Table S2: Whole cell proteomic analysis for CsrB elevation in *E. coli*.

Protein ID	Description	Spectral Counts							TIGR Roles	TIGR Family	TIGR Description
		Induced (Avg)	Stdev	Uninduced (Avg)	Stdev	Fold Change	Variance	Log$_2$ (Fold Change)			
GlgB	glycogen branching enzyme	14.03	1.06	0.84	0.01	16.71	0.01	4.06	Energy metabolism:	TIGR01515 1,4	Biosynthesis and degradation of polysaccharides
CysA	sulfate/thiosulfate transporter subunit	5.82	2.05	0.84	0.01	6.93	0.12	2.79	Transport and bindin	TIGR00968 sul	Anions
YhiI	predicted HlyD family secretion protein	9.75	4.11	1.96	0.49	4.97	0.24	2.31	N/A	N/A	N/A
GlgC	glucose-1-phosphate adenylyltransferase	16.43	0.89	3.65	0.51	4.50	0.02	2.17	Energy metabolism:	TIGR02091 glu	Biosynthesis and degradation of polysaccharides
IaaA	L-asparaginase	5.45	2.30	1.69	0.86	3.23	0.44	1.69	N/A	N/A	N/A
TolC	outer membrane channel; specific toleran	11.48	1.16	3.65	0.51	3.15	0.03	1.65	Transport and bindin	TIGR01844 typ	Porins
AhpC	alkyl hydroperoxide reductase, C22 subun	52.02	4.83	17.6	5.68	2.96	0.11	1.56	Cellular processes:A	TIGR03137 per	Adaptations to atypical conditions
OmpA	outer membrane protein A	183.08	17.70	64.36	11.33	2.84	0.04	1.51	N/A	N/A	N/A
PspA	regulatory protein for phage-shock-protei	24.60	7.50	8.69	1.35	2.83	0.12	1.50	Cellular processes:A	TIGR02977 pha	Adaptations to atypical conditions
DksA	DNA-binding transcriptional regulator of r	9.46	2.95	3.64	0.5	2.60	0.12	1.38	Regulatory functions	TIGR02420 RN	Small molecule interactions
RraA	ribonuclease activity regulator protein Rra	11.43	3.35	4.47	1.23	2.56	0.16	1.35	Regulatory functions	TIGR01935 Rra	Protein interactions
GrpE	heat shock protein	7.43	0.50	3.07	1.26	2.42	0.17	1.28	N/A	N/A	N/A
Pck	phosphoenolpyruvate carboxykinase	21.24	5.81	8.96	1.26	2.37	0.09	1.25	Energy metabolism:	TIGR00224 ph	Glycolysis/gluconeogenesis
CysN	sulfate adenylyltransferase subunit 1	26.17	8.14	12.04	1.3	2.17	0.11	1.12	Central intermediary	TIGR00231 sm	Sulfur metabolism
RplR	50S ribosomal protein L18	5.47	2.88	2.52	0.85	2.17	0.39	1.12	Protein synthesis:Rib	TIGR00060 rib	Ribosomal proteins
SelD	selenophosphate synthetase	7.25	3.95	3.35	0.8	2.16	0.35	1.11	N/A	TIGR00476 sel	N/A
FucU	L-fucose mutarotase	5.40	1.09	2.52	0.82	2.14	0.15	1.10	N/A	N/A	N/A
SecB	export protein SecB	16.38	2.05	7.85	2.17	2.09	0.09	1.06	Protein fate:Protein	TIGR00809 pro	Protein and peptide secretion and trafficking
AllR	DNA-binding transcriptional repressor	5.71	1.67	2.8	0.5	2.04	0.12	1.03	N/A	N/A	N/A
YfgM	hypothetical protein	11.29	4.12	5.6	1	2.02	0.17	1.01	N/A	N/A	N/A
CysD	sulfate adenylyltransferase subunit 2	7.34	1.76	3.64	0.5	2.02	0.08	1.01	Central intermediary	TIGR02039 sul	Sulfur metabolism
SdhB	succinate dehydrogenase, FeS subunit	18.23	2.67	9.25	0.92	1.97	0.03	0.98	Energy metabolism:	TIGR00384 suc	TCA cycle
Gst	glutathionine S-transferase	22.87	5.54	11.76	0.14	1.94	0.06	0.96	N/A	N/A	N/A
UspA	universal stress global response regulator	43.04	14.24	22.4	1.13	1.92	0.11	0.94	N/A	N/A	N/A
HflC	modulator for HflB protease specific for p	16.14	2.16	8.41	1.53	1.92	0.05	0.94	Regulatory functions	TIGR01932 Hfl	Protein interactions
Ssb	single-strand DNA-binding protein	5.31	1.15	2.8	0.5	1.90	0.08	0.92	DNA metabolism:DN	TIGR00621 sin	DNA replication, recombination, and repair
YiiU	hypothetical protein	7.38	0.75	3.91	0.92	1.89	0.07	0.92	N/A	N/A	N/A
ZapA	protein that localizes to the cytokinetic rin	5.77	1.83	3.09	0.52	1.87	0.13	0.90	N/A	N/A	N/A
ManZ	PTS enzyme IID, mannose-specific	6.27	2.43	3.36	0.84	1.87	0.21	0.90	Signal transduction:	TIGR00828 PT	PTS
GlgA	glycogen synthase	9.38	2.38	5.04	2.25	1.86	0.26	0.90	Energy metabolism:	TIGR02095 gly	Biosynthesis and degradation of polysaccharides
b2253	#N/A	15.66	0.46	8.42	1.77	1.86	0.05	0.89	#N/A	#N/A	N/A
PntB	pyridine nucleotide transhydrogenase	10.74	1.12	5.87	1.38	1.83	0.07	0.87	N/A	N/A	N/A
MinD	membrane ATPase of the MinC-MinD-Min	22.34	3.22	12.32	0.46	1.81	0.02	0.86	Cellular processes:C	TIGR01968 sep	Cell division
YaeP	hypothetical protein	7.10	2.33	3.93	0.53	1.81	0.13	0.85	N/A	N/A	N/A
TpiA	triosephosphate isomerase	10.12	4.16	5.61	1.34	1.80	0.23	0.85	Energy metabolism:	TIGR00419 tri	Glycolysis/gluconeogenesis
MinE	cell division topological specificity factor	5.40	1.09	3.07	1.26	1.76	0.21	0.81	Cellular processes:C	TIGR01215 cell	Cell division
YiaD	predicted outer membrane lipoprotien	5.88	3.01	3.35	1.64	1.76	0.50	0.81	N/A	N/A	N/A
PhoP	DNA-binding response regulator in two-co	12.00	3.12	7	1.75	1.71	0.13	0.78	N/A	N/A	N/A
SucD	succinyl-CoA synthetase subunit alpha	31.89	5.92	18.77	1.19	1.70	0.04	0.76	Energy metabolism:	TIGR01019 suc	TCA cycle
CysM	cysteine synthase B (O-acetylserine sulfhy	6.18	1.13	3.64	0.5	1.70	0.05	0.76	Amino acid biosynth	TIGR01136 cys	Serine family
YhcB	orf, hypothetical protein	20.72	4.16	12.32	1.9	1.68	0.06	0.75	N/A	N/A	N/A
SurA	peptidyl-prolyl cis-trans isomerase (PPIase	14.55	3.54	8.68	0.53	1.68	0.06	0.75	N/A	N/A	N/A
TolB	translocation protein TolB precursor	11.68	3.71	7	0.95	1.67	0.12	0.74	Cellular processes:Pa	TIGR02800 Tol	Pathogenesis
YbiC	predicted dehydrogenase	7.47	2.59	4.48	1.29	1.67	0.20	0.74	N/A	N/A	N/A
HflK	modulator for HflB protease specific for p	13.03	3.84	7.84	0.55	1.66	0.09	0.73	N/A	TIGR01933 Hfl	N/A
IhfB	integration host factor subunit beta	11.19	2.73	6.73	1.49	1.66	0.11	0.73	DNA metabolism:DN	TIGR00988 int	DNA replication, recombination, and repair
MraW	S-adenosyl-methyltransferase	11.61	3.04	7	1.32	1.66	0.10	0.73	Cell envelope:Biosyn	TIGR00006 S-a	Biosynthesis and degradation of murein sacculus and peptidoglycan
YfgL	protein assembly complex, lipoprotein co	10.80	3.38	6.73	5.15	1.60	0.68	0.68	Protein fate:Protein	TIGR03300 out	Protein and peptide secretion and trafficking
