Table S1 *Leptospira* proteins identified through iTRAQ analyses.

UniProtKB ID	ORF	Synonym	Protein Identification	Putative Function	COG	EC Number	Predicted Location	Predicted pI	Predicted MW
Q72W82	LIC10055	CysE	Serine O-acetyltransferase	Amino acid transport and metabolism	COG1045,E	2.3.1.30	CYT	8.28	25678.9
Q72W01	LIC10140	AroC	Chorismate synthase	Amino acid transport and metabolism	COG0082,E	4.2.3.5	CYT	6.79	41573.9
Q72VI7	LIC10310	GcvH	Glycine dehydrogenase (decarboxylating), protein H	Amino acid transport and metabolism	COG0509,E	1.4.4.2	CYT	4.41	14118
Q72V62	LIC10440	GlnK	Nitrogen regulatory protein PII	Amino acid transport and metabolism	COG0347,E		CYT	9.79	12761.8
Q72V19	LIC10484	ThrC	Threonine synthase	Amino acid transport and metabolism	COG0498,E	4.2.3.1	CYT	8.27	48665
Q72UC6	LIC10733	PepB	Leucyl aminopeptidase	amino acid transport and metabolism	COG0260,E	3.4.11.-	CYT	9.40	54048.5
Q72U05	LIC10859	TrpB	Tryptophan synthase beta chain	Amino acid transport and metabolism	COG0133,E	4.2.1.20	CYT	9.49	43679.8
Q72SH3	LIC11409		Thiamine pyrophosphate-requiring enzyme	Amino acid transport and metabolism	COG0028,E,H		CYT	6.46	62325.5
Q72SH2	LIC11410	IlvH	Acetolactate synthase, small subunit	Amino acid transport and metabolism	COG0440,E	2.2.1.6	CYT	6.68	17864.7
Q72RZ1	LIC11597	LeuA-3	2-isopropylmalate/homocitrate synthase	Amino acid transport and metabolism	COG0119,E	2.3.3.13	CYT	6.36	57305.2
Q72RL9	LIC11726	LeuA-2	2-isopropylmalate synthase	Amino acid transport and metabolism	COG0119,E	4.1.3.12	CYT	5.75	54946.5
Q72RJ9	LIC11746	ArgC	N-acetyl-gamma-glutamyl-phosphate reductase	Amino acid transport and metabolism	COG0002,E	1.2.1.38	CYT	7.39	37781.4
Q72RH8	LIC11767	ArgD	Acetylornithine aminotransferase	Amino acid transport and metabolism	COG4992,E	2.6.1.11	CYT	4.91	44866.1
Q72RF5	LIC11790		Aspartate/tyrosine/aromatic aminotransferase	Amino acid transport and metabolism	COG0436,E		CYT	7.28	44154.5
Q72RD3	LIC11813	Ggt	Gamma-glutamyltransferase	Amino acid transport and metabolism	COG0405,E	2.3.2.2	PER	9.36	63498.8
Q72RA8	LIC11840	ArgH	Argininosuccinate lyase	Amino acid transport and metabolism	COG0165,E	4.3.2.1	CYT	6.69	53352.2
Q72R96	LIC11852	MetY	O-acetylhomoserine aminocarboxypropyltransferase	Amino acid transport and metabolism	COG2873,E	2.5.1.49	CYT	6.90	47468.1
Q72QN1	LIC12082	CysK-2	Cysteine synthase	Amino acid transport and metabolism	COG0031,E	2.5.1.47	CYT	8.70	33248.2
Q72PY2	LIC12335	GlyA	Glycine hydroxymethyltransferase	Amino acid transport and metabolism	COG0112,E	2.1.2.1	CYT	8.10	44974.3
Q72PR0	LIC12407	GlnA	Glutamate--ammonia ligase	Amino acid transport and metabolism	COG0174,E	6.3.1.2	CYT	6.31	53106.9
Q72P58	LIC12618	LysA	Diaminopimelate decarboxylase	Amino acid transport and metabolism	COG0019,E	4.1.1.20	CYT	6.41	46457.8
Q72NQ9	LIC12771	ProA	Glutamate-5-semialdehyde dehydrogenase	Amino acid transport and metabolism	COG0014,E	1.2.1.41	CYT	6.88	45794.9
Q72MN1	LIC13162	AroF	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	Amino acid transport and metabolism	COG2876,E	2.5.1.54	CYT	6.80	42396.5
P61524	LIC13324	ArgG	Argininosuccinate synthase	Amino acid transport and metabolism	COG0137,E	6.3.4.5	CYT	6.65	45074.6
Q72M38	LIC13353	AofA	Amine oxidase (flavin-containing)	Amino acid transport and metabolism	COG1231,E	1.4.3.4	IM	9.18	49194.1

Q75FI5	LIC20204	CsdB	Selenocysteine lyase	Amino acid transport and metabolism	COG0520,E	4.4.1.16	CYT	5.16	43455.2
Q72TC0	LIC11101	IlvD	Dihydroxy-acid dehydratase	Amino acid transport and metabolism / Carbohydrate transport and metabolism	COG0129,E,G	4.2.1.9	CYT	7.31	59415.6
Q72U22	LIC10842	DapA	Dihydrodipicolinate synthase/N-acetylneuraminate lyase	Amino acid transport and metabolism / Cell envelope biogenesis, outer membrane	COG0329,E,M		CYT	7.11	32035
Q72US5	LIC10582	TrpE	Anthranilate synthase (component I)	Amino acid transport and metabolism / Coenzyme metabolism	COG0147,E,H	4.1.3.27	CYT	4.76	52904.1
Q72M00	LIC13393	IlvC	Ketol-acid reductoisomerase	Amino acid transport and metabolism / Coenzyme metabolism	COG0059,E,H	1.1.1.86	CYT	6.63	36478.5
Q75FE5	LIC20249	AcnA	Aconitate hydratase	carbohydate metabolism, citric acid cycle	COG1048,C	4.2.1.3	CYT	6.84	81983.1
Q72TV3	LIC10913	TktN	Transketolase, N-terminal subunit	Carbohydrate Metabolism; Pentose phosphate pathway	COG3959,G	2.2.1.1	CYT	7.34	30262.6
Q72SM4	LIC11355	TktC	Transketolase, C-terminal subunit	Carbohydrate transport and metabolism	COG3958,G		CYT	6.87	34782
Q72RT8	LIC11652	MipB	Transaldolase	Carbohydrate transport and metabolism	COG0176,G		CYT	4.84	23490.2
Q72RH9	LIC11766	ManB-2	Phosphomannomutase	Carbohydrate transport and metabolism	COG1109,G	5.4.2.8	CYT	9.97	65038.2
Q72QZ8	LIC11954	Eno	Enolase	Carbohydrate transport and metabolism	COG0148,G	4.2.1.11	CYT	6.44	47044.4
Q75FD0	LIC20264	PykF	Pyruvate kinase	Carbohydrate transport and metabolism	COG0469,G	2.7.1.40	CYT	6.34	54101.4
Q72SW4	LIC11258	MreB	Actin-like ATPase involved in cell morphogenesis	Cell division and chromosome partitioning	COG1077,D		CYT	5.08	36835.6
Q72UQ0	LIC10607		Pyridoxal-phosphate-dependent aminotransferase	Cell envelope biogenesis, outer membrane	COG0399,M		CYT	6.53	41487.4
Q72U07	LIC10857		Zinc metalloprotease	Cell envelope biogenesis, outer membrane	COG0750,M		IM	6.07	63974.1
P61656	LIC11541	KdsA	3-deoxy-8-phosphooctulonate synthase	Cell envelope biogenesis, outer membrane	COG2877,M	2.5.1.55	CYT	7.46	31948.6
Q72QC5	LIC12187		pyridoxal-phosphate-dependent aminotransferase	Cell envelope biogenesis, outer membrane	COG0399,M		CYT	7.05	39928.6
Q72Q63	LIC12250	Prc-1	Periplasmic protease	Cell envelope biogenesis, outer membrane	COG0793,M	3.4.21.-	NON-CYT	7.81	67753.2
Q72P56	LIC12620		Membrane carboxypeptidase/Penicillin-binding protein	Cell envelope biogenesis, outer membrane	COG5009,M		IM	8.33	93430
Q72MD8	LIC13250	Lnt	Apolipoprotein N-acyltransferase	Cell envelope biogenesis, outer membrane	COG0815,M	2.3.1.-	IM	9.81	70742.2
Q72UN4	LIC10623	MotB-1	Endoflagellar motor protein	Cell motility and secretion	COG1360,N		IM	7.14	30275.7
Q72U75	LIC10787	FlaA-2	Endoflagellar filament sheath protein	Cell motility and secretion			PER	9.46	27179.9
Q72U74	LIC10788	FlaA-1	Endoflagellar filament sheath protein	Cell motility and secretion			PER	8.03	34888.6
Q72SK9	LIC11370	FliN-1	Endoflagellar motor switch protein	Cell motility and secretion	COG1886,N,U		CYT	4.33	36833.9
Q72SK8	LIC11371	FliO	Endoflagellar biogenesis protein	Cell motility and secretion	COG3190,N		IM	8.93	30038.1
Q72S96	LIC11488	CheX	Inhibitor of MCP methylation	Cell motility and secretion	COG1406,N		CYT	4.74	16724.3
Q72S55	LIC11531	FlaB-1	Endoflagellar filament core protein	Cell motility and secretion	COG1344,N		PER	7.91	31470.8
Q72S54	LIC11532	FlgL-1	Endoflagellar hook-filament protein	Cell motility and secretion	COG1344,N		PER	7.76	31318.4
Q72RN2	LIC11713		Endoflagellar motor protein	Cell motility and secretion	COG1360,N		IM	6.98	39641
Q72R59	LIC11889	FlaB-2	Endoflagellar filament core protein	Cell motility and secretion	COG1344,N		PER	9.26	31257.5
Q72R58	LIC11890	FlaB1	Endoflagellar filament core protein	Cell motility and secretion	COG1344,N		PER	7.10	31305.4
