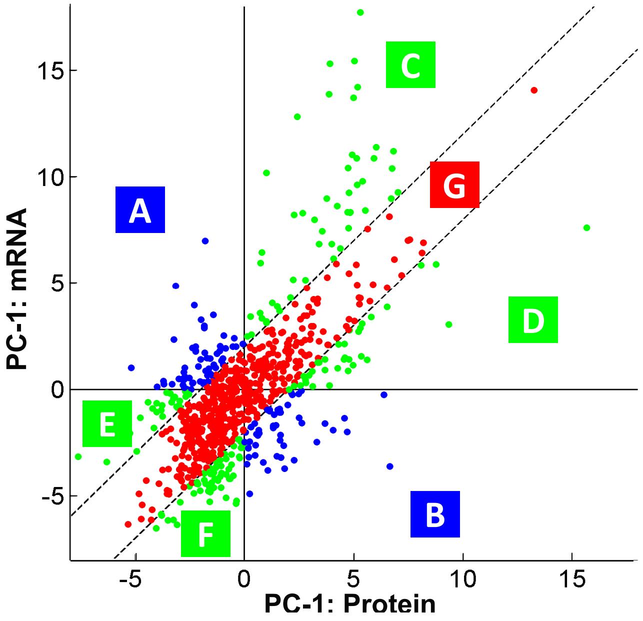
Table S1. List of genes with probable divergent mRNA-protein behavior discovered by PCA

The list shows only data for which at least two unique peptide identifications in mass spectrometry data are available. Please refer to supplementary tables S2 and S3 for complete dataset including proteins with single peptide hits and concordant mRNA-protein behavior.

Column headings

Gene Name:	SCO number from Sanger annotation
Abb.:	Gene abbreviation from Sanger, KEGG, ScoCyc annotations
Category:	Gene category from Sanger annotation
Annotation:	Gene function from Sanger annotation
UPC:	Number of unique peptide count supporting protein identification
TP-m:	Number of time points with mRNA data available
TP-p:	Number of time points with protein data available
PC1 - m:	PCA 1 value from mRNA data
PC2 - m:	PCA 2 value from mRNA data
PC1 - p:	PCA 1 value from protein data
PC2 - p:	PCA 2 value from protein data

Set categories shown in this Table and Tables S2, S3 are defined based on mRNA-protien divergence trends shown below with reference to Figure 4 (genes in set G – those with mRNA-protein concordance – are not shown in Table S1; refer to Tables S2, S3 for complete dataset)



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Gene Name	Abb.	Category	Annotation	UPC	TP-m	TP-p	PC1-m	PC2-m	PC1-p	PC2-p
			Genes in Set A							
SCO1116		Conserved in organism other than Escherichia coli	hypothetical protein	4	8	8	0.27	-0.83	-1.87	0.77
SCO1441	*ribAB*	Riboflavin	3,4-dihydroxy-2-butanone 4-phosphate synthase	2	8	4	1.45	0.22	-0.99	1.17
SCO1484	*pyrAA*	Pyrimidine ribonucleotide biosynthesis	carbamoyl-phosphate synthase, pyrimidine-specific	2	8	4	2.02	1.89	-2.23	-0.39
SCO1793		Gram +ve exported/lipoprotein	hypothetical protein "hypothetical protein (putati	6	8	8	1.17	-0.27	-0.97	-0.41
SCO1831		Not classified (included putative assignments)	putative oxidoreductase	2	8	4	0.12	0.07	-3.99	1.02
SCO1922		Transport/binding proteins	putative ABC transporter ATP-binding subunit	9	8	8	0.22	-0.68	-2.81	-0.14
SCO1958	*uvrA*	DNA - replication, repair, restr./modific'n	ABC excision nuclease subunit A	2	8	6	1.96	-0.29	-2.38	-0.29
SCO2013		Response regulator	putative two-component system response regulator	4	8	6	0.03	-0.80	-2.64	0.41
SCO2077		No homologues	hypothetical protein	4	8	7	0.67	-0.08	-1.68	0.30
SCO2161		Conserved in organism other than Escherichia coli	conserved hypothetical protein	2	8	7	0.54	0.74	-2.51	0.34
SCO2180	*pdhL*	Pyruvate dehydrogenase	putative dihydrolipoamide dehydrogenase	21	8	8	2.03	1.16	-0.53	-0.05
SCO2183	*aceE1*	Pyruvate dehydrogenase	putative pyruvate dehydrogenase E1 component	14	8	8	0.40	-0.48	-3.70	-0.25
SCO2589		Not classified (included putative assignments)	putative glycosyl transferase	2	7	4	0.38	-1.61	-2.02	0.34
SCO2620		Cell division	putative cell division trigger factor	24	8	8	1.02	-0.04	-2.73	0.46
SCO3622		Not classified (included putative assignments)	putative aminotransferase	2	8	7	1.02	0.19	-1.31	0.08
SCO3801		Degradation of proteins, peptides, glycoproteins	putative aminopeptidase	2	7	4	4.88	1.32	-3.14	-0.11
SCO3966		Gram +ve exported/lipoprotein	putative secreted protein	2	8	4	0.63	-1.45	-1.43	-0.70
SCO4068	*purD*	Purine ribonucleotide biosynthesis	phosphoribosylamine-glycine ligase (EC 6.3.4.13)	3	8	8	7.01	0.78	-1.80	-0.66
SCO4071	*purC*	Purine ribonucleotide biosynthesis	phosphoribosylaminoimidazole-succinocarboxamide s	2	8	6	3.51	-3.39	-1.43	0.24
SCO4185		Conserved in organism other than Escherichia coli	conserved hypothetical protein	2	7	4	1.02	-0.59	-5.17	0.92

