Table S1. The *L. pneumophila rpoS* mutant microarray data set

ORF	**Product**	***Gene***	**Category**	**Spot Intensity† (JR32, E Phase)**	**Spot Intensity† (*rpoS*, E Phase)**	**Spot Intensity† (JR32, PE Phase)**	**Spot Intensity† (*rpoS*, PE Phase)**	**T-Test (*rpoS*, JR32) E**	**T-Test (*rpoS*, JR32) PE**	**Ratio* (*rpoS* E/ JR32 E)**	**Ratio* (*rpoS* PE/ JR32 PE)**
lpg0001	chromosomal replication initiator protein DnaA	*dnaA*	Replication and Repair	13.046	13.044	11.044	13.675	9.96E-01	4.57E-04	0.00	2.63
lpg0001	chromosomal replication initiator protein DnaA	*dnaA*	Replication and Repair	12.614	12.683	10.242	12.991	9.40E-01	1.95E-02	0.07	2.75
lpg0002	DNA polymerase III beta chain		Nucleotide Metabolism, Replication an	12.613	12.219	11.063	12.781	5.50E-01	2.67E-03	-0.39	1.72
lpg0002	DNA polymerase III beta chain		Nucleotide Metabolism, Replication an	12.707	12.053	10.802	12.784	2.95E-01	2.40E-03	-0.65	1.98
lpg0003	DNA recombination and repair protein ATPase RecF		Replication and Repair	11.267	9.069	9.617	8.747	1.17E-04	2.44E-01	-2.20	-0.87
lpg0003	DNA recombination and repair protein ATPase RecF		Replication and Repair	11.153	8.917	9.329	9.258	2.37E-02	9.30E-01	-2.24	-0.07
lpg0004	DNA gyrase subunit B	*gyrB*	Replication and Repair	11.975	11.747	11.717	12.141	2.41E-01	7.86E-02	-0.23	0.42
lpg0004	DNA gyrase subunit B	*gyrB*	Replication and Repair	11.877	11.617	11.530	12.083	4.56E-01	1.41E-02	-0.26	0.55
lpg0005	peptidylarginine deiminase		Named proteins of general function	11.591	9.941	10.869	10.871	3.40E-04	9.97E-01	-1.65	0.00
lpg0005	peptidylarginine deiminase		Named proteins of general function	11.500	9.392	10.427	11.081	3.35E-03	1.40E-01	-2.11	0.65
lpg0006	biosynthetic arginine decarboxylase	*speA*	Amino Acid Metabolism	9.700	10.066	8.450	10.752	6.52E-01	1.91E-02	0.37	2.30
lpg0006	biosynthetic arginine decarboxylase	*speA*	Amino Acid Metabolism	10.149	10.026	8.201	10.988	7.13E-01	2.19E-03	-0.12	2.79
lpg0007	probable hydrolase (carbon-nitrogen hydrolase, beta-alanine syntheta		Named proteins of general function	11.774	12.125	11.234	11.844	6.29E-01	3.08E-01	0.35	0.61
lpg0007	probable hydrolase (carbon-nitrogen hydrolase, beta-alanine syntheta		Named proteins of general function	11.161	11.915	10.643	11.815	5.59E-03	5.62E-05	0.75	1.17
lpg0008	ORF		ORFs of unknown function (unique)	11.857	12.578	10.727	11.764	2.75E-01	5.75E-02	0.72	1.04
lpg0008	ORF		ORFs of unknown function (unique)	11.981	12.630	10.757	11.903	2.70E-01	2.90E-02	0.65	1.15
lpg0009	host factor-I protein for bacteriophage Q beta replication	*hfq*	Signal transduction / other regulatory f	9.205	10.762	11.302	9.932	8.38E-02	3.22E-01	1.56	-1.37
lpg0009	host factor-I protein for bacteriophage Q beta replication	*hfq*	Signal transduction / other regulatory f	9.530	10.766	11.410	10.111	1.10E-01	3.53E-01	1.24	-1.30
lpg0010	GTP binding protein HflX (GTPase)		Signal transduction / other regulatory f	11.363	10.233	11.677	11.489	1.32E-02	3.75E-01	-1.13	-0.19
lpg0010	GTP binding protein HflX (GTPase)		Signal transduction / other regulatory f	11.323	10.640	11.766	11.656	5.07E-03	6.54E-01	-0.68	-0.11
lpg0011	thiol-disulfide oxidoreductase ResA (thioredoxin) (cytochr	*resA*	Energy Metabolism	11.797	13.490	11.900	12.967	2.85E-05	4.51E-04	1.69	1.07
lpg0011	thiol-disulfide oxidoreductase ResA (thioredoxin) (cytochr	*resA*	Energy Metabolism	11.732	13.493	11.723	13.006	8.38E-06	5.09E-05	1.76	1.28
lpg0012	ORF	*cegC1*	ORFs of unknown function (unique)	9.908	10.023	11.585	10.141	7.85E-01	9.99E-04	0.12	-1.44
lpg0012	ORF	*cegC1*	ORFs of unknown function (unique)	10.057	11.023	11.669	10.789	1.65E-01	1.54E-01	0.97	-0.88
lpg0013	pirin (metal binding transcription factor or enzyme?)		Transcription factors / DNA binding prc	9.763	9.512	13.037	9.226	8.26E-01	5.56E-03	-0.25	-3.81
lpg0013	pirin (metal binding transcription factor or enzyme?)		Transcription factors / DNA binding prc	10.060	9.447	13.084	9.906	5.81E-01	4.00E-02	-0.61	-3.18
lpg0014	transmembrane protein		Unknown / hypothetical proteins	9.925	9.853	9.880	9.165	9.14E-01	6.33E-01	-0.07	-0.72
lpg0014	transmembrane protein		Unknown / hypothetical proteins	10.044	8.930	9.979	9.473	1.94E-01	6.85E-01	-1.11	-0.51
lpg0015	multidrug resistance protein (efflux pump protein FarA)		Transport and binding	8.555	9.125	9.137	7.225	6.26E-01	2.94E-01	0.57	-1.91
lpg0015	multidrug resistance protein (efflux pump protein FarA)		Transport and binding	8.604	8.187	9.314	8.567	4.84E-01	1.64E-01	-0.42	-0.75
lpg0016	ORF		ORFs of unknown function (unique)	9.995	9.621	10.903	9.172	4.93E-01	3.09E-02	-0.37	-1.73
lpg0016	ORF		ORFs of unknown function (unique)	9.966	9.264	10.546	9.015	1.21E-01	3.82E-02	-0.70	-1.53
lpg0017	ORF		ORFs of unknown function (unique)	8.842	9.002	9.507	8.177	8.49E-01	6.11E-02	0.16	-1.33
lpg0017	ORF		ORFs of unknown function (unique)	9.214	9.403	9.514	8.429	7.79E-01	1.43E-01	0.19	-1.09
lpg0018	outer membrane efflux (channel) protein		Transport and binding	9.312	9.026	10.602	9.213	4.96E-01	1.32E-03	-0.29	-1.39
lpg0018	outer membrane efflux (channel) protein		Transport and binding	8.919	10.346	10.309	10.127	1.50E-01	7.79E-01	1.43	-0.18
lpg0019	hemagglutinin/protease, zinc metalloprotease		Toxin production / other pathogen func	9.985	11.592	10.604	9.474	2.31E-05	2.36E-02	1.61	-1.13
lpg0019	hemagglutinin/protease, zinc metalloprotease		Toxin production / other pathogen func	9.777	11.294	10.541	9.950	3.75E-04	5.06E-02	1.52	-0.59
lpg0020	integral membrane protein		Named proteins of general function	10.822	10.086	10.506	9.706	2.04E-01	1.33E-01	-0.74	-0.80
lpg0020	integral membrane protein		Named proteins of general function	10.808	9.660	10.203	10.008	7.40E-02	6.52E-01	-1.15	-0.20
lpg0021	alpha helix protein		Unknown / hypothetical proteins	10.758	9.143	10.037	8.550	2.70E-04	1.77E-01	-1.62	-1.49
lpg0021	alpha helix protein		Unknown / hypothetical proteins	10.569	9.258	10.095	9.935	4.50E-02	5.25E-01	-1.31	-0.16
lpg0022	conserved hypothetical protein (oxidoreductase, N6-adenine specific		Nucleotide Metabolism	10.223	10.270	10.406	10.952	9.37E-01	4.35E-01	0.05	0.55
lpg0022	conserved hypothetical protein (oxidoreductase, N6-adenine specific		Nucleotide Metabolism	10.219	10.657	10.475	11.425	1.61E-01	6.35E-03	0.44	0.95
lpg0023	transmembrane protein COG4539		Unknown / hypothetical proteins	11.570	11.344	14.051	10.110	7.57E-01	9.74E-05	-0.23	-3.94
lpg0023	transmembrane protein COG4539		Unknown / hypothetical proteins	11.561	11.734	14.098	10.367	8.42E-01	1.18E-03	0.17	-3.73
lpg0024	hemin binding protein Hbp (Legionella pneumophila)		Toxin production / other pathogen func	9.416	10.792	8.553	9.690	4.18E-02	6.64E-02	1.38	1.14
lpg0024	hemin binding protein Hbp (Legionella pneumophila)		Toxin production / other pathogen func	8.803	11.306	8.552	10.115	4.90E-02	5.69E-04	2.50	1.56
lpg0025	Rcp (PagP like gene conferring resistance to cationic antimicrobial pe		Toxin production / other pathogen func	9.708	10.009	9.377	9.286	4.16E-01	9.02E-01	0.30	-0.09
lpg0025	Rcp (PagP like gene conferring resistance to cationic antimicrobial pe		Toxin production / other pathogen func	9.245	8.882	8.922	9.821	7.45E-01	2.89E-01	-0.36	0.90
lpg0026	amino acid permease COG0531		Transport and binding	10.113	11.885	11.264	10.132	6.79E-03	1.46E-01	1.77	-1.13
lpg0026	amino acid permease COG0531		Transport and binding	10.043	12.087	11.239	10.154	4.83E-03	1.44E-01	2.04	-1.08
lpg0027	low affinity inorganic phosphate transporter	*pit*	Transport and binding	10.908	9.455	10.527	10.202	5.85E-02	3.96E-01	-1.45	-0.33
lpg0027	low affinity inorganic phosphate transporter	*pit*	Transport and binding	10.122	11.397	9.283	11.436	1.85E-01	2.00E-02	1.27	2.15
lpg0028	ubiquinone biosynthesis protein COQ7, central metabolic regulatory p		Energy Metabolism	10.685	10.062	9.094	10.105	2.69E-01	3.16E-01	-0.62	1.01
lpg0028	ubiquinone biosynthesis protein COQ7, central metabolic regulatory p		Energy Metabolism	10.925	10.324	8.462	11.159	1.98E-01	1.64E-03	-0.60	2.70
lpg0029	sensory box (GGDEF/EAL domain) regulatory protein (ni	*rre41*	Signal transduction / other regulatory f	8.039	8.921	9.887	9.354	1.60E-01	4.59E-01	0.88	-0.53
lpg0029	sensory box (GGDEF/EAL domain) regulatory protein (ni	*rre41*	Signal transduction / other regulatory f	8.344	10.458	10.154	9.932	9.59E-03	7.25E-01	2.11	-0.22

lpg0030	ORF		ORFs of unknown function (unique)	9.947	10.979	10.396	11.527	1.50E-03	1.49E-03	1.03	1.13
lpg0030	ORF		ORFs of unknown function (unique)	9.846	11.046	9.649	11.499	3.31E-04	1.69E-04	1.20	1.85
lpg0031	ORF		ORFs of unknown function (unique)	10.050	11.301	11.545	11.659	2.15E-01	9.15E-01	1.25	0.11
lpg0031	ORF		ORFs of unknown function (unique)	11.987	13.435	13.220	13.794	7.51E-03	4.50E-01	1.45	0.57
lpg0032	leucine aminopeptidase		Protein fate / hydrolases / secretion	9.673	10.758	9.056	10.650	6.51E-02	1.84E-04	1.08	1.59
lpg0032	leucine aminopeptidase		Protein fate / hydrolases / secretion	9.674	10.688	8.532	10.972	1.06E-01	5.46E-03	1.01	2.44
lpg0033	ORF		ORFs of unknown function (unique)	10.288	11.486	10.172	10.456	7.78E-03	3.43E-01	1.20	0.28
lpg0033	ORF		ORFs of unknown function (unique)	10.275	11.288	9.930	10.395	4.66E-02	2.29E-01	1.01	0.46
lpg0034	unknown protein		Unknown / hypothetical proteins	10.230	8.921	11.810	9.871	1.28E-02	2.31E-03	-1.31	-1.94
lpg0034	unknown protein		Unknown / hypothetical proteins	10.257	9.499	11.734	10.249	4.35E-02	1.25E-05	-0.76	-1.49
lpg0035	small ORF (118aa)		ORFs of unknown function (unique)	8.430	9.006	8.526	8.351	4.70E-01	8.79E-01	0.58	-0.18
lpg0035	small ORF (118aa)		ORFs of unknown function (unique)	9.615	10.852	9.421	10.858	3.99E-01	2.10E-01	1.24	1.44
lpg0036	conserved hypothetical protein		Unknown / hypothetical proteins	9.504	7.933	9.202	8.964	4.07E-02	3.50E-01	-1.57	-0.24
lpg0036	conserved hypothetical protein		Unknown / hypothetical proteins	9.631	9.046	9.073	9.328	1.51E-01	4.10E-01	-0.58	0.26
lpg0037	arginine 3rd transport system periplasmic binding protein	*artJ*	Transport and binding	8.062	10.143	12.710	8.299	1.99E-01	2.37E-02	2.08	-4.41
lpg0037	arginine 3rd transport system periplasmic binding protein	*artJ*	Transport and binding	7.922	10.690	12.757	10.592	7.86E-02	3.37E-01	2.77	-2.16
lpg0038	RIKEN cDNA 4921520G13 gene	*legA10*	Unknown / hypothetical proteins	10.025	11.068	10.707	9.184	1.89E-02	1.61E-02	1.04	-1.52
lpg0038	RIKEN cDNA 4921520G13 gene	*legA10*	Unknown / hypothetical proteins	9.950	11.098	10.420	8.958	3.70E-03	2.47E-02	1.15	-1.46
lpg0039	small ORF (118aa)		ORFs of unknown function (unique)	8.822	7.904	8.729	7.410	1.50E-01	4.61E-01	-0.92	-1.32
lpg0039	small ORF (118aa)		ORFs of unknown function (unique)	7.621	7.345	7.823	8.955	8.70E-01	7.75E-01	-0.28	1.13
lpg0040	integral membrane protein (YhfP-like protein)		Named proteins of general function	9.797	9.149	9.716	9.551	4.22E-01	7.52E-01	-0.65	-0.17
lpg0040	integral membrane protein (YhfP-like protein)		Named proteins of general function	9.645	8.885	9.491	9.341	3.22E-01	8.12E-01	-0.76	-0.15
lpg0041	ORF		ORFs of unknown function (unique)	9.219	9.723	9.242	9.887	2.23E-01	3.74E-01	0.50	0.65
lpg0041	ORF		ORFs of unknown function (unique)	9.197	9.522	8.874	9.849	4.55E-01	2.54E-01	0.32	0.97
lpg0042	ORF		ORFs of unknown function (unique)	10.711	9.466	10.910	10.111	1.47E-01	2.99E-02	-1.25	-0.80
lpg0042	ORF		ORFs of unknown function (unique)	10.702	10.156	10.588	10.331	1.58E-01	3.29E-01	-0.55	-0.26
lpg0043	hypothetical (membrane protein, amino acid transporter?)		Unknown / hypothetical proteins	11.314	11.080	10.696	9.744	4.34E-01	6.50E-02	-0.23	-0.95
lpg0043	hypothetical (membrane protein, amino acid transporter?)		Unknown / hypothetical proteins	11.276	11.019	10.602	9.947	4.34E-01	1.57E-01	-0.26	-0.65
lpg0044	hypothetical (sterol desaturase)		Lipid Metabolism	7.743	8.501	8.889	7.924	3.09E-01	4.16E-01	0.76	-0.96
lpg0044	hypothetical (sterol desaturase)		Lipid Metabolism	8.226	8.624	8.163	7.631	3.57E-01	7.25E-01	0.40	-0.53
lpg0045	small ORF (70aa)		ORFs of unknown function (unique)	11.655	11.683	11.884	11.378	9.00E-01	2.95E-02	0.03	-0.51
lpg0045	small ORF (70aa)		ORFs of unknown function (unique)	11.690	12.289	11.960	11.848	2.64E-01	7.51E-01	0.60	-0.11
lpg0046	small ORF (132aa)		ORFs of unknown function (unique)	9.885	10.886	9.443	10.278	2.98E-02	1.47E-01	1.00	0.84
lpg0046	small ORF (132aa)		ORFs of unknown function (unique)	10.255	10.735	9.336	10.325	1.07E-02	5.26E-02	0.48	0.99
lpg0047	chloramphenicol acetyltransferase (highly similar to antibiotic acetyltra		Detoxification / adaptation	10.121	10.430	10.886	9.129	1.64E-01	1.46E-03	0.31	-1.76
lpg0047	chloramphenicol acetyltransferase (highly similar to antibiotic acetyltra		Detoxification / adaptation	10.209	10.293	10.926	9.230	8.44E-01	1.17E-03	0.08	-1.70
lpg0048	acetyltransferase		Named proteins of general function	8.751	9.875	8.696	9.823	1.67E-01	2.55E-01	1.12	1.13
lpg0048	acetyltransferase		Named proteins of general function	9.488	11.061	9.549	11.042	1.24E-01	1.33E-01	1.57	1.49
lpg0049	amino acid transporter, permease		Transport and binding	7.319	9.567	6.524	9.598	1.32E-02	2.23E-02	2.25	3.07
lpg0049	amino acid transporter, permease		Transport and binding	7.389	10.739	6.799	10.801	6.61E-03	4.01E-05	3.35	4.00
lpg0050	integral membrane protein		Named proteins of general function	8.846	8.571	10.491	8.795	5.61E-01	6.95E-02	-0.28	-1.70
lpg0050	integral membrane protein		Named proteins of general function	8.611	8.811	10.560	9.250	3.26E-01	4.32E-02	0.20	-1.31
lpg0051	hypothetical (membrane associated protein, conserved domain protei		Named proteins of general function	11.632	11.477	9.994	11.040	6.02E-01	4.50E-02	-0.15	1.05
lpg0051	hypothetical (membrane associated protein, conserved domain protei		Named proteins of general function	11.720	11.308	10.442	11.506	1.30E-01	1.90E-02	-0.41	1.06
lpg0052	carboxyphosphoenolpyruvate phosphonomutase (carboxyvinyl-carbo		Carbohydrate Metabolism	12.006	12.221	10.481	12.310	7.79E-01	3.32E-03	0.21	1.83
lpg0052	carboxyphosphoenolpyruvate phosphonomutase (carboxyvinyl-carbo		Carbohydrate Metabolism	11.907	12.319	9.960	12.369	6.16E-01	1.57E-03	0.41	2.41
lpg0053	transferase enzyme		Named proteins of general function	11.006	9.216	10.354	10.065	5.59E-03	5.62E-01	-1.79	-0.29
lpg0053	transferase enzyme		Named proteins of general function	10.770	9.386	10.347	10.322	1.66E-02	9.59E-01	-1.38	-0.03
lpg0054	ORF		ORFs of unknown function (unique)	11.320	10.992	10.347	11.365	4.24E-01	4.07E-02	-0.33	1.02
lpg0054	ORF		ORFs of unknown function (unique)	11.146	11.082	10.267	11.849	9.27E-01	7.10E-03	-0.06	1.58
lpg0055	transcriptional regulator, LysR family		Transcription factors / DNA binding pro	8.251	9.013	8.546	9.185	2.94E-01	2.42E-01	0.76	0.64
lpg0055	transcriptional regulator, LysR family		Transcription factors / DNA binding pro	7.915	9.285	8.204	9.196	1.23E-01	3.97E-01	1.37	0.99
lpg0056	ORF		ORFs of unknown function (unique)	11.045	12.186	13.217	11.147	8.38E-02	5.42E-03	1.14	-2.07
lpg0056	ORF		ORFs of unknown function (unique)	10.978	12.261	13.059	11.183	4.47E-02	1.99E-02	1.28	-1.88
lpg0057	putative regulator, MerR family COG0789 transcription regulators		Transcription factors / DNA binding pro	9.861	9.645	10.278	9.058	3.33E-01	1.74E-02	-0.22	-1.22
lpg0057	putative regulator, MerR family COG0789 transcription regulators		Transcription factors / DNA binding pro	10.035	9.753	10.401	9.423	4.41E-01	2.27E-02	-0.28	-0.98
lpg0058	hypothetical		Unknown / hypothetical proteins	9.553	10.026	11.280	9.587	2.73E-01	4.59E-04	0.47	-1.69
lpg0058	hypothetical		Unknown / hypothetical proteins	9.573	9.822	11.288	9.774	5.08E-01	1.54E-03	0.25	-1.51
lpg0059	ORF		ORFs of unknown function (unique)	8.764	8.396	7.691	8.948	2.69E-01	8.22E-02	-0.37	1.26
lpg0059	ORF		ORFs of unknown function (unique)	8.701	8.341	7.558	9.236	4.07E-01	8.57E-03	-0.36	1.68
lpg0060	methylase		Named proteins of general function	10.915	8.492	9.820	9.257	6.47E-03	2.91E-01	-2.42	-0.56
lpg0060	methylase		Named proteins of general function	11.082	6.411	9.001	8.593	4.41E-04	7.93E-01	-4.67	-0.41
lpg0061	multidrug resistance protein		Transport and binding	12.090	9.875	11.346	10.352	1.98E-02	1.15E-01	-2.21	-0.99
lpg0061	multidrug resistance protein		Transport and binding	12.100	10.521	11.303	10.333	2.08E-03	8.82E-02	-1.58	-0.97

lpg0062	ORF		ORFs of unknown function (unique)	10.921	12.121	10.930	11.655	3.25E-03	5.07E-02	1.20	0.72
lpg0062	ORF		ORFs of unknown function (unique)	10.962	12.142	10.786	11.540	5.66E-03	1.14E-01	1.18	0.75
lpg0063	phospho-2-dehydro-3-deoxyheptonate aldolase (2-keto-3	*aroH*	Amino Acid Metabolism	10.283	8.468	10.417	9.774	2.76E-01	3.16E-01	-1.81	-0.64
lpg0063	phospho-2-dehydro-3-deoxyheptonate aldolase (2-keto-3	*aroH*	Amino Acid Metabolism	11.286	9.000	10.443	10.165	1.68E-02	6.08E-01	-2.29	-0.28
lpg0064	hypothetical		Unknown / hypothetical proteins	12.697	9.193	12.261	11.389	5.57E-07	1.95E-02	-3.50	-0.87
lpg0064	hypothetical		Unknown / hypothetical proteins	12.631	8.991	12.323	11.681	4.83E-06	4.38E-02	-3.64	-0.64
lpg0065	ORF		ORFs of unknown function (unique)	12.176	9.058	11.253	10.470	1.71E-04	4.35E-02	-3.12	-0.78
lpg0065	ORF		ORFs of unknown function (unique)	12.183	9.141	11.268	10.718	1.52E-04	1.73E-01	-3.04	-0.55
lpg0066	carbamoyl phosphate synthase large chain (fusion protein: ligase an		Amino Acid Metabolism, Nucleotide M	12.146	8.604	11.614	10.096	3.68E-05	6.76E-03	-3.54	-1.52
lpg0066	carbamoyl phosphate synthase large chain (fusion protein: ligase an		Amino Acid Metabolism, Nucleotide M	11.965	8.700	11.712	10.243	4.24E-03	1.12E-02	-3.26	-1.47
lpg0067	similar to unknown protein YdeN of Bacillus subtilis		Unknown / hypothetical proteins	10.025	7.573	9.491	9.780	2.77E-02	5.01E-01	-2.45	0.29
lpg0067	similar to unknown protein YdeN of Bacillus subtilis		Unknown / hypothetical proteins	10.051	8.104	9.335	9.767	5.19E-02	3.17E-01	-1.95	0.43
lpg0068	transmembrane protein (ABC transporter (permease, drug/metabolite		Transport and binding	10.645	8.917	10.178	9.252	1.51E-02	7.93E-02	-1.73	-0.93
lpg0068	transmembrane protein (ABC transporter (permease, drug/metabolite		Transport and binding	10.676	9.049	9.744	9.315	5.30E-02	4.74E-01	-1.63	-0.43
lpg0069	tRNA-Asn		tRNA	12.108	11.704	12.424	10.402	4.30E-01	5.73E-05	-0.40	-2.02
lpg0069	tRNA-Asn		tRNA	11.737	12.559	12.406	11.029	3.80E-01	1.75E-01	0.82	-1.38
lpg0070	aspartate aminotransferase A	*aatA*	Amino Acid Metabolism, Energy Metab	9.576	11.177	10.204	10.145	1.30E-03	8.59E-01	1.60	-0.06
lpg0070	aspartate aminotransferase A	*aatA*	Amino Acid Metabolism, Energy Metab	9.417	10.924	10.050	9.999	1.98E-03	8.91E-01	1.51	-0.05
lpg0071	ORF; lpg0079 subseq of,		ORFs of unknown function (unique)	10.762	11.727	12.073	11.790	3.27E-02	5.66E-01	0.97	-0.28
lpg0071	ORF; lpg0079 subseq of,		ORFs of unknown function (unique)	10.569	11.327	11.817	11.547	2.24E-01	5.70E-01	0.76	-0.27
lpg0072	excinuclease ABC subunit B (UvrB)	*uvrB*	DNA/RNA degradation / restriction	10.475	9.922	10.774	11.213	3.48E-01	3.10E-02	-0.55	0.44
lpg0072	excinuclease ABC subunit B (UvrB)	*uvrB*	DNA/RNA degradation / restriction	10.216	10.701	10.947	11.431	2.95E-01	1.32E-02	0.48	0.48
lpg0073	diguanylate cyclase/phosphodiesterase domain 2 (EAL) (sensory box		Signal transduction / other regulatory f	9.828	8.466	12.702	6.870	1.40E-01	5.29E-03	-1.36	-5.83
lpg0073	diguanylate cyclase/phosphodiesterase domain 2 (EAL) (sensory box		Signal transduction / other regulatory f	9.781	8.324	12.609	8.528	1.61E-01	1.51E-03	-1.46	-4.08
lpg0074	glutamate synthase		Energy Metabolism, Amino Acid Metab	10.491	8.131	12.728	8.937	8.69E-02	6.12E-04	-2.36	-3.79
lpg0074	glutamate synthase		Energy Metabolism, Amino Acid Metab	9.739	9.799	12.609	9.599	9.58E-01	4.97E-03	0.06	-3.01
lpg0075	conserved hypothetical protein		Unknown / hypothetical proteins	9.222	10.646	9.343	10.032	1.17E-02	4.96E-01	1.42	0.69
lpg0075	conserved hypothetical protein		Unknown / hypothetical proteins	9.248	10.198	9.031	9.944	1.19E-01	3.58E-01	0.95	0.91
lpg0076	conserved hypothetical protein		Unknown / hypothetical proteins	12.497	13.033	13.327	13.522	5.07E-01	7.78E-01	0.54	0.20
lpg0076	conserved hypothetical protein		Unknown / hypothetical proteins	12.404	14.149	13.313	14.343	7.64E-04	1.64E-02	1.75	1.03
lpg0077	Xaa-Pro aminopeptidase (aminopeptidase PII)	*pepP*	Protein fate / hydrolases / secretion	10.431	10.964	10.046	11.489	7.22E-02	2.93E-03	0.53	1.44
lpg0077	Xaa-Pro aminopeptidase (aminopeptidase PII)	*pepP*	Protein fate / hydrolases / secretion	10.525	10.973	9.831	11.469	7.99E-02	4.11E-04	0.45	1.64
lpg0078	2-octaprenyl-6-methoxyphenol hydroxylase (UbiH protei	*ubiH*	Metabolism of Cofactors and Vitamins	12.177	12.637	12.812	12.271	2.71E-01	6.09E-01	0.46	-0.54
lpg0078	2-octaprenyl-6-methoxyphenol hydroxylase (UbiH protei	*ubiH*	Metabolism of Cofactors and Vitamins	12.249	12.997	12.744	13.335	1.66E-03	1.92E-02	0.75	0.59
lpg0079	2-polyprenyl-6-methoxyphenol hydroxylase (monooxygenase) (oxidor		Metabolism of Cofactors and Vitamins	9.820	10.204	10.315	10.075	3.49E-01	5.20E-01	0.38	-0.24
lpg0079	2-polyprenyl-6-methoxyphenol hydroxylase (monooxygenase) (oxidor		Metabolism of Cofactors and Vitamins	9.691	10.377	10.346	10.189	5.69E-02	6.27E-01	0.69	-0.16
lpg0080	ORF		ORFs of unknown function (unique)	11.379	11.470	11.974	11.810	8.46E-01	7.05E-01	0.09	-0.16
lpg0080	ORF		ORFs of unknown function (unique)	11.270	10.984	11.605	11.591	3.01E-01	9.62E-01	-0.29	-0.01
lpg0081	ORF		ORFs of unknown function (unique)	8.961	10.686	10.524	8.940	2.07E-04	8.49E-03	1.72	-1.58
lpg0081	ORF		ORFs of unknown function (unique)	8.986	10.479	10.589	9.150	1.18E-03	6.58E-03	1.49	-1.44
lpg0082	hypothetical		Unknown / hypothetical proteins	10.222	10.811	10.736	10.470	1.52E-01	4.98E-01	0.59	-0.27
lpg0082	hypothetical		Unknown / hypothetical proteins	10.422	10.996	10.774	10.657	5.77E-02	8.10E-01	0.57	-0.12
lpg0083	COG0189: glutathione synthase/ribosomal protein S6 modification en		Protein fate / hydrolases / secretion, T	11.394	11.068	9.131	11.073	6.01E-01	1.84E-01	-0.33	1.94
lpg0083	COG0189: glutathione synthase/ribosomal protein S6 modification en		Protein fate / hydrolases / secretion, T	11.154	11.760	8.868	12.674	5.62E-01	1.63E-03	0.61	3.81
lpg0084	hypothetical		Unknown / hypothetical proteins	10.855	9.205	8.349	10.470	2.68E-03	1.39E-02	-1.65	2.12
lpg0084	hypothetical		Unknown / hypothetical proteins	11.090	8.953	8.246	10.739	1.82E-04	3.76E-03	-2.14	2.49
lpg0085	uncharacterized conserved protein COG4067		Unknown / hypothetical proteins	10.109	9.978	9.710	11.533	8.74E-01	4.20E-03	-0.13	1.82
lpg0085	uncharacterized conserved protein COG4067		Unknown / hypothetical proteins	10.306	9.390	9.077	11.468	3.30E-01	6.45E-02	-0.92	2.39
lpg0086	ORF		ORFs of unknown function (unique)	9.490	10.022	9.139	9.765	1.77E-01	4.14E-01	0.53	0.63
lpg0086	ORF		ORFs of unknown function (unique)	8.874	10.004	8.519	10.337	2.81E-02	1.20E-01	1.13	1.82
lpg0087	hypothetical		Unknown / hypothetical proteins	9.967	9.941	9.866	10.517	9.69E-01	2.23E-02	-0.03	0.65
lpg0087	hypothetical		Unknown / hypothetical proteins	10.215	10.146	9.467	10.367	8.41E-01	4.92E-02	-0.07	0.90
lpg0088	glutamine ABC transporter (arginine 3rd transport system periplasmic		Transport and binding	10.016	10.449	13.761	9.434	7.24E-01	2.07E-03	0.43	-4.33
lpg0088	glutamine ABC transporter (arginine 3rd transport system periplasmic		Transport and binding	9.936	10.477	13.733	9.632	6.60E-01	3.17E-03	0.54	-4.10
lpg0089	uncharacterized conserved protein COG1671 (YaiI/YqxD family protei		Unknown / hypothetical proteins	9.843	10.256	8.731	9.147	2.83E-02	5.76E-01	0.41	0.42
lpg0089	uncharacterized conserved protein COG1671 (YaiI/YqxD family protei		Unknown / hypothetical proteins	9.836	10.461	9.051	10.051	5.96E-03	3.76E-02	0.62	1.00
lpg0090	ORF		ORFs of unknown function (unique)	11.280	11.174	10.929	11.041	8.72E-01	8.69E-01	-0.11	0.11
lpg0090	ORF		ORFs of unknown function (unique)	11.103	11.435	10.993	11.203	4.05E-01	5.46E-01	0.33	0.21
lpg0091	conserved domain protein		Unknown / hypothetical proteins	11.599	13.396	12.294	12.921	1.63E-05	7.97E-03	1.80	0.63
lpg0091	conserved domain protein		Unknown / hypothetical proteins	11.541	13.410	12.300	12.937	1.51E-06	1.23E-02	1.87	0.64
lpg0092	(exo)ribonuclease R (virulence-associated protein VacB),	*vacB*	Transport and binding, Toxin productio	11.688	11.148	10.584	11.747	3.28E-01	4.59E-03	-0.54	1.16
lpg0092	(exo)ribonuclease R (virulence-associated protein VacB),	*vacB*	Transport and binding, Toxin productio	11.895	11.604	10.546	11.835	5.59E-01	3.02E-03	-0.29	1.29
lpg0093	RNA methyltransferase (tRNA/rRNA methyltransferase)		DNA/RNA degradation / restriction, Tra	12.373	10.850	10.805	12.136	1.96E-03	1.00E-02	-1.52	1.33
lpg0093	RNA methyltransferase (tRNA/rRNA methyltransferase)		DNA/RNA degradation / restriction, Tra	12.171	10.793	10.680	12.251	3.26E-02	1.91E-03	-1.38	1.57

lpg0094	ribose-5-phosphate isomerase A	*rpiA*	Carbohydrate Metabolism, Energy Me	11.458	10.887	10.038	11.812	2.66E-01	2.11E-03	-0.57	1.77
lpg0094	ribose-5-phosphate isomerase A	*rpiA*	Carbohydrate Metabolism, Energy Me	11.676	10.898	10.101	11.932	5.19E-02	3.30E-03	-0.78	1.83
lpg0095	cytosolic IMP-GMP specific 5'-nucleotidase (cytosolic II)		Nucleotide Metabolism	8.817	9.870	8.483	10.003	5.94E-02	2.42E-03	1.05	1.52
lpg0095	cytosolic IMP-GMP specific 5'-nucleotidase (cytosolic II)		Nucleotide Metabolism	9.476	10.329	8.837	10.376	1.79E-02	5.07E-04	0.85	1.54
lpg0096	ORF		ORFs of unknown function (unique)	10.373	10.293	11.219	11.129	9.18E-01	7.64E-01	-0.08	-0.09
lpg0096	ORF		ORFs of unknown function (unique)	10.492	11.013	11.137	11.249	7.52E-02	6.81E-01	0.52	0.11
lpg0097	alkylphosphonate uptake protein PhnA		Named proteins of general function	11.187	10.392	10.183	10.086	3.98E-02	8.41E-01	-0.79	-0.10
lpg0097	alkylphosphonate uptake protein PhnA		Named proteins of general function	11.285	11.462	9.765	11.708	7.68E-01	5.61E-02	0.18	1.94
lpg0098	two component sensor and regulator, sensor/response regulator?? (h		Signal transduction / other regulatory f	12.519	10.936	11.353	11.947	3.78E-02	3.19E-01	-1.58	0.59
lpg0098	two component sensor and regulator, sensor/response regulator?? (h		Signal transduction / other regulatory f	12.350	10.885	11.364	12.169	7.95E-02	1.98E-01	-1.46	0.81
lpg0099	DNA polymerase I	*polI*	Nucleotide Metabolism, Replication an	11.663	10.679	9.905	11.373	3.73E-03	1.34E-02	-0.98	1.47
lpg0099	DNA polymerase I	*polI*	Nucleotide Metabolism, Replication an	11.590	10.666	9.798	11.520	1.34E-02	9.52E-03	-0.92	1.72
lpg0100	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase		Metabolism of Complex Carbohydrate	11.327	12.119	11.291	12.497	3.37E-02	2.24E-02	0.79	1.21
lpg0100	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase		Metabolism of Complex Carbohydrate	11.542	12.063	9.774	12.491	7.59E-02	4.49E-05	0.52	2.72
lpg0101	ORF		ORFs of unknown function (unique)	11.229	11.596	9.678	10.886	3.17E-01	3.24E-02	0.37	1.21
lpg0101	ORF		ORFs of unknown function (unique)	11.181	11.740	9.725	11.088	1.95E-01	5.19E-03	0.56	1.36
lpg0102	3-oxoacyl-[acyl carrier protein] synthase (beta-ketoacyl s	*fabF*	Lipid Metabolism	11.959	11.727	11.020	12.580	8.56E-01	4.33E-02	-0.23	1.56
lpg0102	3-oxoacyl-[acyl carrier protein] synthase (beta-ketoacyl s	*fabF*	Lipid Metabolism	11.881	12.652	10.771	12.656	1.14E-01	1.67E-02	0.77	1.88
lpg0103	N-terminal acetyltransferase, GNAT family (ribosomal pr	*VipF*	Protein fate / hydrolases / secretion	10.617	9.059	9.860	9.667	1.09E-02	6.16E-01	-1.56	-0.19
lpg0103	N-terminal acetyltransferase, GNAT family (ribosomal pr	*VipF*	Protein fate / hydrolases / secretion	10.563	9.305	9.781	9.630	1.42E-02	6.99E-01	-1.26	-0.15
lpg0104	peptide methionine sulfoxide reductase		Detoxification / adaptation	10.654	9.933	8.013	10.145	1.49E-01	1.13E-01	-0.72	2.13
lpg0104	peptide methionine sulfoxide reductase		Detoxification / adaptation	10.347	9.821	7.265	10.606	3.49E-01	3.14E-03	-0.53	3.34
lpg0105	(cytochrome oxidase?) (phosphatidylglycerophosphate synthase?) (C		Named proteins of general function	10.442	11.626	9.469	11.642	1.65E-01	2.70E-05	1.18	2.17
lpg0105	(cytochrome oxidase?) (phosphatidylglycerophosphate synthase?) (C		Named proteins of general function	10.703	11.590	9.225	11.713	1.00E-01	1.39E-04	0.89	2.49
lpg0106	xanthine/uracil permease		Transport and binding	10.052	9.264	9.616	9.718	2.65E-02	7.87E-01	-0.79	0.10
lpg0106	xanthine/uracil permease		Transport and binding	9.816	9.540	9.438	10.013	5.18E-01	2.06E-01	-0.28	0.58
lpg0107	hypothetical (membrane protein required for meiotic division?)		Unknown / hypothetical proteins	11.678	10.328	9.378	12.354	2.76E-01	6.73E-03	-1.35	2.98
lpg0107	hypothetical (membrane protein required for meiotic division?)		Unknown / hypothetical proteins	11.514	11.723	9.765	12.966	7.83E-01	4.09E-04	0.21	3.20
lpg0108	ORF		ORFs of unknown function (unique)	8.997	8.459	9.647	8.520	6.02E-01	4.97E-01	-0.54	-1.13
lpg0108	ORF		ORFs of unknown function (unique)	8.397	8.280	7.481	9.022	8.32E-01	1.13E-02	-0.12	1.54
lpg0109	ORF		ORFs of unknown function (unique)	12.008	9.980	9.504	10.539	3.26E-02	1.05E-01	-2.03	1.04
lpg0109	ORF		ORFs of unknown function (unique)	11.999	10.365	9.353	10.865	4.24E-02	3.09E-02	-1.63	1.51
lpg0110	ORF		ORFs of unknown function (unique)	11.123	10.492	9.222	10.052	1.41E-01	4.36E-01	-0.63	0.83
lpg0110	ORF		ORFs of unknown function (unique)	10.756	10.803	8.979	10.508	9.15E-01	5.61E-02	0.05	1.53
lpg0111	squalene and phytoene synthases (farnesyl-diphosphate	*fdfT*	Lipid Metabolism	10.698	9.358	8.604	10.244	1.17E-01	5.13E-02	-1.34	1.64
lpg0111	squalene and phytoene synthases (farnesyl-diphosphate	*fdfT*	Lipid Metabolism	11.013	10.380	8.683	10.650	1.37E-01	1.62E-02	-0.63	1.97
lpg0112	hypothetical protein		Unknown / hypothetical proteins	10.693	13.645	11.056	11.118	1.25E-09	8.01E-01	2.95	0.06
lpg0112	hypothetical protein		Unknown / hypothetical proteins	10.882	13.594	10.919	11.050	1.84E-07	6.59E-01	2.71	0.13
lpg0113	hypothetical (signal transduction protein), competence pr	*yuxH*	Named proteins of general function	9.349	8.943	8.672	8.075	5.68E-01	6.25E-01	-0.41	-0.60
lpg0113	hypothetical (signal transduction protein), competence pr	*yuxH*	Named proteins of general function	9.550	7.665	8.793	8.648	1.08E-02	8.64E-01	-1.89	-0.14
lpg0114	glycine cleavage system protein P (pyridoxal binding), C-terminal (gly		Amino Acid Metabolism	10.665	11.078	10.319	11.827	7.27E-01	1.77E-02	0.41	1.51
lpg0114	glycine cleavage system protein P (pyridoxal binding), C-terminal (gly		Amino Acid Metabolism	10.455	11.651	10.186	12.026	9.39E-02	6.18E-04	1.20	1.84
lpg0115	conserved hypothetical protein COG2350		Unknown / hypothetical proteins	11.204	13.066	12.306	13.483	2.06E-04	5.53E-03	1.86	1.18
lpg0115	conserved hypothetical protein COG2350		Unknown / hypothetical proteins	11.168	12.784	11.748	13.356	1.44E-03	1.11E-03	1.62	1.61
lpg0116	glycine cleavage system protein P (pyridoxal binding), N-terminal (gly		Amino Acid Metabolism	12.109	13.031	12.226	13.519	1.45E-04	2.26E-04	0.92	1.29
lpg0116	glycine cleavage system protein P (pyridoxal binding), N-terminal (gly		Amino Acid Metabolism	12.031	13.135	12.144	13.578	2.32E-04	4.18E-05	1.10	1.43
lpg0117	glycine cleavage system H protein (carrier of aminometh	*gcvH*	Amino Acid Metabolism	11.915	13.592	12.200	13.012	4.57E-07	8.25E-06	1.68	0.81
lpg0117	glycine cleavage system H protein (carrier of aminometh	*gcvH*	Amino Acid Metabolism	11.655	13.577	11.998	12.973	7.75E-05	7.57E-05	1.92	0.97
lpg0118	glycine cleavage system T protein (aminomethyltransfer	*gcvT1*	Amino Acid Metabolism, Metabolism o	11.030	13.049	10.764	13.269	3.12E-05	8.10E-07	2.02	2.50
lpg0118	glycine cleavage system T protein (aminomethyltransfer	*gcvT1*	Amino Acid Metabolism, Metabolism o	11.111	13.051	10.674	13.266	1.55E-06	2.40E-08	1.94	2.59
lpg0119	ORF transport protein?		Unknown / hypothetical proteins	8.746	9.657	9.961	8.305	4.44E-01	4.35E-01	0.91	-1.66
lpg0119	ORF transport protein?		Unknown / hypothetical proteins	8.601	9.819	8.258	10.273	2.76E-01	1.91E-01	1.22	2.02
lpg0120	IcmL homolog		Transport and binding, Toxin productio	11.332	12.409	12.942	12.523	3.81E-02	4.19E-01	1.08	-0.42
lpg0120	IcmL homolog		Transport and binding, Toxin productio	11.430	12.590	12.952	12.815	2.56E-02	7.71E-01	1.16	-0.14
lpg0121	ABC transporter, permease protein (nitrate permease)		Transport and binding	10.086	10.074	10.300	10.673	9.68E-01	2.59E-01	-0.01	0.37
lpg0121	ABC transporter, permease protein (nitrate permease)		Transport and binding	10.005	10.275	10.020	10.806	4.63E-01	5.74E-02	0.27	0.79
lpg0122	ABC transporter, ATP binding protein (nitrogen transporting)		Transport and binding	11.073	10.798	11.651	11.740	3.46E-01	7.88E-01	-0.28	0.09
lpg0122	ABC transporter, ATP binding protein (nitrogen transporting)		Transport and binding	10.870	11.182	11.647	11.921	1.32E-01	4.65E-01	0.31	0.27
lpg0123	thiol:disulfide interchange protein DsbA (disulfide isomer	*dsbA*	Protein fate / hydrolases / secretion	11.970	13.941	12.406	13.067	3.15E-03	2.36E-01	1.97	0.66
lpg0123	thiol:disulfide interchange protein DsbA (disulfide isomer	*dsbA*	Protein fate / hydrolases / secretion	11.989	13.898	12.049	12.979	2.78E-03	1.58E-03	1.91	0.93
lpg0124	cytochrome c4		Energy Metabolism	8.707	10.599	7.966	10.536	9.74E-03	1.84E-03	1.89	2.57
lpg0124	cytochrome c4		Energy Metabolism	9.242	10.518	6.128	11.006	2.22E-03	8.74E-03	1.28	4.88
lpg0125	GTP binding protein EngB		Signal transduction / other regulatory f	10.599	10.096	9.198	9.805	2.21E-01	2.69E-01	-0.50	0.61
lpg0125	GTP binding protein EngB		Signal transduction / other regulatory f	10.521	10.233	9.074	10.482	7.21E-01	1.35E-01	-0.29	1.41

lpg0126	ninein (GSK3B interacting protein)	*cegC2*	Named proteins of general function	8.768	11.090	9.403	10.018	5.27E-06	1.92E-01	2.32	0.62
lpg0126	ninein (GSK3B interacting protein)	*cegC2*	Named proteins of general function	8.803	11.136	9.273	10.773	5.05E-06	4.23E-02	2.33	1.50
lpg0127	acetyl-coenzyme A synthetase	*acsB*	Carbohydrate Metabolism, Energy Me	9.921	10.446	9.621	10.181	1.25E-01	1.74E-01	0.53	0.56
lpg0127	acetyl-coenzyme A synthetase	*acsB*	Carbohydrate Metabolism, Energy Me	9.923	10.762	9.608	10.654	1.60E-01	1.88E-02	0.84	1.05
lpg0128	3-hydroxyisobutyrate dehydrogenase		Amino Acid Metabolism	11.271	11.705	11.086	10.966	3.34E-02	6.71E-01	0.43	-0.12
lpg0128	3-hydroxyisobutyrate dehydrogenase		Amino Acid Metabolism	11.342	12.109	11.353	11.335	8.78E-02	9.70E-01	0.77	-0.02
lpg0129	methylmalonate-semialdehyde dehydrogenase (malonic	*mmsA*	Carbohydrate Metabolism, Amino Acid	10.533	11.713	10.477	11.596	2.85E-03	6.78E-05	1.18	1.12
lpg0129	methylmalonate-semialdehyde dehydrogenase (malonic	*mmsA*	Carbohydrate Metabolism, Amino Acid	10.434	11.912	10.048	11.382	1.07E-03	6.90E-03	1.48	1.33
lpg0130	ORF		ORFs of unknown function (unique)	11.447	11.296	11.279	9.845	8.31E-01	1.18E-02	-0.15	-1.43
lpg0130	ORF		ORFs of unknown function (unique)	11.089	11.570	11.153	10.044	4.96E-01	1.88E-02	0.48	-1.11
lpg0131	dihydropicolinate reductase	*dapB*	Amino Acid Metabolism	10.388	11.205	10.951	11.317	1.59E-02	5.17E-03	0.82	0.37
lpg0131	dihydropicolinate reductase	*dapB*	Amino Acid Metabolism	10.076	11.603	10.775	11.651	7.20E-02	1.39E-01	1.53	0.88
lpg0132	small ORF (61aa) hypothetical?		Unknown / hypothetical proteins	12.357	11.512	12.648	11.894	6.81E-04	9.57E-03	-0.84	-0.75
lpg0132	small ORF (61aa) hypothetical?		Unknown / hypothetical proteins	12.325	12.046	12.562	12.025	5.17E-01	5.84E-02	-0.28	-0.54
lpg0133	activator of ProP osmoprotectant transporter	*proQm*	Detoxification / adaptation, Signal tran	10.801	10.417	11.020	10.914	7.16E-01	8.51E-01	-0.38	-0.11
lpg0133	activator of ProP osmoprotectant transporter	*proQm*	Detoxification / adaptation, Signal tran	11.679	10.680	10.573	11.225	1.20E-02	3.34E-01	-1.00	0.65
lpg0134	hypothetical		Unknown / hypothetical proteins	10.483	10.123	9.426	11.318	7.62E-01	5.00E-02	-0.36	1.89
lpg0134	hypothetical		Unknown / hypothetical proteins	10.179	10.315	9.503	11.720	8.68E-01	8.12E-03	0.14	2.22
lpg0135	SdhB	*sdhB*	Named proteins of general function	7.659	8.071	10.810	8.022	7.60E-01	4.67E-03	0.41	-2.79
lpg0135	SdhB	*sdhB*	Named proteins of general function	8.331	7.799	11.075	8.563	5.42E-01	2.62E-03	-0.53	-2.51
lpg0136	pyruvate kinase II	*pykA*	Carbohydrate Metabolism, Nucleotide	10.247	10.405	9.451	9.916	6.95E-01	3.68E-01	0.16	0.46
lpg0136	pyruvate kinase II	*pykA*	Carbohydrate Metabolism, Nucleotide	9.949	10.482	9.318	9.984	2.29E-01	2.78E-01	0.53	0.67
lpg0137	phosphoglycerate kinase	*pgk*	Carbohydrate Metabolism, Energy Me	12.017	11.193	10.530	12.078	1.22E-01	4.66E-03	-0.82	1.55
lpg0137	phosphoglycerate kinase	*pgk*	Carbohydrate Metabolism, Energy Me	11.978	11.490	10.193	12.482	5.55E-01	3.02E-03	-0.49	2.29
lpg0138	glyceraldehyde 3-phosphate dehydrogenase	*gap*	Carbohydrate Metabolism, Metabolism	10.439	12.395	9.106	12.705	1.57E-02	5.04E-06	1.96	3.60
lpg0138	glyceraldehyde 3-phosphate dehydrogenase	*gap*	Carbohydrate Metabolism, Metabolism	10.518	12.420	8.326	12.702	9.82E-03	9.66E-05	1.90	4.38
lpg0139	transketolase I	*tktA*	Carbohydrate Metabolism, Energy Me	11.238	11.907	11.103	13.183	4.13E-02	5.65E-06	0.67	2.08
lpg0139	transketolase I	*tktA*	Carbohydrate Metabolism, Energy Me	11.316	11.780	10.888	13.205	1.15E-01	1.07E-05	0.46	2.32
lpg0140	ORF		ORFs of unknown function (unique)	9.667	9.508	9.111	9.278	7.17E-01	7.20E-01	-0.16	0.17
lpg0140	ORF		ORFs of unknown function (unique)	10.148	9.868	9.306	9.869	3.52E-01	5.05E-02	-0.28	0.56
lpg0141	oligopeptidase A (zinc dependent oligopeptidase)		Protein fate / hydrolases / secretion	11.327	10.947	10.364	11.104	6.52E-02	1.75E-01	-0.38	0.74
lpg0141	oligopeptidase A (zinc dependent oligopeptidase)		Protein fate / hydrolases / secretion	11.257	10.836	10.329	11.560	2.01E-01	2.71E-04	-0.42	1.23
lpg0142	; lpg1086; lpg2116; transposase, IS4 family TnpA (Tn5)		Viral functions / Phage / Transposases	10.823	11.010	11.380	11.575	6.46E-01	3.80E-01	0.19	0.19
lpg0142	; lpg1086; lpg2116; transposase, IS4 family TnpA (Tn5)		Viral functions / Phage / Transposases	10.567	11.065	11.189	11.577	1.15E-01	1.32E-01	0.50	0.39
lpg0145	site specific recombinase	*ccrB*	Viral functions / Phage / Transposases	9.610	9.618	8.609	8.971	9.77E-01	5.80E-01	0.01	0.36
lpg0145	site specific recombinase	*ccrB*	Viral functions / Phage / Transposases	9.332	10.042	9.247	10.336	1.72E-01	7.07E-02	0.71	1.09
lpg0146	transposase B, TnpA, ISR508 transposase OrfB protein	*tISRso8b*	Viral functions / Phage / Transposases	10.047	11.547	10.122	11.611	3.58E-03	1.76E-01	1.50	1.49
lpg0146	transposase B, TnpA, ISR508 transposase OrfB protein	*tISRso8b*	Viral functions / Phage / Transposases	11.248	11.226	9.703	11.208	9.82E-01	9.61E-02	-0.02	1.51
lpg0147	transposase (IS911) (IS600)		Viral functions / Phage / Transposases	10.359	10.541	10.149	10.363	6.88E-01	5.85E-01	0.18	0.21
lpg0147	transposase (IS911) (IS600)		Viral functions / Phage / Transposases	10.267	11.107	10.268	10.779	1.27E-01	2.94E-01	0.84	0.51
lpg0148	ORF		ORFs of unknown function (unique)	10.825	10.082	11.079	10.902	2.73E-01	6.72E-01	-0.74	-0.18
lpg0148	ORF		ORFs of unknown function (unique)	10.813	9.950	10.958	10.923	2.03E-01	9.31E-01	-0.86	-0.04
lpg0149	ORF		ORFs of unknown function (unique)	11.486	10.569	10.750	11.561	6.43E-02	1.08E-01	-0.92	0.81
lpg0149	ORF		ORFs of unknown function (unique)	11.193	10.786	10.579	11.956	6.12E-01	3.02E-02	-0.41	1.38
lpg0150	putative phage protein (P-loop ATPase?)		Viral functions / Phage / Transposases	9.800	8.927	8.618	9.806	1.68E-01	9.28E-02	-0.87	1.19
lpg0150	putative phage protein (P-loop ATPase?)		Viral functions / Phage / Transposases	10.417	8.571	8.395	9.782	1.60E-04	3.87E-02	-1.85	1.39
lpg0151	ORF		ORFs of unknown function (unique)	7.918	7.644	10.346	7.303	7.02E-01	2.93E-02	-0.27	-3.04
lpg0151	ORF		ORFs of unknown function (unique)	7.879	6.945	10.565	8.174	2.27E-01	3.38E-02	-0.93	-2.39
lpg0152	hypothetical (GCN5-related N-acetylase, acetyltransferase, GNAT far		Named proteins of general function	10.888	10.842	8.649	10.916	7.39E-01	1.25E-03	-0.05	2.27
lpg0152	hypothetical (GCN5-related N-acetylase, acetyltransferase, GNAT far		Named proteins of general function	10.215	10.954	8.199	11.071	1.15E-01	3.61E-04	0.74	2.87
lpg0153	small ORF (104aa)		ORFs of unknown function (unique)	9.775	9.216	13.069	7.760	4.78E-01	2.00E-05	-0.56	-5.31
lpg0153	small ORF (104aa)		ORFs of unknown function (unique)	9.673	9.387	13.084	9.433	7.46E-01	3.28E-03	-0.29	-3.65
lpg0154	ORF		ORFs of unknown function (unique)	9.687	12.024	10.630	9.314	1.26E-05	7.06E-03	2.34	-1.32
lpg0154	ORF		ORFs of unknown function (unique)	9.806	11.984	10.844	9.793	7.88E-07	1.50E-02	2.18	-1.05
lpg0155	sensory box (GGDEF/EAL domain), regulatory components of sensor		Signal transduction / other regulatory f	7.349	7.631	10.403	6.947	8.66E-01	2.51E-02	0.28	-3.46
lpg0155	sensory box (GGDEF/EAL domain), regulatory components of sensor		Signal transduction / other regulatory f	7.294	7.519	10.504	7.344	8.69E-01	3.57E-02	0.22	-3.16
lpg0156	signal transduction protein (EAL/GGDEF domain protein) - 2 compon		Signal transduction / other regulatory f	9.578	9.381	11.857	9.805	8.13E-01	4.87E-03	-0.20	-2.05
lpg0156	signal transduction protein (EAL/GGDEF domain protein) - 2 compon		Signal transduction / other regulatory f	9.031	9.827	11.760	10.054	1.75E-01	1.10E-02	0.80	-1.71
lpg0157	methionine aminopeptidase	*map-1*	Protein fate / hydrolases / secretion	9.381	9.451	9.688	9.675	7.67E-01	9.67E-01	0.07	-0.01
lpg0157	methionine aminopeptidase	*map-1*	Protein fate / hydrolases / secretion	9.507	9.581	9.442	9.719	7.87E-01	5.49E-01	0.07	0.28
lpg0158	hypothetical		Unknown / hypothetical proteins	9.917	10.114	9.852	10.763	6.10E-01	1.66E-02	0.20	0.91
lpg0158	hypothetical		Unknown / hypothetical proteins	9.858	10.498	9.802	10.839	2.49E-02	6.49E-03	0.64	1.04
lpg0159	small ORF (159aa)		ORFs of unknown function (unique)	8.842	9.246	9.609	9.431	6.12E-01	8.12E-01	0.40	-0.18
lpg0159	small ORF (159aa)		ORFs of unknown function (unique)	8.812	9.226	9.427	9.361	5.99E-01	9.24E-01	0.41	-0.07

lpg0160	ORF		ORFs of unknown function (unique)	10.102	11.905	10.464	12.523	4.31E-02	7.18E-03	1.80	2.06
lpg0160	ORF		ORFs of unknown function (unique)	10.270	12.124	10.151	12.368	2.14E-03	1.32E-02	1.85	2.22
lpg0161	conserved hypothetical protein COG0432		Unknown / hypothetical proteins	9.697	10.224	9.975	9.697	7.79E-02	3.78E-01	0.53	-0.28
lpg0161	conserved hypothetical protein COG0432		Unknown / hypothetical proteins	9.567	10.047	10.006	10.002	2.43E-01	9.88E-01	0.48	0.00
lpg0162	Homolog of sapA		Unknown / hypothetical proteins	10.603	9.823	10.565	10.136	2.73E-03	1.31E-01	-0.78	-0.43
lpg0162	Homolog of sapA		Unknown / hypothetical proteins	10.549	10.294	10.830	10.912	7.49E-01	8.78E-01	-0.26	0.08
lpg0163	hydrolases of the alpha/beta superfamily		Protein fate / hydrolases / secretion	8.907	8.788	11.654	7.765	8.90E-01	7.60E-03	-0.12	-3.89
lpg0163	hydrolases of the alpha/beta superfamily		Protein fate / hydrolases / secretion	8.850	9.213	11.717	8.321	6.83E-01	1.82E-03	0.36	-3.40
lpg0164	ORF		ORFs of unknown function (unique)	8.191	9.454	9.230	9.852	2.05E-02	8.09E-02	1.26	0.62
lpg0164	ORF		ORFs of unknown function (unique)	8.223	9.595	8.668	9.585	8.05E-02	5.55E-02	1.37	0.92
lpg0165	conserved hypothetical protein		Unknown / hypothetical proteins	12.426	12.695	14.055	11.600	4.93E-01	5.17E-05	0.27	-2.46
lpg0165	conserved hypothetical protein		Unknown / hypothetical proteins	12.383	12.647	14.029	11.662	5.46E-01	9.75E-05	0.26	-2.37
lpg0166	hypothetical (integral membrane protein) (methyl-independent misma		Named proteins of general function	8.556	9.352	9.264	9.454	3.34E-01	4.67E-01	0.80	0.19
lpg0166	hypothetical (integral membrane protein) (methyl-independent misma		Named proteins of general function	8.994	9.499	9.150	9.565	2.05E-01	1.20E-01	0.51	0.42
lpg0167	peptide chain release factor		Protein fate / hydrolases / secretion	8.554	9.743	8.599	9.739	1.78E-01	1.96E-02	1.19	1.14
lpg0167	peptide chain release factor		Protein fate / hydrolases / secretion	9.026	9.973	8.678	9.923	9.38E-02	9.03E-04	0.95	1.24
lpg0168	hypothetical protein		Unknown / hypothetical proteins	9.940	8.639	8.994	8.656	7.60E-03	6.13E-01	-1.30	-0.34
lpg0168	hypothetical protein		Unknown / hypothetical proteins	9.655	8.887	8.542	8.763	2.07E-01	7.52E-01	-0.77	0.22
lpg0169	probable transmembrane protein		Unknown / hypothetical proteins	10.760	9.071	9.802	9.341	2.96E-04	1.25E-01	-1.69	-0.46
lpg0169	probable transmembrane protein		Unknown / hypothetical proteins	10.712	9.524	9.622	9.488	1.50E-02	8.67E-01	-1.19	-0.13
lpg0170	probable ABC transport system permease protein		Transport and binding	10.251	8.884	8.862	9.543	2.13E-02	1.31E-01	-1.37	0.68
lpg0170	probable ABC transport system permease protein		Transport and binding	10.130	8.527	8.626	10.190	1.60E-02	1.77E-01	-1.60	1.56
lpg0171	ORF	*legU1*	ORFs of unknown function (unique)	9.055	9.178	8.436	9.337	7.97E-01	3.40E-01	0.12	0.90
lpg0171	ORF	*legU1*	ORFs of unknown function (unique)	8.950	9.810	8.097	10.032	4.04E-02	5.12E-02	0.86	1.94
lpg0172	ORF		ORFs of unknown function (unique)	11.744	10.365	10.225	12.376	3.15E-04	5.28E-03	-1.38	2.15
lpg0172	ORF		ORFs of unknown function (unique)	11.814	10.283	10.179	12.434	1.63E-03	3.60E-03	-1.53	2.26
lpg0173	transcriptional regulator, LysR (cyn operator positive regu	*oxyR*	Detoxification / adaptation, Transcriptio	9.818	8.622	8.119	8.884	2.70E-01	2.83E-01	-1.20	0.76
lpg0173	transcriptional regulator, LysR (cyn operator positive regu	*oxyR*	Detoxification / adaptation, Transcriptio	9.758	9.842	6.945	9.318	8.41E-01	7.85E-02	0.08	2.37
lpg0174	pyoverdine biosynthesis protein PvcA	*pvcA*	Named proteins of general function	9.457	10.964	9.164	10.470	2.84E-03	2.33E-03	1.51	1.31
lpg0174	pyoverdine biosynthesis protein PvcA	*pvcA*	Named proteins of general function	8.824	11.103	9.103	10.574	1.12E-02	1.18E-03	2.28	1.47
lpg0175	pyoverdine biosynthesis protein PvcB		Named proteins of general function	9.380	11.504	7.784	9.902	1.01E-04	2.54E-04	2.12	2.12
lpg0175	pyoverdine biosynthesis protein PvcB		Named proteins of general function	9.465	11.565	7.319	10.075	1.33E-04	1.83E-04	2.10	2.76
lpg0176	FAD monooxygenase, PheA/TfdB family (phenol 2-monooxygenase)		Metabolism of Cofactors and Vitamins	9.627	10.977	8.750	10.760	1.67E-03	3.76E-03	1.35	2.01
lpg0176	FAD monooxygenase, PheA/TfdB family (phenol 2-monooxygenase)		Metabolism of Cofactors and Vitamins	9.997	11.068	8.740	10.760	1.92E-02	1.37E-03	1.07	2.02
lpg0177	chloramphenicol resistance protein (arabinose efflux permease)		Transport and binding	9.672	8.816	9.271	9.347	3.36E-01	9.34E-01	-0.86	0.08
lpg0177	chloramphenicol resistance protein (arabinose efflux permease)		Transport and binding	9.794	10.153	8.972	9.633	7.23E-01	5.83E-01	0.36	0.66
lpg0178	hypothetical		Unknown / hypothetical proteins	10.627	10.460	9.369	11.070	7.30E-01	4.33E-04	-0.17	1.70
lpg0178	hypothetical		Unknown / hypothetical proteins	11.866	10.822	9.513	11.566	2.24E-02	7.79E-04	-1.04	2.05
lpg0179	O-methyltransferase		Named proteins of general function	9.964	9.232	9.930	9.154	8.35E-02	7.15E-02	-0.73	-0.78
lpg0179	O-methyltransferase		Named proteins of general function	9.895	8.575	9.964	9.264	2.70E-02	3.50E-01	-1.32	-0.70
lpg0180	heat shock protein, protease HtpX (metalloprotease, zinc	*htpX*	Detoxification / adaptation, Protein fate	9.117	9.934	10.493	9.822	6.59E-02	3.56E-01	0.82	-0.67
lpg0180	heat shock protein, protease HtpX (metalloprotease, zinc	*htpX*	Detoxification / adaptation, Protein fate	9.514	10.224	10.645	10.373	4.83E-02	5.31E-01	0.71	-0.27
lpg0181	ORF		ORFs of unknown function (unique)	9.323	10.496	8.680	9.859	3.12E-01	3.32E-01	1.17	1.18
lpg0181	ORF		ORFs of unknown function (unique)	9.654	11.325	8.701	10.036	5.15E-02	2.77E-01	1.67	1.33
lpg0182	small ORF (150aa)		ORFs of unknown function (unique)	10.107	9.645	8.549	9.735	3.59E-01	6.35E-02	-0.46	1.19
lpg0182	small ORF (150aa)		ORFs of unknown function (unique)	9.900	9.672	8.185	9.506	6.54E-01	8.37E-02	-0.23	1.32
lpg0183	amine oxidase, flavin containing (dehydrogenase) (cyclopropane fatty		Named proteins of general function	9.543	9.970	8.664	10.560	4.09E-01	2.28E-03	0.43	1.90
lpg0183	amine oxidase, flavin containing (dehydrogenase) (cyclopropane fatty		Named proteins of general function	9.138	10.352	8.391	11.581	3.20E-01	1.28E-02	1.21	3.19
lpg0184	ABC sugar transporter, periplasmic sugar binding protein		Transport and binding	11.869	11.728	11.063	12.338	6.04E-01	1.26E-03	-0.14	1.28
lpg0184	ABC sugar transporter, periplasmic sugar binding protein		Transport and binding	12.475	11.628	10.954	12.351	1.67E-02	1.27E-03	-0.85	1.40
lpg0185	ABC sugar transporter, ATP binding protein		Transport and binding	9.512	10.344	7.899	10.826	1.40E-01	6.92E-03	0.83	2.93
lpg0185	ABC sugar transporter, ATP binding protein		Transport and binding	9.567	10.563	7.261	10.657	2.41E-02	1.32E-02	1.00	3.40
lpg0186	ABC sugar transporter, permease (D-ribose high affinity transport)		Transport and binding	9.018	9.573	8.660	8.686	4.88E-01	9.72E-01	0.55	0.03
lpg0186	ABC sugar transporter, permease (D-ribose high affinity transport)		Transport and binding	9.056	8.988	7.545	8.557	9.55E-01	4.49E-01	-0.07	1.01
lpg0187	L. pneumophila zinc metalloprotein (peptidase, M20/M25/M40 family)		Protein fate / hydrolases / secretion	11.124	12.193	9.930	12.211	3.41E-04	3.03E-04	1.07	2.28
lpg0187	L. pneumophila zinc metalloprotein (peptidase, M20/M25/M40 family)		Protein fate / hydrolases / secretion	11.170	12.087	9.657	12.211	1.30E-01	1.37E-02	0.92	2.55
lpg0188	acyl CoA transferase/carnitine dehydratase (CAIB/BAIF family protein		Named proteins of general function	10.925	10.438	10.735	10.917	1.03E-01	4.73E-01	-0.49	0.18
lpg0188	acyl CoA transferase/carnitine dehydratase (CAIB/BAIF family protein		Named proteins of general function	10.937	10.504	10.696	11.071	5.99E-02	2.38E-01	-0.43	0.38
lpg0189	ORF		ORFs of unknown function (unique)	8.348	9.025	8.812	8.996	1.83E-01	6.05E-01	0.68	0.18
lpg0189	ORF		ORFs of unknown function (unique)	9.235	10.422	8.225	10.150	5.65E-03	5.02E-02	1.19	1.93
lpg0190	small ORF (73aa)?		ORFs of unknown function (unique)	9.366	10.469	9.648	10.143	2.81E-01	5.71E-01	1.10	0.50
lpg0190	small ORF (73aa)?		ORFs of unknown function (unique)	8.999	10.385	9.446	10.144	2.62E-01	3.98E-01	1.39	0.70
lpg0191	ORF		ORFs of unknown function (unique)	10.437	8.890	9.912	10.463	2.31E-02	5.31E-02	-1.55	0.55
lpg0191	ORF		ORFs of unknown function (unique)	10.208	8.869	9.363	10.123	4.23E-02	1.51E-01	-1.34	0.76