Q72NA5	LIC12931	MotA-2	Endoflagellar motor protein	Cell motility and secretion	COG1291,N		IM	7.55	26499.8

Q72MY3	LIC13056	MotB-3	Endoflagellar motor protein	Cell motility and secretion	COG1360,N		IM	9.34	24903.7
Q72W94	LIC10043		Methyl-accepting chemotaxis protein	Cell motility and secretion / Signal transduction mechanisms	COG0840,N,T		IM	5.89	62867.6
Q72T06	LIC11216		Methyl-accepting chemotaxis protein	Cell motility and secretion / Signal transduction mechanisms	COG0840,N,T		IM	4.70	63729.7
Q72S63	LIC11523		Methyl-accepting chemotaxis protein	Cell motility and secretion / Signal transduction mechanisms	COG0840,N,T		IM	5.44	108395
Q72NB4	LIC12921		Methyl-accepting chemotaxis protein	Cell motility and secretion / Signal transduction mechanisms	COG0840,N,T		NON-CYT	4.98	76737.1
Q72LZ9	LIC13394		Methyl-accepting chemotaxis protein	Cell motility and secretion / Signal transduction mechanisms	COG0840,N,T		IM	7.17	59325.8
Q72MM5	LIC13168	Gmd	GDP-mannose 4,6-dehydratase	cell wall biosynthesis	COG1089,M	4.2.1.47	CYT	8.33	38155.5
Q72SM5	LIC11354	MetK	Methionine adenosyltransferase	Coenzyme metabolism	COG0192,H	2.5.1.6	CYT	6.65	42033.6
Q72MN0	LIC13163	PanB	3-methyl-2-oxobutanoate hydroxymethyltransferase	Coenzyme metabolism	COG0413,H	2.1.2.11	CYT	5.65	28913.3
Q72N21	LIC13017		Efflux pump, AcrB family	Defense mechanisms	COG0841,V		IM	9.22	121230
Q72SA5	LIC11479	XerD	Site-specific recombinase XerD	DNA replication, recombination, and repair	COG4974,L		CYT	9.29	35073.1
Q72QK1	LIC12112	Ssb	Single-stranded DNA-binding protein	DNA replication, recombination, and repair	COG0629,L		CYT	4.98	16408
Q72M43	LIC13348		DNA topoisomerase (ATP-hydrolyzing), subunit B	DNA replication, recombination, and repair	COG0187,L	5.99.1.3	CYT	9.11	81524.3
Q72VY3	LIC10162	FumC	Fumarate hydratase	Energy production and conversion	COG0114,C	4.2.1.2	CYT	6.93	50396.4
Q72VD8	LIC10360	EtfA	Electron transfer flavoprotein, alpha subunit	Energy production and conversion	COG2025,C		CYT	9.21	32736.3
Q72TZ0	LIC10874		Fe-S-cluster-containing hydrogenase	Energy production and conversion	COG0437,C		CYT	8.40	112671
Q72TQ9	LIC10958		Zinc-binding alcohol dehydrogenase	Energy production and conversion	COG0604,C		CYT	7.25	36756.4
Q72SY5	LIC11237	AtpB	A Subunit of the H(+)-transporting two-sector ATPase, F0 sector	Energy production and conversion	COG0356,C	3.6.3.14	IM	6.88	39486.7
Q72SY4	LIC11238	AtpE	C subunit of the H(+)-transporting two-sector ATPase, F0 sector	Energy production and conversion	COG0636,C	3.6.3.14	IM	7.54	9678.24
Q72SY3	LIC11239	AtpF	B subunit of the H(+)-transporting two-sector ATPase, FO sector	Energy production and conversion	COG0711,C	3.6.3.14	IM	5.16	19042.3
Q72SY2	LIC11240	AtpH	Delta subunit of the H(+)-transporting two-sector ATPase, F1 sector	Energy production and conversion	COG0712,C	3.6.3.14	CYT	9.33	20751
Q72SY1	LIC11241	AtpA	Alpha subunit of the H(+)-transporting two-sector ATPase, F1 sector	Energy production and conversion	COG0056,C	3.6.3.14	CYT	5.48	55013.2
Q72SY0	LIC11242	AtpG	Gamma subunit of the H(+)-transporting two-sector ATPase, F1 sector	Energy production and conversion	COG0224,C	3.6.3.14	CYT	10.24	31719.7
Q72SX9	LIC11243	AtpD	Beta subunit of the H(+)-transporting two-sector ATPase, F1 sector	Energy production and conversion	COG0055,C	3.6.3.14	CYT	5.54	50565.6
Q72RR8	LIC11674		Alkylglycerone-phosphate synthase	Energy production and conversion	COG0277,C	2.5.1.26	CYT	9.62	64072.2
Q72RP5	LIC11699	GlpA-1	Glycerol-3-phosphate dehydrogenase	Energy production and conversion	COG0578,C	1.1.99.5	CYT	9.72	61772.4
P61975	LIC11781	Mdh	Malate dehydrogenase	Energy production and conversion	COG0039,C	1.1.1.37	CYT	7.45	34918
Q72R51	LIC11897	AcoA	Pyruvate dehydrogenase (lipoamide), alpha subunit	Energy production and conversion	COG1071,C	1.2.4.1	CYT	6.76	36747.6
Q72R50	LIC11898	AcoB	Pyruvate dehydrogenase (lipoamide), beta subunit	Energy production and conversion	COG0022,C	1.2.4.1	CYT	4.58	35744.8
Q72R23	LIC11928		FAD/FMN-containing dehydrogenase	Energy production and conversion	COG0277,C		CYT	10.04	56818
Q72QV6	LIC12002	SdhA	Succinate dehydrogenase/fumarate reductase subunit A	Energy production and conversion	COG1053,C	1.3.99.1	PER	8.60	70442.4
Q72QV5	LIC12003	SdhB	Succinate dehydrogenase/fumarate reductase subunit B	Energy production and conversion	COG0479,C	1.3.99.1	CYT	6.64	26649.6
Q72Q29	LIC12285		Inorganic pyrophosphatase	Energy production and conversion	COG3808,C		IM	5.56	73105.5
Q72PJ7	LIC12474	SucA	Oxoglutarate dehydrogenase (lipoamide), dehydrogenase (E1) component	Energy production and conversion	COG0567,C	1.2.4.2	CYT	6.49	103921
Q72PJ6	LIC12475	LpdA-1	Dihydrolipoamide dehydrogenase	Energy production and conversion	COG1249,C	1.8.1.4	CYT	7.15	50216.9
Q72PA2	LIC12573	SucC	Succinyl-CoA synthetase, beta subunit	Energy production and conversion	COG0045,C	6.2.1.5	CYT	5.73	41890.3
Q72PA1	LIC12574	SucD	Succinyl-CoA synthetase, alpha subunit	Energy production and conversion	COG0074,C	6.2.1.5	CYT	8.61	30193.1
Q72NS9	LIC12750	NuoL	NADH dehydrogenase (ubiquinone), L chain	Energy production and conversion	COG1009,C,P	1.6.5.3	IM	9.33	71217.5

Q72NK5	LIC12829	GltA-1	Citrate (Si)-synthase	Energy production and conversion	COG0372,C	2.3.3.1	CYT	7.10	48237.5
Q72NB1	LIC12925	GltA-2	Citrate synthase	Energy production and conversion	COG0372,C	2.3.3.1	CYT	8.27	48525.2
Q72MG4	LIC13223		Inorganic pyrophosphatase	Energy production and conversion	COG0221,C		CYT	4.94	20444.5
Q72ME4	LIC13244	IcdA	Isocitrate dehydrogenase	Energy production and conversion	COG0538,C	1.1.1.-	CYT	6.80	44762.1
Q72LT0	LIC13470		Reductase	Energy production and conversion	COG0369,P		CYT	8.06	34435.4
Q72NI8	LIC12846	RpoA	DNA-directed RNA polymerase, alpha subunit	Genetic Information Processing; Transcription; RNA polymerase	COG0202,K	2.7.7.6	CYT	4.57	36686.5
Q72SG2	LIC11421		Phosphate permease	Inorganic ion transport and metabolism	COG0306,P		IM	10.05	84071.6
Q72RN3	LIC11712	MgtE	Magnesium transporter	Inorganic ion transport and metabolism	COG2239,P		IM	4.53	51727.5
Q72QS7	LIC12032	KatE	Catalase	Inorganic ion transport and metabolism	COG0753,P	1.11.1.6	CYT	8.62	54676.4
Q72PI5	LIC12486		Membrane protein related to TerC	Inorganic ion transport and metabolism	COG0861,P		IM	9.81	26146.2
Q72SR5	LIC11310	Bfr	Bacterioferritin (cytochrome b1)	inorganic iron binding	COG2193,P		CYT	4.49	18123.7
Q72S17	LIC11570	GspD	Type II secretory pathway component, protein D	Intracellular trafficking and secretion	COG1450,N,U		IM	8.92	66464.3
Q72S14	LIC11573	GspG	Type II secretory pathway component, protein G	Intracellular trafficking and secretion	COG2165,N,U		NON-CYT	8.70	17877.4
Q72RW7	LIC11621		Biopolymer transport protein, TolQ-like	Intracellular trafficking and secretion	COG0811,U		IM	5.38	22022.8
Q72RW6	LIC11622		ExbD-related biopolymer transport protein	Intracellular trafficking and secretion	COG0848,U		NON-CYT	10.35	16660.4
Q72R08	LIC11944	SecA	Preprotein translocase, SecA subunit	Intracellular trafficking and secretion	COG0653,U		CYT	6.63	103529
Q72QX8	LIC11980	TatA	Sec-independent protein secretion pathway component	Intracellular trafficking and secretion	COG1826,U		NON-CYT	10.26	9301.68