SCO4232		Other regulation	putative transcriptional factor regulator	2	8	8	1.84	-0.49	-2.22	-0.55
SCO4266		Fatty acids	putative oxidoreductase	2	8	4	2.14	-1.40	-0.07	-3.58
SCO4583		Menaquinone, ubiquinone	putative polyprenyl diphosphate synthase	3	8	6	0.46	-1.23	-2.77	0.69
SCO4683	*gdhA*	Glutamate	NADP-specific glutamate dehydrogenase	4	8	8	2.41	-0.57	-0.45	0.33
SCO4932	*hutH*	Amino acids	histidine ammonia-lyase	3	8	4	0.38	-0.21	-1.67	-0.52
SCO4934		Gram +ve exported/lipoprotein	putative lipoprotein	5	8	8	1.42	-0.55	-2.00	-0.03
SCO5044	*fumB*	TCA cycle	fumarate hydratase class I	5	8	7	0.97	0.91	-1.62	-0.23
SCO5424	*ackA*	Carbon compounds	acetate kinase	2	8	4	0.49	-0.08	-2.75	0.33
SCO5645		Conserved in organism other than Escherichia coli	conserved hypothetical protein SC6A9.22c	2	8	4	0.26	-0.14	-3.31	0.21
SCO5769	*recA*	Chromosome replication	recombinase A	3	8	7	0.88	-0.82	-1.78	-0.95
SCO5971		Conserved in organism other than Escherichia coli	conserved hypothetical protein	5	8	7	2.88	0.09	-1.84	0.34
SCO6148		No homologues	hypothetical protein SC1A9.12	2	8	6	1.17	1.36	-1.39	0.00
SCO6471		Pool, multipurpose conversions of intermed. met'm	putative citratelyase	2	7	6	1.93	1.30	-0.85	-1.10
SCO6662	*tal1*	Non-oxidative branch, pentose pwy	transaldolase	6	8	6	0.09	-0.10	-2.74	0.50
			Genes in Set B							
SCO1517		Gram +ve exported/lipoprotein	putative secreted protein	4	8	8	-3.13	-0.10	1.49	-0.65
SCO1638	*fkbP*	Protein modification	peptidyl-prolyl cis-trans isomerase	4	8	8	-2.05	1.23	0.67	-0.06
SCO2014	*pyk1*	Glycolysis	pyruvate kinase	5	8	8	-1.67	1.50	1.45	1.63
SCO2094		Other regulation	putative regulatory protein	2	8	6	-0.90	-0.61	1.61	0.49
SCO2389	*acpP*	Fatty acid and phosphatidic acid biosynth	acyl carrier protein	3	8	6	-2.63	0.82	1.81	0.46
SCO2780		Gram +ve exported/lipoprotein	putative secreted protein	2	8	6	-3.50	-0.40	0.12	0.21
SCO3013		Response regulator	putative two-component system response regulator	3	8	8	-2.44	0.59	0.25	0.35
SCO3659		No homologues	hypothetical protein	4	8	8	-2.12	0.84	1.66	0.53
SCO3815	*bkdC1*	Pyruvate dehydrogenase	putative dihydrolipoamide acyltransferase compone	3	8	8	-1.80	0.80	1.33	0.66
SCO3817	*bkdA1*	Pyruvate dehydrogenase	putative branched-chain alpha keto acid dehydroge	3	8	6	-2.01	1.49	0.06	0.34
SCO3977		Degradation of proteins, peptides, glycoproteins	putative protease (putative secreted protein)	5	8	8	-0.21	0.51	2.49	-0.21
SCO4856	*dhsA*	TCA cycle	putative succinate dehydrogenase flavoprotein sub	16	8	8	-3.17	0.52	0.21	-0.85
SCO4885		Gram +ve exported/lipoprotein	putative lipoprotein	18	8	8	-4.90	0.84	0.25	-0.08
SCO4912		Not classified (included putative assignments)	putative aldehyde dehydrogenase	3	8	8	-0.94	1.30	1.15	0.00