lpg0192	heat shock hsp20 (alpha crystallin) proteins family		Named proteins of general function	10.375	10.257	11.150	9.495	7.90E-01	1.15E-02	-0.12	-1.65
lpg0192	heat shock hsp20 (alpha crystallin) proteins family		Named proteins of general function	9.828	9.893	11.214	9.690	9.05E-01	8.52E-03	0.07	-1.52
lpg0193	small ORF (64aa)?		ORFs of unknown function (unique)	8.460	8.991	8.463	8.950	5.09E-01	6.20E-01	0.53	0.49
lpg0193	small ORF (64aa)?		ORFs of unknown function (unique)	8.585	8.917	8.729	9.537	6.88E-01	4.03E-01	0.33	0.81
lpg0194	catalase/(hydro)peroxidase KatG		Amino Acid Metabolism, Energy Meta	10.170	11.336	9.070	11.321	2.93E-04	1.74E-03	1.17	2.25
lpg0194	catalase/(hydro)peroxidase KatG		Amino Acid Metabolism, Energy Meta	10.896	11.006	8.184	11.098	8.93E-01	6.59E-02	0.11	2.91
lpg0195	ORF		ORFs of unknown function (unique)	8.795	9.119	10.082	8.629	3.00E-01	6.25E-03	0.32	-1.45
lpg0195	ORF		ORFs of unknown function (unique)	8.569	8.958	9.698	8.970	4.84E-01	2.73E-01	0.39	-0.73
lpg0196	ORF		ORFs of unknown function (unique)	9.306	9.412	10.657	8.647	7.57E-01	1.41E-02	0.11	-2.01
lpg0196	ORF		ORFs of unknown function (unique)	8.872	9.024	10.619	9.087	6.44E-01	1.17E-02	0.15	-1.53
lpg0197	conserved hypothetical protein		Unknown / hypothetical proteins	10.550	9.635	11.619	10.100	1.84E-01	9.26E-04	-0.92	-1.52
lpg0197	conserved hypothetical protein		Unknown / hypothetical proteins	9.996	9.854	11.683	10.381	7.18E-01	5.42E-03	-0.14	-1.30
lpg0198	hypothetical		Named proteins of general function	9.845	9.080	8.917	9.117	9.58E-02	5.63E-01	-0.77	0.20
lpg0198	hypothetical		Named proteins of general function	10.097	9.030	8.276	8.914	1.47E-03	3.27E-01	-1.07	0.64
lpg0199	cytochrome D ubiquinol oxidase subunit I (cytochrome b	*cydA*	Energy Metabolism	10.059	10.110	11.894	10.116	8.92E-01	2.84E-03	0.05	-1.78
lpg0199	cytochrome D ubiquinol oxidase subunit I (cytochrome b	*cydA*	Energy Metabolism	10.030	10.356	11.952	10.782	3.45E-01	2.26E-02	0.33	-1.17
lpg0200	cytochrome D ubiquinol oxidase subunit II, cyanide insen	*qxtB*	Energy Metabolism	9.832	7.848	11.110	9.598	5.26E-02	8.83E-02	-1.98	-1.51
lpg0200	cytochrome D ubiquinol oxidase subunit II, cyanide insen	*qxtB*	Energy Metabolism	10.218	9.001	10.851	10.052	7.56E-02	1.75E-01	-1.22	-0.80
lpg0201	hypothetical		Unknown / hypothetical proteins	11.160	10.248	11.435	10.305	3.15E-02	5.83E-03	-0.91	-1.13
lpg0201	hypothetical		Unknown / hypothetical proteins	11.173	10.173	11.533	10.564	4.88E-03	1.02E-02	-1.00	-0.97
lpg0202	conserved hypothetical protein		Unknown / hypothetical proteins	10.325	10.300	11.056	10.451	9.68E-01	2.75E-01	-0.02	-0.61
lpg0202	conserved hypothetical protein		Unknown / hypothetical proteins	10.294	10.381	10.002	10.088	8.49E-01	8.81E-01	0.09	0.09
lpg0203	fusion of two types of conserved hypothetical proteins (ki	*yfhG*	Named proteins of general function	11.366	10.597	9.319	10.226	1.47E-01	1.29E-01	-0.77	0.91
lpg0203	fusion of two types of conserved hypothetical proteins (ki	*yfhG*	Named proteins of general function	11.335	10.690	9.409	10.379	2.55E-01	5.33E-02	-0.65	0.97
lpg0204	2-deoxy-D-gluconate-3-dehydrogenase (3-oxoacyl-[acyl carrier protei		Carbohydrate Metabolism	9.414	10.679	8.200	11.278	2.60E-02	8.95E-05	1.27	3.08
lpg0204	2-deoxy-D-gluconate-3-dehydrogenase (3-oxoacyl-[acyl carrier protei		Carbohydrate Metabolism	8.616	11.454	8.385	11.641	2.30E-03	5.47E-05	2.84	3.26
lpg0205	hypothetical		Unknown / hypothetical proteins	11.012	10.932	12.311	11.332	7.23E-01	1.52E-02	-0.08	-0.98
lpg0205	hypothetical		Unknown / hypothetical proteins	11.068	10.761	12.277	11.349	3.36E-01	2.37E-02	-0.31	-0.93
lpg0206	membrane protein		Named proteins of general function	10.473	10.220	10.145	9.616	7.84E-01	6.73E-01	-0.25	-0.53
lpg0206	membrane protein		Named proteins of general function	10.136	9.595	9.427	9.853	4.46E-01	6.72E-01	-0.54	0.43
lpg0207	small ORF (56aa)?		ORFs of unknown function (unique)	9.398	10.310	10.551	10.014	3.85E-01	6.05E-01	0.91	-0.54
lpg0207	small ORF (56aa)?		ORFs of unknown function (unique)	8.808	9.941	9.556	9.918	3.45E-01	6.80E-01	1.13	0.36
lpg0208	serine/threonine-protein kinase	*ceg6/pkn5*	Signal transduction / other regulatory f	9.128	9.099	8.638	9.817	9.66E-01	1.30E-01	-0.03	1.18
lpg0208	serine/threonine-protein kinase	*ceg6/pkn6*	Signal transduction / other regulatory f	8.472	9.263	7.848	9.987	2.82E-01	2.21E-02	0.79	2.14
lpg0209	ORF		ORFs of unknown function (unique)	9.996	9.072	9.486	9.090	1.43E-01	6.02E-01	-0.92	-0.40
lpg0209	ORF		ORFs of unknown function (unique)	9.894	8.463	8.855	9.352	1.02E-01	5.70E-01	-1.43	0.50
lpg0210	ORF		ORFs of unknown function (unique)	9.966	10.891	10.168	10.166	3.79E-02	9.96E-01	0.93	0.00
lpg0210	ORF		ORFs of unknown function (unique)	9.935	11.383	9.977	10.297	1.17E-02	5.78E-01	1.45	0.32
lpg0211	tryptophan rich sensory protein TspO (carotenoid biosynt	*tspO*	Named proteins of general function	9.730	9.019	9.649	9.466	1.01E-01	6.79E-01	-0.71	-0.18
lpg0211	tryptophan rich sensory protein TspO (carotenoid biosynt	*tspO*	Named proteins of general function	10.192	9.632	10.023	9.909	6.18E-01	8.66E-01	-0.56	-0.11
lpg0212	deoxyribodipyrimidine photolyase (DNA photolyase)	*phrB*	DNA/RNA degradation / restriction	10.284	9.566	9.247	10.190	1.99E-02	8.12E-02	-0.72	0.94
lpg0212	deoxyribodipyrimidine photolyase (DNA photolyase)	*phrB*	DNA/RNA degradation / restriction	10.167	10.176	8.858	10.689	9.80E-01	3.93E-03	0.01	1.83
lpg0213	inner membrane protein (LrgB family protein) (serotonin transporter?)		Named proteins of general function	9.293	9.240	11.062	8.665	9.52E-01	5.65E-03	-0.05	-2.40
lpg0213	inner membrane protein (LrgB family protein) (serotonin transporter?)		Named proteins of general function	8.825	9.750	10.443	8.578	3.65E-01	1.34E-01	0.92	-1.86
lpg0214	murein hydrolase exporter (LrgA family protein)		Transport and binding	10.095	10.487	10.887	10.127	3.70E-01	3.95E-01	0.39	-0.76
lpg0214	murein hydrolase exporter (LrgA family protein)		Transport and binding	12.907	11.381	11.714	11.253	7.04E-03	2.27E-01	-1.53	-0.46
lpg0215	transcriptional regulator, LysR family		Transcription factors / DNA binding pr	9.589	9.234	9.394	9.329	4.26E-01	8.73E-01	-0.36	-0.06
lpg0215	transcriptional regulator, LysR family		Transcription factors / DNA binding pr	9.619	9.663	9.358	9.790	9.15E-01	4.89E-01	0.04	0.43
lpg0216	uncharacterized conserved hypothetical protein COG3024		Unknown / hypothetical proteins	11.139	9.484	9.981	9.664	1.06E-01	7.70E-01	-1.66	-0.32
lpg0216	uncharacterized conserved hypothetical protein COG3024		Unknown / hypothetical proteins	11.063	9.409	9.419	9.801	8.79E-02	5.96E-01	-1.65	0.38
lpg0217	phosphoribosylaminoimidazole carboxylase, ATPase sub	*purK*	Nucleotide Metabolism	11.132	11.119	10.959	11.822	9.76E-01	3.29E-03	-0.01	0.86
lpg0217	phosphoribosylaminoimidazole carboxylase, ATPase sub	*purK*	Nucleotide Metabolism	11.312	11.321	10.838	11.891	9.60E-01	6.12E-04	0.01	1.05
lpg0218	phosphoribosylaminoimidazole carboxylase, catalytic su	*purE*	Nucleotide Metabolism	9.923	10.553	10.677	10.956	8.21E-02	3.10E-01	0.63	0.28
lpg0218	phosphoribosylaminoimidazole carboxylase, catalytic su	*purE*	Nucleotide Metabolism	10.038	10.634	10.454	10.867	2.70E-03	6.42E-02	0.60	0.41
lpg0219	hypothetical		Unknown / hypothetical proteins	10.257	12.217	9.570	11.917	3.96E-03	6.34E-05	1.96	2.35
lpg0219	hypothetical		Unknown / hypothetical proteins	10.250	12.453	9.521	11.939	8.78E-04	4.77E-05	2.20	2.42
lpg0220	hypothetical		Unknown / hypothetical proteins	8.600	10.303	8.799	9.973	3.47E-04	2.62E-02	1.70	1.17
lpg0220	hypothetical		Unknown / hypothetical proteins	8.461	10.505	8.834	10.274	2.91E-03	2.76E-02	2.04	1.44
lpg0221	hypothetical		Unknown / hypothetical proteins	6.170	7.612	8.456	7.370	1.41E-01	9.27E-02	1.44	-1.09
lpg0221	hypothetical		Unknown / hypothetical proteins	6.821	7.336	7.536	7.318	7.00E-01	6.05E-01	0.52	-0.22
lpg0222	NADH dehydrogenase subunit 5 (NADH-ubiquinone oxidoreductase		Metabolism of Cofactors and Vitamins	7.633	8.063	8.508	7.686	6.00E-01	4.25E-01	0.43	-0.82
lpg0222	NADH dehydrogenase subunit 5 (NADH-ubiquinone oxidoreductase		Metabolism of Cofactors and Vitamins	8.301	8.082	8.788	8.214	8.41E-01	6.58E-01	-0.22	-0.57
lpg0223	transcriptional regulator, LysR family		Transcription factors / DNA binding pr	11.297	10.067	9.565	10.648	2.35E-03	5.85E-02	-1.23	1.08
lpg0223	transcriptional regulator, LysR family		Transcription factors / DNA binding pr	11.267	10.720	9.462	11.789	5.00E-01	3.20E-02	-0.55	2.33

lpg0224	toxin secretion ABC transporter HlyB/MsbA family ATP-binding protei		Transport and binding	9.760	8.516	9.260	7.659	1.24E-02	1.40E-02	-1.24	-1.60
lpg0224	toxin secretion ABC transporter HlyB/MsbA family ATP-binding protei		Transport and binding	9.732	8.301	8.447	8.010	5.85E-02	6.24E-01	-1.43	-0.44
lpg0225	RND efflux membrane fusion protein		Transport and binding	9.283	8.126	8.834	8.978	3.20E-01	8.17E-01	-1.16	0.14
lpg0225	RND efflux membrane fusion protein		Transport and binding	8.893	8.476	8.281	8.988	5.74E-01	1.67E-01	-0.42	0.71
lpg0226	multidrug efflux protein, outer membrane component		Transport and binding	7.328	8.649	7.882	8.112	6.43E-02	7.65E-01	1.32	0.23
lpg0226	multidrug efflux protein, outer membrane component		Transport and binding	7.861	8.275	8.331	8.627	4.55E-01	6.60E-01	0.41	0.30
lpg0227	ORF	*ceg7*	ORFs of unknown function (unique)	11.790	14.939	12.840	12.700	1.39E-06	5.73E-01	3.15	-0.14
lpg0227	ORF	*ceg7*	ORFs of unknown function (unique)	11.824	14.888	12.797	12.683	3.83E-06	6.57E-01	3.06	-0.11
lpg0228	amino acid permease family protein (amino acid transporter)		Transport and binding	10.160	10.329	10.312	9.616	5.41E-01	4.12E-02	0.17	-0.70
lpg0228	amino acid permease family protein (amino acid transporter)		Transport and binding	10.364	10.197	10.152	9.912	6.28E-01	6.25E-01	-0.17	-0.24
lpg0229	heme oxygenase		Named proteins of general function	11.166	10.904	10.365	11.490	4.20E-01	1.09E-03	-0.26	1.12
lpg0229	heme oxygenase		Named proteins of general function	11.105	10.793	9.548	11.195	3.57E-01	1.97E-02	-0.31	1.65
lpg0230	sensor histidine kinase (two component response regulat	*pleD*	Signal transduction / other regulatory f	11.193	9.423	11.487	9.940	3.31E-04	4.87E-04	-1.77	-1.55
lpg0230	sensor histidine kinase (two component response regulat	*pleD*	Signal transduction / other regulatory f	11.196	9.683	11.692	10.191	1.27E-03	2.99E-05	-1.51	-1.50
lpg0231	heavy metal transporting P-type ATPase (cation transporting) (Cu trar		Transport and binding	8.347	8.892	7.715	8.426	4.10E-01	1.15E-01	0.55	0.71
lpg0231	heavy metal transporting P-type ATPase (cation transporting) (Cu trar		Transport and binding	9.062	9.222	7.875	9.210	7.60E-01	1.63E-01	0.16	1.33
lpg0232	transcriptional regulator np20 (Fur family) (ferric uptake)	*np20*	Transcription factors / DNA binding prc	11.633	11.313	10.452	11.130	1.37E-01	1.25E-01	-0.32	0.68
lpg0232	transcriptional regulator np20 (Fur family) (ferric uptake)	*np20*	Transcription factors / DNA binding prc	11.627	11.323	10.437	11.184	1.47E-01	1.02E-01	-0.30	0.75
lpg0233	benzoylformate decarboxylase	*mdlC*	Biodegradation of Xenobiotics	10.890	10.338	13.071	9.784	3.62E-01	2.32E-03	-0.55	-3.29
lpg0233	benzoylformate decarboxylase	*mdlC*	Biodegradation of Xenobiotics	10.952	10.423	13.095	10.409	4.67E-01	1.67E-02	-0.53	-2.69
lpg0234	SidE	*sidE*	Toxin production / other pathogen func	8.112	8.999	9.005	9.526	4.63E-02	2.09E-01	0.89	0.52
lpg0234	SidE	*sidE*	Toxin production / other pathogen func	8.380	8.991	8.863	9.674	4.54E-02	8.66E-03	0.61	0.81
lpg0235	hypothetical protein		Unknown / hypothetical proteins	10.180	9.124	8.785	8.946	6.86E-02	8.21E-01	-1.06	0.16
lpg0235	hypothetical protein		Unknown / hypothetical proteins	10.056	9.390	8.331	8.813	2.22E-01	7.12E-01	-0.67	0.48
lpg0236	ORF		ORFs of unknown function (unique)	10.330	9.736	10.688	10.303	1.53E-01	3.94E-01	-0.59	-0.39
lpg0236	ORF		ORFs of unknown function (unique)	10.433	9.972	10.558	10.587	3.50E-01	8.83E-01	-0.46	0.03
lpg0237	lipolytic enzyme (3-oxoadipate enol-lactone hydrolase fa	*mhpC*	Protein fate / hydrolases / secretion	11.803	12.420	12.343	12.441	4.70E-03	4.84E-01	0.62	0.10
lpg0237	lipolytic enzyme (3-oxoadipate enol-lactone hydrolase fa	*mhpC*	Protein fate / hydrolases / secretion	11.757	12.606	12.353	12.581	1.26E-03	2.88E-01	0.85	0.23
lpg0238	glycine betaine aldehyde dehydrogenase	*gbsA*	Amino Acid Metabolism	11.508	12.517	12.513	11.974	5.02E-04	1.16E-01	1.01	-0.54
lpg0238	glycine betaine aldehyde dehydrogenase	*gbsA*	Amino Acid Metabolism	11.612	12.466	12.517	12.153	5.50E-03	2.35E-01	0.85	-0.36
lpg0239	4-aminobutyrate aminotransferase	*gabT*	Amino Acid Metabolism, Metabolism o	11.117	10.150	11.812	10.393	1.01E-03	1.39E-03	-0.97	-1.42
lpg0239	4-aminobutyrate aminotransferase	*gabT*	Amino Acid Metabolism, Metabolism o	11.214	9.925	11.848	10.455	9.65E-03	1.17E-03	-1.29	-1.39
lpg0240	DNA repair protein	*recN*	Replication and Repair	11.756	11.745	12.788	12.080	9.78E-01	4.38E-02	-0.01	-0.71
lpg0240	DNA repair protein	*recN*	Replication and Repair	11.725	11.677	12.737	12.068	9.09E-01	4.51E-02	-0.05	-0.67
lpg0241	glutaminase		Amino Acid Metabolism, Metabolism o	10.388	8.973	11.448	9.342	9.92E-04	2.12E-02	-1.41	-2.11
lpg0241	glutaminase		Amino Acid Metabolism, Metabolism o	10.368	9.204	11.118	9.293	1.52E-02	9.22E-02	-1.16	-1.83
lpg0242	D-3-phosphoglycerate dehydrogenase (D-isomer specific	*serA*	Amino Acid Metabolism	10.956	9.981	11.626	10.251	4.34E-03	2.13E-02	-0.98	-1.37
lpg0242	D-3-phosphoglycerate dehydrogenase (D-isomer specific	*serA*	Amino Acid Metabolism	10.824	9.971	11.687	10.604	1.68E-03	1.35E-02	-0.85	-1.08
lpg0243	short chain dehydrogenase/(reductase)		Named proteins of general function	11.865	11.824	11.280	10.997	9.59E-01	4.88E-01	-0.04	-0.28
lpg0243	short chain dehydrogenase/(reductase)		Named proteins of general function	11.019	11.811	10.778	11.138	1.33E-02	3.28E-01	0.79	0.36
lpg0244	pyridine nucleotide-disulfide oxidoreductase, FAD-dependent disulfide		Carbohydrate Metabolism, Amino Acid	9.743	9.073	12.901	9.174	3.57E-01	1.75E-03	-0.67	-3.73
lpg0244	pyridine nucleotide-disulfide oxidoreductase, FAD-dependent disulfide		Carbohydrate Metabolism, Amino Acid	9.687	10.096	12.738	10.343	7.31E-01	9.48E-02	0.41	-2.40
lpg0245	NAD-glutamate dehydrogenase		Named proteins of general function	7.020	8.153	12.177	7.698	6.03E-01	3.22E-02	1.13	-4.48
lpg0245	NAD-glutamate dehydrogenase		Named proteins of general function	8.568	8.644	12.639	8.562	9.49E-01	2.23E-02	0.08	-4.08
lpg0246	ORF		ORFs of unknown function (unique)	10.264	9.593	10.722	9.942	3.01E-02	1.62E-02	-0.67	-0.78
lpg0246	ORF		ORFs of unknown function (unique)	9.800	9.094	10.508	9.958	3.47E-01	4.76E-02	-0.71	-0.55
lpg0247	ORF		ORFs of unknown function (unique)	8.467	8.846	8.672	8.493	6.09E-01	7.67E-01	0.38	-0.18
lpg0247	ORF		ORFs of unknown function (unique)	7.211	8.794	8.037	9.374	1.67E-01	2.05E-01	1.58	1.34
lpg0248	arsenate reductase		Transport and binding, Signal transduc	9.802	10.652	10.237	10.652	2.64E-02	2.50E-01	0.85	0.42
lpg0248	arsenate reductase		Transport and binding, Signal transduc	11.787	11.006	10.491	10.950	3.16E-01	3.26E-01	-0.78	0.46
lpg0249	stearoyl CoA 9-desaturase (fatty acid desaturase)		Lipid Metabolism	10.309	9.497	10.130	9.296	5.62E-02	9.04E-02	-0.81	-0.83
lpg0249	stearoyl CoA 9-desaturase (fatty acid desaturase)		Lipid Metabolism	10.062	9.163	10.028	9.338	3.99E-02	2.54E-01	-0.90	-0.69
lpg0250	ATP-dependent RNA helicase, DEAD box family		DNA/RNA degradation / restriction	11.436	10.389	11.699	10.199	2.29E-03	1.45E-04	-1.05	-1.50
lpg0250	ATP-dependent RNA helicase, DEAD box family		DNA/RNA degradation / restriction	10.954	10.011	11.634	10.160	2.04E-02	1.65E-04	-0.94	-1.47
lpg0251	RNA binding protein (cold-inducible) rrm		DNA/RNA degradation / restriction	12.248	10.145	10.313	10.709	3.56E-04	4.64E-01	-2.10	0.40
lpg0251	RNA binding protein (cold-inducible) rrm		DNA/RNA degradation / restriction	12.219	10.021	10.236	10.741	3.73E-04	3.55E-01	-2.20	0.50
lpg0252	membrane protein		Named proteins of general function	11.532	11.382	10.369	10.828	8.31E-01	5.26E-01	-0.15	0.46
lpg0252	membrane protein		Named proteins of general function	11.538	11.553	10.162	11.514	9.77E-01	4.19E-03	0.02	1.35
lpg0253	acetyltransferase, GNAT family (amino acid acetyltransferase)		Protein fate / hydrolases / secretion	11.129	11.667	12.005	11.731	1.49E-02	2.78E-01	0.54	-0.27
lpg0253	acetyltransferase, GNAT family (amino acid acetyltransferase)		Protein fate / hydrolases / secretion	11.186	11.618	11.940	11.714	5.76E-02	3.37E-01	0.43	-0.23
lpg0254	ORF		ORFs of unknown function (unique)	9.717	9.505	9.813	9.632	3.51E-01	7.20E-01	-0.21	-0.18
lpg0254	ORF		ORFs of unknown function (unique)	9.472	10.242	9.361	9.780	4.51E-01	6.77E-01	0.77	0.42
lpg0255	outer membrane channel protein (outer membrane efflux protein) (mu		Transport and binding	10.071	9.029	8.782	9.200	3.35E-02	4.62E-01	-1.04	0.42
lpg0255	outer membrane channel protein (outer membrane efflux protein) (mu		Transport and binding	9.553	8.640	7.832	9.046	1.79E-01	2.65E-01	-0.91	1.21

lpg0256	conserved domain protein		Unknown / hypothetical proteins	10.113	9.697	9.384	9.798	4.32E-01	5.89E-01	-0.42	0.41
lpg0256	conserved domain protein		Unknown / hypothetical proteins	9.962	9.304	9.135	9.619	8.97E-02	5.61E-01	-0.66	0.48
lpg0257	multidrug resistance secretion protein		Transport and binding	9.972	10.323	11.560	10.515	3.24E-01	7.96E-02	0.35	-1.04
lpg0257	multidrug resistance secretion protein		Transport and binding	9.622	10.657	10.119	10.283	1.88E-01	7.54E-01	1.04	0.16
lpg0258	ORF		ORFs of unknown function (unique)	10.631	10.846	12.014	9.814	7.52E-01	7.04E-03	0.21	-2.20
lpg0258	ORF		ORFs of unknown function (unique)	10.570	10.283	11.705	9.913	5.63E-01	2.57E-02	-0.29	-1.79
lpg0259	hypothetical protein		Unknown / hypothetical proteins	9.606	8.394	11.292	9.430	3.06E-01	3.09E-02	-1.21	-1.86
lpg0259	hypothetical protein		Unknown / hypothetical proteins	9.646	9.251	10.540	9.772	3.71E-01	4.45E-01	-0.39	-0.77
lpg0260	small ORF (132aa)		ORFs of unknown function (unique)	13.764	12.826	12.494	15.272	3.74E-02	2.26E-05	-0.94	2.78
lpg0260	small ORF (132aa)		ORFs of unknown function (unique)	13.967	12.995	12.538	15.341	6.15E-02	1.15E-05	-0.97	2.80
lpg0261	ISSod6 transposase (IS1301)		Viral functions / Phage / Transposases	10.329	8.436	9.389	9.554	1.43E-02	8.55E-01	-1.89	0.17
lpg0261	ISSod6 transposase (IS1301)		Viral functions / Phage / Transposases	10.322	9.276	9.730	10.364	6.98E-02	3.72E-01	-1.05	0.63
lpg0262	bacteriophage related DNA polymerase (uracil DNA glycosylase)		Nucleotide Metabolism, Replication an	10.747	10.953	10.195	11.219	6.83E-01	6.31E-03	0.21	1.02
lpg0262	bacteriophage related DNA polymerase (uracil DNA glycosylase)		Nucleotide Metabolism, Replication an	10.296	10.821	10.108	11.333	1.58E-01	2.51E-02	0.52	1.22
lpg0263	MFS transporter family protein (major facilitator superfamily)		Transport and binding	10.057	10.053	11.194	10.135	9.95E-01	1.25E-01	0.00	-1.06
lpg0263	MFS transporter family protein (major facilitator superfamily)		Transport and binding	9.731	10.190	10.098	10.134	4.20E-01	9.55E-01	0.46	0.04
lpg0264	unknown protein		Unknown / hypothetical proteins	9.893	9.278	9.999	9.383	1.36E-01	1.02E-01	-0.62	-0.62
lpg0264	unknown protein		Unknown / hypothetical proteins	10.014	9.479	9.963	9.541	6.64E-02	3.80E-01	-0.53	-0.42
lpg0265	multicopper oxidase (copper oxidase), copper resistance protein A		Transport and binding	10.629	10.300	9.524	10.821	4.72E-01	5.26E-02	-0.33	1.30
lpg0265	multicopper oxidase (copper oxidase), copper resistance protein A		Transport and binding	10.340	9.968	9.013	10.558	5.72E-01	1.76E-01	-0.37	1.54
lpg0266	small ORF (144aa)		ORFs of unknown function (unique)	9.718	9.453	8.869	10.642	5.20E-01	3.11E-03	-0.26	1.77
lpg0266	small ORF (144aa)		ORFs of unknown function (unique)	9.661	9.876	8.979	11.105	7.27E-01	7.39E-04	0.21	2.13
lpg0267	magnesium and cobalt transport protein CorA	*corA*	Transport and binding	9.802	8.964	11.658	8.481	2.37E-01	7.41E-02	-0.84	-3.18
lpg0267	magnesium and cobalt transport protein CorA	*corA*	Transport and binding	9.718	8.933	11.688	8.784	2.95E-01	1.52E-02	-0.79	-2.90
lpg0268	hypothetical (hydrolase?)		Unknown / hypothetical proteins	10.422	8.765	8.543	9.858	1.35E-02	7.14E-02	-1.66	1.32
lpg0268	hypothetical (hydrolase?)		Unknown / hypothetical proteins	10.263	9.526	8.637	10.496	4.07E-01	1.17E-01	-0.74	1.86
lpg0269	hypothetical (ABC binding protein)		Named proteins of general function	10.396	10.532	10.200	10.371	9.20E-01	9.00E-01	0.14	0.17
lpg0269	hypothetical (ABC binding protein)		Named proteins of general function	8.335	10.364	10.212	10.542	7.65E-02	1.70E-01	2.03	0.33
lpg0270	nicotinate phosphoribosyltransferase		Metabolism of Cofactors and Vitamins	10.994	9.522	11.637	10.012	4.32E-05	4.39E-04	-1.47	-1.63
lpg0270	nicotinate phosphoribosyltransferase		Metabolism of Cofactors and Vitamins	11.104	9.335	11.707	10.145	1.47E-03	1.18E-04	-1.77	-1.56
lpg0271	bifunctional pyrazinamidase/nicotinamidase	*pncA*	Amino Acid Metabolism, Metabolism o	10.939	9.550	11.164	10.537	6.74E-04	4.31E-03	-1.39	-0.63
lpg0271	bifunctional pyrazinamidase/nicotinamidase	*pncA*	Amino Acid Metabolism, Metabolism o	10.974	9.607	11.091	10.831	5.33E-05	3.84E-01	-1.37	-0.26
lpg0272	cysteine transferase		Transport and binding	10.570	11.817	9.738	11.656	6.38E-02	7.85E-04	1.25	1.92
lpg0272	cysteine transferase		Transport and binding	10.508	11.808	9.364	11.676	3.09E-02	3.20E-04	1.30	2.31
lpg0273	major facilitator superfamily transporter (multi-drug resistance transpo		Transport and binding	8.029	8.637	9.244	8.748	5.58E-01	4.77E-01	0.61	-0.50
lpg0273	major facilitator superfamily transporter (multi-drug resistance transpo		Transport and binding	8.658	8.661	8.981	9.110	9.97E-01	8.38E-01	0.00	0.13
lpg0274	transcriptional regulator, LysR family		Transcription factors / DNA binding pro	12.392	11.691	11.022	12.418	7.34E-02	5.58E-03	-0.70	1.40
lpg0274	transcriptional regulator, LysR family		Transcription factors / DNA binding pro	12.410	11.528	10.928	12.421	7.46E-02	3.03E-03	-0.88	1.49
lpg0275	SdbA	*sdbA*	Named proteins of general function	7.849	9.376	8.322	8.286	2.57E-02	9.58E-01	1.53	-0.04
lpg0275	SdbA	*sdbA*	Named proteins of general function	8.094	9.398	7.606	8.019	2.61E-02	7.27E-01	1.30	0.41
lpg0276	ORF	*legG2*	ORFs of unknown function (unique)	11.079	11.368	11.086	9.333	7.71E-01	3.24E-02	0.29	-1.75
lpg0276	ORF	*legG2*	ORFs of unknown function (unique)	10.410	11.345	10.433	9.869	1.71E-02	8.83E-02	0.94	-0.56
lpg0277	sensory box protein (GGDEF family protein) LssE protein (diguanylat		Signal transduction / other regulatory f	11.152	9.823	13.215	10.833	5.49E-02	1.17E-03	-1.33	-2.38
lpg0277	sensory box protein (GGDEF family protein) LssE protein (diguanylat		Signal transduction / other regulatory f	11.563	10.986	13.387	12.097	3.05E-01	8.45E-03	-0.58	-1.29
lpg0278	sensor histidine kinase (two component response regulat	*fixL*	Signal transduction / other regulatory f	8.598	8.069	10.428	7.876	3.72E-01	4.92E-02	-0.53	-2.55
lpg0278	sensor histidine kinase (two component response regulat	*fixL*	Signal transduction / other regulatory f	9.423	9.388	11.556	9.906	9.35E-01	8.60E-03	-0.03	-1.65
lpg0279	hypothetical		Unknown / hypothetical proteins	8.268	8.099	11.370	8.949	8.60E-01	1.04E-02	-0.17	-2.42
lpg0279	hypothetical		Unknown / hypothetical proteins	8.182	9.372	11.299	9.548	2.07E-01	1.13E-01	1.19	-1.75
lpg0280	transcriptional regulator, LysR family		Transcription factors / DNA binding pro	9.125	9.953	11.299	9.727	1.57E-01	6.05E-03	0.83	-1.57
lpg0280	transcriptional regulator, LysR family		Transcription factors / DNA binding pro	9.211	9.995	11.254	9.818	1.70E-01	1.34E-02	0.78	-1.44
lpg0281	(cationic) amino acid transporter (permease)		Transport and binding	10.230	9.919	11.382	9.373	6.09E-01	2.83E-02	-0.31	-2.01
lpg0281	(cationic) amino acid transporter (permease)		Transport and binding	10.036	9.472	10.943	9.386	3.64E-01	1.97E-02	-0.56	-1.56
lpg0282	conserved hypothetical protein		Unknown / hypothetical proteins	11.601	11.670	10.929	11.487	6.88E-01	3.71E-02	0.07	0.56
lpg0282	conserved hypothetical protein		Unknown / hypothetical proteins	11.296	11.730	10.638	11.630	3.72E-01	9.23E-03	0.43	0.99
lpg0283	NAD dependent formate dehydrogenase		Carbohydrate Metabolism, Energy Me	10.977	10.959	12.078	11.157	9.84E-01	2.99E-01	-0.02	-0.92
lpg0283	NAD dependent formate dehydrogenase		Carbohydrate Metabolism, Energy Me	11.015	11.489	12.194	11.755	3.37E-01	2.87E-01	0.47	-0.44
lpg0284	ORF	*ceg10*	ORFs of unknown function (unique)	9.165	9.472	9.733	9.294	3.45E-01	2.45E-01	0.31	-0.44
lpg0284	ORF	*ceg10*	ORFs of unknown function (unique)	8.926	9.397	9.338	9.180	1.20E-01	6.89E-01	0.47	-0.16
lpg0285	ORF		ORFs of unknown function (unique)	10.975	12.458	10.895	12.331	4.64E-04	2.50E-03	1.48	1.44
lpg0285	ORF		ORFs of unknown function (unique)	11.173	12.653	11.077	13.208	4.15E-03	2.42E-03	1.48	2.13
lpg0286	oxidoreductase, short chain dehydrogenase/reductase family		Named proteins of general function	11.432	12.298	11.438	12.226	6.86E-04	3.75E-03	0.87	0.79
lpg0286	oxidoreductase, short chain dehydrogenase/reductase family		Named proteins of general function	11.343	12.246	11.338	12.268	9.05E-04	2.52E-03	0.90	0.93
lpg0287	translation elongation factor P (EF-P)	*efp*	Translation	9.799	12.091	9.519	11.961	1.96E-03	7.39E-04	2.29	2.44
lpg0287	translation elongation factor P (EF-P)	*efp*	Translation	9.781	11.947	8.452	11.834	9.55E-03	1.60E-02	2.17	3.38

lpg0288	L-lysine 2,3-aminomutase (radical SAM domain protein)		Amino Acid Metabolism	10.390	9.884	10.339	11.588	1.81E-01	1.25E-02	-0.51	1.25
lpg0288	L-lysine 2,3-aminomutase (radical SAM domain protein)		Amino Acid Metabolism	10.499	9.864	9.060	11.242	3.78E-02	6.78E-02	-0.64	2.18
lpg0289	polyphosphate kinase (polyphosphoric acid kinase)	*ppk*	Energy Metabolism	10.969	9.242	9.578	9.003	5.73E-04	1.91E-01	-1.73	-0.58
lpg0289	polyphosphate kinase (polyphosphoric acid kinase)	*ppk*	Energy Metabolism	10.878	9.181	9.973	10.062	1.53E-03	8.51E-01	-1.70	0.09
lpg0290	lipoprotein		Named proteins of general function	8.794	8.947	7.794	8.579	6.31E-01	3.78E-01	0.15	0.79
lpg0290	lipoprotein		Named proteins of general function	7.636	10.113	7.599	9.425	9.93E-02	3.02E-01	2.48	1.83
lpg0291	chromate transport protein		Transport and binding	10.873	9.547	9.409	9.433	2.24E-02	9.56E-01	-1.33	0.02
lpg0291	chromate transport protein		Transport and binding	10.595	8.984	8.718	9.724	2.00E-02	3.96E-01	-1.61	1.01
lpg0292	ORF		ORFs of unknown function (unique)	11.169	11.224	9.226	10.740	8.45E-01	2.46E-03	0.05	1.51
lpg0292	ORF		ORFs of unknown function (unique)	10.794	10.678	8.796	10.800	8.48E-01	3.78E-03	-0.12	2.00
lpg0293	long chain acyl-CoA dehydrogenase (oxidoreductase, acyl CoA-dehy		Lipid Metabolism, Metabolism of Com	11.804	11.850	11.099	10.919	8.52E-01	3.50E-01	0.05	-0.18
lpg0293	long chain acyl-CoA dehydrogenase (oxidoreductase, acyl CoA-dehy		Lipid Metabolism, Metabolism of Com	11.674	11.939	10.939	10.873	4.00E-01	8.11E-01	0.26	-0.07
lpg0294	ORF		ORFs of unknown function (unique)	12.161	12.234	12.688	11.930	9.23E-01	9.85E-02	0.07	-0.76
lpg0294	ORF		ORFs of unknown function (unique)	12.201	12.878	12.621	12.093	7.50E-02	2.17E-01	0.68	-0.53
lpg0295	mannose-1-phosphate guanyltransferase (sugar phosphate nucleotid		Carbohydrate Metabolism	9.983	11.568	9.065	10.996	8.12E-02	3.61E-02	1.58	1.93
lpg0295	mannose-1-phosphate guanyltransferase (sugar phosphate nucleotid		Carbohydrate Metabolism	9.931	11.757	9.220	11.996	5.18E-02	3.01E-03	1.83	2.78
lpg0296	(phosphotransferase) hypothetical		Named proteins of general function	9.049	10.463	7.746	11.236	8.23E-02	2.04E-03	1.41	3.49
lpg0296	(phosphotransferase) hypothetical		Named proteins of general function	9.848	10.364	7.052	11.138	2.32E-02	3.63E-03	0.52	4.09
lpg0297	organic solvent tolerance protein	*ostA*	Detoxification / adaptation	10.854	9.327	8.450	11.231	9.01E-02	7.21E-03	-1.53	2.78
lpg0297	organic solvent tolerance protein	*ostA*	Detoxification / adaptation	10.698	10.000	7.875	11.106	5.12E-01	1.51E-02	-0.70	3.23
lpg0298	peptidyl-prolyl cis-trans isomerase D (survival protein Su	*surA*	Toxin production / other pathogen func	12.687	12.798	12.970	13.796	9.30E-01	5.20E-02	0.11	0.83
lpg0298	peptidyl-prolyl cis-trans isomerase D (survival protein Su	*surA*	Toxin production / other pathogen func	12.636	13.922	12.881	13.740	4.37E-04	4.97E-02	1.29	0.86
lpg0299	pyridoxal phosphate biosynthetic protein PdxA (4-hydrox	*pdxA*	Metabolism of Cofactors and Vitamins	10.994	10.569	9.826	11.206	2.01E-01	7.07E-03	-0.43	1.38
lpg0299	pyridoxal phosphate biosynthetic protein PdxA (4-hydrox	*pdxA*	Metabolism of Cofactors and Vitamins	11.010	10.604	9.630	11.059	1.17E-01	2.20E-02	-0.41	1.43
lpg0300	dihydrofolate reductase		Metabolism of Cofactors and Vitamins	11.516	11.339	10.351	11.948	7.16E-01	2.10E-04	-0.18	1.60
lpg0300	dihydrofolate reductase		Metabolism of Cofactors and Vitamins	11.557	11.360	10.170	11.940	5.09E-01	1.22E-04	-0.20	1.77
lpg0301	hypothetical (insect protein?) (CG13321 gene product)		Unknown / hypothetical proteins	11.508	13.219	12.027	12.822	9.02E-04	1.34E-01	1.71	0.80
lpg0301	hypothetical (insect protein?) (CG13321 gene product)		Unknown / hypothetical proteins	11.544	13.255	11.904	12.936	2.19E-03	4.27E-02	1.71	1.03
lpg0302	16S rRNA		rRNA	15.292	15.744	15.685	15.629	1.37E-01	4.48E-01	0.45	-0.06
lpg0302	16S rRNA		rRNA	15.118	15.600	15.664	15.623	1.17E-01	6.85E-01	0.48	-0.04
lpg0303	tRNA-Ala		tRNA	12.745	13.280	12.064	13.974	1.62E-01	5.12E-04	0.54	1.91
lpg0303	tRNA-Ala		tRNA	12.660	13.316	12.010	13.971	1.56E-01	6.25E-04	0.66	1.96
lpg0304	23S rRNA		rRNA	14.636	13.103	15.455	13.282	3.82E-01	2.02E-01	-1.53	-2.17
lpg0304	23S rRNA		rRNA	14.853	14.174	15.555	13.769	6.18E-01	1.83E-01	-0.68	-1.79
lpg0305	; lpg0572; lpg2751; ORF hypothetical (transposase?) global transcrip		Detoxification / adaptation, Transcripti	6.909	8.298	7.641	8.598	3.51E-01	3.88E-01	1.39	0.96
lpg0305	; lpg0572; lpg2751; ORF hypothetical (transposase?) global transcrip		Detoxification / adaptation, Transcripti	7.276	9.407	7.660	9.406	1.79E-02	1.92E-01	2.13	1.75
lpg0306	ORF		ORFs of unknown function (unique)	6.529	8.612	8.814	8.348	1.33E-01	7.14E-01	2.08	-0.47
lpg0306	ORF		ORFs of unknown function (unique)	6.807	8.668	8.588	8.352	2.67E-01	8.40E-01	1.86	-0.24
lpg0307	hypothetical protein		Unknown / hypothetical proteins	9.299	9.530	9.654	9.455	7.74E-01	8.27E-01	0.23	-0.20
lpg0307	hypothetical protein		Unknown / hypothetical proteins	8.316	9.547	8.802	10.072	2.32E-01	1.74E-01	1.23	1.27
lpg0308	cell wall associated hydrolase, putative pseudogene		Named proteins of general function	10.681	13.314	12.643	13.211	2.00E-03	1.27E-01	2.63	0.57
lpg0308	cell wall associated hydrolase, putative pseudogene		Named proteins of general function	10.759	13.382	12.600	13.230	2.14E-03	1.24E-01	2.62	0.63
lpg0309	5S rRNA		rRNA	15.659	14.544	15.732	13.049	3.50E-01	2.82E-01	-1.11	-2.68
lpg0309	5S rRNA		rRNA	15.624	14.505	15.685	13.507	3.84E-01	1.92E-01	-1.12	-2.18
lpg0310	tRNA-Thr		tRNA	13.429	11.643	11.029	12.886	3.33E-02	7.70E-02	-1.79	1.86
lpg0310	tRNA-Thr		tRNA	13.189	11.505	11.071	13.057	1.05E-01	3.81E-02	-1.68	1.99
lpg0311	tRNA-Tyr		tRNA	12.756	12.804	10.302	14.469	9.59E-01	3.72E-04	0.05	4.17
lpg0311	tRNA-Tyr		tRNA	12.931	12.793	10.182	14.476	8.51E-01	3.99E-04	-0.14	4.29
lpg0312	tRNA-Gly		tRNA	14.098	14.265	11.197	15.447	8.13E-01	2.04E-04	0.17	4.25
lpg0312	tRNA-Gly		tRNA	14.100	14.274	10.920	15.410	7.80E-01	5.60E-04	0.17	4.49
lpg0313	tRNA-Thr		tRNA	14.102	13.927	12.153	14.545	9.00E-01	7.86E-02	-0.18	2.39
lpg0313	tRNA-Thr		tRNA	14.035	14.616	11.966	15.267	4.79E-01	3.88E-03	0.58	3.30
lpg0314	elongation factor Tu (EF-Tu)	*tuf2*	Translation	14.907	15.378	13.461	15.645	3.58E-01	2.37E-03	0.47	2.18
lpg0314	elongation factor Tu (EF-Tu)	*tuf2*	Translation	14.778	15.322	13.167	15.694	4.22E-01	2.58E-07	0.54	2.53
lpg0315	tRNA-Trp		tRNA	13.206	12.285	11.027	13.237	4.97E-01	1.14E-01	-0.92	2.21
lpg0315	tRNA-Trp		tRNA	13.546	13.336	10.762	13.323	7.88E-01	7.48E-02	-0.21	2.56
lpg0316	preprotein translocase, SecE subunit	*secE*	Protein fate / hydrolases / secretion	14.086	13.257	10.785	14.080	1.80E-01	3.04E-03	-0.83	3.29
lpg0316	preprotein translocase, SecE subunit	*secE*	Protein fate / hydrolases / secretion	14.011	13.345	10.786	14.188	2.68E-01	3.39E-03	-0.67	3.40
lpg0317	transcription antitermination protein NusG	*nusG*	Transcription	12.999	12.435	10.355	13.320	4.98E-01	3.52E-03	-0.56	2.97
lpg0317	transcription antitermination protein NusG	*nusG*	Transcription	13.156	12.420	10.201	13.256	2.48E-01	3.28E-03	-0.74	3.05
lpg0318	50S ribosomal protein L11	*rplK*	Translation	13.127	12.243	11.207	13.417	2.75E-01	9.44E-03	-0.88	2.21
lpg0318	50S ribosomal protein L11	*rplK*	Translation	13.244	12.010	11.022	13.331	6.20E-02	1.07E-02	-1.23	2.31
lpg0319	50S ribosomal protein L1	*rplA*	Translation	13.492	12.477	11.497	13.419	1.34E-02	9.87E-03	-1.01	1.92
lpg0319	50S ribosomal protein L1	*rplA*	Translation	12.894	12.478	11.568	13.504	5.71E-01	1.06E-02	-0.42	1.94

lpg0320	50S ribosomal protein L10	*rplJ*	Translation	14.565	14.904	12.391	15.491	6.25E-01	1.06E-02	0.34	3.10
lpg0320	50S ribosomal protein L10	*rplJ*	Translation	14.779	14.861	12.147	15.529	9.17E-01	2.69E-03	0.08	3.38
lpg0321	50S ribosomal protein L7/L12	*rplL*	Translation	12.720	13.319	10.375	14.503	5.20E-01	8.31E-04	0.60	4.13
lpg0321	50S ribosomal protein L7/L12	*rplL*	Translation	12.700	13.357	9.589	14.526	4.97E-01	3.24E-03	0.66	4.94
lpg0322	DNA-directed RNA polymerase beta subunit	*rpoB*	Transcription	14.354	13.126	13.136	13.509	7.79E-03	2.77E-01	-1.23	0.37
lpg0322	DNA-directed RNA polymerase beta subunit	*rpoB*	Transcription	14.129	13.166	13.132	13.529	5.56E-03	2.35E-01	-0.96	0.40
lpg0323	DNA-directed RNA polymerase beta' subunit	*rpoC*	Transcription	14.224	13.312	13.307	14.176	2.09E-02	1.33E-02	-0.91	0.87
lpg0323	DNA-directed RNA polymerase beta' subunit	*rpoC*	Transcription	14.000	13.252	13.233	14.136	2.05E-02	1.19E-02	-0.75	0.90
lpg0324	30S ribosomal protein S12		Translation	14.736	13.793	13.501	14.811	1.77E-02	1.21E-02	-0.94	1.31
lpg0324	30S ribosomal protein S12		Translation	15.004	13.836	13.380	14.877	2.52E-05	2.58E-04	-1.17	1.50
lpg0325	30S ribosomal protein S7	*rpS7*	Translation	14.365	13.765	13.090	15.097	2.84E-01	1.15E-03	-0.60	2.01
lpg0325	30S ribosomal protein S7	*rpS7*	Translation	14.248	13.787	13.090	15.111	3.33E-01	2.50E-03	-0.46	2.02
lpg0326	translation elongation factor G (EF-G)	*fusA*	Translation	15.043	14.520	13.651	15.578	1.85E-01	7.54E-04	-0.52	1.93
lpg0326	translation elongation factor G (EF-G)	*fusA*	Translation	15.166	14.505	13.599	15.577	7.77E-02	3.78E-04	-0.66	1.98
lpg0328	30S ribosomal protein S10	*rpsJ*	Translation	13.008	13.344	11.217	14.474	6.93E-01	1.44E-03	0.34	3.26
lpg0328	30S ribosomal protein S10	*rpsJ*	Translation	13.027	13.341	11.028	14.496	6.91E-01	2.64E-03	0.31	3.47
lpg0329	50S ribosomal protein L3	*rplC*	Translation	14.813	14.281	12.671	15.093	3.62E-01	5.35E-03	-0.53	2.42
lpg0329	50S ribosomal protein L3	*rplC*	Translation	14.622	14.233	12.478	15.086	5.42E-01	1.40E-03	-0.39	2.61
lpg0330	50S ribosomal protein L4		Translation	6.876	8.365	7.092	7.620	5.34E-02	7.00E-01	1.49	0.53
lpg0330	50S ribosomal protein L4		Translation	6.505	6.788	6.676	7.526	8.71E-01	6.04E-01	0.28	0.85
lpg0331	50S ribosomal protein L23	*rplW*	Translation	14.328	12.526	12.835	13.445	2.49E-02	3.04E-01	-1.80	0.61
lpg0331	50S ribosomal protein L23	*rplW*	Translation	14.223	12.473	12.854	13.497	3.21E-02	3.20E-01	-1.75	0.64
lpg0332	50S ribosomal protein L2		Translation	14.324	11.842	12.473	13.225	2.86E-02	4.57E-01	-2.48	0.75
lpg0332	50S ribosomal protein L2		Translation	14.292	12.107	12.536	13.544	1.62E-02	2.38E-01	-2.19	1.01
lpg0333	hypothetical?		Unknown / hypothetical proteins	10.480	11.345	9.643	11.661	2.12E-01	2.33E-02	0.86	2.02
lpg0333	hypothetical?		Unknown / hypothetical proteins	10.356	11.087	9.902	12.573	3.12E-01	8.18E-03	0.73	2.67
lpg0334	50S ribosomal protein L22	*rplV*	Translation	14.770	13.272	12.604	14.691	1.87E-02	1.09E-02	-1.50	2.09
lpg0334	50S ribosomal protein L22	*rplV*	Translation	14.559	13.251	12.505	14.664	2.99E-02	8.09E-03	-1.31	2.16
lpg0335	30S ribosomal protein S3	*rpsC*	Translation	14.644	13.321	12.548	14.796	3.34E-02	2.13E-03	-1.32	2.25
lpg0335	30S ribosomal protein S3	*rpsC*	Translation	14.822	13.346	12.457	14.799	2.59E-02	2.17E-03	-1.48	2.34
lpg0336	50S ribosomal protein L16/(L10E)	*rplP*	Translation	14.678	14.587	13.078	15.080	8.68E-01	4.33E-03	-0.09	2.00
lpg0336	50S ribosomal protein L16/(L10E)	*rplP*	Translation	14.804	14.371	12.621	15.131	4.64E-01	5.97E-07	-0.43	2.51
lpg0337	50S ribosomal subunit protein L29	*rpmC*	Translation	13.866	12.189	12.217	13.161	7.39E-02	2.59E-01	-1.68	0.94
lpg0337	50S ribosomal subunit protein L29	*rpmC*	Translation	13.929	12.048	11.969	12.974	6.94E-02	1.95E-01	-1.88	1.01
lpg0338	30S ribosomal protein S17	*rpsQ*	Translation	13.592	12.120	11.752	12.297	8.40E-02	6.09E-01	-1.47	0.54
lpg0338	30S ribosomal protein S17	*rpsQ*	Translation	13.677	12.664	11.816	13.506	2.18E-01	5.01E-02	-1.01	1.69
lpg0339	50S ribosomal protein L14	*rplN*	Translation	14.618	13.110	12.728	14.460	3.20E-02	1.92E-02	-1.51	1.73
lpg0339	50S ribosomal protein L14	*rplN*	Translation	14.705	13.162	12.684	14.497	2.85E-02	1.08E-02	-1.54	1.81
lpg0340	50S ribosomal protein L24	*rplX*	Translation	14.579	12.253	12.163	13.149	2.27E-02	5.20E-01	-2.33	0.99
lpg0340	50S ribosomal protein L24	*rplX*	Translation	14.828	12.645	12.038	13.823	7.11E-03	9.14E-02	-2.18	1.78
lpg0341	50S ribosomal protein L5		Translation	14.595	12.381	11.625	13.976	2.83E-02	6.30E-02	-2.21	2.35
lpg0341	50S ribosomal protein L5		Translation	14.732	12.786	11.630	14.290	2.31E-02	1.41E-02	-1.95	2.66
lpg0342	30S ribosomal protein S14	*rpsN*	Translation	14.685	13.109	12.395	14.986	2.23E-02	2.28E-03	-1.58	2.59
lpg0342	30S ribosomal protein S14	*rpsN*	Translation	14.779	13.080	12.212	15.007	1.66E-02	5.56E-04	-1.70	2.80
lpg0343	30S ribosomal protein S8	*rpsH*	Translation	14.310	13.866	12.508	15.426	5.15E-01	5.05E-04	-0.44	2.92
lpg0343	30S ribosomal protein S8	*rpsH*	Translation	14.765	13.860	12.426	15.439	1.57E-01	2.29E-04	-0.91	3.01
lpg0344	50S ribosomal protein L6/(L9E)	*rplF*	Translation	14.006	13.925	12.263	15.062	9.13E-01	1.58E-03	-0.08	2.80
lpg0344	50S ribosomal protein L6/(L9E)	*rplF*	Translation	14.366	13.711	12.015	15.043	3.62E-01	1.63E-03	-0.65	3.03
lpg0345	50S ribosomal protein L18	*rplR*	Translation	14.534	13.563	12.198	14.287	4.06E-01	9.58E-02	-0.97	2.09
lpg0345	50S ribosomal protein L18	*rplR*	Translation	14.526	14.249	12.364	15.077	7.28E-01	2.09E-03	-0.28	2.71
lpg0346	30S ribosomal protein S5	*rpsE*	Translation	14.903	14.793	13.097	15.438	8.13E-01	2.11E-03	-0.11	2.34
lpg0346	30S ribosomal protein S5	*rpsE*	Translation	14.634	14.778	13.025	15.370	7.70E-01	3.29E-03	0.14	2.35
lpg0347	50S ribosomal protein L30/(L7E)	*rpmD*	Translation	14.808	12.181	11.935	12.701	7.86E-03	5.02E-01	-2.63	0.77
lpg0347	50S ribosomal protein L30/(L7E)	*rpmD*	Translation	14.576	12.726	12.469	13.386	1.17E-02	2.67E-01	-1.85	0.92
lpg0348	50S ribosomal protein L15	*rplO*	Translation	14.434	11.737	11.715	13.621	2.24E-02	5.21E-02	-2.70	1.91
lpg0348	50S ribosomal protein L15	*rplO*	Translation	14.029	12.226	10.736	13.072	7.12E-02	4.80E-03	-1.80	2.34
lpg0349	preprotein translocase (secretion protein SecY)	*secY*	Protein fate / hydrolases / secretion	14.407	12.349	11.768	13.077	1.61E-02	1.20E-01	-2.06	1.31
lpg0349	preprotein translocase (secretion protein SecY)	*secY*	Protein fate / hydrolases / secretion	14.472	11.585	11.091	13.101	2.31E-03	5.77E-02	-2.89	2.01
lpg0350	50S ribosomal protein L36	*rpmJ*	Translation	12.685	10.294	9.332	12.153	5.81E-02	8.40E-03	-2.39	2.82
lpg0350	50S ribosomal protein L36	*rpmJ*	Translation	12.575	11.020	8.197	12.263	3.33E-02	1.08E-02	-1.56	4.07
lpg0351	30S ribosomal protein S13	*rpsM*	Translation	14.713	13.601	12.761	14.297	9.04E-02	3.63E-02	-1.11	1.54
lpg0351	30S ribosomal protein S13	*rpsM*	Translation	14.703	13.622	12.774	14.353	6.46E-02	2.75E-02	-1.08	1.58
lpg0352	30S ribosomal protein S11	*rpsK*	Translation	14.502	13.574	12.046	14.881	2.14E-01	7.70E-04	-0.93	2.84
lpg0352	30S ribosomal protein S11	*rpsK*	Translation	14.693	13.556	11.974	14.865	1.20E-01	1.14E-03	-1.14	2.89