Q72QL8	LIC12095	SecG	Preprotein translocase, SecG subunit	Intracellular trafficking and secretion	COG1314,U		IM	6.77	11700.7
Q72PD4	LIC12537	SecF	Preprotein translocase, SecF subunit	Intracellular trafficking and secretion	COG0341,U		IM	6.13	34318.8
Q72PD3	LIC12538	SecD	Preprotein translocase, SecD subunit	Intracellular trafficking and secretion	COG0342,U		IM	8.67	72161.5
Q72PD1	LIC12540	YajC	Preprotein translocase, YajC subunit	Intracellular trafficking and secretion	COG1862,U		NON-CYT	9.63	12060.1
Q72NI1	LIC12853	SecY	Preprotein translocase, SecY subunit	Intracellular trafficking and secretion	COG0201,U		IM	10.01	50851.4
Q72MZ3	LIC13046	LpxD-2	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	Lipid A biosynthesis; third step	COG1044,M	2.3.1.-	CYT	6.95	36859.7
Q72W46	LIC10094	FadD	Long-chain-fatty-acid--CoA ligase	Lipid metabolism	COG1022,I	6.2.1.3	CYT	9.57	77005.5
Q72VA5	LIC10396	PaaJ-4	Acetyl-CoA C-acetyltransferase	Lipid metabolism	COG0183,I	2.3.1.9	CYT	7.43	41046.2
Q72UU2	LIC10565	CaiD-3	Enoyl-CoA hydratase	Lipid metabolism	COG1024,I		CYT	6.55	28723.4
Q72US4	LIC10583		Acyl-CoA dehydrogenase	Lipid Metabolism	COG1960,I		CYT	6.19	42787.1
Q72TP7	LIC10970		Acyl-CoA dehydrogenase	Lipid metabolism	COG1960,I		CYT	6.77	42596.4
Q72TP3	LIC10974	PaaJ-2	Acetyl-CoA acetyltransferase	Lipid metabolism	COG0183,I	2.3.1.9	CYT	6.79	42957.1
Q72SM9	LIC11350	CaiA-3	Acyl-CoA dehydrogenase	Lipid metabolism	COG1960,I	1.3.99.-	CYT	5.62	65217.4
Q72SM0	LIC11359	MaoC	Acyl dehydratase	Lipid metabolism	COG2030,I		CYT	7.32	44035.2
Q72S69	LIC11517	AccA	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)	Lipid metabolism	COG4799,I	6.4.1.2	CYT	6.52	60320.5
Q72S68	LIC11518	AccC-2	Biotin carboxylase subunit of acetyl CoA carboxylase	Lipid metabolism	COG4770,I		CYT	6.64	102167
Q72RV8	LIC11630		Long-chain-fatty-acid--CoA ligase	Lipid metabolism	COG1022,I	6.2.1.3	CYT	9.00	76147.7
Q72RS0	LIC11672	CaiD-2	Enoyl-CoA hydratase/carnithine racemase	Lipid metabolism	COG1024,I	4.2.1.-	CYT	7.50	28603.1
Q72PH6	LIC12495		Enoyl-CoA hydratase/isomerase family protein	Lipid metabolism	COG1024,I		CYT	5.52	27586.8
Q72PC9	LIC12542	PgsA-1	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	Lipid metabolism	COG0558,I	2.7.8.5	IM	10.23	28118.3
Q72P47	LIC12629		Enoyl-CoA hydratase	Lipid metabolism	COG1024,I	4.2.1.17	CYT	6.53	30572.9
Q72NN7	LIC12795	PaaJ-1	Acetyl-CoA acetyltransferase	Lipid metabolism	COG0183,I	2.3.1.9	CYT	6.33	47280.2
Q72N29	LIC13009		Acyl-CoA dehydrogenase	Lipid metabolism	COG1960,I		CYT	5.79	61463.8
Q72M90	LIC13300	FadB	3-hydroxyacyl-CoA dehydrogenase	Lipid metabolism	COG1250,I	1.1.1.35	CYT	9.09	47837.9
Q72M89	LIC13301	PaaJ-5	Acetyl-CoA acetyltransferase	Lipid metabolism	COG0183,I	2.3.1.9	CYT	8.26	45838.1
Q72M72	LIC13318	FabD	[Acyl-carrier protein] S-malonyltransferase	Lipid metabolism	COG0331,I	2.3.1.39	CYT	6.33	42463.4
Q75FX3	LIC20058	MeaA	Methylmalonyl-CoA mutase	Lipid metabolism	COG2185,I	5.4.99.2	CYT	5.42	74877.5
Q75FW6	LIC20065	AcpP	Acyl carrier protein	Lipid metabolism / Secondary metabolites biosynthesis, transport, and catabolism	COG0236,I,Q		CYT	3.63	8502.39

Q75G05	LIC20010	HemB	Delta-aminolevulinic acid dehydratase	metabolism of cofactors and vitamins, porphyrin and chlorophyll	COG0113,H	4.2.1.24	CYT	7.61	35221.9
Q75G04	LIC20011	HemL	Glutamate-1-semialdehyde aminotransferase	metabolism of cofactors and vitamins, porphyrin and chlorophyll	COG0001,H	5.4.3.8	CYT	8.07	48526.5
Q72NI2	LIC12852	Adk	Adenylate kinase	Metabolism; Nucleotide Metabolism; Purine metabolism	COG0563,F	2.7.4.3	CYT	6.75	20593.7
Q72W72	LIC10065	Dcd	dCTP deaminase	Nucleotide transport and metabolism	COG0717,F	3.5.4.13	CYT	6.52	19527.6
Q72S00	LIC11587	NrdA	Ribonucleoside-triphosphate reductase, alpha subunit	Nucleotide transport and metabolism	COG0209,F	1.17.4.2	CYT	6.45	133918
Q72R32	LIC11919	ImdH	Inosine-5'-monophosphate dehydrogenase	Nucleotide transport and metabolism	COG0516,F	1.1.1.205	CYT	8.65	55880.8
Q72LZ4	LIC13399		Purine-nucleoside phosphorylase	Nucleotide transport and metabolism	COG0005,F	2.4.2.-	CYT	7.18	32069
Q72W26	LIC10115		Protein-disulfide isomerase	Posttranslational modification, protein turnover, chaperones	COG1651,O		IM	8.38	43738.6
Q72VT7	LIC10209	CyoB	Cytochrome C oxidase, subunit I	Posttranslational modification, protein turnover, chaperones	COG0843,C	1.10.3.-	IM	9.12	59012.5
Q72V70	LIC10432		ATP-dependent Zn protease	Posttranslational modification, protein turnover, chaperones	COG0465,O	3.4.24.-	IM	8.88	72543.6
P61444	LIC10525	GrpE	Chaperone protein, GrpE	Posttranslational modification, protein turnover, chaperones	COG0576,O		CYT	4.36	24231.6
Q72UP9	LIC10608	Lon	Endopeptidase La	Posttranslational modification, protein turnover, chaperones	COG0466,O	3.4.21.53	IM	9.41	94786.2
Q72T03	LIC11219	AhpC	Peroxiredoxin	Posttranslational modification, protein turnover, chaperones	COG0450,O	1.6.4.-	CYT	5.87	21516.8
Q72SG7	LIC11416		FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)	Posttranslational modification, protein turnover, chaperones	COG0544,O		CYT	5.48	52144.9
Q72SG6	LIC11417	ClpP-1	Protease subunit of endopeptidase Clp	Posttranslational modification, protein turnover, chaperones	COG0740,O,U	3.4.21.92	CYT	5.74	22112.2
Q72SF9	LIC11424		FKBP-type peptidyl-prolyl cis-trans isomerase	Posttranslational modification, protein turnover, chaperones	COG0545,O		NON-CYT	10.26	14003.3
Q72RY8	LIC11600	HslV	ATP-dependent protease HslVU (ClpYQ), peptidase subunit	Posttranslational modification, protein turnover, chaperones	COG5405,O		CYT	7.41	19584.4
Q72QU2	LIC12017	ClpA-1	Endopeptidase Clp, ATP-dependent proteolytic subunit	Posttranslational modification, protein turnover, chaperones	COG0542,O	3.4.21.92	CYT	6.36	96325
Q72NM1	LIC12812		Trypsin-like serine protease	Posttranslational modification, protein turnover, chaperones	COG0265,O		PER	8.89	41115
Q75FY7	LIC20044	HtpG	HSP90 molecular chaperone	Posttranslational modification, protein turnover, chaperones	COG0326,O		CYT	5.13	69753.1
Q75FI7	LIC20197		Cysteine protease	Posttranslational modification, protein turnover, chaperones	COG4870,O		NON-CYT	8.98	87780.8
Q72QY0	LIC11978	TrxA	Thioredoxin	Posttranslational modification, protein turnover, chaperones / Energy production and conversion	COG3118,O		CYT	4.62	11369.1
Q72R01	LIC11951	ClpP-2	Protease subunit of an ATP-dependent Clp protease	Posttranslational modification, protein turnover, chaperones / Intracellular trafficking and secretion	COG0740,O,U	3.4.21.92	CYT	6.03	21635
Q72MU7	LIC13092	SppA-3	Periplasmic serine protease	Posttranslational modification, protein turnover, chaperones / Intracellular trafficking and secretion	COG0616,O,U		PER	7.49	35093.2

Q75FW7	LIC20064		Short chain dehydrogenase	Secondary metabolites biosynthesis, transport, and catabolism	COG4221,R		CYT	8.48	26062.9
Q72TJ6	LIC11025		Anti-Sigma factor antagonist	Signal transduction mechanism	COG1366,T		CYT	5.78	12913.1
Q72VQ9	LIC10237		cAMP-binding protein	Signal transduction mechanisms	COG0664,T		CYT	9.66	46125.4
Q72VF3	LIC10344		AntiSigma factor antagonist, part (N-term)	Signal transduction mechanisms	COG1366,T		CYT	8.22	9649.04
Q72U02	LIC10862		Adenylate cyclase related protein	Signal transduction mechanisms	COG2114,T		IM	5.25	87381