SCO4919		Not classified (included putative assignments)	putative oxidoreductase	4	8	7	-1.08	-0.10	1.66	-1.20
SCO4926	*pccB*	Fatty acid and phosphatidic acid biosynth	propionyl-CoA carboxylase complex B subunit	2	8	4	-0.24	1.23	2.20	0.27
SCO5113	*bldKB*	Transport/binding proteins	BldKB, putative ABC transport system lipoprotein	25	8	8	-1.90	0.78	0.66	0.01
SCO5169		Not classified (included putative assignments)	putative ATP-binding protein	3	8	6	-3.79	0.31	1.07	0.52
SCO5204		Gram +ve membrane	hypothetical protein (fragment) "putative integral	9	8	7	-1.07	1.25	1.61	-0.56
SCO5464		Conserved in organism other than Escherichia coli	Not Specified	4	8	8	-2.47	1.04	3.33	0.07
SCO5498	*gatC*	Amino acyl tRNA syn; tRNA modific'n	probable Glu-tRNAGln amidotransferase subunit C	2	8	6	-2.75	0.93	0.19	0.77
SCO5541	*cvnD1*	Not classified (included putative assignments)	putative ATP-GTP binding protein	2	8	4	-3.10	-0.40	0.49	-0.19
SCO5744	*dapA*	Lysine	putative dihydrodipicolinate synthase	3	7	7	-1.70	0.26	1.32	0.71
SCO5776	*gluB*	Transport/binding proteins	glutamate binding protein	22	8	8	-1.60	0.13	3.69	0.36
SCO5777	*gluA*	Transport/binding proteins	glutamate uptake system ATP-binding protein	7	7	8	-3.31	0.45	2.28	1.07
SCO5836		DNA - replication, repair, restr./modific'n	DNA gyrase-like protein	3	8	7	-0.96	-0.87	1.54	0.69
SCO5841	*ptsH*	Transport/binding proteins	phosphocarrier protein hpr	2	8	4	-0.96	0.17	1.05	1.08
SCO5869		Conserved in organism other than Escherichia coli	hypothetical protein SC2E9.10	6	8	4	-2.47	0.46	0.02	0.25
SCO6009		Transport/binding proteins	solute-binding protein	14	8	8	-1.91	1.40	4.06	-0.11
SCO6010		Transport/binding proteins	probable ABC-transport system ATP binding protein	2	8	8	-1.57	0.89	2.63	0.96
SCO6011		Transport/binding proteins	probable ABC-type transmembrane transport protein	3	8	7	-1.99	-0.19	4.70	0.40
SCO6124		No homologues	hypothetical protein SC9B2.11	4	8	7	-1.35	0.39	4.58	2.50
SCO6451		Transport/binding proteins	putative substrate binding protein	4	8	7	-2.61	0.38	0.52	-0.81
SCO7463	*cvnA13*	Sensor kinase	putative sensor histidine kinase	2	8	4	-2.08	0.47	0.56	0.76