FabI	enoyl-(acyl carrier protein) reductase	25.11	2.61	15.67	1.95	1.60	0.03	0.68	N/A	N/A	N/A
FabD	acyl carrier protein S-malonyltransferase	8.97	2.04	5.6	1	1.60	0.08	0.68	Fatty acid and phosp	TIGR00128 ma	Biosynthesis
MscS	mechanosensitive channel	9.87	0.98	6.18	1.82	1.60	0.10	0.68	N/A	N/A	N/A
TktA	transketolase 1, thiamin-binding	54.84	2.05	34.47	2.9	1.59	0.01	0.67	Energy metabolism:	TIGR00232 tra	Pentose phosphate pathway
Crp	DNA-binding transcriptional dual regulato	14.22	4.32	8.97	1.04	1.58	0.11	0.66	N/A	N/A	N/A
PepB	putative peptidase	18.99	1.34	12.04	0.89	1.58	0.01	0.66	N/A	N/A	N/A
RplL	50S ribosomal protein L7/L12	53.28	8.55	33.87	3.13	1.57	0.03	0.65	Protein synthesis:Rib	TIGR00855 rib	Ribosomal proteins
CspC	stress protein, member of the CspA-family	11.46	2.07	7.29	1.36	1.57	0.07	0.65	N/A	N/A	N/A
YfgA	hypothetical protein	6.14	0.84	3.92	0.47	1.57	0.03	0.65	N/A	N/A	N/A

YaeT	hypothetical protein	13.11	1.76	8.41	1.49	1.56	0.05	0.64	Protein fate:Protein	TIGR03303 out	Protein and peptide secretion and trafficking
YbiS	hypothetical protein	8.29	3.79	5.33	1.33	1.55	0.27	0.64	N/A	N/A	N/A
LacI	transcriptional repressor of the lac operon	38.62	7.59	25.23	3.19	1.53	0.05	0.61	N/A	N/A	N/A
SdhA	succinate dehydrogenase flavoprotein sub	36.03	6.02	23.8	0.83	1.51	0.03	0.60	Energy metabolism:T	TIGR01812 suc	TCA cycle
TalB	transaldolase B	38.60	2.36	25.51	3.45	1.51	0.02	0.60	Energy metabolism:P	TIGR00874 tra	Pentose phosphate pathway
BasR	DNA-binding response regulator in two-co	4.99	1.52	3.37	0.87	1.48	0.16	0.57	N/A	N/A	N/A
Lrp	DNA-binding transcriptional dual regulator	7.45	2.29	5.03	1.42	1.48	0.17	0.57	N/A	N/A	N/A
UbiE	ubiquinone/menaquinone biosynthesis me	5.40	1.09	3.65	0.51	1.48	0.06	0.57	Biosynthesis of cofac	TIGR01934 ubi	Menaquinone and ubiquinone
IscU	scaffold protein	8.67	0.59	5.87	1.62	1.48	0.08	0.56	Biosynthesis of cofac	TIGR01999 FeS	Other
NlpA	cytoplasmic membrane lipoprotein-28	6.18	1.13	4.19	2.19	1.47	0.31	0.56	Cell envelope:Other	TIGR00363 lipo	Other
CysH	phosphoadenosine phosphosulfate reduct	23.96	2.38	16.26	1.45	1.47	0.02	0.56	Central intermediary	TIGR00434 pho	Sulfur metabolism
Icd	isocitrate dehydrogenase	117.18	3.60	79.82	1.42	1.47	0.00	0.55	Energy metabolism:T	TIGR00183 iso	TCA cycle
HemX	predicted uroporphyrinogen III methylase	9.04	1.70	6.17	1.04	1.47	0.06	0.55	N/A	N/A	N/A
CyoA	cytochrome o ubiquinol oxidase subunit II	10.24	1.23	6.99	1.2	1.46	0.04	0.55	Energy metabolism:E	TIGR01433 ubi	Electron transport
YhbS	predicted acyltransferase with acyl-CoA N-	5.33	1.66	3.64	0.44	1.46	0.11	0.55	N/A	N/A	N/A
InfA	translation initiation factor IF-1	5.31	1.15	3.65	0.51	1.45	0.07	0.54	Protein synthesis:Tra	TIGR00008 tra	Translation factors
YjgF	orf, hypothetical protein	6.49	2.20	4.49	1.01	1.45	0.17	0.53	Transcription:Degrad	TIGR00004 put	Degradation of RNA
AtpG	F0F1 ATP synthase subunit gamma	16.60	3.05	11.49	1.03	1.44	0.04	0.53	Energy metabolism:A	TIGR01146 ATP	ATP-proton motive force interconversion
RplK	50S ribosomal protein L11	12.85	3.10	8.96	0.46	1.43	0.06	0.52	Protein synthesis:Rib	TIGR01632 ribo	Ribosomal proteins
IspG	4-hydroxy-3-methylbut-2-en-1-yl diphosph	12.72	1.09	8.96	0.46	1.42	0.01	0.51	Biosynthesis of cofac	TIGR00612 4-h	Other
SucA	alpha-ketoglutarate decarboxylase	53.90	10.07	38.07	1.67	1.42	0.04	0.50	Energy metabolism:T	TIGR00239 oxo	TCA cycle
YcfF	orf, hypothetical protein	6.67	2.33	4.75	1.24	1.40	0.19	0.49	N/A	N/A	N/A
UspE	stress-induced protein	22.79	3.48	16.25	2.13	1.40	0.04	0.49	N/A	N/A	N/A
MetH	B12-dependent methionine synthase	30.17	7.27	21.57	3	1.40	0.08	0.48	Amino acid biosynth	TIGR02082 me	Aspartate family
InfC	translation initiation factor IF-3	26.92	6.04	19.32	2.97	1.39	0.07	0.48	Protein synthesis:Tra	TIGR00168 tra	Translation factors
TyrS	tyrosyl-tRNA synthetase	23.37	7.15	16.77	4.51	1.39	0.17	0.48	Protein synthesis:tRN	TIGR00234 tyr	tRNA aminoacylation
CysI	sulfite reductase, beta subunit, NAD(P)-bin	43.71	1.68	31.38	5.81	1.39	0.04	0.48	Central intermediary	TIGR02041 sulf	Sulfur metabolism
Pgm	phosphoglucomutase	19.49	4.87	14.01	1.08	1.39	0.07	0.48	Energy metabolism:S	TIGR01132 pho	Sugars
DapA	dihydrodipicolinate synthase	12.46	3.17	8.96	1.01	1.39	0.08	0.48	Amino acid biosynth	TIGR00674 dih	Aspartate family
FumA	fumarate hydratase (fumarase A), aerobic	21.64	6.88	15.7	2.27	1.38	0.12	0.46	N/A	TIGR00722 hyd	N/A
AspC	aspartate aminotransferase, PLP-depende	64.81	5.49	47.06	2.55	1.38	0.01	0.46	N/A	N/A	N/A
ManX	fused mannose-specific PTS enzymes: IIA c	17.31	1.02	12.63	3.16	1.37	0.07	0.45	Signal transduction:P	TIGR00824 PTS	PTS
NlpB	lipoprotein-34	9.94	1.80	7.28	2.11	1.37	0.12	0.45	N/A	N/A	N/A
SucB	dihydrolipoamide acetyltransferase	48.15	2.74	35.27	3.03	1.37	0.01	0.45	Energy metabolism:T	TIGR01347 dih	TCA cycle
RpsF	30S ribosomal protein S6	15.99	3.79	11.76	1.38	1.36	0.07	0.44	Protein synthesis:Rib	TIGR00166 ribo	Ribosomal proteins
Ftn	ferritin iron storage protein (cytoplasmic)	9.87	2.26	7.27	1.21	1.36	0.08	0.44	N/A	N/A	N/A
SucC	succinyl-CoA synthetase subunit beta	59.71	10.49	43.99	3.82	1.36	0.04	0.44	Energy metabolism:T	TIGR01016 suc	TCA cycle
ThrS	threonyl-tRNA synthetase	25.05	1.52	18.46	2.86	1.36	0.03	0.44	Protein synthesis:tRN	TIGR00418 thr	tRNA aminoacylation
YdgA	hypothetical protein	5.31	1.15	3.92	0.47	1.35	0.06	0.44	N/A	N/A	N/A
AcnB	aconitate hydratase	48.57	1.32	36.12	0.47	1.34	0.00	0.43	Energy metabolism:T	TIGR00117 aco	TCA cycle
FabG	3-oxoacyl-[acyl-carrier-protein] reductase	18.45	2.41	13.74	2.26	1.34	0.04	0.43	Fatty acid and phosp	TIGR01830 3-o	Biosynthesis
PntA	NAD(P) transhydrogenase subunit alpha	29.37	7.78	21.87	3.15	1.34	0.09	0.43	Energy metabolism:E	TIGR00561 NA	Electron transport