Q72TW4	LIC10900		Adenylate/guanylate cyclase, part (N-term)	Signal transduction mechanisms	COG2114,T		IM	9.49	52770.8
Q72TW3	LIC10901		Adenylate/guanylate cyclase, part (C-term)	Signal transduction mechanisms	COG2114,T		UNK	10.59	15312.9
Q72TL4	LIC11004		Anti-sigma factor antagonist	Signal transduction mechanisms	COG1366,T		CYT	4.69	12439.2
Q72SF2	LIC11431		cAMP-dependent protein kinase	Signal transduction mechanisms	COG0664,T		CYT	6.25	18260.7
Q72SE6	LIC11437		Adenylate cyclase related protein	Signal transduction mechanisms	COG2114,T		IM	4.91	106645
Q72S40	LIC11546	HprK	HPr Serine kinase	Signal transduction mechanisms	COG1493,T	2.7.1.-	CYT	6.92	36118.7
Q72RN6	LIC11709		Sensor histidine kinase and response regulator of a two component complex	Signal transduction mechanisms	COG4251,T		CYT	5.54	95001
Q72QY1	LIC11977		CAP family transcription factor	Signal transduction mechanisms	COG0664,T		CYT	6.06	82641
Q72PL6	LIC12454		Response regulator, receiver domain	Signal transduction mechanisms	COG2204,T		CYT	5.25	13325.5
Q75FK7	LIC20175	DksA	DnaK suppressor protein	Signal transduction mechanisms	COG1734,T		CYT	4.71	16632.7
Q75FU2	LIC20089		Serine phosphatase RsbU, regulator of sigma subunit	Signal transduction mechanisms / Transcription	COG2208,T,K		CYT	4.62	64925.9
Q75FE0	LIC20254		Response regulator	Signal transduction mechanisms / Transcription	COG0745,T,K		CYT	5.49	27711.7
Q72SK1	LIC11380		RNA polymerase sigma subunit	Transcription	COG1191,K		CYT	4.96	30871.3
P61540	LIC11701	RpoD	DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)	Transcription	COG0568,K		CYT	9.68	67873.1
Q72P40	LIC12636	Rho	Transcription termination factor Rho	Transcription	COG1158,K		CYT	6.76	53790.1
Q72NX2	LIC12706	NusA	Transcription elongation factor	Transcription	COG0195,K		CYT	4.74	50893.1
Q75G28	LIC20021		ParB-like protein	Transcription	COG1475,K		CYT	10.48	26556.9
Q72VM5	LIC10272		Protein-synthesizing GTPase complex, EF-G component	Translation, ribosomal structure and biogenesis	COG0480,J	3.6.1.48	CYT	5.51	79001
Q72V71	LIC10431	Pth-2	Aminoacyl-tRNA hydrolase	Translation, ribosomal structure and biogenesis	COG0193,J	3.1.1.29	CYT	5.10	20992
Q72U13	LIC10851	Tsf	Translation elongation factor Ts	Translation, ribosomal structure and biogenesis	COG0264,J		CYT	5.52	22185.6
Q72U11	LIC10853	Frr	Ribosome recycling factor	Translation, ribosomal structure and biogenesis	COG0233,J		CYT	9.29	20600.7
Q72U06	LIC10858	ProS	Prolyl-tRNA ligase	Translation, ribosomal structure and biogenesis	COG0442,J	6.1.1.15	CYT	5.81	64843.3
Q72TF6	LIC11065	PcnB	tRNA nucleotidyltransferase	Translation, ribosomal structure and biogenesis	COG0617,J		CYT	10.23	57089
Q72T80	LIC11141		Ribonuclease D-related	Translation, ribosomal structure and biogenesis	COG0349,J		CYT	5.82	24748.6
Q72S74	LIC11511	Def	N-formylmethionyl-tRNA deformylase	Translation, ribosomal structure and biogenesis	COG0242,J	3.5.1.31	CYT	4.93	20379.3
Q72R38	LIC11913	LysU	Lysine--tRNA ligase	Translation, ribosomal structure and biogenesis	COG1190,J	6.1.1.6	CYT	5.46	56626.9
Q72PW7	LIC12350	GlyRS	Glycine--tRNA ligase	Translation, ribosomal structure and biogenesis	COG0423,J		CYT	5.84	53770.8
Q72PR7	LIC12400	IleS	Isoleucine--tRNA ligase	Translation, ribosomal structure and biogenesis	COG0060,J	6.1.1.5	CYT	6.66	104366
Q72NX7	LIC12701	Pnp	Polyribonucleotide nucleotidyltransferase	Translation, ribosomal structure and biogenesis	COG1185,J	2.7.7.8	CYT	6.08	76295.9
Q72NX3	LIC12705	InfB	Translation initiation factor 2 (IF-2; GTPase)	Translation, ribosomal structure and biogenesis	COG0532,J		CYT	9.51	92993.5

Q72NF9	LIC12875	TufB	Protein-synthesizing GTPase complex, EF-Tu component	Translation, ribosomal structure and biogenesis	COG0050,J	3.6.1.48	CYT	5.99	43573.9
Q72MR4	LIC13129	MetG	Methionine--tRNA ligase	Translation, ribosomal structure and biogenesis	COG0143,J	6.1.1.10	CYT	6.48	81099.1
Q72MG8	LIC13219	PheT	Phenylalanine--tRNA ligase beta subunit	Translation, ribosomal structure and biogenesis	COG0072,J	6.1.1.20	CYT	6.38	92049.4
Q72M80	LIC13310	PheS	Phenylalanine-tRNA synthetase alpha subunit	Translation, ribosomal structure and biogenesis	COG0016,J	6.1.1.20	CYT	6.52	38626.2
Q72V72	LIC10430	RplY	50S Ribosomal protein L25	Translation, ribosomal structure and biogenesis; transcription	COG1825,J		CYT	10.16	23069.5
P62436	LIC10749	RplK	50S Ribosomal protein L11	Translation, ribosomal structure and biogenesis; transcription	COG0080,J		CYT	10.46	15107.7
Q72UB1	LIC10750	RplA	50S Ribosomal protein L1	Translation, ribosomal structure and biogenesis; transcription	COG0081,J		CYT	10.27	24966.9
Q72UB0	LIC10751	RplJ	50S Ribosomal protein L10	Translation, ribosomal structure and biogenesis; transcription	COG0244,J		CYT	9.93	18851.7
Q72UA9	LIC10752	RplL	50S Ribosomal protein L7/L12	Translation, ribosomal structure and biogenesis; transcription	COG0222,J		CYT	4.98	12807.8
Q72UA6	LIC10755	RpsL	30S Ribosomal protein S12	Translation, ribosomal structure and biogenesis; transcription	COG0048,J		CYT	12.28	13943.3
Q72UA5	LIC10756	RpsG	30S Ribosomal protein S7	Translation, ribosomal structure and biogenesis; transcription	COG0049,J		CYT	10.66	18072.9
Q72UA0	LIC10761	RplM	50S Ribosomal protein L13	Translation, ribosomal structure and biogenesis; transcription	COG0102,J		CYT	10.48	16460.2
Q72U99	LIC10762	RpsI	30S Ribosomal protein S9	Translation, ribosomal structure and biogenesis; transcription	COG0103,J		CYT	11.43	14904.4
Q72U14	LIC10850	RpsB	30S Ribosomal protein S2	Translation, ribosomal structure and biogenesis; transcription	COG0052,J		CYT	5.92	33097.9
P62232	LIC11555	RpsP	30S Ribosomal protein S16	Translation, ribosomal structure and biogenesis; transcription	COG0228,J		CYT	10.79	10103.6
Q72S27	LIC11559	RplS	50S Ribosomal protein L19	Translation, ribosomal structure and biogenesis; transcription	COG0335,J		CYT	10.81	15522
Q72RP1	LIC11704	RpsU	30S Ribosomal protein S21	Translation, ribosomal structure and biogenesis; transcription	COG0828,J		CYT	10.95	7972.47
Q72RI5	LIC11760	RpmB	50S Ribosomal protein L28	Translation, ribosomal structure and biogenesis; transcription	COG0227,J		CYT	12.18	10552.4
Q72QK3	LIC12110	RplI	50S Ribosomal protein L9	Translation, ribosomal structure and biogenesis; transcription	COG0359,J		CYT	10.31	16607.3
Q72QK2	LIC12111	RpsR	30S Ribosomal protein S18	Translation, ribosomal structure and biogenesis; transcription	COG0238,J		CYT	11.50	9603.33
Q72QK0	LIC12113	RpsF	30S Ribosomal protein S6	Translation, ribosomal structure and biogenesis; transcription	COG0360,J		CYT	8.52	10711.2
Q72PM2	LIC12447	RpsA-2	30S Ribosomal protein S1	Translation, ribosomal structure and biogenesis; transcription	COG0539,J		CYT	5.96	63547.8
Q72NQ6	LIC12774	RpmA	50S Ribosomal protein L27	Translation, ribosomal structure and biogenesis; transcription	COG0211,J		CYT	11.54	9102.53
Q72NQ4	LIC12776	RplU	50S Ribosomal protein L21	Translation, ribosomal structure and biogenesis; transcription	COG0261,J		CYT	10.47	11878.6
Q72NI9	LIC12845	RplQ	50S Ribosomal protein L17	Translation, ribosomal structure and biogenesis; transcription	COG0203,J		CYT	11.28	20088.4
Q72NI7	LIC12847	RpsD	30S Ribosomal protein S4	Translation, ribosomal structure and biogenesis; transcription	COG0522,J		CYT	10.61	24043.7