lpg0353	30S ribosomal protein S4	*rpsD*	Translation	14.561	13.823	12.439	14.708	3.92E-01	9.46E-03	-0.74	2.27
lpg0353	30S ribosomal protein S4	*rpsD*	Translation	14.492	14.291	12.428	15.113	7.22E-01	1.17E-03	-0.20	2.69
lpg0354	DNA-directed RNA polymerase alpha subunit RpoA	*rpoA*	Transcription	14.591	13.400	12.595	14.387	4.83E-02	1.33E-02	-1.19	1.79
lpg0354	DNA-directed RNA polymerase alpha subunit RpoA	*rpoA*	Transcription	14.536	13.324	12.559	14.402	3.25E-02	1.89E-02	-1.21	1.84
lpg0355	50S ribosomal protein L17	*rplQ*	Translation	11.728	11.075	9.819	11.414	4.59E-01	4.31E-02	-0.65	1.59
lpg0355	50S ribosomal protein L17	*rplQ*	Translation	11.203	11.223	9.573	11.444	9.86E-01	2.89E-02	0.02	1.87
lpg0356	single strand binding protein	*ssb*	Replication and Repair	13.968	14.159	13.610	13.858	3.26E-01	1.48E-01	0.19	0.25
lpg0356	single strand binding protein	*ssb*	Replication and Repair	13.909	14.169	13.620	13.881	1.81E-01	1.49E-01	0.26	0.26
lpg0357	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	12.010	10.524	10.758	11.040	3.75E-03	4.20E-01	-1.49	0.28
lpg0357	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	11.995	10.352	10.380	10.982	1.93E-03	3.69E-01	-1.64	0.60
lpg0358	glucose-1-dehydrogenase (1-cyclohexenylcarbonyl CoA reductase-sh		Named proteins of general function	12.497	12.370	12.276	12.171	7.34E-01	6.22E-01	-0.13	-0.10
lpg0358	glucose-1-dehydrogenase (1-cyclohexenylcarbonyl CoA reductase-sh		Named proteins of general function	12.539	12.238	12.218	12.174	3.90E-01	8.57E-01	-0.30	-0.04
lpg0359	acyl carrier protein	*acpP*	Named proteins of general function	12.959	11.850	10.127	12.728	1.49E-01	5.95E-03	-1.11	2.60
lpg0359	acyl carrier protein	*acpP*	Named proteins of general function	12.629	12.132	9.838	12.695	6.04E-01	8.96E-03	-0.50	2.86
lpg0360	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier prote	*fabA*	Named proteins of general function	13.252	11.470	10.569	12.947	6.78E-02	1.98E-02	-1.78	2.38
lpg0360	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier prote	*fabA*	Named proteins of general function	13.301	11.482	10.129	12.840	4.38E-02	3.21E-02	-1.82	2.71
lpg0361	3-oxoacyl-[acyl-carrier protein] synthase II (beta-ketoacyl	*fabF*	Lipid Metabolism	11.865	11.364	10.126	12.120	4.00E-01	1.24E-02	-0.50	1.99
lpg0361	3-oxoacyl-[acyl-carrier protein] synthase II (beta-ketoacyl	*fabF*	Lipid Metabolism	12.240	11.394	9.043	12.074	8.98E-02	1.05E-01	-0.85	3.03
lpg0362	3-oxoacyl-[acyl-carrier protein] synthase II (beta-ketoacyl	*fabF*	Lipid Metabolism	11.980	9.215	10.379	10.877	3.17E-04	3.68E-01	-2.77	0.50
lpg0362	3-oxoacyl-[acyl-carrier protein] synthase II (beta-ketoacyl	*fabF*	Lipid Metabolism	12.060	10.611	10.271	11.923	1.14E-01	9.38E-02	-1.45	1.65
lpg0363	lipid A biosynthesis acyltransferase (lauroyl/myristoyl acy	*waaM*	Metabolism of Complex Carbohydrates	10.654	9.174	9.819	9.159	1.49E-03	3.47E-01	-1.48	-0.66
lpg0363	lipid A biosynthesis acyltransferase (lauroyl/myristoyl acy	*waaM*	Metabolism of Complex Carbohydrates	10.671	8.912	8.937	9.368	8.31E-04	6.31E-01	-1.76	0.43
lpg0364	small ORF (101aa)		ORFs of unknown function (unique)	11.733	11.685	12.464	10.860	8.86E-01	2.04E-02	-0.05	-1.60
lpg0364	small ORF (101aa)		ORFs of unknown function (unique)	11.699	11.705	12.459	11.022	9.85E-01	1.70E-02	0.01	-1.44
lpg0365	ORF		ORFs of unknown function (unique)	11.298	13.076	12.017	10.931	8.21E-05	2.48E-02	1.78	-1.09
lpg0365	ORF		ORFs of unknown function (unique)	11.334	13.146	12.041	11.156	8.87E-05	3.61E-02	1.81	-0.89
lpg0366	diaminopimelate epimerase	*dapF*	Amino Acid Metabolism	11.364	11.662	10.990	11.689	2.53E-02	6.63E-02	0.30	0.70
lpg0366	diaminopimelate epimerase	*dapF*	Amino Acid Metabolism	11.399	11.950	10.946	11.668	3.89E-02	1.09E-01	0.55	0.72
lpg0367	anthranilate synthase component I segment?		Amino Acid Metabolism	8.891	9.784	8.859	8.876	4.78E-01	9.81E-01	0.89	0.02
lpg0367	anthranilate synthase component I segment?		Amino Acid Metabolism	9.261	10.317	8.425	8.717	1.17E-01	7.05E-01	1.06	0.29
lpg0368	ORF		ORFs of unknown function (unique)	8.532	8.221	8.916	7.788	5.34E-01	3.35E-02	-0.31	-1.13
lpg0368	ORF		ORFs of unknown function (unique)	8.848	8.272	8.743	7.754	2.05E-01	2.96E-01	-0.58	-0.99
lpg0369	carboxylesterase/phospholipase		Protein fate / hydrolases / secretion	12.518	11.963	9.225	12.578	3.76E-01	3.08E-03	-0.56	3.35
lpg0369	carboxylesterase/phospholipase		Protein fate / hydrolases / secretion	11.537	11.920	9.141	12.550	8.12E-01	1.50E-03	0.38	3.41
lpg0370	oligoketide cyclase/lipid transporter protein COG2867		Transport and binding	12.098	11.739	9.888	12.375	4.28E-01	1.21E-03	-0.36	2.49
lpg0370	oligoketide cyclase/lipid transporter protein COG2867		Transport and binding	12.157	11.871	9.507	12.332	5.43E-01	8.29E-05	-0.29	2.82
lpg0371	hypothetical COG2914		Unknown / hypothetical proteins	11.738	11.144	11.708	10.537	9.27E-02	2.23E-02	-0.59	-1.17
lpg0371	hypothetical COG2914		Unknown / hypothetical proteins	11.783	11.058	11.781	11.098	1.83E-02	1.35E-02	-0.72	-0.68
lpg0372	COG2913 small protein A (tmRNA-binding), outer membr	*smpA*	Signal transduction / other regulatory f	11.698	10.487	8.609	11.108	3.56E-03	1.18E-02	-1.21	2.50
lpg0372	COG2913 small protein A (tmRNA-binding), outer membr	*smpA*	Signal transduction / other regulatory f	11.659	10.571	8.249	11.188	1.05E-02	5.74E-03	-1.09	2.94
lpg0373	components of sensory transduction system (sensory box/GGDEF DI		Signal transduction / other regulatory f	8.160	7.537	7.744	7.424	5.48E-01	8.68E-01	-0.62	-0.32
lpg0373	components of sensory transduction system (sensory box/GGDEF DI		Signal transduction / other regulatory f	8.719	6.898	8.080	7.792	1.58E-01	7.81E-01	-1.82	-0.29
lpg0374	adenylate cyclase? (ATP-pyrophosphate lyase?) lipoprotein?		Unknown / hypothetical proteins	11.969	10.523	8.479	11.324	1.73E-01	8.94E-03	-1.45	2.85
lpg0374	adenylate cyclase? (ATP-pyrophosphate lyase?) lipoprotein?		Unknown / hypothetical proteins	11.769	11.750	7.756	11.998	9.82E-01	8.29E-03	-0.02	4.24
lpg0375	ORF		ORFs of unknown function (unique)	10.025	7.674	7.510	8.245	2.05E-02	2.78E-01	-2.35	0.74
lpg0375	ORF		ORFs of unknown function (unique)	9.697	8.096	7.157	8.093	7.57E-03	2.57E-01	-1.60	0.94
lpg0376	SdhA; GRIP coiled-coil protein GCC185	*sdhA*	Named proteins of general function	11.444	9.725	9.906	10.611	1.93E-03	1.52E-01	-1.72	0.71
lpg0376	SdhA; GRIP coiled-coil protein GCC185	*sdhA*	Named proteins of general function	11.534	9.388	10.300	11.028	2.43E-02	9.92E-02	-2.15	0.73
lpg0377	hypothetical protein		Unknown / hypothetical proteins	11.579	10.215	11.281	9.524	1.02E-01	1.31E-01	-1.36	-1.76
lpg0377	hypothetical protein		Unknown / hypothetical proteins	11.686	9.758	11.223	10.244	6.62E-04	3.55E-02	-1.93	-0.98
lpg0378	A. fulgidus predicted coding region AF2307		Unknown / hypothetical proteins	12.594	11.137	12.255	10.973	2.13E-02	1.31E-01	-1.46	-1.28
lpg0378	A. fulgidus predicted coding region AF2307		Unknown / hypothetical proteins	12.583	11.900	12.252	12.012	3.70E-02	4.45E-01	-0.68	-0.24
lpg0379	ribosomal protein S6 modification protein (glutathione synthase)		Amino Acid Metabolism, Metabolism o	12.666	11.537	12.184	11.571	2.87E-05	6.26E-02	-1.13	-0.61
lpg0379	ribosomal protein S6 modification protein (glutathione synthase)		Amino Acid Metabolism, Metabolism o	12.713	11.494	12.148	11.594	4.94E-04	6.14E-02	-1.22	-0.55
lpg0380	ORF		ORFs of unknown function (unique)	12.515	10.928	12.321	11.347	2.14E-01	1.05E-01	-1.59	-0.97
lpg0380	ORF		ORFs of unknown function (unique)	12.647	11.980	12.545	11.852	1.49E-01	1.55E-02	-0.67	-0.69
lpg0381	hypothetical		Unknown / hypothetical proteins	9.463	8.925	9.068	8.470	2.01E-01	5.03E-01	-0.54	-0.60
lpg0381	hypothetical		Unknown / hypothetical proteins	9.073	8.889	9.260	8.974	6.74E-01	6.92E-01	-0.18	-0.29
lpg0382	osmotically inducible protein Y	*osmY*	Detoxification / adaptation	10.427	10.617	11.080	9.435	6.18E-01	2.54E-03	0.19	-1.64
lpg0382	osmotically inducible protein Y	*osmY*	Detoxification / adaptation	10.397	10.873	10.860	9.511	4.09E-02	5.68E-03	0.48	-1.35
lpg0383	small ORF (160aa) very weak IcmL homolog		Transport and binding, Toxin productio	10.504	9.969	12.893	10.176	4.27E-01	4.87E-03	-0.53	-2.72
lpg0383	small ORF (160aa) very weak IcmL homolog		Transport and binding, Toxin productio	10.472	9.549	12.820	10.300	1.92E-01	9.15E-03	-0.92	-2.52
lpg0384	excinuclease ABC A subunit (UvrA)	*uvrA*	DNA/RNA degradation / restriction	11.338	10.107	10.163	11.298	2.29E-02	3.19E-02	-1.23	1.14
lpg0384	excinuclease ABC A subunit (UvrA)	*uvrA*	DNA/RNA degradation / restriction	11.614	11.054	10.266	11.963	5.33E-01	3.27E-02	-0.56	1.70

lpg0385	LemA protein (cytoplasmic membrane protein)		Toxin production / other pathogen func	11.938	11.573	13.885	10.172	5.40E-01	3.19E-04	-0.36	-3.71
lpg0385	LemA protein (cytoplasmic membrane protein)		Toxin production / other pathogen func	11.959	10.476	13.909	10.271	2.75E-01	4.39E-04	-1.48	-3.64
lpg0386	heat shock protein HtpX (protease) (stress protein)	*htpX*	Detoxification / adaptation, Protein fate	11.706	10.375	11.758	11.443	2.38E-02	2.66E-01	-1.33	-0.31
lpg0386	heat shock protein HtpX (protease) (stress protein)	*htpX*	Detoxification / adaptation, Protein fate	10.214	10.094	11.359	11.067	7.84E-01	5.39E-01	-0.12	-0.29
lpg0387	ABC transporter, permease protein		Transport and binding	11.527	9.585	10.256	9.905	1.18E-05	4.22E-01	-1.94	-0.35
lpg0387	ABC transporter, permease protein		Transport and binding	11.557	9.699	10.310	10.228	2.92E-04	8.48E-01	-1.86	-0.08
lpg0388	ABC transporter, ATP binding component		Transport and binding	10.189	10.827	10.121	9.476	5.53E-02	4.89E-01	0.64	-0.64
lpg0388	ABC transporter, ATP binding component		Transport and binding	9.985	10.610	9.906	10.444	2.63E-01	1.74E-01	0.63	0.54
lpg0389	ORF		ORFs of unknown function (unique)	10.239	8.024	9.391	8.055	2.08E-03	1.39E-01	-2.22	-1.34
lpg0389	ORF		ORFs of unknown function (unique)	8.196	6.383	7.941	7.787	6.51E-02	9.00E-01	-1.81	-0.15
lpg0390	ORF	*vipA*	ORFs of unknown function (unique)	11.960	12.424	11.161	11.022	5.89E-02	5.96E-01	0.46	-0.14
lpg0390	ORF	*vipA*	ORFs of unknown function (unique)	11.658	12.336	10.934	11.060	3.19E-03	7.39E-01	0.68	0.13
lpg0391	SM20-related protein (Ca binding protein)		Transport and binding	10.192	9.468	9.762	9.022	2.08E-01	1.43E-01	-0.72	-0.74
lpg0391	SM20-related protein (Ca binding protein)		Transport and binding	10.077	9.531	9.842	9.169	4.33E-01	1.42E-01	-0.55	-0.67
lpg0392	zinc metalloprotease (metal-dependent hydrolase)		Protein fate / hydrolases / secretion	9.878	7.776	10.397	8.382	5.97E-04	7.85E-03	-2.10	-2.01
lpg0392	zinc metalloprotease (metal-dependent hydrolase)		Protein fate / hydrolases / secretion	10.945	8.159	8.995	8.590	1.66E-02	5.80E-01	-2.79	-0.41
lpg0393	ORF		ORFs of unknown function (unique)	9.281	8.595	9.374	8.663	2.39E-01	7.06E-02	-0.69	-0.71
lpg0393	ORF		ORFs of unknown function (unique)	10.255	9.559	8.601	10.413	3.62E-01	7.65E-02	-0.70	1.81
lpg0394	COG0350 methylated DNA protein cysteine S-methyltransferase		Named proteins of general function	11.448	9.311	9.226	10.456	4.90E-03	1.63E-01	-2.14	1.23
lpg0394	COG0350 methylated DNA protein cysteine S-methyltransferase		Named proteins of general function	11.319	9.135	8.861	10.635	1.55E-03	1.16E-01	-2.18	1.77
lpg0395	50S ribosomal protein L19	*rplS*	Translation	13.655	11.412	11.402	12.988	4.93E-03	4.60E-02	-2.24	1.59
lpg0395	50S ribosomal protein L19	*rplS*	Translation	13.372	11.453	11.248	13.091	2.57E-02	2.44E-02	-1.92	1.84
lpg0396	tRNA (guanine N1) methyltransferase	*trmD*	DNA/RNA degradation / restriction, Tra	11.315	9.161	9.225	11.621	1.25E-02	2.07E-02	-2.15	2.40
lpg0396	tRNA (guanine N1) methyltransferase	*trmD*	DNA/RNA degradation / restriction, Tra	11.964	9.529	8.992	11.617	4.24E-05	1.87E-02	-2.44	2.63
lpg0397	16S rRNA processing protein RimM	*rimM*	DNA/RNA degradation / restriction, Tra	12.380	9.782	8.561	12.972	2.49E-02	4.16E-03	-2.60	4.41
lpg0397	16S rRNA processing protein RimM	*rimM*	DNA/RNA degradation / restriction, Tra	12.299	9.909	7.484	13.135	5.76E-02	6.98E-03	-2.39	5.65
lpg0398	ORF		ORFs of unknown function (unique)	10.243	9.176	8.647	10.593	2.73E-01	3.79E-03	-1.07	1.95
lpg0398	ORF		ORFs of unknown function (unique)	10.195	9.249	8.278	10.367	2.07E-01	5.48E-03	-0.95	2.09
lpg0399	30S ribosomal protein S16	*rpsP*	Translation	14.329	12.927	12.098	14.675	7.56E-02	6.28E-03	-1.40	2.58
lpg0399	30S ribosomal protein S16	*rpsP*	Translation	14.459	13.047	11.685	14.671	4.13E-02	1.59E-03	-1.41	2.99
lpg0400	signal recognition particle protein Ffh (GTP-binding expo	*ffh*	Protein fate / hydrolases / secretion	11.076	11.162	9.881	11.804	8.92E-01	2.47E-02	0.09	1.92
lpg0400	signal recognition particle protein Ffh (GTP-binding expo	*ffh*	Protein fate / hydrolases / secretion	11.047	11.225	9.840	12.183	8.13E-01	8.51E-03	0.18	2.34
lpg0401	ORF		ORFs of unknown function (unique)	8.439	8.270	8.245	10.777	8.51E-01	3.37E-04	-0.17	2.53
lpg0401	ORF		ORFs of unknown function (unique)	8.215	9.203	7.501	10.624	3.08E-02	1.00E-02	0.99	3.12
lpg0402	putative ankyrin-repeat containing protein	*legA9*	Named proteins of general function	9.901	8.624	9.588	9.373	8.31E-02	5.16E-01	-1.28	-0.21
lpg0402	putative ankyrin-repeat containing protein	*legA9*	Named proteins of general function	9.714	9.320	9.138	9.389	1.57E-01	6.44E-01	-0.39	0.25
lpg0403	similar to RIKEN cDNA 1700007B22	*legA7*	Unknown / hypothetical proteins	10.571	9.518	11.432	9.425	9.01E-02	1.43E-02	-1.05	-2.01
lpg0403	similar to RIKEN cDNA 1700007B22	*legA7*	Unknown / hypothetical proteins	10.479	9.821	11.380	9.511	1.09E-01	1.48E-02	-0.66	-1.87
lpg0404	amino acid antiporter (glutamate/gamma-aminobutyrate antiporter)		Transport and binding	11.101	10.630	7.930	9.923	5.49E-01	1.32E-01	-0.47	1.99
lpg0404	amino acid antiporter (glutamate/gamma-aminobutyrate antiporter)		Transport and binding	10.956	10.820	8.516	10.544	8.84E-01	9.63E-02	-0.14	2.03
lpg0405	ORF		ORFs of unknown function (unique)	10.645	9.841	10.307	10.394	1.38E-01	9.34E-01	-0.80	0.09
lpg0405	ORF		ORFs of unknown function (unique)	10.636	9.351	9.411	10.084	4.38E-03	3.30E-01	-1.28	0.67
lpg0406	hypothetical (carboxymuconolactonase decarboxylase family protein)		Named proteins of general function	13.200	14.275	12.554	14.227	6.11E-03	9.24E-05	1.08	1.67
lpg0406	hypothetical (carboxymuconolactonase decarboxylase family protein)		Named proteins of general function	13.124	14.204	12.387	14.156	9.01E-03	6.40E-05	1.08	1.77
lpg0407	ORF		ORFs of unknown function (unique)	11.717	12.383	11.659	12.233	2.76E-02	1.11E-01	0.67	0.57
lpg0407	ORF		ORFs of unknown function (unique)	11.628	12.637	11.720	12.570	1.54E-02	8.95E-03	1.01	0.85
lpg0408	inner (transmembrane) protein (disulfide bond formation protein? (pro		Protein fate / hydrolases / secretion	11.771	10.753	11.915	10.831	5.30E-03	1.29E-02	-1.02	-1.08
lpg0408	inner (transmembrane) protein (disulfide bond formation protein? (pro		Protein fate / hydrolases / secretion	11.709	10.487	11.977	10.979	1.08E-03	2.13E-03	-1.22	-1.00
lpg0409	hypothetical (SURF1 family) (cytochrome c oxidase assembly protein		Energy Metabolism	11.178	11.013	10.142	10.446	4.94E-01	4.73E-01	-0.16	0.30
lpg0409	hypothetical (SURF1 family) (cytochrome c oxidase assembly protein		Energy Metabolism	11.121	10.863	9.613	10.506	3.97E-01	1.41E-01	-0.26	0.89
lpg0410	hypothetical protein		Unknown / hypothetical proteins	11.427	10.506	9.021	9.984	1.62E-02	3.90E-01	-0.92	0.96
lpg0410	hypothetical protein		Unknown / hypothetical proteins	11.111	10.113	8.582	9.896	5.07E-02	2.92E-01	-1.00	1.31
lpg0411	cytochrome c oxidase assembly protein (membrane protein)		Energy Metabolism	11.263	9.820	9.811	10.714	9.40E-03	1.14E-01	-1.44	0.90
lpg0411	cytochrome c oxidase assembly protein (membrane protein)		Energy Metabolism	11.410	10.030	9.602	10.574	3.15E-02	1.13E-01	-1.38	0.97
lpg0412	protoheme IX farnesyltransferase (cytochrome c oxidase assembly fa		Energy Metabolism	10.726	9.521	9.258	10.556	4.94E-03	3.41E-02	-1.21	1.30
lpg0412	protoheme IX farnesyltransferase (cytochrome c oxidase assembly fa		Energy Metabolism	10.746	9.743	9.067	10.776	4.95E-03	4.00E-02	-1.00	1.71
lpg0413	hypothetical (SCO1/SenC family protein)		Named proteins of general function	12.480	12.862	11.841	12.752	1.30E-01	1.12E-03	0.38	0.91
lpg0413	hypothetical (SCO1/SenC family protein)		Named proteins of general function	12.470	12.893	11.784	12.792	9.66E-02	1.04E-03	0.42	1.01
lpg0414	glutathione synthase; ribosomal protein S6 modification protein		Translation	9.731	9.208	10.400	8.692	5.63E-01	1.53E-01	-0.52	-1.71
lpg0414	glutathione synthase; ribosomal protein S6 modification protein		Translation	9.612	8.810	10.295	9.119	2.55E-01	5.79E-02	-0.80	-1.18
lpg0415	ORF		ORFs of unknown function (unique)	9.638	9.690	12.509	9.795	9.31E-01	3.51E-04	0.05	-2.71
lpg0415	ORF		ORFs of unknown function (unique)	9.746	10.190	12.448	10.003	5.93E-01	6.88E-03	0.44	-2.44
lpg0416	glucose-6-phosphate-1-dehydrogenase	*zwf*	Carbohydrate Metabolism, Metabolism	12.273	11.280	14.091	11.614	5.73E-04	1.92E-04	-0.99	-2.48
lpg0416	glucose-6-phosphate-1-dehydrogenase	*zwf*	Carbohydrate Metabolism, Metabolism	12.686	11.216	13.985	11.599	1.27E-03	7.49E-05	-1.47	-2.39

lpg0417	6-phosphogluconolactonase	*pgl*	Carbohydrate Metabolism	11.926	11.746	10.360	12.390	7.45E-01	1.51E-02	-0.18	2.03
lpg0417	6-phosphogluconolactonase	*pgl*	Carbohydrate Metabolism	11.967	11.796	10.210	12.426	7.52E-01	1.18E-02	-0.17	2.22
lpg0418	6-phosphogluconate dehydratase	*edd*	Carbohydrate Metabolism	11.923	11.005	9.767	11.678	3.66E-03	3.10E-02	-0.92	1.91
lpg0418	6-phosphogluconate dehydratase	*edd*	Carbohydrate Metabolism	12.015	11.153	9.542	11.745	9.90E-04	1.10E-02	-0.86	2.20
lpg0419	glucokinase (glucose kinase)	*glk*	Carbohydrate Metabolism, Metabolism	12.966	11.576	12.570	12.495	7.99E-03	8.08E-01	-1.39	-0.07
lpg0419	glucokinase (glucose kinase)	*glk*	Carbohydrate Metabolism, Metabolism	12.998	11.589	12.590	12.529	9.30E-03	8.48E-01	-1.41	-0.06
lpg0420	multifunctional: 2-keto-3-deoxygluconate 6-phosphate al	*eda*	Carbohydrate Metabolism, Amino Acid	12.170	11.148	10.096	12.263	9.52E-03	1.73E-02	-1.02	2.17
lpg0420	multifunctional: 2-keto-3-deoxygluconate 6-phosphate al	*eda*	Carbohydrate Metabolism, Amino Acid	12.068	10.959	9.753	12.156	3.02E-02	1.70E-02	-1.11	2.40
lpg0421	D-xylose (galactose, arabinose)-proton symporter	*ywtG*	Transport and binding	10.288	9.486	9.852	9.091	5.09E-02	2.14E-01	-0.80	-0.76
lpg0421	D-xylose (galactose, arabinose)-proton symporter	*ywtG*	Transport and binding	10.329	9.613	9.859	9.297	2.36E-02	3.42E-01	-0.72	-0.56
lpg0422	glucoamylase (glucan-1,4 alpha glucosidase)	*legY*	Metabolism of Complex Carbohydrates	10.493	8.947	8.588	10.143	8.20E-02	4.22E-02	-1.55	1.55
lpg0422	glucoamylase (glucan-1,4 alpha glucosidase)	*legY*	Metabolism of Complex Carbohydrates	10.695	9.330	8.084	10.067	1.33E-01	1.07E-01	-1.36	1.98
lpg0423	transcriptional regulator (cro family) (HTH-XRE family), p	*yozG*	Transcription factors / DNA binding pro	10.586	10.450	10.649	10.931	7.12E-01	4.66E-01	-0.14	0.28
lpg0423	transcriptional regulator (cro family) (HTH-XRE family), p	*yozG*	Transcription factors / DNA binding pro	10.493	10.272	10.632	10.999	6.08E-01	2.35E-01	-0.22	0.37
lpg0424	hypothetical protein		Unknown / hypothetical proteins	10.492	9.572	9.215	8.926	4.77E-02	7.65E-01	-0.92	-0.29
lpg0424	hypothetical protein		Unknown / hypothetical proteins	10.309	9.717	9.093	9.701	3.30E-01	3.63E-01	-0.59	0.61
lpg0425	ferrochelatase	*hemH*	Metabolism of Cofactors and Vitamins	13.094	12.596	12.455	12.660	2.03E-02	2.07E-01	-0.50	0.21
lpg0425	ferrochelatase	*hemH*	Metabolism of Cofactors and Vitamins	13.126	12.542	12.167	12.648	6.96E-03	1.72E-02	-0.58	0.48
lpg0426	cold shock protein CspH	*cspD*	Detoxification / adaptation	13.365	13.379	13.626	12.634	9.67E-01	1.96E-02	0.01	-0.99
lpg0426	cold shock protein CspH	*cspD*	Detoxification / adaptation	13.384	13.362	13.615	12.728	9.45E-01	2.68E-02	-0.02	-0.89
lpg0427	diadenosine tetraphosphate (Ap4A) hydrolase,histidine triad family pr		Named proteins of general function	10.820	9.711	9.887	9.728	1.22E-01	5.47E-01	-1.11	-0.16
lpg0427	diadenosine tetraphosphate (Ap4A) hydrolase,histidine triad family pr		Named proteins of general function	10.974	10.574	9.703	9.846	1.31E-01	5.44E-01	-0.40	0.14
lpg0428	glyoxylase domain hypothetical protein COG0346		Named proteins of general function	10.515	10.479	11.371	9.794	9.15E-01	3.30E-05	-0.04	-1.58
lpg0428	glyoxylase domain hypothetical protein COG0346		Named proteins of general function	10.363	10.470	11.254	9.718	6.01E-01	4.08E-05	0.11	-1.54
lpg0429	outer membrane efflux protein (multidrug resistance) (RN	*oprM*	Transport and binding	11.844	10.852	11.353	10.889	2.62E-02	5.18E-02	-0.99	-0.46
lpg0429	outer membrane efflux protein (multidrug resistance) (RN	*oprM*	Transport and binding	11.781	11.100	11.307	11.158	1.56E-01	5.40E-01	-0.68	-0.15
lpg0430	multidrug resistance efflux pump PmrA (HlyD family secretion protein)		Transport and binding	9.814	9.273	9.585	8.458	1.29E-01	3.03E-02	-0.54	-1.13
lpg0430	multidrug resistance efflux pump PmrA (HlyD family secretion protein)		Transport and binding	10.058	9.096	9.521	8.675	4.95E-02	2.19E-01	-0.96	-0.85
lpg0431	ORF		ORFs of unknown function (unique)	10.382	7.958	8.511	9.545	1.01E-03	4.64E-01	-2.42	1.03
lpg0431	ORF		ORFs of unknown function (unique)	10.061	9.252	8.601	10.051	7.69E-03	6.92E-02	-0.81	1.45
lpg0432	ORF		ORFs of unknown function (unique)	10.306	9.926	10.302	10.019	3.61E-01	2.40E-01	-0.38	-0.28
lpg0432	ORF		ORFs of unknown function (unique)	10.122	10.804	10.296	10.971	6.58E-03	9.33E-02	0.68	0.67
lpg0433	hypothetical (transcriptional regulator), COG1733		Named proteins of general function	11.542	10.484	11.264	10.045	2.70E-03	9.97E-05	-1.06	-1.22
lpg0433	hypothetical (transcriptional regulator), COG1733		Named proteins of general function	11.580	10.380	11.227	10.048	6.18E-03	3.17E-05	-1.20	-1.18
lpg0434	ORF		ORFs of unknown function (unique)	9.247	8.875	10.109	9.186	7.54E-01	5.71E-02	-0.37	-0.92
lpg0434	ORF		ORFs of unknown function (unique)	9.943	8.144	8.702	9.111	3.83E-03	4.69E-01	-1.80	0.41
lpg0435	SAM-dependent methyltransferase (tellurite resistance protein)		Detoxification / adaptation	12.122	10.842	11.337	10.805	2.02E-02	6.48E-02	-1.28	-0.53
lpg0435	SAM-dependent methyltransferase (tellurite resistance protein)		Detoxification / adaptation	10.713	10.567	10.917	10.396	7.32E-01	1.39E-01	-0.15	-0.52
lpg0436	ORF	*legA11*	ORFs of unknown function (unique)	10.011	12.150	10.904	9.147	2.22E-04	2.28E-03	2.14	-1.76
lpg0436	ORF	*legA11*	ORFs of unknown function (unique)	10.168	12.025	11.038	9.329	1.05E-03	1.95E-03	1.86	-1.71
lpg0437	ORF		ORFs of unknown function (unique)	9.713	9.921	10.071	9.608	5.46E-01	4.06E-01	0.21	-0.46
lpg0437	ORF		ORFs of unknown function (unique)	9.650	10.018	10.054	9.954	3.01E-01	8.74E-01	0.37	-0.10
lpg0438	ORF		ORFs of unknown function (unique)	11.065	8.908	9.190	9.539	2.80E-02	5.05E-01	-2.16	0.35
lpg0438	ORF		ORFs of unknown function (unique)	11.172	8.816	8.764	9.442	7.51E-04	4.27E-01	-2.36	0.68
lpg0439	ORF		ORFs of unknown function (unique)	11.297	11.006	10.606	10.807	5.79E-01	7.10E-01	-0.29	0.20
lpg0439	ORF		ORFs of unknown function (unique)	10.915	11.083	10.352	10.820	8.41E-01	4.61E-01	0.17	0.47
lpg0440	small ORF (70aa)		ORFs of unknown function (unique)	10.911	10.254	10.744	10.518	9.09E-02	6.20E-01	-0.66	-0.23
lpg0440	small ORF (70aa)		ORFs of unknown function (unique)	10.982	10.474	10.531	10.517	2.62E-01	9.77E-01	-0.51	-0.01
lpg0441	IcmT	*icmT*	Transport and binding, Toxin productio	12.008	12.378	12.597	11.661	2.77E-01	3.14E-03	0.37	-0.94
lpg0441	IcmT	*icmT*	Transport and binding, Toxin productio	12.029	12.377	12.634	11.747	2.80E-01	2.27E-03	0.35	-0.89
lpg0442	IcmS	*icmS*	Transport and binding, Toxin productio	12.750	12.247	13.318	11.878	1.93E-02	4.03E-04	-0.50	-1.44
lpg0442	IcmS	*icmS*	Transport and binding, Toxin productio	12.723	12.380	13.280	12.006	5.30E-02	7.76E-04	-0.34	-1.27
lpg0443	IcmR	*icmR*	Transport and binding, Toxin productio	12.460	12.414	12.449	11.104	9.16E-01	5.31E-03	-0.05	-1.34
lpg0443	IcmR	*icmR*	Transport and binding, Toxin productio	12.218	12.410	12.387	11.042	7.22E-01	6.00E-03	0.19	-1.34
lpg0444	IcmQ	*icmQ*	Transport and binding, Toxin productio	12.255	10.538	11.883	11.102	3.15E-03	1.63E-02	-1.72	-0.78
lpg0444	IcmQ	*icmQ*	Transport and binding, Toxin productio	12.385	10.578	11.862	11.185	1.77E-04	1.61E-02	-1.81	-0.68
lpg0445	IcmP (DotM)	*icmP*	Transport and binding, Toxin productio	11.909	10.736	12.557	10.993	1.32E-04	3.60E-04	-1.17	-1.56
lpg0445	IcmP (DotM)	*icmP*	Transport and binding, Toxin productio	11.888	11.349	12.552	11.619	3.82E-01	1.12E-02	-0.54	-0.93
lpg0446	IcmO (DotL) (TrbC)	*icmO*	Transport and binding, Toxin productio	11.157	10.039	11.870	10.550	1.38E-02	1.80E-04	-1.12	-1.32
lpg0446	IcmO (DotL) (TrbC)	*icmO*	Transport and binding, Toxin productio	11.153	9.870	11.765	10.602	1.34E-02	4.31E-04	-1.28	-1.16
lpg0447	LphA (DotK) (OmpA family protein)	*lphA*	Transport and binding, Toxin productio	13.812	12.810	13.886	13.059	2.11E-02	4.46E-02	-1.00	-0.83
lpg0447	LphA (DotK) (OmpA family protein)	*lphA*	Transport and binding, Toxin productio	13.941	12.895	11.959	12.955	3.67E-03	1.10E-01	-1.05	1.00
lpg0448	IcmM (DotJ)	*icmM*	Transport and binding, Toxin productio	13.271	12.246	12.280	12.390	1.09E-02	6.52E-01	-1.03	0.11
lpg0448	IcmM (DotJ)	*icmM*	Transport and binding, Toxin productio	13.251	12.192	12.209	12.350	8.95E-03	5.67E-01	-1.06	0.14

lpg0449	IcmL (DotI)	*icmL*	Transport and binding, Toxin productio	12.944	12.137	12.193	12.330	2.74E-01	8.23E-01	-0.81	0.14
lpg0449	IcmL (DotI)	*icmL*	Transport and binding, Toxin productio	12.949	12.590	11.922	12.720	2.13E-01	5.03E-02	-0.36	0.80
lpg0450	IcmK (DotH) (TraN)	*icmK*	Transport and binding, Toxin productio	12.526	11.591	11.308	11.121	2.77E-01	8.41E-01	-0.94	-0.19
lpg0450	IcmK (DotH) (TraN)	*icmK*	Transport and binding, Toxin productio	12.448	12.304	11.188	11.902	7.80E-01	1.62E-01	-0.14	0.71
lpg0451	IcmE (DotG)	*icmE*	Transport and binding, Toxin productio	11.600	11.362	10.942	11.637	5.93E-01	1.18E-01	-0.24	0.69
lpg0451	IcmE (DotG)	*icmE*	Transport and binding, Toxin productio	11.436	11.405	10.697	11.566	9.48E-01	6.92E-02	-0.03	0.87
lpg0452	IcmG (DotF)	*icmG*	Transport and binding, Toxin productio	12.274	11.653	11.286	12.164	9.48E-02	3.59E-02	-0.62	0.88
lpg0452	IcmG (DotF)	*icmG*	Transport and binding, Toxin productio	12.056	11.608	11.180	12.123	4.37E-01	3.73E-02	-0.45	0.94
lpg0453	IcmC (DotE)	*icmC*	Transport and binding, Toxin productio	13.403	11.766	13.851	12.754	7.62E-07	3.03E-02	-1.64	-1.10
lpg0453	IcmC (DotE)	*icmC*	Transport and binding, Toxin productio	13.410	11.892	13.877	12.904	1.18E-06	1.68E-02	-1.52	-0.97
lpg0454	IcmD (DotP)	*icmD*	Transport and binding, Toxin productio	14.858	13.942	15.105	13.995	6.47E-03	1.84E-04	-0.92	-1.11
lpg0454	IcmD (DotP)	*icmD*	Transport and binding, Toxin productio	14.789	14.002	15.081	14.078	1.27E-03	6.69E-05	-0.79	-1.00
lpg0455	IcmJ (DotN)	*icmJ*	Transport and binding, Toxin productio	13.027	11.876	13.188	11.805	1.26E-04	4.26E-07	-1.15	-1.38
lpg0455	IcmJ (DotN)	*icmJ*	Transport and binding, Toxin productio	12.803	11.477	13.026	11.857	6.14E-03	2.54E-05	-1.33	-1.17
lpg0456	IcmB (DotO) (TraU)	*icmB*	Transport and binding, Toxin productio	10.793	9.353	11.559	10.236	6.92E-05	1.29E-03	-1.44	-1.32
lpg0456	IcmB (DotO) (TraU)	*icmB*	Transport and binding, Toxin productio	10.807	9.886	11.476	10.550	5.42E-02	6.84E-02	-0.92	-0.93
lpg0457	tphA (proP) proline/betaine transporter, MFS family	*tphA*	Transport and binding	9.719	9.031	9.408	8.484	5.43E-01	3.47E-01	-0.69	-0.92
lpg0457	tphA (proP) proline/betaine transporter, MFS family	*tphA*	Transport and binding	9.871	9.426	9.308	8.721	6.78E-01	4.89E-01	-0.45	-0.59
lpg0458	IcmF	*icmF*	Transport and binding, Toxin productio	10.650	10.572	10.443	11.507	7.51E-01	5.65E-03	-0.08	1.06
lpg0458	IcmF	*icmF*	Transport and binding, Toxin productio	10.255	10.722	10.164	11.542	4.16E-01	2.63E-03	0.47	1.38
lpg0459	IcmH (DotU)	*icmH*	Transport and binding, Toxin productio	13.595	13.364	11.525	14.053	4.99E-01	2.21E-04	-0.23	2.53
lpg0459	IcmH (DotU)	*icmH*	Transport and binding, Toxin productio	13.510	13.440	11.535	14.140	8.51E-01	1.86E-04	-0.07	2.61
lpg0460	phosphoribosylamineimidazolecarboxamide formyltransfe	*purH*	Nucleotide Metabolism, Metabolism of	11.269	11.717	10.432	12.351	2.30E-01	1.07E-02	0.45	1.92
lpg0460	phosphoribosylamineimidazolecarboxamide formyltransfe	*purH*	Nucleotide Metabolism, Metabolism of	11.282	11.687	9.489	12.363	2.73E-01	1.75E-02	0.40	2.87
lpg0461	ribosomal protein L11 methyltransferase	*prmA*	Translation	12.262	11.497	11.285	13.350	5.85E-02	7.50E-05	-0.76	2.06
lpg0461	ribosomal protein L11 methyltransferase	*prmA*	Translation	12.327	11.468	11.220	13.285	4.05E-02	3.36E-04	-0.86	2.07
lpg0462	acetyl CoA carboxylase, biotin carboxylase subunit	*accC*	Lipid Metabolism	11.503	11.856	10.365	13.592	7.69E-01	6.49E-04	0.35	3.23
lpg0462	acetyl CoA carboxylase, biotin carboxylase subunit	*accC*	Lipid Metabolism	12.094	11.867	10.019	13.564	6.96E-01	2.65E-05	-0.23	3.54
lpg0463	acetyl CoA carboxylase, biotin carboxyl carrier protein		Carbohydrate Metabolism, Lipid Metak	9.582	10.568	9.671	12.006	4.58E-03	8.98E-05	0.99	2.33
lpg0463	acetyl CoA carboxylase, biotin carboxyl carrier protein		Carbohydrate Metabolism, Lipid Metak	9.824	10.826	9.343	12.100	7.88E-04	1.94E-05	1.00	2.76
lpg0464	3-dehydroquinate dehydratase type	*aroQ*	Amino Acid Metabolism	11.675	10.727	10.031	11.048	4.84E-03	1.81E-01	-0.95	1.02
lpg0464	3-dehydroquinate dehydratase type	*aroQ*	Amino Acid Metabolism	11.763	11.202	10.008	11.278	5.29E-02	1.06E-01	-0.56	1.27
lpg0465	small ORF (79aa)		ORFs of unknown function (unique)	6.899	9.155	7.749	8.203	3.71E-02	5.29E-01	2.26	0.45
lpg0465	small ORF (79aa)		ORFs of unknown function (unique)	6.705	8.831	7.363	7.932	1.11E-01	5.31E-01	2.13	0.57
lpg0466	oxaloacetate decarboxylase alpha subunit (pyruvate carboxylase sub		Carbohydrate Metabolism, Amino Acid	9.825	9.824	9.382	9.987	9.97E-01	1.44E-01	0.00	0.60
lpg0466	oxaloacetate decarboxylase alpha subunit (pyruvate carboxylase sub		Carbohydrate Metabolism, Amino Acid	9.979	9.559	9.325	10.025	3.16E-01	5.28E-02	-0.42	0.70
lpg0467	zinc metalloprotease (hemagglutinin/protease)		Toxin production / other pathogen func	14.040	15.637	12.227	14.793	1.89E-03	5.27E-05	1.60	2.57
lpg0467	zinc metalloprotease (hemagglutinin/protease)		Toxin production / other pathogen func	13.988	15.665	12.246	14.816	4.13E-04	4.08E-05	1.68	2.57
lpg0468	lipase A		Protein fate / hydrolases / secretion	10.701	11.266	9.956	10.191	1.51E-01	6.19E-01	0.57	0.23
lpg0468	lipase A		Protein fate / hydrolases / secretion	10.543	11.313	9.224	10.412	3.41E-02	2.37E-01	0.77	1.19
lpg0469	endonuclease/exonuclease/phosphatase family protein		DNA/RNA degradation / restriction	9.930	8.964	11.646	8.976	8.85E-02	6.43E-05	-0.97	-2.67
lpg0469	endonuclease/exonuclease/phosphatase family protein		DNA/RNA degradation / restriction	9.999	8.736	11.651	9.174	8.98E-03	6.98E-04	-1.26	-2.48
lpg0470	fructose bisphosphate aldolase		Carbohydrate Metabolism, Energy Me	11.656	13.691	11.107	13.574	5.03E-06	3.04E-04	2.03	2.47
lpg0470	fructose bisphosphate aldolase		Carbohydrate Metabolism, Energy Me	11.854	13.676	10.906	13.548	1.48E-06	2.46E-04	1.82	2.64
lpg0471	phenol hydroxylase (ferredoxin-NADP reductase)	*poxF*	Energy Metabolism	9.769	10.837	9.636	11.747	5.28E-03	3.41E-05	1.07	2.11
lpg0471	phenol hydroxylase (ferredoxin-NADP reductase)	*poxF*	Energy Metabolism	9.710	10.830	8.565	11.646	4.70E-04	1.76E-03	1.12	3.08
lpg0472	IcmC homolog (DotV)		Transport and binding, Toxin productio	10.151	10.675	11.586	11.115	6.54E-02	1.75E-01	0.52	-0.47
lpg0472	IcmC homolog (DotV)		Transport and binding, Toxin productio	9.848	10.810	11.708	11.361	2.88E-02	2.93E-01	0.96	-0.35
lpg0473	hypothetical (PhnO related protein) phosphonate metabolism, gene re		Signal transduction / other regulatory f	11.412	10.160	12.197	10.789	6.04E-03	3.15E-03	-1.25	-1.41
lpg0473	hypothetical (PhnO related protein) phosphonate metabolism, gene re		Signal transduction / other regulatory f	11.359	10.513	12.189	10.936	6.55E-03	8.20E-03	-0.85	-1.25
lpg0474	CDP-diacylglycerol-serine-O-phosphatidyltransferase (phosphatidylse		Amino Acid Metabolism, Metabolism o	12.290	12.589	11.042	12.672	5.49E-01	2.10E-03	0.30	1.63
lpg0474	CDP-diacylglycerol-serine-O-phosphatidyltransferase (phosphatidylse		Amino Acid Metabolism, Metabolism o	13.206	12.588	10.684	12.748	1.96E-01	3.79E-03	-0.62	2.06
lpg0475	sugar transport PTS system phosphocarrier HPr protein	*ptsH*	Transport and binding	12.352	11.843	11.225	11.581	3.13E-01	3.18E-01	-0.51	0.36
lpg0475	sugar transport PTS system phosphocarrier HPr protein	*ptsH*	Transport and binding	11.985	11.734	11.113	11.522	7.37E-01	2.40E-01	-0.25	0.41
lpg0476	sigma-54 modulation protein		Transcription factors / DNA binding prc	13.632	12.715	14.624	11.767	1.02E-03	1.80E-06	-0.92	-2.86
lpg0476	sigma-54 modulation protein		Transcription factors / DNA binding prc	13.564	12.620	14.596	11.812	2.50E-03	1.26E-06	-0.94	-2.78
lpg0477	RNA polymerase signma-54 factor RpoN		Transcription factors / DNA binding prc	11.940	11.707	12.771	11.477	4.72E-01	2.86E-02	-0.23	-1.29
lpg0477	RNA polymerase signma-54 factor RpoN		Transcription factors / DNA binding prc	12.035	12.189	12.794	12.202	7.80E-01	2.75E-01	0.15	-0.59
lpg0478	50S ribosomal protein L33	*rpL33*	Translation	12.952	13.113	10.265	13.863	8.84E-01	2.01E-03	0.16	3.60
lpg0478	50S ribosomal protein L33	*rpL33*	Translation	13.079	13.048	9.792	13.813	9.74E-01	3.79E-03	-0.03	4.02
lpg0479	50S ribosomal protein L28	*rpmB*	Translation	13.794	13.752	10.330	14.837	9.70E-01	4.06E-03	-0.04	4.51
lpg0479	50S ribosomal protein L28	*rpmB*	Translation	13.662	13.689	9.893	14.767	9.80E-01	5.62E-03	0.03	4.87
lpg0480	small ORF (53aa)		ORFs of unknown function (unique)	10.227	10.279	9.951	10.133	9.01E-01	7.71E-01	0.05	0.18
lpg0480	small ORF (53aa)		ORFs of unknown function (unique)	10.099	11.207	9.869	10.420	1.66E-02	4.94E-01	1.11	0.55

lpg0481	(S-adenosylmethionine-dependent) methyltransferase [tRNA(guanine		DNA/RNA degradation / restriction, Tra	10.288	10.125	9.205	11.113	6.46E-01	3.02E-03	-0.16	1.91
lpg0481	(S-adenosylmethionine-dependent) methyltransferase [tRNA(guanine		DNA/RNA degradation / restriction, Tra	10.280	10.304	8.169	11.328	9.53E-01	4.38E-02	0.02	3.16
lpg0482	endo-1,4 beta-glucanase or (deblocking) aminopeptidase (zinc metall		Protein fate / hydrolases / secretion	9.226	12.298	10.583	12.644	4.45E-05	2.53E-03	3.07	2.06
lpg0482	endo-1,4 beta-glucanase or (deblocking) aminopeptidase (zinc metall		Protein fate / hydrolases / secretion	9.736	12.234	10.527	12.688	5.21E-05	5.33E-04	2.50	2.16
lpg0483	ORF	*LegA12*	ORFs of unknown function (unique)	11.738	13.750	12.338	12.313	6.89E-02	9.51E-01	2.01	-0.03
lpg0483	ORF	*LegA12*	ORFs of unknown function (unique)	11.779	14.324	12.356	12.517	2.88E-04	4.93E-01	2.54	0.16
lpg0484	HflK protein (phage lambda CII protease?)	*hflK*	Protein fate / hydrolases / secretion, V	13.233	12.968	11.789	13.828	5.52E-01	4.58E-04	-0.27	2.04
lpg0484	HflK protein (phage lambda CII protease?)	*hflK*	Protein fate / hydrolases / secretion, V	13.226	12.931	11.673	13.801	5.45E-01	3.68E-04	-0.30	2.13
lpg0485	HflC protein (phage lambda CII repressor?)	*hflC*	Transcription factors / DNA binding pro	12.899	12.595	10.145	12.917	5.16E-01	1.72E-03	-0.30	2.77
lpg0485	HflC protein (phage lambda CII repressor?)	*hflC*	Transcription factors / DNA binding pro	12.857	12.596	10.050	12.966	5.99E-01	1.80E-03	-0.26	2.92
lpg0486	adenylosuccinate synthetase	*purA*	Nucleotide Metabolism, Amino Acid Me	12.569	12.853	9.997	13.804	6.29E-01	3.11E-04	0.28	3.81
lpg0486	adenylosuccinate synthetase	*purA*	Nucleotide Metabolism, Amino Acid Me	12.600	12.848	9.864	13.836	6.49E-01	1.05E-04	0.25	3.97
lpg0487	hypothetical		Unknown / hypothetical proteins	9.562	9.438	10.511	8.786	9.27E-01	3.30E-01	-0.12	-1.73
lpg0487	hypothetical		Unknown / hypothetical proteins	9.140	8.154	10.622	9.603	3.70E-01	3.69E-01	-0.99	-1.02
lpg0488	transposase (IS4 family, ISSod6)		Viral functions / Phage / Transposases	11.675	12.236	11.962	11.480	1.46E-01	1.98E-01	0.56	-0.48
lpg0488	transposase (IS4 family, ISSod6)		Viral functions / Phage / Transposases	11.649	12.293	11.748	11.624	8.43E-02	7.53E-01	0.64	-0.12
lpg0489	hypothetical (endonuclease?)COG2827		Unknown / hypothetical proteins	11.319	10.670	10.495	10.358	4.50E-02	7.52E-01	-0.65	-0.14
lpg0489	hypothetical (endonuclease?)COG2827		Unknown / hypothetical proteins	11.380	11.199	10.574	10.473	6.50E-01	8.50E-01	-0.18	-0.10
lpg0490	arginine repressor (transcriptional regulator)		Transcription factors / DNA binding pro	9.065	11.861	9.953	7.741	1.55E-06	1.30E-01	2.80	-2.21
lpg0490	arginine repressor (transcriptional regulator)		Transcription factors / DNA binding pro	8.103	11.899	8.576	7.499	3.04E-06	1.55E-01	3.80	-1.08
lpg0491	amino acid (glutamine) ABC transporter, periplasmic amino acid bindi		Transport and binding	6.793	14.296	8.074	6.959	1.32E-03	4.90E-01	7.50	-1.12
lpg0491	amino acid (glutamine) ABC transporter, periplasmic amino acid bindi		Transport and binding	7.595	14.539	7.482	9.037	2.24E-04	1.75E-01	6.94	1.56
lpg0492	amino acid (glutamine) ABC transporter, permease	*yqiY*	Transport and binding	8.362	14.560	8.518	7.652	7.48E-07	1.40E-01	6.20	-0.87
lpg0492	amino acid (glutamine) ABC transporter, permease	*yqiY*	Transport and binding	7.942	14.808	8.291	8.501	2.30E-10	6.72E-01	6.87	0.21
lpg0493	amino acid (glutamine) ABC transporter, ATP binding component		Transport and binding	7.761	14.050	7.964	8.160	1.83E-07	7.81E-01	6.29	0.20
lpg0493	amino acid (glutamine) ABC transporter, ATP binding component		Transport and binding	7.936	14.108	7.655	8.827	2.49E-06	1.04E-02	6.17	1.17
lpg0494	argininosuccinate synthase	*argG*	Amino Acid Metabolism	7.947	14.736	8.279	9.119	8.47E-05	3.06E-01	6.79	0.84
lpg0494	argininosuccinate synthase	*argG*	Amino Acid Metabolism	7.498	15.271	7.146	9.771	1.14E-06	1.78E-01	7.77	2.63
lpg0495	argininosuccinate lyase	*argH*	Amino Acid Metabolism	9.374	14.193	9.426	9.141	3.05E-05	4.90E-01	4.82	-0.28
lpg0495	argininosuccinate lyase	*argH*	Amino Acid Metabolism	9.629	14.101	9.019	9.041	9.51E-05	9.56E-01	4.47	0.02
lpg0496	ornithine carbamoyltransferase	*argF*	Amino Acid Metabolism	9.752	13.545	10.335	10.355	4.35E-03	9.76E-01	3.79	0.02
lpg0496	ornithine carbamoyltransferase	*argF*	Amino Acid Metabolism	9.825	13.784	10.159	10.203	1.08E-03	9.28E-01	3.96	0.04
lpg0497	adenosine deaminase		Nucleotide Metabolism	11.408	13.059	12.181	13.498	2.45E-02	2.55E-02	1.65	1.32
lpg0497	adenosine deaminase		Nucleotide Metabolism	11.589	13.790	12.208	14.076	2.67E-04	3.79E-05	2.20	1.87
lpg0498	leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein		Transport and binding	10.765	10.774	10.703	9.995	9.84E-01	1.50E-01	0.01	-0.71
lpg0498	leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein		Transport and binding	10.786	10.932	10.764	10.444	6.84E-01	3.02E-01	0.15	-0.32
lpg0499	carboxy-terminal protease		Protein fate / hydrolases / secretion	8.202	9.223	11.562	9.197	1.75E-01	5.26E-03	1.02	-2.36
lpg0499	carboxy-terminal protease		Protein fate / hydrolases / secretion	8.554	8.766	11.610	9.310	7.61E-01	2.38E-03	0.21	-2.30
lpg0500	peptidase (M23/M37 family)		Protein fate / hydrolases / secretion	10.825	9.300	10.276	9.153	1.91E-03	9.16E-02	-1.53	-1.12
lpg0500	peptidase (M23/M37 family)		Protein fate / hydrolases / secretion	10.779	8.922	10.235	9.454	1.14E-03	7.13E-02	-1.86	-0.78
lpg0501	phosphoglycerate mutase, 2,3-bisphosphoglycerate inde	*pgm*	Carbohydrate Metabolism	11.112	11.751	11.579	12.822	3.45E-03	3.72E-05	0.64	1.24
lpg0501	phosphoglycerate mutase, 2,3-bisphosphoglycerate inde	*pgm*	Carbohydrate Metabolism	11.061	11.766	11.250	12.707	5.76E-04	3.83E-04	0.70	1.46
lpg0502	phosphatidylcholine hydrolyzing phospholipase		Metabolism of Complex Lipids	10.111	9.412	10.023	9.887	2.40E-02	5.54E-01	-0.70	-0.14
lpg0502	phosphatidylcholine hydrolyzing phospholipase		Metabolism of Complex Lipids	10.049	9.208	9.733	9.770	1.27E-02	9.49E-01	-0.84	0.04
lpg0503	undecaprenyl diphosphate synthetase (undecaprenyl pyr	*uppS*	Named proteins of general function	10.933	10.845	9.446	11.853	8.61E-01	9.55E-04	-0.09	2.41
lpg0503	undecaprenyl diphosphate synthetase (undecaprenyl pyr	*uppS*	Named proteins of general function	11.220	11.031	9.183	11.826	5.98E-01	1.33E-03	-0.19	2.64
lpg0504	phosphatidate cytidyltransferase (CDP diglyceride synthe	*cdsA*	Metabolism of Complex Lipids	12.327	10.844	11.146	10.596	2.41E-02	2.97E-01	-1.48	-0.55
lpg0504	phosphatidate cytidyltransferase (CDP diglyceride synthe	*cdsA*	Metabolism of Complex Lipids	12.351	11.048	11.144	11.187	1.38E-01	9.66E-01	-1.30	0.04
lpg0505	membrane associated zinc metalloprotease	*yaeL*	Protein fate / hydrolases / secretion	10.407	10.242	9.893	10.180	5.75E-01	4.39E-01	-0.17	0.29
lpg0505	membrane associated zinc metalloprotease	*yaeL*	Protein fate / hydrolases / secretion	10.454	10.032	9.859	10.152	1.18E-01	5.05E-01	-0.42	0.29
lpg0506	outer membrane protein (bacterial surface antigen family)		Named proteins of general function	12.096	11.643	9.536	13.105	3.47E-01	2.61E-04	-0.45	3.57
lpg0506	outer membrane protein (bacterial surface antigen family)		Named proteins of general function	12.083	11.685	9.417	13.060	3.72E-01	3.72E-03	-0.40	3.64
lpg0507	outer membrane protein OmpH		Named proteins of general function	14.573	14.531	12.504	15.208	9.51E-01	4.48E-04	-0.04	2.70
lpg0507	outer membrane protein OmpH		Named proteins of general function	14.444	14.511	12.525	15.258	9.19E-01	7.87E-04	0.07	2.73
lpg0508	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-aclytransfe	*lpxD*	Metabolism of Complex Carbohydrates	9.530	10.738	8.588	13.779	2.94E-02	2.31E-08	1.21	5.19
lpg0508	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-aclytransfe	*lpxD*	Metabolism of Complex Carbohydrates	9.210	10.702	7.629	13.751	1.54E-02	2.47E-07	1.49	6.12
lpg0509	ORF sugar transporter family		Transport and binding	9.317	10.598	9.045	10.161	1.10E-01	3.69E-01	1.28	1.12
lpg0509	ORF sugar transporter family		Transport and binding	8.943	10.277	9.096	10.932	1.40E-01	2.85E-02	1.33	1.84
lpg0510	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (	*fabZ*	Metabolism of Complex Carbohydrates	13.240	11.541	10.725	12.782	2.31E-02	6.07E-02	-1.70	2.06
lpg0510	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (	*fabZ*	Metabolism of Complex Carbohydrates	13.313	12.055	10.952	13.267	1.30E-02	7.54E-03	-1.26	2.32
lpg0511	acyl-(acyl carrier protein)-UDP-N-acetylglucosamine acyl	*lpxA*	Metabolism of Complex Carbohydrates	9.340	8.668	8.627	10.880	2.75E-01	2.37E-02	-0.67	2.25
lpg0511	acyl-(acyl carrier protein)-UDP-N-acetylglucosamine acyl	*lpxA*	Metabolism of Complex Carbohydrates	8.834	8.415	7.362	10.476	7.22E-01	7.37E-03	-0.42	3.11
lpg0512	CrcB protein (transmembrane protein), chromosome condensation? c		Detoxification / adaptation, Chemotaxi	12.273	10.359	10.218	11.851	1.23E-01	7.27E-02	-1.91	1.63
lpg0512	CrcB protein (transmembrane protein), chromosome condensation? c		Detoxification / adaptation, Chemotaxi	12.540	11.075	10.222	12.215	6.97E-03	9.33E-03	-1.46	1.99

lpg0513	seryl tRNA synthetase	*serS*	Amino Acid Metabolism, Translation	12.665	12.183	11.093	12.920	2.29E-01	4.13E-05	-0.48	1.83
lpg0513	seryl tRNA synthetase	*serS*	Amino Acid Metabolism, Translation	12.667	12.237	11.019	13.001	2.37E-01	6.30E-05	-0.43	1.98
lpg0514	hypothetical (glutamate rich protein) PLUS acetyltransferase (ribosom		Protein fate / hydrolases / secretion	10.307	7.925	9.164	9.051	1.15E-02	7.99E-01	-2.38	-0.11
lpg0514	hypothetical (glutamate rich protein) PLUS acetyltransferase (ribosom		Protein fate / hydrolases / secretion	10.516	9.192	8.745	9.579	6.91E-02	2.18E-01	-1.32	0.83
lpg0515	protein of ancient origin (eukaryotic?) (CG14688 gene pr	*legD2*	Unknown / hypothetical proteins	9.935	9.600	9.359	9.037	5.01E-01	5.44E-01	-0.33	-0.32
lpg0515	protein of ancient origin (eukaryotic?) (CG14688 gene pr	*legD2*	Unknown / hypothetical proteins	9.603	9.566	9.635	9.687	9.51E-01	9.35E-01	-0.04	0.05
lpg0516	conserved hypothetical protein		Unknown / hypothetical proteins	8.628	8.191	8.753	7.857	2.80E-01	8.17E-02	-0.44	-0.90
lpg0516	conserved hypothetical protein		Unknown / hypothetical proteins	8.101	8.397	8.494	8.764	5.97E-01	6.59E-01	0.30	0.27
lpg0517	COG0656: aldo/keto reductases, related to diketogulonat	*ytbE*	Named proteins of general function	10.963	13.397	11.835	13.475	3.00E-03	4.63E-02	2.43	1.64
lpg0517	COG0656: aldo/keto reductases, related to diketogulonat	*ytbE*	Named proteins of general function	11.077	13.649	11.667	13.803	4.09E-03	1.94E-02	2.57	2.14
lpg0518	ORF		ORFs of unknown function (unique)	12.358	14.414	12.179	13.125	1.08E-07	5.07E-04	2.06	0.95
lpg0518	ORF		ORFs of unknown function (unique)	12.428	14.395	12.136	13.151	5.47E-09	1.96E-04	1.97	1.02
lpg0519	ORF		ORFs of unknown function (unique)	6.663	6.726	7.814	4.822	9.54E-01	1.19E-02	0.06	-2.99
lpg0519	ORF		ORFs of unknown function (unique)	6.284	9.578	6.110	11.627	3.30E-01	3.03E-01	3.29	5.52
lpg0520	methyltransferase (ubiE/COQ5 family)		Metabolism of Cofactors and Vitamins	9.437	9.127	9.476	9.517	4.98E-01	9.23E-01	-0.31	0.04
lpg0520	methyltransferase (ubiE/COQ5 family)		Metabolism of Cofactors and Vitamins	9.487	8.442	9.331	9.461	8.10E-03	7.04E-01	-1.05	0.13
lpg0521	hypothetical protein		Unknown / hypothetical proteins	9.727	8.205	9.471	9.404	5.01E-02	8.98E-01	-1.52	-0.07
lpg0521	hypothetical protein		Unknown / hypothetical proteins	9.666	8.206	8.864	9.106	8.53E-02	8.30E-01	-1.46	0.24
lpg0522	acetyltransferase, GNAT family		Named proteins of general function	11.140	8.508	10.188	8.296	1.01E-02	1.46E-02	-2.63	-1.89
lpg0522	acetyltransferase, GNAT family		Named proteins of general function	10.147	9.009	10.328	8.723	6.04E-04	1.19E-03	-1.14	-1.60
lpg0523	aminoglycoside N(6')-acetyltransferase	*aacA4*	Named proteins of general function	10.564	8.180	9.692	8.227	8.63E-03	2.48E-02	-2.38	-1.47
lpg0523	aminoglycoside N(6')-acetyltransferase	*aacA4*	Named proteins of general function	10.666	9.420	8.888	8.954	2.50E-01	9.46E-01	-1.25	0.07
lpg0524	tRNA-Pro		tRNA	11.026	11.921	10.655	11.170	8.95E-02	5.61E-02	0.90	0.51
lpg0524	tRNA-Pro		tRNA	11.000	12.093	10.789	11.317	1.27E-01	2.46E-01	1.09	0.53
lpg0525	unknown virulence protein		Toxin production / other pathogen func	12.507	11.541	13.289	11.132	1.85E-01	8.62E-05	-0.97	-2.16
lpg0525	unknown virulence protein		Toxin production / other pathogen func	12.419	11.803	13.219	11.132	2.70E-01	8.17E-05	-0.62	-2.09
lpg0526	transmembrane protein?		Unknown / hypothetical proteins	10.958	11.411	10.854	10.121	4.94E-01	5.79E-01	0.45	-0.73
lpg0526	transmembrane protein?		Unknown / hypothetical proteins	11.229	11.941	11.373	11.156	2.72E-01	3.78E-01	0.71	-0.22
lpg0527	signal transduction protein (possible competence protein)		Transport and binding, Signal transduc	9.770	9.073	12.199	9.624	2.81E-01	5.00E-04	-0.70	-2.57
lpg0527	signal transduction protein (possible competence protein)		Transport and binding, Signal transduc	9.747	9.052	12.176	9.828	2.59E-01	1.88E-03	-0.69	-2.35
lpg0528	succinate dehydrogenase cytochrome b556 subunit C	*sdhC*	Carbohydrate Metabolism, Energy Me	13.474	11.992	13.253	12.697	4.29E-07	2.40E-01	-1.48	-0.56
lpg0528	succinate dehydrogenase cytochrome b556 subunit C	*sdhC*	Carbohydrate Metabolism, Energy Me	13.165	11.873	13.076	12.857	4.36E-03	5.63E-01	-1.29	-0.22
lpg0529	succinate dehydrogenase hydrophobic membrane ancho	*sdhD*	Carbohydrate Metabolism, Energy Me	12.449	12.144	12.259	12.622	9.60E-02	4.18E-02	-0.30	0.36
lpg0529	succinate dehydrogenase hydrophobic membrane ancho	*sdhD*	Carbohydrate Metabolism, Energy Me	12.400	12.177	12.214	12.662	2.67E-01	1.31E-02	-0.22	0.45
lpg0530	succinate dehydrogenase flavoprotein subunit A	*sdhA*	Carbohydrate Metabolism, Energy Me	12.928	12.980	12.980	12.781	9.13E-01	8.07E-01	0.05	-0.20
lpg0530	succinate dehydrogenase flavoprotein subunit A	*sdhA*	Carbohydrate Metabolism, Energy Me	12.854	12.364	12.996	13.230	6.56E-02	5.06E-01	-0.49	0.23
lpg0531	succinate dehydrogenase iron-sulfur protein subunit B	*sdhB*	Carbohydrate Metabolism, Energy Me	12.755	12.714	13.564	12.943	8.56E-01	1.91E-02	-0.04	-0.62
lpg0531	succinate dehydrogenase iron-sulfur protein subunit B	*sdhB*	Carbohydrate Metabolism, Energy Me	12.763	12.511	13.497	12.963	3.18E-01	2.79E-02	-0.25	-0.53
lpg0532	2-oxoglutarate dehydrogenase E1 component)	*sucA*	Carbohydrate Metabolism, Amino Acid	13.364	13.347	13.703	13.489	9.44E-01	3.88E-01	-0.02	-0.21
lpg0532	2-oxoglutarate dehydrogenase E1 component)	*sucA*	Carbohydrate Metabolism, Amino Acid	13.338	13.318	13.717	13.511	9.38E-01	3.70E-01	-0.02	-0.21
lpg0533	dihydrolipoamide succinyltransferase (2-oxoglutarate deh	*sucB*	Carbohydrate Metabolism, Amino Acid	9.785	11.236	10.685	12.091	1.70E-01	3.01E-02	1.45	1.41
lpg0533	dihydrolipoamide succinyltransferase (2-oxoglutarate deh	*sucB*	Carbohydrate Metabolism, Amino Acid	9.396	11.757	10.742	12.335	1.59E-03	2.40E-03	2.36	1.59
lpg0534	succinyl CoA synthetase beta chain	*sucC*	Carbohydrate Metabolism, Energy Me	13.139	13.039	13.076	13.197	6.91E-01	8.21E-01	-0.10	0.12
lpg0534	succinyl CoA synthetase beta chain	*sucC*	Carbohydrate Metabolism, Energy Me	13.140	12.881	13.106	13.523	3.34E-01	9.32E-02	-0.26	0.42
lpg0535	succinyl CoA synthetase alpha chain	*sucD*	Carbohydrate Metabolism, Energy Me	11.495	12.283	12.147	12.548	7.12E-03	2.00E-01	0.79	0.40
lpg0535	succinyl CoA synthetase alpha chain	*sucD*	Carbohydrate Metabolism, Energy Me	11.536	12.235	11.787	12.532	4.77E-03	3.22E-03	0.70	0.75
lpg0536	pyridoxamine 5'-phosphate oxidase	*pdxH*	Metabolism of Cofactors and Vitamins	10.649	11.176	8.751	10.957	2.97E-01	3.29E-03	0.53	2.21
lpg0536	pyridoxamine 5'-phosphate oxidase	*pdxH*	Metabolism of Cofactors and Vitamins	10.575	11.507	8.647	11.513	1.29E-01	1.62E-03	0.93	2.87
lpg0537	transmission trait enhancer LetE		Toxin production / other pathogen func	13.877	13.998	13.191	12.174	8.64E-01	1.08E-01	0.12	-1.02
lpg0537	transmission trait enhancer LetE		Toxin production / other pathogen func	13.850	14.048	13.216	12.242	7.56E-01	1.26E-01	0.20	-0.97
lpg0538	small ORF (110aa)		ORFs of unknown function (unique)	8.866	7.983	8.599	7.904	1.18E-01	4.42E-01	-0.88	-0.70
lpg0538	small ORF (110aa)		ORFs of unknown function (unique)	8.140	7.294	6.960	7.855	3.84E-01	5.12E-01	-0.85	0.89
lpg0539	small ORF (129aa)		ORFs of unknown function (unique)	10.671	10.114	10.736	10.289	2.98E-01	1.58E-01	-0.56	-0.45
lpg0539	small ORF (129aa)		ORFs of unknown function (unique)	10.582	10.129	10.405	10.056	3.93E-01	2.97E-01	-0.45	-0.35
lpg0540	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	10.402	11.867	9.528	11.549	2.35E-03	2.69E-03	1.47	2.02
lpg0540	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	10.547	12.008	9.318	11.549	1.75E-03	6.84E-03	1.46	2.23
lpg0541	protein product; similar to probable membrane protein YdgA of Esche		Unknown / hypothetical proteins	12.771	12.406	10.447	12.788	5.68E-01	8.23E-03	-0.36	2.34
lpg0541	protein product; similar to probable membrane protein YdgA of Esche		Unknown / hypothetical proteins	12.062	12.345	10.079	12.802	3.81E-01	2.31E-03	0.28	2.72
lpg0542	DNA binding protein Fis (recombinational enhancer bindi	*fis*	Transcription factors / DNA binding pro	14.542	13.965	12.874	15.144	3.06E-01	1.18E-03	-0.58	2.27
lpg0542	DNA binding protein Fis (recombinational enhancer bindi	*fis*	Transcription factors / DNA binding pro	14.388	13.903	12.735	15.091	3.24E-01	7.19E-04	-0.48	2.36
lpg0543	ribose-phosphate pyrophosphokinase (phosphoribosyl py	*prsA*	Carbohydrate Metabolism, Nucleotide	11.183	11.086	10.335	11.824	7.43E-01	7.88E-03	-0.10	1.49
lpg0543	ribose-phosphate pyrophosphokinase (phosphoribosyl py	*prsA*	Carbohydrate Metabolism, Nucleotide	11.041	11.376	10.079	12.207	3.32E-01	2.85E-03	0.34	2.13
lpg0544	small ORF (62aa)		ORFs of unknown function (unique)	11.390	10.786	10.941	11.887	2.17E-01	2.01E-01	-0.60	0.95
lpg0544	small ORF (62aa)		ORFs of unknown function (unique)	11.442	10.957	9.994	11.802	3.56E-01	8.09E-03	-0.48	1.81