Tpx	thiol peroxidase	26.05	2.78	19.62	1.96	1.33	0.02	0.41	N/A	N/A	N/A
SerA	D-3-phosphoglycerate dehydrogenase	40.45	3.11	30.52	0.92	1.33	0.01	0.41	N/A	N/A	N/A
YadR	hypothetical protein	8.13	2.45	6.15	1.21	1.32	0.13	0.40	Biosynthesis of cofac	TIGR00049 iron	Other
SodB	superoxide dismutase, Fe	19.25	3.05	14.56	2.38	1.32	0.05	0.40	N/A	N/A	N/A
Asd	aspartate-semialdehyde dehydrogenase	42.93	3.24	32.5	4.05	1.32	0.02	0.40	Amino acid biosynth	TIGR01745 asp	Aspartate family
PpiD	peptidyl-prolyl cis-trans isomerase (rotama	18.51	1.96	14.02	3.08	1.32	0.06	0.40	N/A	N/A	N/A
PdxJ	pyridoxal phosphate biosynthetic protein	8.26	0.99	6.44	0.47	1.28	0.02	0.36	Biosynthesis of cofac	TIGR00559 pyr	Pyridoxine
Pnp	polynucleotide phosphorylase/polyadenyl	32.96	2.14	25.75	2.1	1.28	0.01	0.36	Transcription:Degrad	TIGR03591 pol	Degradation of RNA
SseA	putative thiosulfate sulfurtransferase	5.70	1.54	4.48	0.94	1.27	0.12	0.35	N/A	N/A	N/A
FkpA	FKBP-type peptidyl-prolyl cis-trans isomera	10.61	2.30	8.4	0.75	1.26	0.05	0.34	N/A	N/A	N/A
KatG	catalase/hydroperoxidase HPI(I)	26.73	1.15	21.3	1.99	1.26	0.01	0.33	Cellular processes:De	TIGR00198 cat	Detoxification
TrxB	thioredoxin reductase, FAD/NAD(P)-bindin	25.63	4.26	20.46	2.8	1.25	0.05	0.32	Energy metabolism:E	TIGR01292 thio	Electron transport
HtpG	heat shock protein 90	23.78	2.24	19.04	1.88	1.25	0.02	0.32	N/A	N/A	N/A
HlpA	periplasmic chaperone	11.17	1.61	8.95	1.63	1.25	0.05	0.32	N/A	N/A	N/A
Mdh	malate dehydrogenase	76.14	6.03	61.03	7.51	1.25	0.02	0.32	Energy metabolism:T	TIGR01772 ma	TCA cycle
Hns	global DNA-binding transcriptional dual re	42.58	5.25	34.15	7.64	1.25	0.07	0.32	N/A	N/A	N/A
GdhA	glutamate dehydrogenase	34.40	5.40	27.71	2.21	1.24	0.03	0.31	N/A	N/A	N/A
AtpD	F0F1 ATP synthase subunit beta	90.98	1.67	73.37	4.12	1.24	0.00	0.31	Energy metabolism:A	TIGR01039 ATP	ATP-proton motive force interconversion
InfB	translation initiation factor IF-2	45.38	10.25	36.97	3.04	1.23	0.06	0.30	Protein synthesis:Tra	TIGR00231 sma	Translation factors
Ais	hypothetical protein	8.60	1.66	7.01	0.54	1.23	0.04	0.29	N/A	N/A	N/A

FbaA	fructose-bisphosphate aldolase	31.85	5.19	26.04	0.62	1.22	0.03	0.29	Energy metabolism:	TIGR00167 ket	Glycolysis/gluconeogenesis
SlyD	FKBP-type peptidyl prolyl cis-trans isomer	9.93	1.55	8.13	2.18	1.22	0.10	0.29	N/A	N/A	N/A
HupA	HU, DNA-binding transcriptional regulator	38.61	11.00	31.66	3.3	1.22	0.09	0.29	N/A	N/A	N/A
DeoD	purine nucleoside phosphorylase	9.83	1.61	8.11	2.04	1.21	0.09	0.28	Purines, pyrimidines	TIGR00107 pur	Salvage of nucleosides and nucleotides
RplA	50S ribosomal protein L1	27.06	7.69	22.41	1.1	1.21	0.08	0.27	Protein synthesis:Rib	TIGR01169 rib	Ribosomal proteins
Rne	fused ribonucleaseE: endoribonuclease/R	15.57	2.72	12.9	1.9	1.21	0.05	0.27	Transcription:Degrad	TIGR00757 rib	Degradation of RNA
GrxC	glutaredoxin 3	6.07	3.05	5.04	0.78	1.20	0.28	0.27	Energy metabolism:	TIGR02181 glu	Electron transport
TrpB	tryptophan synthase subunit beta	18.90	1.76	15.7	2.27	1.20	0.03	0.27	Amino acid biosynth	TIGR00263 try	Aromatic amino acid family
Lpd	dihydrolipoamide dehydrogenase	79.88	19.65	66.4	3.68	1.20	0.06	0.27	N/A	TIGR01350 dih	N/A
LuxS	S-ribosylhomocysteinase	8.71	2.64	7.27	1.66	1.20	0.14	0.26	N/A	N/A	N/A
CysK	cysteine synthase A, O-acetylserine sulfhy	139.00	6.14	116.49	1.86	1.19	0.00	0.25	Amino acid biosynth	TIGR01136 cys	Serine family
LpcA	phosphoheptose isomerase	7.34	1.76	6.16	1.3	1.19	0.10	0.25	Cell envelope:Biosyn	TIGR00441 ph	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
AcrA	multidrug efflux system	10.67	1.46	8.96	0.86	1.19	0.03	0.25	Transport and bindi	TIGR01730 eff	Unknown substrate
SspA	stringent starvation protein A	14.60	4.64	12.33	0.63	1.18	0.10	0.24	N/A	N/A	N/A
YajQ	orf, hypothetical protein	10.60	2.44	8.96	1.29	1.18	0.07	0.24	N/A	N/A	N/A
LivJ	leucine/isoleucine/valine transporter sub	14.22	4.32	12.04	1.7	1.18	0.11	0.24	N/A	N/A	N/A
YcgK	hypothetical protein	8.26	0.99	7.01	0.54	1.18	0.02	0.24	N/A	N/A	N/A
GpmA	phosphoglyceromutase	42.04	2.25	35.88	4.68	1.17	0.02	0.23	N/A	TIGR01258 ph	N/A
TyrB	tyrosine aminotransferase, tyrosine-repre	17.71	1.67	15.13	1.01	1.17	0.01	0.23	N/A	N/A	N/A
ProA	gamma-glutamyl phosphate reductase	8.19	1.56	7.01	1.34	1.17	0.07	0.22	Amino acid biosynth	TIGR00407 glu	Glutamate family
SerC	phosphoserine aminotransferase	39.77	3.62	34.18	6.31	1.16	0.04	0.22	Amino acid biosynth	TIGR01364 ph	Serine family
PurC	phosphoribosylaminoimidazole-succinoca	13.98	0.68	12.05	1.38	1.16	0.02	0.21	Purines, pyrimidines	TIGR00081 ph	Purine ribonucleotide biosynthesis
Fdx	[2Fe-2S] ferredoxin	6.14	0.84	5.31	1.21	1.16	0.07	0.21	Biosynthesis of cofa	TIGR02007 fer	Other
LysC	aspartate kinase III	35.91	8.12	31.1	1.19	1.15	0.05	0.21	Amino acid biosynth	TIGR00656 asp	Aspartate family
UdhA	putative oxidoreductase	11.93	2.37	10.35	1.71	1.15	0.07	0.20	N/A	N/A	N/A
MetK	S-adenosylmethionine synthetase	26.71	5.43	23.27	3.65	1.15	0.07	0.20	Central intermediary	TIGR01034 me	Other
Pps	phosphoenolpyruvate synthase	23.44	2.46	20.43	1.88	1.15	0.02	0.20	Energy metabolism:	TIGR01418 ph	Glycolysis/gluconeogenesis
YidC	inner membrane protein translocase com	8.67	0.59	7.56	0.76	1.15	0.01	0.20	Protein fate:Protein	TIGR03592 me	Protein and peptide secretion and trafficking
PykF	pyruvate kinase	21.50	2.17	18.77	1.44	1.15	0.02	0.20	Energy metabolism:	TIGR01064 pyr	Glycolysis/gluconeogenesis
AckA	acetate kinase	15.90	5.08	14	1.29	1.14	0.11	0.18	Energy metabolism:	TIGR00016 ace	Fermentation
PflB	pyruvate formate lyase I	17.75	1.26	15.67	1.95	1.13	0.02	0.18	Energy metabolism:	TIGR01255 for	Fermentation
TrpD	bifunctional indole-3-glycerol-phosphate	18.10	2.01	15.98	3.14	1.13	0.05	0.18	Amino acid biosynth	TIGR00566 glu	Aromatic amino acid family