Q72NI6	LIC12848	RpsK	30S Ribosomal protein S11	Translation, ribosomal structure and biogenesis; transcription	COG0100,J		CYT	11.18	14702.1

Q72NI5	LIC12849	RpsM	30S Ribosomal protein S13	Translation, ribosomal structure and biogenesis; transcription	COG0099,J		CYT	11.40	14038.4
Q72NI0	LIC12854	RplO	50S Ribosomal protein L15	Translation, ribosomal structure and biogenesis; transcription	COG0200,J		CYT	11.22	19865.1
Q72NH9	LIC12855	RpmD	50S Ribosomal protein L30	Translation, ribosomal structure and biogenesis; transcription	COG1841,J		CYT	11.82	6693.95
Q72NH8	LIC12856	RpsE	30S Ribosomal protein S5	Translation, ribosomal structure and biogenesis; transcription	COG0098,J		CYT	10.74	18124
Q72NH7	LIC12857	RplR	50S Ribosomal protein L18	Translation, ribosomal structure and biogenesis; transcription	COG0256,J		CYT	11.05	13522.8
Q72NH6	LIC12858	RplF	50S Ribosomal protein L6	Translation, ribosomal structure and biogenesis; transcription	COG0097,J		CYT	10.42	19782.1
Q72NH5	LIC12859	RpsH	30S Ribosomal protein S8	Translation, ribosomal structure and biogenesis; transcription	COG0096,J		CYT	10.56	15118.8
Q72NH3	LIC12861	RplE	50S Ribosomal protein L5	Translation, ribosomal structure and biogenesis; transcription	COG0094,J		CYT	10.37	20620.2
Q72NH2	LIC12862	RplX	50S Ribosomal protein L24	Translation, ribosomal structure and biogenesis; transcription	COG0198,J		CYT	11.16	13800.3
Q72NH0	LIC12864	RpsQ	30S Ribosomal protein S17	Translation, ribosomal structure and biogenesis; transcription	COG0186,J		CYT	11.09	10377.3
Q72NG9	LIC12865	RpmC	50S Ribosomal protein L29	Translation, ribosomal structure and biogenesis; transcription	COG0255,J		CYT	11.78	10958
Q72NG8	LIC12866	RplP	50S Ribosomal protein L16	Translation, ribosomal structure and biogenesis; transcription	COG0197,J		CYT	11.89	15505.2
Q72NG7	LIC12867	RpsC	30S Ribosomal protein S3	Translation, ribosomal structure and biogenesis; transcription	COG0092,J		CYT	10.79	25671.8
Q72NG6	LIC12868	RplV	50S Ribosomal protein L22	Translation, ribosomal structure and biogenesis; transcription	COG0091,J		CYT	11.74	12565.8
Q72NG5	LIC12869	RpsS	30S Ribosomal protein S19	Translation, ribosomal structure and biogenesis; transcription	COG0185,J		CYT	11.18	10668.4
Q72NG4	LIC12870	RplB	50S Ribosomal protein L2	Translation, ribosomal structure and biogenesis; transcription	COG0090,J		CYT	10.96	30650.2
Q72NG3	LIC12871	RplW	50S Ribosomal protein L23	Translation, ribosomal structure and biogenesis; transcription	COG0089,J		CYT	10.98	11803.8
Q72NG2	LIC12872	RplD	50S Ribosomal protein L4	Translation, ribosomal structure and biogenesis; transcription	COG0088,J		CYT	10.73	23325.9
Q72NG1	LIC12873	RplC	50S Ribosomal protein L3	Translation, ribosomal structure and biogenesis; transcription	COG0087,J		CYT	10.77	21838.1
Q72NG0	LIC12874	RpsJ	30S Ribosomal protein S10	Translation, ribosomal structure and biogenesis; transcription	COG0051,J		CYT	10.43	11467.3
Q72W61	LIC10076		Uncharacterized protein	Unknown			CYT	5.22	11004
Q72W45	LIC10095		Uncharacterized protein	Unknown			NON-CYT	9.94	9086.34
Q72VY4	LIC10161		Uncharacterized protein	Unknown			CYT	7.87	81029.9
Q72VU0	LIC10206		Uncharacterized protein	Unknown			CYT	11.15	7812.22
Q72VS7	LIC10219		Uncharacterized protein	Unknown			CYT	7.19	30943.8
Q72VR5	LIC10231		Uncharacterized protein	Unknown			NON-CYT	5.04	37703
Q72VR1	LIC10235		Uncharacterized protein	Unknown			CYT	10.63	10784.6
Q72VQ2	LIC10244		Uncharacterized protein	Unknown			CYT	4.89	29409.7
Q72VD6	LIC10362		Uncharacterized protein	Unknown			IM	9.44	15655.4
Q72V17	LIC10486		Uncharacterized protein	Unknown			CYT	6.16	38999.7
Q72UZ1	LIC10512		Uncharacterized protein	Unknown			NON-CYT	8.92	31872.7
Q72UI5	LIC10672		Uncharacterized protein	Unknown			NON-CYT	9.19	26922.2
Q72U96	LIC10765		Uncharacterized protein	Unknown			NON-CYT	9.66	14506.2
Q72U89	LIC10772		Uncharacterized protein	Unknown			NON-CYT	9.18	30150.6

Q72TK9	LIC11009		Uncharacterized protein	Unknown			NON-CYT	5.47	28365.4
Q72T39	LIC11182		Uncharacterized protein	Unknown			CYT	11.11	19079.6
Q72SV4	LIC11268		Uncharacterized protein	Unknown			OM	8.82	68851.1
Q72SU9	LIC11274		Uncharacterized protein	Unknown			NON-CYT	9.52	43248.1
Q72S95	LIC11489		Uncharacterized protein	Unknown			NON-CYT	5.34	46423.5
Q72S85	LIC11499		Uncharacterized protein	Unknown			CYT	10.81	9059.46
Q72RW3	LIC11625		Uncharacterized protein	Unknown			NON-CYT	8.80	17103.6
Q72RU0	LIC11650		Uncharacterized protein	Unknown			CYT	9.73	41067.6
Q72RQ1	LIC11693		Uncharacterized protein	Unknown			NON-CYT	6.55	18697.7
Q72RG1	LIC11784		Uncharacterized protein	Unknown			NON-CYT	8.63	24207
Q72RC0	LIC11826		Uncharacterized protein	Unknown			CYT	10.02	30612
Q72RA0	LIC11848		Uncharacterized protein	Unknown			NON-CYT	8.57	32021.2
Q72QN8	LIC12075		Uncharacterized protein	Unknown			NON-CYT	9.19	32961.4
Q72QM9	LIC12084		Uncharacterized protein	Unknown			CYT	8.42	40145.4
Q72Q50	LIC12263		Uncharacterized protein	Unknown			NON-CYT	6.69	37517.9
Q72PW8	LIC12349		Uncharacterized protein	Unknown			IM	9.91	64753.7
Q72PS0	LIC12397		Uncharacterized protein	Unknown			CYT	6.57	68916.2
Q72PM3	LIC12446		Uncharacterized protein	Unknown			CYT	9.73	27904
Q72PL1	LIC12460		Uncharacterized protein	Unknown			CYT	3.66	23671.6
Q72NY3	LIC12695		Uncharacterized protein	Unknown			CYT	5.77	50175.3
Q72NM7	LIC12805		Uncharacterized protein	Unknown			IM	7.69	38344.7
Q72NL2	LIC12822		Uncharacterized protein	Unknown			CYT	6.39	30209.3
Q72NA0	LIC12936		Uncharacterized protein	Unknown			NON-CYT	9.51	26876.8
Q72N79	LIC12958		Uncharacterized protein	Unknown			CYT	9.37	11214.2
Q72MR5	LIC13128		Uncharacterized protein	Unknown			CYT	4.74	19312.2
Q72MM7	LIC13166		Uncharacterized protein	Unknown			NON-CYT	8.80	36212.2
Q72MC0	LIC13268		Uncharacterized protein	Unknown			IM	7.78	17199.9
Q72M77	LIC13313		Uncharacterized protein	Unknown			NON-CYT	9.23	42378.3
Q72M28	LIC13363		Uncharacterized protein	Unknown			NON-CYT	9.54	29526.9
Q72LS9	LIC13471		Uncharacterized protein	Unknown			CYT	4.87	8139.24
Q75FR8	LIC20113		Uncharacterized protein	Unknown			CYT	9.77	21575.2
Q75FR4	LIC20118		Uncharacterized protein	Unknown			CYT	9.88	12763.1
Q75FL7	LIC20165		Uncharacterized protein	Unknown			CYT	9.03	44785.8
Q75FI8	LIC20196		Uncharacterized protein	Unknown			NON-CYT	9.36	17174
Q75FI6	LIC20198		Uncharacterized protein	Unknown	COG2200,T		CYT	4.99	52014.6
Q75FC2	LIC20272		Uncharacterized protein	Unknown			CYT	8.63	38802.8
NA	LIC2_SPN3857		Uncharacterized protein	Unknown			CYT	4.49	10326.7
Q72WC8	LIC10009		Uncharacterized lipoprotein	Unknown			NON-CYT	6.73	27700.8
Q72W17	LIC10124		Uncharacterized lipoprotein	Unknown			NON-CYT	6.11	60434.7
Q72UU9	LIC10558		Uncharacterized lipoprotein	Unknown			NON-CYT	10.10	17300.2
Q72TY5	LIC10879		Uncharacterized lipoprotein	Unknown			NON-CYT	8.45	17955.6
NA	LIC13520		Uncharacterized lipoprotein	Unknown			NON-CYT	9.26	58226.4
Q75FL0	LIC20172		Uncharacterized lipoprotein	Unknown	COG5422,T		NON-CYT	5.08	71720.9
NA	LIC2_SPN3853		Uncharacterized lipoprotein	Unknown			NON-CYT	8.50	9766.71
Q72VT5	LIC10211		Uncharacterized lipoprotein	Unknown			NON-CYT	8.76	10845.9
Q72VJ6	LIC10301		Uncharacterized lipoprotein	Unknown			NON-CYT	8.06	13445.6
