ppd-R[e] <=>	Exchange
12ppd-S[e] <=>	Exchange
14glucan[e] <=>	Exchange
15dap[e] <=>	Exchange
23camp[e] <=>	Exchange
23ccmp[e] <=>	Exchange
23cgmp[e] <=>	Exchange
23cump[e] <=>	Exchange
23dappa[e] <=>	Exchange
26dap-M[e] <=>	Exchange
2ddglcn[e] <=>	Exchange
34dhpac[e] <=>	Exchange
3amp[e] <=>	Exchange
3cmp[e] <=>	Exchange
3gmp[e] <=>	Exchange
3hcinnm[e] <=>	Exchange
3hpp[e] <=>	Exchange
3hpppn[e] <=>	Exchange
3ump[e] <=>	Exchange
4abut[e] <=>	Exchange
4hoxpacd[e] <=>	Exchange
5dglcn[e] <=>	Exchange
5mtr[e] <=>	Exchange
ac[e] <=>	Exchange
acac[e] <=>	Exchange
acald[e] <=>	Exchange
acgal[e] <=>	Exchange
acgal1p[e] <=>	Exchange
acgam[e] <=>	Exchange
acgam1p[e] <=>	Exchange
acgam2[e] <=>	Exchange
acmana[e] <=>	Exchange
acmum[e] <=>	Exchange
acnam[e] <=>	Exchange
acser[e] <=>	Exchange
ade[e] <=>	Exchange
adn[e] <=>	Exchange
adocbl[e] <=>	Exchange
ag[e] <=>	Exchange
agm[e] <=>	Exchange
akg[e] <=>	Exchange
alaala[e] <=>	Exchange
ala-B[e] <=>	Exchange
ala-D[e] <=>	Exchange
ala-L[e] <=>	Exchange
all-D[e] <=>	Exchange
alltn[e] <=>	Exchange
amp[e] <=>	Exchange

anhgm[e] <=>	Exchange
arab-L[e] <=>	Exchange
arbt[e] <=>	Exchange
arbtn[e] <=>	Exchange
arbtn-fe3[e] <=>	Exchange
arg-L[e] <=>	Exchange
ascb-L[e] <=>	Exchange
asn-L[e] <=>	Exchange
aso3[e] <=>	Exchange
asp-L[e] <=>	Exchange
btn[e] <=>	Exchange
but[e] <=>	Exchange
butso3[e] <=>	Exchange
ca2[e] <=>	Exchange
cAMP[e] <=>	Exchange
cbi[e] <=>	Exchange
cbl1[e] <=>	Exchange
cd2[e] <=>	Exchange
cellob[e] <=>	Exchange
cgly[e] <=>	Exchange
chol[e] <=>	Exchange
chtbs[e] <=>	Exchange
cit[e] <=>	Exchange
cl[e] <=>	Exchange
cm[e] <=>	Exchange
cmp[e] <=>	Exchange
co2[e] <=>	Exchange
cobalt2[e] <=>	Exchange
cpgn[e] <=>	Exchange
cpgn-un[e] <=>	Exchange
crn[e] <=>	Exchange
crn-D[e] <=>	Exchange
csn[e] <=>	Exchange
cu[e] <=>	Exchange
cu2[e] <=>	Exchange
cyan[e] <=>	Exchange
cynt[e] <=>	Exchange
cys-D[e] <=>	Exchange
cys-L[e] <=>	Exchange
cytd[e] <=>	Exchange
dad-2[e] <=>	Exchange
damp[e] <=>	Exchange
dca[e] <=>	Exchange
dcmp[e] <=>	Exchange
dcyt[e] <=>	Exchange
ddca[e] <=>	Exchange
dgmp[e] <=>	Exchange
dgsn[e] <=>	Exchange

dha[e] <=>	Exchange
dimp[e] <=>	Exchange
din[e] <=>	Exchange
dms[e] <=>	Exchange
dmso[e] <=>	Exchange
dopa[e] <=>	Exchange
doxrbcn[e] <=>	Exchange
dtmp[e] <=>	Exchange
dump[e] <=>	Exchange
duri[e] <=>	Exchange
enter[e] <=>	Exchange
etha[e] <=>	Exchange
ethso3[e] <=>	Exchange
etoh[e] <=>	Exchange
f6p[e] <=>	Exchange
fald[e] <=>	Exchange
fe2[e] <=>	Exchange
fe3[e] <=>	Exchange
fe3dcit[e] <=>	Exchange
fe3dhbzs[e] <=>	Exchange
fe3hox[e] <=>	Exchange
fe3hox-un[e] <=>	Exchange
fecrm[e] <=>	Exchange
fecrm-un[e] <=>	Exchange
feenter[e] <=>	Exchange
feoxam[e] <=>	Exchange
feoxam-un[e] <=>	Exchange
fol[e] <=>	Exchange
for[e] <=>	Exchange
fru[e] <=>	Exchange
frulys[e] <=>	Exchange
fruur[e] <=>	Exchange
fuc-L[e] <=>	Exchange
fum[e] <=>	Exchange
fusa[e] <=>	Exchange
g1p[e] <=>	Exchange
g3pc[e] <=>	Exchange
g3pe[e] <=>	Exchange
g3pg[e] <=>	Exchange
g3pi[e] <=>	Exchange
g3ps[e] <=>	Exchange
g6p[e] <=>	Exchange
gal[e] <=>	Exchange
gal1p[e] <=>	Exchange
gal-bD[e] <=>	Exchange
galct-D[e] <=>	Exchange
galctn-D[e] <=>	Exchange
galctn-L[e] <=>	Exchange

galt[e] <=>	Exchange
galur[e] <=>	Exchange
gam[e] <=>	Exchange
gam6p[e] <=>	Exchange
gbbtn[e] <=>	Exchange
gdp[e] <=>	Exchange
glc-D[e] <=>	Exchange
glcn[e] <=>	Exchange
glcr[e] <=>	Exchange
glcur[e] <=>	Exchange
glcur1p[e] <=>	Exchange
gln-L[e] <=>	Exchange
glu-L[e] <=>	Exchange
gly[e] <=>	Exchange
glyald[e] <=>	Exchange
glyb[e] <=>	Exchange
glyc[e] <=>	Exchange
glyc2p[e] <=>	Exchange
glyc3p[e] <=>	Exchange
glyclt[e] <=>	Exchange
glyc-R[e] <=>	Exchange
gmp[e] <=>	Exchange
gsn[e] <=>	Exchange
gthox[e] <=>	Exchange
gthrd[e] <=>	Exchange
gtp[e] <=>	Exchange
gua[e] <=>	Exchange
h[e] <=>	Exchange
h2[e] <=>	Exchange
h2o[e] <=>	Exchange
h2o2[e] <=>	Exchange
h2s[e] <=>	Exchange
hdca[e] <=>	Exchange
hdcea[e] <=>	Exchange
hg2[e] <=>	Exchange
his-L[e] <=>	Exchange
hom-L[e] <=>	Exchange
hv[c] <=>	Exchange
hxa[e] <=>	Exchange
hxan[e] <=>	Exchange
idon-L[e] <=>	Exchange
ile-L[e] <=>	Exchange
imp[e] <=>	Exchange
indole[e] <=>	Exchange
inost[e] <=>	Exchange
ins[e] <=>	Exchange
isetac[e] <=>	Exchange
k[e] <=>	Exchange

kdo2lipid4[e] <=>	Exchange
lac-D[e] <=>	Exchange
lac-L[e] <=>	Exchange
LalaDglu[e] <=>	Exchange
LalaDgluMdap[e] <=>	Exchange
LalaDgluMdapDala[e] <=>	Exchange
LalaLglu[e] <=>	Exchange
lcts[e] <=>	Exchange
leu-L[e] <=>	Exchange
lipavf[e] <=>	Exchange
lipoate[e] <=>	Exchange
lys-L[e] <=>	Exchange
lyx-L[e] <=>	Exchange
mal-D[e] <=>	Exchange
mal-L[e] <=>	Exchange
malt[e] <=>	Exchange
malthx[e] <=>	Exchange
maltpt[e] <=>	Exchange
malttr[e] <=>	Exchange
maltttr[e] <=>	Exchange
man[e] <=>	Exchange
man6p[e] <=>	Exchange
manglyc[e] <=>	Exchange
melib[e] <=>	Exchange
meoh[e] <=>	Exchange
met-D[e] <=>	Exchange
met-L[e] <=>	Exchange
metsox-R-L[e] <=>	Exchange
metsox-S-L[e] <=>	Exchange
mg2[e] <=>	Exchange
mincyc[e] <=>	Exchange
minohp[e] <=>	Exchange
mmet[e] <=>	Exchange
mn2[e] <=>	Exchange
mnl[e] <=>	Exchange
mobd[e] <=>	Exchange
mso3[e] <=>	Exchange
n2o[e] <=>	Exchange
na1[e] <=>	Exchange
nac[e] <=>	Exchange
nh4[e] <=>	Exchange
ni2[e] <=>	Exchange
nmn[e] <=>	Exchange
no[e] <=>	Exchange
no2[e] <=>	Exchange
no3[e] <=>	Exchange
novbcn[e] <=>	Exchange
o2[e] <=>	Exchange

o2s[e] <=>	Exchange
ocdca[e] <=>	Exchange
ocdcea[e] <=>	Exchange
octa[e] <=>	Exchange
orn[e] <=>	Exchange
orot[e] <=>	Exchange
pacald[e] <=>	Exchange
peamn[e] <=>	Exchange
phe-L[e] <=>	Exchange
pheme[e] <=>	Exchange
pi[e] <=>	Exchange
pnto-R[e] <=>	Exchange
ppa[e] <=>	Exchange
ppal[e] <=>	Exchange
pppn[e] <=>	Exchange
ppt[e] <=>	Exchange
progly[e] <=>	Exchange
pro-L[e] <=>	Exchange
psclys[e] <=>	Exchange
pser-L[e] <=>	Exchange
ptrc[e] <=>	Exchange
pydam[e] <=>	Exchange
pydx[e] <=>	Exchange
pydxn[e] <=>	Exchange
pyr[e] <=>	Exchange
quin[e] <=>	Exchange
r5p[e] <=>	Exchange
rfamp[e] <=>	Exchange
rib-D[e] <=>	Exchange
ribflv[c] <=>	Exchange
rmn[e] <=>	Exchange
sbt-D[e] <=>	Exchange
sel[e] <=>	Exchange
ser-D[e] <=>	Exchange
ser-L[e] <=>	Exchange
skm[e] <=>	Exchange
slnt[e] <=>	Exchange
so2[e] <=>	Exchange
so3[e] <=>	Exchange
so4[e] <=>	Exchange
spmd[e] <=>	Exchange
succ[e] <=>	Exchange
sucr[e] <=>	Exchange
sulfac[e] <=>	Exchange
tartr-D[e] <=>	Exchange
tartr-L[e] <=>	Exchange
taur[e] <=>	Exchange
tcynt[e] <=>	Exchange

thm[e] <=>	Exchange	
thr-L[e] <=>	Exchange	
thrp[e] <=>	Exchange	
thym[e] <=>	Exchange	
thymd[e] <=>	Exchange	
tma[e] <=>	Exchange	
tmao[e] <=>	Exchange	
tre[e] <=>	Exchange	
trp-L[e] <=>	Exchange	
tsul[e] <=>	Exchange	
ttdca[e] <=>	Exchange	
ttdcea[e] <=>	Exchange	
ttrcyc[e] <=>	Exchange	
tungs[e] <=>	Exchange	
tym[e] <=>	Exchange	
tyr-L[e] <=>	Exchange	
tyrp[e] <=>	Exchange	
uacgam[e] <=>	Exchange	
udpacgal[e] <=>	Exchange	
udpg[e] <=>	Exchange	
udpgal[e] <=>	Exchange	
udpglcur[e] <=>	Exchange	
ump[e] <=>	Exchange	
ura[e] <=>	Exchange	
urea[e] <=>	Exchange	
uri[e] <=>	Exchange	
val-L[e] <=>	Exchange	
xan[e] <=>	Exchange	
xmp[e] <=>	Exchange	
xtsn[e] <=>	Exchange	
xyl-D[e] <=>	Exchange	
xylu-L[e] <=>	Exchange	
zn2[e] <=>	Exchange	
2 pi[c] + f6p[p] -> f6p[c] + 2 pi[p]	Transport, Inner Membrane	(VF_A0042
f6p[e] <=> f6p[p]	Transport, Outer Membrane Porin	
dcacoa[c] + h2o[c] -> coa[c] + dca[c] + h[c]	Cell Envelope Biosynthesis	(VF_1577)
ddcacoa[c] + h2o[c] -> coa[c] + ddca[c] + h[c]	Cell Envelope Biosynthesis	(VF_1577)
h2o[c] + tdcoa[c] -> coa[c] + h[c] + ttdca[c]	Cell Envelope Biosynthesis	(VF_1577)
h2o[c] + tdecoa[c] -> coa[c] + h[c] + ttdcea[c]	Cell Envelope Biosynthesis	(VF_1577)
h2o[c] + pmtcoa[c] -> coa[c] + h[c] + hdca[c]	Cell Envelope Biosynthesis	(VF_1577)
h2o[c] + hdcoa[c] -> coa[c] + h[c] + hdcea[c]	Cell Envelope Biosynthesis	(VF_1577)
h2o[c] + stcoa[c] -> coa[c] + h[c] + ocdca[c]	Cell Envelope Biosynthesis	(VF_1577)
h2o[c] + odecoa[c] -> coa[c] + h[c] + ocdcea[c]	Cell Envelope Biosynthesis	(VF_1577)
h2o[c] + hxcoa[c] -> coa[c] + h[c] + hxa[c]	Cell Envelope Biosynthesis	(VF_1577)
h2o[c] + occoa[c] -> coa[c] + h[c] + octa[c]	Cell Envelope Biosynthesis	(VF_1577)
atp[c] + coa[c] + dca[p] + h[p] -> amp[c] + dcac	Cell Envelope Biosynthesis	(VF_1708)
atp[c] + coa[c] + ddca[p] + h[p] -> amp[c] + ddc	Cell Envelope Biosynthesis	(VF_1708)
atp[c] + coa[c] + h[p] + ttdca[p] -> amp[c] + h[c]	Cell Envelope Biosynthesis	(VF_1708)

atp[c] + coa[c] + h[p] + ttdcea[p] -> amp[c] + h[c	Cell Envelope Biosynthesis	(VF_1708)
atp[c] + coa[c] + h[p] + hdca[p] -> amp[c] + h[c]	Cell Envelope Biosynthesis	(VF_1708)
atp[c] + coa[c] + h[p] + hdcea[p] -> amp[c] + h[c	Cell Envelope Biosynthesis	(VF_1708)
atp[c] + coa[c] + h[p] + ocdca[p] -> amp[c] + h[c	Cell Envelope Biosynthesis	(VF_1708)
atp[c] + coa[c] + h[p] + ocdcea[p] -> amp[c] + h[	Cell Envelope Biosynthesis	(VF_1708)
atp[c] + coa[c] + h[p] + hxa[p] -> amp[c] + h[c] +	Cell Envelope Biosynthesis	(VF_1708)
atp[c] + coa[c] + h[p] + octa[p] -> amp[c] + h[c]	Cell Envelope Biosynthesis	(VF_1708)
fad[c] + h[c] + nadh[c] -> fadh2[c] + nad[c]	Cofactor and Prosthetic Group	(VF_0062)
fad[c] + h[c] + nadph[c] -> fadh2[c] + nadp[c]	Cofactor and Prosthetic Group	(VF_0310 a
hmgth[c] + nad[c] <=> Sfglutth[c] + h[c] + nadh[	Cofactor and Prosthetic Group	(VF_0645)
fald[e] <=> fald[p]	Transport, Outer Membrane Porin	
h[c] + ddca[c] + atp[c] + nadph[c] -> ddcald[c] +	Luciferase activity	(VF_A0919
fdp[c] <=> dhap[c] + g3p[c]	Glycolysis/Gluconeogenesis	(VF_0443)
s17bp[c] <=> dhap[c] + e4p[c]	Pentose Phosphate Pathway	(VF_0443)
fdp[c] + h2o[c] -> f6p[c] + pi[c]	Glycolysis/Gluconeogenesis	(VF_0209)
fe2[c] + ppp9[c] -> 2 h[c] + pheme[c]	Cofactor and Prosthetic Group	(VF_0794)
formate[c] + nad[c] -> co2[c] + nadh[c]	Oxidative Phosphorylation	(VF_A0251
2 h[c] + q8[c] + for[p] -> q8h2[c] + co2[p] + h[p]	Oxidative Phosphorylation	(VF_1358 a
2 h[c] + mqn8[c] + for[p] -> mql8[c] + co2[p] + h	Oxidative Phosphorylation	(VF_1358 a
atp[c] + h2o[c] + fe2[p] -> adp[c] + fe2[c] + h[c]	Inorganic Ion Transport and Me	(VF_0834)
fe2[c] + h[p] -> h[c] + fe2[p]	Inorganic Ion Transport and Me	(VF_2341)
fe2[e] <=> fe2[p]	Transport, Outer Membrane Porin	
fe2[p] -> fe2[c]	Inorganic Ion Transport and Metabolism	
atp[c] + h2o[c] + fe3[p] -> adp[c] + fe3[c] + h[c]	Inorganic Ion Transport and Metabolism	
atp[c] + h2o[c] + fe3hox[p] -> adp[c] + fe3hox[c]	Inorganic Ion Transport and Me	(VF_A0158
fe3hox[e] + h[p] -> h[c] + fe3hox[p]	Transport, Outer Membrane	(VF_1223 a
fadh2[c] + 2 fe3[c] -> fad[c] + 2 fe2[c] + 2 h[c]	Cofactor and Prosthetic Group	(VF_0062)
fe3[e] <=> fe3[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + fecrm[p] -> adp[c] + fecrm[c] +	Inorganic Ion Transport and Me	(VF_A0158
fecrm[e] + h[p] -> h[c] + fecrm[p]	Transport, Outer Membrane	(VF_1223 a
enter[p] + h[p] -> h[c] + enter[e]	Inorganic Ion Transport and Me	(VF_2233)
atp[c] + h2o[c] + feoxam[p] -> adp[c] + feoxam[	Inorganic Ion Transport and Me	(VF_A0158
feoxam[e] + h[p] -> h[c] + feoxam[p]	Transport, Outer Membrane	(VF_1223 a
forglu[c] + h[c] + h2o[c] -> frmd[c] + glu-L[c]	Histidine Metabolism	(VF_A0452
2 flxso[c] + nadph[c] -> 2 flxr[c] + h[c] + nadp[c]	Unassigned	(VF_0812 a
h[c] + nadph[c] + ribflv[c] -> nadp[c] + rbflvrd[c]	Cofactor and Prosthetic Group	(VF_0062)
h[c] + nadh[c] + ribflv[c] -> nad[c] + rbflvrd[c]	Cofactor and Prosthetic Group	(VF_0062)
10fthf[c] + mettrna[c] -> fmettrna[c] + h[c] + thf[	tRNA Charging	(VF_2544)
atp[c] + fmn[c] + h[c] -> fad[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0466)
fmn[c] + h[c] + nadh[c] -> fmnh2[c] + nad[c]	Cofactor and Prosthetic Group	(VF_0062)
fmn[c] + h[c] + nadph[c] -> fmnh2[c] + nadp[c]	Cofactor and Prosthetic Group	(VF_0062)
5fthf[c] + h[c] -> h2o[c] + methf[c]	Folate Metabolism	(VF_2104)
nadp[c] + formate[c] <=> nadph[c] + co2[c] + h[	Unassigned	(VF_A0100
for[p] + h[p] -> formate[c] + h[c]	Transport, Inner Membrane	(VF_A0813
for[e] <=> for[p]	Transport, Outer Membrane Porin	
formate[c] -> for[p]	Transport, Inner Membrane	(VF_A0813
fum[c] + mql8[c] -> mqn8[c] + succ[c]	Citric Acid Cycle	(VF_2334 a
2dmmql8[c] + fum[c] -> 2dmmq8[c] + succ[c]	Citric Acid Cycle	(VF_2334 a

frdp[c] + ipdp[c] -> ggdp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0712)
atp[c] + f1p[c] -> adp[c] + fdp[c] + h[c]	Alternate Carbon Metabolism	(VF_A0941
frulys[e] <=> frulys[p]	Transport, Outer Membrane Porin	
pep[c] + fru[p] -> f6p[c] + pyr[c]	Transport, Inner Membrane	(VF_1894 a
pep[c] + fru[p] -> f1p[c] + pyr[c]	Transport, Inner Membrane	(VF_1894 a
fru[e] <=> fru[p]	Transport, Outer Membrane Porin	
fruur[e] <=> fruur[p]	Transport, Outer Membrane Porin	
10fthf[c] + h2o[c] -> formate[c] + h[c] + thf[c]	Folate Metabolism	(VF_1714)
atp[c] + formate[c] + thf[c] <=> 10fthf[c] + adp[c	Folate Metabolism	(VF_1793)
fuc-L[e] <=> fuc-L[p]	Transport, Outer Membrane Porin	
fum[c] + h2o[c] <=> mal-L[c]	Citric Acid Cycle	(VF_1180)
fum[p] + 3 h[p] -> fum[c] + 3 h[c]	Transport, Inner Membrane	(VF_2354)
fum[e] <=> fum[p]	Transport, Outer Membrane Porin	
fusa[e] <=> fusa[p]	Transport, Outer Membrane Porin	
accoa[c] + gam1p[c] -> acgam1p[c] + coa[c] +	Cell Envelope Biosynthesis	(VF_2562)
ctp[c] + g1p[c] <=> ppi[c] + cdpglu[c] + 3h[c]	Alternate Carbon Metabolism	(VF_0182)
g1p[e] <=> g1p[p]	Transport, Outer Membrane Porin	
dttp[c] + g1p[c] + h[c] -> dtdpglu[c] + ppi[c]	Cell Envelope Biosynthesis	(VF_0167)
glu1sa[c] <=> 5aop[c]	Cofactor and Prosthetic Group	(VF_2135)
glyc2p[c] + h2o[c] -> glyc[c] + pi[c]	Alternate Carbon Metabolism	(VF_0614)
ddcaACP[c] + glyc3p[c] -> 1ddecg3p[c] + ACP[	Glycerophospholipid Metabolis	(VF_1739 a
glyc3p[c] + myrsACP[c] -> 1tdecg3p[c] + ACP[c	Glycerophospholipid Metabolis	(VF_1739 a
glyc3p[c] + tdeACP[c] -> 1tdec7eg3p[c] + ACP[	Glycerophospholipid Metabolis	(VF_1739 a
glyc3p[c] + palmACP[c] -> 1hdecg3p[c] + ACP[	Glycerophospholipid Metabolis	(VF_1739 a
glyc3p[c] + hdeACP[c] -> 1hdec9eg3p[c] + AC	Glycerophospholipid Metabolis	(VF_1739 a
glyc3p[c] + ocdcaACP[c] -> 1odecg3p[c] + ACP	Glycerophospholipid Metabolis	(VF_1739 a
glyc3p[c] + octeACP[c] -> 1odec11eg3p[c] + AC	Glycerophospholipid Metabolis	(VF_1739 a
g3pc[e] <=> g3pc[p]	Transport, Outer Membrane Porin	
glyc3p[c] + nadp[c] <=> dhap[c] + h[c] + nadph[	Alternate Carbon Metabolism	(VF_2348)
glyc3p[c] + q8[c] -> dhap[c] + q8h2[c]	Oxidative Phosphorylation	(VF_A0248
glyc3p[c] + mqn8[c] -> dhap[c] + mql8[c]	Oxidative Phosphorylation	(VF_A0248
2dmmq8[c] + glyc3p[c] -> 2dmmql8[c] + dhap[c	Oxidative Phosphorylation	(VF_A0248
g3pe[e] <=> g3pe[p]	Transport, Outer Membrane Porin	
g3pg[e] <=> g3pg[p]	Transport, Outer Membrane Porin	
g3pi[e] <=> g3pi[p]	Transport, Outer Membrane Porin	
g3ps[e] <=> g3ps[p]	Transport, Outer Membrane Porin	
glu5sa[c] -> 1pyr5c[c] + h[c] + h2o[c]	Arginine and Proline Metabolism	
glu5p[c] + h[c] + nadph[c] -> glu5sa[c] + nadp[c	Arginine and Proline Metabolis	(VF_0741)
gam6p[c] + h2o[c] -> f6p[c] + nh4[c]	Alternate Carbon Metabolism	(VF_2357)
g6p[c] + nadp[c] <=> 6pgl[c] + h[c] + nadph[c]	Pentose Phosphate Pathway	(VF_A0468
2 pi[c] + g6p[p] -> g6p[c] + 2 pi[p]	Transport, Inner Membrane	(VF_A0042
g6p[e] <=> g6p[p]	Transport, Outer Membrane Porin	
gal1p[e] <=> gal1p[p]	Transport, Outer Membrane Porin	
galam6p[c] + h2o[c] -> nh4[c] + tag6p-D[c]	Alternate Carbon Metabolism	(VF_A1004
gal-bD[e] <=> gal-bD[p]	Transport, Outer Membrane Porin	
galctn-L[e] <=> galctn-L[p]	Transport, Outer Membrane Porin	
galctn-D[e] <=> galctn-D[p]	Transport, Outer Membrane Porin	
galct-D[e] <=> galct-D[p]	Transport, Outer Membrane Porin	

atp[c] + gal[c] <=> adp[c] + gal1p[c] + h[c]	Alternate Carbon Metabolism	(VF_A0355
gal-bD[p] -> gal[p]	Alternate Carbon Metabolism	(VF_A0356
gal[p] + h[p] -> gal[c] + h[c]	Transport, Inner Membrane	
gal[e] <=> gal[p]	Transport, Outer Membrane Porin	
galt[e] <=> galt[p]	Transport, Outer Membrane Porin	
g1p[c] + h[c] + utp[c] -> ppi[c] + udpg[c]	Cell Envelope Biosynthesis	(VF_0342)
galur[e] <=> galur[p]	Transport, Outer Membrane Porin	
2 pi[c] + gam6p[p] -> gam6p[c] + 2 pi[p]	Transport, Inner Membrane	(VF_A0042
gam6p[e] <=> gam6p[p]	Transport, Outer Membrane Porin	
gam[c] + atp[c] <=> gam6p[c] + adp[c] + [h]	Alternate Carbon Metabolism	(VF_2145)
pep[c] + gam[p] -> gam6p[c] + pyr[c]	Transport, Inner Membrane	(VF_1732 a
gam[e] <=> gam[p]	Transport, Outer Membrane Porin	
g3p[c] + nad[c] + pi[c] <=> 13dpg[c] + h[c] + na	Glycolysis/Gluconeogenesis	(VF_0913)
10fthf[c] + gar[c] <=> fgam[c] + h[c] + thf[c]	Purine and Pyrimidine Biosynt	(VF_1929)
atp[c] + formate[c] + gar[c] -> adp[c] + fgam[c]	Purine and Pyrimidine Biosynt	(VF_1487)
gbbtn[e] <=> gbbtn[p]	Transport, Outer Membrane Porin	
gcald[c] + h2o[c] + nad[c] -> glyclt[c] + 2 h[c] +	Folate Metabolism	
atp[c] + gdp[c] -> amp[c] + h[c] + ppgpp[c]	Cofactor and Prosthetic Group	(VF_2080)
gdp[e] <=> gdp[p]	Transport, Outer Membrane Porin	
gdptp[c] + h2o[c] -> gtp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0104)
f6p[c] + gln-L[c] -> gam6p[c] + glu-L[c]	Cell Envelope Biosynthesis	(VF_2372)
ser-L[c] + thf[c] <=> gly[c] + h2o[c] + mlthf[c]	Glycine and Serine Metabolisn	(VF_0695)
atp[c] + gmp[c] <=> adp[c] + gdp[c]	Nucleotide Salvage Pathway	(VF_0106)
glycogen[c] -> bglycogen[c]	Glycolysis/Gluconeogenesis	(VF_A0808
accoa[c] + glc-D[c] <=> acglc-D[c] + coa[c]	Alternate Carbon Metabolism	(VF_1337)
pep[c] + acgam2[p] -> pyr[c] + acgam26p[c]	Transport, Inner Membrane	(VF_0808 a
glcn[e] <=> glcn[p]	Transport, Outer Membrane Porin	
glycogen[c] + pi[c] -> g1p[c]	Glycolysis/Gluconeogenesis	(VF_A0810
bglycogen[c] + pi[c] -> g1p[c]	Glycolysis/Gluconeogenesis	(VF_A0810
pep[c] + glc-D[p] -> g6p[c] + pyr[c]	Transport, Inner Membrane	(VF_1719 a
glcr[e] <=> glcr[p]	Transport, Outer Membrane Porin	
adpglc[c] -> adp[c] + glycogen[c] + h[c]	Glycolysis/Gluconeogenesis	(VF_A0805
glc-D[p] + h[p] -> glc-D[c] + h[c]	Transport, Inner Membrane	
glc-D[e] <=> glc-D[p]	Transport, Outer Membrane Porin	
glc-D[e] -> glc-D[p]	Transport, Outer Membrane	
glcur1p[e] <=> glcur1p[p]	Transport, Outer Membrane Porin	
glcur[p] + h[p] <=> glcur[c] + h[c]	Transport, Inner Membrane	
glcur[e] <=> glcur[p]	Transport, Outer Membrane Porin	
bglycogen[c] -> glycogen[c]	Glycolysis/Gluconeogenesis	(VF_A0801
atp[c] + g1p[c] + h[c] -> adpglc[c] + ppi[c]	Glycolysis/Gluconeogenesis	(VF_A0806
atp[c] + glu-L[c] + nh4[c] -> adp[c] + gln-L[c] +	Glutamate Metabolism	(VF_0098)
h[p] + gln-L[p] <=> h[c] + gln-L[c]	Transport, Inner Membrane	(VF_0924)
gln-L[e] <=> gln-L[p]	Transport, Outer Membrane Porin	
atp[c] + gln-L[c] + trnagln[c] -> amp[c] + glntrna	tRNA Charging	(VF_0809)
atp[c] + glu-L[c] -> adp[c] + glu5p[c]	Arginine and Proline Metabolis	(VF_0740)
atp[c] + cys-L[c] + glu-L[c] -> adp[c] + glucys[c]	Cofactor and Prosthetic Group	(VF_0543)
glu-L[c] + h[c] -> 4abut[c] + co2[c]	Glutamate Metabolism	(VF_1064)
glu-L[c] + h2o[c] + nad[c] <=> akg[c] + h[c] + na	Glutamate Metabolism	(VF_1284)

gln-L[c] + h2o[c] -> glu-L[c] + nh4[c]	Glutamate Metabolism	(VF_1179)
gln-L[p] + h2o[p] -> glu-L[p] + nh4[p]	Glutamate Metabolism	(VF_1527)
gln-L[c] + h2o[c] + prpp[c] -> glu-L[c] + ppi[c] +	Purine and Pyrimidine Biosynt	(VF_1691)
glu-D[c] <=> glu-L[c]	Cell Envelope Biosynthesis	(VF_2433)
akg[c] + gln-L[c] + h[c] + nadph[c] -> 2 glu-L[c]	Glutamate Metabolism	(VF_2124 a
glu-L[p] + h[p] <=> glu-L[c] + h[c]	Transport, Inner Membrane	(VF_1026)
glu-L[p] + na1[p] -> glu-L[c] + na1[c]	Transport, Inner Membrane	(VF_A0507
glu-L[e] <=> glu-L[p]	Transport, Outer Membrane Porin	
glutrna[c] + h[c] + nadph[c] -> glu1sa[c] + nadp	Cofactor and Prosthetic Group	(VF_0767)
atp[c] + glu-L[c] + trnaglu[c] -> amp[c] + glutrna	Cofactor and Prosthetic Group	(VF_1887)
glyald[e] <=> glyald[p]	Transport, Outer Membrane Porin	
glyald[p] <=> glyald[c]	Transport, Inner Membrane	(VF_A0235
accoa[c] + gly[c] <=> 2aobut[c] + coa[c]	Glycine and Serine Metabolis	(VF_A0418
glyb[p] + h[p] -> glyb[c] + h[c]	Transport, Inner Membrane	(VF_1121)
glyb[e] <=> glyb[p]	Transport, Outer Membrane Porin	
glyc2p[e] <=> glyc2p[p]	Transport, Outer Membrane Porin	
pi[c] + glyc3p[p] -> glyc3p[c] + pi[p]	Transport, Inner Membrane	(VF_0072)
glyc3p[e] <=> glyc3p[p]	Transport, Outer Membrane Porin	
glyc-R[e] <=> glyc-R[p]	Transport, Outer Membrane Porin	
atp[c] + glyc-R[c] -> 3pg[c] + adp[c] + h[c]	Glyoxylate Metabolism	(VF_2157)
gly[c] + nad[c] + thf[c] -> co2[c] + mlthf[c] + nad	Folate Metabolism	(VF_2178 a
glyclt[p] + h[p] <=> glyclt[c] + h[c]	Transport, Inner Membrane	
glyclt[e] <=> glyclt[p]	Transport, Outer Membrane Porin	
glyc[e] <=> glyc[p]	Transport, Outer Membrane Porin	
glyc[c] <=> glyc[p]	Transport, Inner Membrane	(VF_A0235
atp[c] + glyc[c] -> adp[c] + glyc3p[c] + h[c]	Alternate Carbon Metabolism	(VF_A0236
h2o[c] + lgt-S[c] -> gthrd[c] + h[c] + lac-D[c]	Methylglyoxal Metabolism	(VF_1938)
gly[p] + h[p] -> gly[c] + h[c]	Transport, Inner Membrane	(VF_1121)
gly[p] + na1[p] -> gly[c] + na1[c]	Transport, Inner Membrane	(VF_2110)
gly[e] <=> gly[p]	Transport, Outer Membrane Porin	
atp[c] + gly[c] + trnagly[c] -> amp[c] + glytrna[c]	tRNA Charging	(VF_0015 a
atp[c] + gmhep1p[c] + h[c] -> adphep-DD[c] + p	Lipopolysaccharide Biosynthes	(VF_2234)
atp[c] + gmhep7p[c] -> adp[c] + gmhep17bp[c]	Lipopolysaccharide Biosynthes	(VF_2234)
gmhep17bp[c] + h2o[c] -> gmhep1p[c] + pi[c]	Lipopolysaccharide Biosynthes	(VF_0687)
gmp[c] + 2 h[c] + nadph[c] -> imp[c] + nadp[c] +	Purine and Pyrimidine Biosynt	(VF_A0695
atp[c] + gln-L[c] + h2o[c] + xmp[c] -> amp[c] + g	Purine and Pyrimidine Biosynt	(VF_0638)
gmp[e] <=> gmp[p]	Transport, Outer Membrane Porin	
6pgc[c] + nadp[c] -> co2[c] + nadph[c] + ru5p-D	Pentose Phosphate Pathway	(VF_A0470
gp4g[c] + h2o[c] -> 2 gdp[c] + 2 h[c]	Nucleotide Salvage Pathway	(VF_0285)
g3pc[c] + h2o[c] -> chol[c] + glyc3p[c] + h[c]	Glycerophospholipid Metabolis	(VF_A0958
g3pc[p] + h2o[p] -> chol[p] + glyc3p[p] + h[p]	Glycerophospholipid Metabolis	(VF_A0958
g3pe[c] + h2o[c] -> etha[c] + glyc3p[c] + h[c]	Glycerophospholipid Metabolis	(VF_A0958
g3pe[p] + h2o[p] -> etha[p] + glyc3p[p] + h[p]	Glycerophospholipid Metabolis	(VF_A0958
g3ps[c] + h2o[c] -> glyc3p[c] + h[c] + ser-L[c]	Glycerophospholipid Metabolis	(VF_A0958
g3ps[p] + h2o[p] -> glyc3p[p] + h[p] + ser-L[p]	Glycerophospholipid Metabolis	(VF_A0958
g3pg[c] + h2o[c] -> glyc[c] + glyc3p[c] + h[c]	Glycerophospholipid Metabolis	(VF_A0958
g3pg[p] + h2o[p] -> glyc[p] + glyc3p[p] + h[p]	Glycerophospholipid Metabolis	(VF_A0958
g3pi[c] + h2o[c] -> glyc3p[c] + h[c] + inost[c]	Glycerophospholipid Metabolis	(VF_A0958

g3pi[p] + h2o[p] -> glyc3p[p] + h[p] + inost[p]	Glycerophospholipid Metabolis	(VF_A0958
grdp[c] + ipdp[c] -> frdp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0712)
grxox[c] + 2 gthrd[c] -> grxrd[c] + gthox[c]	Unassigned	(VF_1584)
atp[c] + gsn[c] -> adp[c] + gmp[c] + h[c]	Nucleotide Salvage Pathway	(VF_0911)
gsn[p] + h[p] -> gsn[c] + h[c]	Transport, Inner Membrane	
gsn[e] <=> gsn[p]	Transport, Outer Membrane Porin	
gthox[c] + h[c] + nadph[c] <=> 2 gthrd[c] + nad	Cofactor and Prosthetic Group	(VF_2489)
gthox[e] <=> gthox[p]	Transport, Outer Membrane Porin	
atp[c] + gthrd[c] + h2o[c] -> adp[c] + h[c] + pi[c]	Transport, Inner Membrane	(VF_0900 a
gthrd[p] + h2o[p] -> cgly[p] + glu-L[p]	Cofactor and Prosthetic Group	(VF_A0086
gthrd[e] <=> gthrd[p]	Transport, Outer Membrane Porin	
atp[c] + glucys[c] + gly[c] -> adp[c] + gthrd[c] +	Cofactor and Prosthetic Group	(VF_0435)
gtp[c] + h2o[c] -> ahdt[c] + formate[c] + h[c]	Cofactor and Prosthetic Group	(VF_1607)
gtp[c] + 3 h2o[c] -> 25drapp[c] + formate[c] + 2	Cofactor and Prosthetic Group	(VF_1189)
gdptp[c] + h2o[c] -> h[c] + pi[c] + ppgpp[c]	Cofactor and Prosthetic Group	(VF_0054)
atp[c] + gtp[c] -> amp[c] + gdptp[c] + h[c]	Cofactor and Prosthetic Group	(VF_2080)
gtp[e] <=> gtp[p]	Transport, Outer Membrane Porin	
gua[c] + h[c] + h2o[c] -> nh4[c] + xan[c]	Nucleotide Salvage Pathway	(VF_A0969
gua[c] + prpp[c] -> gmp[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_0738)
gua[p] + h[p] -> gua[c] + h[c]	Transport, Inner Membrane	(VF_0116)
gua[e] <=> gua[p]	Transport, Outer Membrane	
h2o2[e] <=> h2o2[p]	Transport, Outer Membrane Porin	
h2o[e] <=> h2o[p]	Transport, Outer Membrane P	(VF_A1100
h2o[p] <=> h2o[c]	Transport, Inner Membrane	(VF_1479)
h2s[e] <=> h2s[p]	Transport, Outer Membrane Porin	
h2[e] <=> h2[p]	Transport, Outer Membrane Porin	
aacoa[c] + h[c] + nadh[c] <=> 3hbcoa[c] + nad[	Membrane Lipid Metabolism	(VF_0025)
3ohcoa[c] + h[c] + nadh[c] <=> 3hhcoa[c] + nad	Membrane Lipid Metabolism	(VF_0025)
3oocoa[c] + h[c] + nadh[c] <=> 3hocoa[c] + nad	Membrane Lipid Metabolism	(VF_0025)
3odcoa[c] + h[c] + nadh[c] <=> 3hdcoa[c] + nad	Membrane Lipid Metabolism	(VF_0025)
3oddcoa[c] + h[c] + nadh[c] <=> 3hddcoa[c] + n	Membrane Lipid Metabolism	(VF_0025)
3otdcoa[c] + h[c] + nadh[c] <=> 3htdcoa[c] + na	Membrane Lipid Metabolism	(VF_0025)
3ohdcoa[c] + h[c] + nadh[c] <=> 3hhdcoa[c] + n	Membrane Lipid Metabolism	(VF_0025)
3oodcoa[c] + h[c] + nadh[c] <=> 3hodcoa[c] + n	Membrane Lipid Metabolism	(VF_0025)
4hbz[c] + octdp[c] -> 3ophb[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_2444)
3hcinnm[e] <=> 3hcinnm[p]	Transport, Outer Membrane Porin	
co2[c] + h2o[c] <=> h[c] + hco3[c]	Unassigned	(VF_2174)
hdca[e] -> hdca[p]	Transport, Outer Membrane	(VF_1543)
hdcea[e] -> hdcea[p]	Transport, Outer Membrane	(VF_1543)
4mhetz[c] + atp[c] -> 4mpetz[c] + adp[c] + h[c]	Cofactor and Prosthetic Group	(VF_A0321
atp[c] + glc-D[c] -> adp[c] + g6p[c] + h[c]	Glycolysis/Gluconeogenesis	(VF_1408)
h[p] + hxa[p] <=> h[c] + hxa[c]	Transport, Inner Membrane	
atp[c] + h2o[c] + hg2[c] -> adp[c] + h[c] + pi[c] +	Inorganic Ion Transport and M	(VF_1522)
hg2[c] + h[p] -> h[c] + hg2[p]	Inorganic Ion Transport and M	(VF_2341)
hg2[e] <=> hg2[p]	Transport, Outer Membrane Porin	
3hmp[c] + nad[c] -> h[c] + mmtsa[c] + nadh[c]	Valine, Leucine, and Isoleucin	(VF_A0173
atp[c] + h2o[c] + his-L[p] -> adp[c] + h[c] + his-L	Transport, Inner Membrane	(VF_1585 a
his-L[c] -> nh4[c] + urcan[c]	Histidine Metabolism	(VF_A0450

h2o[c] + histd[c] + 2 nad[c] -> 3 h[c] + his-L[c] +	Histidine Metabolism	(VF_1013)
his-L[e] <=> his-L[p]	Transport, Outer Membrane Porin	
h2o[c] + hisp[c] -> histd[c] + pi[c]	Histidine Metabolism	(VF_1015)
atp[c] + his-L[c] + trnahis[c] -> amp[c] + histrna[	tRNA Charging	(VF_0630)
h2o[c] + 4 ppbng[c] -> hmbil[c] + 4 nh4[c]	Cofactor and Prosthetic Group	(VF_0066)
4ahmmp[c] + atp[c] -> 4ampm[c] + adp[c] + h[c]	Cofactor and Prosthetic Group	(VF_A0316
hom-L[e] <=> hom-L[p]	Transport, Outer Membrane Porin	
6hmhpt[c] + atp[c] -> 6hmhptpp[c] + amp[c] + h	Cofactor and Prosthetic Group	(VF_2168)
3hpppn[e] <=> 3hpppn[p]	Transport, Outer Membrane Porin	
hom-L[c] + nadp[c] <=> aspsa[c] + h[c] + nadph	Threonine and Lysine Metaboli	(VF_2266)
atp[c] + hom-L[c] -> adp[c] + h[c] + phom[c]	Threonine and Lysine Metaboli	(VF_2117)
hom-L[c] + succoa[c] -> coa[c] + suchms[c]	Methionine Metabolism	(VF_2063)
glu-L[c] + imacp[c] -> akg[c] + hisp[c]	Histidine Metabolism	(VF_1014)
h[e] <=> h[p]	Transport, Outer Membrane Porin	
acgam2[c] + h2o[c] -> 2acgam[c]	Alternate Carbon Metabolism	(VF_2146)
hxa[e] <=> hxa[p]	Transport, Outer Membrane Porin	
accoa[c] + hxa[c] -> ac[c] + hxcoa[c]	Alternate Carbon Metabolism	
hxan[c] + prpp[c] -> imp[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_0738)
hxan[e] <=> hxan[p]	Transport, Outer Membrane Porin	
hxan[p] <=> hxan[c]	Transport, Inner Membrane	
2fe1s[c] + iscssh[c] + iscu[c] -> 4 h[c] + iscs[c] +	Cofactor and Prosthetic Group	(VF_0617 a
fadh2[c] + 2 fe2[c] + 2 iscssh[c] + iscu[c] -> fad[	Cofactor and Prosthetic Group	(VF_0617 a
fadh2[c] + 2 fe2[c] + 2 iscssh[c] + iscu-2fe2s[c]	Cofactor and Prosthetic Group	(VF_0617 a
4 h[c] + iscu-2fe2s[c] -> 2fe2s[c] + iscu[c]	Cofactor and Prosthetic Group	(VF_0618 a
fadh2[c] + 2 h[c] + iscu-2fe2s2[c] -> fad[c] + isc	Cofactor and Prosthetic Group	(VF_0618)
4 h[c] + iscu-4fe4s[c] -> 4fe4s[c] + iscu[c]	Cofactor and Prosthetic Group	(VF_0618 a
icit[c] + nadp[c] <=> akg[c] + co2[c] + nadph[c]	Citric Acid Cycle	(VF_1775)
chor[c] <=> ichor[c]	Cofactor and Prosthetic Group	(VF_1672)
icit[c] -> glx[c] + succ[c]	Anaplerotic Reactions	(VF_1972)
cys-L[c] + iscs[c] -> ala-L[c] + iscssh[c]	Cofactor and Prosthetic Group	(VF_0617)
idon-L[e] <=> idon-L[p]	Transport, Outer Membrane Porin	
gln-L[c] + prlp[c] -> aicar[c] + eig3p[c] + glu-L[c]	Histidine Metabolism	(VF_1016 a
eig3p[c] -> h2o[c] + imacp[c]	Histidine Metabolism	(VF_1015)
2cpr5p[c] + h[c] -> 3ig3p[c] + co2[c] + h2o[c]	Tyrosine, Tryptophan, and Phe	(VF_1029)
atp[c] + h2o[c] + ile-L[p] -> adp[c] + h[c] + ile-L[	Transport, Inner Membrane	(VF_1084)
h[p] + ile-L[p] <=> h[c] + ile-L[c]	Transport, Inner Membrane	(VF_0446)
akg[c] + ile-L[c] <=> 3mop[c] + glu-L[c]	Valine, Leucine, and Isoleucin	(VF_2558)
ile-L[e] <=> ile-L[p]	Transport, Outer Membrane Porin	
atp[c] + ile-L[c] + trnaile[c] -> amp[c] + iletrna[c]	tRNA Charging	(VF_0467)
h2o[c] + imp[c] <=> fprica[c]	Purine and Pyrimidine Biosynt	(VF_2394)
h2o[c] + imp[c] + nad[c] -> h[c] + nadh[c] + xmp	Purine and Pyrimidine Biosynt	(VF_0637)
imp[e] <=> imp[p]	Transport, Outer Membrane Porin	
indole[e] <=> indole[p]	Transport, Outer Membrane Porin	
inost[p] + na1[p] -> inost[c] + na1[c]	Transport, Inner Membrane	(VF_A0351
atp[c] + ins[c] -> adp[c] + h[c] + imp[c]	Nucleotide Salvage Pathway	(VF_0911)
h[p] + ins[p] <=> h[c] + ins[c]	Transport, Inner Membrane	
ins[e] <=> ins[p]	Transport, Outer Membrane	
inost[e] <=> inost[p]	Transport, Outer Membrane Porin	

ipdp[c] <=> dmpp[c]	Cofactor and Prosthetic Group	(VF_0403)
h[c] + h2mb4p[c] + nadh[c] -> h2o[c] + ipdp[c] +	Cofactor and Prosthetic Group	(VF_0470)
3c2hmp[c] + nad[c] -> 3c4mop[c] + h[c] + nadh[	Valine, Leucine, and Isoleucine	(VF_0294)
3c2hmp[c] <=> 2ippm[c] + h2o[c]	Valine, Leucine, and Isoleucine	(VF_0292 ar
2ippm[c] + h2o[c] <=> 3c3hmp[c]	Valine, Leucine, and Isoleucine	(VF_0292 ar
3mob[c] + accoa[c] + h2o[c] -> 3c3hmp[c] + coa	Valine, Leucine, and Isoleucine	(VF_0295)
isetac[e] <=> isetac[p]	Transport, Outer Membrane Porin	
4izp[c] + h2o[c] -> forglu[c] + h[c]	Histidine Metabolism	(VF_A0453
23dhmb[c] + nadp[c] <=> alac-S[c] + h[c] + nad	Valine, Leucine, and Isoleucine	(VF_2528)
2ahbut[c] + h[c] + nadph[c] <=> 23dhmp[c] + na	Valine, Leucine, and Isoleucine	(VF_2528)
acACP[c] + h[c] + malACP[c] -> ACP[c] + actAC	Membrane Lipid Metabolism	(VF_1700) (
accoa[c] + h[c] + malACP[c] -> actACP[c] + co2	Membrane Lipid Metabolism	(VF_1742)
ctp[c] + kdo[c] -> ckdo[c] + ppi[c]	Lipopolysaccharide Biosynthes	(VF_A0427
h2o[c] + kdo8p[c] -> kdo[c] + pi[c]	Lipopolysaccharide Biosynthes	(VF_0391) (
ara5p[c] + h2o[c] + pep[c] -> kdo8p[c] + pi[c]	Lipopolysaccharide Biosynthes	(VF_0772) (
h[p] + k[p] -> h[c] + k[c]	Inorganic Ion Transport and Me	(VF_0027 ar
k[c] + h[p] -> h[c] + k[p]	Inorganic Ion Transport and Me	(VF_0220)
k[e] <=> k[p]	Transport, Outer Membrane Porin	
LalaDglu[e] <=> LalaDglu[p]	Transport, Outer Membrane Porin	
LalaDglu[p] + h[p] -> LalaDglu[c] + h[c]	Transport, Inner Membrane	
LalaLglu[e] <=> LalaLglu[p]	Transport, Outer Membrane Porin	
LalaLglu[p] + h[p] -> LalaLglu[c] + h[c]	Transport, Inner Membrane	(VF_A0124
LalaLglu[c] + h2o[c] -> ala-L[c] + glu-L[c]	Murein Recycling	
h2o[c] + lald-L[c] + nad[c] -> 2 h[c] + lac-L[c] + r	Alternate Carbon Metabolism	(VF_A0124
lcts[e] <=> lcts[p]	Transport, Outer Membrane Po	(VF_0736)
lac-D[c] + nad[c] <=> h[c] + nadh[c] + pyr[c]	Pyruvate Metabolism	
atp[c] + h2o[c] + leu-L[p] -> adp[c] + h[c] + leu-L	Transport, Inner Membrane	
h[p] + leu-L[p] <=> h[c] + leu-L[c]	Transport, Inner Membrane	(VF_1055)
4mop[c] + glu-L[c] -> akg[c] + leu-L[c]	Valine, Leucine, and Isoleucine	(VF_1084) (
leu-L[e] <=> leu-L[p]	Transport, Outer Membrane Po	(VF_0446)
atp[c] + leu-L[c] + trnaleu[c] -> amp[c] + leutrna[	tRNA Charging	(VF_2558)
gthrd[c] + mthgxl[c] -> lgt-S[c]	Methylglyoxal Metabolism	
atp[c] + h2o[c] + lipavf[c] -> adp[c] + h[c] + pi[c]	Lipopolysaccharide Biosynthes	(VF_0753)
atp[c] + h2o[c] + lipavf[p] -> adp[c] + h[c] + pi[c]	Lipopolysaccharide Biosynthes	(VF_0928) (
h[c] + ocACP[c] -> ACP[c] + octapb[c]	Cofactor and Prosthetic Group	(VF_A0424
4fe4s[c] + 2 amet[c] + h[c] + nad[c] + octapb[c]	Cofactor and Prosthetic Group	(VF_0388 ar
lipoate[e] <=> lipoate[p]	Transport, Outer Membrane Po	(VF_0743)
h[p] + lac-L[p] <=> h[c] + lac-L[c]	Transport, Inner Membrane	(VF_0742)
lac-L[e] <=> lac-L[p]	Transport, Outer Membrane Porin	
lipidXvf[c] + u23gavf[c] -> h[c] + lipidAdsvf[c] + u	Lipopolysaccharide Biosynthes	(VF_1949)
1ddecg3p[p] + h2o[p] -> ddca[p] + glyc3p[p] + h	Glycerophospholipid Metabolis	(VF_A1044
1tdecg3p[p] + h2o[p] -> glyc3p[p] + h[p] + ttdca[	Glycerophospholipid Metabolis	(VF_A1044
1tdec7eg3p[p] + h2o[p] -> glyc3p[p] + h[p] + ttd	Glycerophospholipid Metabolis	(VF_A1044
1hdecg3p[p] + h2o[p] -> glyc3p[p] + h[p] + hdca	Glycerophospholipid Metabolis	(VF_A1044
1hdec9eg3p[p] + h2o[p] -> glyc3p[p] + h[p] + hc	Glycerophospholipid Metabolis	(VF_A1044
1odecg3p[p] + h2o[p] -> glyc3p[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_A1044
1odec11eg3p[p] + h2o[p] -> glyc3p[p] + h[p] + c	Glycerophospholipid Metabolis	(VF_A1044
1agpe120[p] + h2o[p] -> ddca[p] + g3pe[p] + h[	Glycerophospholipid Metabolis	(VF_A1044