Genes in Set C

SCO0200		Conserved in organism other than Escherichia coli	conserved hypothetical protein SCJ12.12c	3	5	8	5.18	1.95	2.24	-1.99
SCO0379	*katA*	Detoxification	catalase (EC 1.11.1.6)	8	8	7	6.46	-0.79	0.79	-1.73
SCO0560	*cpeB*	Detoxification	catalase/peroxidase	6	8	8	5.15	1.15	2.80	0.13
SCO0608		Other regulation	putative regulatory protein	7	8	8	8.01	-0.08	3.21	0.31
SCO1340		Conserved in organism other than Escherichia coli	conserved hypothetical protein	2	8	4	3.21	1.08	1.00	0.31

SCO1644	*prcB*	Degradation of proteins, peptides, glycoproteins	20S proteasome beta-subunit precursor	3	8	7	3.61	1.30	0.72	-0.41
SCO1648	*arc*	Chaperones	AAA ATPase	10	8	8	7.60	1.95	4.77	-0.36
SCO2008		Amino acids and amines	putative branched chain amino acid binding protei	25	8	8	11.40	-0.64	6.04	-1.01
SCO2286		Not classified (included putative assignments)	putative alkaline phosphatase	2	8	8	8.32	4.04	2.68	0.24
SCO2517		Response regulator	putative two-component system response regulator	4	8	8	6.18	-0.18	4.08	-1.50
SCO2519		Gram +ve membrane	putative integral membrane protein	8	8	8	14.23	-0.85	5.19	-0.37
SCO3767		Conserved in organism other than Escherichia coli	conserved hypothetical protein	13	8	8	4.32	-1.12	2.12	-0.38
SCO3790		Conserved in organism other than Escherichia coli	conserved hypothetical protein	13	8	8	8.99	3.42	6.72	0.96
SCO4142	*pstS*	Not classified (included putative assignments)	phosphate-binding protein precursor	30	8	8	18.22	2.27	7.18	0.44
SCO4545		Conserved in organism other than Escherichia coli	conserved hypothetical protein	9	8	8	8.44	0.10	5.54	0.38
SCO4881		Polysaccharides - (cytoplasmic)	putative polysaccharide biosynthesis related prot	14	8	8	9.81	2.94	5.42	1.90
SCO5071	*actVI-ORFA*	PKS	hydroxylacyl-CoA dehydrogenase	2	8	6	8.23	-5.56	2.28	-1.71
SCO5073	*actVIORF2*	PKS	putative oxidoreductase	5	8	8	10.44	-6.39	4.75	-3.41
SCO5074	*actVIORF3*	PKS	putative dehydratase	3	8	7	12.84	-6.29	2.43	-2.96
SCO5075	*actVIORF4*	PKS	putative oxidoreductase	2	8	7	8.34	-5.65	4.83	-2.09
SCO5078	*actVA3*	PKS	hypothetical protein	4	8	8	8.64	-5.49	4.26	-1.83
SCO5079	*actVA4*	PKS	conserved hypothetical protein	4	8	8	10.89	-5.66	5.15	-2.39
SCO5080	*actVA5*	PKS	putative hydrolase	7	7	8	8.36	-4.90	4.73	-1.43
SCO5087	*actIORF1*	PKS	actinorhodin polyketide beta-ketoacyl synthase alpha	3	8	6	9.26	-5.94	4.79	-2.39
SCO5088	*actIORF2*	PKS	actinorhodin polyketide beta-ketoacyl synthase beta	4	8	4	9.65	-6.14	5.16	-3.34
SCO5178		Thiamin	putative sulfurylase	7	8	8	3.70	1.24	1.61	-0.33
SCO5396		Transport/binding proteins	putative cellulose-binding protein	8	8	8	2.50	1.01	0.14	0.36
SCO5657		Osmotic adaptation	aldehyde dehydrogenase	5	8	8	2.59	0.58	0.32	0.44
SCO5890	*redN*	PKS	putative 8-amino-7-oxononanoate synthase	7	8	8	10.41	-0.44	6.77	0.05
SCO5893	*redK*	PKS	oxidoreductase	5	8	8	9.00	0.83	3.78	-1.83
SCO5895	*redI*	PKS	putative methyltransferase	11	8	8	11.04	0.99	4.93	-0.97
SCO5896	*redH*	PKS	phosphoenolpyruvate-utilizing enzyme	12	8	8	10.89	1.62	5.93	0.37
SCO5897	*redG*	PKS	putative oxidase	9	8	8	11.21	-0.35	6.83	-0.74
SCO6273		PKS	putative type I polyketide synthase	26	8	8	6.85	3.41	3.43	-0.14
SCO6275		PKS	putative type I polyketide synthase	43	8	8	6.85	2.66	4.01	0.33