lpg0545	tRNA-Gln		tRNA	13.622	11.681	11.691	12.671	2.94E-02	2.51E-01	-1.94	0.98
lpg0545	tRNA-Gln		tRNA	13.516	12.633	11.679	13.487	2.77E-01	4.46E-02	-0.88	1.81
lpg0546	small ORF (56aa)		ORFs of unknown function (unique)	9.002	9.303	9.389	9.471	6.25E-01	8.73E-01	0.30	0.08
lpg0546	small ORF (56aa)		ORFs of unknown function (unique)	8.901	8.758	9.234	9.381	8.95E-01	8.49E-01	-0.14	0.15
lpg0547	outer membrane lipoprotein LolB, anchoring of lipoproteins to periplas		Named proteins of general function	11.538	11.610	11.683	12.087	7.93E-01	1.47E-01	0.07	0.40
lpg0547	outer membrane lipoprotein LolB, anchoring of lipoproteins to periplas		Named proteins of general function	11.645	11.440	11.473	12.124	4.20E-01	2.10E-02	-0.20	0.65
lpg0548	phosphopantetheine adenylyltransferase (lipopolysaccha	*kdtB+G443*	Metabolism of Cofactors and Vitamins	12.818	13.214	11.283	13.911	4.12E-01	1.75E-05	0.40	2.63
lpg0548	phosphopantetheine adenylyltransferase (lipopolysaccha	*kdtB+G443*	Metabolism of Cofactors and Vitamins	13.013	13.189	11.015	13.898	5.85E-01	2.37E-05	0.18	2.88
lpg0549	gamma-glutamyltranspeptidase		Metabolism of Other Amino Acids, Met	10.309	7.580	8.502	8.101	1.95E-02	5.50E-01	-2.73	-0.40
lpg0549	gamma-glutamyltranspeptidase		Metabolism of Other Amino Acids, Met	10.056	8.013	6.769	8.472	2.43E-03	2.06E-01	-2.04	1.70
lpg0550	hypothetical (FAD-dependent oxidoreductase)		Named proteins of general function	8.734	5.034	12.321	6.010	6.54E-02	6.82E-05	-3.70	-6.31
lpg0550	hypothetical (FAD-dependent oxidoreductase)		Named proteins of general function	8.910	7.664	11.497	6.055	1.51E-01	8.60E-03	-1.25	-5.44
lpg0551	1-acyl-sn-glycerol-3-phosphate acetyltransferase	*plsC*	Metabolism of Complex Lipids	10.239	8.061	9.612	9.529	4.41E-02	8.69E-01	-2.18	-0.08
lpg0551	1-acyl-sn-glycerol-3-phosphate acetyltransferase	*plsC*	Metabolism of Complex Lipids	9.637	8.458	9.627	10.209	3.05E-01	1.14E-03	-1.18	0.58
lpg0552	suppressor of GroEL (SugE) chaperonin?, SMR (small dı	*sugE*	Transport and binding, Protein fate / hy	11.094	10.507	10.889	9.734	4.26E-01	1.62E-01	-0.59	-1.16
lpg0552	suppressor of GroEL (SugE) chaperonin?, SMR (small dı	*sugE*	Transport and binding, Protein fate / hy	11.167	11.125	10.847	10.862	9.53E-01	9.80E-01	-0.04	0.02
lpg0553	aminoglycoside phosphotransferase		Named proteins of general function	9.937	10.088	11.707	10.427	6.98E-01	3.47E-03	0.15	-1.28
lpg0553	aminoglycoside phosphotransferase		Named proteins of general function	10.083	9.776	11.541	10.357	6.98E-01	3.25E-02	-0.31	-1.18
lpg0554	DNA-damage inducible protein P (DNA polymerase IV)	*dinP*	Nucleotide Metabolism, Replication an	6.590	6.766	7.882	7.363	8.36E-01	5.24E-01	0.18	-0.52
lpg0554	DNA-damage inducible protein P (DNA polymerase IV)	*dinP*	Nucleotide Metabolism, Replication an	7.340	6.839	7.492	9.633	7.04E-01	7.54E-02	-0.50	2.14
lpg0555	tRNA-Gly		tRNA	13.028	12.636	11.398	12.758	6.64E-01	5.29E-01	-0.39	1.36
lpg0555	tRNA-Gly		tRNA	12.972	12.808	11.219	13.653	8.30E-01	7.77E-02	-0.16	2.43
lpg0556	hypothetical		Unknown / hypothetical proteins	7.916	7.638	8.668	8.612	6.51E-01	8.87E-01	-0.28	-0.06
lpg0556	hypothetical		Unknown / hypothetical proteins	8.587	8.511	8.849	9.304	8.50E-01	8.05E-02	-0.08	0.45
lpg0557	formamidopyrimidine DNA glycosylase	*mutM*	DNA/RNA degradation / restriction	11.830	10.682	12.210	11.911	3.43E-03	1.73E-01	-1.15	-0.30
lpg0557	formamidopyrimidine DNA glycosylase	*mutM*	DNA/RNA degradation / restriction	11.847	10.543	12.177	11.959	2.40E-03	3.54E-01	-1.30	-0.22
lpg0558	stearoyl-CoA-9-desaturase (fatty acid desaturase, type 2:fatty acid de		Lipid Metabolism	13.258	13.777	14.124	12.386	2.47E-01	1.68E-02	0.52	-1.74
lpg0558	stearoyl-CoA-9-desaturase (fatty acid desaturase, type 2:fatty acid de		Lipid Metabolism	13.246	13.191	14.107	12.710	8.88E-01	1.61E-03	-0.05	-1.40
lpg0559	small ORF (132aa)		ORFs of unknown function (unique)	12.539	13.666	11.329	12.579	1.11E-01	7.73E-02	1.13	1.25
lpg0559	small ORF (132aa)		ORFs of unknown function (unique)	12.616	13.221	11.222	12.549	5.19E-01	5.28E-02	0.60	1.33
lpg0560	acetyoacetyl CoA reductase	*phaB*	Carbohydrate Metabolism	13.652	13.512	14.493	12.773	5.13E-01	1.57E-04	-0.14	-1.72
lpg0560	acetyoacetyl CoA reductase	*phaB*	Carbohydrate Metabolism	13.634	13.487	14.481	12.834	4.64E-01	1.37E-04	-0.15	-1.65
lpg0561	acetyoacetyl CoA reductase	*phaB*	Carbohydrate Metabolism	10.772	11.578	10.571	10.229	1.57E-02	4.99E-01	0.81	-0.34
lpg0561	acetyoacetyl CoA reductase	*phaB*	Carbohydrate Metabolism	10.676	10.705	10.650	10.490	9.45E-01	6.87E-01	0.03	-0.16
lpg0562	hypothetical COG5394		Unknown / hypothetical proteins	9.441	11.326	8.870	10.991	3.36E-03	4.49E-04	1.89	2.12
lpg0562	hypothetical COG5394		Unknown / hypothetical proteins	9.275	11.483	8.709	10.920	4.41E-04	7.19E-05	2.21	2.21
lpg0563	ORF		ORFs of unknown function (unique)	8.266	11.164	8.527	8.495	4.12E-04	9.69E-01	2.90	-0.03
lpg0563	ORF		ORFs of unknown function (unique)	8.322	10.992	8.213	8.941	3.52E-04	4.37E-01	2.67	0.73
lpg0564	hypothetical protein		Unknown / hypothetical proteins	9.844	10.850	9.587	10.170	2.06E-02	1.03E-01	1.01	0.58
lpg0564	hypothetical protein		Unknown / hypothetical proteins	10.033	10.380	9.269	10.336	2.34E-01	1.56E-01	0.35	1.07
lpg0565	spore maturation protein B		Chemotaxis / motility / cell division	11.377	11.204	12.003	10.956	4.46E-01	1.83E-02	-0.17	-1.05
lpg0565	spore maturation protein B		Chemotaxis / motility / cell division	11.289	11.539	12.036	11.341	6.04E-01	2.17E-01	0.25	-0.69
lpg0566	spore maturation protein A	*spmB*	Chemotaxis / motility / cell division	10.160	10.559	9.842	10.376	4.02E-01	4.12E-01	0.40	0.53
lpg0566	spore maturation protein A	*spmB*	Chemotaxis / motility / cell division	10.174	10.561	9.284	10.521	4.58E-01	1.30E-01	0.39	1.24
lpg0567	peptidase (M23/M37 family)		Protein fate / hydrolases / secretion	10.917	10.055	10.196	11.309	1.34E-01	1.05E-02	-0.86	1.11
lpg0567	peptidase (M23/M37 family)		Protein fate / hydrolases / secretion	10.652	10.819	10.374	11.832	7.77E-01	8.17E-03	0.17	1.46
lpg0568	tyrosyl tRNA synthetase	*tyrS*	Amino Acid Metabolism, Translation	10.285	12.612	9.954	11.992	3.32E-05	3.16E-03	2.33	2.04
lpg0568	tyrosyl tRNA synthetase	*tyrS*	Amino Acid Metabolism, Translation	10.384	12.606	9.557	11.976	1.96E-05	1.77E-03	2.22	2.42
lpg0577	transferase (carbonic anydrase/transferase/acetyltransfe	*yrdA*	Named proteins of general function	10.959	11.520	11.489	11.923	3.28E-01	3.47E-01	0.56	0.43
lpg0577	transferase (carbonic anydrase/transferase/acetyltransfe	*yrdA*	Named proteins of general function	10.851	11.727	11.368	12.106	3.93E-02	2.42E-02	0.88	0.74
lpg0578	glutathione reductase (glutathione oxidoreductase)	*gor*	Amino Acid Metabolism, Metabolism o	13.082	12.812	13.223	12.866	1.29E-01	4.02E-02	-0.27	-0.36
lpg0578	glutathione reductase (glutathione oxidoreductase)	*gor*	Amino Acid Metabolism, Metabolism o	12.960	12.802	13.123	12.840	3.68E-01	4.56E-02	-0.16	-0.28
lpg0579	ORF		ORFs of unknown function (unique)	8.078	10.121	8.198	10.380	9.40E-02	5.66E-02	2.04	2.18
lpg0579	ORF		ORFs of unknown function (unique)	10.653	10.797	9.178	13.071	7.93E-01	3.63E-04	0.14	3.89
lpg0580	adenosine deaminase	*add*	Nucleotide Metabolism	12.001	13.075	10.137	13.265	7.71E-02	2.88E-03	1.07	3.13
lpg0580	adenosine deaminase	*add*	Nucleotide Metabolism	11.916	13.111	10.158	13.341	4.27E-02	1.33E-03	1.19	3.18
lpg0581	hypothetical		Unknown / hypothetical proteins	10.457	9.192	8.850	9.458	9.08E-02	3.19E-01	-1.27	0.61
lpg0581	hypothetical		Unknown / hypothetical proteins	10.668	9.742	9.101	9.717	5.78E-02	2.46E-01	-0.93	0.62
lpg0582	small ORF (159aa)		ORFs of unknown function (unique)	10.371	9.231	10.458	8.854	1.11E-01	2.28E-02	-1.14	-1.60
lpg0582	small ORF (159aa)		ORFs of unknown function (unique)	10.595	9.066	10.093	8.617	3.17E-03	6.06E-02	-1.53	-1.48
lpg0583	phosphate transporter (phosphate permease)		Transport and binding	10.438	10.771	10.144	10.681	4.14E-02	3.30E-01	0.33	0.54
lpg0583	phosphate transporter (phosphate permease)		Transport and binding	10.173	10.797	9.864	10.491	8.60E-02	3.43E-01	0.62	0.63
lpg0584	hypothetical (phosphate transport regulator?)		Unknown / hypothetical proteins	11.757	12.592	10.548	12.988	5.44E-02	2.70E-04	0.84	2.44
lpg0584	hypothetical (phosphate transport regulator?)		Unknown / hypothetical proteins	11.436	12.680	10.364	13.075	1.03E-02	5.14E-05	1.24	2.71

lpg0585	conserved hypothetical protein		Unknown / hypothetical proteins	10.559	8.666	12.724	8.732	6.68E-02	1.13E-02	-1.89	-3.99
lpg0585	conserved hypothetical protein		Unknown / hypothetical proteins	10.466	9.532	12.761	9.967	4.55E-02	2.33E-04	-0.93	-2.79
lpg0586	transcriptional regulator, alginate biosynthesis?		Transcription factors / DNA binding prc	9.651	9.260	13.488	9.392	5.53E-01	1.43E-03	-0.39	-4.10
lpg0586	transcriptional regulator, alginate biosynthesis?		Transcription factors / DNA binding prc	9.575	10.768	13.519	10.124	3.17E-01	2.10E-02	1.19	-3.40
lpg0587	hypothetical (Holliday junction resolvase, endonuclease i	*yqgF*	Replication and Repair	8.556	7.688	9.409	9.675	1.00E-01	7.77E-01	-0.87	0.27
lpg0587	hypothetical (Holliday junction resolvase, endonuclease i	*yqgF*	Replication and Repair	8.556	8.476	9.321	10.106	9.48E-01	3.53E-01	-0.08	0.79
lpg0588	aspartate carbamoyltransferase	*pyrB*	Nucleotide Metabolism, Amino Acid Me	10.518	10.919	10.836	10.024	2.10E-01	9.93E-02	0.40	-0.81
lpg0588	aspartate carbamoyltransferase	*pyrB*	Nucleotide Metabolism, Amino Acid Me	10.467	11.109	11.013	10.253	2.83E-02	1.25E-02	0.64	-0.76
lpg0589	small ORF (128aa)		ORFs of unknown function (unique)	8.776	6.681	13.129	8.222	1.22E-01	5.11E-07	-2.10	-4.91
lpg0589	small ORF (128aa)		ORFs of unknown function (unique)	9.086	7.582	12.007	8.543	1.16E-01	2.89E-02	-1.50	-3.46
lpg0590	competence related protein ComM (Mg(2+) chelatase) (t	*comM*	Transport and binding, Signal transduc	8.166	9.008	9.433	7.898	1.71E-01	8.02E-02	0.84	-1.53
lpg0590	competence related protein ComM (Mg(2+) chelatase) (t	*comM*	Transport and binding, Signal transduc	8.125	8.973	9.290	8.585	2.08E-01	2.67E-01	0.85	-0.70
lpg0591	hypothetical COG2960		Unknown / hypothetical proteins	11.775	11.546	10.399	10.787	5.64E-01	2.79E-01	-0.23	0.39
lpg0591	hypothetical COG2960		Unknown / hypothetical proteins	11.699	11.767	10.264	10.796	9.15E-01	2.34E-01	0.07	0.53
lpg0592	nitrogen regulatory P-II transcription regulator (nitrogen r	*glnK*	Transcription factors / DNA binding prc	9.429	11.622	8.720	10.900	1.23E-04	1.06E-04	2.19	2.18
lpg0592	nitrogen regulatory P-II transcription regulator (nitrogen r	*glnK*	Transcription factors / DNA binding prc	9.621	11.032	8.764	10.967	1.11E-02	8.62E-03	1.41	2.20
lpg0593	5-formyltetrahydrofolate cyclo-ligase		Metabolism of Cofactors and Vitamins	10.133	9.535	9.246	9.592	7.51E-02	3.91E-01	-0.60	0.35
lpg0593	5-formyltetrahydrofolate cyclo-ligase		Metabolism of Cofactors and Vitamins	9.978	9.403	8.788	9.751	1.35E-02	1.04E-01	-0.57	0.96
lpg0594	ORF		ORFs of unknown function (unique)	12.809	12.704	11.602	13.991	8.51E-01	4.75E-04	-0.11	2.39
lpg0594	ORF		ORFs of unknown function (unique)	12.790	12.685	11.433	13.962	8.64E-01	9.37E-04	-0.10	2.53
lpg0595	4-amino-4-deoxychorismate lyase (branched chain amino acid amino		Amino Acid Metabolism	10.843	11.364	9.480	12.902	4.85E-01	1.49E-05	0.52	3.42
lpg0595	4-amino-4-deoxychorismate lyase (branched chain amino acid amino		Amino Acid Metabolism	10.604	10.802	9.209	12.831	7.80E-01	8.64E-05	0.20	3.62
lpg0596	conserved hypothetical protein		Unknown / hypothetical proteins	11.978	11.141	12.052	11.329	5.69E-02	9.25E-02	-0.84	-0.72
lpg0596	conserved hypothetical protein		Unknown / hypothetical proteins	11.881	10.658	12.019	11.403	1.32E-01	1.65E-01	-1.22	-0.62
lpg0597	2-acylglycerophosphoethanolamine acyltransferase	*aas*	Lipid Metabolism	8.859	6.345	8.549	8.279	2.30E-03	5.15E-01	-2.51	-0.27
lpg0597	2-acylglycerophosphoethanolamine acyltransferase	*aas*	Lipid Metabolism	8.815	9.155	8.049	9.260	8.10E-01	3.92E-01	0.34	1.21
lpg0598	small ORF (139aa) (hypothetical?) COG4446		Unknown / hypothetical proteins	9.656	8.540	9.321	8.717	1.46E-01	2.45E-01	-1.12	-0.60
lpg0598	small ORF (139aa) (hypothetical?) COG4446		Unknown / hypothetical proteins	9.835	9.021	9.200	9.040	2.54E-01	7.40E-01	-0.81	-0.16
lpg0599	poly-beta-hydroxybutyrate polymerase (poly(3-hydroxyalkanoate) pol		Named proteins of general function	10.312	11.387	10.653	11.100	7.19E-03	2.72E-01	1.07	0.45
lpg0599	poly-beta-hydroxybutyrate polymerase (poly(3-hydroxyalkanoate) pol		Named proteins of general function	10.439	11.353	10.494	11.058	8.06E-03	1.35E-01	0.91	0.56
lpg0600	rrf2 family protein (transcriptional regulator)		Transcription factors / DNA binding prc	11.257	10.680	10.637	12.001	1.21E-02	2.31E-03	-0.58	1.36
lpg0600	rrf2 family protein (transcriptional regulator)		Transcription factors / DNA binding prc	10.994	10.440	10.122	11.978	1.08E-01	1.29E-03	-0.55	1.86
lpg0601	ABC transporter, permease	*ycf24*	Transport and binding	10.354	10.938	10.760	11.941	3.06E-02	1.21E-02	0.58	1.18
lpg0601	ABC transporter, permease	*ycf24*	Transport and binding	10.555	11.025	10.633	11.916	7.06E-02	7.04E-03	0.47	1.28
lpg0602	ATP transporter, ABC binding component, ATP-binding protein		Transport and binding	11.742	11.970	11.298	13.019	4.01E-01	1.86E-04	0.23	1.72
lpg0602	ATP transporter, ABC binding component, ATP-binding protein		Transport and binding	11.716	11.942	11.223	13.003	3.86E-01	1.49E-04	0.23	1.78
lpg0603	ABC transporter, permease component		Transport and binding	10.985	10.584	10.746	12.044	3.57E-01	6.96E-03	-0.40	1.30
lpg0603	ABC transporter, permease component		Transport and binding	10.974	10.457	10.639	12.020	2.47E-01	9.90E-04	-0.52	1.38
lpg0604	aminotransferase (cystein desulfurase, selenocysteine lyase)		Metabolism of Other Amino Acids	10.328	9.810	10.212	10.878	8.97E-02	9.70E-02	-0.52	0.67
lpg0604	aminotransferase (cystein desulfurase, selenocysteine lyase)		Metabolism of Other Amino Acids	10.291	10.312	10.289	11.172	9.55E-01	4.88E-03	0.02	0.88
lpg0605	nitrogen fixation protein (Fe-S cluster formation) NifU		Energy Metabolism	10.901	10.672	11.259	11.793	2.23E-01	5.80E-02	-0.23	0.53
lpg0605	nitrogen fixation protein (Fe-S cluster formation) NifU		Energy Metabolism	10.790	10.959	11.311	11.867	6.48E-01	2.58E-02	0.17	0.56
lpg0606	hypothetical (dTDP-4-keto-L-rhamnose reductase, component of ring		Nucleotide Metabolism	11.477	11.538	11.381	12.252	8.13E-01	2.81E-03	0.06	0.87
lpg0606	hypothetical (dTDP-4-keto-L-rhamnose reductase, component of ring		Nucleotide Metabolism	11.432	11.479	11.331	12.258	8.35E-01	5.06E-04	0.05	0.93
lpg0607	lysyl tRNA synthetase		Amino Acid Metabolism, Translation	9.136	9.034	7.947	9.833	7.88E-01	1.03E-02	-0.10	1.89
lpg0607	lysyl tRNA synthetase		Amino Acid Metabolism, Translation	9.025	9.093	7.654	9.649	8.75E-01	2.00E-02	0.07	2.00
lpg0608	hypothetical (SAM-dependent methyltransferase?)		Unknown / hypothetical proteins	9.958	9.288	8.019	11.200	8.54E-02	4.13E-04	-0.67	3.18
lpg0608	hypothetical (SAM-dependent methyltransferase?)		Unknown / hypothetical proteins	9.631	9.092	7.770	11.152	3.21E-01	1.27E-02	-0.54	3.38
lpg0609	alanyl tRNA synthetase	*alaS*	DNA/RNA degradation / restriction, Tra	8.916	12.714	8.224	11.406	1.84E-07	1.58E-05	3.80	3.18
lpg0609	alanyl tRNA synthetase	*alaS*	DNA/RNA degradation / restriction, Tra	8.407	12.594	7.060	10.871	1.52E-06	8.48E-04	4.19	3.81
lpg0610	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	10.337	12.843	10.894	11.081	1.88E-06	5.57E-01	2.51	0.19
lpg0610	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	10.376	12.849	10.761	11.078	1.28E-06	3.68E-01	2.47	0.32
lpg0611	metal ion transporter (magnesium and cobalt efflux protein) (hemolys		Transport and binding	11.262	10.660	10.281	10.826	1.72E-01	9.22E-02	-0.60	0.54
lpg0611	metal ion transporter (magnesium and cobalt efflux protein) (hemolys		Transport and binding	11.206	11.065	10.615	11.410	8.08E-01	1.18E-01	-0.14	0.80
lpg0612	alcohol dehydrogenase (NADP-dependent, zinc-type) (oxidoreductas		Carbohydrate Metabolism, Metabolism	11.034	12.759	11.642	11.733	8.97E-06	7.23E-01	1.72	0.09
lpg0612	alcohol dehydrogenase (NADP-dependent, zinc-type) (oxidoreductas		Carbohydrate Metabolism, Metabolism	10.949	12.847	11.613	11.836	2.20E-07	3.20E-01	1.90	0.22
lpg0613	ORF cytochrome c1 precursor?		Unknown / hypothetical proteins	11.955	12.459	10.162	11.599	4.05E-01	2.26E-02	0.50	1.44
lpg0613	ORF cytochrome c1 precursor?		Unknown / hypothetical proteins	11.910	12.403	9.986	11.665	4.66E-01	1.33E-02	0.49	1.68
lpg0614	hypothetical		Unknown / hypothetical proteins	9.850	8.497	10.903	8.961	1.94E-02	1.02E-03	-1.35	-1.94
lpg0614	hypothetical		Unknown / hypothetical proteins	9.910	8.735	10.791	9.512	2.89E-02	6.87E-02	-1.17	-1.28
lpg0615	polypeptide deformylase (formylmethionine deformylase)		Translation	10.480	9.044	11.339	9.786	3.10E-01	2.96E-03	-1.44	-1.55
lpg0615	polypeptide deformylase (formylmethionine deformylase)		Translation	10.547	9.465	10.906	10.018	1.65E-01	5.00E-02	-1.08	-0.89
lpg0616	GTP cyclohydrolase I PLUS perhaps regulatory protein: fused protein		Named proteins of general function	9.372	10.471	8.548	9.282	3.34E-04	2.68E-01	1.10	0.73
lpg0616	GTP cyclohydrolase I PLUS perhaps regulatory protein: fused protein		Named proteins of general function	9.636	10.357	8.985	9.806	3.61E-02	2.40E-01	0.72	0.82

lpg0617	major outer membrane protein		Toxin production / other pathogen func	10.095	10.132	9.841	9.280	9.19E-01	3.42E-01	0.04	-0.56
lpg0617	major outer membrane protein		Toxin production / other pathogen func	9.805	10.033	9.383	9.591	6.83E-01	7.10E-01	0.23	0.21
lpg0618	3-methyladenine DNA glycosylase	*tag*	DNA/RNA degradation / restriction	10.183	9.187	7.652	9.122	7.64E-04	5.70E-02	-1.00	1.47
lpg0618	3-methyladenine DNA glycosylase	*tag*	DNA/RNA degradation / restriction	10.033	9.805	7.817	10.049	6.87E-01	6.97E-02	-0.23	2.23
lpg0619	glyoxylase (hydroxylase) COG3324		Named proteins of general function	10.517	9.776	10.595	9.812	1.31E-01	8.26E-02	-0.74	-0.78
lpg0619	glyoxylase (hydroxylase) COG3324		Named proteins of general function	10.344	10.186	10.663	10.354	5.26E-01	3.74E-01	-0.16	-0.31
lpg0620	conserved hypothetical protein		Unknown / hypothetical proteins	7.992	7.471	10.809	6.291	5.52E-01	1.23E-03	-0.52	-4.52
lpg0620	conserved hypothetical protein		Unknown / hypothetical proteins	8.743	9.014	11.884	8.286	7.98E-01	2.84E-03	0.27	-3.60
lpg0621	SidA	*sidA*	Toxin production / other pathogen func	9.578	11.116	10.935	10.866	8.76E-03	9.01E-01	1.54	-0.07
lpg0621	SidA	*sidA*	Toxin production / other pathogen func	9.490	11.927	10.949	11.532	3.53E-04	3.01E-01	2.44	0.58
lpg0622	transmembrane protein		Unknown / hypothetical proteins	9.409	7.051	9.283	7.491	3.37E-03	3.53E-02	-2.36	-1.79
lpg0622	transmembrane protein		Unknown / hypothetical proteins	9.173	6.828	9.113	8.629	2.73E-02	1.61E-01	-2.34	-0.48
lpg0623	hypothetical		Unknown / hypothetical proteins	9.849	9.023	12.223	7.516	2.92E-01	5.68E-03	-0.83	-4.71
lpg0623	hypothetical		Unknown / hypothetical proteins	10.002	8.880	12.270	9.232	1.26E-01	1.42E-03	-1.12	-3.04
lpg0624	small ORF (125aa)		ORFs of unknown function (unique)	11.765	11.758	11.157	12.305	9.68E-01	2.24E-04	-0.01	1.15
lpg0624	small ORF (125aa)		ORFs of unknown function (unique)	11.773	11.725	11.091	12.357	8.17E-01	1.05E-04	-0.05	1.27
lpg0625	expressed protein		Named proteins of general function	10.509	9.141	13.885	9.691	1.41E-01	5.64E-04	-1.37	-4.19
lpg0625	expressed protein		Named proteins of general function	10.291	9.118	13.857	10.010	3.47E-01	9.71E-04	-1.17	-3.85
lpg0626	DNA uptake/competence protein ComA (DNA internalization-related c		Transport and binding	10.629	12.364	11.026	8.887	1.30E-04	1.46E-03	1.74	-2.14
lpg0626	DNA uptake/competence protein ComA (DNA internalization-related c		Transport and binding	10.359	12.129	11.188	9.442	5.25E-04	3.38E-03	1.77	-1.75
lpg0627	type IV pilin (competence and adherence associated pilir	*pilE3*	Transport and binding	9.906	9.562	12.800	9.320	6.67E-01	4.78E-04	-0.34	-3.48
lpg0627	type IV pilin (competence and adherence associated pilir	*pilE3*	Transport and binding	9.979	9.382	12.834	10.075	4.75E-01	1.30E-03	-0.60	-2.76
lpg0628	type IV fimbrial biogenesis PilY1-related protein		Transport and binding	9.101	9.141	11.164	9.130	9.41E-01	5.10E-04	0.04	-2.03
lpg0628	type IV fimbrial biogenesis PilY1-related protein		Transport and binding	8.852	9.408	11.123	9.602	4.55E-01	8.39E-03	0.56	-1.52
lpg0629	Tfp pilus assembly protein PilX?		Named proteins of general function	9.165	9.353	11.913	8.877	7.11E-01	1.01E-03	0.19	-3.04
lpg0629	Tfp pilus assembly protein PilX?		Named proteins of general function	10.299	9.946	12.218	9.867	4.84E-01	8.51E-05	-0.35	-2.35
lpg0630	hypothetical (type IV fimbrial biogenesis PilW related protein, transme		Transport and binding	7.284	8.981	10.425	8.648	1.21E-01	1.04E-01	1.70	-1.78
lpg0630	hypothetical (type IV fimbrial biogenesis PilW related protein, transme		Transport and binding	7.502	9.393	10.720	10.046	3.61E-01	6.99E-01	1.89	-0.67
lpg0631	type IV fimbrial biogenesis protein PilV		Transport and binding	10.322	9.134	12.436	8.115	1.58E-01	2.61E-04	-1.19	-4.32
lpg0631	type IV fimbrial biogenesis protein PilV		Transport and binding	10.334	10.595	13.209	10.466	8.30E-01	4.31E-02	0.26	-2.74
lpg0632	type IV pre-pilin (type IV fimbrial pilin; fimbrial biogenesis protein)		Transport and binding	8.963	8.469	13.192	6.815	7.34E-01	5.15E-03	-0.49	-6.38
lpg0632	type IV pre-pilin (type IV fimbrial pilin; fimbrial biogenesis protein)		Transport and binding	9.710	7.534	13.089	7.693	4.02E-02	7.96E-04	-2.18	-5.40
lpg0633	polysaccharide deacetylase (peptidoglycan N-acetylglucosamine dea		Metabolism of Complex Carbohydrate:	10.520	8.003	9.752	8.353	1.13E-03	2.76E-01	-2.52	-1.40
lpg0633	polysaccharide deacetylase (peptidoglycan N-acetylglucosamine dea		Metabolism of Complex Carbohydrate:	10.344	8.100	8.208	7.983	2.87E-04	8.45E-01	-2.24	-0.22
lpg0634	ORF		ORFs of unknown function (unique)	14.256	15.093	13.421	12.561	2.96E-02	1.63E-02	0.84	-0.86
lpg0634	ORF		ORFs of unknown function (unique)	14.350	15.184	13.411	12.582	5.01E-02	2.52E-02	0.83	-0.83
lpg0635	melitin resistance protein (dolichyl phosphate-mannose protein mann		Detoxification / adaptation, Metabolism	9.671	10.184	10.357	8.661	3.10E-01	9.90E-02	0.51	-1.70
lpg0635	melitin resistance protein (dolichyl phosphate-mannose protein mann		Detoxification / adaptation, Metabolism	9.873	10.482	10.090	9.470	3.71E-01	3.51E-01	0.61	-0.62
lpg0636	thymidine kinase	*tdk*	Nucleotide Metabolism	10.850	10.722	10.234	7.928	6.59E-01	1.83E-01	-0.13	-2.31
lpg0636	thymidine kinase	*tdk*	Nucleotide Metabolism	10.731	10.705	10.512	9.926	9.62E-01	1.11E-01	-0.03	-0.59
lpg0637	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	11.788	11.878	11.570	12.365	6.29E-01	1.23E-03	0.09	0.80
lpg0637	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	11.972	11.830	11.388	12.239	3.90E-01	6.85E-04	-0.14	0.85
lpg0638	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	10.618	10.711	10.915	10.636	6.16E-01	3.20E-01	0.09	-0.28
lpg0638	major facilitator family transporter (multidrug efflux transporter)		Transport and binding	10.793	11.312	11.156	11.053	5.69E-01	9.17E-01	0.52	-0.10
lpg0639	phosphopentomutase	*deoB*	Carbohydrate Metabolism, Nucleotide	10.686	10.042	9.625	11.083	1.10E-01	9.22E-02	-0.64	1.46
lpg0639	phosphopentomutase	*deoB*	Carbohydrate Metabolism, Nucleotide	11.230	11.292	10.358	12.107	8.82E-01	9.84E-04	0.06	1.75
lpg0640	heat shock protein, HslVU, proteasome-related peptidase	*hslV*	Detoxification / adaptation, Protein fate	11.741	10.836	12.747	12.283	6.25E-02	1.35E-01	-0.91	-0.46
lpg0640	heat shock protein, HslVU, proteasome-related peptidase	*hslV*	Detoxification / adaptation, Protein fate	11.412	10.363	12.316	12.077	5.00E-02	3.89E-01	-1.05	-0.24
lpg0641	ATP dependent Hsl protease, ATP binding subunit (ATP b	*hslU*	Detoxification / adaptation, Protein fate	12.060	10.962	12.716	12.725	7.72E-02	9.70E-01	-1.10	0.01
lpg0641	ATP dependent Hsl protease, ATP binding subunit (ATP b	*hslU*	Detoxification / adaptation, Protein fate	11.973	11.019	12.654	12.777	9.83E-02	6.02E-01	-0.95	0.12
lpg0642	ORF	*WipB*	ORFs of unknown function (unique)	9.910	9.097	10.929	8.918	4.87E-02	2.51E-02	-0.81	-2.01
lpg0642	ORF	*WipB*	ORFs of unknown function (unique)	10.403	8.663	10.666	9.757	5.05E-02	7.16E-02	-1.74	-0.91
lpg0643	ribonuclease BN (tRNA processing exoribonuclease BN)		DNA/RNA degradation / restriction, Tra	11.279	9.473	11.307	9.379	3.41E-03	2.87E-03	-1.81	-1.93
lpg0643	ribonuclease BN (tRNA processing exoribonuclease BN)		DNA/RNA degradation / restriction, Tra	11.370	9.731	11.356	9.524	5.93E-03	1.22E-03	-1.64	-1.83
lpg0644	membrane protein?		Named proteins of general function	11.116	11.401	14.107	11.060	7.13E-01	7.45E-03	0.28	-3.05
lpg0644	membrane protein?		Named proteins of general function	11.244	11.637	14.155	11.291	6.04E-01	7.26E-03	0.39	-2.86
lpg0645	partial RtxA		Toxin production / other pathogen func	13.146	12.306	14.612	12.253	8.71E-02	6.89E-03	-0.84	-2.36
lpg0645	partial RtxA		Toxin production / other pathogen func	13.193	12.350	14.617	12.488	5.22E-02	2.82E-03	-0.84	-2.13
lpg0646	trp repressor binding protein	*wrbA*	Transcription factors / DNA binding prc	10.584	10.306	10.227	10.974	1.26E-01	3.60E-02	-0.28	0.75
lpg0646	trp repressor binding protein	*wrbA*	Transcription factors / DNA binding prc	10.644	10.245	10.329	11.151	6.85E-02	4.51E-02	-0.40	0.82
lpg0647	hypothetical (Tn5, transposase, IS4 family; ATPase component of ATI		Viral functions / Phage / Transposases	10.899	9.517	10.172	9.515	9.00E-02	2.68E-01	-1.38	-0.66
lpg0647	hypothetical (Tn5, transposase, IS4 family; ATPase component of ATI		Viral functions / Phage / Transposases	11.073	9.500	10.103	9.795	2.93E-04	4.82E-01	-1.57	-0.31
lpg0648	exodeoxyribonuclease III	*xth*	DNA/RNA degradation / restriction	11.302	10.795	11.623	11.034	1.39E-02	5.57E-02	-0.51	-0.59
lpg0648	exodeoxyribonuclease III	*xth*	DNA/RNA degradation / restriction	11.371	10.982	11.516	11.092	1.05E-02	1.36E-01	-0.39	-0.42

lpg0649	exodeoxyribonuclease III	*xthA1*	DNA/RNA degradation / restriction	8.896	9.434	11.194	10.147	1.25E-01	2.45E-01	0.54	-1.05
lpg0649	exodeoxyribonuclease III	*xthA1*	DNA/RNA degradation / restriction	8.606	9.085	8.808	10.252	4.56E-01	4.00E-02	0.48	1.44
lpg0650	50S ribosomal protein L31	*rpmE*	Translation	14.052	14.610	11.010	14.649	5.00E-01	3.99E-03	0.56	3.64
lpg0650	50S ribosomal protein L31	*rpmE*	Translation	14.100	14.479	10.722	14.517	6.50E-01	4.09E-03	0.38	3.80
lpg0651	malate oxidoreductase (malic enzyme)		Carbohydrate Metabolism	11.834	10.309	9.883	11.216	1.28E-03	7.44E-02	-1.52	1.33
lpg0651	malate oxidoreductase (malic enzyme)		Carbohydrate Metabolism	11.438	10.387	8.998	10.990	6.67E-02	1.24E-01	-1.05	1.99
lpg0652	major facilitator family transporter (multidrug efflux transporter, MFS f		Transport and binding	12.257	12.537	12.246	14.131	5.64E-01	1.92E-08	0.28	1.89
lpg0652	major facilitator family transporter (multidrug efflux transporter, MFS f		Transport and binding	12.249	12.527	12.217	14.111	5.66E-01	1.73E-07	0.28	1.89
lpg0653	major facilitator family transporter (multidrug efflux transporter, MFS f		Transport and binding	11.653	10.735	10.029	12.861	1.31E-01	8.99E-05	-0.92	2.83
lpg0653	major facilitator family transporter (multidrug efflux transporter, MFS f		Transport and binding	11.754	10.484	9.680	12.866	3.07E-02	7.40E-05	-1.27	3.19
lpg0654	DNA adenine methylase (DNA-adenine methyltransferas	*dam*	DNA/RNA degradation / restriction	10.665	9.650	9.233	10.357	4.09E-02	8.17E-02	-1.01	1.12
lpg0654	DNA adenine methylase (DNA-adenine methyltransferas	*dam*	DNA/RNA degradation / restriction	10.792	9.599	9.289	10.537	3.37E-02	5.37E-02	-1.19	1.25
lpg0655	tryptophan/tyrosine permease (tyrosine-specific transport protein)		Transport and binding	11.991	12.217	10.940	11.866	3.09E-01	4.06E-03	0.23	0.93
lpg0655	tryptophan/tyrosine permease (tyrosine-specific transport protein)		Transport and binding	12.058	12.318	10.916	11.968	2.53E-01	1.54E-03	0.26	1.05
lpg0656	tryptophan/tyrosine permease (tyrosine-specific transport protein) (ar		Transport and binding	10.754	9.475	10.039	10.030	1.18E-02	9.79E-01	-1.28	-0.01
lpg0656	tryptophan/tyrosine permease (tyrosine-specific transport protein) (ar		Transport and binding	11.044	9.222	9.783	9.984	9.78E-04	7.13E-01	-1.82	0.20
lpg0657	outer membrane protein OmpA?		Toxin production / other pathogen func	12.596	13.735	12.701	14.205	8.48E-05	1.19E-06	1.14	1.50
lpg0657	outer membrane protein OmpA?		Toxin production / other pathogen func	12.549	13.736	12.657	14.211	2.91E-05	8.26E-07	1.19	1.55
lpg0658	HlyD family secretion protein		Protein fate / hydrolases / secretion	11.009	10.258	10.195	10.029	8.73E-03	6.16E-01	-0.75	-0.17
lpg0658	HlyD family secretion protein		Protein fate / hydrolases / secretion	10.764	10.141	10.165	10.209	2.81E-01	8.89E-01	-0.62	0.04
lpg0659	ABC transporter ElsE (ABC transporter ATP binding protein)		Transport and binding	9.439	9.980	8.434	10.381	1.84E-01	8.04E-02	0.54	1.95
lpg0659	ABC transporter ElsE (ABC transporter ATP binding protein)		Transport and binding	7.897	9.962	8.508	10.466	1.20E-01	7.15E-02	2.07	1.96
lpg0660	ABC transporter permease protein		Transport and binding	9.821	8.681	9.356	8.668	1.57E-01	3.71E-01	-1.14	-0.69
lpg0660	ABC transporter permease protein		Transport and binding	10.068	8.106	9.413	9.201	3.04E-02	7.56E-01	-1.96	-0.21
lpg0661	ABC transporter permease protein		Transport and binding	8.821	6.156	8.254	7.648	1.07E-01	4.37E-01	-2.67	-0.61
lpg0661	ABC transporter permease protein		Transport and binding	7.691	8.101	8.189	7.803	7.79E-01	5.86E-01	0.41	-0.39
lpg0662	multidrug efflux MFS outer membrane protein (RND family)		Transport and binding	9.470	8.954	9.575	9.060	5.52E-01	5.32E-01	-0.52	-0.51
lpg0662	multidrug efflux MFS outer membrane protein (RND family)		Transport and binding	9.091	8.634	9.318	8.848	1.13E-01	1.28E-01	-0.46	-0.47
lpg0663	soluble lytic murein transglycosylase		Metabolism of Complex Carbohydrates	10.932	7.729	11.050	8.373	1.13E-04	3.15E-03	-3.20	-2.68
lpg0663	soluble lytic murein transglycosylase		Metabolism of Complex Carbohydrates	10.908	8.181	10.786	8.620	4.36E-05	1.83E-03	-2.73	-2.17
lpg0664	D-ribulose-5-phosphate-3-epimerase	*rpe+G736*	Carbohydrate Metabolism, Energy Me	11.080	10.483	10.887	11.742	6.81E-02	1.40E-03	-0.60	0.86
lpg0664	D-ribulose-5-phosphate-3-epimerase	*rpe+G736*	Carbohydrate Metabolism, Energy Me	11.145	10.653	10.759	11.875	7.13E-03	2.09E-04	-0.49	1.12
lpg0665	putative transmembrane protein COG 2259		Unknown / hypothetical proteins	12.137	11.956	14.225	10.455	6.77E-01	8.61E-06	-0.18	-3.77
lpg0665	putative transmembrane protein COG 2259		Unknown / hypothetical proteins	12.170	11.812	14.199	10.455	3.94E-01	7.41E-06	-0.36	-3.74
lpg0666	conserved hypothetical protein		Unknown / hypothetical proteins	11.212	9.165	12.723	8.745	3.03E-03	3.38E-04	-2.05	-3.98
lpg0666	conserved hypothetical protein		Unknown / hypothetical proteins	11.127	8.684	12.720	9.728	3.04E-03	3.70E-04	-2.44	-2.99
lpg0667	conserved hypothetical protein		Unknown / hypothetical proteins	12.071	11.568	14.566	9.822	4.44E-01	1.46E-05	-0.50	-4.74
lpg0667	conserved hypothetical protein		Unknown / hypothetical proteins	12.042	11.470	14.551	9.984	4.11E-01	8.25E-06	-0.57	-4.57
lpg0668	bromodomain? protein-protein interactions? [overlaps (different frame		Named proteins of general function	13.733	14.375	15.315	12.287	1.45E-01	3.47E-05	0.64	-3.03
lpg0668	bromodomain? protein-protein interactions? [overlaps (different frame		Named proteins of general function	13.673	14.358	15.266	12.313	1.39E-01	2.26E-04	0.68	-2.95
lpg0669	hypothetical exported protein [overlaps (different frame) with previous		Named proteins of general function	13.171	13.892	15.101	11.249	2.37E-01	7.44E-04	0.72	-3.85
lpg0669	hypothetical exported protein [overlaps (different frame) with previous		Named proteins of general function	13.167	13.833	15.267	11.684	2.17E-01	2.06E-05	0.67	-3.58
lpg0670	hypothetical		Unknown / hypothetical proteins	10.787	10.281	13.226	9.155	3.47E-01	9.34E-04	-0.51	-4.07
lpg0670	hypothetical		Unknown / hypothetical proteins	10.713	9.430	13.198	9.564	2.58E-01	4.57E-04	-1.28	-3.63
lpg0671	NADH dehydrogenase transmembrane protein	*ndh*	Energy Metabolism	10.526	9.646	13.747	8.312	3.49E-01	6.18E-04	-0.88	-5.43
lpg0671	NADH dehydrogenase transmembrane protein	*ndh*	Energy Metabolism	10.539	9.199	13.769	8.538	1.54E-01	1.20E-03	-1.34	-5.23
lpg0672	acetoacetate decarboxylase (ADC)		Lipid Metabolism, Carbohydrate Metab	10.788	10.325	14.420	10.601	5.86E-01	4.35E-04	-0.46	-3.82
lpg0672	acetoacetate decarboxylase (ADC)		Lipid Metabolism, Carbohydrate Metab	10.617	10.079	14.279	10.683	5.49E-01	1.99E-03	-0.54	-3.60
lpg0673	signal peptide protein (integral or exported protein?)		Named proteins of general function	10.098	9.855	13.263	9.555	8.18E-01	2.28E-02	-0.24	-3.71
lpg0673	signal peptide protein (integral or exported protein?)		Named proteins of general function	10.219	9.782	13.042	9.429	6.78E-01	5.57E-02	-0.44	-3.61
lpg0674	adenylate cyclase		Nucleotide Metabolism	11.428	11.396	13.113	11.551	9.40E-01	1.03E-02	-0.03	-1.56
lpg0674	adenylate cyclase		Nucleotide Metabolism	11.456	11.357	13.116	11.693	8.21E-01	1.71E-02	-0.10	-1.42
lpg0675	hypothetical protein		Unknown / hypothetical proteins	8.456	8.005	7.865	7.696	5.47E-01	8.25E-01	-0.45	-0.17
lpg0675	hypothetical protein		Unknown / hypothetical proteins	8.739	7.782	6.744	7.900	2.66E-01	5.80E-01	-0.96	1.16
lpg0676	protein product; similar to unknown protein		Unknown / hypothetical proteins	11.481	11.021	10.284	11.299	5.83E-01	2.25E-01	-0.46	1.01
lpg0676	protein product; similar to unknown protein		Unknown / hypothetical proteins	10.808	11.286	9.895	11.242	7.23E-02	7.82E-02	0.48	1.35
lpg0677	small ORF (88aa)		ORFs of unknown function (unique)	11.979	13.164	11.454	11.739	1.04E-02	3.58E-01	1.19	0.29
lpg0677	small ORF (88aa)		ORFs of unknown function (unique)	11.985	13.134	11.358	11.842	1.10E-02	1.20E-01	1.15	0.48
lpg0678	arginine ABC transporter, periplasmic binding protein (arginine 3rd tra		Transport and binding	11.840	10.286	11.833	9.986	1.28E-04	2.31E-05	-1.55	-1.85
lpg0678	arginine ABC transporter, periplasmic binding protein (arginine 3rd tra		Transport and binding	11.855	10.419	11.752	10.105	8.04E-04	9.21E-05	-1.44	-1.65
lpg0679	adenylyl transferase (glutamate-ammonia ligase adenylyltransferase)		Named proteins of general function	10.035	8.865	8.870	9.338	3.73E-02	5.98E-01	-1.17	0.47
lpg0679	adenylyl transferase (glutamate-ammonia ligase adenylyltransferase)		Named proteins of general function	10.311	9.267	8.754	9.615	7.23E-04	2.35E-01	-1.04	0.86
lpg0680	dipeptidyl aminopeptidase/acylaminoacyl peptidase		Protein fate / hydrolases / secretion	12.700	12.522	13.124	12.357	3.12E-01	2.23E-02	-0.18	-0.77
lpg0680	dipeptidyl aminopeptidase/acylaminoacyl peptidase		Protein fate / hydrolases / secretion	12.656	12.560	12.582	12.381	5.52E-01	2.18E-01	-0.10	-0.20

lpg0681	lipoprotein, putative		Named proteins of general function	10.331	7.934	10.166	7.730	6.54E-02	2.42E-03	-2.40	-2.44
lpg0681	lipoprotein, putative		Named proteins of general function	10.260	8.800	10.404	8.324	1.23E-04	1.40E-03	-1.46	-2.08
lpg0682	ABC transporter ATP-binding protein (ABC-type multidrug transport sy		Transport and binding	9.760	9.265	8.976	9.232	2.39E-01	6.12E-01	-0.50	0.26
lpg0682	ABC transporter ATP-binding protein (ABC-type multidrug transport sy		Transport and binding	10.032	9.047	8.955	9.451	1.21E-04	3.39E-01	-0.98	0.50
lpg0683	transmembrane protein COG0842 ABC-type multidrug transport syste		Transport and binding	9.610	8.158	9.823	8.561	4.36E-02	6.68E-02	-1.45	-1.26
lpg0683	transmembrane protein COG0842 ABC-type multidrug transport syste		Transport and binding	9.412	8.908	10.032	9.050	4.43E-01	2.07E-01	-0.50	-0.98
lpg0685	Fe-S oxidoreductase (2-methylthioadenine synthase)		Named proteins of general function	10.599	11.483	10.577	11.908	2.29E-02	4.36E-03	0.88	1.33
lpg0685	Fe-S oxidoreductase (2-methylthioadenine synthase)		Named proteins of general function	10.851	11.435	10.628	12.049	9.53E-02	3.16E-03	0.58	1.42
lpg0686	thiol:disulfide interchange protein DsbD (thioredoxin:cyto	*dsbD*	Protein fate / hydrolases / secretion, E	10.998	10.881	12.323	10.515	6.47E-01	4.52E-03	-0.12	-1.81
lpg0686	thiol:disulfide interchange protein DsbD (thioredoxin:cyto	*dsbD*	Protein fate / hydrolases / secretion, E	10.949	10.914	12.326	10.520	8.94E-01	3.50E-03	-0.03	-1.81
lpg0687	Hsp10, 10 kDa chaperonin (GroES protein)	*htpA*	Detoxification / adaptation, Protein fate	14.921	13.315	15.178	14.287	9.84E-04	7.48E-04	-1.61	-0.89
lpg0687	Hsp10, 10 kDa chaperonin (GroES protein)	*htpA*	Detoxification / adaptation, Protein fate	14.885	13.254	15.120	14.247	9.50E-04	2.22E-03	-1.63	-0.87
lpg0688	Hsp60, 60K heat shock protein HtpB (60 kDa chaperonin	*htpB*	Detoxification / adaptation, Protein fate	14.520	12.583	14.571	13.445	9.45E-04	1.34E-02	-1.94	-1.13
lpg0688	Hsp60, 60K heat shock protein HtpB (60 kDa chaperonin	*htpB*	Detoxification / adaptation, Protein fate	14.322	12.576	14.483	13.432	4.28E-03	1.74E-02	-1.75	-1.05
lpg0689	DNA binding stress protein (ferritin-like, oxidative damage protection)		Detoxification / adaptation, Transcripti	11.821	12.017	13.515	11.558	6.17E-01	9.91E-05	0.20	-1.96
lpg0689	DNA binding stress protein (ferritin-like, oxidative damage protection)		Detoxification / adaptation, Transcripti	11.806	11.977	13.505	11.709	6.32E-01	3.89E-04	0.17	-1.80
lpg0690	hypothetical (integral membrane protein)		Named proteins of general function	10.261	10.294	9.438	11.193	9.50E-01	1.35E-02	0.03	1.76
lpg0690	hypothetical (integral membrane protein)		Named proteins of general function	10.341	10.441	9.339	11.183	8.28E-01	4.00E-02	0.10	1.84
lpg0691	DNA topoisomerase IV subunit B (DNA gyrase subunit B)	*parE*	Replication and Repair	10.182	10.657	10.684	10.787	3.16E-01	8.77E-01	0.48	0.10
lpg0691	DNA topoisomerase IV subunit B (DNA gyrase subunit B)	*parE*	Replication and Repair	10.336	11.129	10.739	11.201	1.14E-02	2.19E-01	0.79	0.46
lpg0692	ABC type dipeptide/oligopeptide/nickel transport, ATPase	*dppF*	Transport and binding	9.841	10.266	9.734	11.003	3.94E-01	1.08E-03	0.42	1.27
lpg0692	ABC type dipeptide/oligopeptide/nickel transport, ATPase	*dppF*	Transport and binding	9.893	10.287	9.583	10.861	3.57E-01	1.15E-04	0.39	1.28
lpg0693	LigA (L. pneumophila infectivity gene) (interaptin)		Toxin production / other pathogen func	10.805	9.965	9.643	9.748	8.37E-03	8.80E-01	-0.84	0.11
lpg0693	LigA (L. pneumophila infectivity gene) (interaptin)		Toxin production / other pathogen func	11.466	9.641	10.033	10.215	3.62E-02	7.44E-01	-1.83	0.18
lpg0694	prolyl-tRNA synthase	*proS*	Amino Acid Metabolism, Translation	10.367	10.087	9.763	11.059	6.32E-01	1.54E-02	-0.28	1.30
lpg0694	prolyl-tRNA synthase	*proS*	Amino Acid Metabolism, Translation	10.364	11.210	9.743	11.377	1.56E-01	7.86E-03	0.85	1.63
lpg0695	hypothetical (inversin? alpha- or delta- latroinsectotoxin)	*LegA8*	Named proteins of general function	8.480	8.313	10.453	7.504	7.65E-01	8.57E-03	-0.17	-2.95
lpg0695	hypothetical (inversin? alpha- or delta- latroinsectotoxin)	*LegA8*	Named proteins of general function	9.672	8.745	10.429	8.370	1.49E-02	2.69E-03	-0.93	-2.06
lpg0696	ORF		ORFs of unknown function (unique)	10.197	10.154	10.879	9.411	8.23E-01	1.19E-02	-0.04	-1.47
lpg0696	ORF		ORFs of unknown function (unique)	10.291	10.921	10.888	10.266	4.34E-01	5.04E-01	0.63	-0.62
lpg0697	sulfate transporter (perhaps also: carbonic anhydrase)	*sul1*	Energy Metabolism	11.305	12.403	11.952	11.419	2.09E-02	4.15E-02	1.10	-0.53
lpg0697	sulfate transporter (perhaps also: carbonic anhydrase)	*sul1*	Energy Metabolism	11.326	12.441	11.890	11.435	1.44E-02	7.93E-02	1.12	-0.46
lpg0698	hypothetical (ATPase)		Named proteins of general function	12.504	11.292	9.485	12.329	7.43E-03	2.00E-03	-1.21	2.84
lpg0698	hypothetical (ATPase)		Named proteins of general function	12.365	11.281	9.406	12.278	3.61E-02	1.10E-02	-1.08	2.87
lpg0699	outer membrane protein TolC (outer membrane channel; specific toler		Transport and binding, Detoxification /	12.070	11.439	9.142	12.575	2.11E-01	3.83E-03	-0.63	3.43
lpg0699	outer membrane protein TolC (outer membrane channel; specific toler		Transport and binding, Detoxification /	11.855	11.448	8.830	12.596	5.20E-01	7.00E-03	-0.41	3.77
lpg0700	protein-L-isoaspartate-O-methyltransferase	*pcm*	Named proteins of general function	11.688	11.866	10.007	11.940	7.67E-01	2.32E-03	0.18	1.93
lpg0700	protein-L-isoaspartate-O-methyltransferase	*pcm*	Named proteins of general function	11.255	11.882	9.686	11.912	5.22E-01	1.40E-03	0.63	2.23
lpg0701	2-amino-3-ketobutyrate coenzyme A ligase (glycine acety	*kbl*	Amino Acid Metabolism	8.285	8.505	9.068	7.997	7.09E-01	3.34E-01	0.22	-1.07
lpg0701	2-amino-3-ketobutyrate coenzyme A ligase (glycine acety	*kbl*	Amino Acid Metabolism	8.102	8.785	8.591	7.978	3.51E-01	5.84E-01	0.68	-0.61
lpg0702	threonine(-3-)dehydrogenase	*tdh*	Amino Acid Metabolism	9.151	11.062	9.114	11.101	9.66E-06	5.44E-03	1.91	1.99
lpg0702	threonine(-3-)dehydrogenase	*tdh*	Amino Acid Metabolism	8.923	11.374	9.047	11.268	7.64E-04	1.27E-03	2.45	2.22
lpg0703	ABC transporter, ABC binding protein		Transport and binding	9.602	10.788	9.775	11.129	1.03E-03	1.90E-04	1.19	1.35
lpg0703	ABC transporter, ABC binding protein		Transport and binding	9.640	10.870	9.657	11.368	1.08E-02	3.86E-05	1.23	1.71
lpg0704	enhanced entry protein EnhA	*enhA*	Toxin production / other pathogen func	10.010	9.812	9.796	9.902	3.41E-01	7.30E-01	-0.20	0.11
lpg0704	enhanced entry protein EnhA	*enhA*	Toxin production / other pathogen func	9.913	9.579	9.479	9.670	2.56E-01	5.98E-01	-0.33	0.19
lpg0705	COG2391 predicted transporter component		Transport and binding	10.044	10.156	9.953	9.865	8.35E-01	8.87E-01	0.11	-0.09
lpg0705	COG2391 predicted transporter component		Transport and binding	10.097	9.789	9.283	9.673	5.35E-01	6.26E-01	-0.31	0.39
lpg0706	COG2391 predicted transporter component		Transport and binding	10.454	10.176	10.127	9.298	5.03E-01	2.29E-01	-0.28	-0.83
lpg0706	COG2391 predicted transporter component		Transport and binding	10.585	10.475	10.492	9.685	7.93E-01	1.92E-01	-0.11	-0.81
lpg0707	(outer) membrane protein (long chain fatty acid transporter?)		Named proteins of general function	12.097	10.991	11.290	11.396	6.44E-02	8.37E-01	-1.11	0.11
lpg0707	(outer) membrane protein (long chain fatty acid transporter?)		Named proteins of general function	12.008	11.350	11.302	11.590	2.37E-01	5.93E-01	-0.66	0.29
lpg0708	IcmL homolog		Toxin production / other pathogen func	12.876	12.655	12.369	12.905	5.22E-01	6.35E-02	-0.22	0.54
lpg0708	IcmL homolog		Toxin production / other pathogen func	12.975	12.691	12.286	12.963	3.47E-01	3.45E-02	-0.28	0.68
lpg0709	formiminoglutamase (arginase family protein)		Amino Acid Metabolism	11.142	11.333	9.955	11.771	7.53E-01	4.19E-03	0.19	1.82
lpg0709	formiminoglutamase (arginase family protein)		Amino Acid Metabolism	11.221	11.708	9.785	11.929	4.37E-01	1.02E-03	0.49	2.14
lpg0710	sepiapterin reductase (short chain dehydrogenase) (benz	*yueD*	Metabolism of Cofactors and Vitamins	11.061	11.909	11.688	12.113	7.83E-02	1.44E-01	0.85	0.43
lpg0710	sepiapterin reductase (short chain dehydrogenase) (benz	*yueD*	Metabolism of Cofactors and Vitamins	11.447	11.659	11.696	12.141	6.84E-01	1.46E-01	0.21	0.45
lpg0711	imidazolonepropionase (imidazolone-5-propionate hydrol	*hutI*	Amino Acid Metabolism	12.376	11.942	12.520	11.948	1.40E-01	1.00E-01	-0.43	-0.57
lpg0711	imidazolonepropionase (imidazolone-5-propionate hydrol	*hutI*	Amino Acid Metabolism	12.251	12.263	12.504	12.376	9.79E-01	8.21E-01	0.01	-0.13
lpg0712	similar to endo-1,4-beta-xylanase	*yjeA*	Metabolism of Complex Carbohydrate	10.309	10.925	10.117	11.195	2.06E-01	5.18E-03	0.62	1.08
lpg0712	similar to endo-1,4-beta-xylanase	*yjeA*	Metabolism of Complex Carbohydrate	9.637	10.886	9.765	11.201	7.52E-02	2.56E-02	1.25	1.44
lpg0713	oligopeptide transporter		Transport and binding	10.056	8.428	9.001	8.931	2.09E-02	8.71E-01	-1.63	-0.07
lpg0713	oligopeptide transporter		Transport and binding	10.091	8.057	8.657	9.105	1.13E-03	4.58E-01	-2.03	0.45