1agpe140[p] + h2o[p] -> g3pe[p] + h[p] + ttdca[	Glycerophospholipid Metabolis	(VF_A1044
1agpe141[p] + h2o[p] -> g3pe[p] + h[p] + ttdcea	Glycerophospholipid Metabolis	(VF_A1044
1agpe160[p] + h2o[p] -> g3pe[p] + h[p] + hdca[	Glycerophospholipid Metabolis	(VF_A1044
1agpe161[p] + h2o[p] -> g3pe[p] + h[p] + hdcea	Glycerophospholipid Metabolis	(VF_A1044
1agpe180[p] + h2o[p] -> g3pe[p] + h[p] + ocdca	Glycerophospholipid Metabolis	(VF_A1044
1agpe181[p] + h2o[p] -> g3pe[p] + h[p] + ocdce	Glycerophospholipid Metabolis	(VF_A1044
1agpg120[p] + h2o[p] -> ddca[p] + g3pg[p] + h[	Glycerophospholipid Metabolis	(VF_A1044
1agpg140[p] + h2o[p] -> g3pg[p] + h[p] + ttdca[	Glycerophospholipid Metabolis	(VF_A1044
1agpg141[p] + h2o[p] -> g3pg[p] + h[p] + ttdcea	Glycerophospholipid Metabolis	(VF_A1044
1agpg160[p] + h2o[p] -> g3pg[p] + h[p] + hdca[	Glycerophospholipid Metabolis	(VF_A1044
1agpg161[p] + h2o[p] -> g3pg[p] + h[p] + hdcea	Glycerophospholipid Metabolis	(VF_A1044
1agpg180[p] + h2o[p] -> g3pg[p] + h[p] + ocdca	Glycerophospholipid Metabolis	(VF_A1044
1agpg181[p] + h2o[p] -> g3pg[p] + h[p] + ocdce	Glycerophospholipid Metabolis	(VF_A1044
2ddecg3p[c] + h2o[c] -> ddca[c] + glyc3p[c] + 2	Glycerophospholipid Metabolis	(VF_2481)
2tdecg3p[c] + h2o[c] -> glyc3p[c] + 2 h[c] + ttdc	Glycerophospholipid Metabolis	(VF_2481)
2tdec7eg3p[c] + h2o[c] -> glyc3p[c] + 2 h[c] + tt	Glycerophospholipid Metabolis	(VF_2481)
2hdecg3p[c] + h2o[c] -> glyc3p[c] + 2 h[c] + hd	Glycerophospholipid Metabolis	(VF_2481)
2hdec9eg3p[c] + h2o[c] -> glyc3p[c] + 2 h[c] +	Glycerophospholipid Metabolis	(VF_2481)
2odecg3p[c] + h2o[c] -> glyc3p[c] + 2 h[c] + oc	Glycerophospholipid Metabolis	(VF_2481)
2odec11eg3p[c] + h2o[c] -> glyc3p[c] + 2 h[c] +	Glycerophospholipid Metabolis	(VF_2481)
2agpe120[c] + pg120[c] -> apg120[c] + g3pe[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpe140[c] + pg140[c] -> apg140[c] + g3pe[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpe141[c] + pg141[c] -> apg141[c] + g3pe[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpe160[c] + pg160[c] -> apg160[c] + g3pe[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpe161[c] + pg161[c] -> apg161[c] + g3pe[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpe180[c] + pg180[c] -> apg180[c] + g3pe[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpe181[c] + pg181[c] -> apg181[c] + g3pe[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpg120[c] + pg120[c] -> apg120[c] + g3pg[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpg140[c] + pg140[c] -> apg140[c] + g3pg[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpg141[c] + pg141[c] -> apg141[c] + g3pg[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpg160[c] + pg160[c] -> apg160[c] + g3pg[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpg161[c] + pg161[c] -> apg161[c] + g3pg[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpg180[c] + pg180[c] -> apg180[c] + g3pg[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpg181[c] + pg181[c] -> apg181[c] + g3pg[c]	Glycerophospholipid Metabolis	(VF_2481)
2agpe120[c] + h2o[c] -> ddca[c] + g3pe[c] + h[c	Glycerophospholipid Metabolis	(VF_2481)
2agpe140[c] + h2o[c] -> g3pe[c] + h[c] + ttdca[c	Glycerophospholipid Metabolis	(VF_2481)
2agpe141[c] + h2o[c] -> g3pe[c] + h[c] + ttdcea	Glycerophospholipid Metabolis	(VF_2481)
2agpe160[c] + h2o[c] -> g3pe[c] + h[c] + hdca[c	Glycerophospholipid Metabolis	(VF_2481)
2agpe161[c] + h2o[c] -> g3pe[c] + h[c] + hdcea	Glycerophospholipid Metabolis	(VF_2481)
2agpe180[c] + h2o[c] -> g3pe[c] + h[c] + ocdca[	Glycerophospholipid Metabolis	(VF_2481)
2agpe181[c] + h2o[c] -> g3pe[c] + h[c] + ocdce	Glycerophospholipid Metabolis	(VF_2481)
2agpg120[c] + h2o[c] -> ddca[c] + g3pg[c] + h[c	Glycerophospholipid Metabolis	(VF_2481)
2agpg140[c] + h2o[c] -> g3pg[c] + h[c] + ttdca[c	Glycerophospholipid Metabolis	(VF_2481)
2agpg141[c] + h2o[c] -> g3pg[c] + h[c] + ttdcea	Glycerophospholipid Metabolis	(VF_2481)
2agpg160[c] + h2o[c] -> g3pg[c] + h[c] + hdca[c	Glycerophospholipid Metabolis	(VF_2481)
2agpg161[c] + h2o[c] -> g3pg[c] + h[c] + hdcea	Glycerophospholipid Metabolis	(VF_2481)
2agpg180[c] + h2o[c] -> g3pg[c] + h[c] + ocdca[	Glycerophospholipid Metabolis	(VF_2481)
2agpg181[c] + h2o[c] -> g3pg[c] + h[c] + ocdce	Glycerophospholipid Metabolis	(VF_2481)

ckdo[c] + 2 udpg[c] + adphep-DD[c] + adphep-L	Lipopolysaccharide Biosynthes	(VF_0138 a
atp[c] + h2o[c] + lpsvf[c] -> adp[c] + h[c] + pi[c]	Lipopolysaccharide Biosynthes	(VF_A0424
atp[c] + h2o[c] + lpsvf[p] -> adp[c] + h[c] + pi[c]	Lipopolysaccharide Biosynthes	(VF_0388 a
o2[c] + ddcald[c] + fmnh2[c] -> h2o[c] + ddca [c	Luciferase activity	(VF_A0920
atp[c] + h2o[c] + lys-L[p] -> adp[c] + h[c] + lys-L	Transport, Inner Membrane	(VF_1585 a
lys-L[c] <=> 36dahx[c]	Threonine and Lysine Metaboli	(VF_2239)
h[c] + lys-L[c] -> 15dap[c] + co2[c]	Threonine and Lysine Metaboli	(VF_2057)
lys-L[e] <=> lys-L[p]	Transport, Outer Membrane Porin	
atp[c] + lys-L[c] + trnalys[c] -> amp[c] + lystrna[	tRNA Charging	(VF_0453)
lyx-L[e] <=> lyx-L[p]	Transport, Outer Membrane Porin	
mnl1p[c] + nad[c] <=> f6p[c] + h[c] + nadh[c]	Alternate Carbon Metabolism	(VF_A0062
macgam26p[c] + h2o[c] -> acgam6p[c] + gam[c	Alternate Carbon Metabolism	(VF_0605)
h[c] + malACP[c] -> acACP[c] + co2[c]	Membrane Lipid Metabolism	(VF_1700)
amet[c] + malcoa[c] -> ahcys[c] + malcoame[c]	Cofactor and Prosthetic Group	(VF_A0746
mal-D[e] <=> mal-D[p]	Transport, Outer Membrane Porin	
accoa[c] + glx[c] + h2o[c] -> coa[c] + h[c] + mal-	Anaplerotic Reactions	(VF_1973)
3 h[p] + mal-L[p] -> 3 h[c] + mal-L[c]	Transport, Inner Membrane	(VF_2064)
atp[c] + h2o[c] + malt[p] -> adp[c] + h[c] + malt[	Transport, Inner Membrane	(VF_A0797
accoa[c] + malt[c] <=> acmalt[c] + coa[c]	Alternate Carbon Metabolism	(VF_1337)
mal-L[e] <=> mal-L[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + malthx[p] -> adp[c] + h[c] + ma	Transport, Inner Membrane	(VF_A0797
malthx[e] -> malthx[p]	Transport, Outer Membrane	
atp[c] + h2o[c] + maltpt[p] -> adp[c] + h[c] + mal	Transport, Inner Membrane	(VF_A0797
pep[c] + malt[p] -> malt6p[c] + pyr[c]	Transport, Inner Membrane	(VF_1719 a
maltpt[e] -> maltpt[p]	Transport, Outer Membrane	
malt[e] -> malt[p]	Transport, Outer Membrane	
atp[c] + h2o[c] + malttr[p] -> adp[c] + h[c] + mal	Transport, Inner Membrane	(VF_A0797
malttr[e] -> malttr[p]	Transport, Outer Membrane	
atp[c] + h2o[c] + maltttr[p] -> adp[c] + h[c] + ma	Transport, Inner Membrane	(VF_A0797
maltttr[e] -> maltttr[p]	Transport, Outer Membrane	
man6p[c] <=> f6p[c]	Alternate Carbon Metabolism	(VF_A0710
2 pi[c] + man6p[p] -> man6p[c] + 2 pi[p]	Transport, Inner Membrane	(VF_A0042
man6p[e] <=> man6p[p]	Transport, Outer Membrane Porin	
manglyc[e] <=> manglyc[p]	Transport, Outer Membrane Porin	
pep[c] + man[p] -> man6p[c] + pyr[c]	Transport, Inner Membrane	(VF_1894 a
man[e] <=> man[p]	Transport, Outer Membrane Porin	
2mcit[c] -> 2mcacn[c] + h2o[c]	Alternate Carbon Metabolism	
micit[c] <=> pyr[c] + succ[c]	Alternate Carbon Metabolism	
h2o[c] + oaa[c] + ppcoa[c] -> 2mcit[c] + coa[c] +	Alternate Carbon Metabolism	
ACP[c] + malcoa[c] <=> coa[c] + malACP[c]	Membrane Lipid Metabolism	(VF_1739 a
cyan[c] + mercppyr[c] -> h[c] + pyr[c] + tcynt[c]	Cysteine Metabolism	(VF_1387)
murein5p5p[p] -> ala-D[p] + murein5px4p[p]	Murein Biosynthesis	(VF_2207)
murein5p5p[p] -> alaala[p] + murein5px3p[p]	Murein Biosynthesis	(VF_2162)
murein5p5p5p[p] -> 2 ala-D[p] + murein5px4px	Murein Biosynthesis	(VF_2207)
h2o[p] + murein5px4p[p] -> ala-D[p] + murein4	Murein Biosynthesis	(VF_0745)
h2o[p] + murein5px4px4p[p] -> ala-D[p] + mure	Murein Biosynthesis	(VF_0745)
h2o[p] + murein5p5p[p] -> ala-D[p] + murein5p	Murein Biosynthesis	(VF_0745)
h2o[p] + murein5p4p[p] -> ala-D[p] + murein4p	Murein Biosynthesis	(VF_0745)

h2o[p] + murein5p3p[p] -> ala-D[p] + murein4p3	Murein Biosynthesis	(VF_0745)
h2o[p] + murein4px4p[p] -> murein4p4p[p]	Murein Recycling	(VF_0474)
h2o[p] + murein3px4p[p] -> murein4p3p[p]	Murein Recycling	(VF_0474)
h2o[p] + murein5px4p[p] -> murein5p4p[p]	Murein Recycling	(VF_0474)
h2o[p] + murein4px4px4p[p] -> murein4px4p4p	Murein Recycling	(VF_0474)
mal-L[c] + nad[c] <=> h[c] + nadh[c] + oaa[c]	Citric Acid Cycle	(VF_0276)
mal-L[c] + nadp[c] <=> h[c] + nadph[c] + oaa[c]	Pyruvate Metabolism	(VF_1252)
mal-L[c] + nad[c] -> co2[c] + nadh[c] + pyr[c]	Anaplerotic Reactions	(VF_1558)
mal-L[c] + nadp[c] -> co2[c] + nadph[c] + pyr[c]	Anaplerotic Reactions	(VF_2272)
2mecdp[c] + 2 flxr[c] + h[c] -> 2 flxso[c] + h2mb	Cofactor and Prosthetic Group	(VF_0629 a
2p4c2me[c] -> 2mecdp[c] + cmp[c]	Cofactor and Prosthetic Group	(VF_2072)
melib[e] <=> melib[p]	Transport, Outer Membrane Porin	
meoh[e] <=> meoh[p]	Transport, Outer Membrane Porin	
meoh[p] <=> meoh[c]	Transport, Inner Membrane	
2me4p[c] + ctp[c] + h[c] -> 4c2me[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_2073)
atp[c] + h2o[c] + met-L[p] -> adp[c] + h[c] + met	Transport, Inner Membrane	(VF_0684 a
atp[c] + h2o[c] + met-L[c] -> amet[c] + pi[c] + pp	Methionine Metabolism	(VF_0439)
atp[c] + h2o[c] + met-D[p] -> adp[c] + h[c] + me	Transport, Inner Membrane	(VF_0684 a
met-D[e] <=> met-D[p]	Transport, Outer Membrane Porin	
5mthf[c] + hcys-L[c] -> h[c] + met-L[c] + thf[c]	Methionine Metabolism	(VF_0337)
metsox-S-L[e] <=> metsox-S-L[p]	Transport, Outer Membrane Porin	
metsox-R-L[e] <=> metsox-R-L[p]	Transport, Outer Membrane Porin	
metsox-S-L[c] + trdrd[c] -> h2o[c] + met-L[c] + t	Methionine Metabolism	(VF_0331 a
metsox-R-L[c] + trdrd[c] -> h2o[c] + met-L[c] + t	Methionine Metabolism	(VF_0909 a
met-L[e] <=> met-L[p]	Transport, Outer Membrane Porin	
atp[c] + met-L[c] + trnamet[c] -> amp[c] + mettr	tRNA Charging	(VF_1754)
2 h[c] + mg2[p] <=> mg2[c] + 2 h[p]	Inorganic Ion Transport and Metabolism	
mg2[e] <=> mg2[p]	Transport, Outer Membrane Porin	
mg2[p] -> mg2[c]	Inorganic Ion Transport and Metabolism	
atp[c] + h2o[c] + mg2[p] -> adp[c] + h[c] + mg2[	Inorganic Ion Transport and Me	(VF_1803)
dhap[c] -> mthgxl[c] + pi[c]	Methylglyoxal Metabolism	(VF_1621)
h2o[c] + mi1p-D[c] -> inost[c] + pi[c]	Cell Envelope Biosynthesis	(VF_0614)
2mcacn[c] + h2o[c] <=> micit[c]	Alternate Carbon Metabolism	(VF_2158)
mincyc[e] <=> mincyc[p]	Transport, Outer Membrane Porin	
h2o[c] + malttr[c] -> glc-D[c] + malt[c]	Alternate Carbon Metabolism	(VF_2049)
h2o[c] + maltttr[c] -> glc-D[c] + malttr[c]	Alternate Carbon Metabolism	(VF_2049)
h2o[c] + maltpt[c] -> glc-D[c] + maltttr[c]	Alternate Carbon Metabolism	(VF_2049)
h2o[c] + malthx[c] -> glc-D[c] + maltpt[c]	Alternate Carbon Metabolism	(VF_2049)
h2o[c] + malthp[c] -> glc-D[c] + malthx[c]	Alternate Carbon Metabolism	(VF_2049)
murein4p4p[p] -> 2 anhgm4p[p]	Murein Recycling	(VF_0651)
murein4p3p[p] -> anhgm3p[p] + anhgm4p[p]	Murein Recycling	(VF_0651)
murein3p3p[p] -> 2 anhgm3p[p]	Murein Recycling	(VF_0420)
murein4px4p4p[p] -> anhgm4p[p] + murein4px	Murein Recycling	(VF_1702)
maltpt[c] + pi[c] <=> g1p[c] + maltttr[c]	Alternate Carbon Metabolism	(VF_A0810
malthx[c] + pi[c] <=> g1p[c] + maltpt[c]	Alternate Carbon Metabolism	(VF_A0810
malthp[c] + pi[c] <=> g1p[c] + malthx[c]	Alternate Carbon Metabolism	(VF_A0810
mmet[e] <=> mmet[p]	Transport, Outer Membrane Porin	
mn2[c] + h[p] -> h[c] + mn2[p]	Inorganic Ion Transport and Me	(VF_2341)

mn2[p] -> mn2[c]	Inorganic Ion Transport and Metabolism	
pep[c] + mnl[p] -> mnl1p[c] + pyr[c]	Transport, Inner Membrane	(VF_1894 a
mnl[e] <=> mnl[p]	Transport, Outer Membrane Porin	
mn2[e] <=> mn2[p]	Transport, Outer Membrane Porin	
iscssh[c] + moadamp[c] + nadh[c] -> amp[c] + is	Cofactor and Prosthetic Group	(VF_0617 a
atp[c] + h2o[c] + mobd[p] -> adp[c] + h[c] + mob	Inorganic Ion Transport and Me	(VF_A0290
mobd[e] <=> mobd[p]	Transport, Outer Membrane Porin	
2 h[c] + mobd[c] + mptamp[c] -> amp[c] + cu2[c	Cofactor and Prosthetic Group	(VF_1608)
gtp[c] + h[c] + moco[c] -> mocogdp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_1405)
3mob[c] + h2o[c] + mlthf[c] -> 2dhp[c] + thf[c]	Cofactor and Prosthetic Group	(VF_2169)
mal-L[c] + o2[c] <=> h2o2[c] + oaa[c]	Citric Acid Cycle	
atp[c] + h[c] + mpt[c] -> mptamp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_A0565
2 uaagmda[c] -> 2 h[c] + 2 udcpdp[c] + murein5	Murein Biosynthesis	(VF_0465 a
uaagmda[c] + murein5p5p[p] -> h[c] + udcpdp[c	Murein Biosynthesis	(VF_0465 a
cpmp[c] + cu2[c] + 2 moadcosh[c] -> 5 h[c] + 2	Cofactor and Prosthetic Group	(VF_0942 a
atp[c] + h[c] + moadcoo[c] -> moadamp[c] + ppi	Cofactor and Prosthetic Group	(VF_1609)
mso3[e] <=> mso3[p]	Transport, Outer Membrane Porin	
5mta[c] + h2o[c] -> 5mtr[c] + ade[c]	Arginine and Proline Metabolis	(VF_2128)
h2o[c] + methf[c] <=> 10fthf[c] + h[c]	Folate Metabolism	(VF_1770)
mlthf[c] + nadp[c] <=> methf[c] + nadph[c]	Folate Metabolism	(VF_1770)
2 h[c] + mlthf[c] + nadh[c] -> 5mthf[c] + nad[c]	Folate Metabolism	(VF_2309)
h2o[c] + mdhdhf[c] -> mththf[c]	Methionine Metabolism	
n2o[e] <=> n2o[p]	Transport, Outer Membrane Porin	
acg5sa[c] + h2o[c] -> ac[c] + glu5sa[c]	Arginine and Proline Metabolis	(VF_2307)
nac[e] <=> nac[p]	Transport, Outer Membrane Porin	
h2o[c] + nad[c] -> amp[c] + 2 h[c] + nmn[c]	Cofactor and Prosthetic Group	(VF_2403)
h[c] + mqn8[c] + nadh[c] -> mql8[c] + nad[c]	Oxidative Phosphorylation	(VF_1143)
h[c] + nadh[c] + q8[c] -> nad[c] + q8h2[c]	Oxidative Phosphorylation	(VF_1143)
2dmmq8[c] + h[c] + nadh[c] -> 2dmmql8[c] + na	Oxidative Phosphorylation	(VF_1143)
atp[c] + nad[c] -> adp[c] + h[c] + nadp[c]	Cofactor and Prosthetic Group	(VF_1997)
atp[c] + dnad[c] + nh4[c] -> amp[c] + h[c] + nad	Cofactor and Prosthetic Group	(VF_A0602
nad[c] + nadph[c] -> nadh[c] + nadp[c]	Oxidative Phosphorylation	(VF_2439)
2 na1[c] + 3 h[p] -> 3 h[c] + 2 na1[p]	Inorganic Ion Transport and Me	(VF_1634)
na1[c] + 2 h[p] -> 2 h[c] + na1[p]	Inorganic Ion Transport and Me	(VF_0887)
na1[e] <=> na1[p]	Transport, Outer Membrane Porin	
atp[c] + gdp[c] <=> adp[c] + gtp[c]	Nucleotide Salvage Pathway	(VF_0793)
atp[c] + udp[c] <=> adp[c] + utp[c]	Nucleotide Salvage Pathway	(VF_0793)
atp[c] + cdp[c] <=> adp[c] + ctp[c]	Nucleotide Salvage Pathway	(VF_0625)
atp[c] + dtdp[c] <=> adp[c] + dttp[c]	Nucleotide Salvage Pathway	(VF_0793)
atp[c] + dgdp[c] <=> adp[c] + dgtp[c]	Nucleotide Salvage Pathway	(VF_0793)
atp[c] + dudp[c] <=> adp[c] + dutp[c]	Nucleotide Salvage Pathway	(VF_0625)
atp[c] + dcdp[c] <=> adp[c] + dctp[c]	Nucleotide Salvage Pathway	(VF_0793)
atp[c] + dadp[c] <=> adp[c] + datp[c]	Nucleotide Salvage Pathway	(VF_0793)
nh4[e] <=> nh4[p]	Transport, Outer Membrane Porin	
nh4[p] <=> nh4[c]	Inorganic Ion Transport and Me	(VF_2152)
h[c] + nadh[c] + 2 no[c] -> h2o[c] + n2o[c] + nac	Nitrogen Metabolism	(VF_1781 a
atp[c] + h2o[c] + ni2[c] -> adp[c] + h[c] + pi[c] +	Inorganic Ion Transport and Metabolism	
ni2[c] + h[p] -> h[c] + ni2[p]	Inorganic Ion Transport and Me	(VF_2341)

ni2[e] <=> ni2[p]	Transport, Outer Membrane Porin	
ni2[p] -> ni2[c]	Inorganic Ion Transport and Metabolism	
atp[c] + h2o[c] + ni2[p] -> adp[c] + h[c] + ni2[c] -	Inorganic Ion Transport and Me	(VF_1803)
atp[c] + h[c] + nmn[c] -> nad[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_A0601
nmn[p] -> nmn[c]	Transport, Inner Membrane	(VF_A0529
nmn[e] <=> nmn[p]	Transport, Outer Membrane Porin	
atp[c] + h[c] + nicrnt[c] <=> dnad[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_A0601
2 h[c] + prpp[c] + quln[c] -> co2[c] + nicrnt[c] + p	Cofactor and Prosthetic Group	(VF_2184)
no2[e] <=> no2[p]	Transport, Outer Membrane Porin	
mql8[c] + no3[p] -> mqn8[c] + h2o[p] + no2[p]	Nitrogen Metabolism	(VF_1903 a
no3[e] <=> no3[p]	Transport, Outer Membrane Porin	
nadh[c] + 2 no[c] + 2 o2[c] -> h[c] + nad[c] + 2 r	Nitrogen Metabolism	(VF_2316)
nadph[c] + 2 no[c] + 2 o2[c] -> h[c] + nadp[c] +	Nitrogen Metabolism	(VF_2316)
no[e] <=> no[p]	Transport, Outer Membrane Porin	
dump[c] + h2o[c] -> duri[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
h2o[c] + xmp[c] -> pi[c] + xtsn[c]	Nucleotide Salvage Pathway	(VF_2070)
h2o[p] + xmp[p] -> pi[p] + xtsn[p]	Nucleotide Salvage Pathway	(VF_0778)
h2o[c] + imp[c] -> ins[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
h2o[p] + imp[p] -> ins[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
dimp[c] + h2o[c] -> din[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
dimp[p] + h2o[p] -> din[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
dump[p] + h2o[p] -> duri[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
h2o[c] + ump[c] -> pi[c] + uri[c]	Nucleotide Salvage Pathway	(VF_2070)
h2o[p] + ump[p] -> pi[p] + uri[p]	Nucleotide Salvage Pathway	(VF_0778)
dcmp[c] + h2o[c] -> dcyt[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
dcmp[p] + h2o[p] -> dcyt[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
cmp[c] + h2o[c] -> cytd[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
cmp[p] + h2o[p] -> cytd[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
dtmp[c] + h2o[c] -> pi[c] + thymd[c]	Nucleotide Salvage Pathway	(VF_2070)
dtmp[p] + h2o[p] -> pi[p] + thymd[p]	Nucleotide Salvage Pathway	(VF_0778)
damp[c] + h2o[c] -> dad-2[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
damp[p] + h2o[p] -> dad-2[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
amp[c] + h2o[c] -> adn[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
amp[p] + h2o[p] -> adn[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
dgmp[c] + h2o[c] -> dgsn[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
dgmp[p] + h2o[p] -> dgsn[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
gmp[c] + h2o[c] -> gsn[c] + pi[c]	Nucleotide Salvage Pathway	(VF_2070)
gmp[p] + h2o[p] -> gsn[p] + pi[p]	Nucleotide Salvage Pathway	(VF_0778)
h2o[c] + itp[c] -> h[c] + idp[c] + pi[c]	Nucleotide Salvage Pathway	(VF_0425)
ditp[c] + h2o[c] -> didp[c] + h[c] + pi[c]	Nucleotide Salvage Pathway	(VF_0425)
h2o[c] + xtp[c] -> h[c] + pi[c] + xdp[c]	Nucleotide Salvage Pathway	(VF_0425)
dgtp[c] + h2o[c] -> dgmp[c] + h[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_2192)
ditp[c] + h2o[c] -> dimp[c] + h[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_0425)
h2o[c] + xtp[c] -> h[c] + ppi[c] + xmp[c]	Nucleotide Salvage Pathway	(VF_0425)
gtp[c] + h2o[c] -> gmp[c] + h[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_2192)
dctp[c] + h2o[c] -> dcmp[c] + h[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_2078)
ctp[c] + h2o[c] -> cmp[c] + h[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_2078)
datp[c] + h2o[c] -> damp[c] + h[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_2078)

atp[c] + h2o[c] -> amp[c] + h[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_2078)
dttp[c] + h2o[c] -> dtmp[c] + h[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_2078)
h2o[c] + utp[c] -> h[c] + ppi[c] + ump[c]	Nucleotide Salvage Pathway	(VF_2078)
h2o[c] + itp[c] -> h[c] + imp[c] + ppi[c]	Nucleotide Salvage Pathway	(VF_0425)
dgtp[c] + h2o[c] -> dgsn[c] + pppi[c]	Nucleotide Salvage Pathway	(VF_1682)
gtp[c] + h2o[c] -> gsn[c] + pppi[c]	Nucleotide Salvage Pathway	(VF_1682)
5 h[c] + 3 nadh[c] + no2[c] -> 2 h2o[c] + 3 nad[c	Oxidative Phosphorylation	(VF_0775 a
3 q8h2[c] + 2 h[p] + no2[p] -> 3 q8[c] + 2 h2o[p]	Nitrogen Metabolism	(VF_1551 a
3 mql8[c] + 2 h[p] + no2[p] -> 3 mqn8[c] + 2 h2	Nitrogen Metabolism	(VF_1551 a
o2s[e] <=> o2s[p]	Transport, Outer Membrane Porin	
o2[e] <=> o2[p]	Transport, Outer Membrane Porin	
o2[p] <=> o2[c]	Inorganic Ion Transport and Metabolism	
h[c] + oaa[c] -> co2[c] + pyr[c]	Pyruvate Metabolism	(VF_0539 a
2obut[c] + coa[c] -> formate[c] + ppcoa[c]	Alternate Carbon Metabolism	(VF_1590 a
cbp[c] + orn[c] <=> citr-L[c] + h[c] + pi[c]	Arginine and Proline Metabolis	(VF_0407)
ocdca[e] -> ocdca[p]	Transport, Outer Membrane	(VF_1543)
ocdcea[e] -> ocdcea[p]	Transport, Outer Membrane	(VF_1543)
octa[e] <=> octa[p]	Transport, Outer Membrane Porin	
frdp[c] + 5 ipdp[c] -> octdp[c] + 5 ppi[c]	Cofactor and Prosthetic Group	(VF_0277)
hgmeACP[c] -> egmeACP[c] + h2o[c]	Cofactor and Prosthetic Group	(VF_1951)
h[c] + nadph[c] + ogmeACP[c] -> hgmeACP[c]	Cofactor and Prosthetic Group	(VF_1740)
h[c] + malACP[c] + malcoame[c] -> co2[c] + co	Cofactor and Prosthetic Group	(VF_1742)
glu-L[c] + ohpb[c] <=> akg[c] + phthr[c]	Cofactor and Prosthetic Group	(VF_0899)
2ohph[c] + amet[c] -> 2omph[c] + ahcys[c] + h[	Cofactor and Prosthetic Group	(VF_1203)
2ombzl[c] + amet[c] -> 2ommbl[c] + ahcys[c] +	Cofactor and Prosthetic Group	(VF_0046)
3c4mop[c] + h[c] -> 4mop[c] + co2[c]	Valine, Leucine, and Isoleucine Metabolism	
2ommbl[c] + 0.5 o2[c] -> 2omhmbl[c]	Cofactor and Prosthetic Group	(VF_0760)
h[c] + orot5p[c] -> co2[c] + ump[c]	Purine and Pyrimidine Biosynt	(VF_1755)
2omph[c] + 0.5 o2[c] -> 2ombzl[c]	Cofactor and Prosthetic Group	(VF_2101)
3ophb[c] + h[c] -> 2oph[c] + co2[c]	Cofactor and Prosthetic Group	(VF_0060 a
2oph[c] + 0.5 o2[c] -> 2ohph[c]	Cofactor and Prosthetic Group	(VF_0048)
2oph[c] + 2 atp[c] + 3 h2o[c] + nad[c] -> 2ohph[	Cofactor and Prosthetic Group Biosynthesis	
hpmeACP[c] -> epmeACP[c] + h2o[c]	Cofactor and Prosthetic Group	(VF_1951)
h[c] + nadph[c] + opmeACP[c] -> hpmeACP[c]	Cofactor and Prosthetic Group	(VF_1740)
gmeACP[c] + h[c] + malACP[c] -> ACP[c] + co2	Cofactor and Prosthetic Group	(VF_1700)
atp[c] + h2o[c] + orn[p] -> adp[c] + h[c] + orn[c]	Transport, Inner Membrane	(VF_1585 a
orn[e] <=> orn[p]	Transport, Outer Membrane Porin	
orot[e] <=> orot[p]	Transport, Outer Membrane Porin	
orot5p[c] + ppi[c] <=> orot[c] + prpp[c]	Purine and Pyrimidine Biosynt	(VF_0112)
1pyr5c[c] + 2 h2o[c] + nad[c] -> glu-L[c] + h[c] +	Arginine and Proline Metabolis	(VF_A0830
1pyr5c[c] + 2 h[c] + nadph[c] -> nadp[c] + pro-L	Arginine and Proline Metabolis	(VF_0429)
atp[c] + h2o[c] + pa120[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pa140[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pa141[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pa160[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pa161[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pa180[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pa181[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424

pacald[e] <=> pacald[p]	Transport, Outer Membrane Porin	
ala-B[c] + atp[c] + pant-R[c] -> amp[c] + h[c] + p	Cofactor and Prosthetic Group	(VF_2170)
h2o[c] + pa120[c] -> 12dgr120[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pa120[p] -> 12dgr120[p] + pi[p]	Glycerophospholipid Metabolis	(VF_1544)
h2o[c] + pa140[c] -> 12dgr140[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pa140[p] -> 12dgr140[p] + pi[p]	Glycerophospholipid Metabolis	(VF_1544)
h2o[c] + pa141[c] -> 12dgr141[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pa141[p] -> 12dgr141[p] + pi[p]	Glycerophospholipid Metabolis	(VF_1544)
h2o[c] + pa160[c] -> 12dgr160[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pa160[p] -> 12dgr160[p] + pi[p]	Glycerophospholipid Metabolis	(VF_1544)
h2o[c] + pa161[c] -> 12dgr161[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pa161[p] -> 12dgr161[p] + pi[p]	Glycerophospholipid Metabolis	(VF_1544)
h2o[c] + pa180[c] -> 12dgr180[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pa180[p] -> 12dgr180[p] + pi[p]	Glycerophospholipid Metabolis	(VF_1544)
h2o[c] + pa181[c] -> 12dgr181[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pa181[p] -> 12dgr181[p] + pi[p]	Glycerophospholipid Metabolis	(VF_1544)
udcpp[c] + ugmda[c] -> uagmda[c] + ump[c]	Cell Envelope Biosynthesis	(VF_2204)
paps[c] + trdrd[c] -> 2 h[c] + pap[c] + so3[c] + tr	Cysteine Metabolism	(VF_0312 a
grxrd[c] + paps[c] -> grxox[c] + 2 h[c] + pap[c] +	Cysteine Metabolism	(VF_0312 a
coa[c] + nad[c] + pyr[c] -> accoa[c] + co2[c] + n	Glycolysis/Gluconeogenesis	(VF_2178 a
dhlam[c] + nad[c] -> h[c] + lpam[c] + nadh[c]	Unassigned	(VF_2301)
o2[c] + pdx5p[c] -> h2o2[c] + pydx5p[c]	Cofactor and Prosthetic Group	(VF_A1161
dxyl5p[c] + nad[c] + phthr[c] -> co2[c] + h[c] + 2	Cofactor and Prosthetic Group	(VF_0287 a
atp[c] + h2o[c] + pe120[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pe140[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pe141[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pe160[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pe161[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pe180[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pe181[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
peamn[e] <=> peamn[p]	Transport, Outer Membrane Porin	
4per[c] + nad[c] <=> h[c] + nadh[c] + ohpb[c]	Cofactor and Prosthetic Group	(VF_1699)
atp[c] + f6p[c] -> adp[c] + fdp[c] + h[c]	Glycolysis/Gluconeogenesis	(VF_2340)
atp[c] + tag6p-D[c] -> adp[c] + h[c] + tagdp-D[c]	Alternate Carbon Metabolism	(VF_2340)
atp[c] + s7p[c] -> adp[c] + h[c] + s17bp[c]	Pentose Phosphate Pathway	(VF_2340)
coa[c] + pyr[c] -> accoa[c] + formate[c]	Pyruvate Metabolism	(VF_1590 a
atp[c] + h2o[c] + pg120[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pg140[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pg141[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pg160[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pg161[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pg180[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pg181[c] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_A0424
gam1p[c] <=> gam6p[c]	Cell Envelope Biosynthesis	(VF_0481)
3pg[c] + nad[c] -> 3php[c] + h[c] + nadh[c]	Glycine and Serine Metabolism	(VF_2106)
g6p[c] <=> f6p[c]	Glycolysis/Gluconeogenesis	(VF_0304)
3pg[c] + atp[c] <=> 13dpg[c] + adp[c]	Glycolysis/Gluconeogenesis	(VF_0442)
6pgl[c] + h2o[c] -> 6pgc[c] + h[c]	Pentose Phosphate Pathway	(VF_A0469

2pglyc[c] + h2o[c] -> glyclt[c] + pi[c]	Alternate Carbon Metabolism	(VF_2287)
2pg[c] <=> 3pg[c]	Glycolysis/Gluconeogenesis	(VF_0202)
g1p[c] <=> g6p[c]	Alternate Carbon Metabolism	(VF_1056)
atp[c] + h2o[c] + pgp120[c] -> adp[c] + h[c] + pi[	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pgp140[c] -> adp[c] + h[c] + pi[	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pgp141[c] -> adp[c] + h[c] + pi[	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pgp160[c] -> adp[c] + h[c] + pi[	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pgp161[c] -> adp[c] + h[c] + pi[	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pgp180[c] -> adp[c] + h[c] + pi[	Transport, Inner Membrane	(VF_A0424
atp[c] + h2o[c] + pgp181[c] -> adp[c] + h[c] + pi[	Transport, Inner Membrane	(VF_A0424
h2o[c] + pgp120[c] -> pg120[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pgp120[p] -> pg120[p] + pi[p]	Glycerophospholipid Metabolis	(VF_0706)
h2o[c] + pgp140[c] -> pg140[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pgp140[p] -> pg140[p] + pi[p]	Glycerophospholipid Metabolis	(VF_0706)
h2o[c] + pgp141[c] -> pg141[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pgp141[p] -> pg141[p] + pi[p]	Glycerophospholipid Metabolis	(VF_0706)
h2o[c] + pgp160[c] -> pg160[c] + pi[c]	Glycerophospholipid Metabolis	(VF_0706)
h2o[p] + pgp160[p] -> pg160[p] + pi[p]	Glycerophospholipid Metabolis	(VF_0706)
h2o[c] + pgp161[c] -> pg161[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pgp161[p] -> pg161[p] + pi[p]	Glycerophospholipid Metabolis	(VF_0706)
h2o[c] + pgp180[c] -> pg180[c] + pi[c]	Glycerophospholipid Metabolis	(VF_0706)
h2o[p] + pgp180[p] -> pg180[p] + pi[p]	Glycerophospholipid Metabolis	(VF_0706)
h2o[c] + pgp181[c] -> pg181[c] + pi[c]	Glycerophospholipid Metabolis	(VF_1544)
h2o[p] + pgp181[p] -> pg181[p] + pi[p]	Glycerophospholipid Metabolis	(VF_0706)
cdpdddecg[c] + glyc3p[c] -> cmp[c] + h[c] + pgp	Glycerophospholipid Metabolis	(VF_1625)
cdpdtdecg[c] + glyc3p[c] -> cmp[c] + h[c] + pgp	Glycerophospholipid Metabolis	(VF_1625)
cdpdtdec7eg[c] + glyc3p[c] -> cmp[c] + h[c] + p	Glycerophospholipid Metabolis	(VF_1625)
cdpdhdecg[c] + glyc3p[c] -> cmp[c] + h[c] + pgp	Glycerophospholipid Metabolis	(VF_1625)
cdpdhdec9eg[c] + glyc3p[c] -> cmp[c] + h[c] + p	Glycerophospholipid Metabolis	(VF_1625)
cdpdodecg[c] + glyc3p[c] -> cmp[c] + h[c] + pgp	Glycerophospholipid Metabolis	(VF_1625)
cdpdodec11eg[c] + glyc3p[c] -> cmp[c] + h[c] +	Glycerophospholipid Metabolis	(VF_1625)
atp[c] + h2o[c] + pheme[c] -> adp[c] + h[c] + pi[	Transport, Inner Membrane	(VF_1820 a
h[p] + phe-L[p] <=> h[c] + phe-L[c]	Transport, Inner Membrane	
akg[c] + phe-L[c] <=> glu-L[c] + phpyr[c]	Tyrosine, Tryptophan, and Phe	(VF_1673)
phe-L[e] <=> phe-L[p]	Transport, Outer Membrane Porin	
atp[c] + phe-L[c] + trnaphe[c] -> amp[c] + phetr	tRNA Charging	(VF_1235 a
h[p] + pi[p] <=> h[c] + pi[c]	Inorganic Ion Transport and Me	(VF_2240)
pi[e] <=> pi[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + pi[p] -> adp[c] + h[c] + 2 pi[c]	Inorganic Ion Transport and Me	(VF_1610 a
h2o[p] + pa120[p] -> 2ddecg3p[p] + ddca[p]	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa140[p] -> 2tdecg3p[p] + ttdca[p]	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa141[p] -> 2tdec7eg3p[p] + ttdcea[p]	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa160[p] -> 2hdecg3p[p] + hdca[p]	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa161[p] -> 2hdec9eg3p[p] + hdcea[p]	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa180[p] -> 2odecg3p[p] + ocdca[p]	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa181[p] -> 2odec11eg3p[p] + ocdcea	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe120[p] -> 2agpe120[p] + ddca[p] + h	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe140[p] -> 2agpe140[p] + h[p] + ttdca	Glycerophospholipid Metabolis	(VF_1556)

h2o[p] + pe141[p] -> 2agpe141[p] + h[p] + ttdce	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe160[p] -> 2agpe160[p] + h[p] + hdca	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe161[p] -> 2agpe161[p] + h[p] + hdce	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe180[p] -> 2agpe180[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe181[p] -> 2agpe181[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg120[p] -> 2agpg120[p] + ddca[p] + h	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg140[p] -> 2agpg140[p] + h[p] + ttdca	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg141[p] -> 2agpg141[p] + h[p] + ttdce	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg160[p] -> 2agpg160[p] + h[p] + hdca	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg161[p] -> 2agpg161[p] + h[p] + hdce	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg180[p] -> 2agpg180[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg181[p] -> 2agpg181[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa120[p] -> 1ddecg3p[p] + ddca[p] + h	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa140[p] -> 1tdecg3p[p] + h[p] + ttdca[	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa141[p] -> 1tdec7eg3p[p] + h[p] + ttd	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa160[p] -> 1hdecg3p[p] + h[p] + hdca	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa161[p] -> 1hdec9eg3p[p] + h[p] + hd	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa180[p] -> 1odecg3p[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pa181[p] -> 1odec11eg3p[p] + h[p] + o	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe120[p] -> 1agpe120[p] + ddca[p] + h	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe140[p] -> 1agpe140[p] + h[p] + ttdca	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe141[p] -> 1agpe141[p] + h[p] + ttdce	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe160[p] -> 1agpe160[p] + h[p] + hdca	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe161[p] -> 1agpe161[p] + h[p] + hdce	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe180[p] -> 1agpe180[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pe181[p] -> 1agpe181[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg120[p] -> 1agpg120[p] + ddca[p] + h	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg140[p] -> 1agpg140[p] + h[p] + ttdca	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg141[p] -> 1agpg141[p] + h[p] + ttdce	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg160[p] -> 1agpg160[p] + h[p] + hdca	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg161[p] -> 1agpg161[p] + h[p] + hdce	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg180[p] -> 1agpg180[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
h2o[p] + pg181[p] -> 1agpg181[p] + h[p] + ocdc	Glycerophospholipid Metabolis	(VF_1556)
man1p[c] <=> man6p[c]	Alternate Carbon Metabolism	(VF_1056)
5aprbu[c] + h2o[c] -> 4r5au[c] + pi[c]	Cofactor and Prosthetic Group Biosynthesis	
h2o[c] + pmeACP[c] -> meoh[c] + pimACP[c]	Cofactor and Prosthetic Group	(VF_0118)
4ampm[c] + atp[c] -> 2mahmp[c] + adp[c]	Cofactor and Prosthetic Group	(VF_A0316
atp[c] + pnto-R[c] -> 4ppan[c] + adp[c] + h[c]	Cofactor and Prosthetic Group	(VF_2424)
pnto-R[e] <=> pnto-R[p]	Transport, Outer Membrane Porin	
h2o[c] + ppi[c] -> h[c] + 2 pi[c]	Anaplerotic Reactions	(VF_A0421
h2o[c] + pppi[c] -> h[c] + pi[c] + ppi[c]	Anaplerotic Reactions	(VF_A0421
ppal[e] <=> ppal[p]	Transport, Outer Membrane Porin	
na1[p] + ppa[p] -> na1[c] + ppa[c]	Transport, Inner Membrane	(VF_A0829
ppa[e] <=> ppa[p]	Transport, Outer Membrane Porin	
2 5aop[c] -> h[c] + 2 h2o[c] + ppbng[c]	Cofactor and Prosthetic Group	(VF_0053)
co2[c] + h2o[c] + pep[c] -> h[c] + oaa[c] + pi[c]	Anaplerotic Reactions	(VF_2308)
4ppcys[c] + h[c] -> co2[c] + pan4p[c]	Cofactor and Prosthetic Group	(VF_0125)
atp[c] + oaa[c] -> adp[c] + co2[c] + pep[c]	Anaplerotic Reactions	(VF_2478)

h2o[c] + ppgpp[c] -> gdp[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0104)
r1p[c] <=> r5p[c]	Alternate Carbon Metabolism	(VF_0506)
2dr1p[c] <=> 2dr5p[c]	Alternate Carbon Metabolism	(VF_0506)
4ppan[c] + ctp[c] + cys-L[c] -> 4ppcys[c] + cmp[	Cofactor and Prosthetic Group	(VF_0125)
nad[c] + pphn[c] -> 34hpp[c] + co2[c] + nadh[c]	Tyrosine, Tryptophan, and Phe	(VF_0554)
h[c] + pphn[c] -> co2[c] + h2o[c] + phpyr[c]	Tyrosine, Tryptophan, and Phe	(VF_0561)
1.5 o2[c] + pppg9[c] -> 3 h2o[c] + ppp9[c]	Cofactor and Prosthetic Group	(VF_0028)
3 fum[c] + pppg9[c] -> ppp9[c] + 3 succ[c]	Cofactor and Prosthetic Group	(VF_0028)
h[p] + pppn[p] <=> h[c] + pppn[c]	Transport, Inner Membrane	(VF_2380)
pppn[e] <=> pppn[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + pyr[c] -> amp[c] + 2 h[c] + pep	Glycolysis/Gluconeogenesis	(VF_1242)
ppt[e] <=> ppt[p]	Transport, Outer Membrane Porin	
atp[c] + gly[c] + pram[c] <=> adp[c] + gar[c] + h	Purine and Pyrimidine Biosynt	(VF_2395)
pran[c] -> 2cpr5p[c]	Tyrosine, Tryptophan, and Phe	(VF_1029)
atp[c] + fpram[c] -> adp[c] + air[c] + 2 h[c] + pi[c	Purine and Pyrimidine Biosynt	(VF_1928)
h2o[c] + prbamp[c] -> prfp[c]	Histidine Metabolism	(VF_1019)
5aizc[c] + asp-L[c] + atp[c] -> 25aics[c] + adp[c]	Purine and Pyrimidine Biosynt	(VF_1498)
h2o[c] + prbatp[c] -> h[c] + ppi[c] + prbamp[c]	Histidine Metabolism	(VF_1019)
atp[c] + fgam[c] + gln-L[c] + h2o[c] -> adp[c] + f	Purine and Pyrimidine Biosynt	(VF_0652)
prfp[c] <=> prlp[c]	Histidine Metabolism	(VF_1017)
atp[c] + h2o[c] + pro-L[p] -> adp[c] + h[c] + pi[c]	Transport, Inner Membrane	(VF_0785 a
fad[c] + pro-L[c] -> 1pyr5c[c] + fadh2[c] + h[c]	Arginine and Proline Metabolis	(VF_A0832
atp[c] + h2o[c] + progly[p] -> adp[c] + h[c] + pi[c	Transport, Inner Membrane	(VF_2516 a
progly[e] <=> progly[p]	Transport, Outer Membrane Porin	
na1[p] + pro-L[p] -> na1[c] + pro-L[c]	Transport, Inner Membrane	(VF_A0829
pro-L[e] <=> pro-L[p]	Transport, Outer Membrane Porin	
atp[c] + pro-L[c] + trnapro[c] -> amp[c] + ppi[c]	tRNA Charging	(VF_0682)
atp[c] + r5p[c] <=> amp[c] + h[c] + prpp[c]	Histidine Metabolism	(VF_0764)
psclys[e] <=> psclys[p]	Transport, Outer Membrane Porin	
pep[c] + skm5p[c] <=> 3psme[c] + pi[c]	Tyrosine, Tryptophan, and Phe	(VF_1761)
h[c] + ps120[c] -> co2[c] + pe120[c]	Glycerophospholipid Metabolis	(VF_2331)
h[c] + ps140[c] -> co2[c] + pe140[c]	Glycerophospholipid Metabolis	(VF_2331)
h[c] + ps141[c] -> co2[c] + pe141[c]	Glycerophospholipid Metabolis	(VF_2331)
h[c] + ps160[c] -> co2[c] + pe160[c]	Glycerophospholipid Metabolis	(VF_2331)
h[c] + ps161[c] -> co2[c] + pe161[c]	Glycerophospholipid Metabolis	(VF_2331)
h[c] + ps180[c] -> co2[c] + pe180[c]	Glycerophospholipid Metabolis	(VF_2331)
h[c] + ps181[c] -> co2[c] + pe181[c]	Glycerophospholipid Metabolis	(VF_2331)
3php[c] + glu-L[c] -> akg[c] + pser-L[c]	Glycine and Serine Metabolis	(VF_0899)
pser-L[e] <=> pser-L[p]	Transport, Outer Membrane Porin	
h2o[c] + pser-L[c] -> pi[c] + ser-L[c]	Glycine and Serine Metabolis	(VF_0509)
cdpdddecg[c] + ser-L[c] -> cmp[c] + h[c] + ps12	Glycerophospholipid Metabolis	(VF_2428)
cdpdtdecg[c] + ser-L[c] -> cmp[c] + h[c] + ps14	Glycerophospholipid Metabolis	(VF_2428)
cdpdtdec7eg[c] + ser-L[c] -> cmp[c] + h[c] + ps	Glycerophospholipid Metabolis	(VF_2428)
cdpdhdecg[c] + ser-L[c] -> cmp[c] + h[c] + ps16	Glycerophospholipid Metabolis	(VF_2428)
cdpdhdec9eg[c] + ser-L[c] -> cmp[c] + h[c] + ps	Glycerophospholipid Metabolis	(VF_2428)
cdpdodecg[c] + ser-L[c] -> cmp[c] + h[c] + ps18	Glycerophospholipid Metabolis	(VF_2428)
cdpdodec11eg[c] + ser-L[c] -> cmp[c] + h[c] + p	Glycerophospholipid Metabolis	(VF_2428)
pi[c] + ppcoa[c] -> coa[c] + ppap[c]	Alternate Carbon Metabolism	(VF_0836)

accoa[c] + pi[c] <=> actp[c] + coa[c]	Pyruvate Metabolism	(VF_0836)
atp[c] + h[c] + pan4p[c] -> dpcoa[c] + ppi[c]	Cofactor and Prosthetic Group	(VF_0132)
atp[c] + h2o[c] + ptrc[p] -> adp[c] + h[c] + pi[c] +	Transport, Inner Membrane	(VF_1315 a
ptrc[e] <=> ptrc[p]	Transport, Outer Membrane Porin	
adn[c] + pi[c] <=> ade[c] + r1p[c]	Nucleotide Salvage Pathway	(VF_0507)
dad-2[c] + pi[c] <=> 2dr1p[c] + ade[c]	Nucleotide Salvage Pathway	(VF_0507)
gsn[c] + pi[c] <=> gua[c] + r1p[c]	Nucleotide Salvage Pathway	(VF_0507)
dgsn[c] + pi[c] <=> 2dr1p[c] + gua[c]	Nucleotide Salvage Pathway	(VF_0507)
ins[c] + pi[c] <=> hxan[c] + r1p[c]	Nucleotide Salvage Pathway	(VF_0507)
din[c] + pi[c] <=> 2dr1p[c] + hxan[c]	Nucleotide Salvage Pathway	(VF_0507)
h2o[c] + o2[c] + pyam5p[c] -> h2o2[c] + nh4[c]	Cofactor and Prosthetic Group	(VF_A1161
pydam[e] <=> pydam[p]	Transport, Outer Membrane Porin	
atp[c] + pydx[c] -> adp[c] + h[c] + pydx5p[c]	Cofactor and Prosthetic Group	(VF_2056)
pydxn[e] <=> pydxn[p]	Transport, Outer Membrane Porin	
h2o[c] + pydx5p[c] -> pi[c] + pydx[c]	Cofactor and Prosthetic Group	(VF_2482)
pydx[e] <=> pydx[p]	Transport, Outer Membrane Porin	
pydx[p] -> pydx[c]	Transport, Inner Membrane	
adp[c] + h[c] + pep[c] -> atp[c] + pyr[c]	Glycolysis/Gluconeogenesis	(VF_A0494
pi[c] + uri[c] <=> r1p[c] + ura[c]	Nucleotide Salvage Pathway	(VF_1521)
h[p] + pyr[p] <=> h[c] + pyr[c]	Transport, Inner Membrane	
pyr[e] <=> pyr[p]	Transport, Outer Membrane Porin	
quin[e] <=> quin[p]	Transport, Outer Membrane Porin	
dhap[c] + iasp[c] -> 2 h2o[c] + pi[c] + quln[c]	Cofactor and Prosthetic Group	(VF_0965)
r5p[e] <=> r5p[p]	Transport, Outer Membrane Porin	
atp[c] + ribflv[c] -> adp[c] + fmn[c] + h[c]	Cofactor and Prosthetic Group	(VF_0466)
4r5au[c] + db4p[c] -> dmlz[c] + 2 h2o[c] + pi[c]	Cofactor and Prosthetic Group	(VF_1414)
2 dmlz[c] -> 4r5au[c] + ribflv[c]	Cofactor and Prosthetic Group	(VF_0703)
atp[c] + rib-D[c] -> adp[c] + h[c] + r5p[c]	Alternate Carbon Metabolism	(VF_1448)
rhcys[c] -> dhptd[c] + hcys-L[c]	Methionine Metabolism	(VF_0545)
atp[c] + h2o[c] + rib-D[p] -> adp[c] + h[c] + pi[c]	Transport, Inner Membrane	(VF_1444 a
rib-D[e] <=> rib-D[p]	Transport, Outer Membrane Porin	
rmn[e] <=> rmn[p]	Transport, Outer Membrane Porin	
adp[c] + trdrd[c] -> dadp[c] + h2o[c] + trdox[c]	Nucleotide Salvage Pathway	(VF_0909 a
gdp[c] + trdrd[c] -> dgdp[c] + h2o[c] + trdox[c]	Nucleotide Salvage Pathway	(VF_0057 a
cdp[c] + trdrd[c] -> dcdp[c] + h2o[c] + trdox[c]	Nucleotide Salvage Pathway	(VF_0057 a
trdrd[c] + udp[c] -> dudp[c] + h2o[c] + trdox[c]	Nucleotide Salvage Pathway	(VF_0057 a
atp[c] + 2 flxr[c] + 2 h[c] -> datp[c] + 2 flxso[c] +	Nucleotide Salvage Pathway	(VF_0812 a
2 flxr[c] + gtp[c] + 2 h[c] -> dgtp[c] + 2 flxso[c] +	Nucleotide Salvage Pathway	(VF_0812 a
ctp[c] + 2 flxr[c] + 2 h[c] -> dctp[c] + 2 flxso[c] +	Nucleotide Salvage Pathway	(VF_0812 a
2 flxr[c] + 2 h[c] + utp[c] -> dutp[c] + 2 flxso[c] +	Nucleotide Salvage Pathway	(VF_0812 a
ru5p-D[c] <=> xu5p-D[c]	Pentose Phosphate Pathway	(VF_2288)
r5p[c] <=> ru5p-D[c]	Pentose Phosphate Pathway	(VF_2105)
s7p[c] -> gmhep7p[c]	Lipopolysaccharide Biosynthes	(VF_1931)
2 h[c] + 2 h2o[c] + sucarg[c] -> co2[c] + 2 nh4[c	Arginine and Proline Metabolis	(VF_A0847
atp[c] + gtp[c] + h2o[c] + so4[c] -> aps[c] + gdp[	Cysteine Metabolism	(VF_0320 a
sbt-D[e] <=> sbt-D[p]	Transport, Outer Membrane Porin	
h2o[c] + sl26da[c] -> 26dap-LL[c] + succ[c]	Threonine and Lysine Metaboli	(VF_1914)
akg[c] + sl26da[c] <=> glu-L[c] + sl2a6o[c]	Threonine and Lysine Metaboli	(VF_2284)

selnp[c] + sertrna[sec][c] -> h[c] + pi[c] + sectrn	tRNA Charging	(VF_2508)
sel[e] <=> sel[p]	Transport, Outer Membrane Porin	
akg[c] + h[c] + ichor[c] -> 2sephchc[c] + co2[c]	Cofactor and Prosthetic Group	(VF_1671)
accoa[c] + ser-L[c] <=> acser[c] + coa[c]	Cysteine Metabolism	(VF_2347)
ser-L[c] -> nh4[c] + pyr[c]	Glycine and Serine Metabolis	(VF_1176)
h[p] + ser-L[p] <=> h[c] + ser-L[c]	Transport, Inner Membrane	(VF_1177)
na1[p] + ser-L[p] -> na1[c] + ser-L[c]	Transport, Inner Membrane	(VF_A0803
ser-L[e] <=> ser-L[p]	Transport, Outer Membrane Porin	
atp[c] + ser-L[c] + trnaser[c] -> amp[c] + ppi[c] +	tRNA Charging	(VF_0908)
atp[c] + ser-L[c] + trnasecys[c] -> amp[c] + ppi[	tRNA Charging	(VF_0908)
Sfglutth[c] + h2o[c] -> formate[c] + gthrd[c] + h[	Cofactor and Prosthetic Group	(VF_0644)
h2o[c] + sucglu[c] -> glu-L[c] + succ[c]	Arginine and Proline Metabolis	(VF_0657 a
h2o[c] + nad[c] + sucgsa[c] -> 2 h[c] + nadh[c] +	Arginine and Proline Metabolis	(VF_2282)
2sephchc[c] -> 2shchc[c] + pyr[c]	Cofactor and Prosthetic Group	(VF_1670)
dscl[c] + nad[c] -> h[c] + nadh[c] + scl[c]	Cofactor and Prosthetic Group Biosynthesis	
fe2[c] + scl[c] -> 3 h[c] + sheme[c]	Cofactor and Prosthetic Group Biosynthesis	
3dhsk[c] + h[c] + nadph[c] <=> nadp[c] + skm[c]	Tyrosine, Tryptophan, and Phe	(VF_2535)
atp[c] + skm[c] -> adp[c] + h[c] + skm5p[c]	Tyrosine, Tryptophan, and Phe	(VF_2292)
cys-L[c] + suchms[c] -> cyst-L[c] + h[c] + succ[	Methionine Metabolism	(VF_2267)
skm[e] <=> skm[p]	Transport, Outer Membrane Porin	
slnt[e] <=> slnt[p]	Transport, Outer Membrane Porin	
so2[e] <=> so2[p]	Transport, Outer Membrane Porin	
so3[e] <=> so3[p]	Transport, Outer Membrane Porin	
h[p] + so4[p] -> h[c] + so4[c]	Inorganic Ion Transport and M	(VF_2173)
so4[e] <=> so4[p]	Transport, Outer Membrane Porin	
akg[c] + sucorn[c] -> glu-L[c] + sucgsa[c]	Arginine and Proline Metabolis	(VF_2284)
pyr[c] + ser-L[c] <=> ala-L[c]+ hpyr[c]	Glycine and Serine Metabolis	(VF_0339)
atp[c] + h2o[c] + spmd[p] -> adp[c] + h[c] + pi[c]	Transport, Inner Membrane	(VF_1315 a
accoa[c] + spmd[c] -> N1aspmd[c] + coa[c] + h[	Arginine and Proline Metabolis	(VF_A0385
accoa[c] + spmd[c] -> coa[c] + h[c] + n8aspmd[	Arginine and Proline Metabolis	(VF_A0385
spmd[e] <=> spmd[p]	Transport, Outer Membrane Porin	
atp[c] + coa[c] + sucbz[c] -> amp[c] + ppi[c] + s	Cofactor and Prosthetic Group	(VF_1666)
2shchc[c] -> h2o[c] + sucbz[c]	Cofactor and Prosthetic Group	(VF_1667)
3 h[p] + succ[p] -> 3 h[c] + succ[c]	Transport, Inner Membrane	(VF_2064)
succ[c] + h[p] -> h[c] + succ[p]	Transport, Inner Membrane	
succ[e] <=> succ[p]	Transport, Outer Membrane Porin	
q8[c] + succ[c] -> fum[c] + q8h2[c]	Oxidative Phosphorylation	(VF_0819 a
atp[c] + coa[c] + succ[c] <=> adp[c] + pi[c] + su	Citric Acid Cycle	(VF_0825 a
pep[c] + sucr[p] -> pyr[c] + suc6p[c]	Transport, Inner Membrane	(VF_1115 ar
sucr[e] <=> sucr[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + so4[p] -> adp[c] + h[c] + pi[c] +	Inorganic Ion Transport and M	(VF_A0290
sulfac[e] <=> sulfac[p]	Transport, Outer Membrane Porin	
5 h[c] + 3 nadph[c] + so3[c] -> 3 h2o[c] + h2s[c]	Cysteine Metabolism	(VF_0310 a
tdec2eACP[c] <=> cdec3eACP[c]	Cell Envelope Biosynthesis	(VF_1292)
tag6p-D[c] + atp[c] -> adp[c] + h[c] + tagdp-D[c]	Alternate Carbon Metabolism	(VF_A1005
g3p[c] + s7p[c] <=> e4p[c] + f6p[c]	Pentose Phosphate Pathway	(VF_A0685
tartr-D[e] <=> tartr-D[p]	Transport, Outer Membrane Porin	
tartr-L[e] <=> tartr-L[p]	Transport, Outer Membrane Porin	