SCO6276		Secondary metabolism	putative secreted protein	36	8	8	15.45	0.32	5.05	-0.16
SCO6277		Secondary metabolism	putative epoxide hydrolase	10	8	8	15.33	1.01	3.92	-0.84
SCO6279		Secondary metabolism	putative diaminobutyrate-pyruvate aminotransferas	25	8	8	13.74	1.72	5.01	-0.82
SCO6282		PKS	putative 3-oxoacyl-[acyl-carrier protein] reducta	40	7	8	17.73	-0.77	5.32	-1.41
SCO6283		Secondary metabolism	conserved hypothetical protein	7	8	8	13.90	0.58	3.89	-1.97
SCO7536		Gram +ve membrane	putative integral membrane protein.	2	8	7	8.36	-2.10	4.84	-0.30

Genes in Set D

SCO0546	*pyc*	Gluconeogenesis	pyruvate carboxylase	3	8	7	0.86	0.64	3.10	1.01
SCO1222		Conserved in organism other than Escherichia coli	conserved hypothetical protein	2	8	7	3.88	1.02	6.53	1.28
SCO1223	*rocD*	Arginine	ornithine aminotransferase	3	8	8	2.15	0.47	4.57	1.18
SCO1640		Conserved in organism other than Escherichia coli	conserved hypothetical protein SCI41.23c	2	8	8	5.90	1.92	8.79	1.66
SCO2582		Conserved in organism other than Escherichia coli	conserved hypothetical protein SCC123.20.	2	8	4	0.87	0.39	4.74	-0.88
SCO2792	*adpA*	AraC	araC-family transcriptional regulator	3	8	7	2.79	1.36	4.81	0.20
SCO2855		No homologues	hypothetical protein SCE20.29.	2	8	7	1.41	0.03	3.68	-0.98
SCO2884		Electron transport	putative cytochrome P450.	8	8	8	3.42	0.23	5.80	0.12
SCO4252		No homologues	hypothetical protein SCD8A.25c	4	8	8	2.73	2.96	5.23	0.83
SCO4253		Conserved in organism other than Escherichia coli	conserved hypothetical protein SCD8A.26c	21	8	8	1.50	2.61	4.60	0.88
SCO4677		Other regulation	putative regulatory protein	3	8	8	7.63	-0.86	15.67	3.17
SCO4875		Polysaccharides - (cytoplasmic)	putative sugar transferase (fragment) "putative tr	2	7	4	1.40	-1.16	5.63	1.06
SCO4877		No homologues	hypothetical protein 2SCK8.03c	3	8	6	3.10	1.35	5.40	1.72
SCO4884		Gram +ve exported/lipoprotein	putative lipoprotein	2	8	8	1.14	0.87	4.98	-0.71
SCO5479		Transport/binding proteins	oligopeptide ABC transporter ATP-binding protein	5	8	8	0.45	1.42	2.79	-0.18
SCO5480		Transport/binding proteins	oligopeptide ABC transporter ATP-binding protein	5	8	8	0.63	0.27	2.71	0.47
SCO5874		Conserved in organism other than Escherichia coli	putative membrane protein	2	8	4	0.01	-0.15	2.06	-0.73
SCO5884		PKS	hypothetical protein SC3F7.04c	2	8	4	3.07	-0.29	9.36	0.20
SCO6445		Phospholipids	putative inositol monophosphatase	5	8	8	1.01	1.19	4.27	1.87
SCO6638		Conserved in organism other than Escherichia coli	hypothetical protein SC4G2.12c	3	8	8	1.27	0.10	3.37	0.22
SCO7057		Not classified (included putative assignments)	putative esterase	2	8	7	1.28	0.18	3.41	1.63
SCO7417		Electron transport	putative cytochrome P450-family	2	8	4	0.20	-1.12	2.58	1.01