Q72UZ6	LIC10507		Uncharacterized lipoprotein	Unknown			NON-CYT	5.48	24021.4
Q72TN2	LIC10985		Uncharacterized lipoprotein	Unknown			NON-CYT	9.36	40107.2
Q72QY9	LIC11966		Uncharacterized lipoprotein	Unknown			NON-CYT	5.98	17836.2
Q72Q81	LIC12231		Uncharacterized lipoprotein	Unknown			NON-CYT	9.15	21453.6
Q72ND9	LIC12895		Uncharacterized lipoprotein	Unknown			NON-CYT	6.94	25565.1
Q72MW3	LIC13076		Uncharacterized lipoprotein	Unknown			NON-CYT	9.83	28159.1
Q72LY3	LIC13410		Uncharacterized lipoprotein	Unknown			NON-CYT	8.66	14227.5
Q72WB0	LIC10027		Conserved uncharacterized protein	Unknown	COG3748,S		IM	9.59	25746.5

Q72W73	LIC10064		Conserved uncharacterized protein	Unknown	COG4731,S		NON-CYT	9.59	17389
Q72W37	LIC10103		Conserved uncharacterized protein	Unknown			CYT	10.15	22854.4
Q72W24	LIC10117		Conserved uncharacterized protein	Unknown	COG4805,S		NON-CYT	9.20	70380.6
Q72VX0	LIC10175		Conserved uncharacterized protein	Unknown			CYT	5.73	54179
Q72VT1	LIC10215		Conserved uncharacterized protein	Unknown	COG4956,R		IM	7.17	36920.7
Q72VI3	LIC10314		Conserved uncharacterized protein	Unknown			NON-CYT	8.90	63679.6
Q72VH9	LIC10318		Conserved uncharacterized protein	Unknown			OM	9.24	72817.3
Q72VC1	LIC10380		Conserved uncharacterized protein	Unknown	COG3449,L		NON-CYT	8.75	20941.7
Q72V90	LIC10411		Conserved uncharacterized protein	Unknown			NON-CYT	7.52	17243.7
Q72V20	LIC10483		Conserved uncharacterized protein	Unknown	COG4260,S		CYT	5.43	36148.3
Q72UV6	LIC10551		Conserved uncharacterized protein	Unknown			NON-CYT	9.15	41570.9
Q72US9	LIC10578		Conserved uncharacterized protein	Unknown	COG1413,C		NON-CYT	9.50	55260.7
Q72UQ6	LIC10601		Conserved uncharacterized protein	Unknown			CYT	6.53	17096.6
Q72UL4	LIC10643		Conserved uncharacterized protein	Unknown			CYT	8.17	50082.8
Q72UJ5	LIC10662		Conserved uncharacterized protein	Unknown			NON-CYT	7.66	20352.4
Q72UA1	LIC10760		Conserved uncharacterized protein	Unknown	COG2353,S		NON-CYT	9.83	23034.5
Q72U97	LIC10764		Conserved uncharacterized protein	Unknown			CYT	9.48	18364.2
Q72TZ1	LIC10873		Conserved uncharacterized protein	Unknown			NON-CYT	8.28	18650.2
Q72TY8	LIC10876		Conserved uncharacterized protein	Unknown			CYT	8.20	20699.9
Q72TY7	LIC10877		Conserved uncharacterized protein	Unknown			CYT	9.21	17732
Q72TY6	LIC10878		Conserved uncharacterized protein	Unknown	COG5557,C		IM	8.89	46373.1
Q72TU8	LIC10918		Conserved uncharacterized protein	Unknown	COG3832,S		CYT	6.51	19141.9
Q72TN3	LIC10984		Conserved uncharacterized protein	Unknown	COG1262,S		NON-CYT	8.65	33245.1
Q72TG2	LIC11059		Conserved uncharacterized protein	Unknown			CYT	4.87	10044.2
Q72T25	LIC11196		Conserved uncharacterized protein	Unknown			CYT	6.53	17317
Q72T13	LIC11209		Conserved uncharacterized protein	Unknown			CYT	5.78	15055.2
Q72SZ8	LIC11224		Conserved uncharacterized protein	Unknown			NON-CYT	7.09	39951.6
Q72SV0	LIC11273		Conserved uncharacterized protein	Unknown	COG1655,S		CYT	8.51	33166.9
Q72SP3	LIC11334		Conserved uncharacterized protein	Unknown	COG2968,S		NON-CYT	9.14	25116.9
Q72SJ3	LIC11389		Conserved uncharacterized protein	Unknown			NON-CYT	4.56	24385.1
Q72SH7	LIC11405		Conserved uncharacterized protein	Unknown			CYT	8.73	76763.4
Q72S33	LIC11553		Conserved uncharacterized protein	Unknown	COG2815,S		NON-CYT	8.57	37007.4
Q72RV3	LIC11635		Conserved uncharacterized protein	Unknown	COG2013,S		CYT	5.71	23638.1
Q72R87	LIC11861		Conserved uncharacterized protein	Unknown	COG4929,S		NON-CYT	8.34	20958.3
Q72QZ7	LIC11955		Conserved uncharacterized protein	Unknown			CYT	3.64	19067.1
Q72QZ4	LIC11958		Conserved uncharacterized protein	Unknown	COG1413,C		NON-CYT	8.60	45451.3
Q72QY5	LIC11972		Conserved uncharacterized protein	Unknown			CYT	7.54	15094.2
Q72QV7	LIC12001		Conserved uncharacterized protein	Unknown			IM	10.31	24960.6
Q72QS2	LIC12040		Conserved uncharacterized protein	Unknown	COG2764,S		CYT	5.01	16484.8
Q72QC4	LIC12188		Conserved uncharacterized protein	Unknown	COG2227,H		CYT	6.74	46218.9
Q72QB9	LIC12193		Conserved uncharacterized protein	Unknown			CYT	5.43	30591.7
Q72Q65	LIC12247		Conserved uncharacterized protein	Unknown			CYT	8.91	18941.6
Q72Q37	LIC12277		Conserved uncharacterized protein	Unknown			NON-CYT	10.44	28580.6
Q72PZ0	LIC12325		Conserved uncharacterized protein	Unknown			CYT	8.38	21029.9
Q72PY9	LIC12326		Conserved uncharacterized protein	Unknown			CYT	4.18	14273
Q72PU6	LIC12371		Conserved uncharacterized protein	Unknown			CYT	4.51	17807.1
Q72PD2	LIC12539		Conserved uncharacterized protein	Unknown			NON-CYT	10.64	27451.1
Q72PA6	LIC12568		Conserved uncharacterized protein	Unknown			CYT	5.91	31874.6
Q72P55	LIC12621		Conserved uncharacterized protein	Unknown	COG1664,M		CYT	5.98	14522.4
Q72MY9	LIC13050		Conserved uncharacterized protein	Unknown			NON-CYT	5.02	39232.9
Q72MR9	LIC13123		Conserved uncharacterized protein	Unknown			NON-CYT	6.81	33139.2
Q72ML0	LIC13183		Conserved uncharacterized protein	Unknown			CYT	6.96	13819.8
Q72MJ7	LIC13196		Conserved uncharacterized protein	Unknown			CYT	9.98	28248.6
Q72MH3	LIC13214		Conserved uncharacterized protein	Unknown			IM	9.61	21664.5

Q72M76	LIC13314		Conserved uncharacterized protein	Unknown			IM	9.19	75562.9
Q72M59	LIC13332		Conserved uncharacterized protein	Unknown			CYT	4.20	8667.69
Q75G12	LIC20001		Conserved uncharacterized protein	Unknown			OM	6.42	90967.8
Q75FZ9	LIC20016		Conserved uncharacterized protein	Unknown			IM	9.63	36104.2
Q75FT5	LIC20096		Conserved uncharacterized protein	Unknown			CYT	9.25	40457.1
Q75FJ1	LIC20191		Conserved uncharacterized protein	Unknown			CYT	9.49	76377.9
Q75FI4	LIC20205		Conserved uncharacterized protein	Unknown	COG1633,S		CYT	10.38	32144.8
Q72UM9	LIC10628		Conserved uncharacterized lipoprotein	Unknown			NON-CYT	8.48	14817.9
Q72R63	LIC11885		conserved uncharacterized lipoprotein	Unknown			OM	6.90	44713.7
Q75G29	LIC20035		Conserved uncharacterized lipoprotein	Unknown	COG2849,S		NON-CYT	8.97	49905.8
Q72RC4	LIC11822	LeuC	3-isopropylmalate dehydratase, large subunit	NA	COG0065,E	4.2.1.33	CYT	6.99	50641.7
Q72RC5	LIC11821	LeuD	3-isopropylmalate dehydratase, small subunit	NA	COG0066,E	4.2.1.33	CYT	5.71	23596.9
Q72RH7	LIC11768	LeuB-1	3-isopropylmalate dehydrogenase	NA	COG0473,C,E	1.1.1.85	CYT	5.84	38870.6
Q72PZ2	LIC12323	FabH	3-oxoacyl-[acyl-carrier protein] synthase	NA	COG0332,I	2.3.1.41	CYT	6.69	35134
Q72RG5	LIC11780	BioF	8-amino-7-oxononanoate synthase	NA	COG0156,H	2.3.1.47	CYT	8.29	41743.8
Q72R12	LIC11940		AcrA-related membrane protein	NA	COG0845,M		IM	8.78	36552.8
Q72NU0	LIC12739		Acyl dehydratase	NA	COG2030,I		CYT	8.75	17088.8
Q72UQ7	LIC10600		Acyl dehydratase, MaoC family	NA	COG2030,I		CYT	7.44	15149.3
Q72TC6	LIC11095		Adenylate/guanylate cyclase, part (C-term)	NA	COG2114,T		IM	7.08	40727.3
Q72PA7	LIC12565		Adenylosuccinate synthase	NA	COG0104,F	6.3.4.4	CYT	7.54	47056.9
P61703	LIC10763	AlaS	Alanine--tRNA ligase	NA	COG0013,J	6.1.1.7	CYT	6.01	108515
Q72QE6	LIC12166		Alcohol dehyodrogenase	NA	COG1454,C		CYT	6.99	39768.8
Q72Q79	LIC12233		Aldolase	NA	COG1830,G		CYT	7.25	37977.1
Q72T81	LIC11140		Alpha-galactosidase	NA	COG3345,G		CYT	9.28	73882.1
Q72PS5	LIC12392		Amidase	NA	COG0154,J		CYT	9.66	54410.6