3 h[p] + tartr-D[p] -> 3 h[c] + tartr-D[c]	Transport, Inner Membrane	(VF_2064)
taur[e] <=> taur[p]	Transport, Outer Membrane Porin	
tcynt[e] <=> tcynt[p]	Transport, Outer Membrane Porin	
dtdp4d6dg[c] -> dtdp4d6dm[c]	Cell Envelope Biosynthesis	(VF_0168)
dtdpglu[c] -> dtdp4d6dg[c] + h2o[c]	Cell Envelope Biosynthesis	(VF_0166)
atp[c] + lipidAdsvf[c] -> adp[c] + h[c] + lipidAvf[c	Lipopolysaccharide Biosynthes	(VF_A0425
dsbdrd[c] + dsbcox[p] -> dsbdox[c] + dsbcrd[p]	Transport, Inner Membrane	(VF_0449 ar
tagdp-D[c] <=> dhap[c] + g3p[c]	Alternate Carbon Metabolism	(VF_A0989
nadh[c] + nadp[c] + 2 h[p] -> 2 h[c] + nad[c] + n	Oxidative Phosphorylation	(VF_A0585
h2o[c] + succoa[c] + thdp[c] -> coa[c] + sl2a6o[	Threonine and Lysine Metaboli	(VF_0576)
h2o[c] + methf[c] -> 5fthf[c] + h[c]	Folate Metabolism	(VF_0695)
h2o2[c] + trdrd[c] -> 2 h2o[c] + trdox[c]	Unassigned	(VF_0057 ar
atp[c] + h2o[c] + thm[p] -> adp[c] + h[c] + pi[c] +	Transport, Inner Membrane	(VF_0267 ar
h[p] + thymd[p] -> h[c] + thymd[c]	Transport, Inner Membrane	(VF_2065)
h[p] + thymd[p] <=> h[c] + thymd[c]	Transport, Inner Membrane	
thymd[e] <=> thymd[p]	Transport, Outer Membrane Porin	
thm[e] <=> thm[p]	Transport, Outer Membrane Porin	
athr-L[c] -> acald[c] + gly[c]	Threonine and Lysine Metaboli	(VF_0695)
atp[c] + h2o[c] + thr-L[p] -> adp[c] + h[c] + pi[c]	Transport, Inner Membrane	(VF_1084)
thr-L[c] -> acald[c] + gly[c]	Threonine and Lysine Metaboli	(VF_0695)
nad[c] + thr-L[c] -> 2aobut[c] + h[c] + nadh[c]	Glycine and Serine Metabolism	(VF_A0417
thr-L[c] -> 2obut[c] + nh4[c]	Valine, Leucine, and Isoleucine	(VF_2560)
thrp[e] <=> thrp[p]	Transport, Outer Membrane Porin	
h2o[c] + phom[c] -> pi[c] + thr-L[c]	Threonine and Lysine Metaboli	(VF_2116)
na1[p] + thr-L[p] -> na1[c] + thr-L[c]	Transport, Inner Membrane	(VF_A0803
thr-L[e] <=> thr-L[p]	Transport, Outer Membrane Porin	
atp[c] + thr-L[c] + trnathr[c] -> amp[c] + ppi[c] +	tRNA Charging	(VF_1214)
thym[c] + h[p] -> h[c] + thym[p]	Transport, Inner Membrane	
thym[e] <=> thym[p]	Transport, Outer Membrane Porin	
atp[c] + dhgly[c] + dxyl5p[c] + h[c] + iscssh[c] +	Cofactor and Prosthetic Group	(VF_0034 ar
r5p[c] + xu5p-D[c] <=> g3p[c] + s7p[c]	Pentose Phosphate Pathway	(VF_A0686
e4p[c] + xu5p-D[c] <=> f6p[c] + g3p[c]	Pentose Phosphate Pathway	(VF_A0686
h[c] + mql8[c] + tmao[c] -> h2o[c] + mqn8[c] + t	Oxidative Phosphorylation	(VF_A0080
mql8[c] + h[p] + tmao[p] -> mqn8[c] + h2o[p] + t	Oxidative Phosphorylation	(VF_A0298
2dmmql8[c] + h[c] + tmao[c] -> 2dmmq8[c] + h2	Oxidative Phosphorylation	(VF_A0080
2dmmql8[c] + h[p] + tmao[p] -> 2dmmq8[c] + h	Oxidative Phosphorylation	(VF_A0298
tmao[e] <=> tmao[p]	Transport, Outer Membrane Porin	
tma[e] <=> tma[p]	Transport, Outer Membrane Porin	
atp[c] + thymd[c] -> adp[c] + dtmp[c] + h[c]	Nucleotide Salvage Pathway	(VF_1599)
pi[c] + thymd[c] <=> 2dr1p[c] + thym[c]	Nucleotide Salvage Pathway	(VF_0505)
dump[c] + mlthf[c] -> dhf[c] + dtmp[c]	Nucleotide Salvage Pathway	(VF_0460)
atp[c] + thm[c] -> adp[c] + h[c] + thmmp[c]	Cofactor and Prosthetic Group	(VF_1141)
atp[c] + thmmp[c] -> adp[c] + thmpp[c]	Cofactor and Prosthetic Group	(VF_0705)
2mahmp[c] + 4mpetz[c] + h[c] -> ppi[c] + thmm	Cofactor and Prosthetic Group	(VF_0033)
dhap[c] <=> g3p[c]	Glycolysis/Gluconeogenesis	(VF_0206)
h[c] + nadph[c] + trdox[c] -> nadp[c] + trdrd[c]	Oxidative Phosphorylation	(VF_0057 ar
tre[e] <=> tre[p]	Transport, Outer Membrane Porin	
3ig3p[c] + ser-L[c] -> g3p[c] + h2o[c] + trp-L[c]	Tyrosine, Tryptophan, and Phe	(VF_1027 ar

indole[c] + ser-L[c] -> h2o[c] + trp-L[c]	Tyrosine, Tryptophan, and Phe	(VF_1027 a
3ig3p[c] -> g3p[c] + indole[c]	Tyrosine, Tryptophan, and Phe	(VF_1027 a
h[p] + trp-L[p] <=> h[c] + trp-L[c]	Transport, Inner Membrane	
trp-L[e] <=> trp-L[p]	Transport, Outer Membrane Porin	
atp[c] + trnatrp[c] + trp-L[c] -> amp[c] + ppi[c] +	tRNA Charging	(VF_2286)
tsul[e] <=> tsul[p]	Transport, Outer Membrane Porin	
ttdca[e] -> ttdca[p]	Transport, Outer Membrane	(VF_1543)
ttdcea[e] -> ttdcea[p]	Transport, Outer Membrane	(VF_1543)
ttrcyc[e] <=> ttrcyc[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + tungs[p] -> adp[c] + h[c] + pi[c]	Inorganic Ion Transport and M	(VF_A0290
tungs[e] <=> tungs[p]	Transport, Outer Membrane Porin	
tym[e] <=> tym[p]	Transport, Outer Membrane Porin	
amet[c] + nadph[c] + tyr-L[c] -> 4crsol[c] + dad-	Cofactor and Prosthetic Group	(VF_0035)
tyrp[e] <=> tyrp[p]	Transport, Outer Membrane Porin	
h[p] + tyr-L[p] <=> h[c] + tyr-L[c]	Transport, Inner Membrane	(VF_1197)
akg[c] + tyr-L[c] <=> 34hpp[c] + glu-L[c]	Tyrosine, Tryptophan, and Phe	(VF_1673)
tyr-L[e] <=> tyr-L[p]	Transport, Outer Membrane Porin	
atp[c] + trnatyr[c] + tyr-L[c] -> amp[c] + ppi[c] +	tRNA Charging	(VF_1727)
3hddecACP[c] + u3hga[c] -> ACP[c] + h[c] + u2	Lipopolysaccharide Biosynthes	(VF_1952)
26dap-M[c] + atp[c] + uamag[c] -> adp[c] + h[c]	Cell Envelope Biosynthesis	(VF_2206)
h2o[p] + udpacgal[p] -> acgal1p[p] + 2 h[p] + ur	Alternate Carbon Metabolism	(VF_0778)
h2o[p] + uacgam[p] -> acgam1p[p] + 2 h[p] + ur	Alternate Carbon Metabolism	(VF_0778)
uacgam[e] <=> uacgam[p]	Transport, Outer Membrane Porin	
uacgam[c] <=> uacmam[c]	Cell Envelope Biosynthesis	(VF_0193)
3hmrsACP[c] + uacgam[c] <=> ACP[c] + u3aga	Lipopolysaccharide Biosynthes	(VF_1739 a
pep[c] + uacgam[c] -> pi[c] + uaccg[c]	Cell Envelope Biosynthesis	(VF_0401)
acgam1p[c] + h[c] + utp[c] -> ppi[c] + uacgam[c	Cell Envelope Biosynthesis	(VF_2562)
uacgam[c] + uagmda[c] -> h[c] + uaagmda[c] +	Cell Envelope Biosynthesis	(VF_2201)
atp[c] + glu-D[c] + uama[c] -> adp[c] + h[c] + pi[	Cell Envelope Biosynthesis	(VF_2203)
ala-L[c] + atp[c] + uamr[c] -> adp[c] + h[c] + pi[c	Cell Envelope Biosynthesis	(VF_2200)
h[c] + nadph[c] + uaccg[c] -> nadp[c] + uamr[c]	Cell Envelope Biosynthesis	(VF_2426)
h2o[c] + udcpdp[c] -> h[c] + pi[c] + udcpp[c]	Cell Envelope Biosynthesis	(VF_1544)
h2o[p] + udcpdp[p] -> h[p] + pi[p] + udcpp[p]	Cell Envelope Biosynthesis	(VF_1544)
frdp[c] + 8 ipdp[c] -> 8 ppi[c] + udcpdp[c]	Cofactor and Prosthetic Group	(VF_1958)
udpacgal[e] <=> udpacgal[p]	Transport, Outer Membrane Porin	
udpg[c] <=> udpgal[c]	Alternate Carbon Metabolism	(VF_A0352
h2o[p] + udpgal[p] -> gal1p[p] + 2 h[p] + ump[p]	Alternate Carbon Metabolism	(VF_0778)
udpgal[e] <=> udpgal[p]	Transport, Outer Membrane Porin	
udpglcur[e] <=> udpglcur[p]	Transport, Outer Membrane Porin	
h2o[p] + udpg[p] -> g1p[p] + 2 h[p] + ump[p]	Alternate Carbon Metabolism	(VF_0778)
udpg[e] <=> udpg[p]	Transport, Outer Membrane Porin	
h2o[p] + udpglcur[p] -> glcur1p[p] + 2 h[p] + um	Alternate Carbon Metabolism	(VF_0778)
gal1p[c] + udpg[c] <=> g1p[c] + udpgal[c]	Alternate Carbon Metabolism	(VF_A0353
alaala[c] + atp[c] + ugmd[c] -> adp[c] + h[c] + pi	Cell Envelope Biosynthesis	(VF_2205)
h2o[c] + u3aga[c] -> ac[c] + u3hga[c]	Lipopolysaccharide Biosynthes	(VF_2195)
LalaDgluMdap[c] + atp[c] + uamr[c] -> adp[c] +	Murein Recycling	(VF_0265)
LalaDgluMdapDala[c] + atp[c] + uamr[c] -> adp	Murein Recycling	(VF_0265)
atp[c] + ump[c] <=> adp[c] + udp[c]	Nucleotide Salvage Pathway	(VF_1960)

ump[e] <=> ump[p]	Transport, Outer Membrane Porin	
2 amet[c] + uppg3[c] -> 2 ahcys[c] + dscl[c] + h	Cofactor and Prosthetic Group	(VF_0064)
hmbil[c] -> h2o[c] + uppg3[c]	Cofactor and Prosthetic Group	(VF_0065)
4 h[c] + uppg3[c] -> 4 co2[c] + cpppg3[c]	Cofactor and Prosthetic Group	(VF_2402)
prpp[c] + ura[c] -> ppi[c] + ump[c]	Nucleotide Salvage Pathway	(VF_1927)
h[p] + ura[p] -> h[c] + ura[c]	Transport, Inner Membrane	(VF_1926)
h[p] + ura[p] <=> h[c] + ura[c]	Transport, Inner Membrane	
ura[e] <=> ura[p]	Transport, Outer Membrane Porin	
h2o[c] + urcan[c] -> 4izp[c]	Histidine Metabolism	(VF_A0451
urea[e] <=> urea[p]	Transport, Outer Membrane Porin	
urea[p] <=> urea[c]	Transport, Inner Membrane	(VF_A0235
gtp[c] + uri[c] -> gdp[c] + h[c] + ump[c]	Nucleotide Salvage Pathway	(VF_1752)
h[p] + uri[p] -> h[c] + uri[c]	Transport, Inner Membrane	(VF_2065)
h[p] + uri[p] <=> h[c] + uri[c]	Transport, Inner Membrane	
uri[e] <=> uri[p]	Transport, Outer Membrane	
h2o[c] + u23gavf[c] -> 2 h[c] + lipidXvf[c] + ump	Lipopolysaccharide Biosynthes	(VF_1602)
atp[c] + h2o[c] + val-L[p] -> adp[c] + h[c] + pi[c]	Transport, Inner Membrane	(VF_1084)
h[p] + val-L[p] <=> h[c] + val-L[c]	Transport, Inner Membrane	(VF_0446)
akg[c] + val-L[c] <=> 3mob[c] + glu-L[c]	Valine, Leucine, and Isoleucin	(VF_2558)
val-L[e] <=> val-L[p]	Transport, Outer Membrane Porin	
atp[c] + trnaval[c] + val-L[c] -> amp[c] + ppi[c] +	tRNA Charging	(VF_0411)
0.000223 10fthf[c] + 2.6e-005 2fe2s[c] + 0.0002	Exchange	
3mob[c] + ala-L[c] <=> pyr[c] + val-L[c]	Valine, Leucine, and Isoleucin	(VF_0014)
2 h[c] + mptamp[c] + tungs[c] -> amp[c] + cu2[c	Cofactor and Prosthetic Group	(VF_1608)
h[p] + xan[p] -> h[c] + xan[c]	Transport, Inner Membrane	(VF_0116)
xan[e] <=> xan[p]	Transport, Outer Membrane Porin	
xmp[e] <=> xmp[p]	Transport, Outer Membrane Porin	
prpp[c] + xan[c] -> ppi[c] + xmp[c]	Nucleotide Salvage Pathway	(VF_0738)
h[p] + xtsn[p] <=> h[c] + xtsn[c]	Transport, Inner Membrane	
xtsn[e] <=> xtsn[p]	Transport, Outer Membrane Porin	
xyl-D[e] <=> xyl-D[p]	Transport, Outer Membrane Porin	
xylu-L[e] <=> xylu-L[p]	Transport, Outer Membrane Porin	
atp[c] + h2o[c] + zn2[c] -> adp[c] + h[c] + pi[c] +	Inorganic Ion Transport and M	(VF_1522)
zn2[c] + h[p] -> h[c] + zn2[p]	Inorganic Ion Transport and M	(VF_2341)
zn2[e] <=> zn2[p]	Transport, Outer Membrane Porin	
zn2[p] -> zn2[c]	Inorganic Ion Transport and Metabolism	
atp[c] + h2o[c] + zn2[p] -> adp[c] + h[c] + pi[c] +	Inorganic Ion Transport and M	(VF_0828 a

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VF_0267 VF	0	0	1000
VF_2065	0	0	1000
	1	-1000	1000
	1	-1000	1000
	1	-1000	1000
VF_0695 VF	0	0	1000
VF_1084 VF	0	0	1000
VF_0695 VF	0	0	1000
VF_A0417	0	0	1000
VF_2560	0	0	1000
	1	-1000	1000
VF_1458 VF	0	0	1000
VF_A0803	0	0	1000
	1	-1000	1000
VF_1214	0	0	1000
	0	0	1000
	1	-1000	1000
VF_0034 VF	0	0	1000
VF_0440 VF	1	-1000	1000
VF_0440 VF	1	-1000	1000
VF_A0080 V	0	0	1000
VF_A0188 V	0	0	1000
VF_A0080 V	0	0	1000
VF_A0188 V	0	0	1000
	1	-1000	1000
	1	-1000	1000
VF_1599	0	0	1000
VF_0505	1	-1000	1000
VF_0460	0	0	1000
VF_1141	0	0	1000
VF_0705	0	0	1000
VF_0033 VF	0	0	1000
VF_0206	1	-1000	1000
VF_0057 VF	0	0	1000
	1	-1000	1000
VF_1027 VF	0	0	1000

VF_1027 VF	0	0	1000
VF_1027 VF	0	0	1000
	1	-1000	1000
	1	-1000	1000
VF_2286	0	0	1000
	1	-1000	1000
VF_1543	0	0	1000
VF_1543	0	0	1000
	1	-1000	1000
VF_A0290 V	0	0	1000
	1	-1000	1000
	1	-1000	1000
VF_0035	0	0	1000
	1	-1000	1000
VF_1171 VF	1	-1000	1000
VF_1488 VF	1	-1000	1000
	1	-1000	1000
VF_1727	0	0	1000
VF_1952	0	0	1000
VF_2206	0	0	1000
VF_0778	0	0	1000
VF_0778	0	0	1000
	1	-1000	1000
VF_0193	1	-1000	1000
VF_1739 VF	1	-1000	1000
VF_0401	0	0	1000
VF_2562	0	0	1000
VF_2201	0	0	1000
VF_2203	0	0	1000
VF_2200	0	0	1000
VF_2426	0	0	1000
VF_1544 VF	0	0	1000
VF_1544 VF	0	0	1000
VF_1958	0	0	1000
	1	-1000	1000
VF_0201 VF	1	-1000	1000
VF_0778	0	0	1000
	1	-1000	1000
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VF_0778	0	0	1000
	1	-1000	1000
VF_0778	0	0	1000
VF_A0353	1	-1000	1000
VF_2205	0	0	1000
VF_2195	0	0	1000
VF_0265	0	0	1000
VF_0265	0	0	1000
VF_1960	1	-1000	1000

	1	-1000	1000
VF_0064 VF	0	0	1000
VF_0065	0	0	1000
VF_2402	0	0	1000
VF_1927	0	0	1000
VF_1926	0	0	1000
	1	-1000	1000
	1	-1000	1000
VF_A0451	0	0	1000
	1	-1000	1000
VF_A0235	1	-1000	1000
VF_1752	0	0	1000
VF_2065	0	0	1000
	1	-1000	1000
	1	-1000	1000
VF_1602	0	0	1000
VF_1084 VF	0	0	1000
VF_0446	1	-1000	1000
VF_2558	1	-1000	1000
	1	-1000	1000
VF_0411	0	0	1000
	0	0	1000
VF_0014	1	-1000	1000
VF_1608	0	0	1000
VF_0116	0	0	1000
	1	-1000	1000
	1	-1000	1000
VF_0738	0	0	1000
	1	-1000	1000
	1	-1000	1000
	1	-1000	1000
	1	-1000	1000
VF_1522	0	0	1000
VF_2341	0	0	1000
	1	-1000	1000
	0	0	1000
VF_0828 VF	0	0	1000

Metabolite Abbreviation	Metabolite Name	Neutral Formula
36dahx[c]	(3S)-3,6-Diaminohexanoate	C6H14N2O2
3hmp[c]	3-Hydroxy-2-methylpropanoa	C4H8O3
4h2oglt[c]	4-Hydroxy-2-oxoglutarate	C5H6O6
4izp[c]	4-Imidazolone-5-propanoate	C6H8N2O3
5cmhm[c]	5-Carboxymethyl-2-hydroxym	C8H8O7
5cohe[c]	5-Carboxy-2-oxohept-3-ened	C8H8O7
6pgg[c]	6-Phospho-beta-D-glucosyl-(	C12H23O14P
acgal6p[c]	N-Acetyl-D-galactosamine 6-	C8H16NO9P
acgam2[c]	Chitobiose	C16H28N2O11
acgam2[e]	Chitobiose	C16H28N2O11
acgam2[p]	Chitobiose	C16H28N2O11
acgam26p[c]	N,N'-diacetylchitobiose 6'-ph	C16H29N2O14P
cdpddglu[c]	CDP-4-dehydro-6-deoxy-D-gl	C15H21N3O16P2
cdpglu[c]	CDP-glucose	C15H23N3O16P2
cellob[e]	Cellobiose	C12H22O11
cellob[p]	Cellobiose	C12H22O11
chols[c]	Choline sulfate	C5H13NO4S
ddcald[c]	Dodecylaldehyde	C12H24O
dhlam[c]	Dihydrolipoamide	C8H17NOS2
ficytc[c]	Ferricytochrome c	C42H51FeN8O6S2
focytc[c]	Ferrocytochrome c	C42H52FeN8O6S2
fol[c]	Folate	C19H19N7O6
forglu[c]	N-Formimidoyl-L-glutamate	C6H10N2O4
formate[c]	Formate	CH2O2
frmd[c]	Formamide	CH3NO
galam6p[c]	D-Galactosamine 6-phosphat	C6H14NO8P
gam[c]	D-Glucosamine	C6H13NO5
ggdp[c]	Geranylgeranyl diphosphate	C20H36O7P2
hv[c]	Luciferase	
lipavf[c]	V. fischeri Endotoxin	C78H140N2O24P2
lipavf[e]	V. fischeri Endotoxin	C78H140N2O24P2
lipavf[p]	V. fischeri Endotoxin	C78H140N2O24P2
lipidAdsvf[c]	V. fischeri Lipid A Disaccharid	C64H123N2O20P
lipidAvf[c]	V. fischeri Lipid A disaccharid	C64H124N2O23P2
lipidXvf[c]	2,3-Bis(3-hydroxydodecanoyl	C32H63NO12P
lpam[c]	Lipoamide	C8H15NOS2
lpsvf[c]	V. fischeri LPS	C34H56O29
lpsvf[e]	V. fischeri LPS	C34H56O29
lpsvf[p]	V. fischeri LPS	C34H56O29
macgam26p[c]	N-monoacetylchitobiose 6'-pl	C14H27N2O13P
mmtsa[c]	(S)-Methylmalonate semialde	C4H6O3
sertrna[sec][c]	L-Seryl-tRNA(Sec)	C3H5NO2R
u23gavf[c]	V. fischeri UDP-2,3-bis(3-hyd	C41H74N3O20P2
urcan[c]	Urocanate	C6H6N2O2
zn2[c]	Zinc	Zn
zn2[e]	Zinc	Zn
zn2[p]	Zinc	Zn

xtp[c]	XTP	C10H15N4O15P3
xdp[c]	XDP	C10H14N4O12P2
xmp[c]	Xanthosine 5'-phosphate	C10H13N4O9P
xmp[e]	Xanthosine 5'-phosphate	C10H13N4O9P
xmp[p]	Xanthosine 5'-phosphate	C10H13N4O9P
xtsn[c]	Xanthosine	C10H12N4O6
xtsn[e]	Xanthosine	C10H12N4O6
xtsn[p]	Xanthosine	C10H12N4O6
xan[c]	Xanthine	C5H4N4O2
xan[e]	Xanthine	C5H4N4O2
xan[p]	Xanthine	C5H4N4O2
utp[c]	UTP	C9H15N2O15P3
uppg3[c]	Uroporphyrinogen III	C40H44N4O16
uri[c]	Uridine	C9H12N2O6
uri[e]	Uridine	C9H12N2O6
uri[p]	Uridine	C9H12N2O6
urea[c]	Urea	CH4N2O
urea[e]	Urea	CH4N2O
urea[p]	Urea	CH4N2O
ura[c]	Uracil	C4H4N2O2
ura[e]	Uracil	C4H4N2O2
ura[p]	Uracil	C4H4N2O2
uagmda[c]	Undecaprenyl-diphospho-N-a	C87H143N7O23P2
uaagmda[c]	Undecaprenyl-diphospho-N-a	C95H156N8O28P2
udcpp[c]	Undecaprenyl phosphate	C55H91O4P
udcpp[p]	Undecaprenyl phosphate	C55H91O4P
unaga[c]	Undecaprenyl diphospho N-a	C63H105NO12P2
udcpdp[c]	Undecaprenyl diphosphate	C55H92O7P2
udcpdp[p]	Undecaprenyl diphosphate	C55H92O7P2
ump[c]	UMP	C9H13N2O9P
ump[e]	UMP	C9H13N2O9P
ump[p]	UMP	C9H13N2O9P
ugmda[c]	UDP-N-acetylmuramoyl-L-ala	C41H65N9O28P2
uamag[c]	UDP-N-acetylmuramoyl-L-ala	C28H43N5O23P2
um4p[c]	UDP-N-acetylmuramoyl-L-ala	C38H60N8O27P2
ugmd[c]	UDP-N-acetylmuramoyl-L-ala	C35H55N7O26P2
uama[c]	UDP-N-acetylmuramoyl-L-ala	C23H36N4O20P2
uamr[c]	UDP-N-acetylmuramate	C20H31N3O19P2
uacmam[c]	UDP-N-acetyl-D-mannosami	C17H27N3O17P2
uacgam[c]	UDP-N-acetyl-D-glucosamine	C17H27N3O17P2
uacgam[e]	UDP-N-acetyl-D-glucosamine	C17H27N3O17P2
uacgam[p]	UDP-N-acetyl-D-glucosamine	C17H27N3O17P2
udpacgal[e]	UDP-N-acetyl-D-galactosami	C17H27N3O17P2
udpacgal[p]	UDP-N-acetyl-D-galactosami	C17H27N3O17P2
uaccg[c]	UDP-N-acetyl-3-O-(1-carboxy	C20H29N3O19P2
udpg[c]	UDPglucose	C15H24N2O17P2
udpg[e]	UDPglucose	C15H24N2O17P2
udpg[p]	UDPglucose	C15H24N2O17P2

udpgal[c]	UDPgalactose	C15H24N2O17P2
udpgal[e]	UDPgalactose	C15H24N2O17P2
udpgal[p]	UDPgalactose	C15H24N2O17P2
udpglcur[e]	UDP-D-glucuronate	C15H22N2O18P2
udpglcur[p]	UDP-D-glucuronate	C15H22N2O18P2
u3aga[c]	UDP-3-O-(3-hydroxytetradec	C31H53N3O19P2
u3hga[c]	UDP-3-O-(3-hydroxytetradec	C29H51N3O18P2
udp[c]	UDP	C9H14N2O12P2
q8[c]	Ubiquinone-8	C49H74O4
q8h2[c]	Ubiquinol-8	C49H76O4
tym[e]	Tyramine	C8H11NO
tym[p]	Tyramine	C8H11NO
murein3p3p[p]	two linked disacharide tripept	C68H108N12O38
murein4p4p[p]	two linked disacharide tetrap	C74H118N14O40
murein4p3p[p]	two linked disacharide tetrap	C71H113N13O39
murein5p5p[p]	two linked disacharide penta	C80H128N16O42
murein5p3p[p]	two linked disacharide penta	C74H118N14O40
murein5p4p[p]	two linked disacharide penta	C77H123N15O41
murein3px4p[p]	two disacharide linked murei	C71H111N13O38
murein4px4p[p]	two disacharide linked murei	C74H116N14O39
murein5px4p[p]	two disacharide linked murei	C77H121N15O40
murein5px3p[p]	two disacharide linked murei	C74H116N14O39
bwco1gdp[c]	tungsten bispterin cofactor m	C30H36N15O20P3S4W
bwcogdp[c]	tungsten bispterin cofactor g	C40H44N20O27P4S4W
bwco[c]	tungsten bispterin cofactor	C20H24N10O13P2S4W
wco[c]	tungsten binding cofactor	C10H12N5O8PS2W
tungs[c]	tungstate	H2O4W1
tungs[e]	tungstate	H2O4W1
tungs[p]	tungstate	H2O4W1
trnaval[c]	tRNA(Val)	R
trnatyr[c]	tRNA(Tyr)	R
trnatrp[c]	tRNA(Trp)	R
trnathr[c]	tRNA(Thr)	R
trnaser[c]	tRNA(Ser)	R
trnasecys[c]	tRNA(SeCys)	R
trnapro[c]	tRNA(Pro)	R
trnaphe[c]	tRNA(Phe)	R
trnamet[c]	tRNA(Met)	R
trnalys[c]	tRNA(Lys)	R
trnaleu[c]	tRNA(Leu)	R
trnaile[c]	tRNA(Ile)	R
trnahis[c]	tRNA(His)	R
trnagly[c]	tRNA(Gly)	R
trnagln[c]	tRNA(Gln)	R
trnacys[c]	tRNA(Cys)	R
trnaasp[c]	tRNA(Asp)	R
trnaasn[c]	tRNA(Asn)	C10H17O10PR2
trnaarg[c]	tRNA(Arg)	R

trnaala[c]	tRNA(Ala)	R
trnaglu[c]	tRNA (Glu)	R
tmao[c]	Trimethylamine N-oxide	C3H9NO
tmao[e]	Trimethylamine N-oxide	C3H9NO
tmao[p]	Trimethylamine N-oxide	C3H9NO
tma[c]	trimethylamine	C3H9N
tma[e]	trimethylamine	C3H9N
tma[p]	trimethylamine	C3H9N
tre[e]	Trehalose	C12H22O11
tre[p]	Trehalose	C12H22O11
td2coa[c]	trans-Tetradec-2-enoyl-CoA	C35H60N7O17P3S
tmrs2eACP[c]	trans-Tetradec-2-enoyl-[acyl-	C25H46N2O8PRS
od2coa[c]	trans-Octadec-2-enoyl-CoA	C39H68N7O17P3S
toctd2eACP[c]	trans-octadec-2-enoyl-[acyl-c	C29H54N2O8PRS
oc2coa[c]	trans-Oct-2-enoyl-CoA	C29H48N7O18P3S
toct2eACP[c]	trans-Oct-2-enoyl-[acyl-carrie	C19H34N2O8PRS
hdd2coa[c]	trans-Hexadec-2-enoyl-CoA	C37H64N7O17P3S
tpalm2eACP[c]	trans-Hexadec-2-enoyl-[acyl-	C27H50N2O8PRS
hx2coa[c]	trans-Hex-2-enoyl-CoA	C27H44N7O17P3S
thex2eACP[c]	trans-Hex-2-enoyl-[acyl-carri	C17H30N2O8PRS
dd2coa[c]	trans-Dodec-2-enoyl-CoA	C33H56N7O17P3S
tddec2eACP[c]	trans-Dodec-2-enoyl-[acyl-ca	C23H42N2O8PRS
dc2coa[c]	trans-Dec-2-enoyl-CoA	C31H52N7O17P3S
tdec2eACP[c]	trans-Dec-2-enoyl-[acyl-carri	C21H38N2O8PRS
t3c9palmeACP[c]	trans-3-cis-9-palmitoleoyl-[ac	C27H48N2O8PRS
t3c7mrseACP[c]	trans-3-cis-7-myristoleoyl-[ac	C25H44N2O8PRS
t3c5ddeceACP[c]	trans-3-cis-5-dodecenoyl-[ac	C23H40N2O8PRS
t3c11vaceACP[c]	trans-3-cis-11-vacceoyl-[acyl-	C29H52N2O8PRS
thym[c]	Thymine	C5H6N2O2
thym[e]	Thymine	C5H6N2O2
thym[p]	Thymine	C5H6N2O2
thymd[c]	Thymidine	C10H14N2O5
thymd[e]	Thymidine	C10H14N2O5
thymd[p]	Thymidine	C10H14N2O5
murein5p5p5p[p]	three linked disacharide pent	C120H192N24O63
murein4px4p4p[p]	three disacharide linked mur	C111H175N21O59
murein4px4px4p[p]	three disacharide linked mur	C111H173N21O58
murein5px4px4p[p]	three disacharide linked mur	C114H178N22O59
tsul[c]	Thiosulfate	H2O3S2
tsul[e]	Thiosulfate	H2O3S2
tsul[p]	Thiosulfate	H2O3S2
tcynt[c]	Thiocyanate	CHNS
tcynt[e]	Thiocyanate	CHNS
tcynt[p]	Thiocyanate	CHNS
thmpp[c]	Thiamine diphosphate	C12H19N4O7P2S
thmmp[c]	Thiamin monophosphate	C12H17N4O4PS
thm[c]	Thiamin	C12H17N4OS
thm[e]	Thiamin	C12H17N4OS

thm[p]	Thiamin	C12H17N4OS
tdecoa[c]	Tetradecenoyl-CoA (n-C14:1(	C35H60N7O17P3S
ttdcea[c]	tetradecenoate (n-C14:1)	C14H26O2
ttdcea[e]	tetradecenoate (n-C14:1)	C14H26O2
ttdcea[p]	tetradecenoate (n-C14:1)	C14H26O2
ttdceap[c]	Tetradecanoyl-phosphate (n-(	C14H27O5P
ttdcap[c]	Tetradecanoyl-phosphate (n-(	C14H29O5P
tdcoa[c]	Tetradecanoyl-CoA (n-C14:0(	C35H62N7O17P3S
ttdca[c]	tetradecanoate (n-C14:0)	C14H28O2
ttdca[e]	tetradecanoate (n-C14:0)	C14H28O2
ttdca[p]	tetradecanoate (n-C14:0)	C14H28O2
ttrcyc[e]	tetracycline	C22H24N2O8
ttrcyc[p]	tetracycline	C22H24N2O8
taur[e]	Taurine	C2H7NO3S
taur[p]	Taurine	C2H7NO3S
o2s[e]	Superoxide anion	O2
o2s[p]	Superoxide anion	O2
so2[c]	sulfur dioxide	O2S
so2[e]	sulfur dioxide	O2S
so2[p]	sulfur dioxide	O2S
sulfac[e]	sulfoacetate	C2H4O5S
sulfac[p]	sulfoacetate	C2H4O5S
so3[c]	Sulfite	H2O3S
so3[e]	Sulfite	H2O3S
so3[p]	Sulfite	H2O3S
so4[c]	Sulfate	H2O4S
so4[e]	Sulfate	H2O4S
so4[p]	Sulfate	H2O4S
suc6p[c]	Sucrose 6-phosphate	C12H23O14P
sucr[e]	Sucrose	C12H22O11
sucr[p]	Sucrose	C12H22O11
succoa[c]	Succinyl-CoA	C25H40N7O19P3S
sucsal[c]	Succinic semialdehyde	C4H6O3
succ[c]	Succinate	C4H6O4
succ[e]	Succinate	C4H6O4
succ[p]	Succinate	C4H6O4
stcoa[c]	Stearoyl-CoA (n-C18:0CoA)	C39H70N7O17P3S
rhcys[c]	S-Ribosyl-L-homocysteine	C9H17NO6S
spmd[c]	Spermidine	C7H19N3
spmd[e]	Spermidine	C7H19N3
spmd[p]	Spermidine	C7H19N3
na1[c]	Sodium	Na
na1[e]	Sodium	Na
na1[p]	Sodium	Na
g3pe[c]	sn-Glycero-3-phosphoethano	C5H14NO6P
g3pe[e]	sn-Glycero-3-phosphoethano	C5H14NO6P
g3pe[p]	sn-Glycero-3-phosphoethano	C5H14NO6P
g3pc[c]	sn-Glycero-3-phosphocholine	C8H20NO6P

g3pc[e]	sn-Glycero-3-phosphocholine	C8H20NO6P
g3pc[p]	sn-Glycero-3-phosphocholine	C8H20NO6P
g3pi[c]	sn-Glycero-3-phospho-1-inos	C9H19O11P
g3pi[e]	sn-Glycero-3-phospho-1-inos	C9H19O11P
g3pi[p]	sn-Glycero-3-phospho-1-inos	C9H17O11P
mmet[e]	S-Methyl-L-methionine	C6H13NO2S
mmet[p]	S-Methyl-L-methionine	C6H13NO2S
scl[c]	sirohydrochlorin	C42H46N4O16
sheme[c]	Siroheme	C42H46FeN4O16
ag[e]	silver	Ag
skm5p[c]	Shikimate 5-phosphate	C7H11O8P
skm[c]	Shikimate	C7H10O5
skm[e]	Shikimate	C7H10O5
skm[p]	Shikimate	C7H10O5
Sfglutth[c]	S-Formylglutathione	C11H17N3O7S
selnp[c]	Selenophosphate	H3O3PSe
slnt[e]	selenite	H2O3Se
slnt[p]	selenite	H2O3Se
sel[e]	Selenate	H2O4Se
sel[p]	Selenate	H2O4Se
s7p[c]	Sedoheptulose 7-phosphate	C7H15O10P
s17bp[c]	Sedoheptulose 1,7-bisphosp	C7H16O13P2
amet[c]	S-Adenosyl-L-methionine	C15H23N6O5S
ahcys[c]	S-Adenosyl-L-homocysteine	C14H20N6O5S
amob[c]	S-Adenosyl-4-methylthio-2-o	C15H20N5O6S
rfamp[e]	rifampin	C43H58N4O12
ribflv[c]	Riboflavin	C17H20N4O6
trdrd[c]	Reduced thioredoxin	XH2
rbflvrd[c]	Reduced riboflavin	C17H22N4O6
gthrd[c]	Reduced glutathione	C10H17N3O6S
gthrd[e]	Reduced glutathione	C10H17N3O6S
gthrd[p]	Reduced glutathione	C10H17N3O6S
fmnh2[c]	Reduced FMN	C17H23N4O9P
3hpalmACP[c]	R-3-hydroxypalmitoyl-[acyl-ca	C27H52N2O9PRS
quln[c]	Quinolinate	C7H5NO4
quin[e]	Quinate	C7H12O6
quin[p]	Quinate	C7H12O6
pyr[c]	Pyruvate	C3H4O3
pyr[e]	Pyruvate	C3H4O3
pyr[p]	Pyruvate	C3H4O3
pdx5p[c]	Pyridoxine 5'-phosphate	C8H12NO6P
pydxn[e]	Pyridoxine	C8H11NO3
pydxn[p]	Pyridoxine	C8H11NO3
pyam5p[c]	Pyridoxamine 5'-phosphate	C8H13N2O5P
pydam[e]	Pyridoxamine	C8H12N2O2
pydam[p]	Pyridoxamine	C8H12N2O2
pydx5p[c]	Pyridoxal 5'-phosphate	C8H10NO6P
pydx[c]	Pyridoxal	C8H9NO3

pydx[e]	Pyridoxal	C8H9NO3
pydx[p]	Pyridoxal	C8H9NO3
ptrc[c]	Putrescine	C4H12N2
ptrc[e]	Putrescine	C4H12N2
ptrc[p]	Putrescine	C4H12N2
psclys[e]	psicoselysine	C12H24N2O7
psclys[p]	psicoselysine	C12H24N2O7
pppg9[c]	Protoporphyrinogen IX	C34H40N4O4
ppp9[c]	Protoporphyrin	C34H34N4O4
pheme[c]	Protoheme	C34H32FeN4O4
pheme[e]	Protoheme	C34H32FeN4O4
pheme[p]	Protoheme	C34H32FeN4O4
dsbcrd[p]	protein disulfide isomerase II	XH2
dsbcox[p]	protein disulfide isomerase II	X
ppa[c]	Propionate (n-C3:0)	C3H6O2
ppa[e]	Propionate (n-C3:0)	C3H6O2
ppa[p]	Propionate (n-C3:0)	C3H6O2
ppcoa[c]	Propanoyl-CoA	C24H40N7O17P3S
ppap[c]	Propanoyl phosphate	C3H7O5P
ppal[e]	Propanal	C3H6O
ppal[p]	Propanal	C3H6O
pphn[c]	Prephenate	C10H10O6
k[c]	potassium	K
k[e]	potassium	K
k[p]	potassium	K
ppbng[c]	Porphobilinogen	C10H14N2O4
pmeACP[c]	Pimeloyl-[acyl-carrier protein]	C8H13O3R
pimACP[c]	Pimeloyl-[acyl-carrier protein]	C7H10O3R
tyrp[e]	Phosphotyrosine	C9H12NO6P
tyrp[p]	Phosphotyrosine	C9H12NO6P
ppt[e]	Phosphonate	H3O3P
ppt[p]	Phosphonate	H3O3P
pep[c]	Phosphoenolpyruvate	C3H5O6P
ps140[c]	phosphatidylserine (ditetrade	C34H66N1O10P1
ps141[c]	phosphatidylserine (ditetrade	C34H62N1O10P1
ps180[c]	phosphatidylserine (dioctade	C42H82N1O10P1
ps181[c]	phosphatidylserine (dioctade	C42H78N1O10P1
ps160[c]	phosphatidylserine (dihexade	C38H74N1O10P1
ps161[c]	phosphatidylserine (dihexade	C38H70N1O10P1
ps120[c]	phosphatidylserine (didodeca	C30H58N1O10P1
pgp140[c]	Phosphatidylglycerophospha	C34H68O13P2
pgp140[p]	Phosphatidylglycerophospha	C34H68O13P2
pgp141[c]	Phosphatidylglycerophospha	C34H64O13P2
pgp141[p]	Phosphatidylglycerophospha	C34H64O13P2
pgp180[c]	Phosphatidylglycerophospha	C42H84O13P2
pgp180[p]	Phosphatidylglycerophospha	C42H84O13P2
pgp181[c]	Phosphatidylglycerophospha	C42H80O13P2
pgp181[p]	Phosphatidylglycerophospha	C42H80O13P2

pgp160[c]	Phosphatidylglycerophosphat	C38H76O13P2
pgp160[p]	Phosphatidylglycerophosphat	C38H76O13P2
pgp161[c]	Phosphatidylglycerophosphat	C38H72O13P2
pgp161[p]	Phosphatidylglycerophosphat	C38H72O13P2
pgp120[c]	Phosphatidylglycerophosphat	C30H60O13P2
pgp120[p]	Phosphatidylglycerophosphat	C30H60O13P2
pg140[c]	Phosphatidylglycerol (ditetrac	C34H67O10P1
pg140[p]	Phosphatidylglycerol (ditetrac	C34H67O10P1
pg141[c]	Phosphatidylglycerol (ditetrac	C34H63O10P1
pg141[p]	Phosphatidylglycerol (ditetrac	C34H63O10P1
pg180[c]	Phosphatidylglycerol (dioctad	C42H83O10P1
pg180[p]	Phosphatidylglycerol (dioctad	C42H83O10P1
pg181[c]	Phosphatidylglycerol (dioctad	C42H79O10P1
pg181[p]	Phosphatidylglycerol (dioctad	C42H79O10P1
pg160[c]	Phosphatidylglycerol (dihexa	C38H75O10P1
pg160[p]	Phosphatidylglycerol (dihexa	C38H75O10P1
pg161[c]	Phosphatidylglycerol (dihexa	C38H71O10P1
pg161[p]	Phosphatidylglycerol (dihexa	C38H71O10P1
pg120[c]	Phosphatidylglycerol (didode	C30H59O10P1
pg120[p]	Phosphatidylglycerol (didode	C30H59O10P1
pe140[c]	phosphatidylethanolamine (di	C33H66N1O8P1
pe140[p]	phosphatidylethanolamine (di	C33H66N1O8P1
pe141[c]	phosphatidylethanolamine (di	C33H62N1O8P1
pe141[p]	phosphatidylethanolamine (di	C33H62N1O8P1
pe180[c]	phosphatidylethanolamine (di	C41H82N1O8P1
pe180[p]	phosphatidylethanolamine (di	C41H82N1O8P1
pe181[c]	phosphatidylethanolamine (di	C41H78N1O8P1
pe181[p]	phosphatidylethanolamine (di	C41H78N1O8P1
pe160[c]	phosphatidylethanolamine (di	C37H74N1O8P1
pe160[p]	phosphatidylethanolamine (di	C37H74N1O8P1
pe161[c]	phosphatidylethanolamine (di	C37H70N1O8P1
pe161[p]	phosphatidylethanolamine (di	C37H70N1O8P1
pe120[c]	phosphatidylethanolamine (di	C29H58N1O8P1
pe120[p]	phosphatidylethanolamine (di	C29H58N1O8P1
pi[c]	Phosphate	H3O4P
pi[e]	Phosphate	H3O4P
pi[p]	Phosphate	H3O4P
phpyr[c]	Phenylpyruvate	C9H8O3
pppn[c]	Phenylpropanoate	C9H10O2
pppn[e]	Phenylpropanoate	C9H10O2
pppn[p]	Phenylpropanoate	C9H10O2
pacald[e]	Phenylacetaldehyde	C8H8O
pacald[p]	Phenylacetaldehyde	C8H8O
peamn[e]	Phenethylamine	C8H11N
peamn[p]	Phenethylamine	C8H11N
dsbard[p]	periplasmic protein disulfide i	XH2
dsbaox[p]	periplasmic protein disulfide i	X
4crsol[c]	p-Cresol	C7H8O

pan4p[c]	Pantetheine 4'-phosphate	C11H23N2O7PS
pmtcoa[c]	Palmitoyl-CoA (n-C16:0CoA)	C37H66N7O17P3S
palmACP[c]	Palmitoyl-ACP (n-C16:0ACP)	C27H52N2O8PRS
ap5a[c]	P1,P5-Bis(5'-adenosyl) penta	C20H29N10O22P5
gp4g[c]	P1,P4-Bis(5'-guanosyl) tetrap	C20H28N10O21P4
ap4a[c]	P1,P4-Bis(5'-adenosyl) tetrap	C20H28N10O19P4
trdox[c]	Oxidized thioredoxin	X
gthox[c]	Oxidized glutathione	C20H32N6O12S2
gthox[e]	Oxidized glutathione	C20H32N6O12S2
gthox[p]	Oxidized glutathione	C20H32N6O12S2
oaa[c]	Oxaloacetate	C4H4O5
suchms[c]	O-Succinyl-L-homoserine	C8H13NO6
sbzcoa[c]	O-Succinylbenzoyl-CoA	C32H44N7O20P3S
sucbz[c]	o-Succinylbenzoate	C11H10O5
orot5p[c]	Orotidine 5'-phosphate	C10H13N2O11P
orot[c]	Orotate	C5H4N2O4
orot[e]	Orotate	C5H4N2O4
orot[p]	Orotate	C5H4N2O4
orn[c]	Ornithine	C5H12N2O2
orn[e]	Ornithine	C5H12N2O2
orn[p]	Ornithine	C5H12N2O2
pser-L[c]	O-Phospho-L-serine	C3H8NO6P
pser-L[e]	O-Phospho-L-serine	C3H8NO6P
pser-L[p]	O-Phospho-L-serine	C3H8NO6P
phom[c]	O-Phospho-L-homoserine	C4H10NO6P
phthr[c]	O-Phospho-4-hydroxy-L-thre	C4H10NO7P
occoa[c]	Octanoyl-CoA (n-C8:0CoA)	C29H50N7O17P3S
ocACP[c]	Octanoyl-ACP (n-C8:0ACP)	C19H36N2O8PRS
octapb[c]	octanoate (protein bound)	C8H14O
octa[c]	octanoate (n-C8:0)	C8H16O2
octa[e]	octanoate (n-C8:0)	C8H16O2
octa[p]	octanoate (n-C8:0)	C8H16O2
odecoa[c]	Octadecenoyl-CoA (n-C18:1	C39H68N7O17P3S
ocdcea[c]	octadecenoate (n-C18:1)	C18H34O2
ocdcea[e]	octadecenoate (n-C18:1)	C18H34O2
ocdcea[p]	octadecenoate (n-C18:1)	C18H34O2
ocdceap[c]	Octadecanoyl-phosphate (n-	C18H35O5P
ocdcap[c]	Octadecanoyl-phosphate (n-	C18H37O5P
ocdcaACP[c]	Octadecanoyl-ACP (n-C18:0	C29H56N2O8PRS
ocdca[c]	octadecanoate (n-C18:0)	C18H36O2
ocdca[e]	octadecanoate (n-C18:0)	C18H36O2
ocdca[p]	octadecanoate (n-C18:0)	C18H36O2
acser[c]	O-Acetyl-L-serine	C5H9NO4
acser[e]	O-Acetyl-L-serine	C5H9NO4
acser[p]	O-Acetyl-L-serine	C5H9NO4
o2[c]	O2	O2
o2[e]	O2	O2
o2[p]	O2	O2

sl26da[c]	N-Succinyl-LL-2,6-diaminohe	C11H18N2O7
sl2a6o[c]	N-Succinyl-2-L-amino-6-oxoh	C11H15NO8
novbcn[e]	novobiocin	C31H36N2O11
nmn[c]	NMN	C11H15N2O8P
nmn[e]	NMN	C11H15N2O8P
nmn[p]	NMN	C11H15N2O8P
n2o[c]	Nitrous oxide	N2O
n2o[e]	Nitrous oxide	N2O
n2o[p]	Nitrous oxide	N2O
no2[c]	Nitrite	HNO2
no2[e]	Nitrite	HNO2
no2[p]	Nitrite	HNO2
no[c]	Nitric oxide	NO
no[e]	Nitric oxide	NO
no[p]	Nitric oxide	NO
no3[c]	Nitrate	HNO3
no3[e]	Nitrate	HNO3
no3[p]	Nitrate	HNO3
nicrnt[c]	Nicotinate D-ribonucleotide	C11H15NO9P
nac[e]	Nicotinate	C6H5NO2
nac[p]	Nicotinate	C6H5NO2
nadph[c]	Nicotinamide adenine dinucle	C21H30N7O17P3
nadp[c]	Nicotinamide adenine dinucle	C21H28N7O17P3
nadh[c]	Nicotinamide adenine dinucle	C21H29N7O14P2
nad[c]	Nicotinamide adenine dinucle	C21H28N7O14P2
ni2[c]	nickel	Ni
ni2[e]	nickel	Ni
ni2[p]	nickel	Ni
fmettrna[c]	N-Formylmethionyl-tRNA	C6H9NO2SR
cbasp[c]	N-Carbamoyl-L-aspartate	C5H8N2O5
acnam[c]	N-Acetylneuraminate	C11H19NO9
acnam[e]	N-Acetylneuraminate	C11H19NO9
acnam[p]	N-Acetylneuraminate	C11H19NO9
acmum6p[c]	N-acetylmuramate 6-phospha	C11H20NO11P
acmum[e]	N-Acetylmuramate	C11H19NO8
acmum[p]	N-Acetylmuramate	C11H19NO8
acg5p[c]	N-Acetyl-L-glutamyl 5-phospl	C7H12NO8P
acg5sa[c]	N-Acetyl-L-glutamate 5-semia	C7H11NO4
acglu[c]	N-Acetyl-L-glutamate	C7H11NO5
acmanap[c]	N-Acetyl-D-mannosamine 6-p	C8H16NO9P
acmana[c]	N-Acetyl-D-mannosamine	C8H15NO6
acmana[e]	N-Acetyl-D-mannosamine	C8H15NO6
acmana[p]	N-Acetyl-D-mannosamine	C8H15NO6
anhgm3p[c]	N-Acetyl-D-glucosamine(anh	C34H54N6O19
anhgm3p[p]	N-Acetyl-D-glucosamine(anh	C34H54N6O19
anhgm4p[c]	N-Acetyl-D-glucosamine(anh	C37H59N7O20
anhgm4p[p]	N-Acetyl-D-glucosamine(anh	C37H59N7O20
anhgm[c]	N-Acetyl-D-glucosamine(anh	C19H30N2O12