lpg0714	sensor histidine kinase (two component sensor)		Signal transduction / other regulatory f	9.183	9.068	8.994	7.969	8.54E-01	3.03E-01	-0.11	-1.03
lpg0714	sensor histidine kinase (two component sensor)		Signal transduction / other regulatory f	9.692	8.570	8.963	8.042	7.53E-02	3.25E-01	-1.12	-0.92
lpg0715	two component response regulator (cobalt-zinc-cadmium resistance)		Signal transduction / other regulatory f	9.066	7.483	7.333	6.719	6.51E-02	5.25E-01	-1.58	-0.61
lpg0715	two component response regulator (cobalt-zinc-cadmium resistance)		Signal transduction / other regulatory f	9.137	8.874	7.178	8.088	6.43E-01	3.13E-01	-0.26	0.91
lpg0716	ORF		ORFs of unknown function (unique)	10.042	9.777	9.350	10.515	5.31E-01	1.12E-02	-0.26	1.16
lpg0716	ORF		ORFs of unknown function (unique)	10.179	9.596	8.878	10.414	2.03E-01	1.41E-01	-0.58	1.54
lpg0717	small ORF (153aa)		ORFs of unknown function (unique)	9.927	9.369	12.140	8.880	4.33E-01	3.48E-03	-0.56	-3.26
lpg0717	small ORF (153aa)		ORFs of unknown function (unique)	9.908	9.416	11.990	9.367	5.22E-01	9.39E-03	-0.49	-2.62
lpg0718	proton/sodium-glutamate symport protein (sodium:dicarboxylate symp		Transport and binding	9.386	9.274	9.852	8.519	7.65E-01	3.93E-02	-0.11	-1.33
lpg0718	proton/sodium-glutamate symport protein (sodium:dicarboxylate symp		Transport and binding	8.969	7.940	9.393	8.291	4.67E-02	3.20E-02	-1.03	-1.10
lpg0719	valyl tRNA synthase	*valS*	Amino Acid Metabolism, Translation	10.834	11.676	8.660	12.503	2.03E-01	4.40E-04	0.84	3.84
lpg0719	valyl tRNA synthase	*valS*	Amino Acid Metabolism, Translation	10.785	12.403	8.556	12.855	5.94E-02	8.12E-04	1.62	4.30
lpg0720	multidrug resistance protein (transporter, AcrB/AcrD/AcrF family) (RN		Transport and binding	11.172	10.841	9.677	10.837	3.94E-01	1.27E-01	-0.33	1.16
lpg0720	multidrug resistance protein (transporter, AcrB/AcrD/AcrF family) (RN		Transport and binding	11.019	10.792	9.387	10.742	6.19E-01	6.06E-02	-0.23	1.35
lpg0721	RND efflux membrane fusion protein (acriflavin resistance protein E)		Transport and binding	12.353	12.679	10.969	12.795	1.08E-01	3.49E-04	0.33	1.83
lpg0721	RND efflux membrane fusion protein (acriflavin resistance protein E)		Transport and binding	11.610	12.533	10.416	12.763	4.22E-03	1.05E-03	0.92	2.35
lpg0722	ORF hypothetical?		Unknown / hypothetical proteins	11.533	13.619	10.249	12.728	8.84E-02	1.02E-03	2.09	2.48
lpg0722	ORF hypothetical?		Unknown / hypothetical proteins	11.830	13.569	8.605	12.664	6.10E-02	4.44E-03	1.74	4.06
lpg0723	small ORF (145aa) zinc finger protein? VrrB? His rich glycoprotein?		Unknown / hypothetical proteins	10.587	10.041	9.668	10.284	4.45E-01	4.01E-01	-0.55	0.62
lpg0723	small ORF (145aa) zinc finger protein? VrrB? His rich glycoprotein?		Unknown / hypothetical proteins	10.934	9.828	9.017	10.403	4.27E-02	1.51E-01	-1.11	1.39
lpg0724	hypothetical lipoprotein; hyperosmotically inducible periplasmic protei		Named proteins of general function	13.856	13.803	12.145	13.781	8.72E-01	7.87E-04	-0.05	1.64
lpg0724	hypothetical lipoprotein; hyperosmotically inducible periplasmic protei		Named proteins of general function	13.847	13.810	12.081	13.778	9.26E-01	1.05E-03	-0.04	1.70
lpg0725	serine hydroxymethyltransferase	*glyA3*	Amino Acid Metabolism, Metabolism o	12.546	13.462	11.777	13.508	2.84E-03	7.12E-05	0.92	1.73
lpg0725	serine hydroxymethyltransferase	*glyA3*	Amino Acid Metabolism, Metabolism o	12.558	13.482	11.828	13.586	2.72E-03	8.52E-05	0.92	1.76
lpg0726	ATP cone and Zn ribbon domains protein (transcriptional regulator), C		Transcription factors / DNA binding pro	11.936	10.690	9.794	10.670	2.68E-03	2.05E-01	-1.25	0.88
lpg0726	ATP cone and Zn ribbon domains protein (transcriptional regulator), C		Transcription factors / DNA binding pro	11.511	10.739	9.427	10.709	7.17E-02	1.57E-01	-0.77	1.28
lpg0727	transcription termination factor NusB (nitrogen utilization	*nusB*	Transcription factors / DNA binding pro	11.086	9.833	9.556	10.876	6.51E-02	1.15E-02	-1.25	1.32
lpg0727	transcription termination factor NusB (nitrogen utilization	*nusB*	Transcription factors / DNA binding pro	10.929	9.792	8.451	10.894	1.11E-01	3.44E-03	-1.14	2.44
lpg0728	thiamine monophosphate kinase (AIR synthase)	*thiL*	Metabolism of Cofactors and Vitamins	10.857	11.487	10.351	12.380	2.58E-01	1.32E-02	0.63	2.03
lpg0728	thiamine monophosphate kinase (AIR synthase)	*thiL*	Metabolism of Cofactors and Vitamins	10.839	10.773	7.686	11.769	7.78E-01	6.18E-02	-0.07	4.08
lpg0729	phosphatidylglycerophosphatase A (PgpA)	*pgpA*	Metabolism of Complex Lipids	10.624	11.286	12.964	10.517	3.09E-01	3.11E-03	0.66	-2.45
lpg0729	phosphatidylglycerophosphatase A (PgpA)	*pgpA*	Metabolism of Complex Lipids	10.658	11.441	13.001	10.648	1.81E-01	3.19E-03	0.78	-2.35
lpg0730	transmembrane permease		Transport and binding	9.981	11.948	10.324	11.203	1.13E-02	1.85E-01	1.97	0.88
lpg0730	transmembrane permease		Transport and binding	9.784	11.912	9.909	11.251	2.71E-02	1.89E-01	2.13	1.34
lpg0731	hypothetical protein		Unknown / hypothetical proteins	12.139	13.061	9.835	13.386	1.71E-01	1.90E-03	0.92	3.55
lpg0731	hypothetical protein		Unknown / hypothetical proteins	12.151	13.008	9.741	13.373	2.19E-01	2.98E-04	0.86	3.63
lpg0732	hypothetical protein		Unknown / hypothetical proteins	11.129	13.105	10.990	13.003	2.92E-03	3.80E-04	1.98	2.01
lpg0732	hypothetical protein		Unknown / hypothetical proteins	10.829	13.066	10.598	12.953	6.92E-03	2.57E-04	2.24	2.35
lpg0733	ORF		ORFs of unknown function (unique)	12.338	12.562	11.845	11.561	4.03E-01	1.20E-02	0.22	-0.28
lpg0733	ORF		ORFs of unknown function (unique)	12.361	12.545	11.797	11.608	5.03E-01	2.22E-01	0.18	-0.19
lpg0734	glutamine dependent NAD+ synthetase (NH3 dependent NAD synthe		Amino Acid Metabolism, Metabolism o	9.757	9.605	9.447	10.210	6.79E-01	2.55E-01	-0.15	0.76
lpg0734	glutamine dependent NAD+ synthetase (NH3 dependent NAD synthe		Amino Acid Metabolism, Metabolism o	9.848	9.914	9.378	10.462	6.69E-01	3.10E-02	0.07	1.08
lpg0735	DNA helicase, SNF2/RAD54 family domain protein		Replication and Repair	9.982	8.988	10.000	9.637	6.87E-02	4.40E-01	-0.99	-0.36
lpg0735	DNA helicase, SNF2/RAD54 family domain protein		Replication and Repair	10.419	8.907	9.729	10.094	4.35E-04	4.22E-01	-1.51	0.37
lpg0736	helicase/SNF2 superfamily (superfamily II DNA/RNA helicases)		Transcription, Replication and Repair	7.575	8.917	8.326	10.007	5.15E-01	2.69E-01	1.34	1.68
lpg0736	helicase/SNF2 superfamily (superfamily II DNA/RNA helicases)		Transcription, Replication and Repair	7.671	8.080	7.928	9.683	6.40E-01	3.08E-01	0.41	1.75
lpg0737	hypothetical signal peptide protein		Named proteins of general function	13.932	14.497	15.198	13.468	1.00E-01	2.70E-03	0.57	-1.73
lpg0737	hypothetical signal peptide protein		Named proteins of general function	13.855	14.483	15.133	13.452	9.27E-02	3.38E-03	0.63	-1.68
lpg0738	replicative DNA helicase	*dnaB*	Replication and Repair	11.345	11.430	11.181	11.705	6.10E-01	6.44E-02	0.09	0.52
lpg0738	replicative DNA helicase	*dnaB*	Replication and Repair	11.242	11.368	10.998	11.637	5.74E-01	8.82E-02	0.13	0.64
lpg0739	alanine racemase		Amino Acid Metabolism, Metabolism o	10.137	8.987	10.624	9.964	3.53E-01	6.35E-01	-1.15	-0.66
lpg0739	alanine racemase		Amino Acid Metabolism, Metabolism o	9.572	8.676	9.323	10.151	4.44E-01	4.06E-01	-0.90	0.83
lpg0740	17kDa common antigen (17kDa surface antigen precurso	*omp*	Named proteins of general function	11.008	13.031	10.966	10.271	3.43E-04	1.24E-01	2.02	-0.70
lpg0740	17kDa common antigen (17kDa surface antigen precurso	*omp*	Named proteins of general function	10.852	13.075	10.912	10.412	1.93E-03	2.82E-01	2.22	-0.50
lpg0741	inosine-5'-monophosphate dehydrogenase (IMP dehydrogenase)		Nucleotide Metabolism	10.297	8.538	11.834	9.283	1.12E-02	9.48E-03	-1.76	-2.55
lpg0741	inosine-5'-monophosphate dehydrogenase (IMP dehydrogenase)		Nucleotide Metabolism	10.221	9.313	11.982	9.649	2.48E-02	3.78E-03	-0.91	-2.33
lpg0742	hypothetical protein		Unknown / hypothetical proteins	11.638	10.694	11.741	10.747	1.76E-01	1.19E-02	-0.94	-0.99
lpg0742	hypothetical protein		Unknown / hypothetical proteins	11.505	10.961	11.333	10.679	5.43E-01	2.12E-01	-0.54	-0.65
lpg0743	glutamate synthetase		Energy Metabolism, Amino Acid Metab	11.268	9.713	11.918	9.960	1.51E-02	1.19E-03	-1.55	-1.96
lpg0743	glutamate synthetase		Energy Metabolism, Amino Acid Metab	11.308	9.709	11.908	10.327	8.32E-03	5.32E-03	-1.60	-1.58
lpg0744	GGDEF domain protein (regulatory components of sensory transduct		Signal transduction / other regulatory f	5.933	8.449	9.401	5.572		8.87E-02	2.52	-3.83
lpg0744	GGDEF domain protein (regulatory components of sensory transduct		Signal transduction / other regulatory f	7.934	10.059	10.010	6.660	4.95E-01	7.88E-02	2.13	-3.35
lpg0745	lipoic acid synthetase (lipoate synthetase) COG0320		Named proteins of general function	10.915	11.987	11.498	11.380	4.51E-04	6.64E-01	1.07	-0.12
lpg0745	lipoic acid synthetase (lipoate synthetase) COG0320		Named proteins of general function	10.685	11.852	11.296	11.424	5.43E-03	6.23E-01	1.17	0.13

lpg0746	IraAB (proton/(oligo)peptide symporter)		Transport and binding	10.241	10.541	8.807	9.653	4.18E-01	9.86E-02	0.30	0.85
lpg0746	IraAB (proton/(oligo)peptide symporter)		Transport and binding	10.427	10.561	8.255	9.719	6.28E-01	6.34E-02	0.13	1.46
lpg0747	hypothetical		Unknown / hypothetical proteins	11.721	10.404	9.660	10.458	5.98E-02	2.49E-01	-1.32	0.80
lpg0747	hypothetical		Unknown / hypothetical proteins	11.374	11.425	9.976	11.036	9.42E-01	1.54E-02	0.05	1.06
lpg0748	LPS biosynthesis protein (pseudaminic acid biosynthesis and flagelli		Cell envelope synthesis, Metabolism	13.943	14.575	12.752	14.164	2.33E-01	3.91E-03	0.63	1.41
lpg0748	LPS biosynthesis protein (pseudaminic acid biosynthesis and flagelli		Cell envelope synthesis, Metabolism	13.922	14.531	12.743	14.171	2.06E-01	2.80E-03	0.61	1.43
lpg0749	imidazole glycerol phosphate synthase, cyclase subunit	*hisF*	Amino Acid Metabolism	11.490	13.083	10.680	13.038	1.01E-02	1.35E-03	1.59	2.36
lpg0749	imidazole glycerol phosphate synthase, cyclase subunit	*hisF*	Amino Acid Metabolism	10.870	13.225	10.034	13.257	2.49E-03	6.35E-04	2.36	3.22
lpg0750	imidazole glycerol phosphate synthase subunit HisH (IG	*hisH*	Amino Acid Metabolism	12.701	12.242	10.727	12.709	4.90E-01	1.46E-02	-0.46	1.98
lpg0750	imidazole glycerol phosphate synthase subunit HisH (IG	*hisH*	Amino Acid Metabolism	12.822	12.310	10.607	12.864	4.13E-01	6.83E-03	-0.51	2.26
lpg0751	CMP-N-acetylneuraminic acid synthetase (N-acylneuram	*neuA*	Metabolism of Complex Carbohydrate	12.509	11.040	10.775	11.398	2.10E-02	2.05E-01	-1.47	0.62
lpg0751	CMP-N-acetylneuraminic acid synthetase (N-acylneuram	*neuA*	Metabolism of Complex Carbohydrate	11.981	10.125	10.570	11.448	5.22E-02	6.54E-02	-1.86	0.88
lpg0752	N-acetylneuraminic acid synthetase (N-acylneuraminic a	*nnaB1*	Carbohydrate Metabolism, Metabolism	12.287	10.108	9.231	10.680	2.97E-03	1.42E-01	-2.18	1.45
lpg0752	N-acetylneuraminic acid synthetase (N-acylneuraminic a	*nnaB1*	Carbohydrate Metabolism, Metabolism	11.806	9.152	8.561	10.444	6.29E-03	7.10E-02	-2.65	1.88
lpg0753	polysialic acid biosynthesis (N-acylglucosamine-2-epimerase) (UDP-		Metabolism of Complex Carbohydrate	12.564	10.935	11.097	11.651	2.62E-02	2.70E-01	-1.63	0.55
lpg0753	polysialic acid biosynthesis (N-acylglucosamine-2-epimerase) (UDP-		Metabolism of Complex Carbohydrate	12.388	11.339	10.966	12.316	3.34E-01	9.24E-02	-1.05	1.35
lpg0754	acetyltransferase (hexapeptide transferase) (serine-O-acetyltransfera		Metabolism of Complex Carbohydrate	14.000	14.926	12.259	14.655	6.14E-02	2.49E-04	0.93	2.40
lpg0754	acetyltransferase (hexapeptide transferase) (serine-O-acetyltransfera		Metabolism of Complex Carbohydrate	14.016	14.961	12.232	14.669	4.44E-02	1.74E-04	0.95	2.44
lpg0755	COG0399: Predicted pyridoxal phosphate-dependent en	*yvfE*	Cell envelope synthesis, Signal transd	12.915	13.809	10.372	13.707	1.88E-01	1.74E-04	0.89	3.33
lpg0755	COG0399: Predicted pyridoxal phosphate-dependent en	*yvfE*	Cell envelope synthesis, Signal transd	12.777	13.912	10.304	13.780	7.75E-02	1.91E-04	1.14	3.48
lpg0756	RmlC protein (dTDP-6-deoxy-D-glucose-3,5-epimerase)		Nucleotide Metabolism	12.880	10.736	11.138	11.262	8.24E-05	7.47E-01	-2.14	0.12
lpg0756	RmlC protein (dTDP-6-deoxy-D-glucose-3,5-epimerase)		Nucleotide Metabolism	12.796	10.883	11.077	11.304	5.88E-05	5.72E-01	-1.91	0.23
lpg0757	dTDP-6-deoxy-L-mannose dehydrogenase (dTDP-4-dehydrorhamno		Nucleotide Metabolism	10.732	9.426	10.116	11.233	4.10E-03	5.86E-02	-1.31	1.12
lpg0757	dTDP-6-deoxy-L-mannose dehydrogenase (dTDP-4-dehydrorhamno		Nucleotide Metabolism	10.733	9.413	9.954	11.162	1.55E-02	9.90E-02	-1.32	1.21
lpg0758	dTDP-glucose 4,6-dehydratase RmlB	*rfbB*	Nucleotide Metabolism, Biosynthesis	13.183	10.839	11.220	12.281	9.51E-05	5.00E-02	-2.34	1.06
lpg0758	dTDP-glucose 4,6-dehydratase RmlB	*rfbB*	Nucleotide Metabolism, Biosynthesis	13.258	10.677	11.165	12.248	6.31E-06	5.50E-02	-2.58	1.08
lpg0759	glucose-6-phosphate isomerase	*pgi*	Carbohydrate Metabolism, Metabolism	11.691	11.543	9.901	12.456	8.65E-01	1.95E-04	-0.15	2.56
lpg0759	glucose-6-phosphate isomerase	*pgi*	Carbohydrate Metabolism, Metabolism	12.064	11.373	9.396	12.114	1.15E-01	2.56E-03	-0.69	2.72
lpg0760	glucose-1-phosphate thymidylyltransferase RmlA	*rfbA*	Nucleotide Metabolism, Biosynthesis	12.930	12.430	12.211	13.159	5.50E-02	6.51E-03	-0.50	0.95
lpg0760	glucose-1-phosphate thymidylyltransferase RmlA	*rfbA*	Nucleotide Metabolism, Biosynthesis	12.813	12.363	12.040	13.171	1.72E-01	8.77E-03	-0.45	1.13
lpg0761	NAD dependent epimerase/dehydratase; UDP-glucose-4-epimerase		Nucleotide Metabolism, Metabolism of	12.318	9.780	9.999	10.319	1.28E-03	6.37E-01	-2.54	0.32
lpg0761	NAD dependent epimerase/dehydratase; UDP-glucose-4-epimerase		Nucleotide Metabolism, Metabolism of	12.162	9.733	9.774	10.458	5.35E-03	3.73E-01	-2.43	0.68
lpg0762	O-antigen initiating glycosyl transferase group 4-UDP-N-acetylmuram		Metabolism of Complex Carbohydrate	10.584	9.192	8.792	9.388	1.05E-01	5.99E-01	-1.39	0.60
lpg0762	O-antigen initiating glycosyl transferase group 4-UDP-N-acetylmuram		Metabolism of Complex Carbohydrate	10.771	8.662	8.205	8.968	7.80E-06	3.75E-01	-2.11	0.76
lpg0763	(L. pneumophila hypothetical protein)		Unknown / hypothetical proteins	12.076	11.190	11.551	10.317	2.06E-02	2.58E-02	-0.89	-1.23
lpg0763	(L. pneumophila hypothetical protein)		Unknown / hypothetical proteins	11.452	10.882	11.278	10.172	1.90E-01	7.04E-02	-0.57	-1.11
lpg0764	hypothetical		Unknown / hypothetical proteins	10.177	9.980	9.854	9.613	5.78E-01	7.11E-01	-0.20	-0.24
lpg0764	hypothetical		Unknown / hypothetical proteins	10.167	10.259	9.906	9.857	7.20E-01	9.34E-01	0.09	-0.05
lpg0765	tetratricopeptide repeat domain 8		Named proteins of general function	13.088	12.918	12.076	12.332	7.48E-01	4.24E-01	-0.17	0.26
lpg0765	tetratricopeptide repeat domain 8		Named proteins of general function	13.111	12.960	12.098	12.430	7.80E-01	2.88E-01	-0.15	0.33
lpg0766	hypothetical		Unknown / hypothetical proteins	11.567	11.145	11.340	11.374	1.63E-01	8.72E-01	-0.42	0.03
lpg0766	hypothetical		Unknown / hypothetical proteins	11.533	11.297	10.919	11.576	5.02E-01	1.15E-01	-0.24	0.66
lpg0767	hypothetical		Unknown / hypothetical proteins	13.493	11.007	10.600	9.819	1.58E-03	3.89E-01	-2.49	-0.78
lpg0767	hypothetical		Unknown / hypothetical proteins	13.543	10.950	10.710	10.215	1.25E-03	5.57E-01	-2.59	-0.50
lpg0768	spore coat polysaccharide biosynthesis protein E (N-acetylneuramina		Cell envelope synthesis, Chemotaxis /	11.284	10.878	11.353	11.930	3.09E-01	9.50E-02	-0.41	0.58
lpg0768	spore coat polysaccharide biosynthesis protein E (N-acetylneuramina		Cell envelope synthesis, Chemotaxis /	11.285	10.846	11.310	11.914	1.17E-01	8.26E-02	-0.44	0.60
lpg0769	hypothetical		Unknown / hypothetical proteins	13.199	13.322	11.125	12.961	8.49E-01	1.16E-02	0.12	1.84
lpg0769	hypothetical		Unknown / hypothetical proteins	13.331	13.396	10.966	13.029	8.84E-01	7.98E-03	0.07	2.06
lpg0770	hypothetical		Unknown / hypothetical proteins	11.630	11.008	10.807	10.930	2.10E-01	6.55E-01	-0.62	0.12
lpg0770	hypothetical		Unknown / hypothetical proteins	11.803	11.163	10.610	11.005	3.75E-02	2.71E-01	-0.64	0.40
lpg0771	hypothetical		Unknown / hypothetical proteins	11.211	10.186	10.741	10.171	1.10E-01	1.30E-01	-1.02	-0.57
lpg0771	hypothetical		Unknown / hypothetical proteins	11.123	10.214	10.899	10.401	2.40E-01	1.61E-01	-0.91	-0.50
lpg0772	polysaccharide ABC transporter, permease protein	*rfbA*	Transport and binding, Protein fate / h	9.997	10.528	9.543	10.355	3.81E-01	2.30E-01	0.53	0.81
lpg0772	polysaccharide ABC transporter, permease protein	*rfbA*	Transport and binding, Protein fate / h	9.914	10.504	9.746	10.569	3.50E-01	1.88E-01	0.59	0.82
lpg0773	polysaccharide ABC transporter, ATP binding protein (O-antigen expo		Transport and binding, Protein fate / h	13.512	11.100	11.559	11.094	1.62E-04	4.10E-01	-2.41	-0.46
lpg0773	polysaccharide ABC transporter, ATP binding protein (O-antigen expo		Transport and binding, Protein fate / h	13.354	10.704	11.349	10.930	3.82E-04	4.82E-01	-2.65	-0.42
lpg0774	hypothetical (Legionella pneumophila)		Unknown / hypothetical proteins	11.796	9.561	10.468	10.141	2.84E-03	5.70E-01	-2.24	-0.33
lpg0774	hypothetical (Legionella pneumophila)		Unknown / hypothetical proteins	12.074	9.328	10.390	10.214	1.05E-03	7.23E-01	-2.75	-0.18
lpg0775	glycosyl transferase (L. pneumophila) COG1216		Named proteins of general function	10.332	7.716	8.726	8.721	1.67E-01	9.92E-01	-2.62	-0.01
lpg0775	glycosyl transferase (L. pneumophila) COG1216		Named proteins of general function	10.448	8.633	8.504	9.605	8.90E-03	2.80E-02	-1.82	1.10
lpg0776	transposase (ORF1 transposase)		Viral functions / Phage / Transposase	9.702	8.090	9.351	8.418	3.09E-01	3.48E-01	-1.61	-0.93
lpg0776	transposase (ORF1 transposase)		Viral functions / Phage / Transposase	9.145	8.451	8.785	8.281	4.95E-01	5.94E-01	-0.69	-0.50
lpg0777	O-acetyltransferase (glycosyltransferase)		Named proteins of general function	11.930	11.090	10.642	10.138	4.54E-02	4.60E-01	-0.84	-0.50
lpg0777	O-acetyltransferase (glycosyltransferase)		Named proteins of general function	12.227	11.036	10.386	10.181	4.26E-03	7.48E-01	-1.19	-0.20

lpg0778	glycosyl transferase		Metabolism of Complex Carbohydrate	11.762	10.182	11.535	9.951	1.16E-03	2.38E-02	-1.58	-1.58
lpg0778	glycosyl transferase		Metabolism of Complex Carbohydrate	11.734	10.169	11.462	10.344	5.76E-03	3.39E-02	-1.57	-1.12
lpg0779	glycosyltransferase		Metabolism of Complex Carbohydrate	11.397	10.912	8.894	11.843	1.19E-01	2.07E-03	-0.48	2.95
lpg0779	glycosyltransferase		Metabolism of Complex Carbohydrate	11.194	10.987	8.288	11.904	6.32E-01	1.85E-03	-0.21	3.62
lpg0780	metallo-beta-lactamase family protein, COG0491: Zn dependent hydr		Protein fate / hydrolases / secretion	13.047	12.464	10.461	12.830	3.58E-01	5.80E-03	-0.58	2.37
lpg0780	metallo-beta-lactamase family protein, COG0491: Zn dependent hydr		Protein fate / hydrolases / secretion	13.193	12.187	9.742	12.815	4.78E-02	8.97E-03	-1.01	3.07
lpg0781	global regulator (carbon storage regulator)	*csrA-2*	Signal transduction / other regulatory f	14.673	12.148	12.389	12.512	1.34E-02	8.48E-01	-2.52	0.12
lpg0781	global regulator (carbon storage regulator)	*csrA-2*	Signal transduction / other regulatory f	14.471	12.137	12.265	12.421	1.33E-02	8.19E-01	-2.33	0.16
lpg0782	O-antigen acetylase (lipopolysaccharide modification acyltransferase)		Cell envelope synthesis, Metabolism o	10.308	8.384	10.038	8.808	8.38E-03	4.21E-02	-1.92	-1.23
lpg0782	O-antigen acetylase (lipopolysaccharide modification acyltransferase)		Cell envelope synthesis, Metabolism o	10.516	8.358	9.350	8.842	6.29E-04	4.69E-01	-2.16	-0.51
lpg0783	biotin operon repressor and biotin [acetyl CoA carboxylas	*birA*	Metabolism of Cofactors and Vitamins	11.036	10.319	10.458	11.011	2.59E-02	2.74E-01	-0.72	0.55
lpg0783	biotin operon repressor and biotin [acetyl CoA carboxylas	*birA*	Metabolism of Cofactors and Vitamins	10.498	10.426	9.563	11.098	9.06E-01	4.62E-03	-0.07	1.54
lpg0784	phosphopantetheine-protein transferase (4'-phosphopantetheinyl tran		Metabolism of Cofactors and Vitamins	10.818	9.738	9.410	10.052	2.56E-02	1.54E-01	-1.08	0.64
lpg0784	phosphopantetheine-protein transferase (4'-phosphopantetheinyl tran		Metabolism of Cofactors and Vitamins	10.776	9.624	9.205	10.152	9.63E-03	1.20E-01	-1.15	0.95
lpg0785	acetyl CoA carboxylase, carboxyltransferase, alpha subu	*accA*	Lipid Metabolism, Biosynthesis of Sec	11.633	10.801	10.819	11.234	5.40E-02	3.91E-01	-0.83	0.41
lpg0785	acetyl CoA carboxylase, carboxyltransferase, alpha subu	*accA*	Lipid Metabolism, Biosynthesis of Sec	11.247	10.800	10.658	11.365	3.96E-01	1.43E-01	-0.45	0.71
lpg0786	cell cycle protein MesJ	*mesJ*	Chemotaxis / motility / cell division	10.455	9.357	9.634	9.645	2.20E-03	9.84E-01	-1.10	0.01
lpg0786	cell cycle protein MesJ	*mesJ*	Chemotaxis / motility / cell division	10.747	10.392	9.751	10.495	7.51E-01	4.43E-01	-0.35	0.74
lpg0787	hypothetical protein		Unknown / hypothetical proteins	9.689	10.088	9.819	8.256	2.99E-01	1.94E-02	0.40	-1.56
lpg0787	hypothetical protein		Unknown / hypothetical proteins	9.359	9.838	9.491	8.310	1.29E-01	4.10E-02	0.48	-1.18
lpg0788	ORF		ORFs of unknown function (unique)	11.793	9.732	9.925	10.572	4.15E-03	3.58E-01	-2.06	0.65
lpg0788	ORF		ORFs of unknown function (unique)	11.914	9.827	9.156	10.737	8.07E-04	1.78E-01	-2.09	1.58
lpg0789	alginate O-acetyltransferase AlgI		Named proteins of general function	10.625	8.763	9.652	8.933	2.08E-02	3.08E-01	-1.86	-0.72
lpg0789	alginate O-acetyltransferase AlgI		Named proteins of general function	10.596	8.965	9.793	9.278	1.47E-02	4.26E-01	-1.63	-0.51
lpg0790	L-serine dehydratase (iron, sulfur-dependent) (L-serine d	*sda-2*	Amino Acid Metabolism	10.626	12.681	11.723	13.016	2.86E-03	4.77E-04	2.06	1.29
lpg0790	L-serine dehydratase (iron, sulfur-dependent) (L-serine d	*sda-2*	Amino Acid Metabolism	10.494	12.648	11.460	12.979	5.35E-03	5.91E-04	2.15	1.52
lpg0791	macrophage infectivity potentiator (mip)	*mip*	Toxin production / other pathogen func	14.368	14.354	13.278	13.548	9.81E-01	6.10E-01	-0.01	0.27
lpg0791	macrophage infectivity potentiator (mip)	*mip*	Toxin production / other pathogen func	14.409	14.349	13.289	13.600	9.10E-01	5.50E-01	-0.06	0.31
lpg0792	beta lactamase induction signal transducer AmpG	*ampG*	Transcription factors / DNA binding pro	12.267	9.479	11.329	10.378	3.22E-05	3.79E-02	-2.79	-0.95
lpg0792	beta lactamase induction signal transducer AmpG	*ampG*	Transcription factors / DNA binding pro	12.303	9.452	11.485	10.675	4.57E-06	3.19E-02	-2.85	-0.81
lpg0793	IS1400 transposase, transposase ORFA, COG2801: transposase an		Viral functions / Phage / Transposase	10.310	8.616	10.672	8.769	9.93E-04	1.25E-02	-1.69	-1.90
lpg0793	IS1400 transposase, transposase ORFA, COG2801: transposase an		Viral functions / Phage / Transposase	9.508	7.541	9.355	8.108	1.34E-02	2.27E-02	-1.97	-1.25
lpg0794	ISI400 transposase B		Viral functions / Phage / Transposase	8.126	6.569	9.287	7.839	9.33E-02	7.11E-02	-1.56	-1.45
lpg0794	ISI400 transposase B		Viral functions / Phage / Transposase	8.458	7.688	9.448	8.012	2.46E-01	1.09E-01	-0.77	-1.44
lpg0795	ISI400 transposase B		Viral functions / Phage / Transposase	7.800	8.073	7.121	6.453	8.35E-01	5.42E-01	0.27	-0.67
lpg0795	ISI400 transposase B		Viral functions / Phage / Transposase	6.202	7.924	6.006	7.394	1.97E-01	4.56E-01	1.72	1.39
lpg0796	ORF		ORFs of unknown function (unique)	8.630	9.552	9.439	9.105	1.33E-01	5.11E-01	0.92	-0.33
lpg0796	ORF		ORFs of unknown function (unique)	9.158	9.596	9.501	9.285	4.41E-01	6.64E-01	0.44	-0.22
lpg0797	tRNA-Met		tRNA	10.857	8.545	9.953	9.665	4.53E-03	6.42E-01	-2.31	-0.29
lpg0797	tRNA-Met		tRNA	10.993	8.889	9.919	10.194	2.32E-03	6.88E-01	-2.10	0.27
lpg0798	small ORF (128aa)		ORFs of unknown function (unique)	10.178	11.297	11.276	9.545	5.16E-03	3.80E-03	1.12	-1.73
lpg0798	small ORF (128aa)		ORFs of unknown function (unique)	10.264	11.086	11.211	10.118	3.21E-02	1.77E-01	0.82	-1.09
lpg0799	quinolinate synthetase A (NadA)	*nadA*	Metabolism of Cofactors and Vitamins	10.618	9.803	9.463	9.330	2.50E-02	8.44E-01	-0.81	-0.13
lpg0799	quinolinate synthetase A (NadA)	*nadA*	Metabolism of Cofactors and Vitamins	10.544	10.122	10.037	10.242	4.22E-01	7.39E-01	-0.42	0.21
lpg0800	L-aspartate oxidase	*nadB1*	Amino Acid Metabolism, Metabolism o	13.608	11.965	12.028	12.891	3.13E-02	1.33E-01	-1.64	0.86
lpg0800	L-aspartate oxidase	*nadB1*	Amino Acid Metabolism, Metabolism o	13.558	12.069	11.912	12.806	1.04E-01	1.56E-01	-1.49	0.89
lpg0801	adenylsuccinate lyase		Nucleotide Metabolism, Amino Acid M	12.493	12.744	10.468	13.582	4.03E-01	4.38E-04	0.25	3.11
lpg0801	adenylsuccinate lyase		Nucleotide Metabolism, Amino Acid M	12.451	12.795	10.365	13.598	2.68E-01	1.50E-04	0.34	3.23
lpg0802	sulfate transporter (sulfate permease)		Transport and binding	12.395	14.051	13.429	14.182	7.55E-04	1.25E-01	1.66	0.75
lpg0802	sulfate transporter (sulfate permease)		Transport and binding	12.383	14.015	13.373	14.203	7.04E-04	8.50E-02	1.63	0.83
lpg0803	acyl CoA dehydrogenase, short chain specific		Lipid Metabolism, Metabolism of Com	9.430	9.875	10.182	8.898	5.71E-01	6.78E-02	0.45	-1.28
lpg0803	acyl CoA dehydrogenase, short chain specific		Lipid Metabolism, Metabolism of Com	9.456	10.316	10.102	9.480	2.93E-01	2.79E-01	0.86	-0.62
lpg0804	choloylglycine hydrolase (penicillin acylase)		Protein fate / hydrolases / secretion	9.449	9.021	10.568	8.307	5.00E-01	5.79E-03	-0.43	-2.26
lpg0804	choloylglycine hydrolase (penicillin acylase)		Protein fate / hydrolases / secretion	9.336	8.200	10.485	8.351	1.99E-01	1.04E-02	-1.14	-2.13
lpg0805	phosphoenolpyruvate synthase		Carbohydrate Metabolism, Energy Me	11.830	11.819	10.847	12.091	9.88E-01	2.08E-02	-0.01	1.24
lpg0805	phosphoenolpyruvate synthase		Carbohydrate Metabolism, Energy Me	11.844	11.993	10.710	12.090	8.29E-01	1.92E-02	0.15	1.38
lpg0806	Na+/H+ antiporter		Transport and binding	11.102	9.360	8.996	9.966	1.08E-02	1.08E-01	-1.74	0.97
lpg0806	Na+/H+ antiporter		Transport and binding	10.956	9.954	9.373	10.540	9.82E-07	4.39E-02	-1.00	1.17
lpg0807	nicotinate-nucleotide pyrophosphorylase	*nadC*	Metabolism of Cofactors and Vitamins	10.691	10.551	10.614	10.947	7.79E-01	2.70E-01	-0.14	0.33
lpg0807	nicotinate-nucleotide pyrophosphorylase	*nadC*	Metabolism of Cofactors and Vitamins	11.300	10.784	10.120	10.905	4.36E-01	9.61E-02	-0.52	0.78
lpg0808	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapepti	*murG*	Metabolism of Complex Carbohydrate	11.472	10.081	10.856	10.776	2.54E-04	8.22E-01	-1.39	-0.08
lpg0808	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapepti	*murG*	Metabolism of Complex Carbohydrate	11.276	9.896	10.779	10.779	9.16E-05	1.00E+00	-1.38	0.00
lpg0809	succinyl-diaminopimelate desuccinylase? (peptidase?) (	*dapE*	Amino Acid Metabolism	11.517	11.307	11.294	11.615	5.72E-01	1.11E-01	-0.21	0.32
lpg0809	succinyl-diaminopimelate desuccinylase? (peptidase?) (	*dapE*	Amino Acid Metabolism	11.443	11.403	11.159	11.570	9.10E-01	5.19E-02	-0.04	0.41

lpg0810	small ORF (105aa) competence protein ComEA (DNA uptake and rel		Transport and binding, Transcription fa	12.242	12.495	10.978	13.660	4.82E-01	8.32E-05	0.25	2.68
lpg0810	small ORF (105aa) competence protein ComEA (DNA uptake and rel		Transport and binding, Transcription fa	12.246	12.516	10.748	13.659	4.74E-01	1.45E-04	0.27	2.91
lpg0811	rod shape determining protein MreB (regulator of FtsI)	*mreB*	Cell envelope synthesis, Signal transd	12.422	12.225	12.005	12.575	8.43E-01	3.81E-01	-0.20	0.57
lpg0811	rod shape determining protein MreB (regulator of FtsI)	*mreB*	Cell envelope synthesis, Signal transd	12.620	13.026	12.173	13.307	3.76E-01	1.29E-02	0.41	1.13
lpg0812	rod shape determining protein MreC (cell shape determir	*mreC*	Cell envelope synthesis	11.153	9.669	9.562	11.044	1.28E-04	3.85E-03	-1.48	1.48
lpg0812	rod shape determining protein MreC (cell shape determir	*mreC*	Cell envelope synthesis	11.255	10.086	9.606	11.219	3.54E-03	1.88E-03	-1.17	1.61
lpg0813	rod shape determining protein MreD (cell shape determir	*mreD*	Cell envelope synthesis	10.677	8.939	9.657	8.358	3.07E-02	8.64E-02	-1.74	-1.30
lpg0813	rod shape determining protein MreD (cell shape determir	*mreD*	Cell envelope synthesis	10.273	8.917	9.673	8.726	6.94E-02	1.37E-01	-1.36	-0.95
lpg0814	pseudouridine synthase (ribosomal large subunit pseudouridine synth		DNA/RNA degradation / restriction, Tra	11.298	11.447	10.281	11.407	5.65E-01	1.17E-02	0.15	1.13
lpg0814	pseudouridine synthase (ribosomal large subunit pseudouridine synth		DNA/RNA degradation / restriction, Tra	11.340	11.381	10.091	11.474	7.89E-01	2.19E-03	0.04	1.38
lpg0815	ORF		ORFs of unknown function (unique)	10.075	10.629	9.588	10.006	2.47E-01	2.62E-01	0.55	0.42
lpg0815	ORF		ORFs of unknown function (unique)	10.602	10.809	9.384	10.724	4.18E-01	5.31E-02	0.21	1.34
lpg0816	isocitrate dehydrogenase, NADP-dependent	*icd*	Carbohydrate Metabolism, Metabolism	13.562	13.838	12.832	14.228	9.94E-02	1.20E-04	0.28	1.40
lpg0816	isocitrate dehydrogenase, NADP-dependent	*icd*	Carbohydrate Metabolism, Metabolism	13.556	13.806	12.792	14.204	1.12E-01	1.08E-04	0.25	1.41
lpg0817	conserved hypothetical protein		Unknown / hypothetical proteins	11.556	12.435	12.724	12.477	3.86E-02	3.58E-01	0.88	-0.25
lpg0817	conserved hypothetical protein		Unknown / hypothetical proteins	11.743	13.152	12.803	13.023	3.19E-02	7.15E-01	1.41	0.22
lpg0818	ATP binding protease component ClpA (ATP dependent (	*cl*	Protein fate / hydrolases / secretion	13.158	13.532	15.011	13.582	4.11E-01	6.74E-03	0.37	-1.43
lpg0818	ATP binding protease component ClpA (ATP dependent (	*cl*	Protein fate / hydrolases / secretion	13.125	13.577	14.981	13.595	3.45E-01	8.82E-03	0.45	-1.39
lpg0819	ORF2 transposase		Viral functions / Phage / Transposases	10.259	9.806	10.708	9.869	3.69E-01	6.97E-02	-0.45	-0.84
lpg0819	ORF2 transposase		Viral functions / Phage / Transposases	10.327	10.358	10.903	10.138	9.19E-01	1.24E-01	0.03	-0.77
lpg0820	hypothetical (endonuclease?)		Unknown / hypothetical proteins	10.002	10.774	10.088	10.686	2.12E-02	5.81E-02	0.77	0.60
lpg0820	hypothetical (endonuclease?)		Unknown / hypothetical proteins	10.010	10.732	9.947	10.979	9.24E-02	2.74E-02	0.72	1.03
lpg0821	lipopolysaccharide biosynthesis glycosyltransferase (beta 1,4-glucosy		Metabolism of Complex Carbohydrates	11.571	12.990	9.633	13.936	2.53E-02	3.70E-04	1.42	4.30
lpg0821	lipopolysaccharide biosynthesis glycosyltransferase (beta 1,4-glucosy		Metabolism of Complex Carbohydrates	11.529	13.068	8.839	14.037	1.92E-02	2.34E-04	1.54	5.20
lpg0822	O-antigen biosynthesis protein		Named proteins of general function	10.481	10.394	9.678	10.668	8.18E-01	2.51E-02	-0.09	0.99
lpg0822	O-antigen biosynthesis protein		Named proteins of general function	10.389	10.163	9.291	10.352	6.36E-01	3.33E-02	-0.23	1.06
lpg0823	Neurogenic locus notch protein homolog precursor		Named proteins of general function	11.828	10.539	11.663	9.905	2.79E-03	2.12E-04	-1.29	-1.76
lpg0823	Neurogenic locus notch protein homolog precursor		Named proteins of general function	11.872	10.708	11.768	10.185	5.66E-03	3.34E-04	-1.16	-1.58
lpg0824	rhomboid family protein (integral membrane protein)		Named proteins of general function	9.697	8.658	9.571	8.977	1.20E-01	3.58E-01	-1.04	-0.59
lpg0824	rhomboid family protein (integral membrane protein)		Named proteins of general function	9.469	9.423	9.922	9.747	9.36E-01	6.97E-01	-0.05	-0.17
lpg0825	peptidase, M23/M37 family		Protein fate / hydrolases / secretion	9.966	10.339	10.767	10.597	2.11E-01	6.44E-01	0.37	-0.17
lpg0825	peptidase, M23/M37 family		Protein fate / hydrolases / secretion	9.873	10.351	10.510	10.750	6.52E-02	5.51E-01	0.48	0.24
lpg0826	exonuclease VII, large subunit	*xseA*	DNA/RNA degradation / restriction	9.986	11.511	9.921	11.538	1.60E-02	1.74E-03	1.53	1.62
lpg0826	exonuclease VII, large subunit	*xseA*	DNA/RNA degradation / restriction	10.279	11.479	9.528	11.490	3.84E-03	1.47E-03	1.20	1.96
lpg0827	agglutination protein, COG1538: membrane protein	*tolC*	Named proteins of general function	11.725	11.883	9.893	12.059	7.66E-01	1.25E-03	0.16	2.17
lpg0827	agglutination protein, COG1538: membrane protein	*tolC*	Named proteins of general function	11.834	12.485	9.796	12.418	3.88E-01	9.19E-04	0.65	2.62
lpg0828	periplasmic protein		Named proteins of general function	10.195	9.061	10.223	9.328	1.87E-01	2.70E-02	-1.13	-0.89
lpg0828	periplasmic protein		Named proteins of general function	10.130	9.079	10.097	9.442	1.68E-01	1.57E-01	-1.05	-0.65
lpg0829	two component histidine kinase, GGDEF domain protein/EAL domain		Signal transduction / other regulatory f	9.657	11.558	9.188	9.518	1.03E-07	6.54E-01	1.90	0.33
lpg0829	two component histidine kinase, GGDEF domain protein/EAL domain		Signal transduction / other regulatory f	9.854	11.655	8.883	9.600	2.91E-07	2.34E-01	1.80	0.72
lpg0830	hypothetical protein		Unknown / hypothetical proteins	11.804	11.639	9.991	11.590	7.62E-01	1.65E-02	-0.16	1.60
lpg0830	hypothetical protein		Unknown / hypothetical proteins	11.161	11.898	9.988	11.743	4.00E-01	1.15E-03	0.74	1.76
lpg0831	flavin containing monooxygenae (dimethylaniline monooxygenase)		Named proteins of general function	12.302	12.452	9.984	12.906	8.20E-01	1.47E-03	0.15	2.92
lpg0831	flavin containing monooxygenae (dimethylaniline monooxygenase)		Named proteins of general function	12.488	12.469	10.025	12.956	9.68E-01	3.51E-04	-0.02	2.93
lpg0832	oxidoreductase dehydrogenase, short chain		Named proteins of general function	10.881	11.577	10.905	12.004	1.04E-04	5.91E-04	0.70	1.10
lpg0832	oxidoreductase dehydrogenase, short chain		Named proteins of general function	10.933	11.592	10.659	11.978	7.62E-04	1.04E-03	0.66	1.32
lpg0833	indole-3-glycerol phosphate synthase	*trpC*	Amino Acid Metabolism	10.740	10.474	10.821	12.092	6.30E-01	2.57E-03	-0.27	1.27
lpg0833	indole-3-glycerol phosphate synthase	*trpC*	Amino Acid Metabolism	10.716	10.502	10.766	12.091	7.05E-01	8.68E-03	-0.21	1.32
lpg0834	anthranilate phosphoribosyltransferase	*trpD*	Amino Acid Metabolism	11.929	10.724	10.930	10.807	7.79E-05	7.04E-01	-1.21	-0.12
lpg0834	anthranilate phosphoribosyltransferase	*trpD*	Amino Acid Metabolism	11.959	10.467	10.790	10.757	1.25E-03	9.28E-01	-1.49	-0.03
lpg0835	anthranilate synthase (component II) (para-aminobenzoa	*pabA*	Amino Acid Metabolism	11.480	10.053	9.875	11.385	1.35E-02	1.47E-02	-1.43	1.51
lpg0835	anthranilate synthase (component II) (para-aminobenzoa	*pabA*	Amino Acid Metabolism	11.004	9.732	9.339	11.181	1.34E-01	2.94E-02	-1.27	1.84
lpg0836	ABC transporter, ATP binding protein		Transport and binding	11.295	9.774	10.599	10.413	1.08E-02	4.87E-01	-1.52	-0.19
lpg0836	ABC transporter, ATP binding protein		Transport and binding	10.543	9.436	9.698	10.283	1.83E-01	2.23E-01	-1.11	0.58
lpg0837	conserved hypothetical protein		Unknown / hypothetical proteins	10.763	10.037	10.543	10.435	2.22E-02	7.27E-01	-0.73	-0.11
lpg0837	conserved hypothetical protein		Unknown / hypothetical proteins	10.818	10.158	10.326	10.552	4.89E-02	5.38E-01	-0.66	0.23
lpg0838	conserved hypothetical protein		Unknown / hypothetical proteins	10.872	10.020	10.427	10.254	2.39E-01	6.47E-01	-0.85	-0.17
lpg0838	conserved hypothetical protein		Unknown / hypothetical proteins	10.971	9.686	10.382	10.389	1.35E-01	9.88E-01	-1.29	0.01
lpg0839	hydrolase, HAD superfamily, subfamily III A (low specificity phosphata		Transport and binding, Protein fate / hy	13.329	12.515	13.042	12.372	3.50E-01	2.99E-01	-0.81	-0.67
lpg0839	hydrolase, HAD superfamily, subfamily III A (low specificity phosphata		Transport and binding, Protein fate / hy	13.359	13.141	12.988	13.064	5.38E-01	7.89E-01	-0.22	0.08
lpg0840	polysialic acid capsule expression protein (carbohydrate isomerase) (		Cell envelope synthesis, Metabolism c	11.208	12.197	10.640	12.339	2.71E-04	1.91E-04	0.99	1.70
lpg0840	polysialic acid capsule expression protein (carbohydrate isomerase) (		Cell envelope synthesis, Metabolism c	11.112	12.285	10.761	12.477	1.11E-03	7.65E-05	1.17	1.72
lpg0841	toluene tolerance ABC transporter, ATP binding protein Ttg2A		Detoxification / adaptation	12.451	11.518	13.622	11.021	1.12E-01	4.00E-03	-0.93	-2.60
lpg0841	toluene tolerance ABC transporter, ATP binding protein Ttg2A		Detoxification / adaptation	12.506	11.838	13.671	11.317	1.09E-01	6.15E-04	-0.67	-2.35

lpg0842	toluene tolerance protein Ttg2B		Transport and binding, Detoxification /	11.219	11.169	12.187	10.225	9.27E-01	7.80E-03	-0.05	-1.96
lpg0842	toluene tolerance protein Ttg2B		Transport and binding, Detoxification /	11.179	11.675	12.167	10.752	3.23E-01	1.23E-02	0.50	-1.41
lpg0843	toluene tolerance protein Ttg2C (mce related protein)		Detoxification / adaptation	12.086	11.562	13.429	10.437	7.57E-02	5.80E-06	-0.52	-2.99
lpg0843	toluene tolerance protein Ttg2C (mce related protein)		Detoxification / adaptation	12.190	11.621	13.396	10.908	5.03E-02	6.37E-06	-0.57	-2.49
lpg0844	signal peptide protein (toluene tolerance protein) Ttg2D		Detoxification / adaptation	12.949	12.286	13.294	12.035	4.84E-02	6.39E-06	-0.66	-1.26
lpg0844	signal peptide protein (toluene tolerance protein) Ttg2D		Detoxification / adaptation	12.992	11.974	13.287	12.053	1.32E-01	1.32E-05	-1.02	-1.23
lpg0845	small ORF (93aa) anti sigma B (or F) factor antagonist??	*rsbV*	Transcription factors / DNA binding pro	12.010	10.752	12.372	10.936	5.63E-05	1.10E-04	-1.26	-1.44
lpg0845	small ORF (93aa) anti sigma B (or F) factor antagonist??	*rsbV*	Transcription factors / DNA binding pro	11.974	11.235	12.354	11.287	1.81E-01	1.14E-02	-0.74	-1.07
lpg0846	hypothetical BolA like protein (predicted transcriptional re	*yrbA*	Cell envelope synthesis, Transcription	12.341	11.618	13.947	12.863	2.06E-01	8.79E-02	-0.72	-1.08
lpg0846	hypothetical BolA like protein (predicted transcriptional re	*yrbA*	Cell envelope synthesis, Transcription	12.353	12.113	13.902	13.242	6.83E-01	1.67E-01	-0.24	-0.66
lpg0847	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (3-	*murA*	Metabolism of Complex Carbohydrate	12.556	11.904	14.720	12.704	2.32E-01	2.87E-03	-0.65	-2.02
lpg0847	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (3-	*murA*	Metabolism of Complex Carbohydrate	12.562	12.133	14.730	12.947	4.99E-01	2.05E-02	-0.43	-1.78
lpg0848	conserved hypothetical protein TIGR00486		Unknown / hypothetical proteins	10.712	9.474	12.628	9.898	3.72E-02	4.41E-04	-1.24	-2.73
lpg0848	conserved hypothetical protein TIGR00486		Unknown / hypothetical proteins	10.785	9.735	12.660	10.148	3.88E-02	9.17E-04	-1.05	-2.51
lpg0849	ABC transporter, ATP binding protein (lipoprotein releasing system)		Transport and binding	9.740	9.776	9.956	10.303	9.33E-01	3.34E-01	0.04	0.35
lpg0849	ABC transporter, ATP binding protein (lipoprotein releasing system)		Transport and binding	9.996	9.873	9.680	10.048	7.43E-01	5.05E-01	-0.12	0.37
lpg0850	ABC transporter, permease protein (lipoprotein releasing system)		Transport and binding	10.014	8.724	10.069	8.238	6.20E-02	1.41E-01	-1.29	-1.83
lpg0850	ABC transporter, permease protein (lipoprotein releasing system)		Transport and binding	9.890	8.379	10.368	9.396	4.68E-02	3.86E-02	-1.51	-0.97
lpg0851	membrane fusion protein (HlyD family secretion protein) secretion of		Protein fate / hydrolases / secretion	12.110	12.825	11.064	12.780	2.02E-02	6.44E-05	0.71	1.72
lpg0851	membrane fusion protein (HlyD family secretion protein) secretion of		Protein fate / hydrolases / secretion	12.216	12.936	11.159	12.944	3.67E-04	2.46E-05	0.72	1.79
lpg0852	ORF		ORFs of unknown function (unique)	12.325	11.349	11.225	11.569	1.39E-01	3.54E-01	-0.98	0.34
lpg0852	ORF		ORFs of unknown function (unique)	12.402	11.447	11.071	11.625	8.52E-02	1.60E-01	-0.95	0.55
lpg0853	transcriptional regulator FleQ (polar flagellar protein FlaK	*fleQ*	Chemotaxis / motility / cell division, Tra	11.015	9.264	10.121	7.312	5.85E-04	5.81E-04	-1.75	-2.81
lpg0853	transcriptional regulator FleQ (polar flagellar protein FlaK	*fleQ*	Chemotaxis / motility / cell division, Tra	10.946	9.623	10.353	7.954	7.25E-03	2.19E-02	-1.32	-2.40
lpg0854	ORF		ORFs of unknown function (unique)	13.094	12.513	14.111	11.533	1.63E-01	6.64E-04	-0.58	-2.58
lpg0854	ORF		ORFs of unknown function (unique)	13.043	12.495	14.069	11.573	2.04E-01	1.32E-03	-0.55	-2.50
lpg0855	signal peptide peptidase SppA (protease IV) (SohB protein)		Protein fate / hydrolases / secretion	11.032	10.417	8.651	11.011	3.64E-01	6.85E-03	-0.61	2.36
lpg0855	signal peptide peptidase SppA (protease IV) (SohB protein)		Protein fate / hydrolases / secretion	11.070	10.129	8.382	11.097	1.84E-01	4.81E-03	-0.94	2.72
lpg0856	heme exporter protein CcmA (ATP binding protein of hem	*ccmA*	Transport and binding	11.833	12.237	10.870	12.267	8.81E-02	2.43E-03	0.40	1.40
lpg0856	heme exporter protein CcmA (ATP binding protein of hem	*ccmA*	Transport and binding	11.855	12.221	10.897	12.330	1.36E-01	9.14E-04	0.37	1.43
lpg0857	heme exporter protein CcmB	*ccmB*	Transport and binding	9.976	9.043	9.016	9.397	1.46E-01	3.10E-01	-0.93	0.38
lpg0857	heme exporter protein CcmB	*ccmB*	Transport and binding	10.312	10.169	8.799	10.329	8.79E-01	1.78E-01	-0.14	1.53
lpg0858	heme exporter protein CcmC	*ccmC*	Transport and binding	10.423	11.696	8.775	11.470	5.07E-02	9.71E-04	1.27	2.70
lpg0858	heme exporter protein CcmC	*ccmC*	Transport and binding	10.837	11.709	8.574	11.475	1.26E-02	1.17E-03	0.87	2.90
lpg0859	cytochrome c-type biogenesis protein CcmD (heme exporter protein		Transport and binding, Energy Metabo	12.683	13.079	12.006	13.168	1.33E-02	4.16E-04	0.40	1.16
lpg0859	cytochrome c-type biogenesis protein CcmD (heme exporter protein		Transport and binding, Energy Metabo	12.701	13.059	11.959	13.158	4.44E-02	1.43E-04	0.36	1.20
lpg0860	cytochrome c-type biogenesis protein CcmE	*ccmE*	Transport and binding, Energy Metabo	11.262	10.609	11.062	10.260	3.88E-05	5.90E-02	-0.65	-0.80
lpg0860	cytochrome c-type biogenesis protein CcmE	*ccmE*	Transport and binding, Energy Metabo	11.204	10.802	11.083	10.982	2.99E-01	7.39E-01	-0.40	-0.10
lpg0861	cytochrome c-type biogenesis protein CcmF	*ccmF*	Energy Metabolism	10.613	9.352	7.981	9.963	2.34E-03	6.96E-03	-1.26	1.98
lpg0861	cytochrome c-type biogenesis protein CcmF	*ccmF*	Energy Metabolism	10.842	9.565	7.784	10.407	1.08E-05	3.39E-02	-1.28	2.62
lpg0862	cytochrome c biogenesis protein CcmG	*dsbE*	Protein fate / hydrolases / secretion, E	11.350	9.505	11.229	9.889	2.11E-03	5.63E-03	-1.84	-1.34
lpg0862	cytochrome c biogenesis protein CcmG	*dsbE*	Protein fate / hydrolases / secretion, E	11.453	10.551	11.256	10.596	2.08E-01	3.97E-01	-0.90	-0.66
lpg0863	c-type cytochrome biogenesis protein CcmH		Energy Metabolism	11.266	10.760	10.179	10.864	2.61E-01	1.66E-01	-0.51	0.68
lpg0863	c-type cytochrome biogenesis protein CcmH		Energy Metabolism	11.313	10.535	9.879	10.846	2.04E-02	1.24E-01	-0.78	0.97
lpg0864	cytochrome c type biogenesis protein CcmH	*cycH*	Energy Metabolism	10.615	14.471	9.453	13.730	4.87E-06	1.58E-06	3.86	4.28
lpg0864	cytochrome c type biogenesis protein CcmH	*cycH*	Energy Metabolism	10.645	14.453	9.280	13.692	2.12E-06	3.56E-06	3.81	4.41
lpg0865	outer membrane lipoprotein		Named proteins of general function	14.217	14.258	12.943	14.227	9.69E-01	1.62E-01	0.04	1.28
lpg0865	outer membrane lipoprotein		Named proteins of general function	14.311	14.700	12.942	14.780	5.95E-01	4.13E-03	0.39	1.84
lpg0866	3-methyladenine DNA glycosylase		DNA/RNA degradation / restriction	10.000	9.254	9.576	9.004	7.70E-02	3.94E-01	-0.75	-0.57
lpg0866	3-methyladenine DNA glycosylase		DNA/RNA degradation / restriction	9.903	9.367	9.777	9.232	5.10E-01	2.42E-01	-0.54	-0.55
lpg0867	ATP-dependent DNA helicase RecQ	*recQ*	Replication and Repair	10.990	10.716	11.561	11.078	5.98E-01	1.84E-01	-0.27	-0.48
lpg0867	ATP-dependent DNA helicase RecQ	*recQ*	Replication and Repair	11.037	10.302	11.273	11.189	1.15E-01	8.48E-01	-0.74	-0.08
lpg0868	acyl CoA dehydrogenase, short chain specific		Lipid Metabolism, Amino Acid Metabol	11.591	11.761	10.406	11.702	8.60E-01	1.70E-01	0.17	1.30
lpg0868	acyl CoA dehydrogenase, short chain specific		Lipid Metabolism, Amino Acid Metabol	11.645	12.345	10.507	12.327	2.16E-01	2.37E-03	0.70	1.82
lpg0869	3-hydroxyisobutyryl Coenzyme A hydrolase (crotonase) (enoyl CoA h		Carbohydrate Metabolism	9.906	11.370	9.680	11.792	1.64E-01	6.18E-03	1.46	2.11
lpg0869	3-hydroxyisobutyryl Coenzyme A hydrolase (crotonase) (enoyl CoA h		Carbohydrate Metabolism	10.113	12.225	9.565	12.254	1.79E-04	1.18E-04	2.11	2.69
lpg0870	3-hydroxyisobutyryl Coenzyme A hydrolase (enoyl CoA hydratase/iso		Lipid Metabolism, Amino Acid Metabol	12.986	13.256	12.601	13.009	2.39E-01	3.86E-02	0.27	0.41
lpg0870	3-hydroxyisobutyryl Coenzyme A hydrolase (enoyl CoA hydratase/iso		Lipid Metabolism, Amino Acid Metabol	12.952	13.151	12.603	13.031	3.87E-01	9.80E-04	0.20	0.43
lpg0871	ORF		ORFs of unknown function (unique)	9.206	9.375	11.333	10.328	8.17E-01	4.82E-02	0.17	-1.01
lpg0871	ORF		ORFs of unknown function (unique)	8.962	9.202	10.948	10.183	7.85E-01	1.88E-01	0.24	-0.77
lpg0872	peptide chain release factor 3	*prfC*	Translation	12.743	11.969	10.939	12.915	3.82E-02	1.01E-03	-0.77	1.98
lpg0872	peptide chain release factor 3	*prfC*	Translation	12.849	12.008	10.884	12.939	9.53E-03	1.57E-03	-0.84	2.06
lpg0873	small ORF (141aa) (60 kDa chaperonin features?)		Protein fate / hydrolases / secretion	14.002	13.218	13.749	13.930	3.48E-01	7.85E-01	-0.78	0.18
lpg0873	small ORF (141aa) (60 kDa chaperonin features?)		Protein fate / hydrolases / secretion	13.893	13.869	13.823	14.480	8.28E-01	6.17E-03	-0.02	0.66

lpg0874	NAD(P) transhydrogenase (beta subunit)	*pntB*	Metabolism of Cofactors and Vitamins	10.252	10.262	10.478	8.339	9.72E-01	1.63E-03	0.01	-2.14
lpg0874	NAD(P) transhydrogenase (beta subunit)	*pntB*	Metabolism of Cofactors and Vitamins	10.045	10.202	10.442	8.876	6.06E-01	1.29E-03	0.16	-1.57
lpg0875	transmembrane NAD(P) transhydrogenase (alpha subun	*pntAb2*	Metabolism of Cofactors and Vitamins	11.351	11.020	11.864	8.944	3.31E-01	6.85E-06	-0.33	-2.92
lpg0875	transmembrane NAD(P) transhydrogenase (alpha subun	*pntAb2*	Metabolism of Cofactors and Vitamins	11.308	11.259	11.818	9.454	8.24E-01	1.03E-05	-0.05	-2.36
lpg0876	alanine dehydrogenase and pyridine nucleotide transhyd	*pntAa*	Metabolism of Cofactors and Vitamins	10.872	11.757	11.306	9.586	8.94E-06	6.16E-04	0.89	-1.72
lpg0876	alanine dehydrogenase and pyridine nucleotide transhyd	*pntAa*	Metabolism of Cofactors and Vitamins	10.861	11.728	11.490	10.836	7.39E-04	7.17E-02	0.87	-0.65
lpg0877	hypothetical transporter		Named proteins of general function	11.925	14.916	12.035	13.955	2.58E-06	4.88E-05	2.99	1.92
lpg0877	hypothetical transporter		Named proteins of general function	11.975	14.969	12.090	14.179	3.56E-06	5.01E-06	2.99	2.09
lpg0878	small ORF (99aa)		ORFs of unknown function (unique)	10.622	9.198	13.988	8.507	1.22E-01	1.06E-04	-1.42	-5.48
lpg0878	small ORF (99aa)		ORFs of unknown function (unique)	10.555	9.639	13.944	8.538	2.20E-01	3.63E-04	-0.92	-5.41
lpg0879	two component response regulator with GGDEF domain (regulatory c		Signal transduction / other regulatory f	9.690	9.415	11.478	9.438	7.10E-01	1.41E-02	-0.27	-2.04
lpg0879	two component response regulator with GGDEF domain (regulatory c		Signal transduction / other regulatory f	10.008	10.475	11.812	10.143	4.41E-01	2.63E-02	0.47	-1.67
lpg0880	ORF		ORFs of unknown function (unique)	12.144	12.176	9.711	11.847	9.59E-01	7.58E-03	0.03	2.14
lpg0880	ORF		ORFs of unknown function (unique)	11.877	12.161	9.403	11.686	7.55E-01	7.46E-03	0.28	2.28
lpg0881	tRNA-Ser		tRNA	10.836	11.697	11.397	11.401	3.19E-01	9.97E-01	0.86	0.00
lpg0881	tRNA-Ser		tRNA	11.261	10.861	11.074	11.249	5.24E-01	8.53E-01	-0.40	0.18
lpg0882	small ORF (144aa)		ORFs of unknown function (unique)	11.962	12.356	12.553	12.281	2.19E-01	4.78E-01	0.39	-0.27
lpg0882	small ORF (144aa)		ORFs of unknown function (unique)	11.950	12.330	12.534	12.411	2.44E-01	7.29E-01	0.38	-0.12
lpg0883	small ORF (148aa)		ORFs of unknown function (unique)	11.562	12.245	12.068	12.014	1.12E-01	8.69E-01	0.68	-0.05
lpg0883	small ORF (148aa)		ORFs of unknown function (unique)	11.569	12.176	12.023	12.018	1.66E-01	9.88E-01	0.61	-0.01
lpg0884	ORF hypothetical?		Unknown / hypothetical proteins	7.276	7.693	6.988	4.766	6.24E-01	1.66E-01	0.42	-2.22
lpg0884	ORF hypothetical?		Unknown / hypothetical proteins	7.577	5.569	8.308	7.526	1.55E-01	4.95E-01	-2.01	-0.78
lpg0885	glycosyl hydrolase (beta-hexosaminidase A) (beta-N-acetylglucosami		Metabolism of Complex Carbohydrate	12.893	11.711	12.028	12.455	5.47E-03	4.67E-01	-1.18	0.43
lpg0885	glycosyl hydrolase (beta-hexosaminidase A) (beta-N-acetylglucosami		Metabolism of Complex Carbohydrate	12.911	11.330	12.041	12.551	9.32E-03	3.32E-01	-1.58	0.51
lpg0886	sodium:dicarboxylate symporter (neutral amino acid (glutamate) trans		Transport and binding	11.201	10.741	10.662	10.314	1.51E-02	1.74E-01	-0.46	-0.35
lpg0886	sodium:dicarboxylate symporter (neutral amino acid (glutamate) trans		Transport and binding	11.281	10.789	10.572	10.377	2.32E-02	5.22E-01	-0.49	-0.19
lpg0887	N-succinyl-diaminopimelate desuccinylase	*dapE*	Amino Acid Metabolism	14.037	15.496	14.673	15.670	1.09E-05	4.09E-03	1.46	1.00
lpg0887	N-succinyl-diaminopimelate desuccinylase	*dapE*	Amino Acid Metabolism	14.082	15.529	14.671	15.804	2.11E-05	1.64E-03	1.45	1.13
lpg0888	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransf	*dapD*	Amino Acid Metabolism	11.938	11.724	10.807	12.571	5.82E-01	5.27E-05	-0.21	1.76
lpg0888	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransf	*dapD*	Amino Acid Metabolism	11.959	11.395	10.583	12.438	2.21E-01	3.48E-04	-0.56	1.85
lpg0889	acyltransferase (endonuclease?)		Named proteins of general function	11.354	11.555	10.557	11.997	3.68E-01	4.93E-03	0.20	1.44
lpg0889	acyltransferase (endonuclease?)		Named proteins of general function	11.308	11.605	10.177	12.078	1.92E-01	1.45E-02	0.30	1.90
lpg0890	cystathionine beta-lyase (cystathionine gamma lyase)	*metC*	Amino Acid Metabolism, Metabolism o	11.027	12.181	10.992	12.353	4.52E-02	1.83E-05	1.15	1.36
lpg0890	cystathionine beta-lyase (cystathionine gamma lyase)	*metC*	Amino Acid Metabolism, Metabolism o	11.200	12.119	10.841	12.366	3.32E-02	2.07E-06	0.92	1.52
lpg0891	sensory box protein/GGDEF/EAL domains		Signal transduction / other regulatory f	6.816	9.234	8.153	10.368	2.81E-03	1.65E-02	2.42	2.22
lpg0891	sensory box protein/GGDEF/EAL domains		Signal transduction / other regulatory f	5.366	9.263	7.613	10.055	2.06E-04	3.75E-02	3.90	2.44
lpg0892	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)		Amino Acid Metabolism	11.131	10.674	12.830	9.813	4.51E-01	1.55E-04	-0.46	-3.02
lpg0892	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)		Amino Acid Metabolism	11.107	10.830	12.777	9.955	5.88E-01	3.69E-04	-0.28	-2.82
lpg0893	hypothetical		Unknown / hypothetical proteins	12.851	10.107	13.893	9.039	3.36E-04	5.84E-05	-2.74	-4.85
lpg0893	hypothetical		Unknown / hypothetical proteins	12.857	10.341	13.911	9.895	3.95E-05	1.60E-06	-2.52	-4.02
lpg0894	cytokinin oxidase (cytokinin dehydrogenase)		Named proteins of general function	9.885	8.985	10.396	8.922	1.82E-01	1.43E-01	-0.90	-1.47
lpg0894	cytokinin oxidase (cytokinin dehydrogenase)		Named proteins of general function	9.645	9.703	10.123	9.783	9.38E-01	7.33E-01	0.06	-0.34
lpg0895	ORF		ORFs of unknown function (unique)	10.424	10.091	10.146	9.963	2.73E-01	6.08E-01	-0.33	-0.18
lpg0895	ORF		ORFs of unknown function (unique)	10.144	9.929	9.485	9.614	6.44E-01	8.12E-01	-0.21	0.13
lpg0896	lipoprotein (enhanced entry protein EnhC?) COG0790		Named proteins of general function	10.286	12.390	9.820	12.258	1.09E-04	2.28E-05	2.10	2.44
lpg0896	lipoprotein (enhanced entry protein EnhC?) COG0790		Named proteins of general function	10.457	12.307	9.698	12.240	2.13E-05	1.06E-06	1.85	2.54
lpg0897	Na/Ca antiporter (sodium/calcium exchange protein)		Transport and binding	9.960	10.045	10.459	9.653	8.75E-01	1.65E-01	0.09	-0.81
lpg0897	Na/Ca antiporter (sodium/calcium exchange protein)		Transport and binding	10.036	10.371	9.962	10.172	5.68E-01	7.42E-01	0.33	0.21
lpg0898	hypothetical	*ceg18*	Unknown / hypothetical proteins	14.437	14.235	14.084	13.685	7.29E-01	5.77E-01	-0.20	-0.40
lpg0898	hypothetical	*ceg18*	Unknown / hypothetical proteins	14.573	14.523	14.076	14.220	9.13E-01	5.95E-01	-0.05	0.14
lpg0899	A/G specific adenine glycosylase		DNA/RNA degradation / restriction	9.713	8.636	9.835	7.714	7.52E-03	1.07E-02	-1.08	-2.12
lpg0899	A/G specific adenine glycosylase		DNA/RNA degradation / restriction	9.430	8.238	9.015	7.877	3.65E-03	6.22E-02	-1.19	-1.14
lpg0900	hypothetical (AsmA?) (outer membrane assembly protein) LPS bioge		Unknown / hypothetical proteins	11.807	10.680	9.372	10.929	1.90E-01	3.59E-02	-1.13	1.56
lpg0900	hypothetical (AsmA?) (outer membrane assembly protein) LPS bioge		Unknown / hypothetical proteins	11.673	10.436	8.782	11.493	1.05E-01	7.10E-03	-1.24	2.71
lpg0901	hypothetical protein NMA0899		Named proteins of general function	10.757	8.884	13.454	8.738	5.29E-02	1.19E-03	-1.87	-4.72
lpg0901	hypothetical protein NMA0899		Named proteins of general function	10.929	10.624	13.572	9.429	6.93E-01	1.29E-03	-0.30	-4.14
lpg0902	ORF		ORFs of unknown function (unique)	10.347	10.515	13.955	9.245	8.51E-01	7.92E-04	0.17	-4.71
lpg0902	ORF		ORFs of unknown function (unique)	10.265	10.520	13.906	9.279	7.80E-01	2.08E-03	0.26	-4.63
lpg0903	DegP protease (Do-like, S2-serine-like) (periplasmic serine protease		Protein fate / hydrolases / secretion	12.133	12.771	12.684	11.785	5.06E-01	1.67E-01	0.64	-0.90
lpg0903	DegP protease (Do-like, S2-serine-like) (periplasmic serine protease		Protein fate / hydrolases / secretion	12.100	13.212	12.697	12.240	3.16E-02	5.71E-02	1.11	-0.46
lpg0904	hydrolase, isochorismatase family		Metabolism of Cofactors and Vitamins	11.554	10.915	11.658	10.548	2.06E-02	2.40E-03	-0.64	-1.11
lpg0904	hydrolase, isochorismatase family		Metabolism of Cofactors and Vitamins	11.435	10.901	11.457	10.542	9.16E-02	2.52E-02	-0.53	-0.92
lpg0905	3-oxoacyl (acyl carrier protein) reductase (short chain dehydrogenase		Lipid Metabolism, Amino Acid Metabol	12.731	12.542	12.068	12.210	5.85E-01	4.32E-01	-0.19	0.14
lpg0905	3-oxoacyl (acyl carrier protein) reductase (short chain dehydrogenase		Lipid Metabolism, Amino Acid Metabol	12.698	12.795	12.014	12.377	6.29E-01	2.05E-02	0.10	0.36