Q72QE4	LIC12168		Aminotransferase	NA	COG0399,M		CYT	6.85	44359.8
Q72V61	LIC10441	AmtB	Ammonia permease	NA	COG0004,P		IM	7.23	45133.3
Q72ML7	LIC13176		Aryl-alcohol dehydrogenase-related oxidoreductase	NA	COG0667,C		CYT	8.54	39715.3
Q72NC5	LIC12909	LysC	Aspartate kinase	NA	COG0527,E	2.7.2.4	CYT	6.44	43059.3
Q75FC8	LIC20266	Asd	Aspartate-semialdehyde dehydrogenase	NA	COG0136,E	1.2.1.11	CYT	8.47	38031.9
Q72VE7	LIC10351		ATP-binding protein of an ABC transporter complex	NA	COG1131,V		CYT	9.60	33388.7
Q72UW9	LIC10538		ATP-binding protein of an ABC transporter complex	NA	COG0488,R		IM	4.99	60875.1
Q72Q04	LIC12311		ATP-binding protein of an ABC transporter complex	NA	COG1136,V		CYT	4.83	24654.2
Q72PE5	LIC12526		ATP-binding protein of an ABC transporter complex	NA	COG1118,P		CYT	6.76	40301.9
Q72M74	LIC13316		ATP-binding protein of an ABC transporter complex	NA	COG1131,V		CYT	7.50	34872.1
Q72VF8	LIC10339	ClpA-3	ATP-dependent Clp protease	NA	COG0542,O		CYT	6.61	95304.8
Q75FT8	LIC20093		Bacterioferritin comigratory protein	NA	COG1225,O		CYT	5.80	17733.1
Q72SG9	LIC11413		Beta-glucosidase-related glycosidase	NA	COG1472,G		NON-CYT	8.50	64962
Q72PD7	LIC12534	RibAB	Bifunctional 3,4-dihydroxy-2-butanone 4-phosphate	NA	COG0108,H	3.5.4.25	CYT	5.86	44361.1
Q72PJ5	LIC12476	AceF	Bifunctional dihydrolipoyllysine-residue	NA	COG0508,C	2.3.1.12	CYT	7.19	45197.9
NA	LIC1_SPN3184		Bifunctional dihydrolipoyllysine-residue	NA	COG0508,C	2.3.1.12	CYT	7.69	49036.7
Q72PA9	LIC12563		Bifunctional glycerol-3-phosphate dehydrogenase /glycerol-3-phosphate acyltransferase	NA	COG0240,C		CYT	8.37	75133.9
Q72N17	LIC13021		cAMP-dependent protein kinase	NA	COG0664,T		CYT	7.14	95355.2
P61442	LIC10524	DnaK	Chaperone protein, Hsp70	NA	COG0443,O		CYT	4.85	69098.7
NA	LIC13522	CheA	Chemotaxis protein histidine kinase	NA	COG0643,N,T		CYT	4.75	119746
Q72PL4	LIC12457	CheW	Chemotaxis signal transduction protein	NA	COG0835,N,T		CYT	4.25	18595.3
Q72T27	LIC11194	CitE	Citrate lyase, beta subunit	NA	COG2301,G	4.1.3.6	CYT	6.51	37061.4
Q72PX6	LIC12341		Component of an ABC transporter system	NA	COG2854,Q		NON-CYT	9.83	22899.3
Q72V96	LIC10405		Conserved uncharacterized protein containing tetratricopeptide repeat (TPR) domains	NA	COG1729,S		NON-CYT	6.20	78007.8
Q72VH2	LIC10325		Conserved uncharacterized protein with tetratricopeptide repeat domain	NA	COG1729,S		NON-CYT	5.98	43370.6
Q72Q11	LIC12303	Prc-2	C-terminal processing periplasmic-protease-3	NA	COG0793,M		PER	8.93	51529.4

Q72U71	LIC10791		Cyclic nucleotide binding protein	NA	COG0664,T		CYT	9.32	23779.8
Q72RC6	LIC11820	CysK-3	Cysteine synthase	NA	COG0031,E	2.5.1.47	CYT	9.19	37012.2
Q72VT8	LIC10208	CyoA	Cytochrome C oxidase subunit II	NA	COG1622,C	1.10.3.-	IM	7.97	37679.3
Q72SC8	LIC11456	LipL31	Cytoplasmic membrane lipoprotein, LipL31	NA			IM	7.35	27620.7
Q72RY6	LIC11602		Dehydrogenase	NA	COG2133,G		CYT	8.98	57645.7
Q72QW6	LIC11992		Dehydrogenase	NA	COG0111,H,E		CYT	7.12	44788.5
Q72W68	LIC10069		Dioxygenase superfamily protein	NA	COG0346,E		CYT	3.89	13657.3
Q72RF4	LIC11791		DNA or RNA helicase of superfamily II	NA	COG1061,K,L		CYT	6.75	64575.7
Q72M44	LIC13347		DNA topoisomerase (ATP-hydrolyzing), subunit A	NA	COG0188,L	5.99.1.3	CYT	8.69	54076.9
Q72UQ1	LIC10606	Dps	DNA-binding ferritin-like protein	NA	COG0783,P		CYT	6.01	18228.6
Q72WD5	LIC10002	DnaN	DNA-directed DNA polymerase, beta subunit	NA	COG0592,L	2.7.7.7	CYT	4.76	41443.1
Q72UA8	LIC10753	RpoB	DNA-directed RNA polymerase, beta subunit	NA	COG0085,K	2.7.7.6	CYT	5.56	137767
Q72UA7	LIC10754	RpoC	DNA-directed RNA polymerase, beta subunit	NA	COG0086,K	2.7.7.6	CYT	6.96	157624
Q72S75	LIC11510		Efflux pump, AcrB family	NA	COG0841,V		IM	6.94	120334
Q72VD7	LIC10361	EftB	Electron transfer flavoprotein, beta subunit	NA	COG2086,C		CYT	5.46	27068
Q72UN3	LIC10624	FliL	Endoflagellar basal body-associated protein	NA	COG1580,N		PER	4.51	19206.1
Q72SI8	LIC11394	FliH	Endoflagellar biosynthesis/type III secretory pathway protein	NA	COG1317,N,U		CYT	4.72	35818.8
Q72NV4	LIC12725		Enoyl-CoA hydratase/carnithine racemase	NA	COG1024,I		CYT	8.45	29764.2
Q72RZ8	LIC11590	XseB	Exodeoxyribonuclease VII, small subunit	NA	COG1722,L	3.1.11.6	CYT	4.50	10854.2
Q72ST1	LIC11294		Fe-S oxidoreductase	NA	COG0247,C		IM	6.51	77136.3
Q72TY9	LIC10875		Fe-S-cluster-containing hydrogenase, membrane component	NA	COG5557,C		IM	7.76	52036.3
Q72T74	LIC11147		Flavin reductase related protein	NA	COG1853,R		CYT	6.22	17397.7
Q72TQ8	LIC10959		Flavoprotein	NA	COG2072,P		NON-CYT	9.71	53881.9
Q75G27	LIC20022		Flavoprotein	NA	COG0431,R		CYT	8.65	22305.5
Q72NY4	LIC12694	GltB	Glutamate synthase (NADH)	NA	COG0069,E	1.4.1.13	CYT	6.58	166269
Q72RE6	LIC11799	GlpK-1	Glycerol kinase	NA	COG0554,C	2.7.1.30	CYT	9.56	55085.9
Q72VI8	LIC10309	GcvP	Glycine dehydrogenase (decarboxylating), protein P	NA	COG1003,E	1.4.4.2	CYT	6.54	106324
Q72V51	LIC10452		Glycosyltransferase	NA	COG0463,M		CYT	9.03	26480.7
Q72UN7	LIC10620		Glycosyltransferase	NA	COG0438,M		CYT	9.85	42432.9
Q72TJ7	LIC11024		Glycosyltransferase	NA	COG0463,M		CYT	9.69	37951
Q72QD3	LIC12179		Glycosyltransferase	NA	COG0463,M		CYT	9.66	35580.4
Q72U26	LIC10838		Glyoxalase	NA	COG3324,R		CYT	4.41	16221
Q72WA0	LIC10037		GMC-family oxidoreductase	NA	COG2303,E		CYT	8.64	58470.7
Q72U73	LIC10789	GreA	greA transcription elongation factor related protein	NA	COG1747,S		CYT	5.62	106948
Q72RB6	LIC11832		GTP cyclohydrolase-1 related protein	NA	COG0780,R		CYT	7.50	15352.6
Q72RA4	LIC11844		HflC membrane associated protease	NA	COG0330,O		IM	5.07	35195.6
Q72RA3	LIC11845		HflC membrane associated protease	NA	COG0330,O		IM	8.88	35083.3
P62359	LIC12564		Histidine biosynthesis protein	NA	COG0124,J		CYT	6.17	39113.5
P62458	LIC11453	HisD	Histidinol dehydrogenase	NA	COG0141,E	1.1.1.23	CYT	9.67	46380.6
Q72NN1	LIC12801		Hydrolase or acyltransferase	NA	COG0596,R		CYT	10.43	34339.8
Q72UW1	LIC10546		Hydrolase or acyltransferase, alpha/beta hydrolase superfamily, lipoprotein	NA	COG3243,I		NON-CYT	8.57	40267
Q72U64	LIC10800		Hydroxyethylthiazole kinase family	NA	COG2145,H		CYT	5.86	27371.6
P61660	LIC10112	HisB	Imidazoleglycerol-phosphate dehydratase or histidinol-phosphatase	NA	COG0131,E	3.1.3.15 ~~~ 4.2.1.19	CYT	6.65	23167.6
Q72M63	LIC13328	LeuB-2	Isocitrate dehydrogenase (NADP+)	NA	COG0473,C,E	1.1.1.42	CYT	7.16	53888
Q72PR6	LIC12401		Leucine-rich-repeat protein	NA	COG4886,S		NON-CYT	8.79	24581.7
Q72MX9	LIC13060	LipL36	LipL36, outer membrane lipoprotein	NA			OM	4.63	37620.1
Q72N71	LIC12966	LipL41	LipL41 lipoprotein	NA			OM	7.96	38938.7
Q72W18	LIC10123		LipL45-related lipoprotein	NA	COG4254,S		NON-CYT	8.85	33712.4
Q72RB4	LIC11834		LipL45-related lipoprotein	NA	COG4254,S		NON-CYT	4.91	34682

Q75FJ7	LIC20185		LipL45-related lipoprotein	NA			NON-CYT	8.45	26204.9
Q72TW2	LIC10902		LipL45-related protein	NA			UNK	9.84	41705.5
Q72TL5	LIC11003	LipL71	LipL71 lipoprotein	NA			NON-CYT	5.34	62027.3
Q72RU5	LIC11643	LipL45	Lipoprotein LipL45	NA	COG4254,S		IM	7.59	42101
Q72VR4	LIC10232	LolE-1	Lipoprotein releasing system, LolE permease component	NA	COG4591,M		IM	9.56	50974.3
Q72SM7	LIC11352	LipL32	Major outer membrane protein (MOMP), LipL32 lipoprotein	NA			OM	6.81	29612.9
Q72QK7	LIC12106		Membrane-associated HD superfamily hydrolase	NA	COG1480,R		IM	8.73	91067.6