			protein.							

Genes in Set E

SCO1505	*rspD*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S4	9	8	8	-4.81	1.42	-1.56	-0.35
SCO1598	*rplT*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L20	6	8	8	-4.09	0.24	-1.10	-0.40
SCO1651		Conserved in organism other than Escherichia coli	conserved hypothetical protein SCI41.34c	3	7	7	-3.21	-0.29	-0.22	-0.01
SCO1655		Transport/binding proteins	putative lipoprotein oligopeptide binding protein	6	8	8	-3.58	0.01	-1.06	0.15
SCO1866		Osmotic adaptation	putative condensing enzyme	2	8	6	-4.56	0.70	-1.58	1.43
SCO1921		Incorporation metal ions	putative aminotransferase	5	8	7	-3.33	0.60	-1.32	-0.39
SCO1998	*rpsA*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S1	23	8	8	-4.25	0.19	-1.83	-0.21
SCO2088	*murF*	Gram +ve peptidoglycan, teichoic acid	putative UDP-N-acetylmuramoylalanyl-D-glutamyl- 2	4	8	7	-4.18	-0.20	-0.69	0.24
SCO2155	*cox1*	Aerobic respiration	putative cytochrome c oxidase subunit I	3	8	8	-4.04	1.02	-0.51	-0.55
SCO2179		Degradation of proteins, peptides, glycoproteins	putative aminopeptidase	16	8	8	-3.15	-0.21	-0.23	-0.09
SCO2387	*fabD*	Fatty acid and phosphatidic acid biosynth	malonyl CoA:acyl carrier protein malonyltransfera	2	8	8	-6.35	-0.01	-3.07	-0.06
SCO2390	*fabF*	Fatty acid and phosphatidic acid biosynth	3-oxoacyl-[acyl-carrier-protein] synthase II	12	8	8	-6.15	0.22	-3.49	0.62
SCO2504	*glyS*	Amino acyl tRNA syn; tRNA modific'n	glycyl-tRNA synthetase	11	8	8	-4.41	-0.35	-1.78	0.16
SCO2593		No homologues	hypothetical protein SCC88.04c	3	8	6	-2.65	0.08	-0.49	-0.55
SCO2677		Transport/binding proteins	putative ABC transpoter ATP-binding protein	8	8	8	-3.26	0.76	-0.84	-0.15
SCO2950	*hup*	Other regulation	DNA-binding protein Hu (hs1)	10	8	8	-5.99	1.30	-2.50	0.27
SCO3123	*prsA2*	Purine ribonucleotide biosynthesis	ribose-phosphate pyrophosphokinase	7	8	8	-4.41	-0.89	-2.18	-0.36
SCO3124		Ribosomal proteins - synthesis, modification	ribosomal L25p family protein	11	8	8	-5.24	-0.17	-0.36	-0.37
SCO3182	*gtaB*	Carbon compounds	UTP-glucose-1-phosphate uridylyltransferase	8	8	8	-6.50	-0.48	-1.54	0.55
SCO3409	*ppa*	Phosphorus compounds	putative inorganic pyrophosphatase	5	8	8	-4.18	0.61	-0.65	0.65
SCO3615	*ask*	Threonine	putative aspartokinase	7	8	8	-3.02	1.42	-0.89	0.15
SCO3877		Oxidative branch, pentose pathway	putative 6-phosphogluconate dehydrogenase	10	8	8	-4.53	0.08	-2.52	1.00
SCO3906	*rpsF*	Ribosomal proteins - synthesis, modification	putative 30S ribosomal protein S6	6	8	8	-3.94	0.27	-1.83	-0.23
SCO3909	*rplI*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L9	11	8	8	-6.13	0.95	-3.24	0.60