lpg0906	hypothetical?		Chemotaxis / motility / cell division	10.164	10.034	12.176	9.299	7.78E-01	3.13E-04	-0.13	-2.88
lpg0906	hypothetical?		Chemotaxis / motility / cell division	10.156	9.488	12.152	9.348	2.36E-01	9.91E-04	-0.67	-2.80
lpg0907	negative regulator of flagellin synthesis (anti sigma factor 28 FlgM)		Chemotaxis / motility / cell division, Sig	9.487	11.673	11.830	10.536	1.14E-02	1.75E-01	2.19	-1.29
lpg0907	negative regulator of flagellin synthesis (anti sigma factor 28 FlgM)		Chemotaxis / motility / cell division, Sig	9.385	11.624	11.673	10.634	9.57E-03	3.24E-01	2.24	-1.04
lpg0908	flagella basal body P-ring formation protein FlgA		Chemotaxis / motility / cell division	10.687	10.207	11.910	9.497	1.58E-01	8.70E-04	-0.48	-2.41
lpg0908	flagella basal body P-ring formation protein FlgA		Chemotaxis / motility / cell division	10.603	10.497	11.674	9.434	8.59E-01	1.34E-02	-0.11	-2.24
lpg0909	cytochrome c5		Named proteins of general function	10.362	10.318	10.513	11.209	9.16E-01	2.79E-02	-0.04	0.70
lpg0909	cytochrome c5		Named proteins of general function	10.434	10.232	10.310	11.094	6.48E-01	1.22E-01	-0.20	0.78
lpg0910	enhanced entry protein EnhA	*enhA*	Toxin production / other pathogen func	11.015	9.940	14.640	11.002	2.97E-01	6.60E-03	-1.07	-3.64
lpg0910	enhanced entry protein EnhA	*enhA*	Toxin production / other pathogen func	11.015	9.930	14.277	10.665	3.43E-01	1.40E-02	-1.08	-3.61
lpg0911	Bvg accessory factor (transcriptional regulatory protein) (32 kDa repli		Transcription factors / DNA binding pro	10.760	11.260	10.662	11.562	2.11E-01	1.58E-02	0.50	0.90
lpg0911	Bvg accessory factor (transcriptional regulatory protein) (32 kDa repli		Transcription factors / DNA binding pro	10.740	11.334	10.620	11.888	6.26E-02	6.06E-04	0.59	1.27
lpg0912	small ORF (35aa)		ORFs of unknown function (unique)	10.716	10.368	9.898	10.711	4.31E-01	2.20E-01	-0.35	0.81
lpg0912	small ORF (35aa)		ORFs of unknown function (unique)	10.606	10.198	9.825	10.760	3.41E-01	1.43E-01	-0.41	0.94
lpg0913	MraZ protein		Named proteins of general function	12.420	12.803	11.715	13.319	2.40E-01	6.43E-05	0.38	1.60
lpg0913	MraZ protein		Named proteins of general function	12.419	12.764	11.697	13.330	2.98E-01	3.38E-05	0.34	1.63
lpg0914	S-adenosylmethyl transferase MraW	*mraW*	Chemotaxis / motility / cell division	12.196	12.146	12.611	12.149	7.82E-01	5.59E-02	-0.05	-0.46
lpg0914	S-adenosylmethyl transferase MraW	*mraW*	Chemotaxis / motility / cell division	12.229	12.215	12.606	12.361	9.40E-01	2.74E-01	-0.01	-0.25
lpg0915	cell division transmembrane protein FtsL		Chemotaxis / motility / cell division	12.032	11.875	12.808	10.916	4.36E-01	2.28E-05	-0.16	-1.89
lpg0915	cell division transmembrane protein FtsL		Chemotaxis / motility / cell division	11.909	11.798	12.747	10.924	7.04E-01	1.96E-05	-0.11	-1.82
lpg0916	penicillin binding protein 3 (transpeptidase) (cell division	*pbpB*	Cell envelope synthesis, Metabolism o	10.236	9.303	8.543	9.954	9.00E-02	5.05E-02	-0.93	1.41
lpg0916	penicillin binding protein 3 (transpeptidase) (cell division	*pbpB*	Cell envelope synthesis, Metabolism o	10.405	9.868	8.419	10.088	1.74E-01	3.76E-02	-0.54	1.67
lpg0917	UDP-N-acetylmuramyl-tripeptide synthetase MurE (meso	*murE*	Amino Acid Metabolism, Metabolism o	10.635	10.890	11.256	11.442	5.60E-01	5.15E-01	0.25	0.19
lpg0917	UDP-N-acetylmuramyl-tripeptide synthetase MurE (meso	*murE*	Amino Acid Metabolism, Metabolism o	10.544	10.825	11.308	11.526	5.57E-01	4.84E-01	0.28	0.22
lpg0918	erythronate-4-phosphate dehydrogenase		Metabolism of Cofactors and Vitamins	11.529	10.494	10.156	11.129	1.09E-03	1.26E-02	-1.04	0.97
lpg0918	erythronate-4-phosphate dehydrogenase		Metabolism of Cofactors and Vitamins	11.535	10.714	10.131	11.172	6.89E-04	4.70E-02	-0.82	1.04
lpg0919	transmembrane protein (Zn dependent protease) (membrane metallo		Protein fate / hydrolases / secretion	10.283	9.799	9.479	9.835	3.84E-01	6.65E-01	-0.48	0.36
lpg0919	transmembrane protein (Zn dependent protease) (membrane metallo		Protein fate / hydrolases / secretion	10.026	10.001	8.928	10.114	9.57E-01	2.71E-01	-0.02	1.19
lpg0920	phosphatidylglycerophosphatase B (Pap2)		Metabolism of Complex Lipids	12.045	12.072	10.027	11.804	9.48E-01	1.37E-03	0.03	1.78
lpg0920	phosphatidylglycerophosphatase B (Pap2)		Metabolism of Complex Lipids	11.908	12.059	9.789	11.713	7.63E-01	6.89E-03	0.15	1.92
lpg0921	ORF		ORFs of unknown function (unique)	11.842	10.569	10.173	9.374	1.62E-02	1.06E-01	-1.27	-0.80
lpg0921	ORF		ORFs of unknown function (unique)	11.865	10.392	10.003	9.485	8.56E-03	3.14E-01	-1.47	-0.52
lpg0922	electron transfer flavoprotein, beta subunit	*etfB*	Energy Metabolism	13.322	12.546	11.421	13.654	1.67E-01	1.81E-03	-0.78	2.23
lpg0922	electron transfer flavoprotein, beta subunit	*etfB*	Energy Metabolism	12.957	12.647	11.055	13.716	7.55E-01	1.67E-03	-0.31	2.66
lpg0923	electron transfer flavoprotein, alpha subunit	*etfA-2*	Energy Metabolism	12.304	11.652	10.581	12.494	2.55E-01	9.98E-03	-0.65	1.91
lpg0923	electron transfer flavoprotein, alpha subunit	*etfA-2*	Energy Metabolism	12.223	11.629	10.341	12.438	3.60E-01	7.74E-03	-0.59	2.10
lpg0924	alanine dehydrogenase	*ald*	Energy Metabolism	13.154	13.118	10.455	13.056	9.64E-01	5.65E-03	-0.04	2.60
lpg0924	alanine dehydrogenase	*ald*	Energy Metabolism	13.151	13.135	10.154	13.090	9.82E-01	1.29E-02	-0.02	2.94
lpg0925	penicillin binding protein 1A (transpeptidase) (peptidogly	*ponA*	Cell envelope synthesis	10.505	10.263	9.632	10.423	4.34E-01	1.10E-01	-0.24	0.79
lpg0925	penicillin binding protein 1A (transpeptidase) (peptidogly	*ponA*	Cell envelope synthesis	10.778	10.432	9.428	10.307	2.90E-01	6.29E-02	-0.35	0.88
lpg0926	ORF		ORFs of unknown function (unique)	14.245	15.704	13.776	14.914	5.51E-05	2.57E-04	1.46	1.14
lpg0926	ORF		ORFs of unknown function (unique)	14.292	15.691	13.763	14.943	5.57E-05	1.68E-04	1.40	1.18
lpg0927	type IV pilus biogenesis protein PilM	*pilM*	Transport and binding	11.634	11.182	11.303	10.823	2.53E-01	1.83E-01	-0.45	-0.48
lpg0927	type IV pilus biogenesis protein PilM	*pilM*	Transport and binding	11.533	11.278	11.117	10.744	5.91E-01	3.65E-01	-0.26	-0.37
lpg0928	type IV pilus biogenesis protein PilN	*pilN*	Transport and binding	9.393	9.687	8.966	9.031	7.00E-01	9.41E-01	0.29	0.06
lpg0928	type IV pilus biogenesis protein PilN	*pilN*	Transport and binding	9.352	9.381	8.037	8.390	9.56E-01	6.81E-01	0.03	0.35
lpg0929	type IV pilus biogenesis protein PilO (membrane protein)	*pilO*	Transport and binding	11.031	9.950	9.428	10.145	2.97E-02	1.16E-01	-1.08	0.72
lpg0929	type IV pilus biogenesis protein PilO (membrane protein)	*pilO*	Transport and binding	10.909	10.291	9.016	10.346	1.63E-01	1.10E-01	-0.62	1.33
lpg0930	type IV pilus biogenesis protein PilP (lipoprotein)	*pilP*	Transport and binding	11.333	10.237	11.686	10.547	4.84E-02	1.32E-02	-1.10	-1.14
lpg0930	type IV pilus biogenesis protein PilP (lipoprotein)	*pilP*	Transport and binding	11.321	11.014	10.923	10.961	2.44E-01	9.53E-01	-0.31	0.04
lpg0931	type IV pilus biogenesis protein PilQ (fimbrial type 4-asse	*pilQ*	Transport and binding	10.839	12.163	10.565	9.795	9.15E-04	1.55E-01	1.32	-0.77
lpg0931	type IV pilus biogenesis protein PilQ (fimbrial type 4-asse	*pilQ*	Transport and binding	11.061	11.949	10.331	9.562	4.38E-02	1.72E-01	0.89	-0.77
lpg0932	shikimate kinase		Amino Acid Metabolism	11.527	11.072	11.253	10.601	2.75E-01	1.60E-01	-0.46	-0.65
lpg0932	shikimate kinase		Amino Acid Metabolism	11.602	11.007	10.973	10.698	2.57E-01	6.94E-01	-0.59	-0.28
lpg0933	3-dehydroquinate synthetase	*aroB*	Amino Acid Metabolism	10.485	11.551	9.789	9.638	1.02E-02	8.25E-01	1.07	-0.15
lpg0933	3-dehydroquinate synthetase	*aroB*	Amino Acid Metabolism	10.087	9.706	9.321	9.678	7.31E-01	7.08E-01	-0.38	0.36
lpg0934	DamX-related protein		Chemotaxis / motility / cell division	10.744	9.239	9.661	9.098	4.28E-02	2.54E-01	-1.51	-0.56
lpg0934	DamX-related protein		Chemotaxis / motility / cell division	10.793	9.514	9.488	9.277	2.05E-02	5.68E-01	-1.28	-0.21
lpg0935	universal stress protein A (UspA)		Detoxification / adaptation	11.629	10.475	12.675	8.676	1.29E-01	3.32E-02	-1.15	-4.00
lpg0935	universal stress protein A (UspA)		Detoxification / adaptation	11.778	10.933	12.784	9.525	2.06E-01	1.96E-03	-0.85	-3.26
lpg0936	riboflavin biosynthesis RibF (riboflavin kinase/FMN aden	*ribF*	Metabolism of Cofactors and Vitamins	10.024	10.527	9.065	10.678	3.86E-01	5.00E-02	0.50	1.61
lpg0936	riboflavin biosynthesis RibF (riboflavin kinase/FMN aden	*ribF*	Metabolism of Cofactors and Vitamins	10.315	11.263	9.415	11.262	3.44E-01	5.66E-02	0.95	1.85
lpg0937	isoleucyl tRNA synthetase	*ileS*	Amino Acid Metabolism, Translation	9.848	10.092	10.849	9.786	7.84E-02	5.95E-03	0.24	-1.06
lpg0937	isoleucyl tRNA synthetase	*ileS*	Amino Acid Metabolism, Translation	9.729	10.288	10.426	10.070	5.75E-02	4.77E-01	0.56	-0.36

lpg0938	lipoprotein signal peptidase	*lspA*	Protein fate / hydrolases / secretion	12.210	11.227	11.138	11.136	7.46E-02	9.97E-01	-0.98	0.00
lpg0938	lipoprotein signal peptidase	*lspA*	Protein fate / hydrolases / secretion	12.239	11.743	11.260	11.826	1.25E-02	1.21E-01	-0.50	0.57
lpg0939	2-dehydro-3-deoxy-phosphogluconate aldolase	*eda*	Carbohydrate Metabolism, Amino Acid	12.620	13.983	11.489	12.765	4.66E-04	1.72E-06	1.36	1.28
lpg0939	2-dehydro-3-deoxy-phosphogluconate aldolase	*eda*	Carbohydrate Metabolism, Amino Acid	12.334	13.935	11.388	12.715	1.94E-03	4.30E-06	1.60	1.33
lpg0940	LidA (translocated substrate of Dot/Icm system) (Uso1 pr	*lidA*	Toxin production / other pathogen func	11.097	12.086	13.320	11.189	2.43E-02	1.30E-03	0.99	-2.13
lpg0940	LidA (translocated substrate of Dot/Icm system) (Uso1 pr	*lidA*	Toxin production / other pathogen func	11.091	11.972	13.275	11.293	3.56E-02	1.62E-03	0.88	-1.98
lpg0941	ORF		ORFs of unknown function (unique)	8.801	9.666	8.571	11.338	2.41E-01	4.03E-03	0.86	2.77
lpg0941	ORF		ORFs of unknown function (unique)	8.926	8.413	6.950	10.000	3.44E-01	2.71E-02	-0.51	3.05
lpg0942	GTP-binding protein Era	*era*	Signal transduction / other regulatory f	10.156	10.400	9.201	9.628	6.03E-01	4.47E-01	0.24	0.43
lpg0942	GTP-binding protein Era	*era*	Signal transduction / other regulatory f	10.463	10.432	9.267	9.946	9.24E-01	2.19E-01	-0.03	0.68
lpg0943	DNA repair protein RecO	*recO*	Replication and Repair	10.808	10.087	11.183	10.429	8.62E-02	1.03E-01	-0.72	-0.75
lpg0943	DNA repair protein RecO	*recO*	Replication and Repair	10.880	10.499	11.116	10.709	3.19E-02	9.03E-02	-0.38	-0.41
lpg0944	ORF		ORFs of unknown function (unique)	10.294	10.041	10.205	11.409	2.61E-01	2.25E-02	-0.25	1.20
lpg0944	ORF		ORFs of unknown function (unique)	10.749	9.737	9.908	11.396	1.68E-01	4.84E-02	-1.01	1.49
lpg0945	Gala protein type 1 or 3 (caspase recruitment domain, le	*legL1*	Toxin production / other pathogen func	10.119	10.243	10.100	9.942	8.11E-01	7.30E-01	0.12	-0.16
lpg0945	Gala protein type 1 or 3 (caspase recruitment domain, le	*legL1*	Toxin production / other pathogen func	10.258	10.291	10.081	10.012	9.31E-01	8.80E-01	0.03	-0.07
lpg0946	pyridoxal phosphate biosynthetic protein PdxJ (pyridoxin	*pdxJ*	Metabolism of Cofactors and Vitamins	10.113	12.363	9.504	12.313	1.25E-02	4.90E-06	2.25	2.81
lpg0946	pyridoxal phosphate biosynthetic protein PdxJ (pyridoxin	*pdxJ*	Metabolism of Cofactors and Vitamins	10.857	12.397	9.295	12.306	5.14E-04	1.68E-04	1.54	3.01
lpg0947	2-oxoglutarate ferredoxin oxidoreductase alpha subunit		Carbohydrate Metabolism, Energy Me	11.433	11.597	11.575	11.871	7.52E-01	2.61E-01	0.16	0.30
lpg0947	2-oxoglutarate ferredoxin oxidoreductase alpha subunit		Carbohydrate Metabolism, Energy Me	11.421	11.230	11.220	11.654	7.76E-01	3.84E-01	-0.19	0.43
lpg0948	2-oxoglutarate ferredoxin oxidoreductase beta subunit	*korB*	Carbohydrate Metabolism, Energy Me	11.241	10.435	11.558	11.172	1.18E-01	4.68E-01	-0.81	-0.39
lpg0948	2-oxoglutarate ferredoxin oxidoreductase beta subunit	*korB*	Carbohydrate Metabolism, Energy Me	11.291	11.417	11.671	11.963	8.37E-01	5.20E-01	0.13	0.29
lpg0949	carrier/transport protein (TEGT family)		Transport and binding	13.322	13.889	13.819	12.745	2.06E-01	8.29E-03	0.57	-1.07
lpg0949	carrier/transport protein (TEGT family)		Transport and binding	12.828	13.777	13.446	12.591	1.06E-01	5.82E-02	0.95	-0.85
lpg0950	nitrilase (carbon-nitrogen hydrolase)		Protein fate / hydrolases / secretion	11.788	11.470	11.504	11.445	1.20E-01	7.84E-01	-0.32	-0.06
lpg0950	nitrilase (carbon-nitrogen hydrolase)		Protein fate / hydrolases / secretion	11.842	11.760	11.511	11.555	7.79E-01	8.16E-01	-0.08	0.04
lpg0951	TldD protein (modulator of DNA gyrase) (suppresses inhi	*tldD*	Signal transduction / other regulatory f	12.123	12.525	12.279	13.049	8.45E-02	6.80E-04	0.40	0.77
lpg0951	TldD protein (modulator of DNA gyrase) (suppresses inhi	*tldD*	Signal transduction / other regulatory f	12.093	12.524	12.192	13.087	5.95E-02	2.06E-04	0.43	0.89
lpg0952	phosphoesterase (serine protease)	*ychK*	Protein fate / hydrolases / secretion	11.552	10.326	11.740	11.242	8.23E-02	2.91E-01	-1.23	-0.50
lpg0952	phosphoesterase (serine protease)	*ychK*	Protein fate / hydrolases / secretion	11.592	10.786	11.648	11.537	2.65E-03	5.36E-01	-0.81	-0.11
lpg0953	AMP-binding protein (long chain fatty acid-CoA ligase) (AMP depende		Lipid Metabolism	10.523	9.304	12.579	9.175	5.13E-02	1.89E-04	-1.22	-3.40
lpg0953	AMP-binding protein (long chain fatty acid-CoA ligase) (AMP depende		Lipid Metabolism	10.469	9.660	12.550	10.080	2.11E-01	3.53E-04	-0.81	-2.47
lpg0954	transcription repair coupling factor	*mfd*	Transcription, Replication and Repair	11.684	10.155	10.093	11.795	1.43E-03	1.64E-02	-1.53	1.70
lpg0954	transcription repair coupling factor	*mfd*	Transcription, Replication and Repair	11.533	9.939	10.027	11.818	1.67E-03	2.26E-02	-1.59	1.79
lpg0955	transmembrane protein (competence-induced protein) (DNA recombi		Replication and Repair	9.718	7.885	8.763	8.599	8.36E-02	7.81E-01	-1.83	-0.16
lpg0955	transmembrane protein (competence-induced protein) (DNA recombi		Replication and Repair	9.660	8.316	8.282	8.553	1.06E-01	7.48E-01	-1.34	0.27
lpg0956	hypothetical protein		Unknown / hypothetical proteins	11.646	12.267	11.132	10.721	5.91E-02	2.44E-01	0.62	-0.41
lpg0956	hypothetical protein		Unknown / hypothetical proteins	11.707	11.944	10.820	10.598	2.45E-01	3.92E-01	0.24	-0.22
lpg0957	hypothetical		Unknown / hypothetical proteins	11.471	10.901	10.195	9.295	4.00E-01	1.20E-01	-0.57	-0.90
lpg0957	hypothetical		Unknown / hypothetical proteins	11.561	11.474	10.066	9.432	7.77E-01	2.61E-01	-0.09	-0.63
lpg0958	DNA ligase (NAD-dependent)	*lig*	Replication and Repair	10.026	9.191	9.496	9.081	2.24E-02	5.20E-01	-0.84	-0.41
lpg0958	DNA ligase (NAD-dependent)	*lig*	Replication and Repair	9.989	9.219	9.718	9.547	8.54E-02	6.72E-01	-0.77	-0.17
lpg0959	bacterial extracellular solute-binding protein (peptide AB	*hbpA*	Transport and binding	9.784	9.731	9.982	9.383	8.92E-01	3.43E-01	-0.05	-0.60
lpg0959	bacterial extracellular solute-binding protein (peptide AB	*hbpA*	Transport and binding	9.742	9.215	8.927	9.637	7.61E-02	2.62E-02	-0.53	0.71
lpg0960	peptide ABC transporter, permease protein (oligopeptide transport) (d		Transport and binding	9.546	9.108	8.947	9.208	2.53E-01	7.58E-01	-0.44	0.26
lpg0960	peptide ABC transporter, permease protein (oligopeptide transport) (d		Transport and binding	9.467	9.506	9.048	9.375	9.28E-01	6.48E-01	0.04	0.33
lpg0961	peptide ABC transporter, permease protein (oligopeptide transport) (d		Transport and binding	10.580	9.618	9.672	9.968	2.00E-02	2.76E-01	-0.96	0.30
lpg0961	peptide ABC transporter, permease protein (oligopeptide transport) (d		Transport and binding	10.400	9.633	9.466	9.859	6.16E-02	1.55E-01	-0.77	0.39
lpg0962	DNA polymerase III, alpha subunit	*dnaE*	Replication and Repair	10.181	9.346	10.584	10.756	3.42E-01	4.21E-01	-0.83	0.17
lpg0962	DNA polymerase III, alpha subunit	*dnaE*	Replication and Repair	10.571	10.497	10.675	11.034	7.42E-01	4.22E-01	-0.07	0.36
lpg0963	ORF		ORFs of unknown function (unique)	11.416	13.501	12.272	10.547	6.62E-04	1.70E-03	2.09	-1.73
lpg0963	ORF		ORFs of unknown function (unique)	11.455	13.765	12.354	10.955	3.94E-04	3.98E-02	2.31	-1.40
lpg0964	4-hydroxybenzoate octaprenyltransferase (UbiA prenyltransferase far		Metabolism of Cofactors and Vitamins	11.894	10.795	11.084	10.238	2.24E-03	3.64E-02	-1.10	-0.85
lpg0964	4-hydroxybenzoate octaprenyltransferase (UbiA prenyltransferase far		Metabolism of Cofactors and Vitamins	11.759	11.325	11.020	10.387	5.99E-01	4.23E-01	-0.43	-0.63
lpg0965	LphB		Named proteins of general function	10.745	9.830	10.688	8.845	4.66E-03	1.14E-02	-0.92	-1.84
lpg0965	LphB		Named proteins of general function	10.869	9.677	10.906	9.481	5.14E-03	2.31E-02	-1.19	-1.42
lpg0966	nucleoside-diphosphate sugar epimerases (epimerase/dehydratase)		Nucleotide Metabolism	11.291	11.498	11.574	11.781	6.00E-01	4.41E-01	0.21	0.21
lpg0966	nucleoside-diphosphate sugar epimerases (epimerase/dehydratase)		Nucleotide Metabolism	11.436	11.353	11.633	11.908	8.45E-01	3.43E-01	-0.08	0.27
lpg0967	ORF		ORFs of unknown function (unique)	9.060	9.670	12.224	9.358	3.15E-01	3.57E-03	0.61	-2.87
lpg0967	ORF		ORFs of unknown function (unique)	8.998	9.667	12.133	9.289	2.14E-01	5.20E-03	0.67	-2.84
lpg0968	ORF		ORFs of unknown function (unique)	10.103	12.759	12.227	9.577	1.54E-04	1.44E-02	2.66	-2.65
lpg0968	ORF		ORFs of unknown function (unique)	10.152	12.717	12.197	9.658	9.41E-04	1.61E-02	2.57	-2.54
lpg0969	ORF		ORFs of unknown function (unique)	11.461	15.219	13.174	11.117	2.72E-05	4.28E-03	3.76	-2.06
lpg0969	ORF		ORFs of unknown function (unique)	11.474	15.318	13.219	11.192	9.61E-06	4.08E-03	3.84	-2.03

lpg0970	amino acid permeases (arginine permease, histidine permease, gam		Transport and binding	10.288	10.434	9.953	10.245	7.68E-01	6.37E-01	0.15	0.29
lpg0970	amino acid permeases (arginine permease, histidine permease, gam		Transport and binding	10.552	10.253	9.962	10.343	4.08E-01	3.81E-01	-0.30	0.38
lpg0971	ecto-ATP diphosphohydrolase II (ectonucleoside triphosphate diphos		Nucleotide Metabolism	9.619	9.772	9.651	8.705	7.81E-01	1.73E-01	0.15	-0.95
lpg0971	ecto-ATP diphosphohydrolase II (ectonucleoside triphosphate diphos		Nucleotide Metabolism	9.477	9.270	9.069	8.920	7.76E-01	8.80E-01	-0.21	-0.15
lpg0972	tRNA-Thr		tRNA	11.139	10.371	10.401	10.290	4.29E-02	7.64E-01	-0.77	-0.11
lpg0972	tRNA-Thr		tRNA	11.005	10.621	10.741	10.983	3.84E-01	4.31E-01	-0.38	0.24
lpg0973	hypothetical		Unknown / hypothetical proteins	11.817	10.690	10.129	10.520	1.92E-01	5.75E-01	-1.13	0.39
lpg0973	hypothetical		Unknown / hypothetical proteins	12.203	10.746	10.196	10.698	1.51E-02	4.28E-01	-1.46	0.50
lpg0974	ORF		ORFs of unknown function (unique)	11.303	9.678	10.583	9.889	2.76E-03	1.97E-01	-1.62	-0.69
lpg0974	ORF		ORFs of unknown function (unique)	11.428	9.945	10.324	9.841	6.65E-03	4.42E-01	-1.48	-0.48
lpg0975	transmembrane protein (transporter, DME family)		Transport and binding	9.369	9.289	9.318	7.846	7.95E-01	1.07E-02	-0.08	-1.47
lpg0975	transmembrane protein (transporter, DME family)		Transport and binding	9.441	8.582	8.688	8.931	1.73E-01	6.27E-01	-0.86	0.24
lpg0976	antirestriction protein		DNA/RNA degradation / restriction, Sig	9.505	10.882	10.147	10.157	5.42E-03	9.77E-01	1.38	0.01
lpg0976	antirestriction protein		DNA/RNA degradation / restriction, Sig	9.493	11.917	10.161	10.797	8.10E-05	1.61E-01	2.42	0.64
lpg0977	single strand DNA binding protein (ssb)		Replication and Repair	10.321	11.117	9.249	11.218	9.25E-02	1.35E-03	0.80	1.97
lpg0977	single strand DNA binding protein (ssb)		Replication and Repair	10.408	11.193	9.075	11.613	1.29E-02	1.87E-06	0.79	2.54
lpg0978	ORF		ORFs of unknown function (unique)	10.551	11.533	10.208	11.560	1.53E-03	6.21E-06	0.98	1.35
lpg0978	ORF		ORFs of unknown function (unique)	10.605	11.254	9.968	11.474	1.94E-02	1.72E-05	0.65	1.51
lpg0979	aminoglycoside N(6')acetyltransferase	*aacA4*	Named proteins of general function	10.947	9.595	11.140	9.662	3.77E-04	6.57E-04	-1.35	-1.48
lpg0979	aminoglycoside N(6')acetyltransferase	*aacA4*	Named proteins of general function	10.829	9.620	10.770	9.824	2.39E-03	1.13E-02	-1.21	-0.95
lpg0980	putative integrase		Viral functions / Phage / Transposases	7.903	8.340	8.456	8.830	5.51E-01	4.82E-01	0.44	0.37
lpg0980	putative integrase		Viral functions / Phage / Transposases	7.655	7.796	8.655	9.147	8.23E-01	4.57E-01	0.14	0.49
lpg0981	ORF		ORFs of unknown function (unique)	6.563	8.537	8.707	7.552	8.81E-02	1.73E-01	1.97	-1.15
lpg0981	ORF		ORFs of unknown function (unique)	7.159	9.519	8.713	9.560	1.43E-01	4.63E-01	2.36	0.85
lpg0982	hypothetical		Unknown / hypothetical proteins	9.850	9.974	11.307	9.691	8.79E-01	9.93E-02	0.12	-1.62
lpg0982	hypothetical		Unknown / hypothetical proteins	9.238	9.597	8.549	9.711	6.99E-01	5.78E-01	0.36	1.16
lpg0983	conjugative coupling factor TraD		Transport and binding	8.996	9.263	8.945	8.846	5.83E-01	8.73E-01	0.27	-0.10
lpg0983	conjugative coupling factor TraD		Transport and binding	9.314	9.625	8.931	9.491	4.00E-01	1.24E-01	0.31	0.56
lpg0984	ORF hypothetical? phosphatidylcholine desaturase? cytochrome b? b		Unknown / hypothetical proteins	8.734	8.853	8.890	8.643	8.40E-01	7.21E-01	0.12	-0.25
lpg0984	ORF hypothetical? phosphatidylcholine desaturase? cytochrome b? b		Unknown / hypothetical proteins	8.513	9.194	8.908	8.921	1.88E-01	9.79E-01	0.68	0.01
lpg0985	small ORF (56aa)		ORFs of unknown function (unique)	13.076	11.136	11.366	11.253	3.57E-03	8.83E-01	-1.94	-0.11
lpg0985	small ORF (56aa)		ORFs of unknown function (unique)	13.091	11.432	11.460	11.524	6.96E-04	9.13E-01	-1.66	0.06
lpg0986	membrane protein		Named proteins of general function	7.389	8.261	9.025	7.277	3.40E-01	2.89E-02	0.87	-1.75
lpg0986	membrane protein		Named proteins of general function	8.730	9.000	8.967	8.201	7.48E-01	4.39E-01	0.27	-0.77
lpg0987	membrane protein?		Named proteins of general function	8.884	8.582	10.922	7.964	6.42E-01	1.09E-02	-0.30	-2.96
lpg0987	membrane protein?		Named proteins of general function	9.310	8.957	11.148	8.992	3.74E-01	4.72E-03	-0.35	-2.16
lpg0988	conserved hypothetical protein		Unknown / hypothetical proteins	8.678	8.746	9.596	8.436	8.65E-01	5.35E-03	0.07	-1.16
lpg0988	conserved hypothetical protein		Unknown / hypothetical proteins	8.975	8.935	9.791	9.268	9.39E-01	1.81E-01	-0.04	-0.52
lpg0989	hypothetical (pilus assembly protein?) Type IV secretory protein VirB4		Transport and binding	8.335	8.480	9.392	8.963	8.11E-01	3.04E-01	0.14	-0.43
lpg0989	hypothetical (pilus assembly protein?) Type IV secretory protein VirB4		Transport and binding	8.108	9.005	9.307	9.155	2.16E-02	7.27E-01	0.90	-0.15
lpg0990	conserved hypothetical protein		Unknown / hypothetical proteins	11.628	12.931	11.009	12.687	1.51E-02	1.66E-06	1.30	1.68
lpg0990	conserved hypothetical protein		Unknown / hypothetical proteins	11.716	13.010	10.837	12.679	7.06E-03	1.10E-05	1.29	1.84
lpg0991	exported protein?		Named proteins of general function	8.333	6.767	10.066	8.316	3.56E-02	1.31E-02	-1.57	-1.75
lpg0991	exported protein?		Named proteins of general function	8.291	8.012	9.168	8.000	5.24E-01	5.29E-02	-0.28	-1.17
lpg0992	conserved hypothetical protein		Unknown / hypothetical proteins	13.590	15.406	14.655	15.367	6.03E-05	1.24E-01	1.82	0.71
lpg0992	conserved hypothetical protein		Unknown / hypothetical proteins	13.611	15.296	14.672	15.397	8.65E-05	9.40E-02	1.69	0.73
lpg0993	conserved hypothetical protein		Unknown / hypothetical proteins	8.406	8.784	9.139	8.567	6.35E-01	4.38E-01	0.38	-0.57
lpg0993	conserved hypothetical protein		Unknown / hypothetical proteins	8.529	8.256	8.685	8.582	7.98E-01	9.10E-01	-0.27	-0.10
lpg0994	ORF		ORFs of unknown function (unique)	8.888	7.948	9.103	7.468	6.82E-02	3.75E-02	-0.94	-1.63
lpg0994	ORF		ORFs of unknown function (unique)	8.108	8.076	8.954	8.818	9.64E-01	7.56E-01	-0.03	-0.14
lpg0995	ORF		ORFs of unknown function (unique)	10.108	9.307	10.799	9.969	8.08E-03	1.00E-01	-0.80	-0.83
lpg0995	ORF		ORFs of unknown function (unique)	10.070	9.509	10.688	10.041	7.38E-02	2.63E-01	-0.56	-0.65
lpg0996	ORF		ORFs of unknown function (unique)	6.331	6.340	8.559	10.137	9.98E-01	3.86E-01	0.01	1.58
lpg0996	ORF		ORFs of unknown function (unique)	7.900	7.771	7.688	10.935	9.75E-01	3.18E-01	-0.13	3.25
lpg0997	small ORF (108aa)		ORFs of unknown function (unique)	7.797	8.021	7.924	7.169	7.55E-01	6.06E-01	0.22	-0.76
lpg0997	small ORF (108aa)		ORFs of unknown function (unique)	8.122	8.260	7.834	7.125	7.99E-01	5.86E-01	0.14	-0.71
lpg0998	conserved hypothetical protein		Unknown / hypothetical proteins	6.791	4.862	7.778	7.977	3.73E-01	8.65E-01	-1.93	0.20
lpg0998	conserved hypothetical protein		Unknown / hypothetical proteins	4.616	7.078	7.253	8.739	2.37E-01	2.75E-01	2.46	1.49
lpg0999	hypothetical		Unknown / hypothetical proteins	11.744	10.946	11.447	10.206	7.28E-02	1.81E-02	-0.80	-1.24
lpg0999	hypothetical		Unknown / hypothetical proteins	11.467	10.338	11.182	10.195	6.08E-02	1.38E-01	-1.13	-0.99
lpg1000	protein product; similar to putative exported protein protein product; s		Unknown / hypothetical proteins	7.371	7.883	8.999	8.124	6.61E-01	2.28E-01	0.51	-0.88
lpg1000	protein product; similar to putative exported protein protein product; s		Unknown / hypothetical proteins	8.471	8.665	8.460	8.448	7.37E-01	9.85E-01	0.19	-0.01
lpg1001	ORF		ORFs of unknown function (unique)	8.074	7.864	7.750	7.461	8.52E-01	7.98E-01	-0.21	-0.29
lpg1001	ORF		ORFs of unknown function (unique)	5.493	7.378	6.780	7.442	5.08E-01	7.86E-01	1.88	0.66

lpg1002	putative exported protein		Unknown / hypothetical proteins	9.166	8.650	9.183	7.957	8.97E-02	1.37E-01	-0.52	-1.23
lpg1002	putative exported protein		Unknown / hypothetical proteins	8.702	9.474	8.815	10.361	5.69E-01	2.06E-01	0.77	1.55
lpg1003	carbon storage regulator	*csrA-2*	Named proteins of general function	8.161	8.730	9.130	8.529	2.13E-01	3.13E-01	0.57	-0.60
lpg1003	carbon storage regulator	*csrA-2*	Named proteins of general function	7.955	8.766	8.718	8.933	1.33E-01	6.54E-01	0.81	0.21
lpg1004	ORF		ORFs of unknown function (unique)	7.849	7.764	8.525	10.057	9.32E-01	4.56E-02	-0.09	1.53
lpg1004	ORF		ORFs of unknown function (unique)	7.452	8.903	8.373	10.127	2.02E-01	4.89E-02	1.45	1.75
lpg1005	LvrA	*lvrA*	Transport and binding	10.452	11.128	10.869	10.953	1.79E-02	8.43E-01	0.68	0.08
lpg1005	LvrA	*lvrA*	Transport and binding	10.535	11.052	10.955	11.059	1.58E-01	8.12E-01	0.52	0.10
lpg1006	cobalt/zinc/cadmium efflux RND transporter, outer membrane protein		Transport and binding	9.219	9.872	8.738	9.849	2.05E-01	2.18E-01	0.65	1.11
lpg1006	cobalt/zinc/cadmium efflux RND transporter, outer membrane protein		Transport and binding	9.228	9.463	8.441	9.706	3.35E-01	2.13E-02	0.23	1.27
lpg1007	cation efflux system HelB (HlyD family secretion protein)		Transport and binding	10.442	9.712	11.179	8.563	1.88E-03	6.24E-04	-0.73	-2.62
lpg1007	cation efflux system HelB (HlyD family secretion protein)		Transport and binding	10.330	9.443	10.486	8.625	3.63E-03	4.37E-04	-0.89	-1.86
lpg1008	cobalt/zinc/cadmium efflux RND transporter, permease protein HelA (		Transport and binding	9.135	7.326	9.081	7.760	6.17E-02	3.06E-01	-1.81	-1.32
lpg1008	cobalt/zinc/cadmium efflux RND transporter, permease protein HelA (		Transport and binding	8.263	9.393	8.621	8.844	1.30E-01	6.44E-01	1.13	0.22
lpg1009	cadmium translocating P-type ATPase CadA (Pb-efflux A	*cadA-1*	Metabolism of Complex Carbohydrate	9.851	9.028	10.475	10.304	3.08E-01	6.92E-01	-0.82	-0.17
lpg1009	cadmium translocating P-type ATPase CadA (Pb-efflux A	*cadA-1*	Metabolism of Complex Carbohydrate	10.049	10.350	10.330	10.782	2.92E-01	1.49E-01	0.30	0.45
lpg1010	cadmium efflux ATPase (cadmium resistance protein)		Transport and binding	9.293	8.121	8.765	9.957	2.57E-02	6.12E-02	-1.17	1.19
lpg1010	cadmium efflux ATPase (cadmium resistance protein)		Transport and binding	9.314	8.277	8.304	10.052	2.87E-02	9.74E-03	-1.04	1.75
lpg1011	uncharacterized conserved protein		Unknown / hypothetical proteins	9.854	9.245	12.504	7.961	3.76E-01	1.96E-03	-0.61	-4.54
lpg1011	uncharacterized conserved protein		Unknown / hypothetical proteins	9.787	8.827	12.529	9.060	2.51E-01	3.27E-02	-0.96	-3.47
lpg1012	small ORF (65aa)		ORFs of unknown function (unique)	10.133	9.771	12.433	7.798	5.82E-01	1.05E-02	-0.36	-4.63
lpg1012	small ORF (65aa)		ORFs of unknown function (unique)	10.050	10.439	12.465	9.249	6.21E-01	3.61E-03	0.39	-3.22
lpg1013	small ORF (83aa)		ORFs of unknown function (unique)	8.775	7.697	8.936	8.576	1.04E-01	5.38E-01	-1.08	-0.36
lpg1013	small ORF (83aa)		ORFs of unknown function (unique)	8.952	8.123	8.913	8.970	4.45E-01	9.20E-01	-0.83	0.06
lpg1014	(dehydrogenase?)		Named proteins of general function	10.063	9.905	10.183	10.418	5.55E-01	5.28E-01	-0.16	0.24
lpg1014	(dehydrogenase?)		Named proteins of general function	9.984	9.622	10.032	10.346	3.26E-01	4.51E-01	-0.36	0.31
lpg1015	unknown Legionella protein, benzil (sepiapterin, ketoacyl	*yueD*	Metabolism of Cofactors and Vitamins	10.277	10.799	12.378	7.842	4.74E-01	2.33E-02	0.52	-4.54
lpg1015	unknown Legionella protein, benzil (sepiapterin, ketoacyl	*yueD*	Metabolism of Cofactors and Vitamins	10.320	10.493	12.572	8.814	7.95E-01	5.21E-03	0.17	-3.76
lpg1016	unknown Legionella protein (putative secreted protein?)		Named proteins of general function	11.231	11.300	10.754	11.485	9.01E-01	2.56E-01	0.07	0.73
lpg1016	unknown Legionella protein (putative secreted protein?)		Named proteins of general function	11.272	11.817	9.830	11.973	3.46E-01	2.10E-02	0.55	2.14
lpg1017	cation efflux transporter (calcium transporting ATPase) (c	*mgtA*	Metabolism of Complex Carbohydrate	10.581	10.529	10.773	9.765	8.80E-01	1.72E-01	-0.05	-1.01
lpg1017	cation efflux transporter (calcium transporting ATPase) (c	*mgtA*	Metabolism of Complex Carbohydrate	10.450	9.490	10.720	10.075	3.58E-01	8.77E-02	-0.96	-0.65
lpg1018	chemiosmotic efflux system B protein C (outer membrane efflux prote		Transport and binding	7.589	7.530	8.806	8.017	9.38E-01	3.94E-01	-0.06	-0.79
lpg1018	chemiosmotic efflux system B protein C (outer membrane efflux prote		Transport and binding	8.365	8.334	9.228	8.671	9.74E-01	5.49E-01	-0.03	-0.56
lpg1019	chemiosmotic efflux system B protein B (heavy metal efflux)		Transport and binding	7.718	7.039	8.860	6.972	2.91E-01	3.15E-02	-0.68	-1.89
lpg1019	chemiosmotic efflux system B protein B (heavy metal efflux)		Transport and binding	7.930	6.746	8.612	8.031	2.70E-01	1.99E-01	-1.18	-0.58
lpg1020	chemiosmotic efflux system B protein A (silver efflux pump)		Transport and binding	7.719	7.662	8.626	6.812	9.46E-01	1.43E-01	-0.06	-1.81
lpg1020	chemiosmotic efflux system B protein A (silver efflux pump)		Transport and binding	8.253	8.392	8.862	9.833	8.89E-01	2.53E-01	0.14	0.97
lpg1021	metallo-beta lactamase family (cleavage and polyadenylation specific		Detoxification / adaptation, Transcripti	8.869	8.552	10.179	7.956	7.30E-01	5.64E-02	-0.32	-2.22
lpg1021	metallo-beta lactamase family (cleavage and polyadenylation specific		Detoxification / adaptation, Transcripti	8.071	9.832	9.886	9.391	2.51E-01	7.03E-01	1.76	-0.50
lpg1022	thymidine phosphorylase (TdRPase) (thymidine/pyrimidi	*deoA*	Nucleotide Metabolism	8.110	9.545	10.032	9.057	1.89E-02	2.30E-01	1.44	-0.98
lpg1022	thymidine phosphorylase (TdRPase) (thymidine/pyrimidi	*deoA*	Nucleotide Metabolism	7.958	9.518	9.933	9.939	6.33E-02	9.92E-01	1.56	0.01
lpg1023	ribose-phosphate pyrophosphokinase (RPPK) (phosphoribosyl pyrop		Carbohydrate Metabolism, Nucleotide	8.763	7.586	9.298	8.260	1.16E-01	3.24E-01	-1.18	-1.04
lpg1023	ribose-phosphate pyrophosphokinase (RPPK) (phosphoribosyl pyrop		Carbohydrate Metabolism, Nucleotide	8.009	7.976	9.589	9.023	9.52E-01	3.55E-01	-0.03	-0.57
lpg1024	copper efflux ATPase (cation transport P-type ATPase) (heavy metal t		Transport and binding	8.696	9.768	10.411	8.692	4.17E-02	3.92E-03	1.07	-1.72
lpg1024	copper efflux ATPase (cation transport P-type ATPase) (heavy metal t		Transport and binding	9.078	9.887	10.358	9.112	6.93E-02	9.60E-02	0.81	-1.25
lpg1025	sensory box/GGDEF/EAL family (membrane protein)	*yegE*	Signal transduction / other regulatory f	8.754	9.676	11.708	8.532	2.66E-01	7.78E-02	0.92	-3.18
lpg1025	sensory box/GGDEF/EAL family (membrane protein)	*yegE*	Signal transduction / other regulatory f	8.467	9.415	11.398	8.649	2.58E-01	1.48E-02	0.95	-2.75
lpg1026	putative outer membrane lipoprotein		Named proteins of general function	10.876	11.088	11.148	10.568	5.37E-01	9.23E-02	0.21	-0.58
lpg1026	putative outer membrane lipoprotein		Named proteins of general function	10.738	11.349	11.065	10.847	7.88E-04	6.54E-01	0.61	-0.22
lpg1027	chemiosmotic efflux system C protein C (metal ion efflux outer membr		Transport and binding	9.824	10.238	11.147	10.609	3.71E-01	1.87E-02	0.41	-0.54
lpg1027	chemiosmotic efflux system C protein C (metal ion efflux outer membr		Transport and binding	9.872	10.594	11.119	11.037	2.47E-01	8.62E-01	0.72	-0.08
lpg1028	chemiosmotic efflux system C protein B		Transport and binding	9.911	9.763	10.937	10.007	7.79E-01	1.27E-02	-0.15	-0.93
lpg1028	chemiosmotic efflux system C protein B		Transport and binding	9.893	9.471	10.921	10.031	4.94E-01	8.17E-03	-0.42	-0.89
lpg1029	chemiosmotic efflux system protein A-like protein		Transport and binding	10.263	9.466	11.868	10.205	4.13E-01	5.43E-03	-0.80	-1.66
lpg1029	chemiosmotic efflux system protein A-like protein		Transport and binding	10.283	10.030	11.798	10.404	7.51E-01	1.99E-03	-0.25	-1.39
lpg1030	hypothetical		Unknown / hypothetical proteins	11.806	12.763	13.480	11.609	2.06E-02	3.01E-03	0.96	-1.87
lpg1030	hypothetical		Unknown / hypothetical proteins	11.870	12.825	13.460	11.707	1.31E-02	4.45E-03	0.95	-1.75
lpg1031	small ORF (114aa)		ORFs of unknown function (unique)	10.479	11.438	11.482	9.283	4.01E-02	8.27E-03	0.96	-2.20
lpg1031	small ORF (114aa)		ORFs of unknown function (unique)	10.659	11.699	12.076	10.435	7.77E-03	3.92E-03	1.04	-1.64
lpg1032	conserved hypothetical protein		Unknown / hypothetical proteins	9.871	9.055	12.273	9.286	1.91E-01	2.15E-04	-0.82	-2.99
lpg1032	conserved hypothetical protein		Unknown / hypothetical proteins	10.127	9.775	12.321	9.575	4.85E-01	4.31E-04	-0.35	-2.75
lpg1033	hypothetical?		Unknown / hypothetical proteins	9.735	9.314	10.021	8.766	4.60E-01	1.56E-02	-0.42	-1.26
lpg1033	hypothetical?		Unknown / hypothetical proteins	10.088	10.229	10.626	9.733	2.93E-01	1.67E-03	0.14	-0.89

lpg1034	small ORF (175aa)		ORFs of unknown function (unique)	11.535	11.327	11.219	11.847	4.70E-01	4.20E-02	-0.21	0.63
lpg1034	small ORF (175aa)		ORFs of unknown function (unique)	11.376	11.352	11.114	11.782	9.39E-01	2.27E-02	-0.02	0.67
lpg1035	copper efflux ATPase (copper resistance protein A) CopA	*pcoA*	Transport and binding	10.538	11.773	9.892	12.360	1.42E-02	8.81E-04	1.23	2.47
lpg1035	copper efflux ATPase (copper resistance protein A) CopA	*pcoA*	Transport and binding	10.458	13.091	9.744	13.586	3.86E-05	8.39E-05	2.63	3.84
lpg1036	outer membrane lipoprotein (L. pneumophila)		Named proteins of general function	9.269	10.144	10.500	9.362	9.25E-02	8.67E-02	0.87	-1.14
lpg1036	outer membrane lipoprotein (L. pneumophila)		Named proteins of general function	9.688	9.575	10.357	9.290	7.60E-01	6.66E-04	-0.11	-1.07
lpg1037	small ORF (55aa)		ORFs of unknown function (unique)	9.868	10.961	11.111	10.220	5.24E-02	7.28E-02	1.09	-0.89
lpg1037	small ORF (55aa)		ORFs of unknown function (unique)	9.948	10.329	10.960	10.250	5.34E-01	1.65E-01	0.38	-0.71
lpg1038	VrrB (contains histidine/glycine rich portion)		Named proteins of general function	9.611	9.233	11.925	9.461	6.96E-01	6.31E-02	-0.38	-2.46
lpg1038	VrrB (contains histidine/glycine rich portion)		Named proteins of general function	10.653	10.173	12.038	10.325	4.44E-01	9.49E-02	-0.48	-1.71
lpg1039	hypothetical		Unknown / hypothetical proteins	11.137	12.839	11.094	12.141	3.68E-04	3.86E-03	1.70	1.05
lpg1039	hypothetical		Unknown / hypothetical proteins	11.170	12.846	10.999	12.066	2.53E-04	5.02E-03	1.68	1.07
lpg1040	hypothetical (transmembrane protein) (nickel-cobalt-cadmium resistar		Transport and binding	8.767	7.809	11.192	8.448	3.74E-01	8.98E-03	-0.96	-2.74
lpg1040	hypothetical (transmembrane protein) (nickel-cobalt-cadmium resistar		Transport and binding	8.613	8.844	11.283	8.916	7.88E-01	9.99E-03	0.23	-2.37
lpg1041	small ORF (166aa) (hypothetical transporter; glycerol-3-phosphate tra		Transport and binding	8.761	8.438	11.292	8.256	6.84E-01	3.37E-02	-0.32	-3.04
lpg1041	small ORF (166aa) (hypothetical transporter; glycerol-3-phosphate tra		Transport and binding	8.550	8.204	11.277	8.762	6.22E-01	3.71E-02	-0.35	-2.52
lpg1042	hypothetical		Unknown / hypothetical proteins	9.476	10.071	11.176	10.736	5.59E-02	1.83E-01	0.60	-0.44
lpg1042	hypothetical		Unknown / hypothetical proteins	9.538	10.068	11.212	11.726	2.94E-01	1.60E-01	0.53	0.51
lpg1043	hypothetical (bll4815 of B. japonicum)		Unknown / hypothetical proteins	10.865	10.845	11.869	10.830	9.48E-01	1.10E-01	-0.02	-1.04
lpg1043	hypothetical (bll4815 of B. japonicum)		Unknown / hypothetical proteins	10.915	10.656	11.972	10.996	6.18E-01	9.60E-02	-0.26	-0.98
lpg1044	oxidoreductase, FAD-binding (ferredoxin oxidoreductase) (iron-sulfur		Energy Metabolism	11.595	11.502	12.443	10.907	8.06E-01	7.11E-04	-0.09	-1.54
lpg1044	oxidoreductase, FAD-binding (ferredoxin oxidoreductase) (iron-sulfur		Energy Metabolism	11.645	10.655	12.476	11.114	3.48E-01	7.56E-04	-0.99	-1.36
lpg1045	small ORF (64aa)?		ORFs of unknown function (unique)	7.724	8.981	9.635	6.850	1.44E-01	8.02E-02	1.26	-2.78
lpg1045	small ORF (64aa)?		ORFs of unknown function (unique)	7.332	8.896	9.699	7.355	1.20E-01	1.08E-02	1.56	-2.34
lpg1046	small ORF (129aa)		ORFs of unknown function (unique)	9.088	9.156	10.893	9.695	9.14E-01	8.65E-02	0.07	-1.20
lpg1046	small ORF (129aa)		ORFs of unknown function (unique)	9.450	8.970	10.772	9.591	3.74E-01	2.99E-02	-0.48	-1.18
lpg1047	ATP synthase gamma subunit C-terminus homolog	*atpG*	Energy Metabolism	8.748	7.500	9.128	7.235	5.18E-02	1.05E-01	-1.25	-1.89
lpg1047	ATP synthase gamma subunit C-terminus homolog	*atpG*	Energy Metabolism	8.831	7.488	9.212	8.321	3.85E-02	1.82E-01	-1.34	-0.89
lpg1048	ATP synthase F1, subunit alpha (F0F1-type ATP synthase alpha subu		Energy Metabolism	10.391	11.776	11.855	10.949	2.26E-02	3.70E-02	1.38	-0.91
lpg1048	ATP synthase F1, subunit alpha (F0F1-type ATP synthase alpha subu		Energy Metabolism	10.325	12.934	11.936	11.179	2.87E-05	7.95E-02	2.61	-0.76
lpg1049	H(+) transporting ATP synthase, subunit B (F0F1-type ATPase subuni		Energy Metabolism	8.550	9.240	9.835	7.988	3.14E-01	6.55E-02	0.69	-1.85
lpg1049	H(+) transporting ATP synthase, subunit B (F0F1-type ATPase subuni		Energy Metabolism	8.271	8.607	9.613	8.420	7.22E-01	4.40E-02	0.34	-1.19
lpg1050	ATP synthase C subunit (H+ transporting ATP synthase) (ATP syntha		Energy Metabolism	9.741	8.388	10.870	9.199	1.87E-01	3.92E-03	-1.35	-1.67
lpg1050	ATP synthase C subunit (H+ transporting ATP synthase) (ATP syntha		Energy Metabolism	9.747	9.128	10.838	9.489	2.23E-01	3.10E-02	-0.62	-1.35
lpg1051	ATP synthase subunit A (F0F1-type ATP synthase F0, su	*atpB*	Energy Metabolism	9.583	8.184	10.379	8.606	2.13E-03	4.58E-03	-1.40	-1.77
lpg1051	ATP synthase subunit A (F0F1-type ATP synthase F0, su	*atpB*	Energy Metabolism	9.607	8.519	10.624	9.073	8.38E-02	1.42E-02	-1.09	-1.55
lpg1052	ATP synthase, putative		Named proteins of general function	9.077	8.866	8.265	7.897	6.63E-01	7.93E-01	-0.21	-0.37
lpg1052	ATP synthase, putative		Named proteins of general function	9.313	7.618	7.677	8.007	6.44E-02	7.58E-01	-1.69	0.33
lpg1053	F0F1-type ATP synthase epsilon subunit??)		Energy Metabolism	10.232	9.326	10.939	9.281	2.09E-02	3.68E-03	-0.91	-1.66
lpg1053	F0F1-type ATP synthase epsilon subunit??)		Energy Metabolism	10.266	9.205	10.840	9.707	1.83E-03	2.88E-02	-1.06	-1.13
lpg1054	ATP synthase F1, beta chain (F0F1-type ATPase beta su	*atpD*	Energy Metabolism	10.335	10.089	10.808	11.123	4.43E-01	1.77E-01	-0.25	0.32
lpg1054	ATP synthase F1, beta chain (F0F1-type ATPase beta su	*atpD*	Energy Metabolism	10.361	10.117	10.257	11.090	3.74E-01	1.13E-01	-0.24	0.83
lpg1055	hypothetical protein		Unknown / hypothetical proteins	10.916	10.547	12.567	10.253	2.49E-01	1.26E-04	-0.37	-2.31
lpg1055	hypothetical protein		Unknown / hypothetical proteins	10.826	10.295	12.532	10.228	5.55E-02	1.98E-04	-0.53	-2.30
lpg1056	guanylate cyclase		Signal transduction / other regulatory f	12.012	11.290	13.126	11.585	6.70E-02	8.53E-04	-0.72	-1.54
lpg1056	guanylate cyclase		Signal transduction / other regulatory f	11.942	11.424	13.088	11.657	1.07E-01	1.22E-03	-0.52	-1.43
lpg1057	sensory box/GGDEF family (diguanylate cyclase/phosphodiesterase (		Signal transduction / other regulatory f	10.549	10.015	11.596	10.882	5.62E-01	2.89E-01	-0.53	-0.71
lpg1057	sensory box/GGDEF family (diguanylate cyclase/phosphodiesterase (		Signal transduction / other regulatory f	10.401	9.663	11.233	10.605	1.10E-01	1.04E-01	-0.74	-0.63
lpg1058	polyhydroxyalkanoic synthase (PHA synthase) (poly(3-hy	*phbC*	Amino Acid Metabolism, Metabolism o	10.820	11.488	12.790	10.868	2.55E-01	4.43E-02	0.67	-1.92
lpg1058	polyhydroxyalkanoic synthase (PHA synthase) (poly(3-hy	*phbC*	Amino Acid Metabolism, Metabolism o	10.930	11.561	12.880	11.206	2.83E-01	8.15E-02	0.63	-1.67
lpg1059	acetoacetyl CoA reductase	*phaB*	Carbohydrate Metabolism	11.017	10.459	11.782	10.531	3.51E-02	1.92E-03	-0.56	-1.25
lpg1059	acetoacetyl CoA reductase	*phaB*	Carbohydrate Metabolism	10.915	10.767	11.724	10.679	4.79E-01	1.66E-03	-0.15	-1.05
lpg1060	cold shock domain family protein, COG1278: cold shock proteins		Detoxification / adaptation	10.076	12.296	10.174	12.177	5.79E-04	3.54E-03	2.22	2.00
lpg1060	cold shock domain family protein, COG1278: cold shock proteins		Detoxification / adaptation	10.167	12.325	10.165	12.217	5.60E-05	3.57E-03	2.16	2.05
lpg1061	ORF hypothetical?		Unknown / hypothetical proteins	10.781	11.303	10.652	11.182	5.28E-01	1.99E-01	0.52	0.53
lpg1061	ORF hypothetical?		Unknown / hypothetical proteins	10.544	11.798	10.471	11.557	1.36E-02	2.23E-03	1.25	1.09
lpg1062	TPR repeat protein (enhanced entry protein EnhC)		Toxin production / other pathogen func	11.886	11.091	11.525	11.106	1.18E-03	1.73E-01	-0.80	-0.42
lpg1062	TPR repeat protein (enhanced entry protein EnhC)		Toxin production / other pathogen func	11.906	10.986	11.511	11.195	8.94E-05	2.42E-01	-0.92	-0.32
lpg1063	proline/betaine transporter (ProP6) (MFS transporter) (lo\	*proP6*	Transport and binding	9.425	10.096	9.907	9.891	1.86E-01	9.48E-01	0.67	-0.02
lpg1063	proline/betaine transporter (ProP6) (MFS transporter) (lo\	*proP6*	Transport and binding	9.515	10.666	9.997	10.407	6.73E-02	3.27E-01	1.15	0.41
lpg1064	polypeptide deformylase (peptide deformylase)		Translation	10.332	10.113	10.875	9.618	5.36E-01	1.00E-03	-0.22	-1.26
lpg1064	polypeptide deformylase (peptide deformylase)		Translation	10.647	10.110	10.989	10.044	8.61E-02	2.27E-03	-0.54	-0.95
lpg1065	ORF		ORFs of unknown function (unique)	10.193	10.541	9.909	10.804	6.77E-01	2.71E-02	0.35	0.89
lpg1065	ORF		ORFs of unknown function (unique)	10.397	10.517	8.819	10.219	8.12E-01	2.33E-01	0.12	1.40