Tdh	L-threonine 3-dehydrogenase	5.40	1.09	4.77	1.8	1.13	0.18	0.18	Energy metabolism:	TIGR00692 L-t	Amino acids and amines
FtsH	protease, ATP-dependent zinc-metallo	27.34	4.01	24.38	3.81	1.12	0.05	0.17	Protein fate:Degrada	TIGR01241 AT	Degradation of proteins, peptides, and glycopeptides
PurR	DNA-binding transcriptional repressor, hy	5.66	2.60	5.06	1.73	1.12	0.33	0.16	N/A	N/A	N/A
HslU	ATP-dependent protease ATP-binding sub	15.34	2.85	13.72	0.89	1.12	0.04	0.16	Protein fate:Protein	TIGR00390 AT	Protein folding and stabilization
AsnS	asparaginyl-tRNA synthetase	26.86	2.41	24.08	0.68	1.12	0.01	0.16	Protein synthesis:tR	TIGR00457 asp	tRNA aminoacylation
AtpA	F0F1 ATP synthase subunit alpha	89.32	10.60	80.63	6.3	1.11	0.02	0.15	Energy metabolism:	TIGR00962 AT	ATP-proton motive force interconversion
FabH	3-oxoacyl-(acyl carrier protein) synthase	9.93	2.37	8.97	1.38	1.11	0.08	0.15	Fatty acid and phosp	TIGR00747 3-o	Biosynthesis
GlmS	D-fructose-6-phosphate amidotransferase	17.65	1.98	15.96	0.67	1.11	0.01	0.15	Central intermediary	TIGR01135 glu	Amino sugars
HscA	chaperone protein HscA	10.81	3.66	9.8	1.26	1.10	0.13	0.14	Protein fate:Protein	TIGR01991 Fe-	Protein folding and stabilization
RpsB	30S ribosomal protein S2	24.62	3.03	22.39	2.14	1.10	0.02	0.14	Protein synthesis:Rib	TIGR01011 rib	Ribosomal proteins
YdhD	hypothetical protein	8.32	2.02	7.57	0.91	1.10	0.07	0.14	Energy metabolism:	TIGR00365 mo	Electron transport
MaeB	malic enzyme	8.30	2.16	7.57	1.49	1.10	0.11	0.13	N/A	N/A	N/A
Crr	glucose-specific PTS system enzyme IIA co	28.82	0.63	26.3	3.19	1.10	0.02	0.13	Signal transduction:	TIGR00830 PTS	PTS
TrpC	N-(5-phosphoribosyl)anthranilate isomera	16.25	4.92	14.85	0.66	1.09	0.09	0.13	N/A	N/A	N/A
RpsI	30S ribosomal protein S9	6.10	1.84	5.61	1.79	1.09	0.19	0.12	N/A	N/A	N/A
Gnd	6-phosphogluconate dehydrogenase	34.09	2.83	31.35	1.56	1.09	0.01	0.12	Energy metabolism:	TIGR00873 6-p	Pentose phosphate pathway
TrpA	tryptophan synthase subunit alpha	27.42	3.77	25.24	6.24	1.09	0.08	0.12	Amino acid biosynth	TIGR00262 try	Aromatic amino acid family
Pgk	phosphoglycerate kinase	79.94	2.24	73.69	4.36	1.08	0.00	0.12	N/A	N/A	N/A
Dps	DNA protection during starvation conditio	6.99	0.34	6.45	1.03	1.08	0.03	0.12	N/A	N/A	N/A
MetQ	DL-methionine transporter subunit	34.90	7.79	32.51	2.31	1.07	0.05	0.10	Cell envelope:Other	TIGR00363 lip	Other
ArcA	DNA-binding response regulator in two-co	10.79	2.18	10.07	0.73	1.07	0.05	0.10	N/A	N/A	N/A
YfbG	hypothetical protein	15.27	1.13	14.28	3.04	1.07	0.05	0.10	N/A	N/A	N/A
SohB	predicted inner membrane peptidase	6.58	0.44	6.16	0.54	1.07	0.01	0.10	N/A	N/A	N/A
SecD	protein export protein SecD	12.28	3.33	11.49	1.82	1.07	0.10	0.10	Protein fate:Protein	TIGR00916 pr	Protein and peptide secretion and trafficking
RpsE	30S ribosomal protein S5	18.83	7.92	17.64	0.9	1.07	0.18	0.09	Protein synthesis:Rib	TIGR01021 rib	Ribosomal proteins
UspG	universal stress protein UP12	12.28	1.67	11.5	4.7	1.07	0.19	0.09	N/A	N/A	N/A
CysJ	sulfite reductase, alpha subunit, flavoprot	36.48	6.51	34.17	3.31	1.07	0.04	0.09	N/A	TIGR01931 sul	N/A
HisF	imidazole glycerol phosphate synthase su	14.60	4.64	13.72	1.31	1.06	0.11	0.09	Amino acid biosynth	TIGR00735 imi	Histidine family
PepQ	proline dipeptidase	12.20	3.67	11.49	2.49	1.06	0.14	0.09	N/A	N/A	N/A
TufA	protein chain elongation factor EF-Tu (du	448.63	29.39	422.86	4.91	1.06	0.00	0.09	Protein synthesis:Tr	TIGR00231 sm	Translation factors

RibE	riboflavin synthase subunit beta	15.64	0.87	14.84	1.18	1.05	0.01	0.08	Biosynthesis of cofac	TIGR00114 6,7	Riboflavin, FMN, and FAD
GalU	glucose-1-phosphate uridylyltransferase	7.38	0.75	7	0.52	1.05	0.02	0.08	Cell envelope:Biosyn	TIGR01099 UT	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
Pta	phosphate acetyltransferase	37.66	4.98	35.86	2.62	1.05	0.02	0.07	Energy metabolism:F	TIGR00651 pho	Fermentation
NudE	ADP-ribose diphosphatase	7.04	1.11	6.71	1.42	1.05	0.07	0.07	N/A	N/A	N/A
MetE	5-methyltetrahydropteroyltriglutamate-- h	98.64	13.04	94.14	5.25	1.05	0.02	0.07	Amino acid biosynth	TIGR01371 5-n	Aspartate family
RplO	50S ribosomal protein L15	16.71	3.90	15.97	1.73	1.05	0.07	0.07	Protein synthesis:Rib	TIGR01071 ribo	Ribosomal proteins
RpsG	30S ribosomal protein S7	30.95	2.05	29.71	2.76	1.04	0.01	0.06	Protein synthesis:Rib	TIGR01029 ribo	Ribosomal proteins
PanB	3-methyl-2-oxobutanoate hydroxymethylt	4.96	0.34	4.76	0.47	1.04	0.01	0.06	Biosynthesis of cofac	TIGR00222 3-n	Pantothenate and coenzyme A
YdgH	hypothetical protein	7.84	0.79	7.56	0.09	1.04	0.01	0.05	N/A	N/A	N/A
DapD	2,3,4,5-tetrahydropyridine-2-carboxylate N	32.17	11.31	31.07	4.26	1.04	0.14	0.05	Amino acid biosynth	TIGR00965 2,3	Aspartate family
ArgD	bifunctional acetylornithine aminotransfer	8.71	1.72	8.41	2.28	1.04	0.11	0.05	Energy metabolism:A	TIGR00707 ace	Amino acids and amines
MoaB	molybdopterin biosynthesis protein B	5.21	6.13	5.04	0.89	1.03	1.41	0.05	Biosynthesis of cofac	TIGR00177 mo	Molybdopterin
YfiO	predicted lipoprotein	5.79	0.88	5.6	2.11	1.03	0.17	0.05	Protein fate:Protein	TIGR03302 out	Protein and peptide secretion and trafficking
AccD	acetyl-CoA carboxylase subunit beta	12.72	1.09	12.33	1.43	1.03	0.02	0.04	Fatty acid and phosp	TIGR00515 ace	Biosynthesis
GuaA	bifunctional GMP synthase/glutamine ami	11.83	2.35	11.48	0.62	1.03	0.04	0.04	Purines, pyrimidines,	TIGR00884 GM	Purine ribonucleotide biosynthesis
HisS	histidyl-tRNA synthetase	20.19	1.62	19.59	1.05	1.03	0.01	0.04	Protein synthesis:tRN	TIGR00442 hist	tRNA aminoacylation
BetB	betaine aldehyde dehydrogenase, NAD-de	6.60	0.76	6.44	1.23	1.02	0.05	0.04	Cellular processes:Ac	TIGR01804 bet	Adaptations to atypical conditions
PurH	bifunctionalphosphoribosylaminoimidazol	19.43	4.07	19.03	3.44	1.02	0.08	0.03	Purines, pyrimidines,	TIGR00355 pho	Purine ribonucleotide biosynthesis