SCO3974		No homologues	hypothetical protein	6	8	7	-3.86	-0.38	-1.74	0.17
SCO4328		Gram +ve exported/lipoprotein	putative lipoprotein	2	8	8	-4.65	0.29	-1.46	-1.26
SCO4647	*nusG*	RNA synthesis, modification, DNA transcript'n	transcription antitermination protein	5	8	8	-5.29	-0.81	-2.93	0.45
SCO4652	*rplJ*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L10	8	8	8	-4.74	-0.30	-2.02	0.22
SCO4653	*rplL*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L7/L12	9	8	8	-5.90	-0.06	-1.64	0.14
SCO4654	*rpoB*	RNA synthesis, modification, DNA transcript'n	DNA-directed RNA polymerase beta chain	50	8	8	-4.37	-0.33	-1.50	-0.50
SCO4655	*rpoC*	RNA synthesis, modification, DNA transcript'n	DNA-directed RNA polymerase beta' chain (fragment	52	8	8	-3.96	-0.49	-1.54	-0.16
SCO4659	*rspL*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S12	7	8	8	-4.28	-0.03	-1.21	-0.48
SCO4660	*rspG*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S7	14	8	8	-4.61	-1.13	-1.39	-0.29
SCO4702	*rplC*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L3	9	8	8	-4.57	-0.81	-1.61	0.06
SCO4708		Ribosomal proteins - synthesis, modification	30S ribosomal protein S3	15	8	8	-3.31	0.25	-1.10	-0.13
SCO4709	*rplP*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L16	6	8	8	-3.58	-0.81	-1.27	-0.61
SCO4716	*rpsH*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S8	10	8	8	-3.65	-0.44	-1.29	-0.48
SCO4719	*rpsE*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S5	17	8	8	-4.18	-0.56	-1.36	-0.02
SCO4721	*rplO*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L15	9	8	8	-3.73	0.77	-0.71	-0.60
SCO4723	*adk*	Purine ribonucleotide biosynthesis	adenylate kinase (fragment) "adenylate kinase"	4	8	4	-2.45	-0.18	-0.17	0.31
SCO4725	*infA*	Proteins - translation and modification	translational initiation factor IF1	4	8	8	-2.74	-1.66	-0.11	0.17
SCO4734	*rplM*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L13	9	8	8	-5.08	-0.62	-0.84	0.01
SCO4735	*rpsI*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S9	8	8	8	-3.92	0.66	-1.03	-0.43
SCO4770	*guaB*	Purine ribonucleotide biosynthesis	inosine 5' monophosphate dehydrogenase	11	8	8	-3.98	-0.17	-0.83	-0.02
SCO4785	*guaA*	Purine ribonucleotide biosynthesis	GMP synthase	5	8	6	-4.88	-0.36	-2.32	-0.03
SCO4886		Transport/binding proteins	putative sugar ABC transporter ATP-binding protei	3	8	4	-3.53	0.03	-0.59	0.13
SCO4965		RNA synthesis, modification, DNA transcript'n	putative transcription elongation factor	3	8	7	-3.69	-0.73	-1.58	0.39