anhgm[e]	N-Acetyl-D-glucosamine(anh	C19H30N2O12
anhgm[p]	N-Acetyl-D-glucosamine(anh	C19H30N2O12
acgam6p[c]	N-Acetyl-D-glucosamine 6-ph	C8H16NO9P
acgam1p[c]	N-Acetyl-D-glucosamine 1-ph	C8H16NO9P
acgam1p[e]	N-Acetyl-D-glucosamine 1-ph	C8H16NO9P
acgam1p[p]	N-Acetyl-D-glucosamine 1-ph	C8H16NO9P
acgam[c]	N-Acetyl-D-glucosamine	C8H15NO6
acgam[e]	N-Acetyl-D-glucosamine	C8H15NO6
acgam[p]	N-Acetyl-D-glucosamine	C8H15NO6
acgal1p[e]	N-Acetyl-D-galactosamine 1-	C8H16NO9P
acgal1p[p]	N-Acetyl-D-galactosamine 1-	C8H16NO9P
acgal[e]	N-Acetyl-D-galactosamine	C8H17NO6
acgal[p]	N-Acetyl-D-galactosamine	C8H15NO6
n8aspmd[c]	N8-Acetylspermidine	C9H21N3O
dcamp[c]	N6-(1,2-Dicarboxyethyl)-AM	C14H18N5O11P
sucorn[c]	N2-Succinyl-L-ornithine	C9H16N2O5
sucgsa[c]	N2-Succinyl-L-glutamate 5-s	C9H13NO6
sucglu[c]	N2-Succinyl-L-glutamate	C9H13NO7
sucarg[c]	N2-Succinyl-L-arginine	C10H18N4O5
fgam[c]	N2-Formyl-N1-(5-phospho-D-	C8H15N2O9P
acorn[c]	N2-Acetyl-L-ornithine	C7H14N2O3
N1aspmd[c]	N1-Acetylspermidine	C9H21N3O
gar[c]	N1-(5-Phospho-D-ribosyl)gly	C7H15N2O8P
chtbs[e]	N,N'-diacetylchitobiose	C16H28N2O11
chtbs[p]	N,N'-diacetylchitobiose	C16H28N2O11
argsuc[c]	N(omega)-(L-Arginino)succin	C10H18N4O6
pran[c]	N-(5-Phospho-D-ribosyl)anth	C12H16NO9P
4ppcys[c]	N-((R)-4-Phosphopantotheno	C12H23N2O9PS
myrsACP[c]	Myristoyl-ACP (n-C14:0ACP)	C25H48N2O8PRS
minohp[e]	myo-Inositol hexakisphospha	C6H18O24P6
inost[c]	myo-Inositol	C6H12O6
inost[e]	myo-Inositol	C6H12O6
inost[p]	myo-Inositol	C6H12O6
mocogdp[c]	molybdopterin guanine dinucl	C20H24N10O15P2S2M
mpt[c]	molybdopterin	C10H12N5O6PS2Cu
moco[c]	molybdenum cofactor	C10H12N5O8PS2Mo
mobd[c]	Molybdate	H2MoO4
mobd[e]	Molybdate	H2MoO4
mobd[p]	Molybdate	H2MoO4
moadcosh[c]	MoaD Protein with thiocarbo	C1H1O1S1X
moadcoo[c]	MoaD Protein with carboxyla	C1O2H1X
moadamp[c]	MoaD Protein with bound AM	C11H13N5O8P1X
mn2[c]	Mn2+	Mn
mn2[e]	Mn2+	Mn
mn2[p]	Mn2+	Mn
mincyc[e]	minocycline	C23H27N3O7
mincyc[p]	minocycline	C23H27N3O7
micit[c]	methylisocitrate	C7H10O7

mthgxl[c]	Methylglyoxal	C3H4O2
meoh[c]	Methanol	CH4O1
meoh[e]	Methanol	CH4O1
meoh[p]	Methanol	CH4O1
mso3[e]	methanesulfonate	CH4O3S
mso3[p]	methanesulfonate	CH4O3S
26dap-M[c]	meso-2,6-Diaminoheptanedic	C7H14N2O4
26dap-M[e]	meso-2,6-Diaminoheptanedic	C7H14N2O4
26dap-M[p]	meso-2,6-Diaminoheptanedic	C7H14N2O4
mercppyr[c]	Mercaptopyruvate	C3H4O3S
mqn8[c]	Menaquinone 8	C51H72O2
mql8[c]	Menaquinol 8	C51H74O2
melib[e]	Melibiose	C12H22O11
melib[p]	Melibiose	C12H22O11
malttr[c]	Maltotriose	C18H32O16
malttr[e]	Maltotriose	C18H32O16
malttr[p]	Maltotriose	C18H32O16
maltttr[c]	Maltotetraose	C24H42O21
maltttr[e]	Maltotetraose	C24H42O21
maltttr[p]	Maltotetraose	C24H42O21
malt6p[c]	Maltose 6'-phosphate	C12H23O14P
malt[c]	Maltose	C12H22O11
malt[e]	Maltose	C12H22O11
malt[p]	Maltose	C12H22O11
maltpt[c]	Maltopentaose	C30H52O26
maltpt[e]	Maltopentaose	C30H52O26
maltpt[p]	Maltopentaose	C30H52O26
malthx[c]	Maltohexaose	C36H62O31
malthx[e]	Maltohexaose	C36H62O31
malthx[p]	Maltohexaose	C36H62O31
malthp[c]	Maltoheptaose	C42H72O36
malcoame[c]	malonyl-CoA methyl ester	C25H40N7O19P3S
malcoa[c]	Malonyl-CoA	C24H38N7O19P3S
malACP[c]	Malonyl-[acyl-carrier protein]	C3H3O3R
mg2[c]	magnesium	Mg
mg2[e]	magnesium	Mg
mg2[p]	magnesium	Mg
xylu-L[e]	L-Xylulose	C5H10O5
xylu-L[p]	L-Xylulose	C5H10O5
valtrna[c]	L-Valyl-tRNA(Val)	C5H9NOR
val-L[c]	L-Valine	C5H11NO2
val-L[e]	L-Valine	C5H11NO2
val-L[p]	L-Valine	C5H11NO2
tyrtrna[c]	L-Tyrosyl-tRNA(Tyr)	C9H9NO2R
tyr-L[c]	L-Tyrosine	C9H11NO3
tyr-L[e]	L-Tyrosine	C9H11NO3
tyr-L[p]	L-Tyrosine	C9H11NO3
trptrna[c]	L-Tryptophanyl-tRNA(Trp)	C11H10N2OR

trp-L[c]	L-Tryptophan	C11H12N2O2
trp-L[e]	L-Tryptophan	C11H12N2O2
trp-L[p]	L-Tryptophan	C11H12N2O2
thrtrna[c]	L-Threonyl-tRNA(Thr)	C4H7NO2R
thrp[e]	L-Threonine O-3-phosphate	C4H10NO6P
thrp[p]	L-Threonine O-3-phosphate	C4H10NO6P
thr-L[c]	L-Threonine	C4H9NO3
thr-L[e]	L-Threonine	C4H9NO3
thr-L[p]	L-Threonine	C4H9NO3
tartr-L[e]	L-tartrate	C4H6O6
tartr-L[p]	L-tartrate	C4H6O6
sertrna[c]	L-Seryl-tRNA(Ser)	C3H5NO2R
ser-L[c]	L-Serine	C3H7NO3
ser-L[e]	L-Serine	C3H7NO3
ser-L[p]	L-Serine	C3H7NO3
sectrna[c]	L-Selenocysteinyl-tRNA(Sec)	C3H5NOSeR
rmn[e]	L-Rhamnose	C6H12O5
rmn[p]	L-Rhamnose	C6H12O5
protrna[c]	L-Prolyl-tRNA(Pro)	C5H9NOR
progly[c]	L-Prolinylglycine	C7H12N2O3
progly[e]	L-Prolinylglycine	C7H12N2O3
progly[p]	L-Prolinylglycine	C7H12N2O3
pro-L[c]	L-Proline	C5H9NO2
pro-L[e]	L-Proline	C5H9NO2
pro-L[p]	L-Proline	C5H9NO2
phetrna[c]	L-Phenylalanyl-tRNA(Phe)	C9H9NOR
phe-L[c]	L-Phenylalanine	C9H11NO2
phe-L[e]	L-Phenylalanine	C9H11NO2
phe-L[p]	L-Phenylalanine	C9H11NO2
mettrna[c]	L-Methionyl-tRNA (Met)	C5H9NOSR
metsox-R-L[c]	L-methionine-R-sulfoxide	C5H11NO3S
metsox-R-L[e]	L-methionine-R-sulfoxide	C5H11NO3S
metsox-R-L[p]	L-methionine-R-sulfoxide	C5H11NO3S
metsox-S-L[c]	L-Methionine Sulfoxide	C5H11NO3S
metsox-S-L[e]	L-Methionine Sulfoxide	C5H11NO3S
metsox-S-L[p]	L-Methionine Sulfoxide	C5H11NO3S
met-L[c]	L-Methionine	C5H11NO2S
met-L[e]	L-Methionine	C5H11NO2S
met-L[p]	L-Methionine	C5H11NO2S
mal-L[c]	L-Malate	C4H6O5
mal-L[e]	L-Malate	C4H6O5
mal-L[p]	L-Malate	C4H6O5
lyx-L[e]	L-Lyxose	C5H10O5
lyx-L[p]	L-Lyxose	C5H10O5
lystrna[c]	L-Lysine-tRNA (Lys)	C6H12N2OR
lys-L[c]	L-Lysine	C6H14N2O2
lys-L[e]	L-Lysine	C6H14N2O2
lys-L[p]	L-Lysine	C6H14N2O2

leutrna[c]	L-Leucyl-tRNA(Leu)	C6H11NOR
leu-L[c]	L-Leucine	C6H13NO2
leu-L[e]	L-Leucine	C6H13NO2
leu-L[p]	L-Leucine	C6H13NO2
lac-L[c]	L-Lactate	C3H6O3
lac-L[e]	L-Lactate	C3H6O3
lac-L[p]	L-Lactate	C3H6O3
lald-L[c]	L-Lactaldehyde	C3H6O2
26dap-LL[c]	LL-2,6-Diaminoheptanedioat	C7H14N2O4
iletrna[c]	L-Isoleucyl-tRNA(Ile)	C6H11NOR
ile-L[c]	L-Isoleucine	C6H13NO2
ile-L[e]	L-Isoleucine	C6H13NO2
ile-L[p]	L-Isoleucine	C6H13NO2
lipopb[c]	lipoate (protein bound)	C8H13OS2
lipoate[e]	Lipoate	C8H14O2S2
lipoate[p]	Lipoate	C8H14O2S2
idon-L[e]	L-Idonate	C6H12O7
idon-L[p]	L-Idonate	C6H12O7
hom-L[c]	L-Homoserine	C4H9NO3
hom-L[e]	L-Homoserine	C4H9NO3
hom-L[p]	L-Homoserine	C4H9NO3
hcys-L[c]	L-Homocysteine	C4H9NO2S
histrna[c]	L-Histidyl-tRNA(His)	C6H7N3OR
hisp[c]	L-Histidinol phosphate	C6H12N3O4P
histd[c]	L-Histidinol	C6H11N3O
his-L[c]	L-Histidine	C6H9N3O2
his-L[e]	L-Histidine	C6H9N3O2
his-L[p]	L-Histidine	C6H9N3O2
glutrna[c]	L-Glutamyl-tRNA(Glu)	C5H7NO3R
glntrna[c]	L-Glutaminyl-tRNA(Gln)	C5H8N2O2R
gln-L[c]	L-Glutamine	C5H10N2O3
gln-L[e]	L-Glutamine	C5H10N2O3
gln-L[p]	L-Glutamine	C5H10N2O3
glu5sa[c]	L-Glutamate 5-semialdehyde	C5H9NO3
glu5p[c]	L-Glutamate 5-phosphate	C5H10NO7P
glu1sa[c]	L-Glutamate 1-semialdehyde	C5H9NO3
glu-L[c]	L-Glutamate	C5H9NO4
glu-L[e]	L-Glutamate	C5H9NO4
glu-L[p]	L-Glutamate	C5H9NO4
galctn-L[e]	L-Galactonate	C6H12O7
galctn-L[p]	L-Galactonate	C6H12O7
fuc-L[e]	L-Fucose	C6H12O5
fuc-L[p]	L-Fucose	C6H12O5
cystrna[c]	L-Cysteinyl-tRNA(Cys)	C3H5NOSR
cys-L[c]	L-Cysteine	C3H7NO2S
cys-L[e]	L-Cysteine	C3H7NO2S
cys-L[p]	L-Cysteine	C3H7NO2S
cyst-L[c]	L-Cystathionine	C7H14N2O4S

citr-L[c]	L-Citrulline	C6H13N3O3
crn[c]	L-Carnitine	C7H15NO3
crn[e]	L-Carnitine	C7H15NO3
crn[p]	L-Carnitine	C7H15NO3
asptrna[c]	L-Aspartyl-tRNA(Asp)	C4H5NO3R
aspsa[c]	L-Aspartate 4-semialdehyde	C4H7NO3
asp-L[c]	L-Aspartate	C4H7NO4
asp-L[e]	L-Aspartate	C4H7NO4
asp-L[p]	L-Aspartate	C4H7NO4
asntrna[c]	L-Asparaginyl-tRNA(Asn)	C14H23N2O12PR2
asn-L[c]	L-Asparagine	C4H8N2O3
asn-L[e]	L-Asparagine	C4H8N2O3
asn-L[p]	L-Asparagine	C4H8N2O3
ascb6p[c]	L-ascorbate-6-phosphate	C6H9O9P
ascb-L[e]	L-Ascorbate	C6H8O6
ascb-L[p]	L-Ascorbate	C6H8O6
argtrna[c]	L-Arginyl-tRNA(Arg)	C6H12N4OR
arg-L[c]	L-Arginine	C6H14N4O2
arg-L[e]	L-Arginine	C6H14N4O2
arg-L[p]	L-Arginine	C6H14N4O2
arab-L[e]	L-Arabinose	C5H10O5
arab-L[p]	L-Arabinose	C5H10O5
athr-L[c]	L-Allo-threonine	C4H9NO3
alatrna[c]	L-Alanyl-tRNA(Ala)	C3H5NOR
LalaLglu[c]	L-alanine-L-glutamate	C8H14N2O5
LalaLglu[e]	L-alanine-L-glutamate	C8H14N2O5
LalaLglu[p]	L-alanine-L-glutamate	C8H14N2O5
LalaDgluMdapDala[c]	L-alanine-D-glutamate-meso-	C18H31N5O9
LalaDgluMdapDala[e]	L-alanine-D-glutamate-meso-	C18H31N5O9
LalaDgluMdapDala[p]	L-alanine-D-glutamate-meso-	C18H31N5O9
LalaDgluMdap[c]	L-alanine-D-glutamate-meso-	C15H26N4O8
LalaDgluMdap[e]	L-alanine-D-glutamate-meso-	C15H26N4O8
LalaDgluMdap[p]	L-alanine-D-glutamate-meso-	C15H26N4O8
LalaDglu[c]	L-alanine-D-glutamate	C8H14N2O5
LalaDglu[e]	L-alanine-D-glutamate	C8H14N2O5
LalaDglu[p]	L-alanine-D-glutamate	C8H14N2O5
ala-L[c]	L-Alanine	C3H7NO2
ala-L[e]	L-Alanine	C3H7NO2
ala-L[p]	L-Alanine	C3H7NO2
lcts[e]	Lactose	C12H22O11
lcts[p]	Lactose	C12H22O11
2aobut[c]	L-2-Amino-3-oxobutanoate	C4H7NO3
kdo2lipid4[e]	KDO(2)-lipid IV(A)	C84H154N2O37P2
itp[c]	ITP	C10H15N4O14P3
ipdp[c]	Isopentenyl diphosphate	C5H12O7P2
icit[c]	Isocitrate	C6H8O7
ichor[c]	Isochorismate	C10H10O6
isetac[e]	Isethionic acid	C2H6O4S

isetac[p]	Isethionic acid	C2H6O4S
iscu-2fe2s2[c]	IscU with two bound [2Fe-2S	H4O2S10Fe4R
iscu-4fe4s[c]	IscU with bound [4Fe-4S] clu	H6O2S10Fe4R
iscu-2fe2s[c]	IscU with bound [2Fe-2S] clu	H6O2S8Fe2R
iscu[c]	IscU scaffold protein	H8O2S6R
iscssh[c]	IscS with bound sulfur	HS2R
iscs[c]	IscS sulfur acceptor protein	HSR
ins[c]	Inosine	C10H12N4O5
ins[e]	Inosine	C10H12N4O5
ins[p]	Inosine	C10H12N4O5
pppi[c]	Inorganic triphosphate	H5O10P3
indole[c]	Indole	C8H7N
indole[e]	Indole	C8H7N
indole[p]	Indole	C8H7N
imp[c]	IMP	C10H13N4O8P
imp[e]	IMP	C10H13N4O8P
imp[p]	IMP	C10H13N4O8P
iasp[c]	Iminoaspartate	C4H5NO4
idp[c]	IDP	C10H14N4O11P2
hxan[c]	Hypoxanthine	C5H4N4O
hxan[e]	Hypoxanthine	C5H4N4O
hxan[p]	Hypoxanthine	C5H4N4O
hpyr[c]	Hydroxypyruvate	C3H4O4
hmgth[c]	hydroxymethylglutathione	C11H19N3O7S
hmbil[c]	Hydroxymethylbilane	C40H46N4O17
hqn[c]	Hydroquinone	C6H6O2
h2s[c]	Hydrogen sulfide	H2S
h2s[e]	Hydrogen sulfide	H2S
h2s[p]	Hydrogen sulfide	H2S
h2o2[c]	Hydrogen peroxide	H2O2
h2o2[e]	Hydrogen peroxide	H2O2
h2o2[p]	Hydrogen peroxide	H2O2
cyan[c]	Hydrogen cyanide	CHN
cyan[e]	Hydrogen cyanide	CHN
cyan[p]	Hydrogen cyanide	CHN
hg2[c]	Hg2+	Hg
hg2[e]	Hg2+	Hg
hg2[p]	Hg2+	Hg
hxcoa[c]	Hexanoyl-CoA (n-C6:0CoA)	C27H46N7O18P3S
hexACP[c]	Hexanoyl-ACP (n-C6:0ACP)	C17H32N2O8PRS
hxa[c]	Hexanoate (n-C6:0)	C6H12O2
hxa[e]	Hexanoate (n-C6:0)	C6H12O2
hxa[p]	Hexanoate (n-C6:0)	C6H12O2
hdcoa[c]	Hexadecenoyl-CoA (n-C16:1	C37H64N7O17P3S
hdcea[c]	Hexadecenoate (n-C16:1)	C16H30O2
hdcea[e]	Hexadecenoate (n-C16:1)	C16H30O2
hdcea[p]	Hexadecenoate (n-C16:1)	C16H30O2
hdceap[c]	Hexadecanoyl-phosphate (n-	C16H31O5P

hdcap[c]	Hexadecanoyl-phosphate (n-	C16H33O5P
hdca[c]	Hexadecanoate (n-C16:0)	C16H32O2
hdca[e]	Hexadecanoate (n-C16:0)	C16H32O2
hdca[p]	Hexadecanoate (n-C16:0)	C16H32O2
h2o[c]	H2O	H2O
h2o[e]	H2O	H2O
h2o[p]	H2O	H2O
h2[e]	H2	H2
h2[p]	H2	H2
h[c]	H+	H
h[e]	H+	H
h[p]	H+	H
gdptp[c]	Guanosine 3'-diphosphate 5'-	C10H18N5O20P5
ppgpp[c]	Guanosine 3',5'-bis(diphosph	C10H17N5O17P4
gsn[c]	Guanosine	C10H13N5O5
gsn[e]	Guanosine	C10H13N5O5
gsn[p]	Guanosine	C10H13N5O5
gua[c]	Guanine	C5H5N5O
gua[e]	Guanine	C5H5N5O
gua[p]	Guanine	C5H5N5O
gtp[c]	GTP	C10H16N5O14P3
gtp[e]	GTP	C10H16N5O14P3
gtp[p]	GTP	C10H16N5O14P3
gmp[c]	GMP	C10H14N5O8P
gmp[e]	GMP	C10H14N5O8P
gmp[p]	GMP	C10H14N5O8P
glx[c]	Glyoxylate	C2H2O3
glytrna[c]	Glycyl-tRNA(Gly)	C2H3NOR
glyclt[c]	Glycolate	C2H4O3
glyclt[e]	Glycolate	C2H4O3
glyclt[p]	Glycolate	C2H4O3
gcald[c]	Glycolaldehyde	C2H4O2
glycogen[c]	glycogen	C6H10O5
glyb[c]	Glycine betaine	C5H11NO2
glyb[e]	Glycine betaine	C5H11NO2
glyb[p]	Glycine betaine	C5H11NO2
gly[c]	Glycine	C2H5NO2
gly[e]	Glycine	C2H5NO2
gly[p]	Glycine	C2H5NO2
g3ps[c]	Glycerophosphoserine	C6H14NO8P
g3ps[e]	Glycerophosphoserine	C6H14NO8P
g3ps[p]	Glycerophosphoserine	C6H14NO8P
g3pg[c]	Glycerophosphoglycerol	C6H15O8P
g3pg[e]	Glycerophosphoglycerol	C6H15O8P
g3pg[p]	Glycerophosphoglycerol	C6H15O8P
glyc3p[c]	Glycerol 3-phosphate	C3H9O6P
glyc3p[e]	Glycerol 3-phosphate	C3H9O6P
glyc3p[p]	Glycerol 3-phosphate	C3H9O6P

glyc2p[c]	Glycerol 2-phosphate	C3H9O6P
glyc2p[e]	Glycerol 2-phosphate	C3H9O6P
glyc2p[p]	Glycerol 2-phosphate	C3H9O6P
glyc[c]	Glycerol	C3H8O3
glyc[e]	Glycerol	C3H8O3
glyc[p]	Glycerol	C3H8O3
g3p[c]	Glyceraldehyde 3-phosphate	C3H7O6P
gmeACP[c]	Glutaryl-[acyl-carrier protein]	C6H9O3R
grxrd[c]	glutaredoxin (reduced)	XH2
grxox[c]	glutaredoxin (oxidized)	X
grdp[c]	Geranyl diphosphate	C10H20O7P2
gdp[c]	GDP	C10H15N5O11P2
gdp[e]	GDP	C10H15N5O11P2
gdp[p]	GDP	C10H15N5O11P2
glucys[c]	gamma-L-Glutamyl-L-cystein	C8H14N2O5S
gbbtn[e]	gamma-butyrobetaine	C7H15NO2
gbbtn[p]	gamma-butyrobetaine	C7H15NO2
galt[e]	Galactitol	C6H14O6
galt[p]	Galactitol	C6H14O6
fusa[e]	fusidic acid	C31H48O5
fusa[p]	fusidic acid	C31H48O5
dsbdrd[c]	fused thiol:disulfide interchan	XH2
dsbdox[c]	fused thiol:disulfide interchan	X
fum[c]	Fumarate	C4H4O4
fum[e]	Fumarate	C4H4O4
fum[p]	Fumarate	C4H4O4
frulys[e]	fructoselysine	C12H24N2O7
frulys[p]	fructoselysine	C12H24N2O7
for[e]	Formate	CH2O2
for[p]	Formate	CH2O2
fald[e]	Formaldehyde	CH2O
fald[p]	Formaldehyde	CH2O
fmn[c]	FMN	C17H21N4O9P
flxso[c]	flavodoxin semi oxidized	XH
flxr[c]	Flavodoxin reduced	XH2
fadh2[c]	Flavin adenine dinucleotide r	C27H35N9O15P2
fad[c]	Flavin adenine dinucleotide o	C27H33N9O15P2
feoxam-un[e]	ferroxamine minus Fe(3)	C25H48N6O8
feoxam[c]	ferroxamine	C25H45FeN6O8
feoxam[e]	ferroxamine	C25H45FeN6O8
feoxam[p]	ferroxamine	C25H45FeN6O8
fecrm-un[e]	Ferrichrome minus Fe(III)	C27H45N9O12
fecrm[c]	Ferrichrome	C27H42FeN9O12
fecrm[e]	Ferrichrome	C27H42FeN9O12
fecrm[p]	Ferrichrome	C27H42FeN9O12
fe3dhbzs[e]	ferric 2,3-dihydroxybenzoylse	C10H8NO6Fe
feenter[e]	Fe-enterobactin	C30H24FeN3O15
fe3[c]	Fe3+	Fe

fe3[e]	Fe3+	Fe
fe3[p]	Fe3+	Fe
fe2[c]	Fe2+	Fe
fe2[e]	Fe2+	Fe
fe2[p]	Fe2+	Fe
fe3hox[c]	Fe(III)hydroxamate	C9H18O6N3Fe
fe3hox[e]	Fe(III)hydroxamate	C9H18O6N3Fe
fe3hox[p]	Fe(III)hydroxamate	C9H18O6N3Fe
fe3hox-un[e]	Fe(III)hydoxamate, unloaded	C9H21O6N3
fe3dcit[e]	Fe(III)dicitrate	C12H13FeO14
frdp[c]	Farnesyl diphosphate	C15H28O7P2
etha[c]	Ethanolamine	C2H7NO
etha[e]	Ethanolamine	C2H7NO
etha[p]	Ethanolamine	C2H7NO
etoh[c]	Ethanol	C2H6O
etoh[e]	Ethanol	C2H6O
etoh[p]	Ethanol	C2H6O
ethso3[e]	ethanesulfonate	C2H6O3S
ethso3[p]	ethanesulfonate	C2H6O3S
enter[e]	Enterochelin	C30H27N3O15
enter[p]	Enterochelin	C30H27N3O15
epmeACP[c]	Enoylpimeloyl-[acyl-carrier pr	C8H11O3R
egmeACP[c]	Enoylglutaryl-[acyl-carrier pro	C6H7O3R
xu5p-D[c]	D-Xylulose 5-phosphate	C5H11O8P
xyl-D[e]	D-Xylose	C5H10O5
xyl-D[p]	D-Xylose	C5H10O5
dutp[c]	dUTP	C9H15N2O14P3
dump[c]	dUMP	C9H13N2O8P
dump[e]	dUMP	C9H13N2O8P
dump[p]	dUMP	C9H13N2O8P
dudp[c]	dUDP	C9H14N2O11P2
dttp[c]	dTTP	C10H17N2O14P3
dtmp[c]	dTMP	C10H15N2O8P
dtmp[e]	dTMP	C10H15N2O8P
dtmp[p]	dTMP	C10H15N2O8P
dtdpglu[c]	dTDPglucose	C16H26N2O16P2
dtdp4d6dm[c]	dTDP-4-dehydro-6-deoxy-L-n	C16H24N2O15P2
dtdp4d6dg[c]	dTDP-4-dehydro-6-deoxy-D-g	C16H24N2O15P2
dtdp[c]	dTDP	C10H16N2O11P2
tartr-D[c]	D-tartrate	C4H6O6
tartr-D[e]	D-tartrate	C4H6O6
tartr-D[p]	D-tartrate	C4H6O6
tag6p-D[c]	D-Tagatose 6-phosphate	C6H13O9P
tagdp-D[c]	D-Tagatose 1,6-biphosphate	C6H14O12P2
sbt-D[e]	D-Sorbitol	C6H14O6
sbt-D[p]	D-Sorbitol	C6H14O6
ser-D[e]	D-Serine	C3H7NO3
ser-D[p]	D-Serine	C3H7NO3

ru5p-D[c]	D-Ribulose 5-phosphate	C5H11O8P
rib-D[c]	D-Ribose	C5H10O5
rib-D[e]	D-Ribose	C5H10O5
rib-D[p]	D-Ribose	C5H10O5
doxrbcn[e]	doxorubicin	C27H29NO11
doxrbcn[p]	doxorubicin	C27H29NO11
dopa[e]	Dopamine	C8H11NO2
dopa[p]	Dopamine	C8H11NO2
ddcacoa[c]	Dodecanoyl-CoA (n-C12:0Co	C33H58N7O17P3S
ddcaACP[c]	Dodecanoyl-ACP (n-C12:0A	C23H44N2O8PRS
ddcap[c]	Dodecanoly-phosphate (n-C1	C12H25O5P1
ddca[c]	Dodecanoate (n-C12:0)	C12H24O2
ddca[e]	Dodecanoate (n-C12:0)	C12H24O2
ddca[p]	Dodecanoate (n-C12:0)	C12H24O2
met-D[c]	D-Methionine	C5H11NO2S
met-D[e]	D-Methionine	C5H11NO2S
met-D[p]	D-Methionine	C5H11NO2S
man6p[c]	D-Mannose 6-phosphate	C6H13O9P
man6p[e]	D-Mannose 6-phosphate	C6H13O9P
man6p[p]	D-Mannose 6-phosphate	C6H13O9P
man1p[c]	D-Mannose 1-phosphate	C6H13O9P
man[e]	D-Mannose	C6H12O6
man[p]	D-Mannose	C6H12O6
mnl1p[c]	D-Mannitol 1-phosphate	C6H15O9P
mnl[e]	D-Mannitol	C6H14O6
mnl[p]	D-Mannitol	C6H14O6
mal-D[e]	D-Malate	C4H6O5
mal-D[p]	D-Malate	C4H6O5
lac-D[c]	D-Lactate	C3H6O3
lac-D[e]	D-Lactate	C3H6O3
lac-D[p]	D-Lactate	C3H6O3
ditp[c]	dITP	C10H15N4O13P3
ppi[c]	Diphosphate	H4O7P2
dimp[c]	dIMP	C10H13N4O7P
dimp[e]	dIMP	C10H13N4O7P
dimp[p]	dIMP	C10H13N4O7P
dmpp[c]	Dimethylallyl diphosphate	C5H12O7P2
dmso[c]	Dimethyl sulfoxide	C2H6OS
dmso[e]	Dimethyl sulfoxide	C2H6OS
dmso[p]	Dimethyl sulfoxide	C2H6OS
dms[c]	Dimethyl sulfide	C2H6S
dms[e]	Dimethyl sulfide	C2H6S
dms[p]	Dimethyl sulfide	C2H6S
dhap[c]	Dihydroxyacetone phosphate	C3H7O6P
dha[e]	Dihydroxyacetone	C3H6O3
dha[p]	Dihydroxyacetone	C3H6O3
dscl[c]	dihydrosirohydrochlorin	C42H48N4O16
dhpt[c]	Dihydropteroate	C14H14N6O3

dhpmp[c]	Dihydroneopterin monophosp	C9H14N5O7P
dhnpt[c]	Dihydroneopterin	C9H13N5O4
dhmpt[c]	Dihydromonapterin	C9H13N5O4
didp[c]	dIDP	C10H14N4O10P2
chtbs6p[c]	diacetylchitobiose-6-phospha	C16H29N2O14P
dgtp[c]	dGTP	C10H16N5O13P3
dgmp[c]	dGMP	C10H14N5O7P
dgmp[e]	dGMP	C10H14N5O7P
dgmp[p]	dGMP	C10H14N5O7P
gmhep7p[c]	D-Glycero-D-manno-heptose	C7H15O10P
gmhep1p[c]	D-Glycero-D-manno-heptose	C7H15O10P
gmhep17bp[c]	D-Glycero-D-manno-heptose	C7H16O13P2
2pg[c]	D-Glycerate 2-phosphate	C3H7O7P
glyald[c]	D-Glyceraldehyde	C3H6O3
glyald[e]	D-Glyceraldehyde	C3H6O3
glyald[p]	D-Glyceraldehyde	C3H6O3
glu-D[c]	D-Glutamate	C5H9NO4
glcur1p[e]	D-Glucuronate 1-phosphate	C6H11O10P
glcur1p[p]	D-Glucuronate 1-phosphate	C6H11O10P
glcur[c]	D-Glucuronate	C6H10O7
glcur[e]	D-Glucuronate	C6H10O7
glcur[p]	D-Glucuronate	C6H10O7
g6p[c]	D-Glucose 6-phosphate	C6H13O9P
g6p[e]	D-Glucose 6-phosphate	C6H13O9P
g6p[p]	D-Glucose 6-phosphate	C6H13O9P
g1p[c]	D-Glucose 1-phosphate	C6H13O9P
g1p[e]	D-Glucose 1-phosphate	C6H13O9P
g1p[p]	D-Glucose 1-phosphate	C6H13O9P
glc-D[c]	D-Glucose	C6H12O6
glc-D[e]	D-Glucose	C6H12O6
glc-D[p]	D-Glucose	C6H12O6
gam6p[c]	D-Glucosamine 6-phosphate	C6H14NO8P
gam6p[e]	D-Glucosamine 6-phosphate	C6H14NO8P
gam6p[p]	D-Glucosamine 6-phosphate	C6H14NO8P
gam1p[c]	D-Glucosamine 1-phosphate	C6H14NO8P
gam[e]	D-Glucosamine	C6H13NO5
gam[p]	D-Glucosamine	C6H13NO5
glcn[e]	D-Gluconate	C6H12O7
glcn[p]	D-Gluconate	C6H12O7
glcr[e]	D-Glucarate	C6H10O8
glcr[p]	D-Glucarate	C6H10O8
dgdp[c]	dGDP	C10H15N5O10P2
galur[e]	D-Galacturonate	C6H10O7
galur[p]	D-Galacturonate	C6H10O7
gal[c]	D-Galactose	C6H12O6
gal[e]	D-Galactose	C6H12O6
gal[p]	D-Galactose	C6H12O6
galctn-D[e]	D-Galactonate	C6H12O7

galctn-D[p]	D-Galactonate	C6H12O7
galct-D[e]	D-Galactarate	C6H10O8
galct-D[p]	D-Galactarate	C6H10O8
fruur[e]	D-Fructuronate	C6H10O7
fruur[p]	D-Fructuronate	C6H10O7
f6p[c]	D-Fructose 6-phosphate	C6H13O9P
f6p[e]	D-Fructose 6-phosphate	C6H13O9P
f6p[p]	D-Fructose 6-phosphate	C6H13O9P
f1p[c]	D-Fructose 1-phosphate	C6H13O9P
fdp[c]	D-Fructose 1,6-bisphosphate	C6H14O12P2
fru[e]	D-Fructose	C6H12O6
fru[p]	D-Fructose	C6H12O6
dtbt[c]	Dethiobiotin	C10H18N2O3
e4p[c]	D-Erythrose 4-phosphate	C4H9O7P
eig3p[c]	D-erythro-1-(Imidazol-4-yl)gly	C6H11N2O6P
dpcoa[c]	Dephospho-CoA	C21H35N7O13P2S
duri[c]	Deoxyuridine	C9H12N2O5
duri[e]	Deoxyuridine	C9H12N2O5
duri[p]	Deoxyuridine	C9H12N2O5
din[c]	Deoxyinosine	C10H12N4O4
din[e]	Deoxyinosine	C10H12N4O4
din[p]	Deoxyinosine	C10H12N4O4
dgsn[c]	Deoxyguanosine	C10H13N5O4
dgsn[e]	Deoxyguanosine	C10H13N5O4
dgsn[p]	Deoxyguanosine	C10H13N5O4
dcyt[c]	Deoxycytidine	C9H13N3O4
dcyt[e]	Deoxycytidine	C9H13N3O4
dcyt[p]	Deoxycytidine	C9H13N3O4
dad-2[c]	Deoxyadenosine	C10H13N5O3
dad-2[e]	Deoxyadenosine	C10H13N5O3
dad-2[p]	Deoxyadenosine	C10H13N5O3
dhgly[c]	dehydroglycine	C2H3NO2
dcacoa[c]	Decanoyl-CoA (n-C10:0CoA)	C31H54N7O17P3S
dcaACP[c]	Decanoyl-ACP (n-C10:0ACP	C21H40N2O8PRS
dca[c]	Decanoate (n-C10:0)	C10H20O2
dca[e]	Decanoate (n-C10:0)	C10H20O2
dca[p]	Decanoate (n-C10:0)	C10H20O2
dnad[c]	Deamino-NAD+	C21H27N6O15P2
cys-D[c]	D-Cysteine	C3H7NO2S
cys-D[e]	D-Cysteine	C3H7NO2S
cys-D[p]	D-Cysteine	C3H7NO2S
dctp[c]	dCTP	C9H16N3O13P3
dcmp[c]	dCMP	C9H14N3O7P
dcmp[e]	dCMP	C9H14N3O7P
dcmp[p]	dCMP	C9H14N3O7P
dcdp[c]	dCDP	C9H15N3O10P2
crn-D[c]	D-Carnitine	C7H15NO3
crn-D[e]	D-Carnitine	C7H15NO3

crn-D[p]	D-Carnitine	C7H15NO3
datp[c]	dATP	C10H16N5O12P3
ara5p[c]	D-Arabinose 5-phosphate	C5H11O8P
damp[c]	dAMP	C10H14N5O6P
damp[e]	dAMP	C10H14N5O6P
damp[p]	dAMP	C10H14N5O6P
all-D[e]	D-Allose	C6H12O6
all-D[p]	D-Allose	C6H12O6
alaala[c]	D-Alanyl-D-alanine	C6H12N2O3
alaala[e]	D-Alanyl-D-alanine	C6H12N2O3
alaala[p]	D-Alanyl-D-alanine	C6H12N2O3
ala-D[c]	D-Alanine	C3H7NO2
ala-D[e]	D-Alanine	C3H7NO2
ala-D[p]	D-Alanine	C3H7NO2
dadp[c]	dADP	C10H15N5O9P2
4ppan[c]	D-4'-Phosphopantothenate	C9H18NO8P
csn[c]	Cytosine	C4H5N3O
csn[e]	Cytosine	C4H5N3O
csn[p]	Cytosine	C4H5N3O
cytd[c]	Cytidine	C9H13N3O5
cytd[e]	Cytidine	C9H13N3O5
cytd[p]	Cytidine	C9H13N3O5
cgly[c]	Cys-Gly	C5H10N2O3S
cgly[e]	Cys-Gly	C5H10N2O3S
cgly[p]	Cys-Gly	C5H10N2O3S
cpg180[c]	cyclopropane phosphatidylgly	C44H83O10P1
cpg160[c]	cyclopropane phosphatidylgly	C40H75O10P1
cpe180[c]	cyclopropane phosphatidyleth	C43H82N1O8P1
cpe160[c]	cyclopropane phosphatidyleth	C39H74N1O8P1
cpmp[c]	cyclic pyranopterin monophos	C10H14N5O8P
cynt[e]	Cyanate	CHNO
cynt[p]	Cyanate	CHNO
cu2[c]	Cu2+	Cu
cu2[e]	Cu2+	Cu
cu2[p]	Cu2+	Cu
cu[c]	Cu+	Cu
cu[e]	Cu+	Cu
cu[p]	Cu+	Cu
ctp[c]	CTP	C9H16N3O14P3
b2coa[c]	Crotonoyl-CoA	C25H40N7O17P3S
ctbt[c]	crotonobetaine	C7H13NO2
ctbt[p]	crotonobetaine	C7H13NO2
cpppg3[c]	Coproporphyrinogen III	C36H44N4O8
cpgn-un[e]	coprogen unloaded (no Fe(III	C35H56N6O13
cpgn[c]	coprogen	C35H53N6O13Fe
cpgn[e]	coprogen	C35H53N6O13Fe
cpgn[p]	coprogen	C35H53N6O13Fe
coa[c]	Coenzyme A	C21H36N7O16P3S

cbi[c]	Cobinamide	C48H72CoN11O8
cbi[e]	Cobinamide	C48H72CoN11O8
cbi[p]	Cobinamide	C48H72CoN11O8
cbl1[c]	Cob(I)alamin	C62H89CoN13O14P
cbl1[e]	Cob(I)alamin	C62H89CoN13O14P
cbl1[p]	Cob(I)alamin	C62H89CoN13O14P
cobalt2[c]	Co2+	Co
cobalt2[e]	Co2+	Co
cobalt2[p]	Co2+	Co
co2[c]	CO2	CO2
co2[e]	CO2	CO2
co2[p]	CO2	CO2
ckdo[c]	CMP-3-deoxy-D-manno-octul	C17H26N3O15P
cmp[c]	CMP	C9H14N3O8P
cmp[e]	CMP	C9H14N3O8P
cmp[p]	CMP	C9H14N3O8P
cit[c]	Citrate	C6H8O7
cit[e]	Citrate	C6H8O7
cit[p]	Citrate	C6H8O7
tdeACP[c]	cis-tetradec-7-enoyl-[acyl-car	C25H46N2O8PRS
octeACP[c]	cis-octadec-11-enoyl-[acyl-ca	C29H54N2O8PRS
hdeACP[c]	cis-hexadec-9-enoyl-[acyl-car	C27H50N2O8PRS
cddec5eACP[c]	cis-dodec-5-enoyl-[acyl-carrie	C23H42N2O8PRS
cdec3eACP[c]	cis-dec-3-enoyl-[acyl-carrier	C21H38N2O8PRS
acon-C[c]	cis-Aconitate	C6H6O6
2mcacn[c]	cis-2-Methylaconitate	C7H8O6
chor[c]	chorismate	C10H10O6
chol[c]	Choline	C5H13NO
chol[e]	Choline	C5H13NO
chol[p]	Choline	C5H13NO
cl[c]	Chloride	Cl
cl[e]	Chloride	Cl
cl[p]	Chloride	Cl
cm[e]	Chloramphenicol	C11H12Cl2N2O5
cm[p]	Chloramphenicol	C11H12Cl2N2O5
cdpdtdecg[c]	CDP-1,2-ditetradecanoylglyc	C40H73N3O15P2
cdpdtdec7eg[c]	CDP-1,2-ditetradec-7-enoylgl	C40H69N3O15P2
cdpdodecg[c]	CDP-1,2-dioctadecanoylglyc	C48H89N3O15P2
cdpdodec11eg[c]	CDP-1,2-dioctadec-11-enoyl	C48H85N3O15P2
cdpdhdecg[c]	CDP-1,2-dihexadecanoylglyc	C44H81N3O15P2
cdpdhdec9eg[c]	CDP-1,2-dihexadec-9-enoylg	C44H77N3O15P2
cdpdddecg[c]	CDP-1,2-didodecanoylglycer	C36H65N3O15P2
cdp[c]	CDP	C9H15N3O11P2
clpn140[p]	cardiolipin (tetratetradecanoy	C65H126O17P2
clpn141[p]	cardiolipin (tetratetradec-7-en	C65H118O17P2
clpn180[p]	cardiolipin (tetraoctadecanoyl	C81H158O17P2
clpn181[p]	cardiolipin (tetraoctadec-11-e	C81H150O17P2
clpn160[p]	cardiolipin (tetrahexadecanoy	C73H142O17P2

clpn161[p]	cardiolipin (tetrahexadec-9-er	C73H134O17P2
clpn120[p]	cardiolipin (tetradodecanoyl,	C57H110O17P2
cbp[c]	Carbamoyl phosphate	CH4NO5P
camp[c]	cAMP	C10H12N5O6P
ca2[c]	Calcium	Ca
ca2[e]	Calcium	Ca
ca2[p]	Calcium	Ca
cd2[c]	Cadmium	Cd
cd2[e]	Cadmium	Cd
cd2[p]	Cadmium	Cd
3ig3p[c]	C'-(3-Indolyl)-glycerol 3-phos	C11H14NO6P
butACP[c]	Butyryl-ACP (n-C4:0ACP)	C15H28N2O8PRS
but[c]	Butyrate (n-C4:0)	C4H8O2
but[e]	Butyrate (n-C4:0)	C4H8O2
but[p]	Butyrate (n-C4:0)	C4H8O2
btcoa[c]	Butanoyl-CoA	C25H42N7O17P3S
butso3[e]	butanesulfonate	C4H10O3S
butso3[p]	butanesulfonate	C4H10O3S
but2eACP[c]	But-2-enoyl-[acyl-carrier prot	C15H26N2O8PRS
bglycogen[c]	branching glycogen	C6H10O5
bmoco1gdp[c]	bis-molybdopterin mono-guar	C30H36N15O20P3S4Mc
bmocogdp[c]	bis-molybdopterin guanine di	C40H48N20O27P4S4Mc
bmoco[c]	bis-molybdenum cofactor	C20H24N10O13P2S4Mc
btn[c]	Biotin	C10H16N2O3S
btn[e]	Biotin	C10H16N2O3S
btn[p]	Biotin	C10H16N2O3S
hco3[c]	Bicarbonate	CH2O3
ala-B[c]	beta-Alanine	C3H7NO2
ala-B[e]	beta-Alanine	C3H7NO2
ala-B[p]	beta-Alanine	C3H7NO2
gal-bD[e]	beta D-Galactose	C6H12O6
gal-bD[p]	beta D-Galactose	C6H12O6
atp[c]	ATP	C10H16N5O13P3
aso3[e]	arsenite	H3AsO3
aso3[p]	arsenite	H3AsO3
arbt6p[c]	Arbutin 6-phosphate	C12H17O10P
arbt[e]	Arbutin	C12H16O7
arbt[p]	Arbutin	C12H16O7
apoACP[c]	apoprotein [acyl carrier protei	RHO
anth[c]	Anthranilate	C7H7NO2
amp[c]	AMP	C10H14N5O7P
amp[e]	AMP	C10H14N5O7P
amp[p]	AMP	C10H14N5O7P
nh4[c]	Ammonium	H3N
nh4[e]	Ammonium	H3N
nh4[p]	Ammonium	H3N
r5p[c]	alpha-D-Ribose 5-phosphate	C5H11O8P
r5p[e]	alpha-D-Ribose 5-phosphate	C5H11O8P

r5p[p]	alpha-D-Ribose 5-phosphate	C5H11O8P
r1p[c]	alpha-D-Ribose 1-phosphate	C5H11O8P
gal1p[c]	alpha-D-Galactose 1-phosph	C6H13O9P
gal1p[e]	alpha-D-Galactose 1-phosph	C6H13O9P
gal1p[p]	alpha-D-Galactose 1-phosph	C6H13O9P
octdp[c]	all-trans-Octaprenyl diphosph	C40H68O7P2
alltn[e]	Allantoin	C4H6N4O3
alltn[p]	Allantoin	C4H6N4O3
agm[c]	Agmatine	C5H14N4
agm[e]	Agmatine	C5H14N4
agm[p]	Agmatine	C5H14N4
arbtn[e]	aerobactin minus Fe3	C22H36N4O13
arbtn-fe3[c]	Aerobactin	C22H33FeN4O13
arbtn-fe3[e]	Aerobactin	C22H33FeN4O13
arbtn-fe3[p]	Aerobactin	C22H33FeN4O13
adprib[c]	ADPribose	C15H23N5O14P2
adphep-LD[c]	ADP-L-glycero-D-manno-hep	C17H27N5O16P2
adpglc[c]	ADPglucose	C16H25N5O15P2
adphep-DD[c]	ADP-D-glycero-D-manno-hep	C17H27N5016P2
adp[c]	ADP	C10H15N5O10P2
mptamp[c]	adenylated molybdopterin	C20H24N10O12P2S2Cu
adocbl[c]	Adenosylcobalamin	C72H100CoN18O17P
adocbl[e]	Adenosylcobalamin	C72H100CoN18O17P
adocbl[p]	Adenosylcobalamin	C72H100CoN18O17P
adocbi[c]	Adenosyl cobinamide	C58H83CoN16O11
aps[c]	Adenosine 5'-phosphosulfate	C10H14N5O10PS
pap[c]	Adenosine 3',5'-bisphosphate	C10H15N5O10P2
adn[c]	Adenosine	C10H13N5O4
adn[e]	Adenosine	C10H13N5O4
adn[p]	Adenosine	C10H13N5O4
ade[c]	Adenine	C5H5N5
ade[e]	Adenine	C5H5N5
ade[p]	Adenine	C5H5N5
apg181[c]	acyl phosphatidylglycerol (n-	C60H111O11P
apg180[c]	acyl phosphatidylglycerol (n-	C60H126O11P
apg161[c]	acyl phosphatidylglycerol (n-	C54H99O11P
apg160[c]	acyl phosphatidylglycerol (n-	C54H105O11P
apg141[c]	acyl phosphatidylglycerol (n-	C48H87O11P
apg140[c]	acyl phosphatidylglycerol (n-	C48H93O11P
apg120[c]	acyl phosphatidylglycerol (n-	C42H81O11P
ACP[c]	acyl carrier protein	C11H22N2O7PRS
acmalt[c]	Acetyl-maltose	C14H24O12
accoa[c]	Acetyl-CoA	C23H38N7O17P3S
acACP[c]	Acetyl-ACP	C13H24N2O8PRS
actp[c]	Acetyl phosphate	C2H5O5P
aacoa[c]	Acetoacetyl-CoA	C25H40N7O18P3S
actACP[c]	Acetoacetyl-ACP	C15H26N2O9PRS
acac[e]	Acetoacetate	C4H6O3

acac[p]	Acetoacetate	C4H6O3
ac[c]	Acetate	C2H4O2
ac[e]	Acetate	C2H4O2
ac[p]	Acetate	C2H4O2
acald[c]	Acetaldehyde	C2H4O
acald[e]	Acetaldehyde	C2H4O
acald[p]	Acetaldehyde	C2H4O
8aonn[c]	8-Amino-7-oxononanoate	C9H17NO3
cdg[c]	7-deaza-7-carboxyguanine	C7H6N4O3
preq0[c]	7-cyano-7-carbaguanine	C7H5N5O
preq1[c]	7-aminomethyl-7-deazaguani	C7H9N5O
dhf[c]	7,8-Dihydrofolate	C19H21N7O6
dann[c]	7,8-Diaminononanoate	C9H20N2O2
6pgl[c]	6-phospho-D-glucono-1,5-lac	C6H11O9P
6pgc[c]	6-Phospho-D-gluconate	C6H13O10P
6hmhptpp[c]	6-hydroxymethyl-dihydropteri	C7H11N5O8P2
6hmhpt[c]	6-hydroxymethyl dihydropteri	C7H9N5O2
cph4[c]	6-carboxy-5,6,7,8-tetrahydro	C7H9N5O3
acglc-D[c]	6-Acetyl-D-glucose	C8H14O7
dmlz[c]	6,7-Dimethyl-8-(1-D-ribityl)lu	C13H18N4O6
5caiz[c]	5-phosphoribosyl-5-carboxya	C9H14N3O9P
pram[c]	5-Phospho-beta-D-ribosylami	C5H12NO7P
prpp[c]	5-Phospho-alpha-D-ribose 1-	C5H13O14P3
3psme[c]	5-O-(1-Carboxyvinyl)-3-phos	C10H13O10P
5mtr[c]	5-Methylthio-D-ribose	C6H12O4S
5mtr[e]	5-Methylthio-D-ribose	C6H12O4S
5mtr[p]	5-Methylthio-D-ribose	C6H12O4S
5mta[c]	5-Methylthioadenosine	C11H15N5O3S
5mthf[c]	5-Methyltetrahydrofolate	C20H25N7O6
5fthf[c]	5-Formyltetrahydrofolate	C20H23N7O7
fprica[c]	5-Formamido-1-(5-phospho-	C10H15N4O9P
5drib[c]	5'-deoxyribose	C5H10O4
dad-5[c]	5'-Deoxyadenosine	C10H13N5O3
5dglcn[e]	5-Dehydro-D-gluconate	C6H10O7
5dglcn[p]	5-Dehydro-D-gluconate	C6H10O7
5apru[c]	5-Amino-6-(5'-phosphoribosy	C9H15N4O9P
5aprbu[c]	5-Amino-6-(5'-phosphoribityl	C9H17N4O9P
5aop[c]	5-Amino-4-oxopentanoate	C5H9NO3
5aizc[c]	5-amino-1-(5-phospho-D-ribo	C9H14N3O9P
aicar[c]	5-Amino-1-(5-Phospho-D-rib	C9H15N4O8P
air[c]	5-amino-1-(5-phospho-D-ribo	C8H14N3O7P
prlp[c]	5-[(5-phospho-1-deoxyribulos	C15H25N5O15P2
thf[c]	5,6,7,8-Tetrahydrofolate	C19H23N7O6
mlthf[c]	5,10-Methylenetetrahydrofola	C20H23N7O6
methf[c]	5,10-Methenyltetrahydrofolat	C20H22N7O6
4pasp[c]	4-Phospho-L-aspartate	C4H8NO7P
4per[c]	4-Phospho-D-erythronate	C4H9O8P
4mpetz[c]	4-Methyl-5-(2-phosphoethyl)-	C6H10NO4PS