IhfA	integration host factor subunit alpha	10.30	0.46	10.09	2.56	1.02	0.07	0.03	DNA metabolism:DN	TIGR00987 inte	DNA replication, recombination, and repair
SerS	seryl-tRNA synthetase	19.14	5.06	18.76	0.6	1.02	0.07	0.03	Protein synthesis:tRN	TIGR00414 ser	tRNA aminoacylation
RpsC	30S ribosomal protein S3	29.99	2.34	29.4	2.93	1.02	0.02	0.03	Protein synthesis:Rib	TIGR01009 ribo	Ribosomal proteins
RpmC	50S ribosomal protein L29	15.42	4.21	15.14	1.85	1.02	0.09	0.03	Protein synthesis:Rib	TIGR00012 ribo	Ribosomal proteins
CarA	carbamoyl-phosphate synthase small subu	10.28	1.68	10.1	2.32	1.02	0.08	0.03	Purines, pyrimidines,	TIGR01368 car	Pyrimidine ribonucleotide biosynthesis
CarB	carbamoyl-phosphate synthase large subu	36.44	4.90	35.87	3.09	1.02	0.03	0.02	Purines, pyrimidines,	TIGR01369 car	Pyrimidine ribonucleotide biosynthesis
YfiF	predicted methyltransferase	5.40	3.11	5.32	0.51	1.02	0.34	0.02	N/A	N/A	N/A
FusA	elongation factor EF-2	119.74	5.59	118.44	9.23	1.01	0.01	0.02	Protein synthesis:Tra	TIGR00231 sma	Translation factors
YidA	predicted hydrolase	5.10	3.70	5.05	0.9	1.01	0.56	0.02	Unknown function:E	TIGR00099 Cof	Enzymes of unknown specificity
HisC	histidinol-phosphate aminotransferase	8.49	3.91	8.41	1.71	1.01	0.25	0.01	Amino acid biosynth	TIGR01141 hist	Histidine family
VacB	putative enzyme	8.19	1.56	8.12	1.29	1.01	0.06	0.01	Transcription:Degrac	TIGR00358 Vac	Degradation of RNA
PurL	phosphoribosylformylglycinamidine synth	21.37	1.67	21.25	5.23	1.01	0.07	0.01	Purines, pyrimidines,	TIGR01735 pho	Purine ribonucleotide biosynthesis
DacA	D-alanyl-D-alanine carboxypeptidase (pen	8.15	2.04	8.12	1.21	1.00	0.09	0.01	N/A	N/A	N/A
PfkB	6-phosphofructokinase II; suppressor of pf	7.03	0.94	7	0.95	1.00	0.04	0.01	N/A	TIGR03168 hex	N/A
ArgB	acetylglutamate kinase (RefSeq)	5.33	1.77	5.31	2.05	1.00	0.26	0.00	Amino acid biosynth	TIGR00761 ace	Glutamate family
LeuS	leucyl-tRNA synthetase	17.12	3.83	17.09	2.96	1.00	0.08	0.00	Protein synthesis:tRN	TIGR00396 leu	tRNA aminoacylation
LeuC	isopropylmalate isomerase large subunit	28.88	1.49	28.83	2.66	1.00	0.01	0.00	Amino acid biosynth	TIGR00170 3-is	Pyruvate family
RpsD	30S ribosomal protein S4	29.08	6.04	29.12	2.54	1.00	0.05	0.00	Protein synthesis:Rib	TIGR01017 ribo	Ribosomal proteins
Pfs	5'-methylthioadenosine/S-adenosylhomoc	5.86	2.26	5.87	0.78	1.00	0.17	0.00	Purines, pyrimidines,	TIGR01704 MT	Salvage of nucleosides and nucleotides
GlyA	serine hydroxymethyltransferase	42.12	4.26	42.26	2.98	1.00	0.02	0.00	N/A	N/A	N/A
NemA	N-ethylmaleimide reductase, FMN-linked	18.95	1.68	19.04	0.74	1.00	0.01	-0.01	N/A	N/A	N/A
PheS	phenylalanyl-tRNA synthetase alpha subur	13.27	2.34	13.45	0.99	0.99	0.04	-0.02	Protein synthesis:tRN	TIGR00468 phe	tRNA aminoacylation
Eda	keto-hydroxyglutarate-aldolase/keto-deox	7.73	2.12	7.84	0.92	0.99	0.09	-0.02	Energy metabolism:E	TIGR01182 2-d	Entner-Doudoroff
MreB	regulator of ftsI, penicillin binding protein	5.79	2.56	5.88	0.78	0.98	0.21	-0.02	Cell envelope:Biosyn	TIGR00904 cell	Biosynthesis and degradation of murein sacculus and peptidoglycan
AspS	aspartyl-tRNA synthetase	37.45	2.85	38.08	0.07	0.98	0.01	-0.02	Protein synthesis:tRN	TIGR00459 asp	tRNA aminoacylation
AtpH	F0F1 ATP synthase subunit delta	11.57	1.77	11.77	2.31	0.98	0.06	-0.02	Energy metabolism:A	TIGR01145 ATI	ATP-proton motive force interconversion
LysS	lysine tRNA synthetase, constitutive	15.40	3.95	15.68	0.78	0.98	0.07	-0.03	Protein synthesis:tRN	TIGR00499 lysi	tRNA aminoacylation
RpsT	30S ribosomal protein S20	8.52	2.80	8.68	0.53	0.98	0.11	-0.03	Protein synthesis:Rib	TIGR00029 ribo	Ribosomal proteins
OppA	oligopeptide transporter subunit	31.06	4.79	31.66	2.82	0.98	0.03	-0.03	N/A	N/A	N/A
NusG	transcription antitermination protein NusG	11.80	3.32	12.03	1.15	0.98	0.09	-0.03	Transcription:Transc	TIGR00922 tra	Transcription factors
ArgH	argininosuccinate lyase	10.71	0.27	10.94	2.61	0.98	0.06	-0.03	Amino acid biosynth	TIGR00838 arg	Glutamate family
AlaS	alanyl-tRNA synthetase	28.77	2.68	29.4	4.42	0.98	0.03	-0.03	Protein synthesis:tRN	TIGR00344 ala	tRNA aminoacylation
RplN	50S ribosomal protein L14	9.30	3.77	9.53	0.56	0.98	0.17	-0.04	Protein synthesis:Rib	TIGR01067 ribo	Ribosomal proteins
DnaK	molecular chaperone DnaK	36.44	5.16	37.55	3.11	0.97	0.03	-0.04	Protein fate:Protein	TIGR02350 cha	Protein folding and stabilization
PpiB	peptidyl-prolyl cis-trans isomerase B (rota	8.43	4.42	8.69	1.99	0.97	0.33	-0.04	N/A	N/A	N/A
RpiA	ribose-5-phosphate isomerase A	9.50	1.06	9.8	0.46	0.97	0.01	-0.04	Energy metabolism:F	TIGR00021 ribo	Pentose phosphate pathway
RpsR	30S ribosomal protein S18	9.45	2.40	9.8	0.46	0.96	0.07	-0.05	Protein synthesis:Rib	TIGR00165 ribo	Ribosomal proteins
LepA	GTP-binding protein LepA	5.36	0.73	5.59	1.91	0.96	0.14	-0.06	Unknown function:G	TIGR00231 sma	General
MurA	UDP-N-acetylglucosamine 1-carboxyvinylt	6.99	0.34	7.29	1.03	0.96	0.02	-0.06	Cell envelope:Biosyn	TIGR01072 UD	Biosynthesis and degradation of murein sacculus and peptidoglycan
AccC	acetyl-CoA carboxylase	9.11	1.34	9.51	1.68	0.96	0.05	-0.06	Fatty acid and phosp	TIGR00514 ace	Biosynthesis
YchF	translation-associated GTPase	7.76	1.38	8.11	1.65	0.96	0.07	-0.06	Unknown function:G	TIGR00092 GTI	General
AhpF	alkyl hydroperoxide reductase, F52a subur	16.60	3.05	17.36	0.4	0.96	0.03	-0.06	Cellular processes:Ad	TIGR03140 alky	Adaptations to atypical conditions
Pgi	glucose-6-phosphate isomerase	12.30	1.47	12.89	2.79	0.95	0.06	-0.07	N/A	N/A	N/A
HemL	glutamate-1-semialdehyde aminotransfera	20.19	1.69	21.27	2.41	0.95	0.02	-0.08	Biosynthesis of cofac	TIGR00713 glu	Heme, porphyrin, and cobalamin

IlvC	ketol-acid reductoisomerase	52.98	11.17	56.54	3.47	0.94	0.05	-0.09	Amino acid biosynth	TIGR00465 ket	Pyruvate family