lpg1066	ORF		ORFs of unknown function (unique)	10.886	11.714	11.083	10.618	3.27E-02	3.16E-01	0.83	-0.46
lpg1066	ORF		ORFs of unknown function (unique)	10.740	12.056	11.065	10.764	4.38E-04	3.49E-01	1.32	-0.30
lpg1067	small ORF (85aa)		ORFs of unknown function (unique)	9.398	9.306	10.804	7.050	8.92E-01	3.84E-03	-0.09	-3.75
lpg1067	small ORF (85aa)		ORFs of unknown function (unique)	9.766	9.907	10.984	8.259	8.22E-01	4.16E-03	0.14	-2.72
lpg1068	small ORF (67aa)		ORFs of unknown function (unique)	11.547	10.979	12.020	10.146	2.61E-01	3.78E-03	-0.57	-1.87
lpg1068	small ORF (67aa)		ORFs of unknown function (unique)	11.497	11.090	12.022	10.166	3.63E-01	2.91E-03	-0.41	-1.86
lpg1069	similar to AbiD phage protein		Viral functions / Phage / Transposases	9.661	8.473	9.008	8.985	2.39E-01	9.54E-01	-1.19	-0.02
lpg1069	similar to AbiD phage protein		Viral functions / Phage / Transposases	10.376	8.993	8.408	9.807	7.77E-02	1.38E-01	-1.38	1.40
lpg1070	integrase (phage related)	*int*	Viral functions / Phage / Transposases	9.209	10.880	9.167	10.912	2.71E-04	1.38E-03	1.67	1.75
lpg1070	integrase (phage related)	*int*	Viral functions / Phage / Transposases	8.700	10.840	8.461	10.857	4.13E-04	1.82E-04	2.14	2.40
lpg1071	transposase TnpA (Uma4)		Viral functions / Phage / Transposases	8.833	9.752	9.738	8.832	1.38E-01	4.64E-01	0.92	-0.91
lpg1071	transposase TnpA (Uma4)		Viral functions / Phage / Transposases	7.907	9.886	8.764	9.650	4.17E-03	1.23E-01	1.98	0.89
lpg1073	ORF		ORFs of unknown function (unique)	10.947	10.925	9.280	10.810	9.67E-01	7.35E-03	-0.02	1.53
lpg1073	ORF		ORFs of unknown function (unique)	10.552	10.994	8.032	10.667	6.25E-01	3.26E-02	0.44	2.64
lpg1074	hypothetical		Unknown / hypothetical proteins	8.840	10.194	9.033	9.523	1.43E-01	2.82E-01	1.35	0.49
lpg1074	hypothetical		Unknown / hypothetical proteins	9.324	10.291	8.947	10.077	1.07E-01	6.74E-02	0.97	1.13
lpg1075	small ORF (113aa)		ORFs of unknown function (unique)	9.924	9.141	9.165	8.678	3.23E-02	3.41E-01	-0.78	-0.49
lpg1075	small ORF (113aa)		ORFs of unknown function (unique)	9.962	8.651	9.162	9.007	3.81E-02	7.92E-01	-1.31	-0.16
lpg1076	small ORF (90aa)		ORFs of unknown function (unique)	6.186	9.112	9.062	9.342	3.57E-01	9.25E-01	2.93	0.28
lpg1076	small ORF (90aa)		ORFs of unknown function (unique)	4.422	5.799	7.062	7.698	7.61E-01	7.89E-01	1.38	0.64
lpg1077	inner membrane protein		Named proteins of general function	7.703	5.501	8.239	6.714	1.39E-02	3.62E-01	-2.20	-1.53
lpg1077	inner membrane protein		Named proteins of general function	7.238	7.111	7.925	8.023	8.89E-01	9.22E-01	-0.13	0.10
lpg1078	small ORF (123aa)		ORFs of unknown function (unique)	10.580	8.928	9.235	8.726	1.65E-03	5.34E-01	-1.65	-0.51
lpg1078	small ORF (123aa)		ORFs of unknown function (unique)	10.507	9.360	9.121	9.053	1.15E-02	9.42E-01	-1.15	-0.07
lpg1079	small ORF (56aa)?		ORFs of unknown function (unique)	8.647	7.903	8.371	6.844	1.13E-01	8.17E-02	-0.74	-1.53
lpg1079	small ORF (56aa)?		ORFs of unknown function (unique)	8.288	6.898	7.151	6.427	1.69E-01	6.84E-01	-1.39	-0.72
lpg1080	deoxyguanosine triphosphate triphosphohydrolase (dGTP triphospho		Nucleotide Metabolism	10.969	12.696	12.706	9.177	3.07E-02	2.11E-03	1.73	-3.53
lpg1080	deoxyguanosine triphosphate triphosphohydrolase (dGTP triphospho		Nucleotide Metabolism	10.996	12.654	12.798	9.393	3.53E-02	1.53E-03	1.66	-3.41
lpg1081	reverse transcriptase		Viral functions / Phage / Transposases	6.744	7.652		7.400	2.33E-01		0.91	
lpg1081	reverse transcriptase		Viral functions / Phage / Transposases	6.556	8.540		7.168	1.09E-01		1.98	
lpg1082	small ORF (135aa)		ORFs of unknown function (unique)	7.048	8.412	7.798	8.192	2.77E-01	6.91E-01	1.36	0.39
lpg1082	small ORF (135aa)		ORFs of unknown function (unique)	7.337	8.472	7.486	7.951	2.83E-01	6.32E-01	1.14	0.47
lpg1083	conserved hypothetical protein		Unknown / hypothetical proteins	9.671	8.790	12.339	8.722	2.88E-01	5.99E-03	-0.88	-3.62
lpg1083	conserved hypothetical protein		Unknown / hypothetical proteins	9.652	8.077	12.393	9.399	2.74E-01	2.65E-02	-1.58	-2.99
lpg1084	hypothetical (cytosolic protein)		Named proteins of general function	11.076	12.191	11.239	11.535	7.27E-06	2.29E-01	1.12	0.30
lpg1084	hypothetical (cytosolic protein)		Named proteins of general function	10.913	13.036	11.025	11.445	3.69E-05	2.13E-01	2.12	0.42
lpg1085	phage related integrase (site specific recombinase)		Viral functions / Phage / Transposases	10.120	11.123	11.375	11.024	2.32E-01	5.45E-01	1.00	-0.35
lpg1085	phage related integrase (site specific recombinase)		Viral functions / Phage / Transposases	10.171	11.801	11.275	11.306	1.84E-05	9.45E-01	1.63	0.03
lpg1087	virulence factor MviN (integral membrane protein, inner membrane), r		Toxin production / other pathogen func	9.981	9.486	9.490	8.717	3.92E-01	1.72E-01	-0.50	-0.77
lpg1087	virulence factor MviN (integral membrane protein, inner membrane), r		Toxin production / other pathogen func	9.918	9.853	9.800	9.087	8.83E-01	2.35E-01	-0.07	-0.71
lpg1088	nucleotidyltransferase PLUS glutamate rich protein GrpB PLUS ribos		Protein fate / hydrolases / secretion	9.329	7.713	8.146	7.177	3.80E-03	2.20E-01	-1.62	-0.97
lpg1088	nucleotidyltransferase PLUS glutamate rich protein GrpB PLUS ribos		Protein fate / hydrolases / secretion	8.818	7.837	7.357	8.389	1.53E-01	1.16E-01	-0.98	1.03
lpg1089	methyltransferase (N-methyltransferase?)		Named proteins of general function	10.337	10.261	11.107	10.047	8.58E-01	1.72E-02	-0.08	-1.06
lpg1089	methyltransferase (N-methyltransferase?)		Named proteins of general function	10.050	12.013	9.467	9.638	6.29E-05	7.76E-01	1.96	0.17
lpg1090	hypothetical		Unknown / hypothetical proteins	7.207	7.661	8.066	6.485	5.48E-01	2.49E-01	0.45	-1.58
lpg1090	hypothetical		Unknown / hypothetical proteins	6.612	7.637	7.522	6.668	1.47E-01	4.31E-01	1.02	-0.85
lpg1091	ORF acetyltransferase?		Unknown / hypothetical proteins	9.606	10.926	8.303	9.330	1.42E-03	2.18E-01	1.32	1.03
lpg1091	ORF acetyltransferase?		Unknown / hypothetical proteins	10.015	11.019	8.061	9.537	1.17E-02	8.57E-02	1.00	1.48
lpg1092	beta-phosphoglucomutase (phosphatase/phosphohexomutase)		Metabolism of Complex Carbohydrate	6.898	5.895	9.134	2.031	4.03E-01	2.85E-02	-1.00	-7.10
lpg1092	beta-phosphoglucomutase (phosphatase/phosphohexomutase)		Metabolism of Complex Carbohydrate	7.585	6.814	10.044	7.634	6.30E-01	1.09E-02	-0.77	-2.41
lpg1093	cation efflux transporter (calcium transporting ATPase) (c	*pacL*	Metabolism of Complex Carbohydrate	9.121	9.569	9.462	8.660	3.66E-01	1.64E-01	0.45	-0.80
lpg1093	cation efflux transporter (calcium transporting ATPase) (c	*pacL*	Metabolism of Complex Carbohydrate	9.097	9.785	9.374	9.652	3.02E-01	7.31E-01	0.69	0.28
lpg1094	chemiosmotic efflux system B protein C (outer membrane efflux prote		Transport and binding	8.813	7.675	9.540	6.638	3.26E-02	1.93E-03	-1.14	-2.90
lpg1094	chemiosmotic efflux system B protein C (outer membrane efflux prote		Transport and binding	8.914	8.067	9.522	7.001	1.82E-01	2.36E-04	-0.85	-2.52
lpg1095	chemiosmotic efflux system B protein B (heavy metal efflux) (cation e		Transport and binding	11.322	11.080	12.754	11.309	6.40E-01	4.35E-03	-0.24	-1.44
lpg1095	chemiosmotic efflux system B protein B (heavy metal efflux) (cation e		Transport and binding	11.585	12.123	12.914	12.463	1.07E-01	2.07E-01	0.54	-0.45
lpg1096	chemiosmotic efflux system B protein A (silver efflux pump) (cation ef		Transport and binding	8.707	8.828	9.676	8.895	8.31E-01	2.09E-01	0.12	-0.78
lpg1096	chemiosmotic efflux system B protein A (silver efflux pump) (cation ef		Transport and binding	8.886	8.995	9.849	9.263	7.81E-01	1.65E-01	0.11	-0.59
lpg1097	polyhydroxyalkanoic synthase (PHA synthase) (poly(3-hy	*phbC*	Carbohydrate Metabolism, Amino Acid	9.096	9.427	11.558	10.251	3.66E-01	4.08E-02	0.33	-1.31
lpg1097	polyhydroxyalkanoic synthase (PHA synthase) (poly(3-hy	*phbC*	Carbohydrate Metabolism, Amino Acid	9.536	9.975	11.659	11.019	1.78E-01	1.08E-01	0.44	-0.64
lpg1098	small ORF (63aa)?		ORFs of unknown function (unique)	10.085	9.762	12.805	8.233	7.42E-01	2.83E-03	-0.32	-4.57
lpg1098	small ORF (63aa)?		ORFs of unknown function (unique)	10.003	9.223	12.749	9.107	5.18E-01	7.47E-03	-0.78	-3.64
lpg1099	small ORF (152aa)		ORFs of unknown function (unique)	10.730	10.672	10.599	10.274	9.42E-01	5.88E-01	-0.06	-0.32
lpg1099	small ORF (152aa)		ORFs of unknown function (unique)	10.831	10.621	10.328	10.347	7.47E-01	9.77E-01	-0.21	0.02

lpg1100	proton transporter (ExoD protein) (exopolysaccharide synthesis prote		Transport and binding, Metabolism of	9.086	7.111	8.997	6.688	6.25E-02	9.52E-03	-1.97	-2.31
lpg1100	proton transporter (ExoD protein) (exopolysaccharide synthesis prote		Transport and binding, Metabolism of	8.987	7.223	8.488	6.543	3.00E-02	1.68E-02	-1.76	-1.94
lpg1101	ORF		ORFs of unknown function (unique)	8.628	9.601	8.827	9.510	6.41E-02	8.60E-02	0.97	0.68
lpg1101	ORF		ORFs of unknown function (unique)	8.693	9.175	8.147	9.633	4.28E-01	1.45E-01	0.48	1.49
lpg1102	ORF		ORFs of unknown function (unique)	8.994	9.576	10.686	9.059	1.22E-01	1.19E-01	0.58	-1.63
lpg1102	ORF		ORFs of unknown function (unique)	8.908	8.716	10.709	9.270	7.72E-01	8.51E-02	-0.19	-1.44
lpg1103	hypothetical (esterase)		Protein fate / hydrolases / secretion	10.304	9.399	9.119	9.625	4.33E-02	4.77E-01	-0.90	0.51
lpg1103	hypothetical (esterase)		Protein fate / hydrolases / secretion	10.059	9.759	7.755	10.187	8.07E-01	2.75E-01	-0.30	2.43
lpg1104	hypothetical protein		Unknown / hypothetical proteins	9.211	10.075	9.242	9.381	1.18E-01	7.76E-01	0.86	0.14
lpg1104	hypothetical protein		Unknown / hypothetical proteins	9.060	10.580	9.084	9.746	8.79E-02	2.82E-01	1.52	0.66
lpg1105	peptide methionine sulfoxide reductase		Detoxification / adaptation	6.604	10.082	7.309	7.891	3.67E-02	6.23E-01	3.48	0.58
lpg1105	peptide methionine sulfoxide reductase		Detoxification / adaptation	7.291	9.192	7.211	8.778	3.17E-02	2.04E-01	1.90	1.57
lpg1106	ORF		ORFs of unknown function (unique)	13.856	15.080	12.643	14.298	3.03E-03	8.18E-07	1.22	1.65
lpg1106	ORF		ORFs of unknown function (unique)	13.866	15.121	12.608	14.323	1.47E-03	4.94E-07	1.26	1.72
lpg1107	bacterial/Archaeal transporter family protein		Transport and binding	10.762	10.294	9.374	9.739	1.72E-01	4.89E-01	-0.47	0.36
lpg1107	bacterial/Archaeal transporter family protein		Transport and binding	10.674	10.502	9.296	9.944	5.34E-01	1.16E-01	-0.17	0.65
lpg1108	putative lipase		Protein fate / hydrolases / secretion	10.054	10.995	10.120	9.871	1.54E-01	7.57E-01	0.94	-0.25
lpg1108	putative lipase		Protein fate / hydrolases / secretion	9.997	11.438	10.046	10.517	6.41E-03	1.66E-01	1.44	0.47
lpg1109	ORF		ORFs of unknown function (unique)	9.678	9.991	10.331	9.961	2.84E-01	2.67E-01	0.31	-0.37
lpg1109	ORF		ORFs of unknown function (unique)	9.716	9.162	9.883	10.081	2.85E-01	7.42E-01	-0.55	0.20
lpg1110	ORF		ORFs of unknown function (unique)	9.720	11.314	9.839	8.739	3.20E-03	2.24E-01	1.59	-1.10
lpg1110	ORF		ORFs of unknown function (unique)	9.951	11.500	9.882	10.176	1.57E-02	5.95E-01	1.55	0.29
lpg1111	ORF		ORFs of unknown function (unique)	13.989	15.509	15.182	13.600	3.44E-03	5.96E-05	1.52	-1.58
lpg1111	ORF		ORFs of unknown function (unique)	13.978	15.465	15.094	13.613	1.26E-02	2.77E-05	1.49	-1.48
lpg1112	small ORF (127aa)		ORFs of unknown function (unique)	9.390	10.248	12.416	8.445	2.52E-01	1.21E-04	0.86	-3.97
lpg1112	small ORF (127aa)		ORFs of unknown function (unique)	7.841	10.730	11.842	9.467	3.80E-02	3.59E-02	2.89	-2.37
lpg1113	hypothetical		Unknown / hypothetical proteins	10.016	9.247	11.756	8.364	6.08E-02	1.82E-03	-0.77	-3.39
lpg1113	hypothetical		Unknown / hypothetical proteins	10.270	9.841	11.653	10.041	2.85E-01	2.43E-04	-0.43	-1.61
lpg1114	sensory box protein (GGDEF domain/EAL domain)		Signal transduction / other regulatory f	8.632	9.371	11.017	8.417	4.34E-01	8.20E-02	0.74	-2.60
lpg1114	sensory box protein (GGDEF domain/EAL domain)		Signal transduction / other regulatory f	8.947	8.766	10.772	8.291	8.62E-01	9.52E-02	-0.18	-2.48
lpg1115	DNA integration/recombination/inversion protein (circadia	*kaiC2*	Replication and Repair	8.938	10.676	11.875	8.766	2.24E-02	2.96E-03	1.74	-3.11
lpg1115	DNA integration/recombination/inversion protein (circadia	*kaiC2*	Replication and Repair	9.474	10.817	11.733	8.688	6.96E-03	2.46E-03	1.34	-3.04
lpg1116	chitinase (exochitinase) aminosugars metabolism?		Protein fate / hydrolases / secretion	12.752	15.096	13.701	12.733	2.41E-04	1.36E-02	2.34	-0.97
lpg1116	chitinase (exochitinase) aminosugars metabolism?		Protein fate / hydrolases / secretion	12.772	15.171	13.695	12.760	6.01E-05	2.02E-02	2.40	-0.94
lpg1117	small ORF (157aa) transcriptional repressor of sporulatio	*paiA*	Protein fate / hydrolases / secretion, C	10.236	11.068	12.658	10.153	1.04E-01	2.86E-04	0.83	-2.50
lpg1117	small ORF (157aa) transcriptional repressor of sporulatio	*paiA*	Protein fate / hydrolases / secretion, C	9.956	11.726	12.467	10.977	5.04E-04	5.12E-03	1.77	-1.49
lpg1118	serine-type D-Ala-D-Ala carboxypeptidase (D-alanyl-D-alanine carbox		Protein fate / hydrolases / secretion	9.361	10.623	10.835	8.060	7.29E-02	9.23E-03	1.26	-2.78
lpg1118	serine-type D-Ala-D-Ala carboxypeptidase (D-alanyl-D-alanine carbox		Protein fate / hydrolases / secretion	8.917	10.405	11.570	9.122	4.55E-02	6.04E-04	1.49	-2.45
lpg1119	major acid phosphatase (L. pneumophila)	*Acph-1*	Named proteins of general function	12.301	11.858	12.259	11.769	7.36E-01	4.83E-01	-0.44	-0.49
lpg1119	major acid phosphatase (L. pneumophila)	*Acph-1*	Named proteins of general function	12.385	12.991	12.366	12.239	4.84E-02	6.63E-01	0.61	-0.13
lpg1120	hypothetical protein		Unknown / hypothetical proteins	9.479	8.938	7.443	10.483	4.73E-01	1.22E-03	-0.54	3.04
lpg1120	hypothetical protein		Unknown / hypothetical proteins	8.095	9.501	7.574	10.615	2.06E-02	1.51E-03	1.41	3.04
lpg1121	ORF		ORFs of unknown function (unique)	10.532	9.737	10.791	9.804	1.00E-01	1.02E-01	-0.80	-0.99
lpg1121	ORF		ORFs of unknown function (unique)	10.488	9.564	10.998	10.306	8.23E-02	8.51E-02	-0.92	-0.69
lpg1122	membrane bound lytic murein transglycosylase D		Metabolism of Complex Carbohydrate	8.604	8.581	9.294	8.655	9.59E-01	2.25E-01	-0.02	-0.64
lpg1122	membrane bound lytic murein transglycosylase D		Metabolism of Complex Carbohydrate	8.629	8.240	9.112	8.523	7.09E-01	3.60E-01	-0.39	-0.59
lpg1123	Peb1 (arginine binding periplasmic protein (amino acid A	*artJ*	Transport and binding	9.670	10.315	11.551	10.013	4.45E-01	3.88E-02	0.65	-1.54
lpg1123	Peb1 (arginine binding periplasmic protein (amino acid A	*artJ*	Transport and binding	9.712	10.209	11.106	9.790	5.53E-01	2.08E-01	0.50	-1.32
lpg1124	ORF		ORFs of unknown function (unique)	9.391	9.108	9.920	5.875	8.19E-01	3.97E-02	-0.28	-4.05
lpg1124	ORF		ORFs of unknown function (unique)	9.479	9.900	9.731	8.429	3.53E-01	7.84E-02	0.42	-1.30
lpg1125	cystine/glutamine-binding periplasmic protein (glutamine ABC transpo		Transport and binding	13.990	11.745	12.336	12.838	5.26E-03	4.57E-01	-2.25	0.50
lpg1125	cystine/glutamine-binding periplasmic protein (glutamine ABC transpo		Transport and binding	13.794	11.834	12.283	12.876	6.40E-03	3.69E-01	-1.96	0.59
lpg1126	calcium-transporting ATPase		Transport and binding	11.282	11.382	11.555	9.584	8.46E-01	1.97E-03	0.10	-1.97
lpg1126	calcium-transporting ATPase		Transport and binding	11.504	11.633	11.560	9.714	7.25E-01	6.16E-03	0.13	-1.85
lpg1127	acyl CoA synthetase, long chain fatty acid:CoA ligase (feruloyl CoA sy		Lipid Metabolism	10.250	8.572	12.851	8.646	6.12E-02	2.35E-04	-1.68	-4.20
lpg1127	acyl CoA synthetase, long chain fatty acid:CoA ligase (feruloyl CoA sy		Lipid Metabolism	10.390	9.434	12.912	9.350	1.22E-01	2.16E-04	-0.96	-3.56
lpg1128	cytidine/deoxycytidylate deaminase		Nucleotide Metabolism	9.941	9.910	10.808	9.753	9.25E-01	3.89E-02	-0.03	-1.06
lpg1128	cytidine/deoxycytidylate deaminase		Nucleotide Metabolism	10.151	10.252	10.837	10.121	7.60E-01	8.48E-02	0.10	-0.72
lpg1129	ORF		ORFs of unknown function (unique)	8.658	8.966	9.083	8.282	7.91E-01	6.06E-01	0.31	-0.80
lpg1129	ORF		ORFs of unknown function (unique)	8.784	8.084	9.438	9.160	6.20E-02	5.00E-01	-0.70	-0.28
lpg1130	adenylate cyclase (adenylate cyclase/guanylate cyclase	*cyaA4*	Nucleotide Metabolism	10.801	11.158	11.326	10.511	5.55E-01	1.09E-01	0.36	-0.82
lpg1130	adenylate cyclase (adenylate cyclase/guanylate cyclase	*cyaA4*	Nucleotide Metabolism	10.869	11.043	11.321	10.908	7.47E-01	1.83E-01	0.17	-0.41
lpg1131	cyclopropane fatty acid synthase (cyclopropane fatty acy	*cfa*	Lipid Metabolism, Metabolism of Com	10.740	10.770	12.458	10.401	9.59E-01	1.44E-04	0.03	-2.06
lpg1131	cyclopropane fatty acid synthase (cyclopropane fatty acy	*cfa*	Lipid Metabolism, Metabolism of Com	10.719	10.502	12.333	10.361	7.63E-01	2.06E-04	-0.22	-1.97

lpg1132	small ORF (126aa)		ORFs of unknown function (unique)	9.007	9.917	10.680	7.968	4.05E-01	1.90E-02	0.91	-2.71
lpg1132	small ORF (126aa)		ORFs of unknown function (unique)	9.394	9.873	10.467	9.451	6.84E-01	4.01E-01	0.48	-1.02
lpg1133	small ORF (59aa)?		ORFs of unknown function (unique)	9.583	9.170	9.594	9.865	2.87E-01	4.81E-01	-0.41	0.27
lpg1133	small ORF (59aa)?		ORFs of unknown function (unique)	9.250	9.820	8.605	10.471	3.55E-01	2.53E-03	0.57	1.87
lpg1134	nitropropane dioxygenase/(trans-enoyl-CoA reductase)		Named proteins of general function	10.297	10.414	12.798	9.833	8.81E-01	2.21E-03	0.12	-2.97
lpg1134	nitropropane dioxygenase/(trans-enoyl-CoA reductase)		Named proteins of general function	10.424	11.136	12.891	10.235	4.51E-01	5.27E-03	0.71	-2.66
lpg1135	bacterial regulatory proteins, TetR family		Transcription factors / DNA binding prc	8.753	9.483	12.350	9.077	4.88E-01	1.02E-02	0.73	-3.27
lpg1135	bacterial regulatory proteins, TetR family		Transcription factors / DNA binding prc	8.669	9.797	12.386	9.147	3.07E-01	1.10E-02	1.13	-3.24
lpg1136	hypothetical (lipoprotein)		Named proteins of general function	9.646	10.684	10.672	9.834	9.35E-02	4.66E-02	1.04	-0.84
lpg1136	hypothetical (lipoprotein)		Named proteins of general function	9.480	10.373	10.432	9.925	1.37E-01	2.84E-01	0.89	-0.51
lpg1137	ORF		ORFs of unknown function (unique)	10.394	10.773	10.791	11.383	3.25E-01	9.23E-02	0.38	0.59
lpg1137	ORF		ORFs of unknown function (unique)	9.994	10.901	10.815	11.455	1.02E-02	4.58E-02	0.91	0.64
lpg1138	spermidine/putrescine-binding periplasmic protein PotD		Transport and binding	11.791	9.025	11.333	10.509	3.87E-04	6.14E-02	-2.77	-0.82
lpg1138	spermidine/putrescine-binding periplasmic protein PotD		Transport and binding	11.843	8.697	11.243	10.497	2.63E-03	7.46E-02	-3.15	-0.75
lpg1139	spermidine/putrescine ABC transporter permease protein	*potC*	Transport and binding	9.513	9.783	9.710	9.822	7.35E-01	8.76E-01	0.27	0.11
lpg1139	spermidine/putrescine ABC transporter permease protein	*potC*	Transport and binding	9.688	9.919	9.160	9.876	7.74E-01	7.32E-02	0.23	0.72
lpg1140	spermidine/putrescine ABC transporter permease protein	*potB*	Transport and binding	10.845	10.913	10.617	10.921	9.08E-01	5.82E-01	0.07	0.30
lpg1140	spermidine/putrescine ABC transporter permease protein	*potB*	Transport and binding	10.879	10.651	10.282	10.841	6.56E-01	2.60E-01	-0.23	0.56
lpg1141	spermidine/putrescine ABC transporter, ATP-binding protein PotA		Transport and binding	10.035	4.586	8.169	8.570	4.16E-06	6.47E-01	-5.45	0.40
lpg1141	spermidine/putrescine ABC transporter, ATP-binding protein PotA		Transport and binding	10.041	6.790	8.467	9.720	2.90E-02	1.75E-01	-3.25	1.25
lpg1142	ORF Hypothetical COG2827		Unknown / hypothetical proteins	10.261	9.434	10.167	9.932	9.01E-02	6.80E-01	-0.83	-0.23
lpg1142	ORF Hypothetical COG2827		Unknown / hypothetical proteins	10.072	9.742	9.958	9.989	4.29E-01	9.52E-01	-0.33	0.03
lpg1143	short chain type dehydrogenase/reductase (retinol dehydrogenase)		Lipid Metabolism	8.362	7.192	11.214	6.669	3.17E-01	1.72E-03	-1.17	-4.54
lpg1143	short chain type dehydrogenase/reductase (retinol dehydrogenase)		Lipid Metabolism	8.382	7.058	11.141	7.806	1.47E-01	6.89E-03	-1.32	-3.34
lpg1144	ORF	*cegC3*	ORFs of unknown function (unique)	9.375	10.924	11.254	10.901	2.77E-03	3.67E-01	1.55	-0.35
lpg1144	ORF	*cegC3*	ORFs of unknown function (unique)	9.034	11.104	10.473	10.579	6.41E-04	7.94E-01	2.07	0.11
lpg1145	ORF		ORFs of unknown function (unique)	10.206	10.748	13.292	8.967	6.45E-01	1.58E-03	0.54	-4.32
lpg1145	ORF		ORFs of unknown function (unique)	10.361	11.551	13.303	9.571	3.34E-01	3.07E-03	1.19	-3.73
lpg1146	thermostable carboxypeptidase 1		DNA/RNA degradation / restriction	10.385	10.489	11.057	10.016	8.45E-01	1.49E-01	0.10	-1.04
lpg1146	thermostable carboxypeptidase 1		DNA/RNA degradation / restriction	10.155	9.852	10.708	9.811	3.64E-01	1.50E-01	-0.30	-0.90
lpg1147	acetyltransferase? streptothricin acetyltransferase		Named proteins of general function	12.210	11.765	13.428	11.470	2.60E-01	1.02E-03	-0.44	-1.96
lpg1147	acetyltransferase? streptothricin acetyltransferase		Named proteins of general function	12.177	11.721	13.354	11.619	2.21E-01	1.49E-03	-0.46	-1.74
lpg1148	ORF		ORFs of unknown function (unique)	10.464	11.615	12.108	9.800	3.53E-03	3.78E-04	1.15	-2.31
lpg1148	ORF		ORFs of unknown function (unique)	10.468	11.829	12.093	10.004	3.68E-03	7.94E-04	1.36	-2.09
lpg1149	ORF		ORFs of unknown function (unique)	10.833	9.994	10.570	10.111	3.76E-01	5.49E-01	-0.84	-0.46
lpg1149	ORF		ORFs of unknown function (unique)	10.963	9.482	9.567	9.736	2.58E-03	7.23E-01	-1.48	0.17
lpg1150	transcription regulator protein (methylated DNA protein cysteine meth		Detoxification / adaptation, Transcriptic	8.562	8.866	9.752	8.519	7.56E-01	2.78E-02	0.30	-1.23
lpg1150	transcription regulator protein (methylated DNA protein cysteine meth		Detoxification / adaptation, Transcriptic	8.599	9.517	9.500	9.646	1.98E-01	8.32E-01	0.92	0.15
lpg1151	ORF		ORFs of unknown function (unique)	9.533	8.261	11.060	8.588	2.20E-01	1.19E-03	-1.27	-2.47
lpg1151	ORF		ORFs of unknown function (unique)	9.500	9.915	11.081	8.666	5.10E-01	1.65E-03	0.41	-2.41
lpg1152	ORF		ORFs of unknown function (unique)	9.741	11.246	9.714	11.667	5.98E-03	9.66E-02	1.50	1.95
lpg1152	ORF		ORFs of unknown function (unique)	9.700	11.258	8.836	10.928	7.22E-02	2.18E-01	1.56	2.09
lpg1153	amine oxidase		Amino Acid Metabolism, Biosynthesis	9.915	9.372	8.922	8.513	1.32E-01	5.44E-01	-0.54	-0.41
lpg1153	amine oxidase		Amino Acid Metabolism, Biosynthesis	9.145	8.784	8.576	8.496	5.29E-02	8.81E-01	-0.36	-0.08
lpg1154	ORF		ORFs of unknown function (unique)	11.163	12.454	13.788	8.446	1.07E-01	4.50E-05	1.29	-5.34
lpg1154	ORF		ORFs of unknown function (unique)	11.221	12.871	13.826	9.182	4.62E-02	3.61E-04	1.65	-4.64
lpg1155	pyruvate decarboxylase		Carbohydrate Metabolism	10.597	10.114	12.151	10.231	5.27E-01	3.30E-02	-0.48	-1.92
lpg1155	pyruvate decarboxylase		Carbohydrate Metabolism	10.633	10.665	12.242	10.339	9.56E-01	1.79E-02	0.03	-1.90
lpg1156	aminopeptidase (leucine aminopeptidase)		Protein fate / hydrolases / secretion	10.763	11.974	12.272	12.180	1.62E-02	7.92E-01	1.21	-0.09
lpg1156	aminopeptidase (leucine aminopeptidase)		Protein fate / hydrolases / secretion	10.904	12.178	12.470	12.383	1.49E-02	7.92E-01	1.27	-0.09
lpg1157	lipase B (conserved hypothetical protein-putative ATP/GTP-binding pr		Protein fate / hydrolases / secretion, S	8.900	6.361	7.290	4.838	8.53E-04	2.27E-01	-2.54	-2.45
lpg1157	lipase B (conserved hypothetical protein-putative ATP/GTP-binding pr		Protein fate / hydrolases / secretion, S	8.883	7.849	7.294	7.076	2.87E-01	8.68E-01	-1.03	-0.22
lpg1158	ORF		ORFs of unknown function (unique)	8.694	8.105	11.328	8.029	4.43E-01	7.14E-03	-0.59	-3.30
lpg1158	ORF		ORFs of unknown function (unique)	8.668	9.170	11.686	8.844	6.04E-01	5.24E-03	0.50	-2.84
lpg1159	hypothetical (transporter?)		Unknown / hypothetical proteins	9.714	10.303	10.735	9.583	4.91E-01	8.06E-02	0.59	-1.15
lpg1159	hypothetical (transporter?)		Unknown / hypothetical proteins	9.623	10.378	10.557	9.669	4.30E-01	2.84E-01	0.76	-0.89
lpg1160	ORF		ORFs of unknown function (unique)	10.541	12.242	13.945	10.518	1.20E-06	2.84E-02	1.70	-3.43
lpg1160	ORF		ORFs of unknown function (unique)	10.571	12.237	13.860	10.632	7.46E-06	3.80E-02	1.67	-3.23
lpg1161	phosphoribosyltransferase		Nucleotide Metabolism	10.385	9.513	12.427	9.199	1.32E-01	1.43E-03	-0.87	-3.23
lpg1161	phosphoribosyltransferase		Nucleotide Metabolism	10.394	9.360	12.448	9.666	7.08E-02	4.81E-03	-1.03	-2.78
lpg1162	ompA-like transmembrane domain protein		Named proteins of general function	13.120	13.200	10.971	12.789	8.91E-01	7.43E-03	0.08	1.82
lpg1162	ompA-like transmembrane domain protein		Named proteins of general function	13.240	13.102	10.946	12.810	8.27E-01	6.37E-03	-0.14	1.86
lpg1163	MFS transporter (sugar transporter transmembrane protein) (citrate-p		Transport and binding	10.163	8.732	9.136	8.605	5.63E-02	5.73E-01	-1.43	-0.53
lpg1163	MFS transporter (sugar transporter transmembrane protein) (citrate-p		Transport and binding	10.279	9.022	8.924	9.400	3.00E-03	5.24E-01	-1.26	0.48

lpg1164	acetylornithine deacetylase (acetylornithinase)	*argE*	Amino Acid Metabolism	10.515	9.379	9.700	10.493	6.55E-03	2.30E-02	-1.14	0.79
lpg1164	acetylornithine deacetylase (acetylornithinase)	*argE*	Amino Acid Metabolism	10.429	9.880	9.505	10.871	1.57E-01	3.84E-03	-0.55	1.37
lpg1165	uridine kinase	*udk*	Nucleotide Metabolism	11.071	11.691	9.467	10.736	2.40E-01	4.05E-02	0.62	1.27
lpg1165	uridine kinase	*udk*	Nucleotide Metabolism	11.045	11.178	9.199	10.729	8.24E-01	1.73E-02	0.13	1.53
lpg1166	hypothetical protein		Unknown / hypothetical proteins	6.211	6.670	7.222	6.842	7.85E-01	9.03E-01	0.46	-0.38
lpg1166	hypothetical protein		Unknown / hypothetical proteins	6.019	6.310	4.275	6.266	9.35E-01	3.55E-01	0.29	1.99
lpg1167	hypothetical (cytoplasmic protein)		Named proteins of general function	12.102	10.097	9.461	9.976	1.06E-03	6.17E-01	-2.00	0.52
lpg1167	hypothetical (cytoplasmic protein)		Named proteins of general function	12.449	9.961	8.480	9.712	3.33E-05	2.58E-01	-2.49	1.23
lpg1168	sensory box protein (GGDEF domain/EAL domain)		Signal transduction / other regulatory f	9.445	9.272	10.793	9.516	8.91E-01	3.25E-01	-0.17	-1.28
lpg1168	sensory box protein (GGDEF domain/EAL domain)		Signal transduction / other regulatory f	9.457	9.778	10.821	9.561	7.69E-01	3.32E-01	0.32	-1.26
lpg1169	hypothetical (dioxygenase)		Named proteins of general function	8.308	10.484	11.854	10.560	7.84E-02	1.81E-01	2.18	-1.29
lpg1169	hypothetical (dioxygenase)		Named proteins of general function	8.685	10.808	11.786	11.125	3.02E-02	3.01E-01	2.12	-0.66
lpg1170	pyruvate formate lyase-activating enzyme PflA		Chemotaxis / motility / cell division	8.691	10.208	10.075	9.191	2.41E-02	4.89E-01	1.52	-0.88
lpg1170	pyruvate formate lyase-activating enzyme PflA		Chemotaxis / motility / cell division	9.224	10.635	10.552	10.672	1.73E-01	8.97E-01	1.41	0.12
lpg1171	small ORF (139aa)		ORFs of unknown function (unique)	9.150	8.904	9.877	9.711	5.45E-01	6.29E-01	-0.25	-0.17
lpg1171	small ORF (139aa)		ORFs of unknown function (unique)	9.063	9.297	10.053	10.000	7.79E-01	8.93E-01	0.23	-0.05
lpg1172	TPR repeat protein (enhanced entry protein EnhC)		Toxin production / other pathogen func	10.299	10.156	11.375	9.909	7.67E-01	7.62E-03	-0.14	-1.47
lpg1172	TPR repeat protein (enhanced entry protein EnhC)		Toxin production / other pathogen func	9.895	10.106	11.226	9.929	3.86E-01	1.44E-02	0.21	-1.30
lpg1173	sensor protein PilS (pilin transcriptional activator) (senso	*pilS*	Protein fate / hydrolases / secretion, S	11.290	10.677	11.537	10.060	1.76E-02	1.03E-04	-0.61	-1.48
lpg1173	sensor protein PilS (pilin transcriptional activator) (senso	*pilS*	Protein fate / hydrolases / secretion, S	11.344	10.564	11.549	10.279	9.67E-04	2.00E-03	-0.78	-1.27
lpg1174	two component response regulator PilR (type 4 fimbriae	*pilR*	Protein fate / hydrolases / secretion, S	9.809	9.890	11.026	10.023	8.65E-01	2.71E-02	0.08	-1.00
lpg1174	two component response regulator PilR (type 4 fimbriae	*pilR*	Protein fate / hydrolases / secretion, S	10.079	10.111	10.951	10.079	9.17E-01	3.38E-02	0.03	-0.87
lpg1175	hydrolase (alpha/beta fold family) (aromatic hydrocarbon catabolism)		Protein fate / hydrolases / secretion	9.769	10.845	10.413	10.347	4.68E-05	8.30E-01	1.08	-0.07
lpg1175	hydrolase (alpha/beta fold family) (aromatic hydrocarbon catabolism)		Protein fate / hydrolases / secretion	9.769	10.697	10.309	10.348	9.09E-04	8.95E-01	0.93	0.04
lpg1176	Zn-dependent protease (zinc metalloprotease)		Protein fate / hydrolases / secretion	7.524	9.133	8.549	8.875	6.10E-02	4.93E-01	1.61	0.33
lpg1176	Zn-dependent protease (zinc metalloprotease)		Protein fate / hydrolases / secretion	8.226	9.705	8.251	9.268	1.64E-02	1.42E-01	1.48	1.02
lpg1177	riboflavin biosynthesis protein RibD	*ribD*	Metabolism of Cofactors and Vitamins	8.303	10.257	8.288	10.119	8.06E-02	1.41E-01	1.95	1.83
lpg1177	riboflavin biosynthesis protein RibD	*ribD*	Metabolism of Cofactors and Vitamins	9.259	10.629	6.697	10.293	2.01E-03	4.96E-03	1.37	3.60
lpg1178	riboflavin synthase, alpha subunit RibE	*ribE*	Metabolism of Cofactors and Vitamins	11.523	11.719	10.932	11.468	5.33E-01	7.14E-02	0.20	0.54
lpg1178	riboflavin synthase, alpha subunit RibE	*ribE*	Metabolism of Cofactors and Vitamins	11.577	11.852	10.780	11.490	2.42E-01	4.95E-02	0.27	0.71
lpg1179	riboflavin biosynthesis protein RibA (GTP cyclohydrolase	*ribA*	Metabolism of Cofactors and Vitamins	10.671	11.877	10.492	11.655	5.02E-03	6.07E-03	1.21	1.16
lpg1179	riboflavin biosynthesis protein RibA (GTP cyclohydrolase	*ribA*	Metabolism of Cofactors and Vitamins	10.836	12.090	10.470	11.851	1.02E-02	1.54E-03	1.25	1.38
lpg1180	riboflavin synthase, beta subunit RibB (6,7-dimethyl-8-rib	*ribH*	Metabolism of Cofactors and Vitamins	11.964	11.061	11.899	11.116	2.98E-02	1.52E-03	-0.90	-0.78
lpg1180	riboflavin synthase, beta subunit RibB (6,7-dimethyl-8-rib	*ribH*	Metabolism of Cofactors and Vitamins	12.008	11.287	11.756	11.223	2.16E-02	1.70E-02	-0.72	-0.53
lpg1181	CTP synthase PyrG	*pyrG*	Nucleotide Metabolism	12.191	12.885	11.820	12.542	3.40E-01	3.58E-01	0.69	0.72
lpg1181	CTP synthase PyrG	*pyrG*	Nucleotide Metabolism	12.202	12.896	11.834	12.578	3.43E-01	3.18E-01	0.69	0.74
lpg1182	2-dehydro-3-deoxyphosphonooctonate aldolase	*kdsA*	Metabolism of Complex Carbohydrate	10.472	11.405	10.007	11.067	1.18E-01	6.70E-02	0.93	1.06
lpg1182	2-dehydro-3-deoxyphosphonooctonate aldolase	*kdsA*	Metabolism of Complex Carbohydrate	10.360	11.466	9.769	10.898	1.04E-01	2.30E-02	1.11	1.13
lpg1183	ORF		Unknown / hypothetical proteins	9.061	10.812	10.498	8.210	7.01E-06	2.83E-03	1.75	-2.29
lpg1183	ORF		Unknown / hypothetical proteins	8.927	10.054	10.049	8.622	6.54E-02	2.31E-02	1.13	-1.43
lpg1184	outer membrane protein RomA		Named proteins of general function	9.342	9.955	10.421	8.964	1.04E-01	1.90E-03	0.61	-1.46
lpg1184	outer membrane protein RomA		Named proteins of general function	9.490	9.474	10.117	8.863	9.87E-01	1.36E-02	-0.02	-1.25
lpg1185	tRNA-Ser		tRNA	11.764	10.659	11.633	11.485	1.32E-03	6.20E-01	-1.11	-0.15
lpg1185	tRNA-Ser		tRNA	11.660	10.301	11.555	11.465	1.34E-02	7.98E-01	-1.36	-0.09
lpg1186	competence lipoprotein ComL		Transport and binding	10.997	10.940	9.850	11.594	9.53E-01	2.76E-02	-0.06	1.74
lpg1186	competence lipoprotein ComL		Transport and binding	10.869	11.985	9.985	12.353	2.35E-02	5.76E-04	1.12	2.37
lpg1187	exonuclease involved in removal of stalled replication for	*rdgC*	Replication and Repair	11.245	10.858	10.542	11.396	6.14E-01	1.38E-01	-0.39	0.85
lpg1187	exonuclease involved in removal of stalled replication for	*rdgC*	Replication and Repair	11.152	11.432	10.443	11.896	3.95E-01	1.18E-03	0.28	1.45
lpg1188	Kup system potassium uptake protein	*kup2*	Transport and binding	10.973	11.510	9.518	12.298	2.02E-01	1.71E-03	0.54	2.78
lpg1188	Kup system potassium uptake protein	*kup2*	Transport and binding	11.023	11.530	9.477	12.291	2.82E-01	1.17E-04	0.51	2.81
lpg1189	ORF		ORFs of unknown function (unique)	11.686	13.366	10.818	12.292	6.70E-05	4.80E-04	1.68	1.47
lpg1189	ORF		ORFs of unknown function (unique)	11.733	13.359	10.848	12.362	1.48E-04	4.72E-04	1.63	1.51
lpg1190	SAM-dependent methyltransferase		Named proteins of general function	9.392	9.657	9.114	9.661	4.63E-01	7.04E-02	0.26	0.55
lpg1190	SAM-dependent methyltransferase		Named proteins of general function	9.515	9.913	8.810	9.775	1.66E-01	4.32E-02	0.40	0.96
lpg1191	glycosyl hydrolase family 3 (anhydromuramoyl peptide exo beta-N-ac		Metabolism of Complex Carbohydrate	9.961	9.222	9.688	8.036	1.90E-01	1.78E-02	-0.74	-1.65
lpg1191	glycosyl hydrolase family 3 (anhydromuramoyl peptide exo beta-N-ac		Metabolism of Complex Carbohydrate	9.863	9.653	9.587	10.913	6.26E-01	3.97E-01	-0.21	1.33
lpg1192	ThiJ/PfpI family (transcriptional regulator, AraC family), isonitrile hydra		Transcription factors / DNA binding pro	9.327	9.491	9.972	8.889	6.48E-01	5.63E-02	0.16	-1.08
lpg1192	ThiJ/PfpI family (transcriptional regulator, AraC family), isonitrile hydra		Transcription factors / DNA binding pro	9.741	9.474	10.033	9.350	3.35E-01	7.38E-02	-0.27	-0.68
lpg1193	phosphoribosyl-ATP pyrophosphatase/phosphoribosyl A	*hisI*	Amino Acid Metabolism	11.678	12.775	10.152	12.424	7.26E-02	8.75E-04	1.10	2.27
lpg1193	phosphoribosyl-ATP pyrophosphatase/phosphoribosyl A	*hisI*	Amino Acid Metabolism	11.828	12.771	9.970	12.407	2.98E-02	2.16E-03	0.94	2.44
lpg1194	imidazoleglycerol-phosphate synthase, cyclase subunit HisF		Amino Acid Metabolism	6.555	9.758	8.039	10.251	1.93E-02	9.91E-03	3.20	2.21
lpg1194	imidazoleglycerol-phosphate synthase, cyclase subunit HisF		Amino Acid Metabolism	6.857	9.316	7.294	9.886	8.90E-03	1.89E-04	2.46	2.59
lpg1195	phosphoribosylformimino-5-aminoimidazole carboxamide	*hisA*	Amino Acid Metabolism	9.802	10.288	10.874	10.833	2.37E-01	9.09E-01	0.49	-0.04
lpg1195	phosphoribosylformimino-5-aminoimidazole carboxamide	*hisA*	Amino Acid Metabolism	9.902	10.957	10.945	11.111	1.98E-01	7.17E-01	1.05	0.17

lpg1196	amidotransferase HisH (glutamine amidotransferase)	*hisH_2*	Amino Acid Metabolism	9.268	8.428	8.279	8.941	5.61E-02	3.50E-01	-0.84	0.66
lpg1196	amidotransferase HisH (glutamine amidotransferase)	*hisH_2*	Amino Acid Metabolism	9.498	8.756	7.733	9.560	7.83E-02	7.09E-02	-0.74	1.83
lpg1197	histidinol phosphatase and imidazoleglycerol-phosphate dehydratase		Amino Acid Metabolism	10.394	10.628	11.277	11.099	6.25E-01	6.89E-01	0.23	-0.18
lpg1197	histidinol phosphatase and imidazoleglycerol-phosphate dehydratase		Amino Acid Metabolism	10.406	10.270	11.124	11.080	8.41E-01	9.18E-01	-0.14	-0.04
lpg1198	histidinol-phosphate aminotransferase	*hisC*	Amino Acid Metabolism	9.676	9.481	9.609	9.380	7.58E-01	8.24E-01	-0.19	-0.23
lpg1198	histidinol-phosphate aminotransferase	*hisC*	Amino Acid Metabolism	9.925	8.717	9.441	9.735	2.37E-03	6.80E-01	-1.21	0.29
lpg1199	histidinol dehydrogenase		Amino Acid Metabolism	9.567	8.621	8.390	10.289	3.55E-02	2.20E-04	-0.95	1.90
lpg1199	histidinol dehydrogenase		Amino Acid Metabolism	10.173	9.537	8.163	10.308	3.02E-01	3.61E-02	-0.64	2.15
lpg1200	ATP phosphoribosyltransferase HisG	*hisG*	Amino Acid Metabolism	10.203	9.251	9.098	10.384	1.70E-01	1.68E-01	-0.95	1.29
lpg1200	ATP phosphoribosyltransferase HisG	*hisG*	Amino Acid Metabolism	10.238	9.477	8.804	10.782	1.14E-01	2.93E-02	-0.76	1.98
lpg1201	hypothetical COG4496		Unknown / hypothetical proteins	10.266	11.892	8.463	10.297	6.24E-03	1.95E-03	1.63	1.83
lpg1201	hypothetical COG4496		Unknown / hypothetical proteins	9.786	10.417	8.124	10.097	3.93E-01	1.05E-01	0.63	1.97
lpg1202	cytochrome D ubiquinol oxidase, subunit I	*cydA-2*	Energy Metabolism	12.821	13.735	11.225	12.729	7.88E-02	1.36E-03	0.91	1.50
lpg1202	cytochrome D ubiquinol oxidase, subunit I	*cydA-2*	Energy Metabolism	12.902	13.753	10.931	12.759	4.92E-02	1.27E-03	0.85	1.83
lpg1203	cytochrome D ubiquinol oxidase, subunit II	*cydB*	Energy Metabolism	13.049	13.858	12.296	12.643	2.92E-02	7.62E-02	0.81	0.35
lpg1203	cytochrome D ubiquinol oxidase, subunit II	*cydB*	Energy Metabolism	13.014	13.888	12.285	12.680	3.24E-02	4.55E-02	0.87	0.40
lpg1204	orotate phosphoribosyltransferase	*pyrE*	Nucleotide Metabolism	11.357	12.394	11.292	13.301	4.26E-03	1.47E-04	1.04	2.01
lpg1204	orotate phosphoribosyltransferase	*pyrE*	Nucleotide Metabolism	11.235	12.442	11.108	13.250	1.04E-03	3.43E-04	1.21	2.14
lpg1205	cold shock domain family protein CspA		Detoxification / adaptation	15.024	14.235	13.128	14.393	1.33E-01	1.23E-02	-0.79	1.27
lpg1205	cold shock domain family protein CspA		Detoxification / adaptation	15.017	14.211	13.113	14.404	1.64E-01	1.44E-02	-0.81	1.29
lpg1206	sigma 54 modulation protein YhbH		Signal transduction / other regulatory f	10.871	11.512	14.524	9.485	4.18E-01	4.28E-04	0.64	-5.04
lpg1206	sigma 54 modulation protein YhbH		Signal transduction / other regulatory f	10.866	11.670	14.501	10.104	3.26E-01	1.76E-03	0.80	-4.40
lpg1207	conserved hypothetical protein COG2606		Unknown / hypothetical proteins	10.972	10.601	14.040	9.349	5.94E-01	1.54E-04	-0.37	-4.69
lpg1207	conserved hypothetical protein COG2606		Unknown / hypothetical proteins	10.971	10.694	14.044	9.575	6.62E-01	8.40E-04	-0.28	-4.47
lpg1208	transcriptional regulator MarR family		Transcription factors / DNA binding pro	10.295	9.862	10.953	9.880	3.26E-01	1.00E-02	-0.43	-1.07
lpg1208	transcriptional regulator MarR family		Transcription factors / DNA binding pro	10.371	9.436	10.822	9.850	1.59E-01	2.42E-02	-0.93	-0.97
lpg1209	conserved hypothetical protein		Unknown / hypothetical proteins	10.109	11.208	11.094	11.725	2.42E-02	1.56E-01	1.10	0.63
lpg1209	conserved hypothetical protein		Unknown / hypothetical proteins	9.863	11.313	10.797	11.690	1.01E-02	1.63E-02	1.45	0.89
lpg1210	acetyltransferase (ribosomal-protein alanine acetyltransferase)		Named proteins of general function	10.790	10.618	9.425	11.598	6.36E-01	1.05E-03	-0.17	2.17
lpg1210	acetyltransferase (ribosomal-protein alanine acetyltransferase)		Named proteins of general function	10.795	10.694	9.254	11.626	8.13E-01	3.00E-03	-0.10	2.37
lpg1211	transporter, LysE family (threonine efflux)		Transport and binding	10.404	9.401	10.476	9.485	1.74E-04	3.25E-02	-1.00	-0.99
lpg1211	transporter, LysE family (threonine efflux)		Transport and binding	10.232	9.745	10.406	9.704	2.18E-01	1.46E-01	-0.49	-0.70
lpg1212	IAA acetyltransferase/MarR transcriptional regulatory protein - fused		Transcription factors / DNA binding pro	10.500	9.294	9.488	9.802	1.55E-02	5.27E-01	-1.21	0.31
lpg1212	IAA acetyltransferase/MarR transcriptional regulatory protein - fused		Transcription factors / DNA binding pro	10.477	10.502	9.086	10.120	9.76E-01	7.13E-02	0.03	1.03
lpg1213	hypothetical (ATPase)		Named proteins of general function	10.741	9.595	9.264	9.766	7.82E-02	3.33E-01	-1.15	0.50
lpg1213	hypothetical (ATPase)		Named proteins of general function	10.444	10.515	8.757	10.319	9.45E-01	2.27E-01	0.07	1.56
lpg1214	2-acylglycerophosphoethanolamine acyltransferase (aas) (transporte		Lipid Metabolism	12.186	11.740	12.062	12.712	1.34E-01	5.10E-02	-0.45	0.65
lpg1214	2-acylglycerophosphoethanolamine acyltransferase (aas) (transporte		Lipid Metabolism	12.173	11.737	11.983	12.713	1.33E-01	3.41E-02	-0.44	0.73
lpg1215	oxygen-dependent coproporphyrinogen III oxidase	*hemF*	Metabolism of Cofactors and Vitamins	11.633	11.236	10.376	10.472	2.60E-01	8.68E-01	-0.40	0.10
lpg1215	oxygen-dependent coproporphyrinogen III oxidase	*hemF*	Metabolism of Cofactors and Vitamins	11.720	11.234	10.637	10.785	1.18E-01	7.19E-01	-0.49	0.15
lpg1216	flagellar basal body rod protein FlgB	*flgB*	Chemotaxis / motility / cell division	10.739	11.261	12.385	10.773	3.72E-01	6.24E-03	0.52	-1.61
lpg1216	flagellar basal body rod protein FlgB	*flgB*	Chemotaxis / motility / cell division	10.832	12.012	12.425	11.612	6.29E-03	1.74E-02	1.18	-0.81
lpg1217	flagellar basal body rod protein FlgC	*flgC*	Chemotaxis / motility / cell division	11.076	12.025	13.065	11.133	8.96E-02	1.11E-02	0.95	-1.93
lpg1217	flagellar basal body rod protein FlgC	*flgC*	Chemotaxis / motility / cell division	11.018	11.358	13.067	11.186	7.38E-01	1.27E-02	0.34	-1.88
lpg1218	flagellar basal body rod modification protein FlgD	*flgD*	Chemotaxis / motility / cell division	9.830	10.558	12.304	8.835	3.45E-01	4.03E-04	0.73	-3.47
lpg1218	flagellar basal body rod modification protein FlgD	*flgD*	Chemotaxis / motility / cell division	9.933	10.319	12.332	9.230	5.86E-01	1.42E-03	0.39	-3.10
lpg1219	flagellar hook protein FlgE	*flgE*	Chemotaxis / motility / cell division	9.074	9.282	11.585	8.647	7.92E-01	3.24E-02	0.21	-2.94
lpg1219	flagellar hook protein FlgE	*flgE*	Chemotaxis / motility / cell division	8.726	9.528	11.479	9.067	3.99E-01	4.14E-02	0.80	-2.41
lpg1220	flagellar basal body rod protein FlgF	*flgF*	Chemotaxis / motility / cell division	10.312	11.290	13.059	10.890	1.65E-01	5.87E-03	0.98	-2.17
lpg1220	flagellar basal body rod protein FlgF	*flgF*	Chemotaxis / motility / cell division	10.379	11.636	13.201	11.432	1.86E-01	4.12E-02	1.26	-1.77
lpg1221	flagellar basal body rod protein FlgG	*flgG*	Chemotaxis / motility / cell division	9.751	9.789	11.076	7.978	9.40E-01	1.31E-03	0.04	-3.10
lpg1221	flagellar basal body rod protein FlgG	*flgG*	Chemotaxis / motility / cell division	9.815	9.720	11.008	8.460	8.46E-01	5.70E-03	-0.10	-2.55
lpg1222	flagellar L-ring protein FlgH	*flgH*	Chemotaxis / motility / cell division	10.275	11.200	11.612	10.541	4.60E-02	2.64E-02	0.92	-1.07
lpg1222	flagellar L-ring protein FlgH	*flgH*	Chemotaxis / motility / cell division	9.882	11.072	11.443	10.544	2.93E-02	4.55E-02	1.19	-0.90
lpg1223	flagellar P-ring protein (precursor) FlgI	*flgI*	Chemotaxis / motility / cell division	9.385	9.100	11.078	8.962	6.50E-01	2.16E-03	-0.28	-2.12
lpg1223	flagellar P-ring protein (precursor) FlgI	*flgI*	Chemotaxis / motility / cell division	9.091	9.273	11.151	9.294	7.56E-01	4.10E-03	0.18	-1.86
lpg1224	muramidase, peptidoglycan hydrolase FlgJ (flagellar protein)		Protein fate / hydrolases / secretion, C	9.484	8.330	10.967	6.117	1.54E-01	1.10E-02	-1.15	-4.85
lpg1224	muramidase, peptidoglycan hydrolase FlgJ (flagellar protein)		Protein fate / hydrolases / secretion, C	11.282	9.563	11.030	9.028	7.83E-02	7.02E-02	-1.72	-2.00
lpg1225	flagellar hook associated protein 1 FlgK	*flgK*	Chemotaxis / motility / cell division	11.234	10.928	12.384	11.228	4.85E-01	6.26E-03	-0.31	-1.16
lpg1225	flagellar hook associated protein 1 FlgK	*flgK*	Chemotaxis / motility / cell division	11.136	11.193	12.266	11.213	8.77E-01	1.02E-02	0.06	-1.05
lpg1226	flagellar hook associated protein type 3 FlgL	*flgL*	Chemotaxis / motility / cell division	9.786	9.269	12.310	9.182	4.29E-01	2.55E-04	-0.52	-3.13
lpg1226	flagellar hook associated protein type 3 FlgL	*flgL*	Chemotaxis / motility / cell division	9.667	9.164	12.282	9.913	3.98E-01	5.06E-03	-0.50	-2.37
lpg1227	unknown	*vpdB*	Unknown / hypothetical proteins	9.171	8.403	10.192	7.696	4.76E-01	4.35E-02	-0.77	-2.50
lpg1227	unknown	*vpdB*	Unknown / hypothetical proteins	7.111	7.655	9.698	7.646	7.89E-01	1.41E-01	0.54	-2.05

lpg1228	hypothetical COG4804		Unknown / hypothetical proteins	11.302	10.013	9.573	11.003	4.11E-01	7.38E-02	-1.29	1.43
lpg1228	hypothetical COG4804		Unknown / hypothetical proteins	11.278	11.447	9.460	11.571	2.50E-01	3.69E-04	0.17	2.11
lpg1229	site specific recombinase (phage integrase)		Viral functions / Phage / Transposases	11.741	13.134	11.428	12.746	1.20E-03	1.42E-01	1.39	1.32
lpg1229	site specific recombinase (phage integrase)		Viral functions / Phage / Transposases	11.999	13.257	10.894	12.812	4.61E-04	1.28E-04	1.26	1.92
lpg1230	hypothetical		Unknown / hypothetical proteins	9.265	12.902	10.858	12.097	1.18E-03	2.98E-01	3.64	1.24
lpg1230	hypothetical		Unknown / hypothetical proteins	9.281	12.029	10.981	12.762	5.61E-02	3.61E-02	2.75	1.78
lpg1231	SOS response transcriptional regulator (SOS mutagenes	*umuD*	Detoxification / adaptation, Transcripti	9.647	9.876	10.822	10.157	5.94E-01	7.81E-02	0.23	-0.67
lpg1231	SOS response transcriptional regulator (SOS mutagenes	*umuD*	Detoxification / adaptation, Transcripti	9.269	9.536	10.509	10.771	4.81E-01	5.82E-01	0.27	0.26
lpg1232	hypothetical (SOS mutagenesis and repair) RumB (Umu	*umuC*	Replication and Repair	9.594	8.995	9.717	9.864	2.88E-01	7.43E-01	-0.60	0.15
lpg1232	hypothetical (SOS mutagenesis and repair) RumB (Umu	*umuC*	Replication and Repair	9.122	7.792	9.019	9.916	2.75E-01	8.73E-02	-1.33	0.90
lpg1233	ORF		ORFs of unknown function (unique)	9.774	10.380	9.386	7.669	2.64E-01	1.09E-01	0.61	-1.72
lpg1233	ORF		ORFs of unknown function (unique)	9.226	10.167	9.377	8.574	1.77E-01	3.68E-01	0.94	-0.80
lpg1234	hypothetical		Unknown / hypothetical proteins	10.882	10.275	12.945	10.076	5.18E-01	2.70E-03	-0.61	-2.87
lpg1234	hypothetical		Unknown / hypothetical proteins	10.911	11.105	12.924	10.311	8.35E-01	2.69E-03	0.19	-2.61
lpg1235	patch repair protein (DNA mismatch endonuclease)	*vsr*	Replication and Repair	9.169	9.423	10.901	8.721	7.17E-01	2.68E-02	0.25	-2.18
lpg1235	patch repair protein (DNA mismatch endonuclease)	*vsr*	Replication and Repair	9.035	8.818	10.377	8.681	7.75E-01	1.74E-01	-0.22	-1.70
lpg1236	modification methylase (Eco47II, Sau96I) (site-specific DNA-methyltra		DNA/RNA degradation / restriction	12.634	13.772	13.201	13.002	4.41E-03	5.11E-01	1.14	-0.20
lpg1236	modification methylase (Eco47II, Sau96I) (site-specific DNA-methyltra		DNA/RNA degradation / restriction	12.602	13.811	13.197	13.017	2.23E-03	5.50E-01	1.21	-0.18
lpg1237	type II restriction enzyme (Eco47II, Sau96I)		DNA/RNA degradation / restriction	11.890	13.286	10.047	14.085	1.20E-01	1.52E-05	1.40	4.04
lpg1237	type II restriction enzyme (Eco47II, Sau96I)		DNA/RNA degradation / restriction	12.094	13.252	9.541	14.128	8.49E-02	2.20E-05	1.16	4.59
lpg1238	ORF		ORFs of unknown function (unique)	9.701	9.183	7.676	9.273	4.68E-01	3.16E-01	-0.52	1.60
lpg1238	ORF		ORFs of unknown function (unique)	9.590	9.779	8.312	10.236	6.41E-01	1.65E-02	0.19	1.92
lpg1239	TraD (weak homology)		Transport and binding	11.633	12.588	12.442	11.983	1.58E-03	1.28E-02	0.96	-0.46
lpg1239	TraD (weak homology)		Transport and binding	11.672	12.244	12.335	11.925	2.77E-03	5.11E-02	0.57	-0.41
lpg1240	ORF		ORFs of unknown function (unique)	9.989	9.141	9.279	8.420	2.09E-01	5.24E-01	-0.85	-0.86
lpg1240	ORF		ORFs of unknown function (unique)	10.035	9.470	9.395	9.843	3.26E-01	6.09E-01	-0.56	0.45
lpg1241	conjugal transfer protein TraA	*traA*	Transport and binding, Viral functions	7.119	7.586	7.187	7.739	5.78E-01	6.97E-01	0.47	0.55
lpg1241	conjugal transfer protein TraA	*traA*	Transport and binding, Viral functions	8.283	8.604	7.851	8.694	6.22E-01	4.80E-01	0.32	0.84
lpg1242	; lpg2421; transposase (ISSod13) (integrase)		Viral functions / Phage / Transposases	11.272	10.600	10.552	10.828	3.64E-01	5.24E-01	-0.67	0.28
lpg1242	; lpg2421; transposase (ISSod13) (integrase)		Viral functions / Phage / Transposases	10.738	11.062	10.548	10.942	9.07E-02	3.72E-01	0.32	0.39
lpg1243	hypothetical		Unknown / hypothetical proteins	9.405	8.712	10.263	8.159	4.98E-02	1.00E-01	-0.69	-2.10
lpg1243	hypothetical		Unknown / hypothetical proteins	10.038	9.334	10.308	9.066	5.13E-02	9.46E-02	-0.70	-1.24
lpg1244	LvrE	*lvrE*	Transport and binding, Protein fate / hy	10.592	10.201	11.921	10.770	4.10E-01	7.42E-03	-0.39	-1.15
lpg1244	LvrE	*lvrE*	Transport and binding, Protein fate / hy	10.546	10.663	11.817	10.951	6.37E-01	9.73E-02	0.12	-0.87
lpg1245	LvhD4 (VirD4)	*virD4*	Transport and binding, Protein fate / hy	7.336	8.110	8.508	8.267	5.46E-01	6.43E-01	0.77	-0.24
lpg1245	LvhD4 (VirD4)	*virD4*	Transport and binding, Protein fate / hy	7.460	8.856	8.660	8.568	7.86E-02	8.13E-01	1.40	-0.09
lpg1246	LvhB11 (VirB11)	*virB11*	Transport and binding, Protein fate / hy	8.894	10.295	9.790	10.390	2.90E-03	3.09E-01	1.40	0.60
lpg1246	LvhB11 (VirB11)	*virB11*	Transport and binding, Protein fate / hy	8.957	10.192	9.699	10.379	2.15E-02	3.11E-01	1.23	0.68
lpg1247	LvhB10 (type IV secretion system protein B10)		Transport and binding, Protein fate / hy	8.918	9.255	10.257	8.898	4.06E-01	5.33E-02	0.34	-1.36
lpg1247	LvhB10 (type IV secretion system protein B10)		Transport and binding, Protein fate / hy	9.078	9.461	10.064	9.120	5.69E-02	5.16E-02	0.38	-0.94
lpg1248	LvhB9 (probable conjugal transfer protein TrbG)	*virB9*	Transport and binding, Protein fate / hy	7.936	6.389	8.845	6.588	3.56E-02	3.34E-02	-1.55	-2.26
lpg1248	LvhB9 (probable conjugal transfer protein TrbG)	*virB9*	Transport and binding, Protein fate / hy	8.379	8.275	9.566	7.848	8.84E-01	1.78E-02	-0.10	-1.72
lpg1249	LvhB8 (conjugal transfer protein)	*virB8*	Transport and binding, Protein fate / hy	8.539	10.749	10.617	9.441	2.10E-05	7.43E-02	2.21	-1.18
lpg1249	LvhB8 (conjugal transfer protein)	*virB8*	Transport and binding, Protein fate / hy	8.159	9.664	9.891	9.123	3.67E-02	1.23E-01	1.50	-0.77
lpg1250	LvhB6 (conjugal transfer protein)	*virB6*	Transport and binding, Protein fate / hy	8.829	8.705	10.686	7.902	8.27E-01	1.36E-02	-0.12	-2.78
lpg1250	LvhB6 (conjugal transfer protein)	*virB6*	Transport and binding, Protein fate / hy	9.208	9.641	10.066	8.227	3.70E-01	7.63E-02	0.43	-1.84
lpg1251	LvrD	*lvrD*	Transport and binding, Protein fate / hy	9.617	10.178	10.515	9.955	1.70E-01	3.08E-01	0.56	-0.56
lpg1251	LvrD	*lvrD*	Transport and binding, Protein fate / hy	8.990	9.981	8.023	9.830	6.13E-02	2.23E-01	0.99	1.81
lpg1252	LvhB7		Transport and binding, Protein fate / hy	8.387	8.934	9.408	9.288	3.14E-01	8.27E-01	0.55	-0.12
lpg1252	LvhB7		Transport and binding, Protein fate / hy	8.235	8.966	8.942	9.214	1.69E-01	5.66E-01	0.73	0.27
lpg1253	LvhB5 (plasmid-related export protein)	*virB5*	Transport and binding, Protein fate / hy	7.028	6.566	8.466	10.221	7.29E-01	1.22E-01	-0.46	1.76
lpg1253	LvhB5 (plasmid-related export protein)	*virB5*	Transport and binding, Protein fate / hy	5.397	15.086	8.423	14.896	1.37E-01	3.44E-03	9.69	6.47
lpg1254	LvhB4 (type IV secretion system protein B4)	*virB4*	Transport and binding, Protein fate / hy	9.376	10.065	9.644	8.741	1.55E-01	1.13E-01	0.69	-0.90
lpg1254	LvhB4 (type IV secretion system protein B4)	*virB4*	Transport and binding, Protein fate / hy	10.066	9.944	9.870	9.279	6.84E-01	2.50E-01	-0.12	-0.59
lpg1255	LvhB3 (type IV secretion system protein B3)		Transport and binding, Protein fate / hy	8.585	8.181	9.714	7.372	8.63E-01	1.35E-01	-0.40	-2.34
lpg1255	LvhB3 (type IV secretion system protein B3)		Transport and binding, Protein fate / hy	8.278	8.542	9.017	9.050	8.59E-01	9.73E-01	0.26	0.03
lpg1256	ORF		ORFs of unknown function (unique)	7.550	9.451	9.109	9.383	2.19E-01	7.07E-01	1.90	0.27
lpg1256	ORF		ORFs of unknown function (unique)	8.329	9.495	9.543	10.204	2.33E-01	5.15E-01	1.17	0.66
lpg1257	LvrC (carbon storage regulator)	*csrA*	Transport and binding, Protein fate / hy	7.756	8.954	8.609	7.855	2.61E-01	4.45E-01	1.20	-0.75
lpg1257	LvrC (carbon storage regulator)	*csrA*	Transport and binding, Protein fate / hy	7.802	7.115	8.022	7.563	5.32E-01	5.15E-01	-0.69	-0.46
lpg1258	LvrB	*lvrB*	Transport and binding, Protein fate / hy	9.889	12.568	11.741	13.531	1.21E-01	1.54E-01	2.68	1.79
lpg1258	LvrB	*lvrB*	Transport and binding, Protein fate / hy	10.942	15.319	12.499	15.429	5.95E-04	5.55E-05	4.38	2.93
lpg1259	LvrA	*lvrA*	Transport and binding, Protein fate / hy	9.013	10.776	10.058	10.252	8.29E-03	4.56E-01	1.76	0.19
lpg1259	LvrA	*lvrA*	Transport and binding, Protein fate / hy	9.557	10.991	9.935	10.670	2.64E-02	1.59E-01	1.43	0.74