4mhetz[c]	4-Methyl-5-(2-hydroxyethyl)-t	C6H9NOS
4mop[c]	4-Methyl-2-oxopentanoate	C6H10O3
4hoxpacd[e]	4-Hydroxyphenylacetaldehyd	C8H8O2
4hoxpacd[p]	4-Hydroxyphenylacetaldehyd	C8H8O2
4hthr[c]	4-Hydroxy-L-threonine	C4H9NO4
4hbz[c]	4-Hydroxybenzoate	C7H6O3
4abut[c]	4-Aminobutanoate	C4H9NO2
4abut[e]	4-Aminobutanoate	C4H9NO2
4abut[p]	4-Aminobutanoate	C4H9NO2
4abz[c]	4-Aminobenzoate	C7H7NO2
4ahmmp[c]	4-Amino-5-hydroxymethyl-2-r	C6H9N3O
4adcho[c]	4-amino-4-deoxychorismate	C10H11NO5
4ampm[c]	4-Amino-2-methyl-5-phospho	C6H10N3O4P
dhptd[c]	4,5-dihydroxy-2,3-pentanedio	C5H8O4
4c2me[c]	4-(cytidine 5'-diphospho)-2-C	C14H25N3O14P2
4r5au[c]	4-(1-D-Ribitylamino)-5-amino	C9H16N4O6
3ump[e]	3'-UMP	C9H13N2O9P
3ump[p]	3'-UMP	C9H13N2O9P
3sala[c]	3-Sulfino-L-alanine	C3H7NO4S
3php[c]	3-Phosphohydroxypyruvate	C3H5O7P
13dpg[c]	3-Phospho-D-glyceroyl phosp	C3H8O10P2
3pg[c]	3-Phospho-D-glycerate	C3H7O7P
paps[c]	3'-Phosphoadenylyl sulfate	C10H15N5O13P2S
3otdcoa[c]	3-Oxotetradecanoyl-CoA	C35H60N7O18P3S
3omrsACP[c]	3-Oxotetradecanoyl-[acyl-car	C25H46N2O9PRS
opmeACP[c]	3-Oxo-pimeloyl-[acyl-carrier p	C8H11O4R
3oocoa[c]	3-Oxooctanoyl-CoA	C29H48N7O18P3S
3ooctACP[c]	3-Oxooctanoyl-[acyl-carrier p	C19H34N2O9PRS
3oodcoa[c]	3-Oxooctadecanoyl-CoA	C39H68N7O18P3S
3ooctdACP[c]	3-Oxooctadecanoyl-[acyl-carr	C29H54N2O9PRS
3ohcoa[c]	3-Oxohexanoyl-CoA	C27H44N7O18P3S
3ohexACP[c]	3-Oxohexanoyl-[acyl-carrier p	C17H30N2O9PRS
3ohdcoa[c]	3-Oxohexadecanoyl-CoA	C37H64N7O18P3S
3opalmACP[c]	3-Oxohexadecanoyl-[acyl-car	C27H50N2O9PRS
ogmeACP[c]	3-Oxo-glutaryl-[acyl-carrier pr	C6H7O4R
3oddcoa[c]	3-Oxododecanoyl-CoA	C33H56N7O18P3S
3oddecACP[c]	3-Oxododecanoyl-[acyl-carrie	C23H42N2O9PRS
3odcoa[c]	3-Oxodecanoyl-CoA	C31H52N7O18P3S
3odecACP[c]	3-Oxodecanoyl-[acyl-carrier p	C21H38N2O9PRS
3ocvac11eACP[c]	3-oxo-cis-vacc-11-enoyl-[acyl	C29H52N2O9PRS
3ocpalm9eACP[c]	3-oxo-cis-palm-9-eoyl-[acyl-c	C27H48N2O9PRS
3ocmrs7eACP[c]	3-oxo-cis-myristol-7-eoyl-[acy	C25H44N2O9PRS
3ocddec5eACP[c]	3-oxo-cis-dodec-5-enoyl-[acy	C23H40N2O9PRS
3ophb[c]	3-Octaprenyl-4-hydroxybenzo	C47H70O3
3mob[c]	3-Methyl-2-oxobutanoate	C5H8O3
3hpp[e]	3-Hydroxypropanoate	C3H6O3
3hpp[p]	3-Hydroxypropanoate	C3H6O3
hpmeACP[c]	3-Hydroxypimeloyl-[acyl-carri	C8H13O4R

hgmeACP[c]	3-Hydroxyglutaryl-[acyl-carrie	C6H9O4R
3hcinnm[e]	3-hydroxycinnamic acid	C9H8O3
3hcinnm[p]	3-hydroxycinnamic acid	C9H8O3
3gmp[e]	3'-GMP	C10H14N5O8P
3gmp[p]	3'-GMP	C10H14N5O8P
kdo8p[c]	3-Deoxy-D-manno-octuloson	C8H15O11P
kdo[c]	3-Deoxy-D-manno-2-octulos	C8H14O8
3dhsk[c]	3-Dehydroshikimate	C7H8O5
3dhq[c]	3-Dehydroquinate	C7H10O6
3cmp[e]	3'-cmp	C9H14N3O8P
3cmp[p]	3'-cmp	C9H14N3O8P
3c4mop[c]	3-Carboxy-4-methyl-2-oxope	C7H10O5
3c3hmp[c]	3-Carboxy-3-hydroxy-4-meth	C7H12O5
3c2hmp[c]	3-Carboxy-2-hydroxy-4-meth	C7H12O5
3amp[e]	3'-AMP	C10H14N5O7P
3amp[p]	3'-AMP	C10H14N5O7P
34dhpac[e]	3,4-Dihydroxyphenylacetalde	C8H8O3
34dhpac[p]	3,4-Dihydroxyphenylacetalde	C8H8O3
db4p[c]	3,4-dihydroxy-2-butanone 4-	C4H9O6P
imacp[c]	3-(Imidazol-4-yl)-2-oxopropyl	C6H9N2O5P
34hpp[c]	3-(4-Hydroxyphenyl)pyruvate	C9H8O4
3hpppn[e]	3-(3-hydroxy-phenyl)propion	C9H10O3
3hpppn[p]	3-(3-hydroxy-phenyl)propion	C9H10O3
2tdecg3p[c]	2-tetradecanoyl-sn-glycerol 3	C17H35O7P1
2tdecg3p[p]	2-tetradecanoyl-sn-glycerol 3	C17H35O7P1
2tdec7eg3p[c]	2-tetradec-7-enoyl-sn-glycer	C17H33O7P1
2tdec7eg3p[p]	2-tetradec-7-enoyl-sn-glycer	C17H33O7P1
2shchc[c]	2-Succinyl-6-hydroxy-2,4-cyc	C11H12O6
2sephchc[c]	2-succinyl-5-enolpyruvyl-6-hy	C14H16O9
2pglyc[c]	2-Phosphoglycolate	C2H5O6P
2p4c2me[c]	2-phospho-4-(cytidine 5'-diph	C14H26N3O17P3
akg[c]	2-Oxoglutarate	C5H6O5
akg[e]	2-Oxoglutarate	C5H6O5
akg[p]	2-Oxoglutarate	C5H6O5
2obut[c]	2-Oxobutanoate	C4H6O3
ohpb[c]	2-Oxo-3-hydroxy-4-phospho	C4H7O8P
2oph[c]	2-Octaprenylphenol	C46H70O
2omph[c]	2-Octaprenyl-6-methoxyphen	C47H72O2
2ombzl[c]	2-Octaprenyl-6-methoxy-1,4-	C47H72O3
2ohph[c]	2-Octaprenyl-6-hydroxyphen	C46H70O2
2ommbl[c]	2-Octaprenyl-3-methyl-6-met	C48H74O3
2omhmbl[c]	2-Octaprenyl-3-methyl-5-hyd	C48H74O4
2odecg3p[c]	2-octadecanoyl-sn-glycerol 3	C21H43O7P1
2odecg3p[p]	2-octadecanoyl-sn-glycerol 3	C21H43O7P1
2odec11eg3p[c]	2-octadec-11-enoyl-sn-glycer	C21H41O7P1
2odec11eg3p[p]	2-octadec-11-enoyl-sn-glycer	C21H41O7P1
2mcit[c]	2-Methylcitrate	C7H10O7
2mahmp[c]	2-Methyl-4-amino-5-hydroxy	C6H11N3O7P2

2ippm[c]	2-Isopropylmaleate	C7H10O4
2hdecg3p[c]	2-hexadecanoyl-sn-glycerol 3	C19H39O7P1
2hdecg3p[p]	2-hexadecanoyl-sn-glycerol 3	C19H39O7P1
2hdec9eg3p[c]	2-hexadec-9-enoyl-sn-glycer	C19H37O7P1
2hdec9eg3p[p]	2-hexadec-9-enoyl-sn-glycer	C19H37O7P1
2ddecg3p[c]	2-dodecanoyl-sn-glycerol 3-p	C15H31O7P1
2ddecg3p[p]	2-dodecanoyl-sn-glycerol 3-p	C15H31O7P1
2dr5p[c]	2-Deoxy-D-ribose 5-phospha	C5H11O7P
2dr1p[c]	2-Deoxy-D-ribose 1-phospha	C5H11O7P
2dmmq8[c]	2-Demethylmenaquinone 8	C50H70O2
2dmmql8[c]	2-Demethylmenaquinol 8	C50H72O2
2dhp[c]	2-Dehydropantoate	C6H10O4
2ddg6p[c]	2-Dehydro-3-deoxy-D-glucon	C6H11O9P
2ddglcn[c]	2-Dehydro-3-deoxy-D-glucon	C6H10O6
2ddglcn[e]	2-Dehydro-3-deoxy-D-glucon	C6H10O6
2ddglcn[p]	2-Dehydro-3-deoxy-D-glucon	C6H10O6
2dda7p[c]	2-Dehydro-3-deoxy-D-arabin	C7H13O10P
2me4p[c]	2-C-methyl-D-erythritol 4-pho	C5H13O7P
2mecdp[c]	2-C-methyl-D-erythritol 2,4-cy	C5H12O9P2
ahdt[c]	2-Amino-4-hydroxy-6-(erythr	C9H16N5O13P3
2agpg181[c]	2-Acyl-sn-glycero-3-phospho	C24H47O9P1
2agpg181[p]	2-Acyl-sn-glycero-3-phospho	C24H47O9P1
2agpg180[c]	2-Acyl-sn-glycero-3-phospho	C24H49O9P1
2agpg180[p]	2-Acyl-sn-glycero-3-phospho	C24H49O9P1
2agpg161[c]	2-Acyl-sn-glycero-3-phospho	C22H43O9P1
2agpg161[p]	2-Acyl-sn-glycero-3-phospho	C22H43O9P1
2agpg160[c]	2-Acyl-sn-glycero-3-phospho	C22H45O9P1
2agpg160[p]	2-Acyl-sn-glycero-3-phospho	C22H45O9P1
2agpg141[c]	2-Acyl-sn-glycero-3-phospho	C20H39O9P1
2agpg141[p]	2-Acyl-sn-glycero-3-phospho	C20H39O9P1
2agpg140[c]	2-Acyl-sn-glycero-3-phospho	C20H41O9P1
2agpg140[p]	2-Acyl-sn-glycero-3-phospho	C20H41O9P1
2agpg120[c]	2-Acyl-sn-glycero-3-phospho	C18H37O9P1
2agpg120[p]	2-Acyl-sn-glycero-3-phospho	C18H37O9P1
2agpe181[c]	2-Acyl-sn-glycero-3-phospho	C23H46NO7P1
2agpe181[p]	2-Acyl-sn-glycero-3-phospho	C23H46NO7P1
2agpe180[c]	2-Acyl-sn-glycero-3-phospho	C23H48NO7P1
2agpe180[p]	2-Acyl-sn-glycero-3-phospho	C23H48NO7P1
2agpe161[c]	2-Acyl-sn-glycero-3-phospho	C21H42NO7P1
2agpe161[p]	2-Acyl-sn-glycero-3-phospho	C21H42NO7P1
2agpe160[c]	2-Acyl-sn-glycero-3-phospho	C21H44NO7P1
2agpe160[p]	2-Acyl-sn-glycero-3-phospho	C21H44NO7P1
2agpe141[c]	2-Acyl-sn-glycero-3-phospho	C19H38NO7P1
2agpe141[p]	2-Acyl-sn-glycero-3-phospho	C19H38NO7P1
2agpe140[c]	2-Acyl-sn-glycero-3-phospho	C19H40NO7P1
2agpe140[p]	2-Acyl-sn-glycero-3-phospho	C19H40NO7P1
2agpe120[c]	2-Acyl-sn-glycero-3-phospho	C17H36NO7P1
2agpe120[p]	2-Acyl-sn-glycero-3-phospho	C17H36NO7P1

25drapp[c]	2,5-Diamino-6-(ribosylamino)	C9H16N5O8P
23dhdp[c]	2,3-Dihydrodipicolinate	C7H7NO4
23dappa[e]	2,3-diaminopropionate	C3H8N2O2
23dappa[p]	2,3-diaminopropionate	C3H8N2O2
23cump[e]	2',3'-Cyclic UMP	C9H11N2O8P
23cump[p]	2',3'-Cyclic UMP	C9H11N2O8P
23cgmp[e]	2',3'-Cyclic GMP	C10H12N5O7P
23cgmp[p]	2',3'-Cyclic GMP	C10H12N5O7P
23ccmp[e]	2',3'-Cyclic CMP	C9H12N3O7P
23ccmp[p]	2',3'-Cyclic CMP	C9H12N3O7P
23camp[e]	2',3'-Cyclic AMP	C10H12N5O6P
23camp[p]	2',3'-Cyclic AMP	C10H12N5O6P
thdp[c]	2,3,4,5-Tetrahydrodipicolinate	C7H9NO4
fpram[c]	2-(Formamido)-N1-(5-phosph	C8H16N3O8P
manglyc[e]	2(alpha-D-Mannosyl)-D-glyce	C9H16O9
manglyc[p]	2(alpha-D-Mannosyl)-D-glyce	C9H16O9
1tdecg3p[c]	1-tetradecanoyl-sn-glycerol 3	C17H35O7P1
1tdecg3p[p]	1-tetradecanoyl-sn-glycerol 3	C17H35O7P1
1tdec7eg3p[c]	1-tetradec-7-enoyl-sn-glycero	C17H33O7P1
1tdec7eg3p[p]	1-tetradec-7-enoyl-sn-glycero	C17H33O7P1
1pyr5c[c]	1-Pyrroline-5-carboxylate	C5H7NO2
1odecg3p[c]	1-octadecanoyl-sn-glycerol 3-	C21H43O7P1
1odecg3p[p]	1-octadecanoyl-sn-glycerol 3-	C21H43O7P1
1odec11eg3p[c]	1-octadec-11-enoyl-sn-glycer	C21H41O7P1
1odec11eg3p[p]	1-octadec-11-enoyl-sn-glycer	C21H41O7P1
h2mb4p[c]	1-hydroxy-2-methyl-2-(E)-but	C5H12O8P2
1hdecg3p[c]	1-hexadecanoyl-sn-glycerol 3	C19H39O7P1
1hdecg3p[p]	1-hexadecanoyl-sn-glycerol 3	C19H39O7P1
1hdec9eg3p[c]	1-hexadec-9-enoyl-sn-glycero	C19H37O7P1
1hdec9eg3p[p]	1-hexadec-9-enoyl-sn-glycero	C19H37O7P1
1ddecg3p[c]	1-dodecanoyl-sn-glycerol 3-p	C15H31O7P1
1ddecg3p[p]	1-dodecanoyl-sn-glycerol 3-p	C15H31O7P1
mi1p-D[c]	1D-myo-Inositol 1-phosphate	C6H13O9P
dxyl5p[c]	1-deoxy-D-xylulose 5-phosph	C5H11O7P
1agpg181[p]	1-Acyl-sn-glycero-3-phospho	C24H47O9P1
1agpg180[p]	1-Acyl-sn-glycero-3-phospho	C24H48O9P1
1agpg161[p]	1-Acyl-sn-glycero-3-phospho	C22H43O9P1
1agpg160[p]	1-Acyl-sn-glycero-3-phospho	C22H45O9P1
1agpg141[p]	1-Acyl-sn-glycero-3-phospho	C20H39O9P1
1agpg140[p]	1-Acyl-sn-glycero-3-phospho	C20H41O9P1
1agpg120[p]	1-Acyl-sn-glycero-3-phospho	C18H37O9P1
1agpe181[p]	1-Acyl-sn-glycero-3-phospho	C23H46NO7P1
1agpe180[p]	1-Acyl-sn-glycero-3-phospho	C23H48NO7P1
1agpe161[p]	1-Acyl-sn-glycero-3-phospho	C21H42NO7P1
1agpe160[p]	1-Acyl-sn-glycero-3-phospho	C21H44NO7P1
1agpe141[p]	1-Acyl-sn-glycero-3-phospho	C19H38NO7P1
1agpe140[p]	1-Acyl-sn-glycero-3-phospho	C19H40NO7P1
1agpe120[p]	1-Acyl-sn-glycero-3-phospho	C17H36NO7P1

10fthf[c]	10-Formyltetrahydrofolate	C20H23N7O7
anhm3p[c]	1,6-anhydrous-N-Acetylmura	C26H41N5O14
anhm4p[c]	1,6-anhydrous-N-Acetylmura	C29H46N6O15
anhm[c]	1,6-anhydrous-N-Acetylmura	C11H17NO7
15dap[c]	1,5-Diaminopentane	C5H14N2
15dap[e]	1,5-Diaminopentane	C5H14N2
15dap[p]	1,5-Diaminopentane	C5H14N2
14dhncoa[c]	1,4-dihydroxy-2-napthoyl-Co	C32H38N7O19P3S
dhna[c]	1,4-Dihydroxy-2-naphthoate	C11H8O4
14glucan[c]	1,4-alpha-D-glucan	C36H62O31
14glucan[e]	1,4-alpha-D-glucan	C36H62O31
14glucan[p]	1,4-alpha-D-glucan	C36H62O31
pa140[c]	1,2-ditetradecanoyl-sn-glycer	C31H61O8P1
pa140[p]	1,2-ditetradecanoyl-sn-glycer	C31H61O8P1
pa141[c]	1,2-ditetradec-7-enoyl-sn-gly	C31H57O8P1
pa141[p]	1,2-ditetradec-7-enoyl-sn-gly	C31H57O8P1
pa180[c]	1,2-dioctadecanoyl-sn-glycer	C39H77O8P1
pa180[p]	1,2-dioctadecanoyl-sn-glycer	C39H77O8P1
pa181[c]	1,2-dioctadec-11-enoyl-sn-gl	C39H73O8P1
pa181[p]	1,2-dioctadec-11-enoyl-sn-gl	C39H73O8P1
pa160[c]	1,2-dihexadecanoyl-sn-glyce	C35H69O8P1
pa160[p]	1,2-dihexadecanoyl-sn-glyce	C35H69O8P1
pa161[c]	1,2-dihexadec-9-enoyl-sn-gly	C35H67O8P1
pa161[p]	1,2-dihexadec-9-enoyl-sn-gly	C35H67O8P1
pa120[c]	1,2-didodecanoyl-sn-glycerol	C27H53O8P1
pa120[p]	1,2-didodecanoyl-sn-glycerol	C27H53O8P1
12dgr140[c]	1,2-Diacyl-sn-glycerol (ditetra	C31H60O5
12dgr140[p]	1,2-Diacyl-sn-glycerol (ditetra	C31H60O5
12dgr141[c]	1,2-Diacyl-sn-glycerol (ditetra	C31H56O5
12dgr141[p]	1,2-Diacyl-sn-glycerol (ditetra	C31H56O5
12dgr180[c]	1,2-Diacyl-sn-glycerol (diocta	C39H76O5
12dgr180[p]	1,2-Diacyl-sn-glycerol (diocta	C39H76O5
12dgr181[c]	1,2-Diacyl-sn-glycerol (diocta	C39H72O5
12dgr181[p]	1,2-Diacyl-sn-glycerol (diocta	C39H72O5
12dgr160[c]	1,2-Diacyl-sn-glycerol (dihex	C35H68O5
12dgr160[p]	1,2-Diacyl-sn-glycerol (dihex	C35H68O5
12dgr161[c]	1,2-Diacyl-sn-glycerol (dihex	C35H64O5
12dgr161[p]	1,2-Diacyl-sn-glycerol (dihex	C35H64O5
12dgr120[c]	1,2-Diacyl-sn-glycerol (didod	C27H52O5
12dgr120[p]	1,2-Diacyl-sn-glycerol (didod	C27H52O5
prbatp[c]	1-(5-Phosphoribosyl)-ATP	C15H25N5O20P4
prbamp[c]	1-(5-Phosphoribosyl)-AMP	C15H23N5O14P2
prfp[c]	1-(5-Phosphoribosyl)-5-[(5-p	C15H25N5O15P2
2cpr5p[c]	1-(2-Carboxyphenylamino)-1	C12H16NO9P
4fe4s[c]	[4Fe-4S] iron-sulfur cluster	S4Fe4
2fe2s[c]	[2Fe-2S] iron-sulfur cluster	S2Fe2
2fe1s[c]	[2Fe-1S] desulfurated iron-su	SFe2
12ppd-S[e]	(S)-Propane-1,2-diol	C3H8O2

12ppd-S[p]	(S)-Propane-1,2-diol	$C_3H_8O_2$
dhor-S[c]	(S)-Dihydroorotate	$C_5H_6N_2O_4$
3mop[c]	(S)-3-Methyl-2-oxopentanoat	$C_6H_{10}O_3$
3htdcoa[c]	(S)-3-Hydroxytetradecanoyl-	$C_{35}H_{62}N_7O_{18}P_3S$
3hocoa[c]	(S)-3-Hydroxyoctanoyl-CoA	$C_{29}H_{50}N_7O_{18}P_3S$
3hodcoa[c]	(S)-3-Hydroxyoctadecanoyl-C	$C_{39}H_{70}N_7O_{18}P_3S$
3hhcoa[c]	(S)-3-Hydroxyhexanoyl-CoA	$C_{27}H_{46}N_7O_{18}P_3S$
3hhdcoa[c]	(S)-3-Hydroxyhexadecanoyl-	$C_{37}H_{66}N_7O_{18}P_3S$
3hddcoa[c]	(S)-3-Hydroxydodecanoyl-Co	$C_{33}H_{58}N_7O_{18}P_3S$
3hdcoa[c]	(S)-3-Hydroxydecanoyl-CoA	$C_{31}H_{54}N_7O_{18}P_3S$
3hbcoa[c]	(S)-3-Hydroxybutanoyl-CoA	$C_{25}H_{42}N_7O_{18}P_3S$
alac-S[c]	(S)-2-Acetolactate	$C_5H_8O_4$
2ahbut[c]	(S)-2-Aceto-2-hydroxybutano	$C_6H_{10}O_4$
25aics[c]	(S)-2-[5-Amino-1-(5-phospho	$C_{13}H_{19}N_4O_{12}P$
lgt-S[c]	(R)-S-Lactoylglutathione	$C_{13}H_{21}N_3O_8S$
12ppd-R[e]	(R)-Propane-1,2-diol	$C_3H_8O_2$
pnto-R[c]	(R)-Pantothenate	$C_9H_{17}NO_5$
pnto-R[e]	(R)-Pantothenate	$C_9H_{17}NO_5$
pnto-R[p]	(R)-Pantothenate	$C_9H_{17}NO_5$
pant-R[c]	(R)-Pantoate	$C_6H_{12}O_4$
glyc-R[c]	(R)-Glycerate	$C_3H_6O_4$
glyc-R[e]	(R)-Glycerate	$C_3H_6O_4$
glyc-R[p]	(R)-Glycerate	$C_3H_6O_4$
3hmrsACP[c]	(R)-3-Hydroxytetradecanoyl-[	$C_{25}H_{48}N_2O_9PRS$
3hoctACP[c]	(R)-3-Hydroxyoctanoyl-[acyl-	$C_{19}H_{36}N_2O_9PRS$
3hoctaACP[c]	(R)-3-Hydroxyoctadecanoyl-[	$C_{29}H_{56}N_2O_9PRS$
3hhexACP[c]	(R)-3-Hydroxyhexanoyl-[acyl-	$C_{17}H_{32}N_2O_9PRS$
3hddecACP[c]	(R)-3-Hydroxydodecanoyl-[ac	$C_{23}H_{44}N_2O_9PRS$
3hdecACP[c]	(R)-3-Hydroxydecanoyl-[acyl-	$C_{21}H_{40}N_2O_9PRS$
3hcvac11eACP[c]	(R)-3-hydroxy-cis-vacc-11-en	$C_{29}H_{54}N_2O_9PRS$
3hcpalm9eACP[c]	(R)-3-hydroxy-cis-palm-9-eoy	$C_{27}H_{50}N_2O_9PRS$
3hcmrs7eACP[c]	(R)-3-hydroxy-cis-myristol-7-	$C_{25}H_{46}N_2O_9PRS$
3hcddec5eACP[c]	(R)-3-hydroxy-cis-dodec-5-en	$C_{23}H_{42}N_2O_9PRS$
23dhmp[c]	(R)-2,3-Dihydroxy-3-methylp	$C_6H_{12}O_4$
23dhmb[c]	(R)-2,3-Dihydroxy-3-methylb	$C_5H_{10}O_4$
3haACP[c]	(3R)-3-Hydroxyacyl-[acyl-car	$C_{15}H_{28}N_2O_9PRS$
mdhdhf[c]	(2R,4S)-2-methyl-2,4-dihydro	$C_5H_8O_4$
mththf[c]	(2R,4S)-2-methyl-2,3,3,4-tetr	$C_5H_{10}O_5$

Charged Formula	Charge	Compartment	KEGG ID	CAS Number	Alternate Names
C6H15N2O2	1	Cytosol	C01142		L-beta-Lysine
C4H7O3	-1	Cytosol	C01188	2068-83-9	3-Hydroxyisobutyrate
C5H4O6	-2	Cytosol	C01127		4-Hydroxy-2-oxogluta
C6H7N2O3	-1	Cytosol	C03680		4-Imidazolone-5-prop
C8H5O7	-3	Cytosol	C04186		
C8H5O7	-3	Cytosol	C04052		5-Oxopent-3-ene-1,2,
C12H21O14P	-2	Cytosol	C04534		Cellobiose 6'-phosph
C8H16NO9P	0	Cytosol	C06376		
C16H28N2O11	0	Cytosol	C01674	35061-50-8	Diacetylchitobiose/ N,
C16H28N2O11	0	Extra-organism	C01674	35061-50-8	Diacetylchitobiose/ N,
C16H28N2O11	0	Periplasm	C01674	35061-50-8	Diacetylchitobiose/ N,
C16H27N2O14P	-2	Cytosol	C21152		
C15H21N3O16P2	0	Cytosol	C01219		
C15H23N3O16P2	0	Cytosol	C00501		CDP-D-Glucose
C12H22O11	0	Extra-organism		16462-44-5	1-beta-D-Glucopyran
C12H22O11	0	Periplasm	C00185	16462-44-5	1-beta-D-Glucopyran
C5H13NO4S	0	Cytosol	C00919	4858-96-2	
C12H24O	0	Cytosol	C02278	112-54-9	Dodecyl aldehyde/ D
C8H17NOS2	0	Cytosol	C00579	3884-47-7	Dihydrothioctamide
C42H52FeN8O6S2	1	Cytosol	C00923		
C42H53FeN8O6S2	1	Cytosol	C00924		
C19H18N7O6	-1	Cytosol	C00504	59-30-3	Pteroylglutamic acid/
C6H9N2O4	-1	Cytosol	C00439		N-Formimidoyl-L-glut
CH1O2	-1	Cytosol	C00058	64-18-6	Hydrogencarboxylic
CH3NO	0	Cytosol	C00488	75-12-7	Methanamide
C6H14NO8P	0	Cytosol	C06377		
C6H13NO5	1	Cytosol	C00329	3416-24-8	Chitosamine/ 2-Amin
C20H33O7P2	-3	Cytosol	C00353	6699-20-3	Geranylgeranyl pyrop
	0	Cytosol			
C78H136N2O24P2	-4	Cytosol			
C78H136N2O24P2	-4	Extra-organism			
C78H136N2O24P2	-4	Periplasm			
C64H121N2O20P	-2	Cytosol			
C64H120N2O23P2	-4	Cytosol			
C32H61NO12P	-2	Cytosol			
C8H15NOS2	0	Cytosol	C00248	940-69-2	Thioctic acid amide
C34H55O29	-1	Cytosol			
C34H55O29	-1	Extra-organism			
C34H55O29	-1	Periplasm			
C14H26N2O13P	-1	Cytosol			
C4H5O3	-1	Cytosol	C06002		
C3H6NO2R	1	Cytosol	C06481		
C41H72N3O20P2	-2	Cytosol			
C6H5N2O2	-1	Cytosol	C00785	104-98-3	Urocanic acid
Zn	2	Cytosol	C00038	7440-66-6	Zn2+/ Zn(II)
Zn	2	Extra-organism	C00038	7440-66-6	Zn2+/ Zn(II)
Zn	2	Periplasm	C00038	7440-66-6	Zn2+/ Zn(II)

C10H11N4O15P3	-4	Cytosol	C00700		
C10H11N4O12P2	-3	Cytosol	C01337		
C10H11N4O9P	-2	Cytosol	C00655	523-98-8	XMP/ Xanthylic acid/
C10H11N4O9P	-2	Extra-organism	C00655	523-98-8	XMP/ Xanthylic acid/
C10H11N4O9P	-2	Periplasm	C00655	523-98-8	XMP/ Xanthylic acid/
C10H12N4O6	0	Cytosol	C01762	146-80-5	
C10H12N4O6	0	Extra-organism	C01762	146-80-5	
C10H12N4O6	0	Periplasm	C01762	146-80-5	
C5H4N4O2	0	Cytosol	C00385	69-89-6	2,6-Dioxopurine
C5H4N4O2	0	Extra-organism	C00385	69-89-6	2,6-Dioxopurine
C5H4N4O2	0	Periplasm	C00385	69-89-6	2,6-Dioxopurine
C9H11N2O15P3	-4	Cytosol	C00075	63-39-8	Uridine 5'-triphosphat
C40H36N4O16	-8	Cytosol	C01051	1976-85-8	
C9H12N2O6	0	Cytosol	C00299	58-96-8	
C9H12N2O6	0	Extra-organism	C00299	58-96-8	
C9H12N2O6	0	Periplasm	C00299	58-96-8	
CH4N2O	0	Cytosol	C00086	57-13-6	Carbonyl diamine/ Ca
CH4N2O	0	Extra-organism	C00086	57-13-6	Carbonyl diamine/ Ca
CH4N2O	0	Periplasm	C00086	57-13-6	Carbonyl diamine/ Ca
C4H4N2O2	0	Cytosol	C00106	66-22-8	2,4-dioxy pyrimidine/
C4H4N2O2	0	Extra-organism	C00106	66-22-8	2,4-dioxy pyrimidine/
C4H4N2O2	0	Periplasm	C00106	66-22-8	2,4-dioxy pyrimidine/
C87H139N7O23P2	-4	Cytosol	C05897		N-acetylmuramoyl-L-
C95H152N8O28P2	-4	Cytosol	C05898		Peptidoglycan Unit (t
C55H89O4P	-2	Cytosol	C00348		di-trans-poly-cis-unde
C55H89O4P	-2	Periplasm	C00348		di-trans-poly-cis-unde
C63H103NO12P2	-2	Cytosol	C01289		Lipid I in Enterobacte
C55H89O7P2	-3	Cytosol	C04574		Undecaprenyl pyroph
C55H89O7P2	-3	Periplasm	C04574		Undecaprenyl pyroph
C9H11N2O9P	-2	Cytosol	C00105	58-97-9	Uridylic acid/ Uridine
C9H11N2O9P	-2	Extra-organism	C00105	58-97-9	Uridylic acid/ Uridine
C9H11N2O9P	-2	Periplasm	C00105	58-97-9	Uridylic acid/ Uridine
C41H61N9O28P2	-4	Cytosol	C04882		UDP-N-acetylmuram
C28H39N5O23P2	-4	Cytosol	C00692		
C38H56N8O27P2	-4	Cytosol	C04804		UDP-N-acetylmuram
C35H51N7O26P2	-4	Cytosol	C04877		UDP-N-acetylmuram
C23H33N4O20P2	-3	Cytosol	C01212		common abbr: UDP-
C20H28N3O19P2	-3	Cytosol	C01050		UDP-MurNac/ comm
C17H25N3O17P2	-2	Cytosol	C01170		UDP-ManNAc
C17H25N3O17P2	-2	Cytosol	C00043		UDP-N-acetylglucosa
C17H25N3O17P2	-2	Extra-organism	C00043		UDP-N-acetylglucosa
C17H25N3O17P2	-2	Periplasm	C00043		UDP-N-acetylglucosa
C17H25N3O17P2	-2	Extra-organism	C00203		UDP-GalNAc
C17H25N3O17P2	-2	Periplasm	C00203		UDP-GalNAc
C20H26N3O19P2	-3	Cytosol	C04631		UDP-N-acetyl-3-(1-c
C15H22N2O17P2	-2	Cytosol	C00029		UDP-D-glucose
C15H22N2O17P2	-2	Extra-organism	C00029		UDP-D-glucose
C15H22N2O17P2	-2	Periplasm	C00029		UDP-D-glucose

C15H22N2O17P2	-2	Cytosol	C00052		UDP-D-galactopyran
C15H22N2O17P2	-2	Extra-organism	C00052		UDP-D-galactopyran
C15H22N2O17P2	-2	Periplasm	C00052		UDP-D-galactopyran
C15H19N2O18P2	-3	Extra-organism	C00167		UDPglucuronate/ UD
C15H19N2O18P2	-3	Periplasm	C00167		UDPglucuronate/ UD
C31H51N3O19P2	-2	Cytosol	C04738		UDP-3-O-(beta-hydro
C29H50N3O18P2	-1	Cytosol	C06022		UDP-3-O-(beta-hydro
C9H11N2O12P2	-3	Cytosol	C00015	58-98-0	Uridine 5'-diphosphat
C49H74O4	0	Cytosol	C00399	1339-63-5	
C49H76O4	0	Cytosol	C00390		
C8H12NO	1	Extra-organism	C00483	51-67-2	2-(p-Hydroxyphenyl)e
C8H12NO	1	Periplasm	C00483	51-67-2	2-(p-Hydroxyphenyl)e
C68H104N12O38	-4	Periplasm			
C74H114N14O40	-4	Periplasm			
C71H109N13O39	-4	Periplasm			
C80H124N16O42	-4	Periplasm			GlcNac-MurNac-pent
C74H114N14O40	-4	Periplasm			
C77H119N15O41	-4	Periplasm			
C71H107N13O38	-4	Periplasm			
C74H112N14O39	-4	Periplasm			
C77H117N15O40	-4	Periplasm			
C74H112N14O39	-4	Periplasm			
C30H32N15O20P3S4W	-4	Cytosol			
C40H44N20O27P4S4W	-4	Cytosol			
C20H20N10O13P2S4W	-4	Cytosol			bis-wco
C10H10N5O8PS2W	-2	Cytosol			
O4W1	-2	Cytosol			
O4W1	-2	Extra-organism			
O4W1	-2	Periplasm			
R	0	Cytosol	C01653		
R	0	Cytosol	C00787		
R	0	Cytosol	C01652		
R	0	Cytosol	C01651		
R	0	Cytosol	C01650		
R	0	Cytosol			L-Selenocysteinyl-tR
R	0	Cytosol	C01649		
R	0	Cytosol	C01648		
R	0	Cytosol	C01647		
R	0	Cytosol	C01646		
R	0	Cytosol	C01645		
R	0	Cytosol	C01644		
R	0	Cytosol	C01643		
R	0	Cytosol	C01642		
R	0	Cytosol	C01640		
R	0	Cytosol	C01639		
R	0	Cytosol	C01638		
C10H17O10PR2	0	Cytosol	C01637		
R	0	Cytosol	C01636		

R	0	Cytosol	C01635		
R	0	Cytosol	C01641		
C3H9NO	0	Cytosol	C01104	1184-78-7	(CH3)3NO
C3H9NO	0	Extra-organism	C01104	1184-78-7	(CH3)3NO
C3H9NO	0	Periplasm	C01104	1184-78-7	(CH3)3NO
C3H10N	1	Cytosol	C00565	75-50-3	N/ (CH3)3N/ N-Dimet
C3H10N	1	Extra-organism	C00565	75-50-3	N/ (CH3)3N/ N-Dimet
C3H10N	1	Periplasm	C00565	75-50-3	N/ (CH3)3N/ N-Dimet
C12H22O11	0	Extra-organism	C01083	99-20-7	alpha,alpha-Trehalos
C12H22O11	0	Periplasm	C01083	99-20-7	alpha,alpha-Trehalos
C35H56N7O17P3S	-4	Cytosol	C05273		
C25H45N2O8PRS	-1	Cytosol	C05760		trans-Tetradec-2-eno
C39H64N7O17P3S	-4	Cytosol	C16218		elaidic acid coenzym
C29H53N2O8PRS	-1	Cytosol	C16221		trans-octadec-2-enoy
C29H44N7O17P3S	-4	Cytosol	C05276		
C19H33N2O8PRS	-1	Cytosol	C05751		trans-Oct-2-enoyl-[ac
C37H60N7O17P3S	-4	Cytosol	C05272		
C27H49N2O8PRS	-1	Cytosol	C05763		trans-Hexadec-2-eno
C27H40N7O17P3S	-4	Cytosol	C05271		
C17H29N2O8PRS	-1	Cytosol	C05748		trans-Hex-2-enoyl-[ac
C33H52N7O17P3S	-4	Cytosol	C03221		2-trans-Dodecenoyl-
C23H41N2O8PRS	-1	Cytosol	C05758		trans-Dodec-2-enoyl-
C31H48N7O17P3S	-4	Cytosol	C05275		(2E)-Decenoyl-CoA
C21H37N2O8PRS	-1	Cytosol	C05754		trans-Dec-2-enoyl-[ac
C27H47N2O8PRS	-1	Cytosol			
C25H43N2O8PRS	-1	Cytosol			
C23H39N2O8PRS	-1	Cytosol			
C29H51N2O8PRS	-1	Cytosol			
C5H6N2O2	0	Cytosol	C00178	65-71-4	T/ 2,4-Dihydroxy-5-m
C5H6N2O2	0	Extra-organism	C00178	65-71-4	T/ 2,4-Dihydroxy-5-m
C5H6N2O2	0	Periplasm	C00178	65-71-4	T/ 2,4-Dihydroxy-5-m
C10H14N2O5	0	Cytosol	C00214	50-89-5	dT/ 2'-Deoxythymidin
C10H14N2O5	0	Extra-organism	C00214	50-89-5	dT/ 2'-Deoxythymidin
C10H14N2O5	0	Periplasm	C00214	50-89-5	dT/ 2-Deoxythymidine
C120H186N24O63	-6	Periplasm			GlcNac-MurNac-pent
C111H169N21O59	-6	Periplasm			
C111H167N21O58	-6	Periplasm			
C114H172N22O59	-6	Periplasm			
O3S2	-2	Cytosol	C00320		Hyposulfite
O3S2	-2	Extra-organism	C00320		Hyposulfite
O3S2	-2	Periplasm	C00320		Hyposulfite
CNS	-1	Cytosol	C01755	463-56-9	Thiocyanate/ Thiocya
CNS	-1	Extra-organism	C01755	463-56-9	Thiocyanate/ Thiocya
CNS	-1	Periplasm	C01755	463-56-9	Thiocyanate/ Thiocya
C12H16N4O7P2S	-2	Cytosol	C00068	154-87-0	cocarboxylase/ Thiam
C12H16N4O4PS	-1	Cytosol	C01081	532-40-1	Thiamin phosphate/
C12H17N4OS	1	Cytosol	C00378	67-03-8	Thiamine/ Vitamin B1
C12H17N4OS	1	Extra-organism	C00378	67-03-8	Thiamine/ Vitamin B1

C12H17N4OS	1	Periplasm	C00378	67-03-8	Thiamine/ Vitamin B1
C35H56N7O17P3S	-4	Cytosol			
C14H25O2	-1	Cytosol			tetradecenoic acid
C14H25O2	-1	Extra-organism			tetradecenoic acid
C14H25O2	-1	Periplasm			tetradecenoic acid
C14H26O5P	-1	Cytosol			
C14H28O5P	-1	Cytosol			
C35H58N7O17P3S	-4	Cytosol	C02593		Myristoyl-CoA
C14H27O2	-1	Cytosol	C06424	544-63-8	Tetradecanoate/ neo-
C14H27O2	-1	Extra-organism	C06424	544-63-8	Tetradecanoate/ neo-
C14H27O2	-1	Periplasm	C06424	544-63-8	Tetradecanoate/ neo-
C22H24N2O8	0	Extra-organism	C06570	60-54-8	
C22H24N2O8	0	Periplasm	C06570	60-54-8	
C2H7NO3S	0	Extra-organism	C00245	107-35-7	2-Aminoethanesulfon
C2H7NO3S	0	Periplasm	C00245	107-35-7	2-Aminoethanesulfon
O2	-1	Extra-organism	C00704		O2.-/ o2-/ O2 free rad
O2	-1	Periplasm	C00704		O2.-/ o2-/ O2 free rad
O2S	0	Cytosol	C09306		
O2S	0	Extra-organism	C09306		
O2S	0	Periplasm	C09306		
C2H2O5S	-2	Extra-organism	C14179		
C2H2O5S	-2	Periplasm	C14179		
O3S	-2	Cytosol	C00094	7782-99-2	Sulfurous acid
O3S	-2	Extra-organism	C00094	7782-99-2	Sulfurous acid
O3S	-2	Periplasm	C00094	7782-99-2	Sulfurous acid
O4S	-2	Cytosol	C00059	7664-93-9	Sulfuric acid
O4S	-2	Extra-organism	C00059	7664-93-9	Sulfuric acid
O4S	-2	Periplasm	C00059	7664-93-9	Sulfuric acid
C12H21O14P	-2	Cytosol	C02591		Sugar 1-phosphate
C12H22O11	0	Extra-organism	C00089	57-50-1	Cane sugar/ Sacchar
C12H22O11	0	Periplasm	C00089	57-50-1	Cane sugar/ Sacchar
C25H35N7O19P3S	-5	Cytosol	C00091	604-98-8	succino-1-yl-coenzym
C4H5O3	-1	Cytosol	C00232	692-29-5	4-Oxobutanoate/ Suc
C4H4O4	-2	Cytosol	C00042	110-15-6	Succinic acid/ Butane
C4H4O4	-2	Extra-organism	C00042	110-15-6	Succinic acid/ Butane
C4H4O4	-2	Periplasm	C00042	110-15-6	Succinic acid/ Butane
C39H66N7O17P3S	-4	Cytosol	C00412	362-66-3	Stearyl-CoA/ Octade
C9H17NO6S	0	Cytosol	C03539	37558-16-0	S-Ribosyl-L-homocys
C7H22N3	3	Cytosol	C00315	124-20-9	N-(3-Aminopropyl)-1,
C7H22N3	3	Extra-organism	C00315	124-20-9	N-(3-Aminopropyl)-1,
C7H22N3	3	Periplasm	C00315	124-20-9	N-(3-Aminopropyl)-1,
Na	1	Cytosol	C01330	7440-23-5	Natrium/ Na
Na	1	Extra-organism	C01330	7440-23-5	Natrium/ Na
Na	1	Periplasm	C01330	7440-23-5	Natrium/ Na
C5H14NO6P	0	Cytosol	C01233		Glycerophosphoetha
C5H14NO6P	0	Extra-organism	C01233		Glycerophosphoetha
C5H14NO6P	0	Periplasm	C01233		Glycerophosphoetha
C8H20NO6P	0	Cytosol	C00670		Glycerophosphocholi

C8H20NO6P	0	Extra-organism	C00670		Glycerophosphocholi
C8H20NO6P	0	Periplasm	C00670		Glycerophosphocholi
C9H18O11P	-1	Cytosol	C01225		
C9H18O11P	-1	Extra-organism	C01225		
C9H18O11P	-1	Periplasm	C01225		
C6H14NO2S	1	Extra-organism	C03172		
C6H14NO2S	1	Periplasm	C03172		
C42H39N4O16	-7	Cytosol	C05778		
C42H36FeN4O16	-8	Cytosol	C00748		Sirohaem
Ag	1	Extra-organism	C06710	7440-22-4	Argentum/ Ag/ Ag+
C7H8O8P	-3	Cytosol	C03175		Shikimate 3-phospha
C7H9O5	-1	Cytosol	C00493	138-59-0	Shikimic acid/ 3,4,5-T
C7H9O5	-1	Extra-organism	C00493	138-59-0	Shikimic acid/ 3,4,5-T
C7H9O5	-1	Periplasm	C00493	138-59-0	Shikimic acid/ 3,4,5-T
C11H16N3O7S	-1	Cytosol	C01031		
H2O3PSe	-1	Cytosol	C05172		Selenophosphate
O3Se	-2	Extra-organism	C05684		Selenite
O3Se	-2	Periplasm	C05684		Selenite
O4Se	-2	Extra-organism	C05697		Selenate/ Selenic aci
O4Se	-2	Periplasm	C05697		Selenate/ Selenic aci
C7H13O10P	-2	Cytosol	C05382		altro-Heptulose 7-pho
C7H12O13P2	-4	Cytosol	C00447		altro-Heptulose 1,7-bi
C15H23N6O5S	1	Cytosol	C00019	29908-03-0	S-Adenosylmethionin
C14H20N6O5S	0	Cytosol	C00021	979-92-0	S-Adenosylhomocyst
C15H19N5O6S	0	Cytosol	C04425		
C43H58N4O12	0	Extra-organism	C06688	13292-46-1	rifampicin
C17H20N4O6	0	Cytosol	C00255	83-88-5	Lactoflavin/ Vitamin B
XH2	0	Cytosol	C00342		
C17H22N4O6	0	Cytosol	C01007		
C10H16N3O6S	-1	Cytosol	C00051	70-18-8	Glutathione/ 5-L-Glut
C10H16N3O6S	-1	Extra-organism	C00051	70-18-8	Glutathione/ 5-L-Glut
C10H16N3O6S	-1	Periplasm	C00051	70-18-8	Glutathione/ 5-L-Glut
C17H21N4O9P	-2	Cytosol	C01847	67-63-0	Reduced flavin mono
C27H51N2O9PRS	-1	Cytosol	C04633		(R)-3-Hydroxypalmito
C7H3NO4	-2	Cytosol	C03722	89-00-9	Pyridine-2,3-dicarbox
C7H12O6	0	Extra-organism	C00296	77-95-2	Quinic acid/ Kinic aci
C7H12O6	0	Periplasm	C00296	77-95-2	Quinic acid/ Kinic aci
C3H3O3	-1	Cytosol	C00022	127-17-3	Pyruvic acid/ 2-Oxopr
C3H3O3	-1	Extra-organism	C00022	127-17-3	Pyruvic acid/ 2-Oxopr
C3H3O3	-1	Periplasm	C00022	127-17-3	Pyruvic acid/ 2-Oxopr
C8H10NO6P	-2	Cytosol	C00627	447-05-2	Pyridoxine phosphate
C8H11NO3	0	Extra-organism	C00314	65-23-6	Pyridoxol/ vitamin b6
C8H11NO3	0	Periplasm	C00314	65-23-6	Pyridoxol/ vitamin b6
C8H12N2O5P	-1	Cytosol	C00647	529-96-4	Pyridoxamine 5-phos
C8H13N2O2	1	Extra-organism	C00534	85-87-0	PM
C8H13N2O2	1	Periplasm	C00534	85-87-0	PM
C8H8NO6P	-2	Cytosol	C00018	54-47-7	Pyridoxal 5-phosphat
C8H9NO3	0	Cytosol	C00250	66-72-8	

C8H9NO3	0	Extra-organism	C00250	66-72-8	
C8H9NO3	0	Periplasm	C00250	66-72-8	
C4H14N2	2	Cytosol	C00134	110-60-1	1,4-Diaminobutane/ 1
C4H14N2	2	Extra-organism	C00134	110-60-1	1,4-Diaminobutane/ 1
C4H14N2	2	Periplasm	C00134	110-60-1	1,4-Diaminobutane/ 1
C12H25N2O7	1	Extra-organism			
C12H25N2O7	1	Periplasm			
C34H38N4O4	-2	Cytosol	C01079		
C34H32N4O4	-2	Cytosol	C02191	553-12-8	Protoporphyrin IX/ Po
C34H30FeN4O4	-2	Cytosol	C00032	14875-96-8	Heme/ Haem/ Heme
C34H30FeN4O4	-2	Extra-organism	C00032	14875-96-8	Heme/ Haem/ Heme
C34H30FeN4O4	-2	Periplasm	C00032	14875-96-8	Heme/ Haem/ Heme
XH2	0	Periplasm			gene product of dsbC
X	0	Periplasm			gene product of dsbC
C3H5O2	-1	Cytosol	C00163	79-09-4	Propanoate/ Propano
C3H5O2	-1	Extra-organism	C00163	79-09-4	Propanoate/ Propano
C3H5O2	-1	Periplasm	C00163	79-09-4	Propanoate/ Propano
C24H36N7O17P3S	-4	Cytosol	C00100	317-66-8	Propionyl-CoA/ Propi
C3H5O5P	-2	Cytosol	C02876		Propanoyl phosphate
C3H6O	0	Extra-organism	C00479	123-38-6	Propionaldehyde
C3H6O	0	Periplasm	C00479	123-38-6	Propionaldehyde
C10H8O6	-2	Cytosol	C00254	126-49-8	Prephenic acid
K	1	Cytosol	C00238		Potassium/ K+
K	1	Extra-organism	C00238		Potassium/ K+
K	1	Periplasm	C00238		Potassium/ K+
C10H13N2O4	-1	Cytosol	C00931	487-90-1	
C19H33N2O10PRS	-1	Cytosol			
C18H31N2O10PRS	-1	Cytosol			
C9H10NO6P	-2	Extra-organism	C06501		Phosphonotyrosine
C9H10NO6P	-2	Periplasm	C06501		Phosphonotyrosine
HO3P	-2	Extra-organism	C06701	13598-36-2	Phosphonate/ Phosph
HO3P	-2	Periplasm	C06701	13598-36-2	Phosphonate/ Phosph
C3H2O6P	-3	Cytosol	C00074	138-08-9	Phosphoenolpyruvic
C34H65N1O10P1	-1	Cytosol	C02737		Phosphatidyl-L-serine
C34H61N1O10P1	-1	Cytosol	C02737		Phosphatidyl-L-serine
C42H81N1O10P1	-1	Cytosol	C02737		Phosphatidyl-L-serine
C42H77N1O10P1	-1	Cytosol	C02737		1,2-Diacyl-sn-glycerol
C38H73N1O10P1	-1	Cytosol	C02737		1,2-Diacyl-sn-glycerol
C38H69N1O10P1	-1	Cytosol	C02737		Phosphatidyl-L-serine
C30H57N1O10P1	-1	Cytosol	C02737		Phosphatidyl-L-serine
C34H65O13P2	-3	Cytosol	C03892		3(3-sn-Phosphatidyl)-
C34H65O13P2	-3	Periplasm	C03892		3(3-sn-Phosphatidyl)-
C34H61O13P2	-3	Cytosol	C03892		3(3-sn-Phosphatidyl)-
C34H61O13P2	-3	Periplasm	C03892		3(3-sn-Phosphatidyl)-
C42H81O13P2	-3	Cytosol	C03892		3(3-sn-Phosphatidyl)-
C42H81O13P2	-3	Periplasm	C03892		3(3-sn-Phosphatidyl)-
C42H77O13P2	-3	Cytosol	C03892		3(3-sn-Phosphatidyl)-
C42H77O13P2	-3	Periplasm	C03892		3(3-sn-Phosphatidyl)-

C38H73O13P2	-3	Cytosol	C03892		3(3-sn-Phosphatidyl)-
C38H73O13P2	-3	Periplasm	C03892		3(3-sn-Phosphatidyl)-
C38H69O13P2	-3	Cytosol	C03892		3(3-sn-Phosphatidyl)-
C38H69O13P2	-3	Periplasm	C03892		3(3-sn-Phosphatidyl)-
C30H57O13P2	-3	Cytosol	C03892		3(3-sn-Phosphatidyl)-
C30H57O13P2	-3	Periplasm	C03892		3(3-sn-Phosphatidyl)-
C34H66O10P1	-1	Cytosol	C00344		3(3-Phosphatidyl-)gly
C34H66O10P1	-1	Periplasm	C00344		3(3-Phosphatidyl-)gly
C34H62O10P1	-1	Cytosol	C00344		PtdGro/ Phosphatidyl
C34H62O10P1	-1	Periplasm	C00344		PtdGro/ Phosphatidyl
C42H82O10P1	-1	Cytosol	C00344		3(3-Phosphatidyl-)gly
C42H82O10P1	-1	Periplasm	C00344		3(3-Phosphatidyl-)gly
C42H78O10P1	-1	Cytosol	C00344		PtdGro/ 3(3-Phospha
C42H78O10P1	-1	Periplasm	C00344		PtdGro/ 3(3-Phospha
C38H74O10P1	-1	Cytosol	C00344		3(3-Phosphatidyl-)gly
C38H74O10P1	-1	Periplasm	C00344		3(3-Phosphatidyl-)gly
C38H70O10P1	-1	Cytosol	C00344		Phosphatidylglycerol/
C38H70O10P1	-1	Periplasm	C00344		Phosphatidylglycerol/
C30H58O10P1	-1	Cytosol	C00344		Phosphatidylglycerol/
C30H58O10P1	-1	Periplasm	C00344		Phosphatidylglycerol/
C33H66N1O8P1	0	Cytosol	C00350		(3-Phosphatidyl)ethar
C33H66N1O8P1	0	Periplasm	C00350		(3-Phosphatidyl)ethar
C33H62N1O8P1	0	Cytosol	C00350		(3-Phosphatidyl)ethar
C33H62N1O8P1	0	Periplasm	C00350		(3-Phosphatidyl)ethar
C41H82N1O8P1	0	Cytosol	C00350		Cephalin/ (3-Phospha
C41H82N1O8P1	0	Periplasm	C00350		Cephalin/ (3-Phospha
C41H78N1O8P1	0	Cytosol	C00350		(3-Phosphatidyl)-etha
C41H78N1O8P1	0	Periplasm	C00350		(3-Phosphatidyl)-etha
C37H74N1O8P1	0	Cytosol	C00350		Cephalin/ (3-Phospha
C37H74N1O8P1	0	Periplasm	C00350		Cephalin/ (3-Phospha
C37H70N1O8P1	0	Cytosol	C00350		(3-Phosphatidyl)ethar
C37H70N1O8P1	0	Periplasm	C00350		(3-Phosphatidyl)ethar
C29H58N1O8P1	0	Cytosol	C00350		Cephalin/ (3-Phospha
C29H58N1O8P1	0	Periplasm	C00350		Cephalin/ (3-Phospha
HO4P	-2	Cytosol	C00009	14265-44-2	Orthophosphate/ Pi/ F
HO4P	-2	Extra-organism	C00009	14265-44-2	Orthophosphate/ Pi/ F
HO4P	-2	Periplasm	C00009	14265-44-2	Orthophosphate/ Pi/ F
C9H7O3	-1	Cytosol	C00166	156-06-9	Phenylpyruvic acid/ a
C9H9O2	-1	Cytosol	C05629	2628-17-3	Phenylpropanoate/ 3-
C9H9O2	-1	Extra-organism	C05629	2628-17-3	Phenylpropanoate/ 3-
C9H9O2	-1	Periplasm	C05629	2628-17-3	Phenylpropanoate/ 3-
C8H8O	0	Extra-organism	C00601	122-78-1	alpha-Tolualdehyde
C8H8O	0	Periplasm	C00601	122-78-1	alpha-Tolualdehyde
C8H12N	1	Extra-organism	C05332	64-04-0	Phenethylamine/ 2-Pl
C8H12N	1	Periplasm	C05332	64-04-0	Phenethylamine/ 2-Pl
XH2	0	Periplasm			gene product of dsbA
X	0	Periplasm			gene product of dsbA
C7H8O	0	Cytosol	C01468	106-44-5	4-Cresol/ p-Cresol/ 4-