ValS	valyl-tRNA synthetase	23.11	2.26	24.66	1.54	0.94	0.01	-0.09	Protein synthesis:tR	TIGR00422 val	tRNA aminoacylation
RpoB	DNA-directed RNA polymerase subunit be	70.83	8.67	76.16	3.59	0.93	0.02	-0.10	Transcription:DNA-d	TIGR02013 DN	DNA-dependent RNA polymerase
PfkA	6-phosphofructokinase	17.14	5.96	18.47	1.47	0.93	0.13	-0.11	Energy metabolism:	TIGR02482 6-p	Glycolysis/gluconeogenesis
PrsA	ribose-phosphate pyrophosphokinase	28.01	2.03	30.24	2.1	0.93	0.01	-0.11	Purines, pyrimidines	TIGR01251 rib	Purine ribonucleotide biosynthesis
b2511	putative GTP-binding factor	7.77	2.92	8.4	1.4	0.93	0.17	-0.11	Protein synthesis:Ot	TIGR00231 sm	Other
DegP	serine endoprotease (protease Do), memb	6.99	0.34	7.56	0.86	0.92	0.02	-0.11	Protein fate:Degrada	TIGR02037 pro	Degradation of proteins, peptides, and glycopeptides
PepP	proline aminopeptidase P II	8.26	0.99	8.95	1.64	0.92	0.05	-0.12	N/A	N/A	N/A
B2294	orf, hypothetical protein	11.87	1.83	12.86	2.54	0.92	0.06	-0.12	N/A	N/A	N/A
Tsf	elongation factor Ts	25.29	4.64	27.43	4	0.92	0.05	-0.12	Protein synthesis:Tra	TIGR00116 tra	Translation factors
PtsI	PEP-protein phosphotransferase of PTS sy	56.15	3.74	61.36	3.74	0.92	0.01	-0.13	N/A	TIGR01417 ph	N/A
GroS	co-chaperonin GroES	17.12	5.92	18.77	1.19	0.91	0.12	-0.13	N/A	N/A	N/A
RpsJ	30S ribosomal protein S10	23.16	5.53	25.5	5.71	0.91	0.11	-0.14	Protein synthesis:Rib	TIGR01049 rib	Ribosomal proteins
FabF	3-oxoacyl-(acyl carrier protein) synthase	18.56	2.24	20.45	1.45	0.91	0.02	-0.14	Fatty acid and phosp	TIGR03150 bet	Biosynthesis
PurD	phosphoribosylamine--glycine ligase	6.58	0.44	7.27	1.21	0.91	0.03	-0.14	Purines, pyrimidines	TIGR00877 ph	Purine ribonucleotide biosynthesis
ArgS	arginyl-tRNA synthetase	7.60	4.25	8.39	1.59	0.91	0.35	-0.14	Protein synthesis:tR	TIGR00456 arg	tRNA aminoacylation
TyrA	fused chorismate mutase T/prephenate de	60.39	4.44	66.94	1.28	0.90	0.01	-0.15	Amino acid biosynth	TIGR01799 ch	Aromatic amino acid family
Frr	ribosome releasing factor	5.77	1.39	6.43	2.06	0.90	0.16	-0.16	Protein synthesis:Tra	TIGR00496 rib	Translation factors
ThrA	bifunctional aspartokinase I/homeserine	25.50	1.19	28.56	3.35	0.89	0.02	-0.16	Amino acid biosynth	TIGR00657 asp	Aspartate family
DapB	dihydrodipicolinate reductase	7.75	2.38	8.69	1.35	0.89	0.12	-0.17	Amino acid biosynth	TIGR00036 dih	Aspartate family
HisJ	histidine/lysine/arginine/ornithine transp	9.94	1.80	11.2	0.55	0.89	0.04	-0.17	Transport and bindi	TIGR01096 lys	Amino acids, peptides and amines
BipA	GTP-binding protein	16.80	2.67	19.04	3.49	0.88	0.06	-0.18	Protein synthesis:Tra	TIGR00231 sm	Translation factors
CysP	thiosulfate transporter subunit	20.98	1.93	23.78	4.38	0.88	0.04	-0.18	Transport and bindi	TIGR00971 sul	Anions
RplP	50S ribosomal protein L16	15.73	2.64	17.92	1.63	0.88	0.04	-0.19	Protein synthesis:Rib	TIGR01164 rib	Ribosomal proteins
RplJ	50S ribosomal protein L10	25.46	1.43	29.1	5.53	0.87	0.04	-0.19	N/A	N/A	N/A
Upp	uracil phosphoribosyltransferase	8.56	1.92	9.79	0.85	0.87	0.06	-0.19	Purines, pyrimidines	TIGR01091 ura	Salvage of nucleosides and nucleotides
GlnS	glutaminyl-tRNA synthetase	7.06	2.21	8.11	1.89	0.87	0.15	-0.20	Protein synthesis:tR	TIGR00440 glu	tRNA aminoacylation
Tig	trigger factor	49.35	8.13	56.81	4.9	0.87	0.03	-0.20	Protein fate:Protein	TIGR00115 trig	Protein folding and stabilization
ClpB	protein disaggregation chaperone	35.94	3.05	41.42	5.53	0.87	0.03	-0.20	Protein fate:Protein	TIGR03346 AT	Protein folding and stabilization
RpsA	30S ribosomal protein S1	45.85	6.72	52.9	7.71	0.87	0.04	-0.21	Protein synthesis:Rib	TIGR00717 rib	Ribosomal proteins
RpoC	DNA-directed RNA polymerase subunit be	63.56	5.57	73.37	1.19	0.87	0.01	-0.21	Transcription:DNA-d	TIGR02386 DN	DNA-dependent RNA polymerase
PurB	adenylosuccinate lyase	9.71	3.91	11.21	2.17	0.87	0.20	-0.21	Purines, pyrimidines	TIGR00928 ad	Purine ribonucleotide biosynthesis
IscS	cysteine desulfurase	20.47	2.75	23.79	2.71	0.86	0.03	-0.22	Protein synthesis:tR	TIGR02006 cys	tRNA and rRNA base modification
TrpE	anthranilate synthase component I	9.83	1.61	11.47	1.6	0.86	0.05	-0.22	Amino acid biosynth	TIGR00565 ant	Aromatic amino acid family
ThrC	threonine synthase	20.01	4.97	23.52	2.09	0.85	0.07	-0.23	Amino acid biosynth	TIGR00260 thr	Aspartate family
AdhE	fused acetaldehyde-CoA dehydrogenase/i	26.36	3.75	31.07	2.68	0.85	0.03	-0.24	N/A	N/A	N/A
HisG	ATP phosphoribosyltransferase	7.36	1.71	8.68	2.58	0.85	0.14	-0.24	Amino acid biosynth	TIGR00070 AT	Histidine family
GshA	glutamate--cysteine ligase	4.96	0.34	5.88	1.42	0.84	0.06	-0.25	Biosynthesis of cofa	TIGR01434 glu	Glutathione and analogs
AccA	acetyl-CoA carboxylase subunit alpha	18.15	2.08	21.58	3.38	0.84	0.04	-0.25	Fatty acid and phosp	TIGR00513 ace	Biosynthesis
DppA	dipeptide transporter	22.61	1.64	26.89	0.32	0.84	0.01	-0.25	N/A	N/A	N/A
RplM	50S ribosomal protein L13	8.71	1.72	10.37	2.16	0.84	0.08	-0.25	Protein synthesis:Rib	TIGR01066 rib	Ribosomal proteins
YfbF	undecaprenyl phosphate-L-Ara4FN transfe	5.40	1.09	6.44	1.29	0.84	0.08	-0.25	N/A	N/A	N/A
NuoC	NADH:ubiquinone oxidoreductase, chain	8.67	0.59	10.36	1.74	0.84	0.03	-0.26	Energy metabolism:	TIGR01961 NA	Electron transport
PurT	phosphoribosylglycinamide formyltransfe	5.84	4.17	7.01	1.35	0.83	0.55	-0.26	Purines, pyrimidines	TIGR01142 ph	Purine ribonucleotide biosynthesis
NusA	transcription elongation factor NusA	17.64	1.46	21.26	2.7	0.83	0.02	-0.27	Transcription:Transc	TIGR01953 tra	Transcription factors
RfaE	fused heptose 7-phosphate kinase/heptos	9.50	1.06	11.47	1.6	0.83	0.03	-0.27	Cell envelope:Biosyn	TIGR00125 cyt	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