SCO5031	*ahpD*	Detoxification	alkyl hydroperoxide reductase system hypothetical	4	8	8	-4.77	0.65	-1.65	-0.02
SCO5032	*ahpC*	Detoxification	alkyl hydroperoxide reductase	9	8	8	-5.91	0.70	-3.79	0.24
SCO5293		Not classified (included putative assignments)	putative oxygenase subunit	4	8	6	-2.35	-0.04	-0.23	0.45
SCO5367	*atpB*	ATP-proton motive force	ATP synthase A chain	2	8	7	-5.36	-0.67	-0.38	-0.80
SCO5371	*atpA*	ATP-proton motive force	ATP synthase alpha chain	34	8	8	-3.05	0.04	-0.59	-0.46
SCO5374	*atpC*	ATP-proton motive force	ATP synthase epsilon chain	4	8	8	-2.33	-0.11	-0.28	-0.41
SCO5572		Degradation of RNA	ribonuclease III	3	8	4	-4.51	-0.69	-1.62	0.10
SCO5591	*rpsP*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S16	15	8	8	-3.87	-2.06	-1.80	-0.20
SCO5624	*rpsB*	Ribosomal proteins - synthesis, modification	30S ribosomal protein S2	24	8	8	-4.61	-0.58	-1.06	-0.05
SCO5676	*gabT*	Pool, multipurpose conversions of intermed. met'm	putative 4-aminobutyrate aminotransferase	10	8	8	-5.84	-0.53	-3.80	-0.05
SCO5737	*gpsI*	RNA synthesis, modification, DNA transcript'n	guanosine pentaphosphate synthetase/polyribonucle	26	8	8	-4.36	1.19	-2.17	0.13
SCO5745		Conserved in organism other than Escherichia coli	conserved hypothetical protein SC9A10.09	5	8	7	-3.86	0.25	-1.59	-0.27
SCO5805	*nrdJ*	DNA - replication, repair, restr./modific'n	ribonucleotide reductase	8	8	8	-6.51	-0.38	-4.04	-0.53
SCO7000	*idh*	Glyoxylate bypass	isocitrate dehydrogenase	29	8	8	-3.89	0.75	-1.40	0.12
SCO7510	*cypH*	Proteins - translation and modification	peptidyl-prolyl cis-trans isomerase	7	8	8	-3.71	1.40	-1.35	-0.33

Genes in Set F

SCO0888		Gram +ve exported/lipoprotein	putative secreted protein	2	8	8	-2.01	-0.23	-5.49	0.86
SCO1089		No homologues	hypothetical protein 2SCG4.05c	3	8	4	-3.40	-1.73	-6.30	-0.96
SCO1483	*pyrA*	Pyrimidine ribonucleotide biosynthesis	carbamoylphosphate synthetase large chain	7	8	7	-1.26	0.16	-3.74	-0.70
SCO1486	*pyrC*	Pyrimidine ribonucleotide biosynthesis	dihydroorotase	2	8	7	-2.04	-1.37	-5.24	0.25
SCO1599	*rpmI*	Ribosomal proteins - synthesis, modification	50S ribosomal protein L35	2	8	7	-0.60	-1.74	-4.41	0.47
SCO1661		Aerobic respiration	putative glycerol-3-phosphate dehydrogenase	2	8	4	-0.64	-0.75	-4.01	0.04
SCO2606	*orfsyn*	Conserved in organism other than Escherichia coli	hypothetical protein	2	8	4	-0.84	-1.80	-3.05	0.25
SCO2612	*ndk*	Nucleotide interconversions	nucleoside diphosphate kinase	2	8	7	-1.80	0.83	-4.14	-0.13
SCO3381	*nadC*	Pyridine nucleotide	nicotinate-nucleotide pyrophophorylase	2	8	4	-0.33	-0.41	-2.69	-0.16
SCO3670	*grpE*	Chaperones	heat chock protein	6	8	8	-0.35	2.18	-3.18	0.80
SCO4077		No homologues	hypothetical protein SCD25.13	3	8	7	-0.19	-0.84	-3.39	0.01

SCO4469	*hemL*	Heme, porphyrin	glutamate-1-semialdehyde 2,1-aminomutase	2	8	4	-0.86	-0.61	-2.93	0.25
SCO5283		Response regulator	putative two-component system response regulator	3	8	8	-0.80	-0.56	-3.10	-0.84
SCO5472	*gcvT*	Amino acids	aminomethyltransferase	3	8	7	-1.92	-0.50	-5.29	-0.54
SCO5556		Basic proteins - synthesis, modification	histone-like DNA binding protein	4	8	6	-3.14	-0.96	-7.61	-0.35
SCO6564	*fabH2*	Fatty acid and phosphatidic acid biosynthesis	3-oxoacyl-[acyl-carrier-protein] synthase II	2	8	6	-1.05	0.17	-4.01	1.02