C11H21N2O7PS	-2	Cytosol	C01134		4'-Phosphopantethein
C37H62N7O17P3S	-4	Cytosol	C00154		Hexadecanoyl-CoA
C27H51N2O8PRS	-1	Cytosol	C05764		Hexadecanoyl-[acp]/
C20H24N10O22P5	-5	Cytosol	C04058	4637-56-3	Bis(5'-adenosyl) pent
C20H24N10O21P4	-4	Cytosol	C01261		GppppG/ Bis(5'-guan
C20H24N10O19P4	-4	Cytosol	C01260		5',5'''-diadenosine tetr
X	0	Cytosol	C00343		
C20H30N6O12S2	-2	Cytosol	C00127		L-Glutathione oxidize
C20H30N6O12S2	-2	Extra-organism	C00127		L-Glutathione oxidize
C20H30N6O12S2	-2	Periplasm	C00127		L-Glutathione oxidize
C4H2O5	-2	Cytosol	C00036	328-42-7	Oxalacetic acid/ Oxal
C8H12NO6	-1	Cytosol	C01118	1492-23-5	
C32H39N7O20P3S	-5	Cytosol	C03160		2-Succinylbenzoyl-Co
C11H8O5	-2	Cytosol	C02730		2-Succinylbenzoate/
C10H10N2O11P	-3	Cytosol	C01103	2149-82-8	Orotidylic acid
C5H3N2O4	-1	Cytosol	C00295	65-86-1	Orotic acid/ Uracil-6-c
C5H3N2O4	-1	Extra-organism	C00295	65-86-1	Orotic acid/ Uracil-6-c
C5H3N2O4	-1	Periplasm	C00295	65-86-1	Orotic acid/ Uracil-6-c
C5H13N2O2	1	Cytosol	C01602	70-26-8	2,5-Diaminovaleric ac
C5H13N2O2	1	Extra-organism	C01602	70-26-8	2,5-Diaminovaleric ac
C5H13N2O2	1	Periplasm	C01602	70-26-8	2,5-Diaminovaleric ac
C3H6NO6P	-2	Cytosol	C01005	407-41-0	3-Phosphoserine
C3H6NO6P	-2	Extra-organism	C01005	407-41-0	3-Phosphoserine
C3H6NO6P	-2	Periplasm	C01005	407-41-0	3-Phosphoserine
C4H8NO6P	-2	Cytosol	C01102		
C4H8NO7P	-2	Cytosol	C06055		4-(Phosphonooxy)-thr
C29H46N7O17P3S	-4	Cytosol	C01944		
C19H35N2O8PRS	-1	Cytosol	C05752		Octanoyl-[acyl-carrier
C8H15O	1	Cytosol			
C8H15O2	-1	Cytosol	C06423	124-07-2	Caprylic acid/ Octano
C8H15O2	-1	Extra-organism	C06423	124-07-2	Caprylic acid/ Octano
C8H15O2	-1	Periplasm	C06423	124-07-2	Caprylic acid/ Octano
C39H64N7O17P3S	-4	Cytosol	C00510		Oleoyl-CoA
C18H33O2	-1	Cytosol	C00712		Oleic acid/ octadecen
C18H33O2	-1	Extra-organism	C00712		Oleic acid/ octadecen
C18H33O2	-1	Periplasm			Oleic acid/ octadecen
C18H34O5P	-1	Cytosol			
C18H36O5P	-1	Cytosol			
C29H55N2O8PRS	-1	Cytosol	C04088		stearoyl-ACP
C18H35O2	-1	Cytosol	C01530	57-11-4	Stearate/ Stearic acid
C18H35O2	-1	Extra-organism	C01530	57-11-4	Stearate/ Stearic acid
C18H35O2	-1	Periplasm	C01530	57-11-4	Stearate/ Stearic acid
C5H9NO4	0	Cytosol	C00979	66638-22-0	O3-Acetyl-L-serine
C5H9NO4	0	Extra-organism	C00979	66638-22-0	O3-Acetyl-L-serine
C5H9NO4	0	Periplasm	C00979	66638-22-0	O3-Acetyl-L-serine
O2	0	Cytosol	C00007	7782-44-7	Oxygen/ dioxygen
O2	0	Extra-organism	C00007	7782-44-7	Oxygen/ dioxygen
O2	0	Periplasm	C00007	7782-44-7	Oxygen/ dioxygen

C11H16N2O7	-2	Cytosol	C04421		N-Succinyl-LL-2,6-dia
C11H12NO8	-3	Cytosol	C04462		N-Succinyl-L-2-amino
C31H36N2O11	0	Extra-organism	C05080	303-81-1	
C11H14N2O8P	-1	Cytosol	C00455	1094-61-7	Nicotinamide D-ribon
C11H14N2O8P	-1	Extra-organism	C00455	1094-61-7	Nicotinamide D-ribon
C11H14N2O8P	-1	Periplasm	C00455	1094-61-7	Nicotinamide D-ribon
N2O	0	Cytosol	C00887	10024-97-2	Dinitrogen monoxide/
N2O	0	Extra-organism	C00887	10024-97-2	Dinitrogen monoxide/
N2O	0	Periplasm	C00887	10024-97-2	Dinitrogen monoxide/
NO2	-1	Cytosol	C00088	7697-37-2	Nitric acid
NO2	-1	Extra-organism	C00088	7697-37-2	Nitric acid
NO2	-1	Periplasm	C00088	7697-37-2	Nitric acid
NO	0	Cytosol	C00533	10102-43-9	NO/ Nitrogen monoxi
NO	0	Extra-organism	C00533	10102-43-9	NO/ Nitrogen monoxi
NO	0	Periplasm	C00533	10102-43-9	NO/ Nitrogen monoxi
NO3	-1	Cytosol	C00244		Nitric acid
NO3	-1	Extra-organism	C00244		Nitric acid
NO3	-1	Periplasm	C00244		Nitric acid
C11H12NO9P	-2	Cytosol	C01185		Nicotinate ribonucleo
C6H4NO2	-1	Extra-organism	C00253	59-67-6	Niacin/ Nicotinic acid/
C6H4NO2	-1	Periplasm	C00253	59-67-6	Niacin/ Nicotinic acid/
C21H26N7O17P3	-4	Cytosol	C00005	2646-71-1	TPNH/ beta-triphosp
C21H25N7O17P3	-3	Cytosol	C00006	53-59-8	beta-Nicotinamide ad
C21H27N7O14P2	-2	Cytosol	C00004	58-68-4	DPNH/ NADH
C21H26N7O14P2	-1	Cytosol	C00003	53-84-9	NAD+/ NAD/ beta-Di
Ni	2	Cytosol	C00291		Nickel/ Ni2+
Ni	2	Extra-organism	C00291		Nickel/ Ni2+
Ni	2	Periplasm	C00291		Nickel/ Ni2+
C6H9NO2SR	0	Cytosol	C03294		
C5H6N2O5	-2	Cytosol	C00438		
C11H18NO9	-1	Cytosol	C00270	131-48-6	5-Acetamido-3,5-dide
C11H18NO9	-1	Extra-organism	C00270	131-48-6	5-Acetamido-3,5-dide
C11H18NO9	-1	Periplasm	C00270	131-48-6	5-Acetamido-3,5-dide
C11H17NO11P	-3	Cytosol	C16698		N-Acetylmuramate-6-
C11H18NO8	-1	Extra-organism	C02713	61633-75-8	N-Acetylmuramate/ N
C11H18NO8	-1	Periplasm	C02713	61633-75-8	N-Acetylmuramate/ N
C7H9NO8P	-3	Cytosol	C04133		N-Acetyl-L-glutamate
C7H10NO4	-1	Cytosol	C01250		2-Acetamido-5-oxope
C7H9NO5	-2	Cytosol	C00624	1188-37-0	N-Acetyl-L-glutamic a
C8H14NO9P	-2	Cytosol	C04257	157296-99-6	N-Acetyl-D-mannosa
C8H15NO6	0	Cytosol	C00645	3615-17-6	2-Acetamido-2-deoxy
C8H15NO6	0	Extra-organism	C00645	3615-17-6	2-Acetamido-2-deoxy
C8H15NO6	0	Periplasm	C00645	3615-17-6	2-Acetamido-2-deoxy
C34H52N6O19	-2	Cytosol			GlcNAc(anh)MurNAc
C34H52N6O19	-2	Periplasm			GlcNAc(anh)MurNAc
C37H57N7O20	-2	Cytosol			GlcNAc(anh)MurNAc
C37H57N7O20	-2	Periplasm			GlcNAc(anh)MurNAc
C19H29N2O12	-1	Cytosol			GlcNAc(anh)MurNAc

C19H29N2O12	-1	Extra-organism			GlcNAc(anh)MurNAc
C19H29N2O12	-1	Periplasm			GlcNAc(anh)MurNAc
C8H14NO9P	-2	Cytosol	C00357	102029-88-9	
C8H14NO9P	-2	Cytosol	C04256		
C8H14NO9P	-2	Extra-organism	C04256		
C8H14NO9P	-2	Periplasm	C04256		
C8H15NO6	0	Cytosol	C00140	7512-17-6	N-Acetylchitosamine/
C8H15NO6	0	Extra-organism	C00140	7512-17-6	N-Acetylchitosamine/
C8H15NO6	0	Periplasm	C00140	7512-17-6	N-Acetylchitosamine/
C8H14NO9P	-2	Extra-organism	C18060		
C8H14NO9P	-2	Periplasm	C18060		
C8H15NO6	0	Extra-organism	C01132	14215-68-0	N-Acetyl-D-chondros
C8H15NO6	0	Periplasm	C01132	14215-68-0	N-Acetyl-D-chondros
C9H23N3O	2	Cytosol	C01029	34450-15-2	
C14H14N5O11P	-4	Cytosol	C03794		Adenylosuccinate/ Ad
C9H15N2O5	-1	Cytosol	C03415	80102-04-1	N2-Succinyl-L-ornithi
C9H11NO6	-2	Cytosol	C05932		N2-Succinyl-L-glutam
C9H10NO7	-3	Cytosol	C05931	33981-72-5	N2-Succinyl-L-glutam
C10H17N4O5	-1	Cytosol	C03296	1758-80-1	N2-Succinyl-L-argini
C8H13N2O9P	-2	Cytosol	C04376		5'-Phosphoribosyl-N-
C7H14N2O3	0	Cytosol	C00437		
C9H23N3O	2	Cytosol	C00612	34450-16-3	
C7H14N2O8P	-1	Cytosol	C03838		5'-Phosphoribosylgly
C16H28N2O11	0	Extra-organism	C01674	35061-50-8	
C16H28N2O11	0	Periplasm	C01674	35061-50-8	
C10H17N4O6	-1	Cytosol	C03406		N-(L-Arginino)succina
C12H13NO9P	-3	Cytosol	C04302		N-(5-Phospho-beta-D
C12H20N2O9PS	-3	Cytosol	C04352		(R)-4'-Phosphopantot
C25H47N2O8PRS	-1	Cytosol	C05761		Tetradecanoyl-[acyl-c
C6H6O24P6	-12	Extra-organism	C01204		Inositol 1,2,3,4,5,6-he
C6H12O6	0	Cytosol	C00137	87-89-8	D-myo-Inositol/ 1D-m
C6H12O6	0	Extra-organism	C00137	87-89-8	D-myo-Inositol/ 1D-m
C6H12O6	0	Periplasm	C00137	87-89-8	D-myo-Inositol/ 1D-m
C20H22N10O15P2S2Mc	-2	Cytosol			MGD
C10H10N5O6PS2Cu	-2	Cytosol	C05924		Molybdopterin
C10H10N5O8PS2Mo	-2	Cytosol	C18237		Molybdenum cofactor
MoO4	-2	Cytosol	C06232		
MoO4	-2	Extra-organism	C06232		
MoO4	-2	Periplasm	C06232		
C1H1O1S1X	0	Cytosol			
C1O2X	-1	Cytosol			
C11H12N5O8P1X	-1	Cytosol			
Mn	2	Cytosol	C00034		Manganese dication/
Mn	2	Extra-organism	C00034		Manganese dication/
Mn	2	Periplasm	C00034		Manganese dication/
C23H27N3O7	0	Extra-organism	C07225	10118-90-8	
C23H27N3O7	0	Periplasm	C07225	10118-90-8	
C7H7O7	-3	Cytosol	C04593	20298-95-7	Methylisocitric acid/ (

C3H4O2	0	Cytosol	C00546	78-98-8	Pyruvaldehyde/ Pyruv
CH4O1	0	Cytosol	C00132	67-56-1	Methyl alcohol
CH4O1	0	Extra-organism	C00132	67-56-1	Methyl alcohol
CH4O1	0	Periplasm	C00132	67-56-1	Methyl alcohol
CH3O3S	-1	Extra-organism	C11145		MethaneSulfonic Acid
CH3O3S	-1	Periplasm	C11145		MethaneSulfonic Acid
C7H14N2O4	0	Cytosol	C00680		meso-2,6-Diaminopim
C7H14N2O4	0	Extra-organism	C00680		meso-2,6-Diaminopim
C7H14N2O4	0	Periplasm	C00680		meso-2,6-Diaminopim
C3H3O3S	-1	Cytosol	C00957		3-Mercaptopyruvate
C51H72O2	0	Cytosol	C00828	84-81-1	Vitamin K2
C51H74O2	0	Cytosol	C05819		
C12H22O11	0	Extra-organism	C05402	585-99-9	6-O-(alpha-D-Galacto
C12H22O11	0	Periplasm	C05402	585-99-9	6-O-(alpha-D-Galacto
C18H32O16	0	Cytosol	C01835	1109-28-0	Maltotriose/ Amylotrio
C18H32O16	0	Extra-organism	C01835	1109-28-0	Maltotriose/ Amylotrio
C18H32O16	0	Periplasm	C01835	1109-28-0	Maltotriose/ Amylotrio
C24H42O21	0	Cytosol	C02052	34612-38-9	Maltotetraose
C24H42O21	0	Extra-organism	C02052	34612-38-9	Maltotetraose
C24H42O21	0	Periplasm	C02052	34612-38-9	Maltotetraose
C12H21O14P	-2	Cytosol	C02995		
C12H22O11	0	Cytosol	C00208	69-79-4	Malt sugar/ 1-alpha-D
C12H22O11	0	Extra-organism	C00208	69-79-4	Malt sugar/ 1-alpha-D
C12H22O11	0	Periplasm	C00208	69-79-4	Malt sugar/ 1-alpha-D
C30H52O26	0	Cytosol			
C30H52O26	0	Extra-organism			
C30H52O26	0	Periplasm			
C36H62O31	0	Cytosol	C01936	34620-77-4	Maltohexaose
C36H62O31	0	Extra-organism	C01936	34620-77-4	Maltohexaose
C36H62O31	0	Periplasm	C01936	34620-77-4	Maltohexaose
C42H72O36	0	Cytosol			
C25H36N7O19P3S	-4	Cytosol			
C24H33N7O19P3S	-5	Cytosol	C00083	524-14-1	Malonyl coenzyme A
C14H22N2O10PRS	-2	Cytosol	C01209		
Mg	2	Cytosol	C00305		Mg
Mg	2	Extra-organism	C00305		Mg
Mg	2	Periplasm	C00305		Mg
C5H10O5	0	Extra-organism	C00312	527-50-4	L-threo-Pentulose/ L-
C5H10O5	0	Periplasm	C00312	527-50-4	L-threo-Pentulose/ L-
C5H10NOR	1	Cytosol	C02554		
C5H11NO2	0	Cytosol	C00183	72-18-4	2-Aminoisovaleric aci
C5H11NO2	0	Extra-organism	C00183	72-18-4	2-Aminoisovaleric aci
C5H11NO2	0	Periplasm	C00183	72-18-4	2-Aminoisovaleric aci
C9H10NO2R	1	Cytosol	C02839		
C9H11NO3	0	Cytosol	C00082	60-18-4	(S)-3-(p-Hydroxypher
C9H11NO3	0	Extra-organism	C00082	60-18-4	(S)-3-(p-Hydroxypher
C9H11NO3	0	Periplasm	C00082	60-18-4	(S)-3-(p-Hydroxypher
C11H11N2OR	1	Cytosol	C03512		

C11H12N2O2	0	Cytosol	C00078	73-22-3	(S)-alpha-amino-beta
C11H12N2O2	0	Extra-organism	C00078	73-22-3	(S)-alpha-amino-beta
C11H12N2O2	0	Periplasm	C00078	73-22-3	(S)-alpha-amino-beta
C4H8NO2R	1	Cytosol	C02992		
C4H8NO6P	-2	Extra-organism	C12147		L-Threonine phospha
C4H8NO6P	-2	Periplasm	C12147		L-Threonine phospha
C4H9NO3	0	Cytosol	C00188	72-19-5	Thr/ 2-Amino-3-hydro
C4H9NO3	0	Extra-organism	C00188	72-19-5	Thr/ 2-Amino-3-hydro
C4H9NO3	0	Periplasm	C00188	72-19-5	Thr/ 2-Amino-3-hydro
C4H4O6	-2	Extra-organism	C00898	87-69-4	L-Tartaric acid/ (R,R)-
C4H4O6	-2	Periplasm	C00898	87-69-4	L-Tartaric acid/ (R,R)-
C3H6NO2R	1	Cytosol	C02553		
C3H7NO3	0	Cytosol	C00065	56-45-1	L-2-Amino-3-hydroxy
C3H7NO3	0	Extra-organism	C00065	56-45-1	L-2-Amino-3-hydroxy
C3H7NO3	0	Periplasm	C00065	56-45-1	L-2-Amino-3-hydroxy
C3H6NOSeR	1	Cytosol	C06482		
C6H12O5	0	Extra-organism	C00507	3615-41-6	6-Deoxy-L-mannose/
C6H12O5	0	Periplasm	C00507	3615-41-6	6-Deoxy-L-mannose/
C5H8NOR	1	Cytosol	C02702		
C7H12N2O3	0	Cytosol			Pro-Gly/ L-Pro-GLy
C7H12N2O3	0	Extra-organism			Pro-Gly/ L-Pro-GLy
C7H12N2O3	0	Periplasm			Pro-Gly/ L-Pro-GLy
C5H9NO2	0	Cytosol	C00148	147-85-3	Pro/ 2-Pyrrolidinecar
C5H9NO2	0	Extra-organism	C00148	147-85-3	Pro/ 2-Pyrrolidinecar
C5H9NO2	0	Periplasm	C00148	147-85-3	Pro/ 2-Pyrrolidinecar
C9H10NOR	1	Cytosol	C03511		
C9H11NO2	0	Cytosol	C00079	63-91-2	(S)-Phenylalanine/ 3-
C9H11NO2	0	Extra-organism	C00079	63-91-2	(S)-Phenylalanine/ 3-
C9H11NO2	0	Periplasm	C00079	63-91-2	(S)-Phenylalanine/ 3-
C5H10NOSR	1	Cytosol	C02430		L-Methionyl-tRNA
C5H11NO3S	0	Cytosol	C15998		
C5H11NO3S	0	Extra-organism	C15998		
C5H11NO3S	0	Periplasm	C15998		
C5H11NO3S	0	Cytosol	C02989		L-methionine-S-sulfo
C5H11NO3S	0	Extra-organism	C02989		L-methionine-S-sulfo
C5H11NO3S	0	Periplasm	C02989		L-methionine-S-sulfo
C5H11NO2S	0	Cytosol	C00073	63-68-3	Met/ L-2-Amino-4met
C5H11NO2S	0	Extra-organism	C00073	63-68-3	Met/ L-2-Amino-4met
C5H11NO2S	0	Periplasm	C00073	63-68-3	Met/ L-2-Amino-4met
C4H4O5	-2	Cytosol	C00149	97-67-6	(S)-Malate/ L-Apple a
C4H4O5	-2	Extra-organism	C00149	97-67-6	(S)-Malate/ L-Apple a
C4H4O5	-2	Periplasm	C00149	97-67-6	(S)-Malate/ L-Apple a
C5H10O5	0	Extra-organism	C01508	1949-78-6	L-Lyxose
C5H10O5	0	Periplasm	C01508	1949-78-6	L-Lyxose
C6H14N2OR	2	Cytosol	C01931		L-Lysyl-tRNA
C6H15N2O2	1	Cytosol	C00047	56-87-1	Lys/ 2,6-diaminohexa
C6H15N2O2	1	Extra-organism	C00047	56-87-1	Lys/ 2,6-diaminohexa
C6H15N2O2	1	Periplasm	C00047	56-87-1	Lys/ 2,6-diaminohexa

C6H12NOR	1	Cytosol	C02047		L-Leucyl-tRNA
C6H13NO2	0	Cytosol	C00123	61-90-5	2-amino-4-methylvale
C6H13NO2	0	Extra-organism	C00123	61-90-5	2-amino-4-methylvale
C6H13NO2	0	Periplasm	C00123	61-90-5	2-amino-4-methylvale
C3H5O3	-1	Cytosol	C00186	79-33-4	Hydroxypropionic aci
C3H5O3	-1	Extra-organism	C00186	79-33-4	Hydroxypropionic aci
C3H5O3	-1	Periplasm	C00186	79-33-4	Hydroxypropionic aci
C3H6O2	0	Cytosol	C00424	598-35-6	(S)-Lactaldehyde/ L-2
C7H14N2O4	0	Cytosol	C00666	583-93-7	LL-2,6-Diaminopimeli
C6H12NOR	1	Cytosol	C03127		
C6H13NO2	0	Cytosol	C00407	73-32-5	2-Amino-3-methylvale
C6H13NO2	0	Extra-organism	C00407	73-32-5	2-Amino-3-methylvale
C6H13NO2	0	Periplasm	C00407	73-32-5	2-Amino-3-methylvale
C8H12OS2	1	Cytosol			
C8H14O2S2	0	Extra-organism	C00725		
C8H14O2S2	0	Periplasm	C00725		
C6H11O7	-1	Extra-organism	C00770	1114-17-6	
C6H11O7	-1	Periplasm	C00770	1114-17-6	
C4H9NO3	0	Cytosol	C00263	672-15-1	2-Amino-4-hydroxybu
C4H9NO3	0	Extra-organism	C00263	672-15-1	2-Amino-4-hydroxybu
C4H9NO3	0	Periplasm	C00263	672-15-1	2-Amino-4-hydroxybu
C4H9NO2S	0	Cytosol	C00155	6027-13-0	L-2-Amino-4-mercapt
C6H8N3OR	1	Cytosol	C02988		
C6H11N3O4P	-1	Cytosol	C01100	25679-93-0	
C6H12N3O	1	Cytosol	C00860		
C6H9N3O2	0	Cytosol	C00135	71-00-1	His/ Glyoxaline-5-ala
C6H9N3O2	0	Extra-organism	C00135	71-00-1	His/ Glyoxaline-5-ala
C6H9N3O2	0	Periplasm	C00135	71-00-1	His/ Glyoxaline-5-ala
C5H7NO3R	0	Cytosol	C02987		
C5H9N2O2R	1	Cytosol	C02282		Glutaminyl-tRNA
C5H10N2O3	0	Cytosol	C00064	56-85-9	Gln/ L-2-Aminoglutar
C5H10N2O3	0	Extra-organism	C00064	56-85-9	Gln/ L-2-Aminoglutar
C5H10N2O3	0	Periplasm	C00064	56-85-9	Gln/ L-2-Aminoglutar
C5H9NO3	0	Cytosol	C01165		L-Glutamate gamma-
C5H8NO7P	-2	Cytosol	C03287		L-Glutamyl 5-phosph
C5H9NO3	0	Cytosol	C03741		(S)-4-Amino-5-oxope
C5H8NO4	-1	Cytosol	C00025	56-86-0	L-Glutamic acid/ L-Gl
C5H8NO4	-1	Extra-organism	C00025	56-86-0	L-Glutamic acid/ L-Gl
C5H8NO4	-1	Periplasm	C00025	56-86-0	L-Glutamic acid/ L-Gl
C6H11O7	-1	Extra-organism	C15930		L-Galactonic acid
C6H11O7	-1	Periplasm	C15930		L-Galactonic acid
C6H12O5	0	Extra-organism	C01019	2438-80-4	6-Deoxy-L-galactose
C6H12O5	0	Periplasm	C01019	2438-80-4	6-Deoxy-L-galactose
C3H6NOSR	1	Cytosol	C03125		
C3H7NO2S	0	Cytosol	C00097	52-90-4	Cys/ L-2-Amino-3-me
C3H7NO2S	0	Extra-organism	C00097	52-90-4	Cys/ L-2-Amino-3-me
C3H7NO2S	0	Periplasm	C00097	52-90-4	Cys/ L-2-Amino-3-me
C7H14N2O4S	0	Cytosol	C02291	56-88-2	

C6H13N3O3	0	Cytosol	C00327	372-75-8	2-Amino-5-ureidovale
C7H15NO3	0	Cytosol	C00318	541-15-1	L-gamma-Trimethyl-b
C7H15NO3	0	Extra-organism	C00318	541-15-1	L-gamma-Trimethyl-b
C7H15NO3	0	Periplasm	C00318	541-15-1	L-gamma-Trimethyl-b
C4H5NO3R	0	Cytosol	C02984		
C4H7NO3	0	Cytosol	C00441		Aspartate beta-semia
C4H6NO4	-1	Cytosol	C00049	56-84-8	2-aminosuccinic acid/
C4H6NO4	-1	Extra-organism	C00049	56-84-8	2-aminosuccinic acid/
C4H6NO4	-1	Periplasm	C00049	56-84-8	2-aminosuccinic acid/
C14H24N2O12PR2	1	Cytosol	C03402		
C4H8N2O3	0	Cytosol	C00152	70-47-3	Arg/ 2-Amino-3-carba
C4H8N2O3	0	Extra-organism	C00152	70-47-3	Arg/ 2-Amino-3-carba
C4H8N2O3	0	Periplasm	C00152	70-47-3	Arg/ 2-Amino-3-carba
C6H7O9P	-2	Cytosol	C16186		
C6H8O6	0	Extra-organism	C00072	50-81-7	Ascorbate/ Ascorbic a
C6H8O6	0	Periplasm	C00072	50-81-7	Ascorbate/ Ascorbic a
C6H14N4OR	2	Cytosol	C02163		L-Arginyl-tRNA
C6H15N4O2	1	Cytosol	C00062	74-79-3	(S)-2-Amino-5-guanid
C6H15N4O2	1	Extra-organism	C00062	74-79-3	(S)-2-Amino-5-guanid
C6H15N4O2	1	Periplasm	C00062	74-79-3	(S)-2-Amino-5-guanid
C5H10O5	0	Extra-organism	C00259	147-81-9	
C5H10O5	0	Periplasm	C00259	147-81-9	
C4H9NO3	0	Cytosol	C05519	28954-12-3	L-Allothreonine
C3H6NOR	1	Cytosol	C00886		L-Alanyl-tRNA
C8H13N2O5	-1	Cytosol			ala-L-glu-L
C8H13N2O5	-1	Extra-organism			ala-L-glu-L
C8H13N2O5	-1	Periplasm			ala-L-glu-L
C18H30N5O9	-1	Cytosol			ala-L-glu-D-A2pm-ala
C18H30N5O9	-1	Extra-organism			ala-L-glu-D-A2pm-ala
C18H30N5O9	-1	Periplasm			ala-L-glu-D-A2pm-ala
C15H25N4O8	-1	Cytosol			ala-L-glu-D-A2pm
C15H25N4O8	-1	Extra-organism			ala-L-glu-D-A2pm
C15H25N4O8	-1	Periplasm			ala-L-glu-D-A2pm
C8H13N2O5	-1	Cytosol			ala-L-glu-D/ alaglu
C8H13N2O5	-1	Extra-organism			ala-L-glu-D/ alaglu
C8H13N2O5	-1	Periplasm			ala-L-glu-D/ alaglu
C3H7NO2	0	Cytosol	C00041	56-41-7	L-2-Aminopropionic a
C3H7NO2	0	Extra-organism	C00041	56-41-7	L-2-Aminopropionic a
C3H7NO2	0	Periplasm	C00041	56-41-7	L-2-Aminopropionic a
C12H22O11	0	Extra-organism	C00243	63-42-3	lactobiose/ 1-beta-D-
C12H22O11	0	Periplasm	C00243	63-42-3	lactobiose/ 1-beta-D-
C4H7NO3	0	Cytosol	C03508		L-2-Amino-acetoaceta
C84H148N2O37P2	-6	Extra-organism	C06025		
C10H11N4O14P3	-4	Cytosol	C00081	132-06-9	Inosine 5'-triphosphat
C5H9O7P2	-3	Cytosol	C00129		delta3-Isopentenyl di
C6H5O7	-3	Cytosol	C00311	30810-51-6	Isocitric acid/ 1-Hydro
C10H8O6	-2	Cytosol	C00885		Isochorismic acid
C2H5O4S	-1	Extra-organism	C05123	107-36-8	2-Hydroxyethanesulfo

C2H5O4S	-1	Periplasm	C05123	107-36-8	2-Hydroxyethanesulf
O2S10Fe4R	-4	Cytosol			
H4O2S10Fe4R	-2	Cytosol			
H4O2S8Fe2R	-2	Cytosol			
H8O2S6R	0	Cytosol			
HS2R	0	Cytosol			
HSR	0	Cytosol			
C10H12N4O5	0	Cytosol	C00294	58-63-9	Hypoxanthine ribonuc
C10H12N4O5	0	Extra-organism	C00294	58-63-9	Hypoxanthine ribonuc
C10H12N4O5	0	Periplasm	C00294	58-63-9	Hypoxanthine ribonuc
HO10P3	-4	Cytosol	C00536		
C8H7N	0	Cytosol	C00463	120-72-9	2,3-Benzopyrrole
C8H7N	0	Extra-organism	C00463	120-72-9	2,3-Benzopyrrole
C8H7N	0	Periplasm	C00463	120-72-9	2,3-Benzopyrrole
C10H11N4O8P	-2	Cytosol	C00130	131-99-7	Inosinic acid/ Inosine
C10H11N4O8P	-2	Extra-organism	C00130	131-99-7	Inosinic acid/ Inosine
C10H11N4O8P	-2	Periplasm	C00130	131-99-7	Inosinic acid/ Inosine
C4H3NO4	-2	Cytosol	C05840		
C10H11N4O11P2	-3	Cytosol	C00104	86-04-4	5'-inosinate diphosph
C5H4N4O	0	Cytosol	C00262	68-94-0	1,7-Dihydro-6H-purin-
C5H4N4O	0	Extra-organism	C00262	68-94-0	1,7-Dihydro-6H-purin-
C5H4N4O	0	Periplasm	C00262	68-94-0	1,7-Dihydro-6H-purin-
C3H3O4	-1	Cytosol	C00168	1113-60-6	Hydroxypyruvic acid/
C11H18N3O7S	-1	Cytosol	C14180		HMGSH/ GS-CH2-O
C40H38N4O17	-8	Cytosol	C01024	73023-76-4	
C6H6O2	0	Cytosol	C00530	123-31-9	Quinol/ p-Benzenedic
H2S	0	Cytosol	C00283		H2S/ Hydrogen-sulfid
H2S	0	Extra-organism	C00283		H2S/ Hydrogen-sulfid
H2S	0	Periplasm	C00283		H2S/ Hydrogen-sulfid
H2O2	0	Cytosol	C00027	7722-84-1	peroxide/ hydrogen d
H2O2	0	Extra-organism	C00027	7722-84-1	peroxide/ hydrogen d
H2O2	0	Periplasm	C00027	7722-84-1	peroxide/ hydrogen d
CHN	0	Cytosol	C01326	57-12-5	CN-/ Cyano
CHN	0	Extra-organism	C01326	57-12-5	CN-/ Cyano
CHN	0	Periplasm	C01326	57-12-5	CN-/ Cyano
Hg	2	Cytosol	C00703		HHg/ mercury(II)/ me
Hg	2	Extra-organism	C00703		HHg/ mercury(II)/ me
Hg	2	Periplasm	C00703		HHg/ mercury(II)/ me
C27H42N7O17P3S	-4	Cytosol	C05270		
C17H31N2O8PRS	-1	Cytosol	C05749		Hexanoyl-[acp]/ Hexa
C6H11O2	-1	Cytosol	C01585	142-62-1	Hexylic acid/ Hexanoi
C6H11O2	-1	Extra-organism	C01585	142-62-1	Hexylic acid/ Hexanoi
C6H11O2	-1	Periplasm	C01585	142-62-1	Hexylic acid/ Hexanoi
C37H60N7O17P3S	-4	Cytosol	C05272		palmitoleic coenzyme
C16H29O2	-1	Cytosol	C08362		cis-9-Hexadecenoic a
C16H29O2	-1	Extra-organism	C08362		cis-9-Hexadecenoic a
C16H29O2	-1	Periplasm	C08362		cis-9-Hexadecenoic a
C16H30O5P	-1	Cytosol			

C16H32O5P	-1	Cytosol			
C16H31O2	-1	Cytosol	C00249	57-10-3	palmitate/ Palmitic ac
C16H31O2	-1	Extra-organism	C00249	57-10-3	palmitate/ Palmitic ac
C16H31O2	-1	Periplasm	C00249	57-10-3	palmitate/ Palmitic ac
H2O	0	Cytosol	C00001	7732-18-5	Water/ Dihydrogen ox
H2O	0	Extra-organism	C00001	7732-18-5	Water/ Dihydrogen ox
H2O	0	Periplasm	C00001	7732-18-5	Water/ Dihydrogen ox
H2	0	Extra-organism	C00282	1333-74-0	Hydrogen
H2	0	Periplasm	C00282	1333-74-0	Hydrogen
H	1	Cytosol	C00080	12408-02-5	Proton/ Hydrogen Ion
H	1	Extra-organism	C00080	12408-02-5	Proton/ Hydrogen Ion
H	1	Periplasm	C00080	12408-02-5	Proton/ Hydrogen Ion
C10H11N5O20P5	-7	Cytosol	C04494		guanosine 5'-diphosp
C10H11N5O17P4	-6	Cytosol	C01228		Guanosine 3'-diphosp
C10H13N5O5	0	Cytosol	C00387	118-00-3	rG/ Guanine riboside
C10H13N5O5	0	Extra-organism	C00387	118-00-3	rG/ Guanine riboside
C10H13N5O5	0	Periplasm	C00387	118-00-3	rG/ Guanine riboside
C5H5N5O	0	Cytosol	C00242	73-40-5	2-Aminohypoxanthine
C5H5N5O	0	Extra-organism	C00242	73-40-5	2-Aminohypoxanthine
C5H5N5O	0	Periplasm	C00242	73-40-5	2-Aminohypoxanthine
C10H12N5O14P3	-4	Cytosol	C00044	86-01-1	Guanosine 5'-triphosp
C10H12N5O14P3	-4	Extra-organism	C00044	86-01-1	Guanosine 5'-triphosp
C10H12N5O14P3	-4	Periplasm	C00044	86-01-1	Guanosine 5'-triphosp
C10H12N5O8P	-2	Cytosol	C00144	85-32-5	Guanosine 5'-phosph
C10H12N5O8P	-2	Extra-organism	C00144	85-32-5	Guanosine 5'-phosph
C10H12N5O8P	-2	Periplasm	C00144	85-32-5	Guanosine 5'-phosph
C2H1O3	-1	Cytosol	C00048	298-12-4	Acetic acid/ Glyoxalat
C2H4NOR	1	Cytosol	C02412		
C2H3O3	-1	Cytosol	C00160	79-14-1	Glycolic acid/ Hydroxy
C2H3O3	-1	Extra-organism	C00160	79-14-1	Glycolic acid/ Hydroxy
C2H3O3	-1	Periplasm	C00160	79-14-1	Glycolic acid/ Hydroxy
C2H4O2	0	Cytosol	C00266		Hydroxyacetaldehyde
C6H10O5	0	Cytosol	C00182		
C5H11NO2	0	Cytosol	C00719	107-43-7	Trimethylaminoacetat
C5H11NO2	0	Extra-organism	C00719	107-43-7	Trimethylaminoacetat
C5H11NO2	0	Periplasm	C00719	107-43-7	Trimethylaminoacetat
C2H5NO2	0	Cytosol	C00037	56-40-6	Aminoacetic acid/ Gly
C2H5NO2	0	Extra-organism	C00037	56-40-6	Aminoacetic acid/ Gly
C2H5NO2	0	Periplasm	C00037	56-40-6	Aminoacetic acid/ Gly
C6H13NO8P	-1	Cytosol			
C6H13NO8P	-1	Extra-organism			
C6H13NO8P	-1	Periplasm			
C6H14O8P	-1	Cytosol	C03274	11034-93-8	Glycerophosphoglyce
C6H14O8P	-1	Extra-organism	C03274	11034-93-8	Glycerophosphoglyce
C6H14O8P	-1	Periplasm	C03274	11034-93-8	Glycerophosphoglyce
C3H7O6P	-2	Cytosol	C00093		Glycerophosphoric ac
C3H7O6P	-2	Extra-organism	C00093		Glycerophosphoric ac
C3H7O6P	-2	Periplasm	C00093		Glycerophosphoric ac

C3H7O6P	-2	Cytosol	C02979	3249-68-1	
C3H7O6P	-2	Extra-organism	C02979	3249-68-1	
C3H7O6P	-2	Periplasm	C02979	3249-68-1	
C3H8O3	0	Cytosol	C00116	56-81-5	1,2,3-trihydroxypropa
C3H8O3	0	Extra-organism	C00116	56-81-5	1,2,3-trihydroxypropa
C3H8O3	0	Periplasm	C00116	56-81-5	1,2,3-trihydroxypropa
C3H5O6P	-2	Cytosol	C00661	142-10-9	D-glyceraldehyde 3-p
C17H29N2O10PRS	-1	Cytosol			
XH2	0	Cytosol	C07292		
X	0	Cytosol	C07293		
C10H17O7P2	-3	Cytosol	C00341		GPP
C10H12N5O11P2	-3	Cytosol	C00035	146-91-8	Guanosine 5'-diphosp
C10H12N5O11P2	-3	Extra-organism	C00035	146-91-8	Guanosine 5'-diphosp
C10H12N5O11P2	-3	Periplasm	C00035	146-91-8	Guanosine 5'-diphosp
C8H13N2O5S	-1	Cytosol	C00669	686-58-8	L-gamma-Glutamylcy
C7H15NO2	0	Extra-organism	C01181		Butyrobetaine [MeSH
C7H15NO2	0	Periplasm	C01181		Butyrobetaine [MeSH
C6H14O6	0	Extra-organism	C01697	608-66-2	Dulcitol/ Dulcose
C6H14O6	0	Periplasm	C01697	608-66-2	Dulcitol/ Dulcose
C31H48O5	0	Extra-organism	C06694		
C31H48O5	0	Periplasm	C06694		
XH2	0	Cytosol			gene product of dsbD
X	0	Cytosol			gene product of dsbD
C4H2O4	-2	Cytosol	C00122	110-17-8	boletic acid/ allomalei
C4H2O4	-2	Extra-organism	C00122	110-17-8	boletic acid/ allomalei
C4H2O4	-2	Periplasm	C00122	110-17-8	boletic acid/ allomalei
C12H25N2O7	1	Extra-organism	C16488		N-epsilon-(1-deoxyfru
C12H25N2O7	1	Periplasm	C16488		N-epsilon-(1-deoxyfru
CH1O2	-1	Extra-organism	C00058	64-18-6	Hydrogencarboxylic a
CH1O2	-1	Periplasm	C00058	64-18-6	Hydrogencarboxylic a
CH2O	0	Extra-organism	C00067	50-00-0	Formalin/ Methanal/
CH2O	0	Periplasm	C00067	50-00-0	Formalin/ Methanal/
C17H19N4O9P	-2	Cytosol	C00061	146-17-8	Riboflavin-5-phospha
XH	0	Cytosol	C02869		
XH	-1	Cytosol	C02745		
C27H33N9O15P2	-2	Cytosol	C01352		flavin adenine dinucle
C27H31N9O15P2	-2	Cytosol	C00016	146-14-5	FAD/ Flavin adenine
C25H46N6O8	-2	Extra-organism			
C25H46FeN6O8	1	Cytosol	C07597		Ferrioxamine B
C25H46FeN6O8	1	Extra-organism	C07597		Ferrioxamine B
C25H46FeN6O8	1	Periplasm	C07597		Ferrioxamine B
C27H42N9O12	-3	Extra-organism			
C27H42FeN9O12	0	Cytosol	C06228		
C27H42FeN9O12	0	Extra-organism	C06228		
C27H42FeN9O12	0	Periplasm	C06228		
C10H10NO6Fe	2	Extra-organism			
C30H27FeN3O15	3	Extra-organism	C06230		Fe-enterochlin
Fe	3	Cytosol	C14819		Iron trication/ Fe(III)

Fe	3	Extra-organism	C14819		Iron trication/ Fe(III)
Fe	3	Periplasm	C14819		Iron trication/ Fe(III)
Fe	2	Cytosol	C00023		Reduced Iron/ Iron di
Fe	2	Extra-organism	C00023		Reduced Iron/ Iron di
Fe	2	Periplasm	C00023		Reduced Iron/ Iron di
C9H18O6N3Fe	0	Cytosol	C06227		Fe(III)hydroxamic aci
C9H18O6N3Fe	0	Extra-organism	C06227		Fe(III)hydroxamic aci
C9H18O6N3Fe	0	Periplasm	C06227		Fe(III)hydroxamic aci
C9H18O6N3	-3	Extra-organism			
C12H10FeO14	-3	Extra-organism	C06229		Iron(III)dicitrate
C15H25O7P2	-3	Cytosol	C00448	13058-04-3	Farnesyl pyrophosph
C2H8NO	1	Cytosol	C00189	141-43-5	Aminoethanol/ Hydro
C2H8NO	1	Extra-organism	C00189	141-43-5	Aminoethanol/ Hydro
C2H8NO	1	Periplasm	C00189	141-43-5	Aminoethanol/ Hydro
C2H6O	0	Cytosol	C00469	64-17-5	Ethyl alcohol/ Methyl
C2H6O	0	Extra-organism	C00469	64-17-5	Ethyl alcohol/ Methyl
C2H6O	0	Periplasm	C00469	64-17-5	Ethyl alcohol/ Methyl
C2H5O3S	-1	Extra-organism			
C2H5O3S	-1	Periplasm			
C30H27N3O15	0	Extra-organism	C05821		tri-(2,3-dihydroxy-N-b
C30H27N3O15	0	Periplasm	C05821		tri-(2,3-dihydroxy-N-b
C19H31N2O10PRS	-1	Cytosol			
C17H27N2O10PRS	-1	Cytosol			
C5H9O8P	-2	Cytosol	C00231		
C5H10O5	0	Extra-organism	C00181	58-86-6	Wood sugar
C5H10O5	0	Periplasm	C00181	58-86-6	Wood sugar
C9H11N2O14P3	-4	Cytosol	C00460		2'-Deoxyuridine 5'-tri
C9H11N2O8P	-2	Cytosol	C00365	964-26-1	Deoxyuridylic acid/ D
C9H11N2O8P	-2	Extra-organism	C00365	964-26-1	Deoxyuridylic acid/ D
C9H11N2O8P	-2	Periplasm	C00365	964-26-1	Deoxyuridylic acid/ D
C9H11N2O11P2	-3	Cytosol	C01346		2'-Deoxyuridine 5'-dip
C10H13N2O14P3	-4	Cytosol	C00459		Thymidine triphosph
C10H13N2O8P	-2	Cytosol	C00364	365-07-1	Thymidine 5'-phosph
C10H13N2O8P	-2	Extra-organism	C00364	365-07-1	Thymidine 5'-phosph
C10H13N2O8P	-2	Periplasm	C00364	365-07-1	Thymidine 5'-phosph
C16H24N2O16P2	-2	Cytosol	C00842	2009-24-7	dTDP-D-glucose
C16H22N2O15P2	-2	Cytosol	C00688		dTDP-4-oxo-L-rhamn
C16H22N2O15P2	-2	Cytosol	C00687		dTDP-4-oxo-6-deoxy-
C10H13N2O11P2	-3	Cytosol	C00363		Thymidine 5'-diphosp
C4H4O6	-2	Cytosol	C02107	147-71-7	D-Tartrate/ (S,S)-Tart
C4H4O6	-2	Extra-organism	C02107	147-71-7	D-Tartrate/ (S,S)-Tart
C4H4O6	-2	Periplasm	C02107	147-71-7	D-Tartrate/ (S,S)-Tart
C6H11O9P	-2	Cytosol	C01097		
C6H10O12P2	-4	Cytosol	C03785		
C6H14O6	0	Extra-organism	C00794	50-70-4	D-Sorbitol/ Gulitol/ D-
C6H14O6	0	Periplasm	C00794	50-70-4	D-Sorbitol/ Gulitol/ D-
C3H7NO3	0	Extra-organism	C00740	312-84-5	D-2-Amino-3-hydroxy
C3H7NO3	0	Periplasm	C00740	312-84-5	D-2-Amino-3-hydroxy

C5H9O8P	-2	Cytosol	C00199	4151-19-3	
C5H10O5	0	Cytosol	C00121	50-69-1	
C5H10O5	0	Extra-organism	C00121	50-69-1	
C5H10O5	0	Periplasm	C00121	50-69-1	
C27H29NO11	0	Extra-organism	C01661	23214-92-8	adriamycin
C27H29NO11	0	Periplasm	C01661	23214-92-8	adriamycin
C8H12NO2	1	Extra-organism	C03758	51-61-6	4-(2-Aminoethyl)-1,2-
C8H12NO2	1	Periplasm	C03758	51-61-6	4-(2-Aminoethyl)-1,2-
C33H54N7O17P3S	-4	Cytosol	C01832	6244-92-4	Lauroyl-CoA/ Lauroyl
C23H43N2O8PRS	-1	Cytosol	C05223		Dodecanoyl-[acyl-car
C12H24O5P1	-1	Cytosol			
C12H23O2	-1	Cytosol	C02679	143-07-7	Dodecylcarboxylate/ L
C12H23O2	-1	Extra-organism	C02679	143-07-7	Dodecylcarboxylate/ L
C12H23O2	-1	Periplasm	C02679	143-07-7	Dodecylcarboxylate/ L
C5H10NO2S	0	Cytosol	C00855	348-67-4	D-2-Amino-4-(methylt
C5H10NO2S	0	Extra-organism	C00855	348-67-4	D-2-Amino-4-(methylt
C5H10NO2S	0	Periplasm	C00855	348-67-4	D-2-Amino-4-(methylt
C6H11O9P	-2	Cytosol	C00275		
C6H11O9P	-2	Extra-organism	C00275		
C6H11O9P	-2	Periplasm	C00275		
C6H11O9P	-2	Cytosol	C00636		alpha-D-Mannose 1-p
C6H12O6	0	Extra-organism	C00159	3458-28-4	Mannose/ Seminose/
C6H12O6	0	Periplasm	C00159	3458-28-4	Mannose/ Seminose/
C6H13O9P	-2	Cytosol	C00644		
C6H14O6	0	Extra-organism	C00392	69-65-8	
C6H14O6	0	Periplasm	C00392	69-65-8	
C4H4O5	-2	Extra-organism	C00497	636-61-3	D-Hydroxysuccinic ac
C4H4O5	-2	Periplasm	C00497	636-61-3	D-Hydroxysuccinic ac
C3H5O3	-1	Cytosol	C00256	10326-41-7	(R)-Lactate/ D-Lactic
C3H5O3	-1	Extra-organism	C00256	10326-41-7	(R)-Lactate/ D-Lactic
C3H5O3	-1	Periplasm	C00256	10326-41-7	(R)-Lactate/ D-Lactic
C10H11N4O13P3	-4	Cytosol	C01345		2'-Deoxyinosine-5'-tri
HO7P2	-3	Cytosol	C00013		Pyrophosphate/ Pyro
C10H11N4O7P	-2	Cytosol	C06196		2'-Deoxyinosine 5'-ph
C10H11N4O7P	-2	Extra-organism	C06196		2'-Deoxyinosine 5'-ph
C10H11N4O7P	-2	Periplasm	C06196		2'-Deoxyinosine 5'-ph
C5H9O7P2	-3	Cytosol	C00235	358-71-4	2-Isopentenyl diphos
C2H6OS	0	Cytosol	C11143		
C2H6OS	0	Extra-organism	C11143		
C2H6OS	0	Periplasm	C11143		
C2H6S	0	Cytosol	C00580	75-18-3	Methyl sulfide/ Methyl
C2H6S	0	Extra-organism	C00580	75-18-3	Methyl sulfide/ Methyl
C2H6S	0	Periplasm	C00580	75-18-3	Methyl sulfide/ Methyl
C3H5O6P	-2	Cytosol	C00111	57-04-5	Glycerone phosphate
C3H6O3	0	Extra-organism	C00184	96-26-4	Glycerone/ 1/ 3-Dihyd
C3H6O3	0	Periplasm	C00184	96-26-4	Glycerone/ 1/ 3-Dihyd
C42H41N4O16	-7	Cytosol	C02463	65207-12-7	Precorrin 2
C14H13N6O3	-1	Cytosol	C00921		7,8-Dihydropteroate

C9H12N5O7P	-2	Cytosol	C05925		Dihydroneopterin pho
C9H13N5O4	0	Cytosol	C04874		2-Amino-4-hydroxy-6-
C9H13N5O4	0	Cytosol			
C10H11N4O10P2	-3	Cytosol	C01344		2'-Deoxyinosine-5'-di
C16H27N2O14P	-2	Cytosol			chitobiose-6-phospha
C10H12N5O13P3	-4	Cytosol	C00286	2564-35-4	2'-Deoxyguanosine 5'
C10H12N5O7P	-2	Cytosol	C00362	902-04-5	2'-Deoxyguanosine 5'
C10H12N5O7P	-2	Extra-organism	C00362	902-04-5	2'-Deoxyguanosine 5'
C10H12N5O7P	-2	Periplasm	C00362	902-04-5	2'-Deoxyguanosine 5'
C7H13O10P	-2	Cytosol	C07836		
C7H13O10P	-2	Cytosol	C07838		
C7H12O13P2	-4	Cytosol	C11472		
C3H4O7P	-3	Cytosol	C00631		2-Phospho-D-glycera
C3H6O3	0	Cytosol	C00577	453-17-8	(R)-glyceraldehyde
C3H6O3	0	Extra-organism	C00577	453-17-8	(R)-glyceraldehyde
C3H6O3	0	Periplasm	C00577	453-17-8	(R)-glyceraldehyde
C5H8NO4	-1	Cytosol	C00217	6893-26-1	D-Glutamic acid/ D-G
C6H8O10P	-3	Extra-organism	C05385		GlcA-1P
C6H8O10P	-3	Periplasm	C05385		GlcA-1P
C6H9O7	-1	Cytosol	C00191		Glucuronic acid/ Gluc
C6H9O7	-1	Extra-organism	C00191		Glucuronic acid/ Gluc
C6H9O7	-1	Periplasm	C00191		Glucuronic acid/ Gluc
C6H11O9P	-2	Cytosol	C00092	56-73-5	Glucose 6-phosphate
C6H11O9P	-2	Extra-organism	C00092	56-73-5	Glucose 6-phosphate
C6H11O9P	-2	Periplasm	C00092	56-73-5	Glucose 6-phosphate
C6H11O9P	-2	Cytosol	C00103	59-56-3	Cori ester/ alpha-D-G
C6H11O9P	-2	Extra-organism	C00103	59-56-3	Cori ester/ alpha-D-G
C6H11O9P	-2	Periplasm	C00103	59-56-3	Cori ester/ alpha-D-G
C6H12O6	0	Cytosol	C00031	50-99-7	alpha-D-Glucose/ bet
C6H12O6	0	Extra-organism	C00031	50-99-7	alpha-D-Glucose/ bet
C6H12O6	0	Periplasm	C00031	50-99-7	alpha-D-Glucose/ bet
C6H13NO8P	-1	Cytosol	C00352	3616-42-0	D-Glucosamine phos
C6H13NO8P	-1	Extra-organism	C00352	3616-42-0	D-Glucosamine phos
C6H13NO8P	-1	Periplasm	C00352	3616-42-0	D-Glucosamine phos
C6H13NO8P	-1	Cytosol	C06156		
C6H14NO5	1	Extra-organism	C00329	3416-24-8	Chitosamine/ 2-Amin
C6H14NO5	1	Periplasm	C00329	3416-24-8	Chitosamine/ 2-Amin
C6H11O7	-1	Extra-organism	C00257	526-95-4	D-Gluconic acid/ D-G
C6H11O7	-1	Periplasm	C00257	526-95-4	D-Gluconic acid/ D-G
C6H8O8	-2	Extra-organism	C00818	87-73-0	L-Gularic acid/ D-Glu
C6H8O8	-2	Periplasm	C00818	87-73-0	L-Gularic acid/ D-Glu
C10H12N5O10P2	-3	Cytosol	C00361		2'-Deoxyguanosine 5'
C6H9O7	-1	Extra-organism	C00333	685-73-4	alpha-D-galacturonop
C6H9O7	-1	Periplasm	C00333	685-73-4	alpha-D-galacturonop
C6H12O6	0	Cytosol	C00124	59-23-4	alpha-Galactose(D)/
C6H12O6	0	Extra-organism	C00124	59-23-4	alpha-Galactose(D)/
C6H12O6	0	Periplasm	C00124	59-23-4	alpha-Galactose(D)/
C6H11O7	-1	Extra-organism	C00880		D-Galactonic acid