GlyS	glycyl-tRNA synthetase subunit beta	17.12	3.83	20.71	4.84	0.83	0.10	-0.27	Protein synthesis:tR	TIGR00211 gly	tRNA aminoacylation
GlnA	glutamine synthetase	9.02	2.78	10.92	1.68	0.83	0.12	-0.28	Amino acid biosynth	TIGR00653 glu	Glutamate family
YgfZ	putative global regulator	6.71	2.96	8.13	0.58	0.83	0.20	-0.28	Protein synthesis:tR	TIGR03317 fol	tRNA and rRNA base modification
DadA	D-amino acid dehydrogenase small subun	5.75	0.40	6.99	3.39	0.82	0.24	-0.28	N/A	N/A	N/A
RplQ	50S ribosomal protein L17	15.18	2.07	18.47	1.47	0.82	0.02	-0.28	Protein synthesis:Rib	TIGR00059 rib	Ribosomal proteins
RbfA	ribosome-binding factor A	5.29	1.54	6.44	1	0.82	0.11	-0.28	Transcription:RNA p	TIGR00082 rib	RNA processing
RplF	50S ribosomal protein L6	24.38	3.58	29.69	3.44	0.82	0.03	-0.28	Protein synthesis:Rib	TIGR03654 rib	Ribosomal proteins
YibN	predicted rhodanese-related sulfurtransfe	5.71	1.67	7	0.93	0.82	0.10	-0.29	N/A	N/A	N/A
HisB	imidazoleglycerolphosphate dehydratase	4.99	1.52	6.15	1.21	0.81	0.13	-0.30	Amino acid biosynth	TIGR01261 his	Histidine family
AceE	pyruvate dehydrogenase subunit E1	77.27	12.78	95.2	2.46	0.81	0.03	-0.30	N/A	TIGR00759 pyr	N/A
Zwf	glucose-6-phosphate 1-dehydrogenase	12.22	2.91	15.12	1.36	0.81	0.06	-0.31	Energy metabolism:	TIGR00871 glu	Pentose phosphate pathway
IleS	isoleucyl-tRNA synthetase	20.73	6.08	25.75	4.02	0.80	0.11	-0.31	Protein synthesis:tR	TIGR00392 iso	tRNA aminoacylation
RpsP	30S ribosomal protein S16	8.95	3.46	11.21	1.09	0.80	0.16	-0.32	Protein synthesis:Rib	TIGR00002 rib	Ribosomal proteins
GyrB	DNA gyrase subunit B	8.71	1.72	10.93	1.54	0.80	0.06	-0.33	DNA metabolism:DN	TIGR01059 DN	DNA replication, recombination, and repair
AtpF	F0F1 ATP synthase subunit B	11.15	0.76	14.01	1.43	0.80	0.02	-0.33	Energy metabolism:	TIGR01144 AT	ATP-proton motive force interconversion
YebL	putative adhesin	23.96	2.38	30.26	1.8	0.79	0.01	-0.34	N/A	N/A	N/A

GroEL	chaperonin GroEL	101.82	3.08	128.79	4.86	0.79	0.00	-0.34	Protein fate:Protein	TIGR02348 cha	Protein folding and stabilization
Rho	transcription termination factor Rho	39.16	10.14	49.59	2.17	0.79	0.07	-0.34	Transcription:Transc	TIGR00767 tra	Transcription factors
PepD	aminoacyl-histidine dipeptidase (peptidas	7.73	2.12	9.79	2.03	0.79	0.12	-0.34	N/A	TIGR01893 am	N/A
GlnH	glutamine ABC transporter periplasmic pr	7.49	1.75	9.52	0.91	0.79	0.06	-0.35	N/A	N/A	N/A
SolA	N-methyltryptophan oxidase, FAD-binding	5.29	1.54	6.73	0.9	0.79	0.10	-0.35	N/A	N/A	N/A
TrxA	thioredoxin 1	10.28	1.68	13.17	1.42	0.78	0.04	-0.36	Energy metabolism:	TIGR01068 thi	Electron transport
Ppc	phosphoenolpyruvate carboxylase	36.92	3.34	47.33	3.81	0.78	0.01	-0.36	N/A	N/A	N/A
RpoA	DNA-directed RNA polymerase subunit alp	39.25	6.35	50.41	7.74	0.78	0.05	-0.36	Transcription:DNA-d	TIGR02027 DN	DNA-dependent RNA polymerase
AceF	dihydrolipoamide acetyltransferase	37.16	2.52	47.88	3.42	0.78	0.01	-0.37	Energy metabolism:	TIGR01348 dih	Pyruvate dehydrogenase
YeeZ	predicted epimerase, with NAD(P)-binding	7.80	1.71	10.09	2.26	0.77	0.10	-0.37	N/A	N/A	N/A
PyrG	CTP synthetase	12.35	0.96	15.97	0.19	0.77	0.01	-0.37	Purines, pyrimidines	TIGR00337 CT	Pyrimidine ribonucleotide biosynthesis
PanC	pantoate--beta-alanine ligase	6.49	2.20	8.4	0.76	0.77	0.12	-0.37	Biosynthesis of cofa	TIGR00018 pa	Pantothenate and coenzyme A
PykA	pyruvate kinase	19.91	3.52	25.77	4.05	0.77	0.06	-0.37	Energy metabolism:	TIGR01064 py	Glycolysis/gluconeogenesis
YjjK	fused predicted transporter subunits of A	10.32	0.89	13.44	1.68	0.77	0.02	-0.38	N/A	TIGR03719 AT	N/A
HupB	HU, DNA-binding transcriptional regulator	6.88	4.21	8.96	1.26	0.77	0.39	-0.38	N/A	N/A	N/A
PurA	adenylosuccinate synthetase	24.46	6.12	31.92	1.96	0.77	0.07	-0.38	Purines, pyrimidines	TIGR00184 ad	Purine ribonucleotide biosynthesis
GltA	citrate synthase	49.59	6.37	64.72	2.95	0.77	0.02	-0.38	Energy metabolism:	TIGR01798 cit	TCA cycle
LeuB	3-isopropylmalate dehydrogenase	32.57	2.02	42.87	3.76	0.76	0.01	-0.40	Amino acid biosynth	TIGR00169 3-i	Pyruvate family
YciK	short chain dehydrogenase	6.14	0.84	8.12	2.11	0.76	0.09	-0.40	N/A	N/A	N/A
AroG	3-deoxy-D-arabino-heptulosonate-7-phos	28.53	7.56	37.81	2.64	0.75	0.08	-0.41	Amino acid biosynth	TIGR00034 3-d	Aromatic amino acid family
Tas	predicted oxidoreductase, NADP(H)-depe	5.25	2.29	7.01	2.15	0.75	0.28	-0.42	N/A	N/A	N/A
PheT	phenylalanyl-tRNA synthetase beta subun	50.42	6.42	67.54	11.1	0.75	0.04	-0.42	Protein synthesis:tR	TIGR00472 ph	tRNA aminoacylation
NrdA	ribonucleotide-diphosphate reductase alp	8.74	2.57	11.77	0.95	0.74	0.09	-0.43	Purines, pyrimidines	TIGR02506 rib	2'-Deoxyribonucleotide metabolism
LeuD	isopropylmalate isomerase small subunit	13.18	0.33	17.93	0.6	0.74	0.00	-0.44	Amino acid biosynth	TIGR00171 3-i	Pyruvate family
RpsK	30S ribosomal protein S11	13.79	5.05	18.77	2.2	0.73	0.15	-0.44	Protein synthesis:Rib	TIGR03632 30	Ribosomal proteins
Adk	adenylate kinase	12.33	3.07	17.11	2.76	0.72	0.09	-0.47	Purines, pyrimidines	TIGR01351 ad	Nucleotide and nucleoside interconversions
Apt	adenine phosphoribosyltransferase	7.36	2.25	10.34	3.35	0.71	0.20	-0.49	Purines, pyrimidines	TIGR01090 ad	Salvage of nucleosides and nucleotides
GlmM	phosphoglucosamine mutase	6.56	1.74	9.25	1.71	0.71	0.10	-0.50	Central intermediary	TIGR01455 ph	Amino sugars
MetG	methionyl-tRNA synthetase	15.99	1.42	22.69	2.51	0.70	0.02	-0.50	Protein synthesis:tR	TIGR00398 me	tRNA aminoacylation
HisA	N-(5'-phospho-L-ribosyl-formimino)-5-am	9.49	1.43	13.71	1.12	0.69	0.03	-0.53	Amino acid biosynth	TIGR00007 1-(	Histidine family
ClpP	ATP-dependent Clp protease proteolytic s	5.81	1.03	8.41	1.71	0.69	0.07	-0.53	Protein fate:Degrada	TIGR00493 AT	Degradation of proteins, peptides, and glycopeptides
AroF	3-deoxy-D-arabino-heptulosonate-7-phos	104.36	23.91	151.44	14.01	0.69	0.06	-0.54	Amino acid biosynth	TIGR00034 3-d	Aromatic amino acid family