Q72LR2	LIC13491	ArgE	Metallopeptidase	NA	COG0624,E		CYT	8.73	53758
Q72QH2	LIC12141		N-acetyl glucosamine/N-acetyl galactosamine epimerase	NA	COG1086,M,G		CYT	8.57	38942
Q72W91	LIC10046	PntA	NAD(P)(+) transhydrogenase (AB-specific), alpha subunit	NA	COG3288,C	1.6.1.2	IM	10.11	41418.8
Q72VK7	LIC10290	PntB	NAD(P)(+) transhydrogenase , beta component	NA	COG1282,C	1.6.1.2	IM	5.41	49189.7
Q72NT7	LIC12742	NuoB	NADH dehydrogenase (ubiquinone), B chain	NA	COG0377,C	1.6.5.3	CYT	7.82	20577.8
Q72NT6	LIC12743	NuoC	NADH dehydrogenase (ubiquinone), C chain	NA	COG0852,C	1.6.5.3	CYT	5.63	20599.5
Q72NT5	LIC12744	NuoD	NADH dehydrogenase (ubiquinone), D chain	NA	COG0649,C	1.6.5.3	CYT	6.09	46117
Q72NT4	LIC12745	NuoE	NADH dehydrogenase (ubiquinone), E chain	NA	COG1905,C	1.6.5.3	CYT	4.72	18209.6
Q72NT3	LIC12746	NuoF	NADH dehydrogenase (ubiquinone), F chain	NA	COG1894,C	1.6.5.3	CYT	7.47	48529.6
Q72NT2	LIC12747	NuoH	NADH dehydrogenase (ubiquinone), H chain	NA	COG1005,C	1.6.5.3	IM	8.28	38964.3
Q72NU9	LIC12730		NHL repeat protein	NA	COG3391,S		OM	9.72	76452.1
Q72M65	LIC13326	Ndk	Nucleoside-diphosphate kinase	NA	COG0105,F	2.7.4.6	CYT	7.67	15254.4
Q72QB0	LIC12202		Nucleoside-diphosphate-sugar epimerase	NA	COG0451,M,G		CYT	6.69	36606.6
Q72VV5	LIC10191		OmpA-family lipoprotein	NA	COG2885,M		NON-CYT	8.98	20912.5
Q72UR5	LIC10592		OmpA-family protein	NA	COG2885,M		OM	9.42	53006
Q75FE4	LIC20250		OmpA-family protein	NA	COG2885,M		OM	10.09	44251
Q72T26	LIC11195	ArgF	Ornithine carbamoyltransferase	NA	COG0078,E	2.1.3.3	CYT	6.52	35415.7
Q72LZ8	LIC13395		OsmC/Ohr family protein	NA	COG1764,O		CYT	6.95	17725.1
Q72UY1	LIC10522		Oxidoreductase	NA	COG0673,R		CYT	6.76	36036.5
Q72RG3	LIC11782		Oxidoreductase	NA	COG1651,O		CYT	7.92	39757.4
Q72VS6	LIC10220		ParA-like protein	NA	COG1192,D		CYT	6.68	28607.1
Q72LR5	LIC13488		ParB-like protein	NA	COG1475,K		CYT	10.18	32511.6
Q72RA9	LIC11839	PpiB-2	Peptidylprolyl isomerase	NA	COG0652,O	5.2.1.8	CYT	8.56	32428.1
Q72RF2	LIC11793	SppA-2	Periplasmic serine protease (ClpP class)	NA	COG0616,O,U	3.4.21.-	NON-CYT	9.29	36644.1
Q72LX7	LIC13416		Permease	NA	COG3329,R		IM	7.14	34684.4
Q72VT0	LIC10216	PckA	Phosphoenolpyruvate carboxykinase (ATP)	NA	COG1866,C	4.1.1.49	CYT	7.25	59174.3
P62414	LIC12091	Pgk	Phosphoglycerate kinase	NA	COG0126,G	2.7.2.3	CYT	10.06	43002
Q72MW8	LIC13071		Phospholipid binding protein	NA	COG1881,R		NON-CYT	9.55	19958.8
Q72UH7	LIC10680	PurS	Phosphoribosylformylglycinamidine synthase	NA	COG1828,F	6.3.5.3	CYT	7.35	9299.86
Q75FP0	LIC20142		Phosphoribosyltransferase	NA	COG0503,F		CYT	6.54	19281.6
Q72VY8	LIC10157	YidC	Preprotein translocase, YidC subunit	NA	COG0706,U		IM	9.33	71489.4
Q72TF8	LIC11063	Lgt	Prolipoprotein diacylglyceryltransferase	NA	COG0682,M	2.4.99.-	IM	8.18	36707.9
P62217	LIC11745	RecA	RecA recombinase	NA	COG0468,L		CYT	6.95	39686.6
Q72UV0	LIC10557		Receiver component of a response regulator	NA	COG2204,T		CYT	6.80	26017.3
Q72MV1	LIC13088		Receiver component of a two-component response regulator	NA	COG2197,T,K		CYT	7.16	24519.3
Q72V73	LIC10429	PrsA	Ribose-phosphate diphosphokinase	NA	COG0462,FE	2.7.6.1	CYT	7.18	33846.9
Q72SG0	LIC11423		RNA binding protein	NA	COG0724,R		CYT	10.20	12996.6
Q72VS1	LIC10225		RNA polymerase sigma subunit	NA	COG1595,K		CYT	5.88	35445.4
Q72QX3	LIC11985		RNA-binding protein	NA	COG0724,R		CYT	9.55	10151.5
Q75FU8	LIC20083	SahH	S-adenosylhomocysteine hydrolase	NA	COG0499,H	3.3.1.1	CYT	6.08	48233.3
Q72W77	LIC10060		Serine phosphatase RsbU, regulator of sigma subunit	NA	COG2208,T,K		IM	6.46	122167
Q72NL3	LIC12821		Shape determination protein	NA	COG1664,M		UNK	9.06	15851.2

Q72UF7	LIC10700		Short chain dehydrogenase	NA	COG1028,I,Q,R		CYT	8.44	27169.2
Q72SL5	LIC11364		Short chain dehydrogenase	NA	COG0300,R		CYT	10.04	28597.3
Q72R22	LIC11929		Short chain dehydrogenase	NA	COG0300,R		CYT	10.35	26948.5
Q72PZ5	LIC12320		Short chain dehydrogenase	NA	COG1028,I,Q,R		CYT	7.98	27134.4
Q75G18	LIC20026		Short chain dehydrogenase	NA	COG0300,R		CYT	10.74	26881.4
Q75FT4	LIC20097		Short chain dehydrogenase	NA	COG4221,R		CYT	10.15	29414.5
Q72SY9	LIC11233	LepB-2	Signal peptidase I	NA	COG0681,U	3.4.21.89	IM	6.20	38431.6
Q72QN5	LIC12078		Signal transduction protein	NA	COG1639,T		CYT	7.19	55889.8
Q75FT1	LIC20100		Signal transduction protein	NA	COG1639,T		CYT	7.03	31588.6
Q72PZ1	LIC12324		Signal transduction protein with multiple domains	NA	COG3899,R		CYT	6.00	201611
Q72QA2	LIC12210	IbpA-1	Small heat shock protein (molecular chaperone)	NA	COG0071,O		CYT	6.81	15588.6
Q72QA1	LIC12211	IbpA-2	Small heat shock protein (molecular chaperone)	NA	COG0071,O		CYT	5.39	14999.9
NA	LIC2_SPN3825	SpeE	Spermidine synthase	NA	COG0421,E	2.5.1.16	CYT	6.28	31956.8
Q72TK6	LIC11013		Substrate binding protein of an ABC transporter complex	NA	COG0747,E		PER	8.85	70146
Q72SV5	LIC11267		Substrate binding protein of an ABC transporter complex	NA	COG1613,P		PER	9.66	37478.6
Q72QB5	LIC12197		Sugar pyridoxal-phosphate-dependent aminotransferase	NA	COG0399,M		CYT	6.80	41048.9
Q72QB4	LIC12198		Sugar pyridoxal-phosphate-dependent aminotransferase	NA	COG0399,M		CYT	6.99	41248.4
Q72M24	LIC13367	CysI	Sulfite reductase (NADPH), alpha subunit	NA	COG0155,P	1.8.1.2	CYT	6.62	62467.7
Q72PZ4	LIC12321		Thioesterase	NA	COG0824,R		CYT	9.73	32907.3
Q72TA6	LIC11115	SseA	Thiosulfate sulfurtransferase	NA	COG2897,P	2.8.1.1	CYT	9.51	31821.3
Q72PK6	LIC12465	ThrS	Threonine--tRNA ligase	NA	COG0441,J	6.1.1.3	CYT	6.71	73786
Q72Q80	LIC12232		Thymidylate synthase	NA	COG1351,F		CYT	7.18	60923.1
Q72PA0	LIC12575		TolC-like protein	NA	COG1538,M,U		OM	9.51	59860.3
Q75FH3	LIC20216	ExbB	TolQ-like transport protein	NA	COG0811,U		IM	8.84	22190.9
Q72W16	LIC10125		TPR-repeat-containing lipoprotein	NA			NON-CYT	9.48	135262
Q72QW8	LIC11990		TPR-repeat-containing protein	NA			OM	4.19	133846
Q72UB3	LIC10748	NusG	Transcription antiterminator	NA	COG0250,K		CYT	7.51	20454.6
Q72W09	LIC10132		Transcriptional regulator	NA	COG3604,K,T		CYT	5.29	78157.9
Q72VT2	LIC10214		Transcriptional regulator	NA	COG1329,K		CYT	9.22	20555.8
Q72QU3	LIC12016		Transcriptional regulator	NA	COG1476,K		CYT	9.98	16502.3
Q72PN0	LIC12438		Transcriptional regulator	NA			CYT	8.91	16753.1
Q72PL8	LIC12452		Transcriptional regulator	NA	COG1386,K		CYT	4.66	19707.8
Q72PC7	LIC12544		Transcriptional regulator	NA	COG1426,S		CYT	5.02	41529.1
Q72RX1	LIC11617		Transcriptional regulator, ArsR family	NA	COG0640,K		CYT	10.47	11178
Q72QB8	LIC12194	TktC	Transketolase, C-terminal subunit	NA	COG3958,G		CYT	5.92	34219.8
Q72QL9	LIC12094	TpiA	Triosephosphate isomerase	NA	COG0149,G	5.3.1.1	CYT	7.56	27237.2
Q75FN9	LIC20143		Trypsin-like serine protease	NA	COG0265,O		NON-CYT	8.66	56920.9
Q72QB3	LIC12199	GalE	UDP-glucose 4-epimerase	NA	COG0451,MG	5.1.3.2	CYT	6.64	36998.2
Q72UV9	LIC10548		Uracil-DNA glycosylase	NA	COG1573,L	3.2.2.-	CYT	9.23	22821.5
Q72M95	LIC13293		Zinc dependent protease	NA	COG4783,R		NON-CYT	8.75	74852.5
Q72VP3	LIC10253		Zinc-binding dehydrogenase	NA	COG1064,R		CYT	7.59	45516.2
Q72MD1	LIC13257		Zn-dependent oxidoreductase	NA	COG0604,C		CYT	9.88	37404.6
Q72U93	LIC10768		Zn-dependent peptidase	NA	COG0612,R		NON-CYT	8.45	62280.5
Q72U92	LIC10769		Zn-dependent peptidase	NA	COG0612,R		NON-CYT	9.71	64109.1