C6H11O7	-1	Periplasm	C00880		D-Galactonic acid
C6H8O8	-2	Extra-organism	C00879	526-99-8	D-Mucic acid/ D-Gala
C6H8O8	-2	Periplasm	C00879	526-99-8	D-Mucic acid/ D-Gala
C6H9O7	-1	Extra-organism	C00905	669-90-9	
C6H9O7	-1	Periplasm	C00905	669-90-9	
C6H11O9P	-2	Cytosol	C00085	643-13-0	D-Fructose 6-phosph
C6H11O9P	-2	Extra-organism	C00085	643-13-0	D-Fructose 6-phosph
C6H11O9P	-2	Periplasm	C00085	643-13-0	D-Fructose 6-phosph
C6H11O9P	-2	Cytosol	C02976	15978-08-2	Fructose 1-phosphate
C6H10O12P2	-4	Cytosol	C00354	488-69-7	fructose-1,6-bisphosp
C6H12O6	0	Extra-organism	C00095	57-48-7	Levulose/ Fruit sugar/
C6H12O6	0	Periplasm	C00095	57-48-7	Levulose/ Fruit sugar/
C10H17N2O3	-1	Cytosol	C01909		Desthiobiotin
C4H7O7P	-2	Cytosol	C00279	585-18-2	4-phospho D-erythros
C6H9N2O6P	-2	Cytosol	C04666		D-erythro-Imidazole-g
C21H33N7O13P2S	-2	Cytosol	C00882		
C9H12N2O5	0	Cytosol	C00526	951-78-0	2-Deoxyuridine/ 2'-De
C9H12N2O5	0	Extra-organism	C00526	951-78-0	2-Deoxyuridine/ 2'-De
C9H12N2O5	0	Periplasm	C00526	951-78-0	2-Deoxyuridine/ 2'-De
C10H12N4O4	0	Cytosol	C05512	890-38-0	2'-deoxy-inosine
C10H12N4O4	0	Extra-organism	C05512	890-38-0	2'-deoxy-inosine
C10H12N4O4	0	Periplasm	C05512	890-38-0	2'-deoxy-inosine
C10H13N5O4	0	Cytosol	C00330	961-07-9	2'-deoxyguanosine he
C10H13N5O4	0	Extra-organism	C00330	961-07-9	2'-deoxyguanosine he
C10H13N5O4	0	Periplasm	C00330	961-07-9	2'-deoxyguanosine he
C9H13N3O4	0	Cytosol	C00881	951-77-9	2'-Deoxycytidine/ dC
C9H13N3O4	0	Extra-organism	C00881	951-77-9	2'-Deoxycytidine/ dC
C9H13N3O4	0	Periplasm	C00881	951-77-9	2'-Deoxycytidine/ dC
C10H13N5O3	0	Cytosol	C00559	958-09-8	2'-Deoxyadenosine/ d
C10H13N5O3	0	Extra-organism	C00559	958-09-8	2'-Deoxyadenosine/ d
C10H13N5O3	0	Periplasm	C00559	958-09-8	2'-Deoxyadenosine/ d
C2H2NO2	-1	Cytosol	C15809		2-iminoacetate
C31H50N7O17P3S	-4	Cytosol	C05274		
C21H39N2O8PRS	-1	Cytosol	C05755		Decanoyl-[acyl-carrier
C10H19O2	-1	Cytosol	C01571	334-48-5	n-Capric acid/ Decylic
C10H19O2	-1	Extra-organism	C01571	334-48-5	n-Capric acid/ Decylic
C10H19O2	-1	Periplasm	C01571	334-48-5	n-Capric acid/ Decylic
C21H24N6O15P2	-2	Cytosol	C00857		Deamido-NAD+
C3H7NO2S	0	Cytosol	C00793	921-01-7	D-Amino-3-mercaptop
C3H7NO2S	0	Extra-organism	C00793	921-01-7	D-Amino-3-mercaptop
C3H7NO2S	0	Periplasm	C00793	921-01-7	D-Amino-3-mercaptop
C9H12N3O13P3	-4	Cytosol	C00458	2056-98-6	Deoxycytidine 5'-triph
C9H12N3O7P	-2	Cytosol	C00239	1032-65-1	Deoxycytidylic acid/ D
C9H12N3O7P	-2	Extra-organism	C00239	1032-65-1	Deoxycytidylic acid/ D
C9H12N3O7P	-2	Periplasm	C00239	1032-65-1	Deoxycytidylic acid/ D
C9H12N3O10P2	-3	Cytosol	C00705		2'-Deoxycytidine diph
C7H15NO3	0	Cytosol	C00487		gamma-Trimethyl-hyd
C7H15NO3	0	Extra-organism	C00487		gamma-Trimethyl-hyd

C7H15NO3	0	Periplasm	C00487		gamma-Trimethyl-hy
C10H12N5O12P3	-4	Cytosol	C00131	1927-31-7	2'-Deoxyadenosine 5'
C5H9O8P	-2	Cytosol	C01112		
C10H12N5O6P	-2	Cytosol	C00360	653-63-4	2'-Deoxyadenosine 5'
C10H12N5O6P	-2	Extra-organism	C00360	653-63-4	2'-Deoxyadenosine 5'
C10H12N5O6P	-2	Periplasm	C00360	653-63-4	2'-Deoxyadenosine 5'
C6H12O6	0	Extra-organism	C01487	2595-97-3	D-Allose
C6H12O6	0	Periplasm	C01487	2595-97-3	D-Allose
C6H12N2O3	0	Cytosol	C00993	923-16-0	DalaDala/ D-ala-D-al
C6H12N2O3	0	Extra-organism	C00993	923-16-0	DalaDala/ D-ala-D-al
C6H12N2O3	0	Periplasm	C00993	923-16-0	DalaDala/ D-ala-D-al
C3H7NO2	0	Cytosol	C00133	338-69-2	D-2-Aminopropionic
C3H7NO2	0	Extra-organism	C00133	338-69-2	D-2-Aminopropionic
C3H7NO2	0	Periplasm	C00133	338-69-2	D-2-Aminopropionic
C10H12N5O9P2	-3	Cytosol	C00206		2'-Deoxyadenosine 5'
C9H15NO8P	-3	Cytosol	C03492		(R)-4'-Phosphopantot
C4H5N3O	0	Cytosol	C00380	71-30-7	
C4H5N3O	0	Extra-organism	C00380	71-30-7	
C4H5N3O	0	Periplasm	C00380	71-30-7	
C9H13N3O5	0	Cytosol	C00475	65-46-3	4-amino-1-beta-D-rib
C9H13N3O5	0	Extra-organism	C00475	65-46-3	4-amino-1-beta-D-rib
C9H13N3O5	0	Periplasm	C00475	65-46-3	4-amino-1-beta-D-rib
C5H10N2O3S	0	Cytosol	C01419	19246-18-5	L-Cysteinyl-glycine/
C5H10N2O3S	0	Extra-organism	C01419	19246-18-5	L-Cysteinyl-glycine/
C5H10N2O3S	0	Periplasm	C01419	19246-18-5	L-Cysteinyl-glycine/
C44H82O10P1	-1	Cytosol			
C40H74O10P1	-1	Cytosol			
C43H82N1O8P1	0	Cytosol			
C39H74N1O8P1	0	Cytosol			
C10H13N5O8P	-1	Cytosol	C18239		precursor-Z/ cPMP/ p
CNO	-1	Extra-organism	C01417	420-05-3	Cyanate/ Cyanic acid
CNO	-1	Periplasm	C01417	420-05-3	Cyanate/ Cyanic acid
Cu	2	Cytosol	C00070		Copper
Cu	2	Extra-organism	C00070		Copper
Cu	2	Periplasm	C00070		Copper
Cu	1	Cytosol	C00070		Copper
Cu	1	Extra-organism	C00070		Copper
Cu	1	Periplasm	C00070		Copper
C9H12N3O14P3	-4	Cytosol	C00063	65-47-4	Cytidine 5'-triphospha
C25H36N7O17P3S	-4	Cytosol	C00877	102680-35-3	Crotonyl-CoA/ 2-Bute
C7H13NO2	0	Cytosol	C04114	6666-46-2	4-(Trimethylammonio
C7H13NO2	0	Periplasm	C04114	6666-46-2	4-(Trimethylammonio
C36H40N4O8	-4	Cytosol	C03263	2624-63-7	
C35H52N6O13	-4	Extra-organism			
C35H52N6O13Fe	-1	Cytosol			
C35H52N6O13Fe	-1	Extra-organism			
C35H52N6O13Fe	-1	Periplasm			
C21H32N7O16P3S	-4	Cytosol	C00010	85-61-0	CoA-SH/ CoA/ CoAS

C48H72CoN11O8	0	Cytosol	C05774	1867-62-5	Cobinamide
C48H72CoN11O8	0	Extra-organism	C05774	1867-62-5	Cobinamide
C48H72CoN11O8	0	Periplasm	C05774	1867-62-5	Cobinamide
C62H88CoN13O14P	-1	Cytosol	C00853	18534-66-2	Cbl/ Vitamin B12s
C62H88CoN13O14P	-1	Extra-organism	C00853	18534-66-2	Cbl/ Vitamin B12s
C62H88CoN13O14P	-1	Periplasm	C00853	18534-66-2	Cbl/ Vitamin B12s
Co	2	Cytosol	C00175	7440-48-4	Cobalt
Co	2	Extra-organism	C00175	7440-48-4	Cobalt
Co	2	Periplasm	C00175	7440-48-4	Cobalt
CO2	0	Cytosol	C00011	124-38-9	Carbon dioxide/ Carb
CO2	0	Extra-organism	C00011	124-38-9	Carbon dioxide/ Carb
CO2	0	Periplasm	C00011	124-38-9	Carbon dioxide/ Carb
C17H24N3O15P	-2	Cytosol			CMP-KDO
C9H12N3O8P	-2	Cytosol	C00055		Cytidine-5'-monophos
C9H12N3O8P	-2	Extra-organism	C00055		Cytidine-5'-monophos
C9H12N3O8P	-2	Periplasm	C00055		Cytidine-5'-monophos
C6H5O7	-3	Cytosol	C00158	77-92-9	Citric acid/ 2-Hydroxy
C6H5O7	-3	Extra-organism	C00158	77-92-9	Citric acid/ 2-Hydroxy
C6H5O7	-3	Periplasm	C00158	77-92-9	Citric acid/ 2-Hydroxy
C25H45N2O8PRS	-1	Cytosol			cis-myristol-7-eoyl-[a
C29H53N2O8PRS	-1	Cytosol			cis-vacc-11-enoyl-[ac
C27H49N2O8PRS	-1	Cytosol			cis-palmitol-9-eoyl-[a
C23H41N2O8PRS	-1	Cytosol			
C21H37N2O8PRS	-1	Cytosol			
C6H3O6	-3	Cytosol	C00417	585-84-2	cis-1,2,3-Propenetric
C7H5O6	-3	Cytosol	C04225	99-98-9	(Z)-But-2-ene-1,2,3-tr
C10H8O6	-2	Cytosol	C00251	55508-12-8	chorismic acid
C5H14NO	1	Cytosol	C00114	123-41-1	Bilineurine
C5H14NO	1	Extra-organism	C00114	123-41-1	Bilineurine
C5H14NO	1	Periplasm	C00114	123-41-1	Bilineurine
Cl	-1	Cytosol	C00698		Cl-
Cl	-1	Extra-organism	C00698		Cl-
Cl	-1	Periplasm	C00698		Cl-
C11H12Cl2N2O5	0	Extra-organism	C00918	56-75-7	
C11H12Cl2N2O5	0	Periplasm	C00918	56-75-7	
C40H71N3O15P2	-2	Cytosol	C00269		CDP-1,2-diacylglycer
C40H67N3O15P2	-2	Cytosol	C00269		CDPdiacylglycerol/ C
C48H87N3O15P2	-2	Cytosol	C00269		1,2-Diacyl-sn-glycero-
C48H83N3O15P2	-2	Cytosol	C00269		CDPdiacylglycerol/ 1,
C44H79N3O15P2	-2	Cytosol	C00269		CDP-1,2-diacylglycer
C44H75N3O15P2	-2	Cytosol	C00269		1,2-Diacyl-sn-glycero-
C36H63N3O15P2	-2	Cytosol	C00269		CDP-1,2-diacylglycer
C9H12N3O11P2	-3	Cytosol	C00112	63-38-7	Cytidine 5'-diphospha
C65H124O17P2	-2	Periplasm	C05980		1',3'-Bis(1,2-diacyl-sn
C65H116O17P2	-2	Periplasm	C05980		1',3'-Bis(1,2-diacyl-sn
C81H156O17P2	-2	Periplasm	C05980		Diphosphatidylglycer
C81H148O17P2	-2	Periplasm	C05980		1',3'-Bis(1,2-diacyl-sn
C73H140O17P2	-2	Periplasm	C05980		Diphosphatidylglycer

C73H132O17P2	-2	Periplasm	C05980		Diphosphatidylglycerc
C57H108O17P2	-2	Periplasm	C05980		Diphosphatidylglycerc
CH2NO5P	-2	Cytosol	C00169		
C10H11N5O6P	-1	Cytosol	C00575		Adenosine 3',5'-cyclic
Ca	2	Cytosol	C00076	7440-70-2	Ca2+
Ca	2	Extra-organism	C00076	7440-70-2	Ca2+
Ca	2	Periplasm	C00076	7440-70-2	Ca2+
Cd	2	Cytosol	C01413		
Cd	2	Extra-organism	C01413		
Cd	2	Periplasm	C01413		
C11H12NO6P	-2	Cytosol	C03506		Indoleglycerol phosph
C15H27N2O8PRS	-1	Cytosol	C05745		Butyryl-[acp]/ Butyryl-
C4H7O2	-1	Cytosol	C00246	107-92-6	Butanoate/ Butyric ac
C4H7O2	-1	Extra-organism	C00246	107-92-6	Butanoate/ Butyric ac
C4H7O2	-1	Periplasm	C00246	107-92-6	Butanoate/ Butyric ac
C25H38N7O17P3S	-4	Cytosol	C00136		Butyryl-CoA
C4H9O3S	-1	Extra-organism			
C4H9O3S	-1	Periplasm			
C15H25N2O8PRS	-1	Cytosol	C04246	128-33-6	
C6H10O5	0	Cytosol			
C30H32N15O20P3S4Mc	-4	Cytosol			
C40H44N20O27P4S4Mc	-4	Cytosol			bis-MGD
C20H20N10O13P2S4Mc	-4	Cytosol			bis-moco
C10H15N2O3S	-1	Cytosol	C00120	58-85-5	Vitamin B7/ D-Biotin/
C10H15N2O3S	-1	Extra-organism	C00120	58-85-5	Vitamin B7/ D-Biotin/
C10H15N2O3S	-1	Periplasm	C00120	58-85-5	Vitamin B7/ D-Biotin/
CHO3	-1	Cytosol	C00288	71-52-3	Acid carbonate/ HCO
C3H7NO2	0	Cytosol	C00099	107-95-9	3-aminopropionic acic
C3H7NO2	0	Extra-organism	C00099	107-95-9	3-aminopropionic acic
C3H7NO2	0	Periplasm	C00099	107-95-9	3-aminopropionic acic
C6H12O6	0	Extra-organism	C01582	33419-42-0	
C6H12O6	0	Periplasm	C01582	33419-42-0	
C10H12N5O13P3	-4	Cytosol	C00002	56-65-5	Adenosine 5'-triphosp
AsO3	-3	Extra-organism	C06697		arsenite
AsO3	-3	Periplasm	C06697		arsenite
C12H15O10P	-2	Cytosol	C06187		Arbutin-6P
C12H16O7	0	Extra-organism	C06186	497-76-7	Ursin/ Uvasol
C12H16O7	0	Periplasm	C06186	497-76-7	Ursin/ Uvasol
RHO	0	Cytosol	C03688		
C7H6NO2	-1	Cytosol	C00108	118-92-3	Vitamin L/ Anthranilic
C10H12N5O7P	-2	Cytosol	C00020	61-19-8	Adenosine 5'-monoph
C10H12N5O7P	-2	Extra-organism	C00020	61-19-8	Adenosine 5'-monoph
C10H12N5O7P	-2	Periplasm	C00020	61-19-8	Adenosine 5'-monoph
H4N	1	Cytosol	C01342	14798-03-9	NH3
H4N	1	Extra-organism	C01342	14798-03-9	NH3
H4N	1	Periplasm	C01342	14798-03-9	NH3
C5H9O8P	-2	Cytosol	C00117	4300-28-1	D-Ribose 5-phosphat
C5H9O8P	-2	Extra-organism	C00117	4300-28-1	D-Ribose 5-phosphat

C5H9O8P	-2	Periplasm	C00117	4300-28-1	D-Ribose 5-phosphat
C5H9O8P	-2	Cytosol	C00442	58459-37-3	Ribose 1-phosphate/
C6H11O9P	-2	Cytosol	C00446	2255-14-3	D-Galactose 1-phosp
C6H11O9P	-2	Extra-organism	C00446	2255-14-3	D-Galactose 1-phosp
C6H11O9P	-2	Periplasm	C00446	2255-14-3	D-Galactose 1-phosp
C40H65O7P2	-3	Cytosol	C04146		Farnesylfarnesylgera
C4H6N4O3	0	Extra-organism	C01551	97-59-6	5-Ureidohydantoin/ G
C4H6N4O3	0	Periplasm	C01551	97-59-6	5-Ureidohydantoin/ G
C5H16N4	2	Cytosol	C00179	306-60-5	(4-Aminobutyl) guani
C5H16N4	2	Extra-organism	C00179	306-60-5	(4-Aminobutyl) guani
C5H16N4	2	Periplasm	C00179	306-60-5	(4-Aminobutyl) guani
C22H33N4O13	-3	Extra-organism	C05554		aerobactin - a sidero
C22H33FeN4O13	0	Cytosol		61-33-6	
C22H33FeN4O13	0	Extra-organism		61-33-6	
C22H33FeN4O13	0	Periplasm		61-33-6	
C15H21N5O14P2	-2	Cytosol	C00301		ADP-D-ribose/ ADP-r
C17H25N5O16P2	-2	Cytosol	C06398		
C16H23N5O15P2	-2	Cytosol	C00498		Adenosine diphosph
C17H25N5O16P2	-2	Cytosol	C06397	119-61-9	ADP-D-glycero-D-ma
C10H12N5O10P2	-3	Cytosol	C00008	58-64-0	Adenosine 5'-diphos
C20H22N10O12P2S2Cu	-2	Cytosol			
C72H100CoN18O17P	0	Cytosol	C00194	13870-90-1	
C72H100CoN18O17P	0	Extra-organism	C00194	13870-90-1	
C72H100CoN18O17P	0	Periplasm	C00194	13870-90-1	
C58H84CoN16O11	1	Cytosol	C06508		Adenosyl cobinamide
C10H12N5O10PS	-2	Cytosol	C00224		APS/ Adenylylsulfate
C10H11N5O10P2	-4	Cytosol	C00054	1053-73-2	PAP/ 3'-Phosphoade
C10H13N5O4	0	Cytosol	C00212	58-61-7	9-beta-D-Ribofurano
C10H13N5O4	0	Extra-organism	C00212	58-61-7	9-beta-D-Ribofurano
C10H13N5O4	0	Periplasm	C00212	58-61-7	9-beta-D-Ribofurano
C5H5N5	0	Cytosol	C00147	73-24-5	A/ Ade/ 1H-Purin-6-a
C5H5N5	0	Extra-organism	C00147	73-24-5	A/ Ade/ 1H-Purin-6-a
C5H5N5	0	Periplasm	C00147	73-24-5	A/ Ade/ 1H-Purin-6-a
C60H110O11P	-1	Cytosol			X-3-phosphatidyl-1'-(
C60H116O11P	-1	Cytosol			X-3-phosphatidyl-1'-(
C54H98O11P	-1	Cytosol			X-3-phosphatidyl-1'-(
C54H104O11P	-1	Cytosol			X-3-phosphatidyl-1'-(
C48H86O11P	-1	Cytosol			X-3-phosphatidyl-1'-(
C48H92O11P	-1	Cytosol			3-sn-phosphatidyl-1'-
C42H80O11P	-1	Cytosol			X-3-phosphatidyl-1'-(
C11H21N2O7PRS	-1	Cytosol	C00229		
C14H24O12	0	Cytosol	C02130		
C23H34N7O17P3S	-4	Cytosol	C00024	72-89-9	Acetyl coenzyme A
C13H23N2O8PRS	-1	Cytosol	C03939		
C2H3O5P	-2	Cytosol	C00227	19926-71-7	
C25H36N7O18P3S	-4	Cytosol	C00332	1420-36-6	3-ketobutanoyl-CoA/
C15H25N2O9PRS	-1	Cytosol	C05744		
C4H5O3	-1	Extra-organism	C00164	541-50-4	Acetoacetic acid/ bet

C4H5O3	-1	Periplasm	C00164	541-50-4	Acetoacetic acid/ bet
C2H3O2	-1	Cytosol	C00033	71-50-1	vinegar/ Ethylic acid/
C2H3O2	-1	Extra-organism	C00033	71-50-1	vinegar/ Ethylic acid/
C2H3O2	-1	Periplasm	C00033	71-50-1	vinegar/ Ethylic acid/
C2H4O	0	Cytosol	C00084	75-07-0	Aldehyde C(2)/ acetyl
C2H4O	0	Extra-organism	C00084	75-07-0	Aldehyde C(2)/ acetyl
C2H4O	0	Periplasm	C00084	75-07-0	Aldehyde C(2)/ acetyl
C9H17NO3	0	Cytosol	C01092		7-keto-8-aminopelarg
C7H5N4O3	-1	Cytosol			
C7H5N5O	0	Cytosol	C15996		PreQ0
C7H10N5O	1	Cytosol	C01449		queuine/ PreQ1
C19H19N7O6	-2	Cytosol	C00415	4033-27-6	7,8-Dihydrofolic acid/
C9H21N2O2	1	Cytosol	C01037		
C6H9O9P	-2	Cytosol	C01236		D-Glucono-1,5-lacton
C6H10O10P	-3	Cytosol	C00345		6-phosphogluconic a
C7H8N5O8P2	-3	Cytosol			6-hydroxymethyl-7,8-
C7H9N5O2	0	Cytosol			6-hydroxymethyl-7,8-
C7H8N5O3	-1	Cytosol			
C8H14O7	0	Cytosol	C02655	107-85-7	
C13H18N4O6	0	Cytosol	C04332		
C9H11N3O9P	-3	Cytosol	C15667		NCAIR
C5H11NO7P	-1	Cytosol	C03090		5-Phosphoribosylami
C5H8O14P3	-5	Cytosol	C00119		5-Phosphoribosyl 1-p
C10H9O10P	-4	Cytosol	C01269		O5-(1-Carboxyvinyl)-
C6H12O4S	0	Cytosol	C03089		S5-Methyl-5-thio-D-ri
C6H12O4S	0	Extra-organism	C03089		S5-Methyl-5-thio-D-ri
C6H12O4S	0	Periplasm	C03089		S5-Methyl-5-thio-D-ri
C11H15N5O3S	0	Cytosol	C00170	2457-80-9	5'-S-Methylthioadeno
C20H24N7O6	-1	Cytosol	C00440		N5-methyl-tetrahydro
C20H21N7O7	-2	Cytosol	C03479	58-05-9	L(-)-5-Formyl-5,6,7,8-
C10H13N4O9P	-2	Cytosol	C04734		1-(5'-Phosphoribosyl)
C5H10O4	0	Cytosol			
C10H13N5O3	0	Cytosol	C05198		
C6H9O7	-1	Extra-organism	C01062		5-k-gluconate/ 5-keto
C6H9O7	-1	Periplasm	C01062		5-k-gluconate/ 5-keto
C9H13N4O9P	-2	Cytosol	C01268		5-Amino-6-(ribosylam
C9H15N4O9P	-2	Cytosol	C04454		5-amino-6-ribitylamin
C5H9NO3	0	Cytosol	C00430	106-60-5	5-Aminolevulinate/ 5-
C9H11N3O9P	-3	Cytosol	C04751		1-(5-Phospho-D-ribos
C9H13N4O8P	-2	Cytosol	C04677	3031-94-5	5-Phosphoribosyl-4-c
C8H12N3O7P	-2	Cytosol	C03373	25635-88-5	Aminoimidazole riboti
C15H21N5O15P2	-4	Cytosol	C04916		N-(5'-Phosphoribulos
C19H21N7O6	-2	Cytosol	C00101	135-16-0	(6S)-Tetrahydrofolic a
C20H21N7O6	-2	Cytosol	C00143		N5,N10-methylene-te
C20H20N7O6	-1	Cytosol	C00445		5,10-methenyltetrahy
C4H6NO7P	-2	Cytosol	C03082		L-4-Aspartyl phospha
C4H6O8P	-3	Cytosol	C03393		
C6H8NO4PS	-2	Cytosol	C04327		4-Methyl-5-(2-phosph

C6H9NOS	0	Cytosol	C04294	137-00-8	5-(2-Hydroxyethyl)-4-
C6H9O3	-1	Cytosol	C00233		alpha-ketoisocaproate
C8H8O2	0	Extra-organism	C03765	60-11-7	2-(4-Hydroxyphenyl)a
C8H8O2	0	Periplasm	C03765	60-11-7	2-(4-Hydroxyphenyl)a
C4H9NO4	0	Cytosol	C06056		
C7H5O3	-1	Cytosol	C00156	99-96-7	Hydroxybenzenecarb
C4H9NO2	0	Cytosol	C00334	56-12-2	GABA/ 4-Aminobutan
C4H9NO2	0	Extra-organism	C00334	56-12-2	GABA/ 4-Aminobutan
C4H9NO2	0	Periplasm	C00334	56-12-2	GABA/ 4-Aminobutan
C7H6NO2	-1	Cytosol	C00568	150-13-0	p-Aminobenzoate/ 4-
C6H9N3O	0	Cytosol	C01279	73-67-6	Toxopyrimidine/ 4-Am
C10H10NO5	-1	Cytosol	C11355		
C6H8N3O4P	-2	Cytosol	C04556		4-Amino-5-phosphom
C5H8O4	0	Cytosol	C11838		
C14H23N3O14P2	-2	Cytosol	C11435		
C9H16N4O6	0	Cytosol	C04732		4-(1-D-Ribitylamino)-
C9H11N2O9P	-2	Extra-organism	C01368	35170-03-7	Uridine 3'-monophosp
C9H11N2O9P	-2	Periplasm	C01368	35170-03-7	Uridine 3'-monophosp
C3H5NO4S	-2	Cytosol	C00606	1115-65-7	L-Cysteinesulfinic aci
C3H2O7P	-3	Cytosol	C03232		3-Phosphohydroxypy
C3H4O10P2	-4	Cytosol	C00236		1,3-bis-phosphoglyce
C3H4O7P	-3	Cytosol	C00197		D-Glycerate 3-phosph
C10H11N5O13P2S	-4	Cytosol	C00053	482-67-7	3'-Phosphoadenosine
C35H56N7O18P3S	-4	Cytosol	C05261		
C25H45N2O9PRS	-1	Cytosol	C05759		3-Oxotetradecanoyl-[a
C19H31N2O11PRS	-1	Cytosol			
C29H44N7O18P3S	-4	Cytosol	C05267		
C19H33N2O9PRS	-1	Cytosol	C05750		3-Oxooctanoyl-[acp]
C39H64N7O18P3S	-4	Cytosol	C16216		
C29H53N2O9PRS	-1	Cytosol	C16219		3-Oxooctadecanoyl-[a
C27H40N7O18P3S	-4	Cytosol	C05269	5096-70-8	3-ketohexanoyl-CoA
C17H29N2O9PRS	-1	Cytosol	C05746		3-Oxohexanoyl-[acp]
C37H60N7O18P3S	-4	Cytosol	C05259		
C27H49N2O9PRS	-1	Cytosol	C05762		3-Oxohexadecanoyl-[
C17H27N2O11PRS	-1	Cytosol			
C33H52N7O18P3S	-4	Cytosol	C05263		
C23H41N2O9PRS	-1	Cytosol	C05756		3-Oxododecanoyl-[ac
C31H48N7O18P3S	-4	Cytosol	C05265		
C21H37N2O9PRS	-1	Cytosol	C05753		3-Oxodecanoyl-[acp]
C29H51N2O9PRS	-1	Cytosol			
C27H47N2O9PRS	-1	Cytosol			
C25H43N2O9PRS	-1	Cytosol			
C23H39N2O9PRS	-1	Cytosol			
C47H69O3	-1	Cytosol	C05809		
C5H7O3	-1	Cytosol	C00141		2-Oxoisovalerate/ alp
C3H5O3	-1	Extra-organism	C01013	503-66-2	3-Hydroxyisobutyric a
C3H5O3	-1	Periplasm	C01013	503-66-2	3-Hydroxyisobutyric a
C19H33N2O11PRS	-1	Cytosol			

C17H29N2O11PRS	-1	Cytosol			
C9H7O3	-1	Extra-organism			3-hydroxycinnamate
C9H7O3	-1	Periplasm			3-hydroxycinnamate
C10H12N5O8P	-2	Extra-organism	C06193		Guanosine 3'-phosph
C10H12N5O8P	-2	Periplasm	C06193		Guanosine 3'-phosph
C8H12O11P	-3	Cytosol	C04478		2-Dehydro-3-deoxy-D
C8H13O8	-1	Cytosol	C01187		3-Deoxy-D-manno-oc
C7H7O5	-1	Cytosol	C02637		
C7H9O6	-1	Cytosol	C00944		5-Dehydroquinate/ 3-
C9H12N3O8P	-2	Extra-organism	C05822		cytidine-3'-phosphate
C9H12N3O8P	-2	Periplasm	C05822		cytidine-3'-phosphate
C7H8O5	-2	Cytosol	C04236		2-Oxo-4-methyl-3-car
C7H10O5	-2	Cytosol	C02504		2-Isopropylmalate/ 2-
C7H10O5	-2	Cytosol	C04411		3-Isopropylmalate/ 2-
C10H12N5O7P	-2	Extra-organism	C01367	84-21-9	3'-Adenylic acid/ 3'-A
C10H12N5O7P	-2	Periplasm	C01367	84-21-9	3'-Adenylic acid/ 3'-A
C8H8O3	0	Extra-organism	C04043		3,4-Dihydroxyphenyla
C8H8O3	0	Periplasm	C04043		3,4-Dihydroxyphenyla
C4H7O6P	-2	Cytosol	C15556		
C6H7N2O5P	-2	Cytosol	C01267		Imidazole-acetol phos
C9H7O4	-1	Cytosol	C01179		4-Hydroxyphenylpyru
C9H9O3	-1	Extra-organism	C11457		
C9H9O3	-1	Periplasm	C11457		
C17H34O7P1	-1	Cytosol	C03974		2-Acyl-sn-glycerol 3-p
C17H34O7P1	-1	Periplasm	C03974		2-Acyl-sn-glycerol 3-p
C17H32O7P1	-1	Cytosol	C03974		2-Acyl-sn-glycerol 3-p
C17H32O7P1	-1	Periplasm	C03974		2-Acyl-sn-glycerol 3-p
C11H10O6	-2	Cytosol	C05817		
C14H13O9	-3	Cytosol	C16519		
C2H2O6P	-3	Cytosol	C00988		Phosphoglycolic acid/
C14H22N3O17P3	-4	Cytosol	C11436		2C-methyl-D-erythrito
C5H4O5	-2	Cytosol	C00026	328-50-7	alpha-Ketoglutarate/
C5H4O5	-2	Extra-organism	C00026	328-50-7	alpha-Ketoglutarate/
C5H4O5	-2	Periplasm	C00026	328-50-7	alpha-Ketoglutarate/
C4H5O3	-1	Cytosol	C00109	600-18-0	2-Ketobutyric acid/ 2-
C4H4O8P	-3	Cytosol	C06054		alpha-Keto-3-hydroxy
C46H70O	0	Cytosol	C05810		
C47H72O2	0	Cytosol	C05812		
C47H72O3	0	Cytosol			
C46H70O2	0	Cytosol	C05811		
C48H74O3	0	Cytosol			
C48H74O4	0	Cytosol			
C21H42O7P1	-1	Cytosol	C03974		2-Acyl-sn-glycerol 3-p
C21H42O7P1	-1	Periplasm	C03974		2-Acyl-sn-glycerol 3-p
C21H40O7P1	-1	Cytosol	C03974		2-Acyl-sn-glycerol 3-p
C21H40O7P1	-1	Periplasm	C03974		2-Acyl-sn-glycerol 3-p
C7H7O7	-3	Cytosol	C02225	96-17-3	
C6H8N3O7P2	-3	Cytosol	C04752	745-65-3	4-amino-2-methyl 5-h

C7H8O4	-2	Cytosol	C02631		beta-isopropylmaleate
C19H38O7P1	-1	Cytosol	C03974		2-Acyl-sn-glycerol 3-p
C19H38O7P1	-1	Periplasm	C03974		2-Acyl-sn-glycerol 3-p
C19H36O7P1	-1	Cytosol	C03974		2-Acyl-sn-glycerol 3-p
C19H36O7P1	-1	Periplasm	C03974		2-Acyl-sn-glycerol 3-p
C15H30O7P1	-1	Cytosol	C03974		2-Acyl-sn-glycerol 3-p
C15H30O7P1	-1	Periplasm	C03974		2-Acyl-sn-glycerol 3-p
C5H9O7P	-2	Cytosol	C00673	102916-66-5	
C5H9O7P	-2	Cytosol	C00672		Deoxy-ribose 1-phosp
C50H70O2	0	Cytosol	C05818		
C50H72O2	0	Cytosol			
C6H9O4	-1	Cytosol	C00966		alpha-ketopantoate
C6H8O9P	-3	Cytosol	C04442		2-Dehydro-3-deoxy-6
C6H9O6	-1	Cytosol	C00204		2-Keto-3-deoxy-D-glu
C6H9O6	-1	Extra-organism	C00204		2-Keto-3-deoxy-D-glu
C6H9O6	-1	Periplasm	C00204		2-Keto-3-deoxy-D-glu
C7H10O10P	-3	Cytosol	C04691		
C5H11O7P	-2	Cytosol	C11434		
C5H10O9P2	-2	Cytosol	C11453		
C9H12N5O13P3	-4	Cytosol	C04895		7,8-Dihydroneopterin
C24H46O9P1	-1	Cytosol			2-acyl-glycerophosph
C24H46O9P1	-1	Periplasm			2-acyl-glycerophosph
C24H48O9P1	-1	Cytosol			2-acyl-glycerophosph
C24H48O9P1	-1	Periplasm			2-acyl-glycerophosph
C22H42O9P1	-1	Cytosol			L-1-Lysophosphatidyl
C22H42O9P1	-1	Periplasm			L-1-Lysophosphatidyl
C22H44O9P1	-1	Cytosol			L-1-Lysophosphatidyl
C22H44O9P1	-1	Periplasm			L-1-Lysophosphatidyl
C20H38O9P1	-1	Cytosol			2-acyl-glycerophosph
C20H38O9P1	-1	Periplasm			2-acyl-glycerophosph
C20H40O9P1	-1	Cytosol			2-acyl-glycerophosph
C20H40O9P1	-1	Periplasm			2-acyl-glycerophosph
C18H36O9P1	-1	Cytosol			2-acyl-glycerophosph
C18H36O9P1	-1	Periplasm			2-acyl-glycerophosph
C23H46NO7P1	0	Cytosol	C05973		L-1-Lysophosphatidyl
C23H46NO7P1	0	Periplasm	C05973		L-1-Lysophosphatidyl
C23H48NO7P1	0	Cytosol	C05973		L-1-Lysophosphatidyl
C23H48NO7P1	0	Periplasm	C05973		L-1-Lysophosphatidyl
C21H42NO7P1	0	Cytosol	C05973		L-1-Lysophosphatidyl
C21H42NO7P1	0	Periplasm	C05973		L-1-Lysophosphatidyl
C21H44NO7P1	0	Cytosol	C05973		L-1-Lysophosphatidyl
C21H44NO7P1	0	Periplasm	C05973		L-1-Lysophosphatidyl
C19H38NO7P1	0	Cytosol	C05973		L-1-Lysophosphatidyl
C19H38NO7P1	0	Periplasm	C05973		L-1-Lysophosphatidyl
C19H40NO7P1	0	Cytosol	C05973		L-1-Lysophosphatidyl
C19H40NO7P1	0	Periplasm	C05973		L-1-Lysophosphatidyl
C17H36NO7P1	0	Cytosol	C05973		L-1-Lysophosphatidyl
C17H36NO7P1	0	Periplasm	C05973		L-1-Lysophosphatidyl

C9H14N5O8P	-2	Cytosol	C01304	
C7H5NO4	-2	Cytosol	C03340	Dihydrodipicolinic aci
C3H9N2O2	1	Extra-organism	C06393	2,3-Diaminopropionic
C3H9N2O2	1	Periplasm	C06393	2,3-Diaminopropionic
C9H10N2O8P	-1	Extra-organism	C02355	
C9H10N2O8P	-1	Periplasm	C02355	
C10H11N5O7P	-1	Extra-organism	C06194	
C10H11N5O7P	-1	Periplasm	C06194	
C9H11N3O7P	-1	Extra-organism	C02354	
C9H11N3O7P	-1	Periplasm	C02354	
C10H11N5O6P	-1	Extra-organism	C02353	Adenosine-2’,3’-cycli
C10H11N5O6P	-1	Periplasm	C02353	Adenosine-2’,3’-cycli
C7H7NO4	-2	Cytosol	C03972	(R)-2,3,4,5-tetrahydro
C8H15N3O8P	-1	Cytosol	C04640	2-(Formamido)-N1-(5
C9H15O9	-1	Extra-organism	C11544	2-O-alpha-mannosyl-
C9H15O9	-1	Periplasm	C11544	2-O-alpha-mannosyl-
C17H33O7P1	-2	Cytosol	C00681	1-Acyl-sn-glycerol 3-p
C17H33O7P1	-2	Periplasm	C00681	1-Acyl-sn-glycerol 3-p
C17H31O7P1	-2	Cytosol	C00681	1-Acyl-sn-glycerol 3-p
C17H31O7P1	-2	Periplasm	C00681	1-Acyl-sn-glycerol 3-p
C5H6NO2	-1	Cytosol	C03912	(S)-1-Pyrroline-5-carb
C21H41O7P1	-2	Cytosol	C00681	1-Acyl-sn-glycerol 3-p
C21H41O7P1	-2	Periplasm	C00681	1-Acyl-sn-glycerol 3-p
C21H39O7P1	-2	Cytosol	C00681	1-Acyl-sn-glycerol 3-p
C21H39O7P1	-2	Periplasm	C00681	1-Acyl-sn-glycerol 3-p
C5H9O8P2	-3	Cytosol	C11811	
C19H37O7P1	-2	Cytosol	C00681	1-Acyl-sn-glycerol 3-p
C19H37O7P1	-2	Periplasm	C00681	1-Acyl-sn-glycerol 3-p
C19H35O7P1	-2	Cytosol	C00681	1-Acyl-sn-glycerol 3-p
C19H35O7P1	-2	Periplasm	C00681	1-Acyl-sn-glycerol 3-p
C15H29O7P1	-2	Cytosol	C00681	1-Acyl-sn-glycerol 3-p
C15H29O7P1	-2	Periplasm	C00681	1-Acyl-sn-glycerol 3-p
C6H11O9P	-2	Cytosol	C01177	Inositol 1-phosphate/
C5H9O7P	-2	Cytosol	C11437	
C24H46O9P1	-1	Periplasm	C018126	1-acyl-glycerophosph
C24H48O9P1	-1	Periplasm	C018126	1-acyl-glycerophosph
C22H42O9P1	-1	Periplasm	C018126	1-acyl-glycerophosph
C22H44O9P1	-1	Periplasm	C018126	L-2-lysophosphatidylg
C20H38O9P1	-1	Periplasm	C018126	1-acyl-glycerophosph
C20H40O9P1	-1	Periplasm	C018126	L-2-lysophosphatidylg
C18H36O9P1	-1	Periplasm	C018126	L-2-lysophosphatidylg
C23H46NO7P1	0	Periplasm	C04438	1-Acyl-sn-glycero-3-p
C23H48NO7P1	0	Periplasm	C04438	1-Acyl-sn-glycero-3-p
C21H42NO7P1	0	Periplasm	C04438	1-Acyl-sn-glycero-3-p
C21H44NO7P1	0	Periplasm	C04438	1-Acyl-sn-glycero-3-p
C19H38NO7P1	0	Periplasm	C04438	1-Acyl-sn-glycero-3-p
C19H40NO7P1	0	Periplasm	C04438	1-Acyl-sn-glycero-3-p
C17H36NO7P1	0	Periplasm	C04438	L-2-Lysophosphatidyl

C20H21N7O7	-2	Cytosol	C00234		10-Formyl-THF
C26H39N5O14	-2	Cytosol			(anh)MurNAcLalaDgl
C29H44N6O15	-2	Cytosol			(anh)MurNAcLalaDgl
C11H16NO7	-1	Cytosol			(anh)MurNAc/ 1,6-an
C5H16N2	2	Cytosol	C01672	462-94-2	Cadaverine/ 1,5-Pent
C5H16N2	2	Extra-organism	C01672	462-94-2	Cadaverine/ 1,5-Pent
C5H16N2	2	Periplasm	C01672	462-94-2	Cadaverine/ 1,5-Pent
C32H38N7O19P3S	-4	Cytosol	C15547		
C11H7O4	-1	Cytosol	C03657		
C36H62O31	0	Cytosol	C00718		
C36H62O31	0	Extra-organism	C00718		
C36H62O31	0	Periplasm	C00718		
C31H59O8P1	-2	Cytosol	C00416		Phosphatidic acid/ Ph
C31H59O8P1	-2	Periplasm	C00416		Phosphatidic acid/ Ph
C31H55O8P1	-2	Cytosol	C00416		Phosphatidate/ Phos
C31H55O8P1	-2	Periplasm	C00416		Phosphatidate/ Phos
C39H75O8P1	-2	Cytosol	C00416		Phosphatidate/ 1,2-D
C39H75O8P1	-2	Periplasm	C00416		Phosphatidate/ 1,2-D
C39H71O8P1	-2	Cytosol	C00416		1,2-Diacyl-sn-glycerol
C39H71O8P1	-2	Periplasm	C00416		1,2-Diacyl-sn-glycerol
C35H67O8P1	-2	Cytosol	C00416		1,2-Diacyl-sn-glycerol
C35H67O8P1	-2	Periplasm	C00416		1,2-Diacyl-sn-glycerol
C35H63O8P1	-2	Cytosol	C00416		Phosphatidate/ 1,2-D
C35H63O8P1	-2	Periplasm	C00416		Phosphatidate/ 1,2-D
C27H51O8P1	-2	Cytosol	C00416		Phosphatidate/ Phos
C27H51O8P1	-2	Periplasm	C00416		Phosphatidate/ Phos
C31H60O5	0	Cytosol	C00641		D-1,2-Diacylglycerol/
C31H60O5	0	Periplasm	C00641		D-1,2-Diacylglycerol/
C31H56O5	0	Cytosol	C00641		D-1,2-Diacylglycerol/
C31H56O5	0	Periplasm	C00641		D-1,2-Diacylglycerol/
C39H76O5	0	Cytosol	C00641		D-1,2-Diacylglycerol/
C39H76O5	0	Periplasm	C00641		D-1,2-Diacylglycerol/
C39H72O5	0	Cytosol	C00641		1,2-Diacylglycerol/ D-
C39H72O5	0	Periplasm	C00641		1,2-Diacylglycerol/ D-
C35H68O5	0	Cytosol	C00641		D-1,2-Diacylglycerol/
C35H68O5	0	Periplasm	C00641		D-1,2-Diacylglycerol/
C35H64O5	0	Cytosol	C00641		D-1,2-Diacylglycerol/
C35H64O5	0	Periplasm	C00641		D-1,2-Diacylglycerol/
C27H52O5	0	Cytosol	C00641		1,2-Diacylglycerol/ D-
C27H52O5	0	Periplasm	C00641		1,2-Diacylglycerol/ D-
C15H19N5O20P4	-6	Cytosol	C02739		Phosphoribosyl-ATP/
C15H19N5O14P2	-4	Cytosol	C02741		Phosphoribosyl)-AM
C15H21N5O15P2	-4	Cytosol	C04896		
C12H13NO9P	-3	Cytosol	C01302		
S4Fe4	2	Cytosol			
S2Fe2	2	Cytosol			
SFe2	2	Cytosol			
C3H8O2	0	Extra-organism	C02917	4254-14-3	(S)-1,2-Propanediol/

C3H8O2	0	Periplasm	C02917	4254-14-3	(S)-1,2-Propanediol/ (
C5H5N2O4	-1	Cytosol	C00337	5988-19-2	L-Dihydroorotate/ L-D
C6H9O3	-1	Cytosol	C00671		(R)-2-oxo-3-methylpe
C35H58N7O18P3S	-4	Cytosol	C05260		
C29H46N7O18P3S	-4	Cytosol	C05266		(S)-Hydroxyoctanoyl-
C39H66N7O18P3S	-4	Cytosol	C16217		
C27H42N7O18P3S	-4	Cytosol	C05268		(S)-Hydroxyhexanoyl-
C37H62N7O18P3S	-4	Cytosol	C05258		
C33H54N7O18P3S	-4	Cytosol	C05262		
C31H50N7O18P3S	-4	Cytosol	C05264		(S)-Hydroxydecanoyl-
C25H38N7O18P3S	-4	Cytosol	C01144		L-3-hydroxybutyryl-Co
C5H7O4	-1	Cytosol	C06010		(S)-2-Hydroxy-2-meth
C6H9O4	-1	Cytosol	C06006		
C13H15N4O12P	-4	Cytosol	C04823		1-(5'-Phosphoribosyl)
C13H20N3O8S	-1	Cytosol	C03451	59-85-8	
C3H8O2	0	Extra-organism	C02912	4254-14-2	(R)-1,2-Propanediol/ (
C9H16NO5	-1	Cytosol	C00864	79-83-4	Pantothenate/ Pantot
C9H16NO5	-1	Extra-organism	C00864	79-83-4	Pantothenate/ Pantot
C9H16NO5	-1	Periplasm	C00864	79-83-4	Pantothenate/ Pantot
C6H11O4	-1	Cytosol	C00522	470-29-1	D-pantoate/ Pantoate
C3H5O4	-1	Cytosol	C00258	473-81-4	D-Glycerate/ Glycera
C3H5O4	-1	Extra-organism	C00258	473-81-4	D-Glycerate/ Glycera
C3H5O4	-1	Periplasm	C00258	473-81-4	D-Glycerate/ Glycera
C25H47N2O9PRS	-1	Cytosol	C04688		(3R)-3-Hydroxytetrad
C19H35N2O9PRS	-1	Cytosol	C04620		(3R)-3-Hydroxyoctano
C29H55N2O9PRS	-1	Cytosol	C16220		
C17H31N2O9PRS	-1	Cytosol	C05747		(R)-3-Hydroxyhexano
C23H43N2O9PRS	-1	Cytosol	C05757		(R)-3-Hydroxydodeca
C21H39N2O9PRS	-1	Cytosol	C04619	320-77-4	(3R)-3-Hydroxydecan
C29H53N2O9PRS	-1	Cytosol			
C27H49N2O9PRS	-1	Cytosol			
C25H45N2O9PRS	-1	Cytosol			
C23H41N2O9PRS	-1	Cytosol			
C6H11O4	-1	Cytosol	C06007		2,3-Dihydroxy-3-meth
C5H9O4	-1	Cytosol	C04272		(R)-2,3-Dihydroxy-iso
C15H27N2O9PRS	-1	Cytosol	C01271		(R)-3-Hydroxyacyl-[ac
C5H8O4	0	Cytosol			Pro-AI-2
C5H10O5	0	Cytosol			AI-2

:/ 3-Hydroxyisobutyric acid
aric acid
pionic acid/ 4,5-Dihydro-4-oxo-5-imidazolepropanoate

,5-tricarboxylate
ate/ Cellobiose 6-phosphate

,N'-Diacetylchitobiose
,N'-Diacetylchitobiose
,N'-Diacetylchitobiose

osyl-4-D-glucopyranose
osyl-4-D-glucopyranose

odecanal/ Lauraldehyde

Folic acid
amate
acid/ aminic acid/ Methanoic acid/ Formic acid

o-2-deoxy-D-glucose
phosphate/ all-trans-Geranylgeranyl diphosphate/ all-trans-Geranylgeranyl pyrophosphate/ (2E,6E,

(9-D-Ribosylxanthine)-5'-phosphate
(9-D-Ribosylxanthine)-5'-phosphate
(9-D-Ribosylxanthine)-5-phosphate

te/ Uridine triphosphate/ rUTP/ 5'-uridylate triphosphate

arbamimidic acid/ aquadrate/ Isourea/ Carbamide
arbamimidic acid/ aquadrate/ Isourea/ Carbamide
arbamimidic acid/ aquadrate/ Isourea/ Carbamide
2,4-Dihydroxypyrimidine/ U/ 2,4(1H,3H)-Pyrimidinedione
2,4-Dihydroxypyrimidine/ U/ 2,4(1H,3H)-Pyrimidinedione
2,4-Dihydroxypyrimidine/ U/ 2,4(1H,3H)-Pyrimidinedione
alanyl-D-glutamyl-meso-2,6-diaminoheptane- D-alanyl-D-alanine-diphosphoundecaprenol
v)
ecaprenyl-phosphate
ecaprenyl-phosphate
rial Common Antigen
osphate
osphate
monophosphate/ Uridine 5'-monophosphate/ 5'Uridylic acid
monophosphate/ Uridine 5'-monophosphate/ 5'Uridylic acid
monophosphate/ Uridine 5-monophosphate/ 5Uridylic acid
oyl-L-alanyl-D-glutamyl-6-carboxy-L-lysyl-D-alanyl-D-alanine

oyl-tetrapeptide
oyl-L-alanyl-D-gamma-glutamyl-meso-2,6-diaminoheptanedioate/ UDP-MurNac-tripeptide
NAcMur-(L)-Ala
on abbr: UDP-NAcMur

amine/ common abbr: UDP-NAcGlc/ UDP-GlcNAc
amine/ common abbr: UDP-NAcGlc/ UDP-GlcNAc
amine/ common abbr: UDP-NAcGlc/ UDP-GlcNAc

arboxyvinyl)-D-glucosamine/ UDP-N-acetylglucosamine-3-O-pyruvateether/ common abbr: UDP-N

ɔse/ UDP-D-galactose
ɔse/ UDP-D-galactose
ɔse/ UDP-D-galactose
P-GlcA
P-GlcA
ɔxymyristoyl)-N-acetylglucosamine
ɔxymyristoyl)-D-glucosamine
:e/ uridine diphosphate/ 5'-uridylate diphosphate

ethylamine
ethylamine

apeptide (x2)/ [GlcNac-MurNac-pentapeptide(beta1->4)GlcNac-MurNac-pentapeptide] unit

NA

hylmethanamine
hylmethanamine
hylmethanamine
e/ alpha, alpha'-Trehalose
e/ alpha, alpha-Trehalose

yl-[acp]
e A
l-[acp]

p]

yl-[acp]

cp]
CoA
[acp]

cp]

ethylpyrimidine/ Thy
ethylpyrimidine/ Thy
ethylpyrimidine/ Thy
e/ Deoxythymidine
e/ Deoxythymidine
e/ Deoxythymidine
apeptide (x3)/ [GlcNac-MurNac-pentapeptide(beta1->4)GlcNac-MurNac-pentapeptide(beta1->4)G

nic acid
nic acid
nic acid
in diphosphate/ TPP/ ThPP/ Thiamin pyrophosphate
Thiamine phosphate/ TMP/ Thiamine monophosphate
/ Aneurin/ Antiberiberi factor
/ Aneurin/ Antiberiberi factor

/ Aneurin/ Antiberiberi factor

fat 14/ univol u 3165/ emery 655/ hydrofol acid 1495/ Myristic Acid/ n-tetradecoic acid/ 1-tridecane
fat 14/ univol u 3165/ emery 655/ hydrofol acid 1495/ Myristic Acid/ n-tetradecoic acid/ 1-tridecane
fat 14/ univol u 3165/ emery 655/ hydrofol acid 1495/ Myristic Acid/ n-tetradecoic acid/ 1-tridecane

ic acid
ic acid
dical
dical

ose/ Sugar/ 1-alpha-D-glucopyranosyl-2-beta-D-fructofuranoside
ose/ Sugar/ 1-alpha-D-glucopyranosyl-2-beta-D-fructofuranoside
eA/ Succinyl coenzyme A
cinate semialdehyde
dionic acid/ Ethylenesuccinic acid
dionic acid/ Ethylenesuccinic acid
dionic acid/ Ethylenesuccinic acid
canoyl-CoA
steine/ S-D-Ribosyl-L-homocysteine
4-butane-diamine
4-butane-diamine
4-butane-diamine

nolamine
nolamine
nolamine
ne

ne
ne

te
rihydroxy-1-cyclohexenecarboxylic acid
rihydroxy-1-cyclohexenecarboxylic acid
rihydroxy-1-cyclohexenecarboxylic acid

d
d
sphate
iphosphate
e/ Acylcarnitine
eine

2/ 7,8-Dimethyl-10-ribitylisoalloxazine

amyl-L-cysteinylglycine/ N-(N-gamma-L-Glutamyl-L-cysteinyl)glycine/ gamma-L-Glutamyl-L-cystei
amyl-L-cysteinylglycine/ N-(N-gamma-L-Glutamyl-L-cysteinyl)glycine/ gamma-L-Glutamyl-L-cystei
amyl-L-cysteinylglycine/ N-(N-gamma-L-Glutamyl-L-cysteinyl)glycine/ gamma-L-Glutamyl-L-cystei
nucleotide
yl-[acyl-carrier protein]/ (3R)-3-Hydroxyhexadecanoyl-[acyl-carrier protein]/ (R)-3-Hydroxyhexadec
ylate/ Quinolinic acid/ 2,3-Pyridinedicarboxylic acid
d/ Chinic acid
d/ Chinic acid
ropanoate/ 2-Oxopropanoic acid/ Pyroracemic acid/ alpha-Ketopropionic acid/ 2-Ketopropionic Ac
ropanoate/ 2-Oxopropanoic acid/ Pyroracemic acid/ alpha-Ketopropionic acid/ 2-Ketopropionic Ac
ropanoate/ 2-Oxopropanoic acid/ Pyroracemic acid/ alpha-Ketopropionic acid/ 2-Ketopropionic Ac
e/ Pyridoxine 5-phosphate

phate/ Pyridoxamine phosphate

e/ Pyridoxal phosphate

,4-Butanediamine/ Tetramethylenediamine
,4-Butanediamine/ Tetramethylenediamine
,4-Butanediamine/ Tetramethylenediamine

rphyrinogen IX
B/ hemeB
B/ hemeB
B/ hemeB

ic acid/ Propionic acid
ic acid/ Propionic acid
ic acid/ Propionic acid
onyl coenzyme A
/ Propionyl phosphate

horous acid/ Phosphonic acid/ Phosphite
horous acid/ Phosphonic acid/ Phosphite
acid/ PEP
/ O3-Phosphatidyl-L-serine/ 1,2-Diacyl-sn-glycerol 3-phospho-L-serine/ 3-O-sn-Phosphatidyl-L-se
/ 1,2-Diacyl-sn-glycerol 3-phospho-L-serine/ O3-Phosphatidyl-L-serine/ 3-O-sn-Phosphatidyl-L-se
/ 1,2-Diacyl-sn-glycerol 3-phospho-L-serine/ O3-Phosphatidyl-L-serine/ 3-O-sn-Phosphatidyl-L-se
l 3-phospho-L-serine/ Phosphatidyl-L-serine/ O3-Phosphatidyl-L-serine/ 3-O-sn-Phosphatidyl-L-se
l 3-phospho-L-serine/ O3-Phosphatidyl-L-serine/ Phosphatidyl-L-serine/ 3-O-sn-Phosphatidyl-L-se
/ 3-O-sn-Phosphatidyl-L-serine/ 1,2-Diacyl-sn-glycerol 3-phospho-L-serine/ O3-Phosphatidyl-L-se
/ 3-O-sn-Phosphatidyl-L-serine/ 1,2-Diacyl-sn-glycerol 3-phospho-L-serine/ O3-Phosphatidyl-L-se
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos

-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
-sn-glycerol 1-phosphate/ 3(3-Phosphatidyl-)L-glycerol 1-phosphate/ 1,2-Diacyl-sn-glycero-3-phos
cerol/ PtdGro/ 3-(3-sn-Phosphatidyl)glycerol/ Phosphatidylglycerol
cerol/ PtdGro/ 3-(3-sn-Phosphatidyl)glycerol/ Phosphatidylglycerol
lglycerol/ 3(3-Phosphatidyl-)glycerol/ 3-(3-sn-Phosphatidyl)glycerol
lglycerol/ 3(3-Phosphatidyl-)glycerol/ 3-(3-sn-Phosphatidyl)glycerol
cerol/ 3-(3-sn-Phosphatidyl)glycerol/ Phosphatidylglycerol/ PtdGro
cerol/ 3-(3-sn-Phosphatidyl)glycerol/ Phosphatidylglycerol/ PtdGro
tidyl-)glycerol/ Phosphatidylglycerol
tidyl-)glycerol/ Phosphatidylglycerol
cerol/ Phosphatidylglycerol/ PtdGro/ 3-(3-sn-Phosphatidyl)glycerol
cerol/ Phosphatidylglycerol/ PtdGro/ 3-(3-sn-Phosphatidyl)glycerol
3(3-Phosphatidyl-)glycerol/ PtdGro/ 3-(3-sn-Phosphatidyl)glycerol
3(3-Phosphatidyl-)glycerol/ PtdGro/ 3-(3-sn-Phosphatidyl)glycerol
3-(3-sn-Phosphatidyl)glycerol/ 3(3-Phosphatidyl-)glycerol/ PtdGro
3-(3-sn-Phosphatidyl)glycerol/ 3(3-Phosphatidyl-)glycerol/ PtdGro
nolamine/ Cephalin/ (3-Phosphatidyl)-ethanolamine
nolamine/ Cephalin/ (3-Phosphatidyl)-ethanolamine
nolamine/ (3-Phosphatidyl)-ethanolamine/ Cephalin
nolamine/ (3-Phosphatidyl)-ethanolamine/ Cephalin
atidyl)-ethanolamine/ (3-Phosphatidyl)ethanolamine
atidyl)-ethanolamine/ (3-Phosphatidyl)ethanolamine
anolamine/ (3-Phosphatidyl)ethanolamine/ Cephalin
anolamine/ (3-Phosphatidyl)ethanolamine/ Cephalin
atidyl)-ethanolamine/ (3-Phosphatidyl)ethanolamine
atidyl)-ethanolamine/ (3-Phosphatidyl)ethanolamine
nolamine/ (3-Phosphatidyl)-ethanolamine/ Cephalin
nolamine/ (3-Phosphatidyl)-ethanolamine/ Cephalin
atidyl)ethanolamine/ (3-Phosphatidyl)-ethanolamine
atidyl)ethanolamine/ (3-Phosphatidyl)-ethanolamine
Phosphoric acid
Phosphoric acid
Phosphoric acid
lpha-Ketohydrocinnamic acid/ keto-Phenylpyruvate/ 3-Phenyl-2-oxopropanoate
-phenylpropionate
-phenylpropionate
-phenylpropionate

henylethylamine/ beta-Phenylethylamine/ Phenylethylamine
henylethylamine/ beta-Phenylethylamine/ Phenylethylamine

-Hydroxytoluene

ne/ Phosphopantetheine

Hexadecanoyl-[acyl-carrier protein]/ hexadecanoyl-ACP/ fa8-ACP
aphosphate/ P1,P5-Bis(5'-adenosyl) pentaphosphate
osyl) tetraphosphate
raphosphate/ AppppA

d/ Glutathione disulfide
d/ Glutathione disulfide
d/ Glutathione disulfide
oacetic acid/ 2-oxobutanedioic acid/ Oxosuccinic acid

oA/ Succinylbenzoyl-CoA
Succinylbenzoate

carboxylic acid
carboxylic acid
carboxylic acid
cid/ 2,5-Diaminopentanoic acid/ 2,5-Diaminopentanoate/ L-Ornithine
cid/ 2,5-Diaminopentanoic acid/ 2,5-Diaminopentanoate/ L-Ornithine
cid/ 2,5-Diaminopentanoic acid/ 2,5-Diaminopentanoate/ L-Ornithine

reonine/ 4-(Phosphonooxy)-L-threonine

protein]/ Octanoyl-[acp]

oic acid/ Octylic acid
oic acid/ Octylic acid
oic acid/ Octylic acid

noic acid/ oleate/ (9Z)-Octadecenoic acid/ (Z)-Octadec-9-enoic acid
noic acid/ oleate/ (9Z)-Octadecenoic acid/ (Z)-Octadec-9-enoic acid
noic acid/ oleate/ (9Z)-Octadecenoic acid/ (Z)-Octadec-9-enoic acid

d/ Octadecanoic acid
d/ Octadecanoic acid
d/ Octadecanoic acid

aminopimelate/ N-Succinyl-L-2,6-diaminoheptanedioate/ N-Succinyl-L-2,6-diaminopimelate
o-6-oxoheptanedioate/ N-Succinyl-L-2-amino-6-oxopimelate/ N-Succinyl-2-amino-6-oxo-L-pimelic a

ucleotide/ Nicotinamide mononucleotide/ Nicotinamide ribonucleotide
ucleotide/ Nicotinamide mononucleotide/ Nicotinamide ribonucleotide
ucleotide/ Nicotinamide mononucleotide/ Nicotinamide ribonucleotide
/ Dinitrogen oxide
/ Dinitrogen oxide
/ Dinitrogen oxide

de
de
de

tide/ Nicotinic acid ribonucleotide/ beta-Nicotinate D-ribonucleotide
/ 3-Pyridinecarboxylic acid
/ 3-Pyridinecarboxylic acid
nopyridine nucleotide/ NADPH
denine dinucleotide phosphate/ NADP/ NADP+

phosphopyridine Nucleotide/ beta-NAD/ beta-Nicotinamide adenine dinucleotide

eoxy-D-glycero-D-galacto-2-nonulosonic acid/ N-Acetylneuraminic acid/ Neu5Ac
eoxy-D-glycero-D-galacto-2-nonulosonic acid/ N-Acetylneuraminic acid/ Neu5Ac
eoxy-D-glycero-D-galacto-2-nonulosonic acid/ N-Acetylneuraminic acid/ Neu5Ac
-phosphate/ MurNAc-6-p
I-Acetylmuramic acid
I-Acetylmuramic acid
5-phosphate
entanoate
acid
mine 6-phosphate/ N-Acetylmannosamine 6-phosphate
-D-monnose
-D-monnose
-D-monnose
LalaDgluMdap
LalaDgluMdap
LalaDgluMdapDala
LalaDgluMdapDala

2-Acetamido-2-deoxy-D-glucose/ GlcNAc
2-Acetamido-2-deoxy-D-glucose/ GlcNAc
2-Acetamido-2-deoxy-D-glucose/ GlcNAc

amine/ 2-Acetamido-2-deoxy-D-galactose/ GalNAc
amine/ 2-Acetamido-2-deoxy-D-galactose/ GalNAc

lenylosuccinic acid
ne
ate 5-semialdehyde
ate
e
formylglycinamide/ N-Formyl-GAR/ N-Formylglycinamide ribonucleotide

cinamide/ GAR/ Glycinamide ribonucleotide

ate/ L-Argininosuccinate/ L-Argininosuccinic acid/ L-Arginosuccinic acid
-ribosyl)anthranilate/ N-(5-Phosphoribosyl)anthranilic acid
thenoyl-L-cysteine
carrier protein]/ Tetradecanoyl-[acp]/ Fatty acid C14:0 ACP
exakisphosphate/ D-myo-Inositol 1,2,3,4,5,6-hexakisphosphate/ Phytic acid/ Phytate/ myo-Inositol
yo-Inositol/ L-myo-Inositol/ 1L-myo-Inositol/ meso-Inositol/ Inositol/ Dambose/ Cyclohexitol/ Meat
yo-Inositol/ L-myo-Inositol/ 1L-myo-Inositol/ meso-Inositol/ Inositol/ Dambose/ Cyclohexitol/ Meat
yo-Inositol/ L-myo-Inositol/ 1L-myo-Inositol/ meso-Inositol/ Inositol/ Dambose/ Cyclohexitol/ Meat

/ Molybdoenzyme molybdenum cofactor

Manganese/ Mn(II)
Manganese/ Mn(II)
Manganese/ Mn(II)

2S,3R)-3-Hydroxybutane-1,2,3-tricarboxylate/ Methylisocitrate vic aldehyde/ 2-Ketopropionaldehyde/ 2-Oxopropanal

d
d
nelic acid/ meso-2,6-Diaminopimelate
nelic acid/ meso-2,6-Diaminopimelate
nelic acid/ meso-2,6-Diaminopimelate

pyranosyl)-D-glucopyranose
pyranosyl)-D-glucopyranose
se
se
se

-Glucopyranosyl-4-alpha-D-glucopyranose
-Glucopyranosyl-4-alpha-D-glucopyranose
-Glucopyranosyl-4-alpha-D-glucopyranose

Lyxulose
Lyxulose

id/ Val/ 2-Amino-3-methylbutyric acid
id/ Val/ 2-Amino-3-methylbutyric acid
id/ Val/ 2-Amino-3-methylbutyric acid

yl)alanine/ (S)-2-Amino-3-(p-hydroxyphenyl)propionic acid
yl)alanine/ (S)-2-Amino-3-(p-hydroxyphenyl)propionic acid
yl)alanine/ (S)-2-Amino-3-(p-hydroxyphenyl)propionic acid

-(3-indolyl)-propionic acid
-(3-indolyl)-propionic acid
-(3-indolyl)-propionic acid

te
te
xybutyric acid
xybutyric acid
xybutyric acid
-Tartrate/ (R,R)-Tartaric acid
-Tartrate/ (R,R)-Tartaric acid

propionic acid/ L-3-Hydroxy-alanine/ Ser
propionic acid/ L-3-Hydroxy-alanine/ Ser
propionic acid/ L-3-Hydroxy-alanine/ Ser

L-Mannomethylose
L-Mannomethylose

oxylic acid
oxylic acid
oxylic acid

phenylalanine/ (S)-alpha-amino-beta-phenylpropionic acid
phenylalanine/ (S)-alpha-amino-beta-phenylpropionic acid
phenylalanine/ (S)-alpha-amino-beta-phenylpropionic acid

xide/ L-methionine S-oxide/ methionine sulfoxide
xide/ L-methionine S-oxide/ methionine sulfoxide
xide/ L-methionine S-oxide/ methionine sulfoxide
hylthiobutyric acid
hylthiobutyric acid
hylthiobutyric acid
cid/ L-Malic acid/ L-2-Hydroxybutanedioic acid/ Malate
cid/ L-Malic acid/ L-2-Hydroxybutanedioic acid/ Malate
cid/ L-Malic acid/ L-2-Hydroxybutanedioic acid/ Malate

noic acid/ Lysine acid
noic acid/ Lysine acid
noic acid/ Lysine acid

eric acid/ Leu
eric acid/ Leu
eric acid/ Leu
d/ (S)-Lactate/ L-Lactic acid
d/ (S)-Lactate/ L-Lactic acid
d/ (S)-Lactate/ L-Lactic acid
2-Hydroxypropionaldehyde
ic acid/ LL-2,6-Diaminopimelate

eric acid/ Ile
eric acid/ Ile
eric acid/ Ile

utyric acid
utyric acid
utyric acid
obutyric acid/ L-Homocysteine

nine/ (S)-alpha-Amino-1H-imidazole-4-propionic acid
nine/ (S)-alpha-Amino-1H-imidazole-4-propionic acid
nine/ (S)-alpha-Amino-1H-imidazole-4-propionic acid

amic acid
amic acid
amic acid
-semialdehyde
ate
ntanoate
utaminic acid/ Glu
utaminic acid/ Glu
utaminic acid/ Glu

rcaptopropionic acid
rcaptopropionic acid
rcaptopropionic acid

eric acid/ N5-(aminocarbonyl)-L-Ornithine/ Citrulline
eta-hydroxybutyrobetaine/ Vitamin BT/ (S)-Carnitine/ 3-Carboxy-2-hydroxy-N/ N-trimethyl-1-propa
eta-hydroxybutyrobetaine/ Vitamin BT/ (S)-Carnitine/ 3-Carboxy-2-hydroxy-N/ N-trimethyl-1-propa
eta-hydroxybutyrobetaine/ Vitamin BT/ (S)-Carnitine/ 3-Carboxy-2-hydroxy-N/ N-trimethyl-1-propa

ldehyde/ L-Aspartic 4-semialdehyde
/ L-Aspartic acid/ Asp
/ L-Aspartic acid/ Asp
/ L-Aspartic acid/ Asp

moylpropanoic acid/ 2-Aminosuccinamic acid
moylpropanoic acid/ 2-Aminosuccinamic acid
moylpropanoic acid/ 2-Aminosuccinamic acid

cid/ L-Ascorbic acid/ Vitamin C
cid/ L-Ascorbic acid/ Vitamin C

inovaleric acid/ Arginine/ Arg
inovaleric acid/ Arginine/ Arg
inovaleric acid/ Arginine/ Arg

-D
-D
-D

cid/ L-alpha-Alanine
cid/ L-alpha-Alanine
cid/ L-alpha-Alanine
Galactopyranosyl-4-alpha-D-glucopyranose/ Milk sugar
Galactopyranosyl-4-alpha-D-glucopyranose/ Milk sugar
ate

te/ Inosine triphosphate/ Inosine tripolyphosphate
phosphate/ delta3-methyl-3-butenyl diphosphate/ Isopentenyl pyrophosphate/ Isoprenyl pyrophosp
xytricarballylic acid/ 2/ 3-tricarboxylic acid/ 1-Hydroxypropane-1

nate/ 2-Hydroxyethanesulfonic acid/ 2-Hydroxyethane-1-sulfonic acid/ Isethionate

onate/ 2-Hydroxyethanesulfonic acid/ 2-Hydroxyethane-1-sulfonic acid/ Isethionate

cleoside
cleoside
cleoside

monophosphate/ Inosine 5'-monophosphate/ Inosine 5'-phosphate/ 5'-Inosinate/ 5'-Inosinic acid/ 5
monophosphate/ Inosine 5'-monophosphate/ Inosine 5'-phosphate/ 5'-Inosinate/ 5'-Inosinic acid/ 5
monophosphate/ Inosine 5'-monophosphate/ Inosine 5'-phosphate/ 5'-Inosinate/ 5'-Inosinic acid/ 5

ate/ Inosine 5'-diphosphate/ Inosine diphosphate
-6-one/ Purine-6-ol/ 6-Hydroxypurine
-6-one/ Purine-6-ol/ 6-Hydroxypurine
-6-one/ Purine-6-ol/ 6-Hydroxypurine
3-Hydroxypyruvate/ 3-Hydroxypyruvic acid
H/ S-(hydroxymethyl)glutathione/ HM-GSH

ol/ 4-Benzenediol/ Benzene-1/ 4-Dihydroxybenzene/ 1/ 4-diol
le/ sulfide
le/ sulfide
le/ sulfide
ioxide/ H2O2
ioxide/ H2O2
ioxide/ H2O2

rcury
rcury
rcury

anoyl-[acyl-carrier protein]
ic acid/ n-Caproic acid
ic acid/ n-Caproic acid
ic acid/ n-Caproic acid
e A/ trans-Hexadec-2-enoyl-CoA/ trans-2-Hexadecenoyl-CoA/ (2E)-Hexadecenoyl-CoA
acid/ Palmitoleic acid/ hexadecenoic acid/ (9Z)-Hexadecenoic acid
acid/ Palmitoleic acid/ hexadecenoic acid/ (9Z)-Hexadecenoic acid
acid/ Palmitoleic acid/ hexadecenoic acid/ (9Z)-Hexadecenoic acid

id/ Hexadecylic acid/ Cetylic acid/ Hexadecanoic acid
id/ Hexadecylic acid/ Cetylic acid/ Hexadecanoic acid
id/ Hexadecylic acid/ Cetylic acid/ Hexadecanoic acid
ide
ide
ide

hate 3'-triphosphate/ pppGpp
hate 5'-diphosphate/ Guanosine 5'-diphosphate,3'-diphosphate/ gdpdp/ ppGpp

/ G/ 2-Amino-6-hydroxypurine
/ G/ 2-Amino-6-hydroxypurine
/ G/ 2-Amino-6-hydroxypurine
hate
hate
hate
ate/ Guanosine monophosphate/ Guanosine 5'-monophosphate/ Guanylic acid
ate/ Guanosine monophosphate/ Guanosine 5'-monophosphate/ Guanylic acid
ate/ Guanosine monophosphate/ Guanosine 5'-monophosphate/ Guanylic acid
te/ Glyoxylic acid

yacetic acid
yacetic acid
yacetic acid

te/ Betaine
te/ Betaine
te/ Betaine
/
/
/

rol
rol
rol
cid/ sn-Gro-1-P/ Phosphatidyl glycerol/ sn-Glycerol 3-phosphate
cid/ sn-Gro-1-P/ Phosphatidyl glycerol/ sn-Glycerol 3-phosphate
cid/ sn-Gro-1-P/ Phosphatidyl glycerol/ sn-Glycerol 3-phosphate

ne/ 3-propanetriol/ Glycerin
ne/ 3-propanetriol/ Glycerin
ne/ 3-propanetriol/ Glycerin
hosphate/ (2R)-2-Hydroxy-3-(phosphonooxy)-propanal

hate/ Guanosine diphosphate
hate/ Guanosine diphosphate
hate/ Guanosine diphosphate
ysteine/ 5-L-Glutamyl-L-cysteine
l: butyrobetaine]/ gamma-Butyrobetain/ 4-(trimethylammonio)butanoate/ gamma-butyrobetaine [Me
l: butyrobetaine]/ gamma-Butyrobetain/ 4-(trimethylammonio)butanoate/ gamma-butyrobetaine [Me

)
)
ic acid/ Fumaric acid/ Trans-butenedioic acid
ic acid/ Fumaric acid/ Trans-butenedioic acid
ic acid/ Fumaric acid/ Trans-butenedioic acid
ctose)-lysine
ctose)-lysine
acid/ aminic acid/ Methanoic acid/ Formic acid
acid/ aminic acid/ Methanoic acid/ Formic acid
Oxomethane/ Oxomethylene/ Methylene oxide
Oxomethane/ Oxomethylene/ Methylene oxide
te/ Flavin mononucleotide

eotide (reduced form)
dinucleotide/ Riboflavine 5'-adenosine diphosphate

cation/ Iron/ Fe(II)
cation/ Iron/ Fe(II)
cation/ Iron/ Fe(II)
d
d
d

ate/ 2-trans,6-trans-Farnesyl diphosphate/ trans,trans-Farnesyl diphosphate/ FPP
xyethylamine
xyethylamine
xyethylamine
carbinol
carbinol
carbinol

enzoyl-L-serine)-ester/ Enterobactin/ tri-(N-(2,3-dihydroxybenzoyl)-L-serine)-ester
enzoyl-L-serine)-ester/ Enterobactin/ tri-(N-(2,3-dihydroxybenzoyl)-L-serine)-ester

phosphate
eoxyuridine monophosphate/ Deoxyuridine 5'-phosphate/ 2'-Deoxyuridine 5'-phosphate
eoxyuridine monophosphate/ Deoxyuridine 5'-phosphate/ 2'-Deoxyuridine 5'-phosphate
eoxyuridine monophosphate/ Deoxyuridine 5'-phosphate/ 2'-Deoxyuridine 5'-phosphate
phosphate
ate/ Thymidine 5'-triphosphate/ TTP
ate/ Deoxythymidine 5'-phosphate/ Thymidylic acid/ 5'-Thymidylic acid/ Thymidine monophosphate
ate/ Deoxythymidine 5'-phosphate/ Thymidylic acid/ 5'-Thymidylic acid/ Thymidine monophosphate
ate/ Deoxythymidine 5'-phosphate/ Thymidylic acid/ 5'-Thymidylic acid/ Thymidine monophosphate

nose/ dTDP-4-oxo-6-deoxy-L-mannose
-D-glucose
hate
rate/ D-Tartaric acid/ (S,S)-Tartaric acid
rate/ D-Tartaric acid/ (S,S)-Tartaric acid
rate/ D-Tartaric acid/ (S,S)-Tartaric acid

-Sorbit/ Sorbite/ D-Glucitol/ Glucitol/ Clucitol/ L-gulitol
-Sorbit/ Sorbite/ D-Glucitol/ Glucitol/ Clucitol/ L-gulitol
ypropanoic acid
ypropanoic acid

-benzenediol/ 4-(2-Aminoethyl)benzene-1,2-diol/ 3,4-Dihydroxyphenethylamine/ 2-(3,4-Dihydroxyp
-benzenediol/ 4-(2-Aminoethyl)benzene-1,2-diol/ 3,4-Dihydroxyphenethylamine/ 2-(3,4-Dihydroxyp
coenzyme A
rier protein]/ Dodecanoyl-[acp]/ Fatty Acid C12 ACP/ Lauroyl ACP

Lauric acid/ Dodecanoic acid
Lauric acid/ Dodecanoic acid
Lauric acid/ Dodecanoic acid
thio)butyric acid
thio)butyric acid
thio)butyric acid

hosphate
Carubinose
Carubinose

cid/ (R)-Malate/ D-Malic acid
cid/ (R)-Malate/ D-Malic acid
acid/ D-2-Hydroxypropanoic acid/ D-2-Hydroxypropionic acid
acid/ D-2-Hydroxypropanoic acid/ D-2-Hydroxypropionic acid
acid/ D-2-Hydroxypropanoic acid/ D-2-Hydroxypropionic acid
phosphate/ 2'-Deoxyinosine 5'-triphosphate
phosphoric acid/ PPi
osphate
osphate
osphate
phate/ delta2-Isopentenyl diphosphate/ Prenyl diphosphate/ dimethylallyl pyrophosphate

l thioether
l thioether
l thioether
e
droxyacetone/ 3-Dihydroxy-2-propanone/ 3-Dihydroxypropan-2-one
droxyacetone/ 3-Dihydroxy-2-propanone/ 3-Dihydroxypropan-2-one

sphate/ 7' 8-dihydronepterin 3'-phosphate/ 2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)
-(D-erythro-1,2,3-trihydroxypropyl)-7,8-dihydropteridine/ 7,8-dihydronepterin

phosphate/ 2'-Deoxyinosine 5'-diphosphate
te
'-triphosphate/ Deoxyguanosine 5'-triphosphate/ Deoxyguanosine triphosphate
'-monophosphate/ 2'-Deoxyguanosine 5'-phosphate/ Deoxyguanylic acid/ Deoxyguanosine monop
'-monophosphate/ 2'-Deoxyguanosine 5'-phosphate/ Deoxyguanylic acid/ Deoxyguanosine monop
'-monophosphate/ 2'-Deoxyguanosine 5'-phosphate/ Deoxyguanylic acid/ Deoxyguanosine monop

te/ 2-phosphoglyceric acid

lutaminic acid/ D-2-Aminoglutaric acid/ Glu

uronate/ GlcA
uronate/ GlcA
uronate/ GlcA
/ Robinson ester/ alpha-D-Glucose 6-phosphate
/ Robinson ester/ alpha-D-Glucose 6-phosphate
/ Robinson ester/ alpha-D-Glucose 6-phosphate
lucose 1-phosphate/ Glucose 1-phosphate
lucose 1-phosphate/ Glucose 1-phosphate
lucose 1-phosphate/ Glucose 1-phosphate
a-D-Glucose/ Grape sugar/ Dextrose/ Glucose
a-D-Glucose/ Grape sugar/ Dextrose/ Glucose
a-D-Glucose/ Grape sugar/ Dextrose/ Glucose
phate
phate
phate

o-2-deoxy-D-glucose/ GlcN
o-2-deoxy-D-glucose/ GlcN
luco-hexonic acid/ Dextronic Acid
luco-hexonic acid/ Dextronic Acid
cosaccharic acid/ D-Glucaric acid/ D-Saccharic acid
cosaccharic acid/ D-Glucaric acid/ D-Saccharic acid
'-diphosphate
yranose/ D-Galacturonic acid
yranose/ D-Galacturonic acid
Galactose
Galactose
Galactose

ctaric acid
ctaric acid

oric acid/ Neuberg ester/ beta-D-Fructose 6-phosphate
oric acid/ Neuberg ester/ beta-D-Fructose 6-phosphate
oric acid/ Neuberg ester/ beta-D-Fructose 6-phosphate
e/ Fructofuranose 1-phosphate
hate/ fructose diphosphate/ beta-D-fructofuranose-1,6-diphosphate/ fbp
/ D-Arabino-hexulose
/ D-Arabino-hexulose

se
glycerol 3-phosphate/ D-erythro-Imidazole-glycerol phosphate

eoxyuridine
eoxyuridine
eoxyuridine

emihydrate/ 2'-Deoxyguanosine
emihydrate/ 2'-Deoxyguanosine
emihydrate/ 2'-Deoxyguanosine

dA
dA
dA

r protein]/ Decanoyl-[acp]
c acid/ decylate/ decoate/ caprate/ n-decanoate/ n-decoate/ caprinate/ decanoate/ n-caprate/ capr
c acid/ decylate/ decoate/ caprate/ n-decanoate/ n-decoate/ caprinate/ decanoate/ n-caprate/ capr
c acid/ decylate/ decoate/ caprate/ n-decanoate/ n-decoate/ caprinate/ decanoate/ n-caprate/ capr

propionic acid
propionic acid
propionic acid
osphate/ Deoxycytidine triphosphate/ 2'-Deoxycytidine 5'-triphosphate
eoxycytidine monophosphate/ Deoxycytidylate/ 2'-Deoxycytidine 5'-monophosphate
eoxycytidine monophosphate/ Deoxycytidylate/ 2'-Deoxycytidine 5'-monophosphate
eoxycytidine monophosphate/ Deoxycytidylate/ 2'-Deoxycytidine 5'-monophosphate
osphate/ 2'-Deoxycytidine 5'-diphosphate
droxybutyrobetaine/ Carnitine/ 3-Hydroxy-4-trimethylammoniobutanoate
droxybutyrobetaine/ Carnitine/ 3-Hydroxy-4-trimethylammoniobutanoate

droxybutyrobetaine/ Carnitine/ 3-Hydroxy-4-trimethylammoniobutanoate
'-triphosphate/ Deoxyadenosine 5'-triphosphate/ Deoxyadenosine triphosphate

'-phosphate/ 2'-Deoxyadenosine 5'-monophosphate/ Deoxyadenylic acid/ Deoxyadenosine monop
'-phosphate/ 2'-Deoxyadenosine 5'-monophosphate/ Deoxyadenylic acid/ Deoxyadenosine monop
'-phosphate/ 2'-Deoxyadenosine 5'-monophosphate/ Deoxyadenylic acid/ Deoxyadenosine monop

a
a
a
acid
acid
acid
'-diphosphate
thenate

ofuranosyl-2(1H)-pyrimidinone/ 1-beta-ribofuranosylosine/ cytosine riboside
ofuranosyl-2(1H)-pyrimidinone/ 1-beta-ribofuranosylosine/ cytosine riboside
ofuranosyl-2(1H)-pyrimidinone/ 1-beta-ribofuranosylosine/ cytosine riboside
CRIS 2905/ Cysteinylglycine [MeSH: cysteinylglycine]/ cysteinyl-glycine [MeSH: cysteinyl-glycine]
CRIS 2905/ Cysteinylglycine [MeSH: cysteinylglycine]/ cysteinyl-glycine [MeSH: cysteinyl-glycine]
CRIS 2905/ Cysteinylglycine [MeSH: cysteinylglycine]/ cysteinyl-glycine [MeSH: cysteinyl-glycine]

recursor Z

ate/ Cytidine triphosphate
enoyl-CoA/ But-2-enoyl-CoA/ trans-But-2-enoyl-CoA
)but-2-enoate
)but-2-enoate

H

onic anhydride
onic anhydride
onic anhydride

sphate/ Cytidylic acid/ 3'-Cytidylic Acid/ Cytidine-2'(3')-monophosphoric acid/ Cytidine-2[(3[)-monop
sphate/ Cytidylic acid/ 3'-Cytidylic Acid/ Cytidine-2'(3')-monophosphoric acid/ Cytidine-2[(3[)-monop
sphate/ Cytidylic acid/ 3'-Cytidylic Acid/ Cytidine-2'(3')-monophosphoric acid/ Cytidine-2[(3[)-monop
tricarballylic acid/ 2/ 2-Hydroxy-1/ 3-propanetricarboxylic acid
tricarballylic acid/ 2/ 2-Hydroxy-1/ 3-propanetricarboxylic acid
tricarballylic acid/ 2/ 2-Hydroxy-1/ 3-propanetricarboxylic acid
cyl-carrier protein] (n-C14:1)/ Tetradecenoyl-ACP (n-C14:1ACP)
yl-carrier protein] (n-C18:1)/ Octadecenoyl-ACP (n-C18:1ACP)
cyl-carrier protein] (n-C16:1)/ Hexadecenoyl-ACP (n-C16:1ACP)

arboxylic acid/ (Z)-1-Propene-1,2,3-tricarboxylic acid/ cis-Aconitic acid
icarboxylate/ cis-2-Methylaconitate

ol/ 1,2-Diacyl-sn-glycero-3-cytidine-5'-diphosphate/ CDPdiacylglycerol
DP-1,2-diacylglycerol/ 1,2-Diacyl-sn-glycero-3-cytidine-5'-diphosphate
-3-cytidine-5'-diphosphate/ CDPdiacylglycerol/ CDP-1,2-diacylglycerol
,2-Diacyl-sn-glycero-3-cytidine-5'-diphosphate/ CDP-1,2-diacylglycerol
ol/ CDPdiacylglycerol/ 1,2-Diacyl-sn-glycero-3-cytidine-5'-diphosphate
-3-cytidine-5'-diphosphate/ CDP-1,2-diacylglycerol/ CDPdiacylglycerol
ol/ CDPdiacylglycerol/ 1,2-Diacyl-sn-glycero-3-cytidine-5'-diphosphate
te/ Cytidine diphosphate
-glycero-3-phospho)-sn-glycerol/ Diphosphatidylglycerol
-glycero-3-phospho)-sn-glycerol/ Diphosphatidylglycerol
ol/ 1',3'-Bis(1,2-diacyl-sn-glycero-3-phospho)-sn-glycerol
-glycero-3-phospho)-sn-glycerol/ Diphosphatidylglycerol
ol/ 1',3'-Bis(1,2-diacyl-sn-glycero-3-phospho)-sn-glycerol

ol/ 1',3'-Bis(1,2-diacyl-sn-glycero-3-phospho)-sn-glycerol
ol/ 1',3'-Bis(1,2-diacyl-sn-glycero-3-phospho)-sn-glycerol

c phosphate/ Cyclic adenylic acid/ 3',5'-Cyclic AMP/ Adenosine 3',5'-phosphate/ Cyclic AMP

nate/ 1-(Indol-3-yl)glycerol 3-phosphate/ (3-Indolyl)-glycerol phosphate
-[acyl-carrier protein]
cid/ Butanoic acid
cid/ Butanoic acid
cid/ Butanoic acid

Vitamin H/ Coenzyme R
Vitamin H/ Coenzyme R
Vitamin H/ Coenzyme R
3-/ Hydrogencarbonate
d/ 3-Aminopropanoate
d/ 3-Aminopropanoate
d/ 3-Aminopropanoate

phate/ 5'-adenylate triphosphate

acid/ o-Aminobenzoic acid/ Vitamin L1/ 2-Aminobenzoate
nosphate/ Adenylic acid/ Adenylate/ 5'-AMP/ 5'-Adenylic acid/ 5'-Adenosine monophosphate/ Aden
nosphate/ Adenylic acid/ Adenylate/ 5'-AMP/ 5'-Adenylic acid/ 5'-Adenosine monophosphate/ Aden
nosphate/ Adenylic acid/ Adenylate/ 5'-AMP/ 5'-Adenylic acid/ 5'-Adenosine monophosphate/ Aden

e/ D-Ribose-5-phosphate/ Ribose 5-phosphate
e/ D-Ribose-5-phosphate/ Ribose 5-phosphate

e/ D-Ribose-5-phosphate/ Ribose 5-phosphate
D-Ribose 1-phosphate
hate/ alpha-D-Galactose 1-phosphate
hate/ alpha-D-Galactose 1-phosphate
hate/ alpha-D-Galactose 1-phosphate
niol
lyoxyldiureide/ Ureidohydantoin/ Paxyl/ Hemocane
lyoxyldiureide/ Ureidohydantoin/ Paxyl/ Hemocane
dine
dine
dine
hore (Fe3 -scavenging molecule)

ibose/ adenosine diphosphate ribose/ adenine-diphosphate-ribose

glucose
nno-heptose
hate

e

ylate/ Phosphoadenosine phosphate
syladenine/ Adenocard/ 9-B-D-ribofuranosyl-9H-purin-6-amine/ rA/ Adenine riboside
syladenine/ Adenocard/ 9-B-D-ribofuranosyl-9H-purin-6-amine/ rA/ Adenine riboside
syladenine/ Adenocard/ 9-B-D-ribofuranosyl-9H-purin-6-amine/ rA/ Adenine riboside
mine/ Adeninimine/ Vitamin B4/ 6-Aminopurine
mine/ Adeninimine/ Vitamin B4/ 6-Aminopurine
mine/ Adeninimine/ Vitamin B4/ 6-Aminopurine
3'-acyl)-glycerol/ 3-sn-phosphatidyl-1'-(3'-acyl)-glycerol
3'-acyl)-glycerol/ 3-sn-phosphatidyl-1'-(3'-acyl)-glycerol
3'-acyl)-glycerol/ 3-sn-phosphatidyl-1'-(3'-acyl)-glycerol
3'-acyl)-glycerol/ 3-sn-phosphatidyl-1'-(3'-acyl)-glycerol
3'-acyl)-glycerol/ 3-sn-phosphatidyl-1'-(3'-acyl)-glycerol
(3'-acyl)-glycerol/ X-3-phosphatidyl-1'-(3'-acyl)-glycerol
3'-acyl)-glycerol/ 3-sn-phosphatidyl-1'-(3'-acyl)-glycerol

3-oxobutyroyl-CoA/ 3-acetoacetyl-CoA/ 3-ketobutyroyl-CoA/ Acetoacetyl coenzyme A/ 3-oxobutan

a-Ketobutyric acid/ 3-Oxobutanoic acid

a-Ketobutyric acid/ 3-Oxobutanoic acid
Vinegar acid/ Methanecarboxylic acid/ Acetic acid/ Ethanoic acid
Vinegar acid/ Methanecarboxylic acid/ Acetic acid/ Ethanoic acid
Vinegar acid/ Methanecarboxylic acid/ Acetic acid/ Ethanoic acid
laldehyde/ Aceteldehyde/ Acetic aldehyde/ Ethyl aldehyde/ Aldehyde/ Ethanal
laldehyde/ Aceteldehyde/ Acetic aldehyde/ Ethyl aldehyde/ Aldehyde/ Ethanal
laldehyde/ Aceteldehyde/ Acetic aldehyde/ Ethyl aldehyde/ Aldehyde/ Ethanal
onate

Dihydrofolate/ Dihydrofolic acid

e 6-phosphate
cid/ D-gluconate 6-phosphate
dihydropterin pyrophosphate
dihydropterin

ne/ 5-Phospho-D-ribosylamine/ 5-Phosphoribosyl-1-amine
yrophosphate/ 5-Phosphoribosyl diphosphate/ PRPP
3-phosphoshikimate/ 3-Phosphate-shikimate
bose
bose
bose
sine/ 5'-Methylthioadenosine/ Methylthioadenosine/ 5'-Deoxy-5'-(methylthio)adenosine
folate/ N5-methyl-5,6,7,8-tetrahydrofolate/ 5-methyl-5,6,7,8-tetrahydrofolate
-tetrahydrofolic acid/ Folinic acid/ 5-formyl-tetrahydrofolate
-5-formamido-4-imidazolecarboxamide/ 5'-Phosphoribosyl-5-formamido-4-imidazolecarboxamide/

gluconate/ 5-Dehydrogluconate/ 5-keto-D-gluconate
gluconate/ 5-Dehydrogluconate/ 5-keto-D-gluconate
ino)-2,4-(1H,3H)-pyrimidinedione 5'-phosphate
o-2,4(1H,3H)-pyrimidinedione 5'-phosphate
Amino-4-oxovaleric acid
syl)-5-amino-4-imidazolecarboxylate/ 1-(5'-Phosphoribosyl)-5-amino-4-imidazolecarboxylate/ 1-(5'-
arbamoyl-5-aminoimidazole/ 1-(5'-Phosphoribosyl)-5-amino-4-imidazolecarboxamide/ 5'-Phosphor
ide/ AIR/ 1-(5'-Phosphoribosyl)-5-aminoimidazole/ 5'-Phosphoribosyl-5-aminoimidazole/ 1-(5-Phos
ylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imidazolecarboxamide/ N-(5'-Phospho-D-1'-ribulosy
acid/ (6S)-THFA/ Tetrahydrofolic acid/ THF/ Tetrahydrofolate/ (6S)-Tetrahydrofolate
trahydrofolate/ N5,N10-methylene-5,6,7,8-tetrahydrofolate/ 5,10-methylene-5,6,7,8-tetrahydrofola
drofolate/ N5,N10-methenyl-5,6,7,8-tetrahydrofolate/ N5,N10-methenyl-tetrahydrofolate/ (6R)-5,10
te

ono-oxyethyl)-thiazole/ 4-methyl-5-(b-hydroxyethyl)thiazole phosphate

methylthiazole/ 4-Methyl-5-(2'-hydroxyethyl)-thiazole
e/ 2-Oxoisocaproate
cetaldehyde
cetaldehyde

oxylic acid/ Hydroxybenzoic acid/ 4-Hydroxybenzoic acid
oic acid/ 4-Aminobutylate/ 4-Aminobutyric acid/ gamma-Aminobutyric acid/ (4-Aminobutyl)guanidi
oic acid/ 4-Aminobutylate/ 4-Aminobutyric acid/ gamma-Aminobutyric acid/ (4-Aminobutyl)guanidi
oic acid/ 4-Aminobutylate/ 4-Aminobutyric acid/ gamma-Aminobutyric acid/ (4-Aminobutyl)guanidi
Aminobenzoic acid/ 4-Aminobenzoate/ ABEE/ p-Aminobenzoic acid/ PABA
ino-2-methyl-5-pyrimidinemethanol

ethyl-2-methylpyrimidine/ 4-amino-2-methyl 5-hydroxymethylpyrimidine phosphate/ HMP-P

5-amino-2,6-dihydroxypyrimidine/ 5-amino-6-ribitylamino-2,4(1H,3H)-pyrimidinedione
hate/ Uridine 3'-phosphate
hate/ Uridine 3'-phosphate
d/ 3-sulphino-L-alanine/ 3-Sulfinoalanine/ L-Cysteine sulfinic acid
ruvic acid/ 3-Phosphonooxypyruvate/ 3-Phosphonooxypyruvic acid
erate/ 3-Phospho-D-glyceroyl phosphate/ 1,3-bisphosphoglycerate/ (R)-2-Hydroxy-3-(phosphonoox
hate/ 3-Phosphoglycerate/ 3-phosphoglyceric acid
e 5'-phosphosulfate/ 3'-Phospho-5-adenylyl sulfate/ PAPS

acp]

acp]

[acp]

p]

ha-Ketovaline/ 2-Oxo-3-methylbutanoate/ 2-Oxoisopentanoate/ 3-Methyl-2-oxobutyric acid/ 2-Ket
cid/ 3-Hydroxypropionic acid/ 3-Hydroxypropanoic acid/ 3-Hydroxypropionate/ 3-Hydroxyisobutyra
cid/ 3-Hydroxypropionic acid/ 3-Hydroxypropanoic acid/ 3-Hydroxypropionate/ 3-Hydroxyisobutyra

ate/ 3'-Guanylic acid/ Guo-3'-P/ Gp
ate/ 3'-Guanylic acid/ Guo-3'-P/ Gp
-octonate 8-phosphate
tulosonate/ KDO/ 2-Dehydro-3-deoxy-D-octonate/ 3-Deoxyoctulosonic acid

Dehydroquinic acid/ 5-Dehydroquinic acid
/ cytidine-3'-monophosphate
/ cytidine-3'-monophosphate
boxypentanoate/ (2S)-2-Isopropyl-3-oxosuccinate
Isopropylmalic acid/ 3-Carboxy-3-hydroxy-isocaproate/ 3-Carboxy-3-hydroxyisocaproate
D-threo-hydroxy-3-carboxy-isocaproate
denosine monophosphate/ AMP 3'-phosphate/ Adenosine-3'-monophosphate/ Adenosine 3'-phosp
denosine monophosphate/ AMP 3'-phosphate/ Adenosine-3'-monophosphate/ Adenosine 3'-phosp
acetaldehyde/ Protocatechuatealdehyde
acetaldehyde/ Protocatechuatealdehyde

sphate
vate/ p-Hydroxyphenylpyruvic acid

hosphate (n-C14:0)
hosphate (n-C14:0)
hosphate (n-C14:1)
hosphate (n-C14:1)

/ 2-phosphoglycolic acid
l 2,4-cyclodiphosphate
Oxoglutaric acid/ 2-Ketoglutaric acid/ alpha-Ketoglutaric Acid
Oxoglutaric acid/ 2-Ketoglutaric acid/ alpha-Ketoglutaric Acid
Oxoglutaric acid/ 2-Ketoglutaric acid/ alpha-Ketoglutaric Acid
Oxobutyric acid/ 2-Oxobutyrate/ 2-Oxobutanoic acid/ alpha-Ketobutyrate
-4-phosphobutyrate

hosphate (n-C18:0)
hosphate (n-C18:0)
hosphate (n-C18:1)
hosphate (n-C18:1)

ydroxymethylpyrimidine pyrophosphate/ HMP-PP

e
phosphate (n-C16:0)
phosphate (n-C16:0)
phosphate (n-C16:1)
phosphate (n-C16:1)
phosphate (n-C12:0)
phosphate (n-C12:0)

phate

-phospho-D-gluconate/ 6-Phospho-2-dehydro-3-deoxy-D-gluconate/ 2-Keto-3-deoxy-6-phosphoglu
uconate
uconate
uconate

3'-triphosphate/ 6-(L-erythro-1,2-Dihydroxypropyl 3-triphosphate)-7,8-dihydropterin/ 2-Amino-4-hy
hoglycerol/ L-1-Lysophosphatidylglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
lglycerol/ 2-acyl-glycerophosphoglycerol
lglycerol/ 2-acyl-glycerophosphoglycerol
lglycerol/ 2-acyl-glycerophosphoglycerol
lglycerol/ 2-acyl-glycerophosphoglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
hoglycerol/ L-1-Lysophosphatidylglycerol
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
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lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine
lethanolamine/ 2-acyl-glycerophosphoethanolamine

d
acid/ 2,3-Diaminopropanoate/ 2,3-Diaminopropanoic acid/ 2,3-Diaminopropionate
acid/ 2,3-Diaminopropanoate/ 2,3-Diaminopropanoic acid/ 2,3-Diaminopropionate

monophosphate
monophosphate
pyridine-2,6-dicarboxylate/ delta1-Piperidine-2,6-dicarboxylate
'-phosphoribosyl)acetamidine/ 1-(5'-Phosphoribosyl)-N-formylglycinamidine/ 5'-Phosphoribosyl-N-
D-glycerate/ alpha-Mannosylglycerate
D-glycerate/ alpha-Mannosylglycerate
phosphate (n-C14:0)
phosphate (n-C14:0)
phosphate (n-C14:1)
phosphate (n-C14:1)
boxylate/ L-1-Pyrroline-5-carboxylate/ 1-Pyrroline-5-carboxylic acid
phosphate (n-C18:0)
phosphate (n-C18:0)
phosphate (n-C18:1)
phosphate (n-C18:1)

phosphate (n-C16:0)
phosphate (n-C16:0)
phosphate (n-C16:1)
phosphate (n-C16:1)
phosphate (n-C12:0)
phosphate (n-C12:0)
D-myo-Inositol 1-phosphate/ L-myo-Inositol 1-phosphate/ myo-Inositol 1-phosphate/ 1D-myo-Inos

oglycerol/ L-2-lysophosphatidylglycerol
oglycerol/ L-2-lysophosphatidylglycerol
oglycerol/ L-2-lysophosphatidylglycerol
glycerol/ 1-acyl-glycerophosphoglycerol
oglycerol/ L-2-lysophosphatidylglycerol
glycerol/ 1-acyl-glycerophosphoglycerol
glycerol/ 1-acyl-glycerophosphoglycerol
phosphoethanolamine/ L-2-Lysophosphatidylethanolamine
phosphoethanolamine/ L-2-Lysophosphatidylethanolamine
phosphoethanolamine/ L-2-Lysophosphatidylethanolamine
phosphoethanolamine/ L-2-Lysophosphatidylethanolamine
phosphoethanolamine/ L-2-Lysophosphatidylethanolamine
phosphoethanolamine/ L-2-Lysophosphatidylethanolamine
lethanolamine/ 1-Acyl-sn-glycero-3-phosphoethanolamine

uMdap
uMdapDala
hydrous-N-Acetylmuramic acid
:anediamine/ Pentamethylenediamine
:anediamine/ Pentamethylenediamine
:anediamine/ Pentamethylenediamine

ıosphatidate/ 3-sn-Phosphatidate/ 1,2-Diacyl-sn-glycerol 3-phosphate
ıosphatidate/ 3-sn-Phosphatidate/ 1,2-Diacyl-sn-glycerol 3-phosphate
phatidic acid/ 1,2-Diacyl-sn-glycerol 3-phosphate/ 3-sn-Phosphatidate
phatidic acid/ 1,2-Diacyl-sn-glycerol 3-phosphate/ 3-sn-Phosphatidate
iacyl-sn-glycerol 3-phosphate/ 3-sn-Phosphatidate/ Phosphatidic acid
iacyl-sn-glycerol 3-phosphate/ 3-sn-Phosphatidate/ Phosphatidic acid
l 3-phosphate/ Phosphatidate/ Phosphatidic acid/ 3-sn-Phosphatidate
l 3-phosphate/ Phosphatidate/ Phosphatidic acid/ 3-sn-Phosphatidate
l 3-phosphate/ Phosphatidate/ Phosphatidic acid/ 3-sn-Phosphatidate
l 3-phosphate/ Phosphatidate/ Phosphatidic acid/ 3-sn-Phosphatidate
iacyl-sn-glycerol 3-phosphate/ 3-sn-Phosphatidate/ Phosphatidic acid
iacyl-sn-glycerol 3-phosphate/ 3-sn-Phosphatidate/ Phosphatidic acid
phatidic acid/ 1,2-Diacyl-sn-glycerol 3-phosphate/ 3-sn-Phosphatidate
phatidic acid/ 1,2-Diacyl-sn-glycerol 3-phosphate/ 3-sn-Phosphatidate
1,2-Diacylglycerol
1,2-Diacylglycerol
1,2-Diacylglycerol
1,2-Diacylglycerol
1,2-Diacylglycerol
1,2-Diacylglycerol
-1,2-Diacylglycerol
-1,2-Diacylglycerol
1,2-Diacylglycerol
1,2-Diacylglycerol
1,2-Diacylglycerol
1,2-Diacylglycerol
-1,2-Diacylglycerol
-1,2-Diacylglycerol
N1-(5-Phospho-D-ribosyl)-ATP
ɔ

(S)-Propylene glycol/ L-1,2-propanediol

(S)-Propylene glycol/ L-1,2-propanediol
ihydroorotic acid/ Dihydro-L-orotic acid/ (S)-4/ 5-Dihydroorotate
ntanoate/ 2-oxo-3-methylpentanoate/ alpha-keto-beta-methylvalerate/ (S)-2-oxo-3-methylpentano

CoA

-CoA

-CoA
oA/ (S)-3-Hydroxybutyryl-CoA
yl-3-oxobutanoate

-5-amino-4-(N-succinocarboxamide)-imidazole/ 1-(5'-Phosphoribosyl)-4-(N-succinocarboxamide)-

(R)-Propylene glycol/ D-1,2-propanediol
henic acid/ D-Pantothenate
henic acid/ D-Pantothenate
henic acid/ D-Pantothenate
/ Pantoic acid
te/ Glyceric acid
te/ Glyceric acid
te/ Glyceric acid
ecanoyl-[acyl-carrier protein]/ HMA/ beta-Hydroxymyristyl-[acyl-carrier protein]
oyl-[acyl-carrier protein]

yl-[acp]/ D-3-Hydroxyhexanoyl-[acp]/ D-3-Hydroxyhexanoyl-[acyl-carrier protein]
anoyl-[acp]/ D-3-Hydroxydodecanoyl-[acp]/ D-3-Hydroxydodecanoyl-[acyl-carrier protein]
noyl-[acyl-carrier protein]

ylvalerate
valeric acid/ (R)-2,3-Dihydroxy-isovalerate
cyl-carrier protein]

10E)-3,7,11,15-Tetramethylhexadeca-2,6,10,14-tetraen-1-yl diphosphate

AcGlc-enolpyruvate

lcNac-MurNac-pentapeptide] unit

carboxylic acid/ crodacid/ Myristate/ hystrene 9014/ n-Tetradecanoic Acid
carboxylic acid/ crodacid/ Myristate/ hystrene 9014/ n-Tetradecanoic Acid
carboxylic acid/ crodacid/ Myristate/ hystrene 9014/ n-Tetradecanoic Acid

nyl-glycine
nyl-glycine
nyl-glycine

canoyl-[acyl-carrier protein]/ (3R)-3-Hydroxypalmitoyl-[acyl-carrier protein]

d
d
d

erine
erine
erine
erine
erine
erine
erine
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
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pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate
pho-sn-glycerol 3'-phosphate

acid/ N-Succinyl-epsilon-keto-L-aminopimelic acid

1,2,3,4,5,6-hexakisphosphate/ 1D-myo-Inositol 1,2,3,4,5,6-hexakisphosphate
sugar/ Bios I
sugar/ Bios I
sugar/ Bios I

naminium
naminium
naminium

hate

5'-Inosine monophosphate
5'-Inosine monophosphate
5'-Inosine monophosphate

eSH: gamma-butyrobetaine]/ N-Trimethyl-gamma-aminobutyric acid/ 4-Butyrobetaine/ Deoxycarnit

eSH: gamma-butyrobetaine]/ N-Trimethyl-gamma-aminobutyric acid/ 4-Butyrobetaine/ Deoxycarnit

e/ Deoxythymidylic acid/ Thymidylate
e/ Deoxythymidylic acid/ Thymidylate
e/ Deoxythymidylic acid/ Thymidylate

henyl)ethylamine

henyl)ethylamine

hosphate
hosphate
hosphate

ynate/ Decanoic acid
ynate/ Decanoic acid
ynate/ Decanoic acid

hosphate
hosphate
hosphate

/ Glycine, N-cysteinyl/ 19246-18-5/ Cys-Gly [MeSH: Cys-Gly]/ BRN 1724689/ L-Cysteinylglycine
/ Glycine, N-cysteinyl/ 19246-18-5/ Cys-Gly [MeSH: Cys-Gly]/ BRN 1724689/ L-Cysteinylglycine
/ Glycine, N-cysteinyl/ 19246-18-5/ Cys-Gly [MeSH: Cys-Gly]/ BRN 1724689/ L-Cysteinylglycine

phosphoric acid
phosphoric acid
phosphoric acid

osine 5'-phosphate
osine 5'-phosphate
osine 5'-phosphate

oyl-CoA

5-Formamido-1-(5-phosphoribosyl)imidazole-4-carboxamide

Phosphoribosyl)-5-amino-4-carboxyimidazole/ 5'-Phosphoribosyl-4-carboxy-5-aminoimidazole/ 1-(
ribosyl-5-amino-4-imidazolecarboxamide/ AICAR/ 5'-Phospho-ribosyl-5-amino-4-imidazole carboxa
pho-D-ribosyl)-5-aminoimidazole
lformimino)-5-amino-1-(5''-phospho-D-ribosyl)-4-imidazolecarboxamide/ Phosphoribulosyl-formimi

te
-methenyltetrahydrofolate

ne
ne
ne

‹y)-1-monoanhydride with phosphoric propanoic acid

›valine/ 2-Keto-3-methylbutyric acid
ate/ 3-Hydropropenoate/ Hydracrylic acid/ 3-Hydropropionic acid
ate/ 3-Hydropropenoate/ Hydracrylic acid/ 3-Hydropropionic acid

hate
hate

uconate

droxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate/ 6-[(1S,2R)-1,2-Dihydroxy-3-

formylglycinamidine/ 5'-Phosphoribosylformylglycinamidine

itol 1-monophosphate/ 1L-myo-Inositol 1-phosphate midazolecarboxamide / 5-(5-Phospho-D-ribosylaminoformimino)-1-(5-phosphoribosyl)-imidazole-4-

ate/ ketoisoleucine/ alpha-oxo-beta-methylvalerate

5-aminoimidazole/ 5'-Phosphoribosyl-4-(N-succinocarboxamide)-5-aminoimidazole

ine [MeSH: deoxycarnitine]/ gamma-Butyrobetain [German]/ Actinine/ 4-(N-Trimethylamino)butyrat

ine [MeSH: deoxycarnitine]/ gamma-Butyrobetain [German]/ Actinine/ 4-(N-Trimethylamino)butyrat

Dimethylbenzimidazolyl-Co-5'-deoxy-5'-adenosylcobamide/ 5'-Deoxy-5'-adenosyl-5/ 6-dimethylben

Dimethylbenzimidazolyl-Co-5'-deoxy-5'-adenosylcobamide/ 5'-Deoxy-5'-adenosyl-5/ 6-dimethylben
Dimethylbenzimidazolyl-Co-5'-deoxy-5'-adenosylcobamide/ 5'-Deoxy-5'-adenosyl-5/ 6-dimethylben

5'-Phosphoribosyl)-4-carboxy-5-aminoimidazole/ 5'-Phosphoribosyl-5-amino-4-imidazolecarboxyla
amide/ 5-Aminoimidazole-4-carboxamide ribotide

ino-AICAR-phosphate

triphosphooxypropyl]-7,8-dihydropterin/ dihydroneopterin triphosphate/ H2-neopterin triphosphate

-carboxamide/ 5-[(5-Phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)in

te
te

zimidazolyl)cobamide coenzyme/ 6-dimethylbenzimidazolylcobamide/ 5'-Deoxy-5'-adenosyl vitami

zimidazolyl)cobamide coenzyme/ 6-dimethylbenzimidazolylcobamide/ 5'-Deoxy-5'-adenosyl vitami

zimidazolyl)cobamide coenzyme/ 6-dimethylbenzimidazolylcobamide/ 5'-Deoxy-5'-adenosyl vitami

ıte

nidazole-4-carboxamide/ N-(5'-Phospho-D-ribosylformimino)-5-amino-1-(5''-phospho-D-ribosyl)-4-i