RplI	50S ribosomal protein L9	31.89	5.92	47.33	5.62	0.67	0.05	-0.57	Protein synthesis:Rib	TIGR00158 rib	Ribosomal proteins
GutQ	orf, hypothetical protein	8.63	0.99	12.88	0.33	0.67	0.01	-0.58	Energy metabolism:	TIGR00393 sug	Sugars
NarL	DNA-binding response regulator in two-co	8.23	0.29	12.31	2.01	0.67	0.03	-0.58	N/A	N/A	N/A
YcdW	putative dehydrogenase	5.80	2.95	8.69	1.35	0.67	0.28	-0.58	N/A	N/A	N/A
Eno	phosphopyruvate hydratase	66.88	5.09	100.49	5.76	0.67	0.01	-0.59	Energy metabolism:	TIGR01060 ph	Glycolysis/gluconeogenesis
PotD	spermidine/putrescine ABC transporter pe	6.14	0.84	9.24	0.74	0.66	0.02	-0.59	N/A	N/A	N/A
GuaB	inositol-5-monophosphate dehydrogenas	11.90	2.10	17.94	2.3	0.66	0.05	-0.59	Purines, pyrimidines	TIGR01302 ino	Purine ribonucleotide biosynthesis
IlvB	acetolactate synthase large subunit	9.99	2.64	15.11	2.1	0.66	0.09	-0.60	Amino acid biosynth	TIGR00118 ace	Pyruvate family
ProS	prolyl-tRNA synthetase	20.22	2.83	30.79	2.23	0.66	0.02	-0.61	Protein synthesis:tR	TIGR00409 pro	tRNA aminoacylation
AcnA	aconitate hydratase	11.04	1.75	16.82	1.65	0.66	0.03	-0.61	Energy metabolism:	TIGR01341 ac	TCA cycle
RplB	50S ribosomal protein L2	27.62	1.87	42.31	2.24	0.65	0.01	-0.62	Protein synthesis:Rib	TIGR01171 rib	Ribosomal proteins
RplE	50S ribosomal protein L5	25.48	1.47	40.04	3.14	0.64	0.01	-0.65	N/A	N/A	N/A
StpA	DNA binding protein, nucleoid-associated	8.56	1.92	13.46	2.36	0.64	0.08	-0.65	N/A	N/A	N/A
IlvE	branched-chain amino acid aminotransfer	11.93	0.91	18.77	1.48	0.64	0.01	-0.65	Amino acid biosynth	TIGR01122 bra	Pyruvate family
RfaD	ADP-L-glycero-D-mannoheptose-6-epime	9.56	2.10	15.11	1.51	0.63	0.06	-0.66	Cell envelope:Biosyn	TIGR02197 AD	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
FabZ	(3R)-hydroxymyristoyl ACP dehydratase	6.51	2.32	10.37	0.54	0.63	0.13	-0.67	Fatty acid and phosp	TIGR01750 bet	Biosynthesis
YliJ	putative transferase	8.40	6.13	13.45	2.32	0.62	0.56	-0.68	N/A	N/A	N/A
FabB	3-oxoacyl-(acyl carrier protein) synthase	18.29	5.51	29.39	2.72	0.62	0.10	-0.68	N/A	N/A	N/A
MoeA	molybdopterin biosynthesis protein	5.31	1.15	8.68	1.72	0.61	0.09	-0.71	N/A	TIGR00177 mo	N/A
ArgG	argininosuccinate synthase	12.61	3.51	20.73	1.09	0.61	0.08	-0.72	Amino acid biosynth	TIGR00032 arg	Glutamate family
IlvD	dihydroxy-acid dehydratase	40.47	2.99	66.66	2.25	0.61	0.01	-0.72	Amino acid biosynth	TIGR00110 dih	Pyruvate family
RplY	50S ribosomal protein L25	15.62	1.31	25.74	3.95	0.61	0.03	-0.72	N/A	N/A	N/A
FtsZ	cell division protein FtsZ	14.72	2.39	24.38	1.91	0.60	0.03	-0.73	Cellular processes:C	TIGR00065 cel	Cell division
YbeZ	predicted protein with nucleoside tripho	7.47	2.59	12.6	1.68	0.59	0.14	-0.75	N/A	N/A	N/A
Usg	hypothetical protein	12.61	3.51	21.29	2.21	0.59	0.09	-0.76	N/A	N/A	N/A
KdsA	2-dehydro-3-deoxyphosphooctonate aldo	9.76	2.72	16.54	1.45	0.59	0.09	-0.76	Cell envelope:Biosyn	TIGR01362 3-d	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides
GltB	glutamate synthase, large subunit	35.03	1.13	59.94	1.09	0.58	0.00	-0.77	N/A	N/A	N/A
RplC	50S ribosomal protein L3	15.01	4.37	25.75	2.1	0.58	0.09	-0.78	N/A	TIGR03625 50	N/A
RplD	50S ribosomal protein L4	15.27	2.69	26.88	0.62	0.57	0.03	-0.82	Protein synthesis:Rib	TIGR03953 50	Ribosomal proteins
NadE	NAD synthetase	6.99	0.34	12.32	1.19	0.57	0.01	-0.82	Biosynthesis of cofa	TIGR00552 NA	Pyridine nucleotides

YbiB	hypothetical protein	5.36	0.73	9.52	0.91	0.56	0.03	-0.83	N/A	N/A	N/A
GyrA	DNA gyrase subunit A	6.92	2.89	12.33	1.83	0.56	0.20	-0.83	DNA metabolism:DN	TIGR01063 DN	DNA replication, recombination, and repair
LeuA	2-isopropylmalate synthase	10.65	1.20	19.32	4.43	0.55	0.07	-0.86	Amino acid biosynth	TIGR00973 2-i	Pyruvate family
FolE	GTP cyclohydrolase I	14.33	2.08	26.04	3.79	0.55	0.04	-0.86	Biosynthesis of cofa	TIGR00063 GT	Folic acid
Ndk	nucleoside diphosphate kinase	11.37	3.59	20.73	0.46	0.55	0.10	-0.87	N/A	N/A	N/A
NuoG	NADH:ubiquinone oxidoreductase, chain	9.56	2.10	17.93	1.17	0.53	0.05	-0.91	Energy metabolism:	TIGR01973 NA	Electron transport
MetF	5,10-methylenetetrahydrofolate reductas	7.01	1.40	13.17	1.42	0.53	0.05	-0.91	Amino acid biosynth	TIGR00676 5,1	Aspartate family
RpsM	30S ribosomal protein S13	5.77	1.83	11.22	2.2	0.51	0.14	-0.96	Protein synthesis:Rib	TIGR03631 30	Ribosomal proteins
SecA	translocase	11.06	1.54	21.58	1.96	0.51	0.03	-0.96	Protein fate:Protein	TIGR00963 pre	Protein and peptide secretion and trafficking
RpoD	RNA polymerase sigma factor	7.03	0.94	13.74	2.57	0.51	0.05	-0.97	Transcription:Transc	TIGR02393 RN	Transcription factors
GshB	glutathione synthetase	7.01	1.40	13.71	2.8	0.51	0.08	-0.97	Biosynthesis of cofa	TIGR01380 glu	Glutathione and analogs
PepN	aminopeptidase N	6.99	0.34	13.98	2.4	0.50	0.03	-1.00	Protein fate:Degrada	TIGR02414 am	Degradation of proteins, peptides, and glycopeptides
GltX	glutamyl-tRNA synthetase	6.29	2.62	12.62	1.82	0.50	0.19	-1.01	Protein synthesis:tR	TIGR00464 glu	tRNA aminoacylation
GapA	glyceraldehyde-3-phosphate dehydrogena	18.47	1.26	37.55	3.37	0.49	0.01	-1.02	Energy metabolism:	TIGR01534 gly	Glycolysis/gluconeogenesis
RplV	50S ribosomal protein L22	13.05	3.38	27.45	1.32	0.48	0.07	-1.07	Protein synthesis:Rib	TIGR01044 rib	Ribosomal proteins
RplS	50S ribosomal protein L19	5.45	2.30	11.77	2.31	0.46	0.22	-1.11	Protein synthesis:Rib	TIGR01024 rib	Ribosomal proteins
GltD	glutamate synthase, 4Fe-4S protein, small	5.44	2.26	12.89	2.05	0.42	0.20	-1.25	N/A	TIGR01318 glu	N/A
TrpS	tryptophanyl-tRNA synthetase	6.14	0.84	16.52	1.83	0.37	0.03	-1.43	Protein synthesis:tR	TIGR00233 try	tRNA aminoacylation
IlvA	threonine dehydratase	6.29	2.62	18.21	0.7	0.35	0.18	-1.53	Amino acid biosynth	TIGR01124 thr	Pyruvate family