lpg1260	phage repressor (putative repressor protein of prophage)	*prpA*	Transcription factors / DNA binding pro	9.610	11.682	8.816	11.351	2.75E-04	4.58E-04	2.07	2.54
lpg1260	phage repressor (putative repressor protein of prophage)	*prpA*	Transcription factors / DNA binding pro	9.692	11.458	8.017	11.662	2.83E-03	5.37E-04	1.77	3.64
lpg1261	small ORF (129aa)		ORFs of unknown function (unique)	9.085	8.480	8.857	8.994	5.35E-01	8.60E-01	-0.60	0.14
lpg1261	small ORF (129aa)		ORFs of unknown function (unique)	8.476	8.808	8.894	9.170	7.33E-01	6.56E-01	0.33	0.28
lpg1262	small ORF (112aa)		ORFs of unknown function (unique)	10.778	10.795	10.214	9.850	9.46E-01	1.98E-01	0.02	-0.36
lpg1262	small ORF (112aa)		ORFs of unknown function (unique)	10.935	10.735	10.123	9.897	2.96E-01	6.46E-01	-0.20	-0.23
lpg1263	ORF		ORFs of unknown function (unique)	9.567	10.038	10.516	9.163	4.67E-01	9.75E-02	0.47	-1.35
lpg1263	ORF		ORFs of unknown function (unique)	9.451	10.097	9.991	9.933	4.42E-01	9.54E-01	0.65	-0.06
lpg1264	proton/peptide symporter family protein		Transport and binding	10.192	9.944	9.858	10.573	7.73E-01	3.03E-01	-0.25	0.71
lpg1264	proton/peptide symporter family protein		Transport and binding	10.283	9.632	9.874	11.203	5.72E-01	4.17E-02	-0.65	1.33
lpg1265	ORF		ORFs of unknown function (unique)	9.540	8.387	8.807	8.008	1.18E-01	4.00E-01	-1.15	-0.80
lpg1265	ORF		ORFs of unknown function (unique)	8.945	8.976	9.189	8.705	9.68E-01	3.40E-01	0.03	-0.48
lpg1266	methylase		Named proteins of general function	8.853	9.021	8.412	8.407	8.53E-01	9.96E-01	0.17	0.00
lpg1266	methylase		Named proteins of general function	9.262	9.144	8.759	8.816	8.26E-01	9.36E-01	-0.12	0.06
lpg1267	hypothetical (dGTP triphosphohydrolase?) (nucleotidyltransferase?)		Unknown / hypothetical proteins	8.490	7.572	9.881	6.842	4.47E-01	2.70E-02	-0.92	-3.04
lpg1267	hypothetical (dGTP triphosphohydrolase?) (nucleotidyltransferase?)		Unknown / hypothetical proteins	8.700	7.721	9.964	8.956	5.45E-01	4.81E-03	-0.98	-1.01
lpg1268	ORF		ORFs of unknown function (unique)	10.433	9.349	9.713	9.560	6.83E-02	7.67E-01	-1.08	-0.15
lpg1268	ORF		ORFs of unknown function (unique)	10.781	9.809	9.762	9.874	1.15E-02	7.92E-01	-0.97	0.11
lpg1269	hypothetical		Unknown / hypothetical proteins	10.445	10.496	9.568	10.615	8.65E-01	1.00E-01	0.05	1.05
lpg1269	hypothetical		Unknown / hypothetical proteins	10.771	10.004	9.485	11.048	2.29E-01	5.00E-02	-0.77	1.56
lpg1270	small ORF (152aa)		ORFs of unknown function (unique)	10.454	10.928	8.285	11.957	3.00E-01	1.45E-03	0.47	3.67
lpg1270	small ORF (152aa)		ORFs of unknown function (unique)	10.766	11.354	8.330	12.240	5.50E-02	4.30E-03	0.59	3.91
lpg1271	ISSod6 transposase, IS1301, COG3293		Viral functions / Phage / Transposases	7.931	7.318	8.183	7.664	2.54E-01	4.86E-01	-0.61	-0.52
lpg1271	ISSod6 transposase, IS1301, COG3293		Viral functions / Phage / Transposases	8.409	6.044	7.778	7.493	8.96E-02	7.73E-01	-2.37	-0.28
lpg1272	tRNA-Arg		tRNA	9.742	8.495	9.344	7.162	7.41E-02	4.37E-02	-1.25	-2.18
lpg1272	tRNA-Arg		tRNA	9.445	8.559	9.710	7.960	3.97E-01	4.39E-02	-0.89	-1.75
lpg1273	ORF		ORFs of unknown function (unique)	11.408	11.008	10.671	10.985	1.81E-01	3.94E-01	-0.40	0.31
lpg1273	ORF		ORFs of unknown function (unique)	11.216	10.967	10.477	10.949	5.03E-01	3.31E-01	-0.25	0.47
lpg1274	hypothetical		Unknown / hypothetical proteins	10.988	7.678	12.904	6.308	2.57E-03	1.28E-04	-3.31	-6.60
lpg1274	hypothetical		Unknown / hypothetical proteins	10.865	8.602	13.235	6.912	1.40E-02	3.01E-04	-2.26	-6.32
lpg1275	transporter, TrkA family (ion transport) (di- and tricarboxylate transpor		Transport and binding	9.527	8.371	10.514	9.365	3.84E-01	3.00E-01	-1.16	-1.15
lpg1275	transporter, TrkA family (ion transport) (di- and tricarboxylate transpor		Transport and binding	8.888	8.938	9.054	8.545	9.35E-01	5.28E-01	0.05	-0.51
lpg1276	electron transferring flavoprotein dehydrogenase (electron transfer fla		Energy Metabolism	11.518	11.526	12.017	11.919	9.64E-01	7.00E-01	0.01	-0.10
lpg1276	electron transferring flavoprotein dehydrogenase (electron transfer fla		Energy Metabolism	11.359	11.538	12.000	12.060	5.23E-01	7.93E-01	0.18	0.06
lpg1277	ABC transporter ATP binding protein (abcT3) (multidrug r	*abcT3*	Transport and binding	11.080	10.962	11.077	11.046	7.63E-01	9.15E-01	-0.12	-0.03
lpg1277	ABC transporter ATP binding protein (abcT3) (multidrug r	*abcT3*	Transport and binding	11.098	11.001	10.361	11.073	6.78E-01	1.68E-01	-0.10	0.71
lpg1278	small ORF (105aa) hypothetical		Unknown / hypothetical proteins	10.990	10.484	11.221	10.351	2.05E-01	1.04E-01	-0.51	-0.87
lpg1278	small ORF (105aa) hypothetical		Unknown / hypothetical proteins	10.869	10.911	11.237	10.443	7.03E-01	1.48E-01	0.04	-0.79
lpg1279	small ORF (123aa) hypothetical		Unknown / hypothetical proteins	11.541	11.113	12.551	10.063	1.38E-01	6.98E-05	-0.43	-2.49
lpg1279	small ORF (123aa) hypothetical		Unknown / hypothetical proteins	11.534	10.761	12.543	10.159	6.28E-02	1.51E-04	-0.77	-2.38
lpg1280	malate oxidoreductase (NAD linked malic enzyme) (mala	*sfcA*	Carbohydrate Metabolism	11.212	10.866	8.930	11.129	6.00E-01	4.83E-02	-0.35	2.20
lpg1280	malate oxidoreductase (NAD linked malic enzyme) (mala	*sfcA*	Carbohydrate Metabolism	10.904	11.575	9.077	12.060	2.88E-01	1.10E-04	0.67	2.98
lpg1281	hypothetical (L. pneumophila unknown protein)		Unknown / hypothetical proteins	11.283	11.511	11.069	11.760	5.26E-01	1.32E-01	0.23	0.69
lpg1281	hypothetical (L. pneumophila unknown protein)		Unknown / hypothetical proteins	10.993	11.238	10.859	11.707	7.05E-01	7.55E-02	0.24	0.85
lpg1282	stationary phase surival protein SurE (acid phosphatase)	*surE*	Biodegradation of Xenobiotics, Metabo	11.977	11.691	10.061	11.777	5.62E-01	4.10E-03	-0.29	1.72
lpg1282	stationary phase surival protein SurE (acid phosphatase)	*surE*	Biodegradation of Xenobiotics, Metabo	12.057	11.722	9.814	11.778	3.98E-01	4.86E-03	-0.34	1.96
lpg1283	lipoprotein NlpD		Named proteins of general function	11.498	11.163	10.179	11.498	1.50E-01	1.07E-02	-0.33	1.32
lpg1283	lipoprotein NlpD		Named proteins of general function	11.452	11.136	10.136	11.457	2.01E-01	1.06E-02	-0.32	1.32
lpg1284	stationary phase specific sigma factor (RNA polymerase	*rpoS*	Toxin production / other pathogen func	12.356	12.493	12.228	12.342	6.96E-01	6.34E-01	0.14	0.11
lpg1284	stationary phase specific sigma factor (RNA polymerase	*rpoS*	Toxin production / other pathogen func	12.266	12.639	12.180	12.589	2.97E-01	1.57E-02	0.37	0.41
lpg1285	homogentisate 1,2-dioxygenase (homogentisicase)		Amino Acid Metabolism, Biodegradatio	11.356	12.923	10.138	12.594	5.18E-06	8.98E-04	1.57	2.46
lpg1285	homogentisate 1,2-dioxygenase (homogentisicase)		Amino Acid Metabolism, Biodegradatio	11.263	12.650	9.841	12.613	2.18E-04	2.41E-03	1.39	2.77
lpg1286	YebC (L. pneumophila) hypothetical (cytosolic protein?) TIGR01033		Named proteins of general function	11.594	11.661	11.192	11.730	7.60E-01	7.27E-02	0.07	0.54
lpg1286	YebC (L. pneumophila) hypothetical (cytosolic protein?) TIGR01033		Named proteins of general function	11.303	11.843	11.136	11.697	2.42E-01	8.20E-02	0.54	0.56
lpg1287	crossover junction endodeoxyribonuclease RuvC (Hollida	*ruvC*	Replication and Repair	10.836	10.537	8.316	11.285	4.69E-01	7.66E-03	-0.30	2.97
lpg1287	crossover junction endodeoxyribonuclease RuvC (Hollida	*ruvC*	Replication and Repair	10.358	10.513	7.937	11.263	8.57E-01	2.41E-02	0.15	3.33
lpg1288	Holliday junction DNA helicase RuvA	*ruvA*	Replication and Repair	10.556	11.286	11.114	11.063	2.23E-01	8.77E-01	0.73	-0.05
lpg1288	Holliday junction DNA helicase RuvA	*ruvA*	Replication and Repair	10.486	11.987	10.998	11.676	1.44E-01	3.90E-01	1.50	0.68
lpg1289	small ORF (106aa)		ORFs of unknown function (unique)	11.054	11.971	11.372	10.155	1.45E-03	3.03E-03	0.92	-1.22
lpg1289	small ORF (106aa)		ORFs of unknown function (unique)	10.865	11.929	11.287	10.366	7.96E-03	1.53E-02	1.06	-0.92
lpg1290	hypothetical protein		Unknown / hypothetical proteins	9.727	9.279	13.065	9.414	5.95E-01	2.15E-03	-0.45	-3.65
lpg1290	hypothetical protein		Unknown / hypothetical proteins	9.613	9.606	13.070	10.308	9.92E-01	4.85E-03	-0.01	-2.76
lpg1291	two component sensor kinase (transmembrane sensor histidine kinas		Signal transduction / other regulatory f	7.523	8.383	9.084	8.059	2.73E-01	5.12E-01	0.86	-1.02
lpg1291	two component sensor kinase (transmembrane sensor histidine kinas		Signal transduction / other regulatory f	8.151	8.660	9.261	9.322	5.79E-01	9.41E-01	0.51	0.06

lpg1292	DNA-binding response regulator (two component)		Signal transduction / other regulatory f	12.344	11.399	13.359	11.217	1.42E-01	6.51E-05	-0.94	-2.14
lpg1292	DNA-binding response regulator (two component)		Signal transduction / other regulatory f	12.375	11.759	13.332	11.572	1.39E-01	1.36E-04	-0.62	-1.76
lpg1293	intracellular septation protein A	*ispZ*	Chemotaxis / motility / cell division	12.691	10.844	13.093	10.498	3.51E-04	3.89E-06	-1.85	-2.60
lpg1293	intracellular septation protein A	*ispZ*	Chemotaxis / motility / cell division	12.604	11.048	13.001	10.492	6.38E-04	3.38E-05	-1.56	-2.51
lpg1294	membrane bound lytic murein transglycosylase D		Cell envelope synthesis, Metabolism o	10.242	10.306	9.424	9.376	8.71E-01	9.44E-01	0.06	-0.05
lpg1294	membrane bound lytic murein transglycosylase D		Cell envelope synthesis, Metabolism o	10.034	10.223	9.382	9.812	6.66E-01	2.95E-01	0.19	0.43
lpg1295	hydroxyacylglutathione hydrolase GloB		Carbohydrate Metabolism	10.595	9.117	9.742	10.278	2.25E-02	3.37E-01	-1.48	0.54
lpg1295	hydroxyacylglutathione hydrolase GloB		Carbohydrate Metabolism	10.553	9.316	9.792	10.506	1.42E-01	3.31E-01	-1.24	0.71
lpg1296	protein involved in catabolism of external DNA		DNA/RNA degradation / restriction	10.265	8.266	10.056	9.431	6.72E-03	1.65E-01	-2.00	-0.62
lpg1296	protein involved in catabolism of external DNA		DNA/RNA degradation / restriction	10.592	8.912	10.043	10.125	1.42E-03	6.90E-01	-1.68	0.08
lpg1297	5,10-methylenetetrahydrofolate dehydrogenase (NADP)/	*folD*	Carbohydrate Metabolism, Metabolism	9.777	9.329	10.588	8.623	3.53E-01	1.63E-03	-0.45	-1.97
lpg1297	5,10-methylenetetrahydrofolate dehydrogenase (NADP)/	*folD*	Carbohydrate Metabolism, Metabolism	9.742	9.875	10.301	8.530	5.73E-01	2.01E-02	0.13	-1.77
lpg1298	small ORF (65aa) weak eukaryotic hits?		Unknown / hypothetical proteins	9.147	8.350	12.285	8.455	2.83E-01	1.18E-03	-0.80	-3.83
lpg1298	small ORF (65aa) weak eukaryotic hits?		Unknown / hypothetical proteins	9.800	9.648	12.724	10.011	8.13E-01	1.67E-02	-0.15	-2.71
lpg1299	transmembrane protein FimV (twitching motility) (LysM domain protei		Chemotaxis / motility / cell division, Me	11.544	11.174	10.851	11.236	2.77E-01	3.34E-01	-0.37	0.39
lpg1299	transmembrane protein FimV (twitching motility) (LysM domain protei		Chemotaxis / motility / cell division, Me	11.562	11.314	10.745	11.204	3.53E-01	2.98E-01	-0.25	0.46
lpg1300	integral membrane protein COG5528		Named proteins of general function	11.080	10.921	11.164	10.703	6.65E-01	1.57E-01	-0.16	-0.46
lpg1300	integral membrane protein COG5528		Named proteins of general function	11.032	11.178	11.045	10.908	7.45E-01	6.77E-01	0.15	-0.14
lpg1301	oxidoreductase (NADH dehydrogenase/oxidoreductase) NolA		Metabolism of Cofactors and Vitamins	9.286	9.692	9.112	8.078	2.56E-01	3.05E-02	0.41	-1.03
lpg1301	oxidoreductase (NADH dehydrogenase/oxidoreductase) NolA		Metabolism of Cofactors and Vitamins	9.182	9.651	8.922	8.873	4.35E-01	9.13E-01	0.47	-0.05
lpg1302	tRNA pseudouridine synthase A		DNA/RNA degradation / restriction, Tra	12.140	11.331	10.653	11.379	2.70E-02	1.70E-01	-0.81	0.73
lpg1302	tRNA pseudouridine synthase A		DNA/RNA degradation / restriction, Tra	12.226	11.253	10.495	11.334	8.82E-03	1.33E-01	-0.97	0.84
lpg1303	phosphoribosyl anthranilate isomerase (N-5'-phosphoribo	*trpF*	Amino Acid Metabolism	13.103	12.847	11.495	13.429	4.65E-01	4.12E-04	-0.26	1.93
lpg1303	phosphoribosyl anthranilate isomerase (N-5'-phosphoribo	*trpF*	Amino Acid Metabolism	13.010	12.759	11.047	13.358	6.06E-01	8.83E-04	-0.25	2.31
lpg1304	tryptophan synthetase, beta subunit		Amino Acid Metabolism	11.951	11.365	10.177	11.835	2.66E-01	1.43E-02	-0.59	1.66
lpg1304	tryptophan synthetase, beta subunit		Amino Acid Metabolism	11.800	10.718	9.904	12.083	2.72E-01	1.86E-02	-1.08	2.18
lpg1305	tryptophan synthetase (alpha chain) TrpA	*trpA*	Amino Acid Metabolism	11.179	11.117	9.222	11.795	9.22E-01	2.60E-03	-0.06	2.57
lpg1305	tryptophan synthetase (alpha chain) TrpA	*trpA*	Amino Acid Metabolism	11.178	10.335	8.717	11.812	4.02E-01	2.42E-03	-0.84	3.10
lpg1306	glutaminyl-tRNA synthetase	*glnS*	Amino Acid Metabolism, Translation	12.671	11.289	11.072	12.835	3.45E-03	1.60E-03	-1.38	1.76
lpg1306	glutaminyl-tRNA synthetase	*glnS*	Amino Acid Metabolism, Translation	12.800	11.276	10.904	12.837	2.88E-04	2.13E-03	-1.52	1.93
lpg1307	cysteinyl-tRNA synthetase	*cysS*	Amino Acid Metabolism, Translation	12.759	12.077	11.194	12.975	2.62E-02	1.75E-03	-0.68	1.78
lpg1307	cysteinyl-tRNA synthetase	*cysS*	Amino Acid Metabolism, Translation	12.727	12.066	10.979	13.200	3.29E-02	3.74E-04	-0.66	2.22
lpg1308	sulfatase domain protein		Named proteins of general function	10.229	10.333	10.379	10.202	7.05E-01	6.26E-01	0.10	-0.18
lpg1308	sulfatase domain protein		Named proteins of general function	9.083	10.151	10.363	10.320	3.59E-01	8.87E-01	1.07	-0.04
lpg1309	small ORF (104aa)		ORFs of unknown function (unique)	10.771	10.517	12.429	10.269	7.00E-01	3.35E-02	-0.25	-2.16
lpg1309	small ORF (104aa)		ORFs of unknown function (unique)	10.790	13.035	12.444	13.235	2.92E-03	2.86E-01	2.25	0.79
lpg1310	small ORF (97aa)		ORFs of unknown function (unique)	7.657	8.170	7.141	8.217	6.48E-01	5.54E-01	0.51	1.08
lpg1310	small ORF (97aa)		ORFs of unknown function (unique)	6.255	8.083	6.348	9.063	2.71E-01	1.37E-01	1.83	2.71
lpg1311	small ORF (89aa)		ORFs of unknown function (unique)	9.221	11.499	10.574	11.194	2.18E-02	3.68E-01	2.28	0.62
lpg1311	small ORF (89aa)		ORFs of unknown function (unique)	9.322	11.451	10.394	11.092	3.13E-02	3.47E-01	2.13	0.70
lpg1312	erythrocyte membrane-associated antigen	*LegC1*	Named proteins of general function	7.503	7.647	7.270	6.725	7.13E-01	6.73E-01	0.14	-0.54
lpg1312	erythrocyte membrane-associated antigen	*LegC1*	Named proteins of general function	7.502	8.949	6.832	7.413	3.74E-01	8.21E-01	1.45	0.58
lpg1313	transposase		Viral functions / Phage / Transposases	9.382	8.352	8.472	7.713	1.40E-01	1.28E-01	-1.03	-0.76
lpg1313	transposase		Viral functions / Phage / Transposases	9.155	7.922	9.302	9.206	1.26E-01	8.59E-01	-1.23	-0.10
lpg1314	hypothetical (endonuclease?)		Unknown / hypothetical proteins	10.785	9.812	10.666	10.005	4.15E-02	5.42E-02	-0.97	-0.66
lpg1314	hypothetical (endonuclease?)		Unknown / hypothetical proteins	10.969	10.791	10.676	10.525	8.25E-01	7.72E-01	-0.18	-0.15
lpg1315	transposase (ISSod6)		Viral functions / Phage / Transposases	10.562	11.063	11.316	11.287	4.32E-01	9.73E-01	0.50	-0.03
lpg1315	transposase (ISSod6)		Viral functions / Phage / Transposases	10.095	11.047	10.027	11.194	1.31E-01	3.15E-01	0.95	1.17
lpg1316	ORF		ORFs of unknown function (unique)	10.842	9.370	11.264	9.767	3.62E-02	1.52E-02	-1.47	-1.50
lpg1316	ORF		ORFs of unknown function (unique)	10.829	10.170	11.171	10.113	2.08E-01	3.01E-02	-0.66	-1.06
lpg1317	ORF		ORFs of unknown function (unique)	10.358	10.685	11.584	10.582	5.90E-01	4.41E-02	0.33	-1.00
lpg1317	ORF		ORFs of unknown function (unique)	10.456	10.926	11.648	10.844	3.95E-01	7.24E-02	0.47	-0.80
lpg1318	ORF		ORFs of unknown function (unique)	9.443	8.370	11.758	5.653	2.10E-01	1.80E-03	-1.07	-6.10
lpg1318	ORF		ORFs of unknown function (unique)	8.828	8.207	10.941	7.676	5.61E-01	4.41E-02	-0.62	-3.27
lpg1319	type II secretory pathway protein E (ATPase EpsE)		Protein fate / hydrolases / secretion	10.078	9.251	9.570	10.258	4.70E-01	2.03E-01	-0.83	0.69
lpg1319	type II secretory pathway protein E (ATPase EpsE)		Protein fate / hydrolases / secretion	10.540	7.886	9.209	10.381	9.92E-03	1.42E-01	-2.65	1.17
lpg1320	type II protein secretion LspD (general secretion pathway D transmen		Protein fate / hydrolases / secretion	10.334	9.104	8.916	9.314	6.04E-02	5.31E-01	-1.23	0.40
lpg1320	type II protein secretion LspD (general secretion pathway D transmen		Protein fate / hydrolases / secretion	10.497	7.964	8.192	8.865	3.86E-02	5.83E-01	-2.53	0.67
lpg1321	oxidoreductase (dehydrogenase)		Named proteins of general function	9.731	9.764	9.517	8.370	9.42E-01	2.62E-01	0.03	-1.15
lpg1321	oxidoreductase (dehydrogenase)		Named proteins of general function	9.907	10.713	9.597	9.684	4.29E-01	9.54E-01	0.81	0.09
lpg1322	adenylate cyclase 1 protein	*cyaA*	Nucleotide Metabolism	7.998	8.470	8.246	7.774	5.82E-01	5.02E-01	0.47	-0.47
lpg1322	adenylate cyclase 1 protein	*cyaA*	Nucleotide Metabolism	7.574	6.262	7.437	7.989	4.67E-01	8.12E-01	-1.31	0.55
lpg1323	drug resistance transporter, Bcr/CflA (MFS transporter)		Transport and binding	8.895	8.445	9.457	8.213	5.95E-01	1.46E-01	-0.45	-1.24
lpg1323	drug resistance transporter, Bcr/CflA (MFS transporter)		Transport and binding	9.322	9.623	10.032	8.997	7.35E-01	8.94E-02	0.30	-1.04

lpg1324	multidrug resistance efflux pump (permease MDR) (major facilitator fa		Transport and binding	8.920	8.328	9.189	8.677	1.52E-01	4.37E-01	-0.59	-0.51
lpg1324	multidrug resistance efflux pump (permease MDR) (major facilitator fa		Transport and binding	8.911	9.207	9.483	9.482	7.02E-01	9.97E-01	0.30	0.00
lpg1325	siderophore biosynthetic enzyme FrgA	*frgA*	Toxin production / other pathogen func	8.655	8.322	8.751	9.592	4.96E-01	1.03E-01	-0.33	0.84
lpg1325	siderophore biosynthetic enzyme FrgA	*frgA*	Toxin production / other pathogen func	8.815	8.298	8.548	9.825	4.44E-01	3.07E-02	-0.52	1.28
lpg1326	conserved hypothetical protein		Unknown / hypothetical proteins	8.092	9.882	8.205	8.949	5.09E-02	3.71E-01	1.79	0.74
lpg1326	conserved hypothetical protein		Unknown / hypothetical proteins	8.333	9.119	7.394	8.891	5.04E-02	6.51E-02	0.79	1.50
lpg1327	small ORF (104aa) hypothetical		Unknown / hypothetical proteins	9.089	8.941	9.549	7.781	7.05E-01	9.26E-02	-0.15	-1.77
lpg1327	small ORF (104aa) hypothetical		Unknown / hypothetical proteins	8.865	8.845	9.322	7.684	9.51E-01	2.14E-01	-0.02	-1.64
lpg1328	conserved repeat domain protein	*legT*	Unknown / hypothetical proteins	9.625	8.365	8.710	8.499	7.54E-03	8.37E-01	-1.26	-0.21
lpg1328	conserved repeat domain protein	*legT*	Unknown / hypothetical proteins	9.554	8.054	8.294	8.721	3.75E-01	7.73E-01	-1.50	0.43
lpg1329	hypothetical protein		Unknown / hypothetical proteins	10.218	7.746	8.665	8.512	1.37E-02	8.53E-01	-2.47	-0.15
lpg1329	hypothetical protein		Unknown / hypothetical proteins	10.191	8.564	8.525	8.584	9.09E-03	9.53E-01	-1.63	0.06
lpg1330	tRNA-Met		tRNA	10.475	10.403	10.447	10.875	7.86E-01	2.12E-01	-0.07	0.43
lpg1330	tRNA-Met		tRNA	10.317	10.505	10.401	11.082	6.80E-01	1.53E-02	0.19	0.68
lpg1331	protease DO (periplasmic serine endoprotease)	*htrA*	Protein fate / hydrolases / secretion	12.987	12.959	11.655	13.043	9.27E-01	5.27E-02	-0.03	1.39
lpg1331	protease DO (periplasmic serine endoprotease)	*htrA*	Protein fate / hydrolases / secretion	12.833	12.890	11.669	13.152	8.88E-01	2.41E-02	0.06	1.48
lpg1332	hypothetical (inner membrane protein)		Named proteins of general function	11.901	10.663	11.272	10.658	1.18E-03	1.82E-01	-1.24	-0.61
lpg1332	hypothetical (inner membrane protein)		Named proteins of general function	11.930	11.297	11.686	11.176	3.04E-01	3.06E-01	-0.63	-0.51
lpg1333	ribosomal large subunit pseudouridine synthase D, RluD	*rluD*	DNA/RNA degradation / restriction, Tra	10.870	10.103	10.688	10.689	1.18E-01	9.99E-01	-0.77	0.00
lpg1333	ribosomal large subunit pseudouridine synthase D, RluD	*rluD*	DNA/RNA degradation / restriction, Tra	11.122	10.719	10.758	11.587	2.92E-01	6.34E-02	-0.40	0.83
lpg1334	tRNA thiotransferase (tRNA-i(6) A37 modification enzyme MiaB)		DNA/RNA degradation / restriction, Tra	12.714	13.662	12.196	13.183	1.47E-04	3.56E-03	0.95	0.99
lpg1334	tRNA thiotransferase (tRNA-i(6) A37 modification enzyme MiaB)		DNA/RNA degradation / restriction, Tra	12.715	13.731	12.260	13.268	2.26E-04	1.46E-03	1.02	1.01
lpg1335	major facilitator family transporter (permease) (multidrug efflux transp		Transport and binding	12.695	12.814	12.321	11.977	8.09E-01	2.00E-01	0.12	-0.34
lpg1335	major facilitator family transporter (permease) (multidrug efflux transp		Transport and binding	12.687	13.627	12.363	12.446	1.24E-02	7.95E-01	0.94	0.08
lpg1336	enhanced entry protein EnhA	*enhA*	Toxin production / other pathogen func	10.357	10.604	13.683	9.555	8.05E-01	1.04E-02	0.25	-4.13
lpg1336	enhanced entry protein EnhA	*enhA*	Toxin production / other pathogen func	9.994	9.924	12.922	9.136	9.32E-01	4.69E-02	-0.07	-3.79
lpg1337	flagellar protein FliS	*fliS*	Chemotaxis / motility / cell division	9.464	7.783	11.798	7.926	1.02E-01	5.49E-02	-1.68	-3.87
lpg1337	flagellar protein FliS	*fliS*	Chemotaxis / motility / cell division	9.352	8.096	11.736	8.714	1.40E-01	6.33E-02	-1.26	-3.02
lpg1338	flagellar hook associated protein 2 (flagellar cap protein F	*fliD*	Chemotaxis / motility / cell division	10.407	10.334	13.927	10.099	9.36E-01	1.27E-03	-0.07	-3.83
lpg1338	flagellar hook associated protein 2 (flagellar cap protein F	*fliD*	Chemotaxis / motility / cell division	10.473	11.365	13.936	11.742	3.27E-01	2.93E-02	0.89	-2.19
lpg1339	small ORF (93aa)		ORFs of unknown function (unique)	10.637	10.420	13.593	10.987	8.27E-01	2.05E-02	-0.22	-2.61
lpg1339	small ORF (93aa)		ORFs of unknown function (unique)	10.534	10.115	13.510	10.960	7.42E-01	2.39E-02	-0.42	-2.55
lpg1340	flagellin	*fliC*	Chemotaxis / motility / cell division	11.389	13.133	14.606	12.293	7.02E-02	4.55E-02	1.74	-2.31
lpg1340	flagellin	*fliC*	Chemotaxis / motility / cell division	11.154	13.264	14.511	12.632	5.23E-02	1.35E-01	2.11	-1.88
lpg1341	acetyl CoA carboxylase, carboxyltransferase, beta subun	*accD*	Lipid Metabolism, Biosynthesis of Sec	10.887	11.210	10.349	11.632	4.40E-01	2.03E-02	0.32	1.28
lpg1341	acetyl CoA carboxylase, carboxyltransferase, beta subun	*accD*	Lipid Metabolism, Biosynthesis of Sec	10.576	11.782	10.499	12.070	3.84E-02	1.20E-02	1.21	1.57
lpg1342	FolC bifunctional protein (folylpolyglutamate synthase/dil	*folC*	Metabolism of Cofactors and Vitamins	11.833	10.541	10.068	10.546	1.14E-01	5.90E-01	-1.29	0.48
lpg1342	FolC bifunctional protein (folylpolyglutamate synthase/dil	*folC*	Metabolism of Cofactors and Vitamins	11.811	10.386	8.872	10.385	5.65E-02	1.31E-01	-1.42	1.51
lpg1343	ORF		ORFs of unknown function (unique)	10.630	11.861	10.965	11.320	3.95E-02	2.75E-01	1.23	0.36
lpg1343	ORF		ORFs of unknown function (unique)	10.365	11.677	10.795	11.179	1.48E-02	2.58E-01	1.31	0.38
lpg1344	colicin V (bacteriocin) production protein (membrane prot	*dedE*	Toxin production / other pathogen func	11.455	10.595	10.624	9.262	4.44E-02	2.19E-03	-0.86	-1.36
lpg1344	colicin V (bacteriocin) production protein (membrane prot	*dedE*	Toxin production / other pathogen func	11.398	10.753	10.552	9.838	1.77E-01	5.61E-02	-0.65	-0.71
lpg1345	nicotinate-nucleotide adenylyltransferase (cytidylyltransferase)		Metabolism of Cofactors and Vitamins	10.849	9.649	9.486	10.134	1.12E-03	2.05E-01	-1.20	0.65
lpg1345	nicotinate-nucleotide adenylyltransferase (cytidylyltransferase)		Metabolism of Cofactors and Vitamins	10.668	9.471	9.296	10.222	9.92E-03	2.22E-01	-1.20	0.93
lpg1346	DNA polymerase III, delta subunit	*holA*	Nucleotide Metabolism, Replication an	11.599	10.059	9.625	11.933	1.15E-02	5.13E-03	-1.54	2.31
lpg1346	DNA polymerase III, delta subunit	*holA*	Nucleotide Metabolism, Replication an	11.592	11.768	9.748	12.770	7.16E-01	1.59E-03	0.18	3.02
lpg1347	rare lipoprotein B		Named proteins of general function	10.868	10.635	9.494	10.566	7.93E-01	9.06E-02	-0.23	1.07
lpg1347	rare lipoprotein B		Named proteins of general function	10.911	11.901	9.499	11.649	3.69E-01	5.06E-02	0.99	2.15
lpg1348	leucyl tRNA synthetase	*leuS*	Amino Acid Metabolism, Translation	12.687	12.817	10.254	13.541	8.34E-01	1.52E-03	0.13	3.29
lpg1348	leucyl tRNA synthetase	*leuS*	Amino Acid Metabolism, Translation	12.845	12.806	10.187	13.524	9.45E-01	1.28E-03	-0.04	3.34
lpg1349	apolipoprotein N-acyltransferase	*cutE*	Named proteins of general function	11.138	10.878	9.254	9.863	6.65E-01	3.20E-01	-0.26	0.61
lpg1349	apolipoprotein N-acyltransferase	*cutE*	Named proteins of general function	11.389	10.659	9.221	10.202	9.81E-02	7.39E-02	-0.73	0.98
lpg1350	L-lysine dehydrogenase (dehydrogenase) (saccharopine dehydrogen		Amino Acid Metabolism	13.893	14.022	12.010	13.591	8.07E-01	1.12E-02	0.13	1.58
lpg1350	L-lysine dehydrogenase (dehydrogenase) (saccharopine dehydrogen		Amino Acid Metabolism	13.983	14.015	11.902	13.563	9.53E-01	1.13E-02	0.03	1.66
lpg1351	piperidine-6-carboxylate dehydrogenase (aldehyde dehydrogenase)		Carbohydrate Metabolism, Lipid Metab	11.521	12.309	10.385	11.656	9.94E-02	5.65E-02	0.79	1.27
lpg1351	piperidine-6-carboxylate dehydrogenase (aldehyde dehydrogenase)		Carbohydrate Metabolism, Lipid Metab	11.563	12.463	10.324	11.689	4.20E-02	3.10E-02	0.90	1.37
lpg1352	3-hydroxyacyl CoA dehydrogenase oxidoreductase prote	*fadB*	Lipid Metabolism, Amino Acid Metabol	13.891	14.489	13.364	13.491	2.03E-02	5.68E-01	0.60	0.13
lpg1352	3-hydroxyacyl CoA dehydrogenase oxidoreductase prote	*fadB*	Lipid Metabolism, Amino Acid Metabol	14.224	14.499	13.410	13.635	1.96E-01	3.85E-01	0.27	0.22
lpg1353	3-ketoacyl CoA thiolase (thiolase)	*fadA*	Lipid Metabolism, Amino Acid Metabol	12.414	13.444	12.660	12.308	4.04E-03	1.23E-01	1.03	-0.35
lpg1353	3-ketoacyl CoA thiolase (thiolase)	*fadA*	Lipid Metabolism, Amino Acid Metabol	12.491	13.379	12.655	12.306	5.88E-03	1.09E-01	0.89	-0.35
lpg1354	ORF		ORFs of unknown function (unique)	9.526	8.997	10.645	8.394	1.24E-01	1.69E-02	-0.53	-2.25
lpg1354	ORF		ORFs of unknown function (unique)	9.748	9.637	10.294	9.311	7.53E-01	1.19E-01	-0.11	-0.98
lpg1355	SidG, LepC, Vng0394c	*sidG*	Named proteins of general function	8.334	6.635	12.875	7.360	1.59E-01	6.42E-04	-1.70	-5.52
lpg1355	SidG, LepC, Vng0394c	*sidG*	Named proteins of general function	8.376	7.823	11.727	7.581	5.71E-01	1.88E-02	-0.55	-4.15

lpg1356	TPR repeat protein (enhanced entry protein EnhC)		Toxin production / other pathogen func	10.860	10.938	14.027	11.212	9.03E-01	3.98E-03	0.08	-2.82
lpg1356	TPR repeat protein (enhanced entry protein EnhC)		Toxin production / other pathogen func	10.975	11.042	14.025	11.282	9.12E-01	3.28E-03	0.07	-2.74
lpg1357	inner membrane protein PLUS sensory box protein LssE		Signal transduction / other regulatory f	7.935	9.219	9.995	8.212	1.95E-01	1.13E-01	1.28	-1.78
lpg1357	inner membrane protein PLUS sensory box protein LssE		Signal transduction / other regulatory f	9.104	8.478	10.066	8.306	4.69E-01	3.10E-02	-0.63	-1.76
lpg1358	general secretion pathway protein LspK	*xcpX*	Protein fate / hydrolases / secretion	10.764	9.996	9.851	9.856	1.10E-02	9.92E-01	-0.77	0.00
lpg1358	general secretion pathway protein LspK	*xcpX*	Protein fate / hydrolases / secretion	10.553	10.188	9.753	10.525	2.60E-01	9.60E-02	-0.36	0.77
lpg1359	general secretion pathway protein LspJ	*xcpW*	Protein fate / hydrolases / secretion	9.176	8.896	8.815	6.786	4.60E-01	1.38E-01	-0.28	-2.03
lpg1359	general secretion pathway protein LspJ	*xcpW*	Protein fate / hydrolases / secretion	9.393	9.062	9.468	8.422	3.53E-01	2.22E-01	-0.33	-1.05
lpg1360	general secretion pathway protein LspI		Protein fate / hydrolases / secretion	10.778	10.412	10.587	10.528	3.73E-01	8.56E-01	-0.37	-0.06
lpg1360	general secretion pathway protein LspI		Protein fate / hydrolases / secretion	10.852	10.252	10.460	10.429	1.23E-01	9.13E-01	-0.60	-0.03
lpg1361	general secretion pathway protein LspH	*xcpU*	Protein fate / hydrolases / secretion	10.976	11.169	10.559	10.878	6.37E-01	6.00E-01	0.19	0.32
lpg1361	general secretion pathway protein LspH	*xcpU*	Protein fate / hydrolases / secretion	10.958	11.666	10.704	11.153	3.11E-01	6.35E-01	0.71	0.45
lpg1362	type II protein secretion LspG (general secretion pathway	*gspG*	Protein fate / hydrolases / secretion	13.045	14.039	12.918	13.394	1.22E-03	6.26E-02	0.99	0.48
lpg1362	type II protein secretion LspG (general secretion pathway	*gspG*	Protein fate / hydrolases / secretion	12.998	14.045	12.790	13.355	1.37E-03	4.91E-02	1.05	0.56
lpg1363	type II protein secretion LspF (general secretion pathway	*gspF*	Protein fate / hydrolases / secretion	11.520	11.003	9.503	11.447	2.78E-01	3.76E-03	-0.52	1.94
lpg1363	type II protein secretion LspF (general secretion pathway	*gspF*	Protein fate / hydrolases / secretion	10.915	11.406	9.389	11.390	4.18E-01	3.36E-03	0.49	2.00
lpg1364	glutamine synthetase, type I (glutamate-ammonia ligase)	*glnA*	Amino Acid Metabolism, Metabolism o	12.276	14.818	11.320	13.816	4.00E-04	6.29E-03	2.54	2.50
lpg1364	glutamine synthetase, type I (glutamate-ammonia ligase)	*glnA*	Amino Acid Metabolism, Metabolism o	12.175	13.989	11.005	14.084	8.20E-02	5.08E-04	1.81	3.08
lpg1365	hypothetical		Unknown / hypothetical proteins	13.557	12.784	12.148	12.773	2.78E-02	7.43E-02	-0.77	0.63
lpg1365	hypothetical		Unknown / hypothetical proteins	13.473	12.752	12.119	12.771	4.98E-02	7.73E-02	-0.72	0.65
lpg1366	hypothetical (cytoplasmic protein) (highly similar to unknown protein Y		Named proteins of general function	8.205	9.622	9.493	9.516	8.80E-02	9.53E-01	1.42	0.02
lpg1366	hypothetical (cytoplasmic protein) (highly similar to unknown protein Y		Named proteins of general function	8.733	10.095	9.791	10.092	4.12E-02	6.07E-01	1.36	0.30
lpg1367	1-aminocyclopropane-1-carboxylate deaminase		Carbohydrate Metabolism	10.608	9.378	10.978	9.825	4.24E-04	5.14E-03	-1.23	-1.15
lpg1367	1-aminocyclopropane-1-carboxylate deaminase		Carbohydrate Metabolism	10.595	9.705	10.951	10.113	1.15E-01	3.72E-02	-0.89	-0.84
lpg1368	ORF		ORFs of unknown function (unique)	9.821	9.950	14.097	8.831	9.04E-01	1.50E-03	0.13	-5.27
lpg1368	ORF		ORFs of unknown function (unique)	10.141	10.188	14.123	9.547	9.62E-01	1.06E-03	0.05	-4.58
lpg1369	chaperone Hsp90 HtpG (heat shock protein)	*htpG*	Detoxification / adaptation, Protein fate	11.965	11.690	12.666	11.939	4.17E-01	4.47E-02	-0.28	-0.73
lpg1369	chaperone Hsp90 HtpG (heat shock protein)	*htpG*	Detoxification / adaptation, Protein fate	11.938	11.724	12.699	12.130	5.40E-01	2.58E-02	-0.21	-0.57
lpg1370	small ORF (98aa) DNA binding protein Fis (recombinatio	*fis*	Transcription factors / DNA binding pro	13.971	12.987	13.508	10.744	1.73E-02	1.40E-05	-0.98	-2.76
lpg1370	small ORF (98aa) DNA binding protein Fis (recombinatio	*fis*	Transcription factors / DNA binding pro	13.950	12.938	13.437	10.830	1.95E-02	4.11E-05	-1.01	-2.61
lpg1371	lipid A disaccharide synthase	*lpxB*	Metabolism of Complex Carbohydrates	10.876	10.350	12.172	10.382	5.82E-02	9.99E-06	-0.53	-1.79
lpg1371	lipid A disaccharide synthase	*lpxB*	Metabolism of Complex Carbohydrates	10.858	10.215	11.511	10.264	7.95E-02	1.01E-03	-0.64	-1.25
lpg1372	oxidoreductase (NADH dependent dehydrogenase) (myo-inositol-2-de		Carbohydrate Metabolism, Metabolism	10.617	11.576	10.391	11.243	2.19E-01	1.70E-02	0.96	0.85
lpg1372	oxidoreductase (NADH dependent dehydrogenase) (myo-inositol-2-de		Carbohydrate Metabolism, Metabolism	10.965	11.523	9.965	10.899	2.83E-01	1.00E-01	0.56	0.93
lpg1373	ribonuclease HII	*rnhB*	DNA/RNA degradation / restriction	10.042	8.229	8.804	9.490	4.01E-02	3.34E-01	-1.81	0.69
lpg1373	ribonuclease HII	*rnhB*	DNA/RNA degradation / restriction	9.726	7.892	8.678	9.676	4.29E-02	1.62E-01	-1.83	1.00
lpg1374	rod shape determining protein RodA	*rodA*	Cell envelope synthesis	10.777	10.076	10.643	7.977	2.40E-01	2.89E-04	-0.70	-2.67
lpg1374	rod shape determining protein RodA	*rodA*	Cell envelope synthesis	10.728	10.472	10.863	9.295	6.79E-01	2.65E-02	-0.26	-1.57
lpg1375	penicillin binding protein 2 (cell elongation, e phase; pept	*pbpA*	Cell envelope synthesis, Metabolism o	10.176	9.056	9.275	8.436	1.38E-01	2.08E-01	-1.12	-0.84
lpg1375	penicillin binding protein 2 (cell elongation, e phase; pept	*pbpA*	Cell envelope synthesis, Metabolism o	10.239	8.479	8.937	9.421	1.03E-01	3.99E-01	-1.76	0.48
lpg1376	hypothetical COG1576		Unknown / hypothetical proteins	10.443	8.268	10.251	9.649	7.63E-05	1.99E-01	-2.18	-0.60
lpg1376	hypothetical COG1576		Unknown / hypothetical proteins	10.315	7.573	10.031	10.322	2.27E-02	5.82E-01	-2.74	0.29
lpg1377	hypothetical COG0799		Unknown / hypothetical proteins	12.296	11.002	14.121	11.201	1.01E-01	1.09E-04	-1.29	-2.92
lpg1377	hypothetical COG0799		Unknown / hypothetical proteins	12.357	9.979	11.671	11.039	6.82E-02	2.95E-01	-2.38	-0.63
lpg1378	proton/peptide symporter (POT) family protein (proton/oligopeptide tra		Transport and binding	11.874	12.786	12.186	10.238	5.44E-02	5.75E-03	0.91	-1.95
lpg1378	proton/peptide symporter (POT) family protein (proton/oligopeptide tra		Transport and binding	11.743	12.999	12.124	11.209	5.80E-02	1.58E-01	1.26	-0.92
lpg1379	urocanate hydratase (urocanase)		Amino Acid Metabolism	11.643	11.886	11.193	11.716	4.28E-01	1.27E-01	0.24	0.52
lpg1379	urocanate hydratase (urocanase)		Amino Acid Metabolism	11.805	12.233	11.148	11.834	3.43E-01	1.10E-01	0.43	0.69
lpg1380	histidine ammonia lyase		Amino Acid Metabolism, Energy Metab	11.788	12.417	12.222	12.701	2.47E-01	2.74E-01	0.63	0.48
lpg1380	histidine ammonia lyase		Amino Acid Metabolism, Energy Metab	11.823	12.440	12.177	12.675	1.76E-01	2.69E-01	0.62	0.50
lpg1381	aldehyde dehydrogenase (NAD dependent) (coniferyl adehyde dehyd		Named proteins of general function	11.780	11.753	11.868	11.576	9.20E-01	2.56E-01	-0.03	-0.29
lpg1381	aldehyde dehydrogenase (NAD dependent) (coniferyl adehyde dehyd		Named proteins of general function	11.806	11.699	11.652	11.478	6.68E-01	5.19E-01	-0.11	-0.17
lpg1382	dehydrogenase, short chain (dhs-6C) (hydroxysteroid dehydrogenase		Lipid Metabolism	10.788	12.157	11.207	11.626	1.63E-04	5.77E-02	1.37	0.42
lpg1382	dehydrogenase, short chain (dhs-6C) (hydroxysteroid dehydrogenase		Lipid Metabolism	10.642	12.269	11.100	11.779	9.33E-05	7.03E-03	1.63	0.68
lpg1383	ribonuclease HI	*rnhA*	DNA/RNA degradation / restriction	10.115	11.295	8.900	10.844	5.91E-03	1.26E-02	1.18	1.94
lpg1383	ribonuclease HI	*rnhA*	DNA/RNA degradation / restriction	9.159	11.205	8.835	10.859	8.59E-02	7.15E-03	2.05	2.02
lpg1384	DNA polymerase III, epsilon subunit	*dnaQ*	Nucleotide Metabolism, Replication an	10.931	10.750	9.653	10.634	8.27E-01	1.02E-01	-0.18	0.98
lpg1384	DNA polymerase III, epsilon subunit	*dnaQ*	Nucleotide Metabolism, Replication an	11.101	11.186	9.478	10.837	8.67E-01	1.59E-02	0.08	1.36
lpg1385	small ORF (125aa)		ORFs of unknown function (unique)	10.347	10.017	14.303	9.071	7.68E-01	6.83E-04	-0.33	-5.23
lpg1385	small ORF (125aa)		ORFs of unknown function (unique)	10.533	10.096	14.351	9.281	6.76E-01	3.92E-04	-0.44	-5.07
lpg1386	enhanced entry protein EnhA (ErfK/YbiS/YcfS/YnhG family protein)		Toxin production / other pathogen func	7.949	7.062	12.642	7.665	6.16E-01	2.36E-03	-0.89	-4.98
lpg1386	enhanced entry protein EnhA (ErfK/YbiS/YcfS/YnhG family protein)		Toxin production / other pathogen func	8.248	7.556	12.586	8.555	6.46E-01	4.07E-03	-0.69	-4.03
lpg1387	ORF		ORFs of unknown function (unique)	10.644	10.149	13.364	9.038	5.03E-01	3.11E-04	-0.50	-4.33
lpg1387	ORF		ORFs of unknown function (unique)	10.899	10.910	13.534	10.187	9.90E-01	4.47E-03	0.01	-3.35

lpg1388	hypothetical (HesB/YadR/YfhF family protein)		Named proteins of general function	11.429	10.027	11.002	9.151	9.54E-02	1.09E-02	-1.40	-1.85
lpg1388	hypothetical (HesB/YadR/YfhF family protein)		Named proteins of general function	11.219	10.241	10.924	9.699	2.81E-01	5.30E-02	-0.98	-1.22
lpg1389	tRNA (5 methylaminomethyl-2-thiouridylate) methyltransferase (tRNA		DNA/RNA degradation / restriction, Tra	11.424	11.116	10.021	11.249	2.31E-01	3.56E-03	-0.31	1.23
lpg1389	tRNA (5 methylaminomethyl-2-thiouridylate) methyltransferase (tRNA		DNA/RNA degradation / restriction, Tra	11.491	11.122	9.752	11.210	1.53E-01	9.79E-03	-0.37	1.46
lpg1390	small ORF (142aa)		ORFs of unknown function (unique)	11.311	10.756	10.799	10.490	1.63E-01	2.75E-01	-0.55	-0.31
lpg1390	small ORF (142aa)		ORFs of unknown function (unique)	11.381	10.989	10.843	10.653	4.86E-01	7.15E-01	-0.39	-0.19
lpg1391	50S ribosomal protein L32	*rpmF*	Translation	14.653	15.068	13.096	14.721	5.27E-01	2.06E-02	0.42	1.63
lpg1391	50S ribosomal protein L32	*rpmF*	Translation	14.544	14.866	12.542	14.672	6.57E-01	1.60E-03	0.32	2.13
lpg1392	fatty acid/phospholipid synthesis protein PlsX	*plsX*	Lipid Metabolism, Metabolism of Comp	12.840	11.603	10.804	12.149	1.79E-01	2.48E-01	-1.24	1.35
lpg1392	fatty acid/phospholipid synthesis protein PlsX	*plsX*	Lipid Metabolism, Metabolism of Comp	12.933	11.596	10.156	11.947	1.07E-01	2.59E-01	-1.34	1.79
lpg1393	3-oxoacyl-(acyl carrier protein) synthase II FabH	*fabH*	Lipid Metabolism	13.920	13.073	11.389	13.344	1.54E-01	1.27E-02	-0.85	1.95
lpg1393	3-oxoacyl-(acyl carrier protein) synthase II FabH	*fabH*	Lipid Metabolism	13.967	13.037	11.268	13.360	1.68E-01	1.42E-02	-0.93	2.09
lpg1394	S-malonyl transferase (malonyl CoA-acyl carrier protein transacylase)		Lipid Metabolism	12.516	10.959	10.823	11.534	2.59E-02	2.59E-01	-1.56	0.71
lpg1394	S-malonyl transferase (malonyl CoA-acyl carrier protein transacylase)		Lipid Metabolism	12.518	11.315	10.842	11.795	7.69E-02	1.14E-01	-1.20	0.95
lpg1395	3-oxoacyl-(acyl carrier protein) reductase	*fabG*	Lipid Metabolism	9.807	8.700	10.194	7.555	2.79E-02	3.73E-02	-1.11	-2.64
lpg1395	3-oxoacyl-(acyl carrier protein) reductase	*fabG*	Lipid Metabolism	10.126	8.432	10.392	7.849	2.89E-04	2.68E-02	-1.69	-2.54
lpg1396	acyl carrier protein (ACP)	*acpP*	Named proteins of general function	14.027	14.090	12.316	14.805	8.89E-01	1.85E-03	0.06	2.49
lpg1396	acyl carrier protein (ACP)	*acpP*	Named proteins of general function	14.006	14.081	12.311	14.811	8.72E-01	1.10E-03	0.07	2.50
lpg1397	beta-ketoacyl-acyl carrier protein synthase II (3-oxoacyl [	*fabF1*	Lipid Metabolism	14.892	13.826	13.298	14.626	1.68E-02	3.79E-03	-1.07	1.33
lpg1397	beta-ketoacyl-acyl carrier protein synthase II (3-oxoacyl [	*fabF1*	Lipid Metabolism	14.841	13.893	13.298	14.672	3.06E-02	5.40E-03	-0.95	1.37
lpg1398	aminodeoxychorismate lyase (thymidylate kinase?)		Named proteins of general function	10.913	6.982	10.698	9.054	2.70E-03	1.05E-02	-3.93	-1.64
lpg1398	aminodeoxychorismate lyase (thymidylate kinase?)		Named proteins of general function	11.025	8.137	10.687	9.640	1.44E-03	4.00E-02	-2.89	-1.05
lpg1399	thymidylate kinase (dTMP kinase)		Nucleotide Metabolism	12.088	10.336	10.715	12.126	7.27E-03	5.47E-02	-1.75	1.41
lpg1399	thymidylate kinase (dTMP kinase)		Nucleotide Metabolism	12.248	10.357	10.252	12.183	4.76E-04	8.49E-02	-1.89	1.93
lpg1400	DNA polymerase III, delta prime subunit	*holB*	Nucleotide Metabolism, Replication an	12.185	10.370	10.730	11.863	4.08E-03	2.08E-02	-1.81	1.13
lpg1400	DNA polymerase III, delta prime subunit	*holB*	Nucleotide Metabolism, Replication an	12.048	10.323	10.585	11.810	1.41E-02	1.37E-02	-1.73	1.22
lpg1401	type 4 fimbrial biogenesis protein PilZ	*pilZ*	Transport and binding	11.191	9.747	11.764	9.693	7.19E-03	1.62E-03	-1.44	-2.07
lpg1401	type 4 fimbrial biogenesis protein PilZ	*pilZ*	Transport and binding	11.177	10.022	11.734	10.168	1.46E-02	2.93E-03	-1.15	-1.57
lpg1402	deoxyribonuclease TatD		DNA/RNA degradation / restriction	12.241	11.485	12.488	11.890	1.16E-03	1.14E-04	-0.76	-0.60
lpg1402	deoxyribonuclease TatD		DNA/RNA degradation / restriction	12.174	11.436	12.312	11.845	5.12E-04	1.07E-02	-0.74	-0.47
lpg1403	hypothetical (transcriptional repressor?) (molecular chaperone?) COG		Unknown / hypothetical proteins	12.414	10.693	11.640	10.935	5.98E-04	1.02E-02	-1.72	-0.70
lpg1403	hypothetical (transcriptional repressor?) (molecular chaperone?) COG		Unknown / hypothetical proteins	12.392	10.679	11.379	10.724	1.78E-03	1.32E-01	-1.71	-0.66
lpg1404	major facilitator family transporter		Transport and binding	11.913	10.304	11.133	9.549	1.07E-02	5.84E-04	-1.61	-1.58
lpg1404	major facilitator family transporter		Transport and binding	11.988	10.217	11.062	9.886	8.48E-04	8.27E-04	-1.77	-1.18
lpg1405	multidrug translocase MdfA (sugar transport protein) (pro	*cmr*	Transport and binding	11.063	11.116	11.280	10.674	8.70E-01	4.51E-01	0.05	-0.61
lpg1405	multidrug translocase MdfA (sugar transport protein) (pro	*cmr*	Transport and binding	11.211	11.698	11.612	11.519	1.50E-01	8.64E-01	0.49	-0.09
lpg1406	glycosyltransferase (dolichol phosphate mannosyltransferase) (polyp		Metabolism of Complex Carbohydrate	12.689	9.376	10.321	8.797	8.50E-04	2.00E-01	-3.31	-1.52
lpg1406	glycosyltransferase (dolichol phosphate mannosyltransferase) (polyp		Metabolism of Complex Carbohydrate	12.649	11.007	10.517	9.855	1.98E-01	6.99E-01	-1.64	-0.66
lpg1407	dolichol monophosphate mannose synthase		Metabolism of Complex Carbohydrate	9.757	7.829	8.975	7.640	1.46E-01	2.47E-01	-1.93	-1.33
lpg1407	dolichol monophosphate mannose synthase		Metabolism of Complex Carbohydrate	9.458	9.130	9.127	8.196	2.52E-01	2.08E-02	-0.33	-0.93
lpg1408	choline kinase (cholinephosphate cytidylyltransferase)	*licA*	Metabolism of Other Amino Acids, Met	11.157	12.394	10.853	11.222	4.94E-03	2.70E-01	1.24	0.37
lpg1408	choline kinase (cholinephosphate cytidylyltransferase)	*licA*	Metabolism of Other Amino Acids, Met	11.147	12.599	10.889	11.634	6.07E-03	1.73E-01	1.45	0.74
lpg1409	hypothetical		Unknown / hypothetical proteins	10.854	11.029	10.824	10.893	5.24E-01	8.52E-01	0.18	0.07
lpg1409	hypothetical		Unknown / hypothetical proteins	10.817	11.045	10.569	11.036	3.57E-01	5.74E-02	0.23	0.47
lpg1410	transcriptional regulatory protein (lipoprotein)		Transcription factors / DNA binding pro	11.757	11.577	10.528	11.414	8.44E-01	9.89E-02	-0.18	0.89
lpg1410	transcriptional regulatory protein (lipoprotein)		Transcription factors / DNA binding pro	13.133	11.586	10.067	11.400	1.30E-02	1.76E-02	-1.55	1.33
lpg1411	adenylate kinase (ATP-AMP transphosphorylase)	*adK*	Nucleotide Metabolism	12.828	13.605	12.244	13.164	2.64E-03	4.01E-03	0.78	0.92
lpg1411	adenylate kinase (ATP-AMP transphosphorylase)	*adK*	Nucleotide Metabolism	12.868	13.663	12.284	13.258	4.06E-03	1.13E-03	0.79	0.97
lpg1412	thioredoxin	*trxA3*	Named proteins of general function	10.397	8.864	10.090	8.888	1.89E-02	6.36E-02	-1.53	-1.20
lpg1412	thioredoxin	*trxA3*	Named proteins of general function	10.154	8.691	9.891	8.784	1.06E-01	6.26E-02	-1.46	-1.11
lpg1413	glycerol-3-phosphate dehydrogenase	*glpD*	Metabolism of Complex Lipids	11.504	11.824	12.771	11.174	5.57E-01	9.61E-04	0.32	-1.60
lpg1413	glycerol-3-phosphate dehydrogenase	*glpD*	Metabolism of Complex Lipids	11.490	11.415	12.044	10.665	7.43E-01	5.79E-04	-0.08	-1.38
lpg1414	glycerol kinase (probable carbohydrate kinase)		Metabolism of Complex Lipids	9.621	10.245	10.131	10.196	3.36E-01	9.37E-01	0.62	0.06
lpg1414	glycerol kinase (probable carbohydrate kinase)		Metabolism of Complex Lipids	9.976	10.321	10.263	10.355	3.83E-01	8.50E-01	0.34	0.09
lpg1415	citrate synthase	*gltA*	Carbohydrate Metabolism	11.642	11.496	13.903	12.292	8.41E-01	1.74E-02	-0.15	-1.61
lpg1415	citrate synthase	*gltA*	Carbohydrate Metabolism	11.615	12.588	13.937	13.067	1.71E-01	1.55E-01	0.97	-0.87
lpg1416	purine nucleoside phosphorylase II (uridine phosphorylase Udp2)		Nucleotide Metabolism	12.289	12.473	11.835	12.179	6.01E-01	5.13E-01	0.18	0.34
lpg1416	purine nucleoside phosphorylase II (uridine phosphorylase Udp2)		Nucleotide Metabolism	12.380	12.820	11.742	12.313	2.88E-01	4.28E-01	0.44	0.57
lpg1417	DNA gyrase, A subunit	*gyrA*	Replication and Repair	12.951	13.017	11.658	12.968	8.76E-01	8.74E-04	0.07	1.31
lpg1417	DNA gyrase, A subunit	*gyrA*	Replication and Repair	12.877	13.038	11.623	12.977	7.32E-01	4.87E-04	0.16	1.35
lpg1418	3-phosphoserine aminotransferase (phosphoserine trans	*serC*	Amino Acid Metabolism, Metabolism o	12.731	10.294	11.385	10.618	2.51E-03	1.97E-01	-2.44	-0.77
lpg1418	3-phosphoserine aminotransferase (phosphoserine trans	*serC*	Amino Acid Metabolism, Metabolism o	12.775	10.196	11.363	10.702	1.15E-03	2.44E-01	-2.58	-0.66
lpg1419	3-phosphoshikimate 1-carboxyvinyltransferase (5-enolpyruvoylshikim		Amino Acid Metabolism	12.200	10.438	10.180	12.025	2.99E-03	1.47E-02	-1.76	1.85
lpg1419	3-phosphoshikimate 1-carboxyvinyltransferase (5-enolpyruvoylshikim		Amino Acid Metabolism	12.209	10.173	10.274	12.136	3.24E-03	1.25E-02	-2.04	1.86

lpg1420	cytidylate kinase	*cmk*	Nucleotide Metabolism	13.724	13.415	10.468	14.132	8.29E-01	8.73E-03	-0.31	3.66
lpg1420	cytidylate kinase	*cmk*	Nucleotide Metabolism	14.242	13.309	10.525	14.263	3.47E-01	4.95E-03	-0.93	3.74
lpg1421	30S ribosomal protein S1	*rpsA*	Translation	14.417	13.646	14.099	14.567	2.65E-04	1.02E-01	-0.77	0.47
lpg1421	30S ribosomal protein S1	*rpsA*	Translation	14.502	13.669	14.055	14.528	2.35E-03	7.80E-02	-0.83	0.47
lpg1422	hypothetical COG3771: membrane protein		Unknown / hypothetical proteins	12.418	10.914	11.463	11.322	5.91E-04	8.09E-01	-1.50	-0.14
lpg1422	hypothetical COG3771: membrane protein		Unknown / hypothetical proteins	12.361	10.838	10.748	11.116	3.35E-04	6.08E-01	-1.52	0.37
lpg1423	TPR domain protein (heat shock protein) N-acetylglucosaminyl transf		Detoxification / adaptation, Protein fate	12.648	11.867	11.572	12.263	8.34E-02	9.58E-02	-0.78	0.69
lpg1423	TPR domain protein (heat shock protein) N-acetylglucosaminyl transf		Detoxification / adaptation, Protein fate	12.587	11.678	11.257	12.128	3.74E-02	8.84E-02	-0.91	0.87
lpg1424	aminotransferase (amino sugar biosynthesis protein) (lipopolysacchar		Metabolism of Complex Lipids	11.936	11.866	9.744	11.668	8.48E-01	2.65E-02	-0.07	1.92
lpg1424	aminotransferase (amino sugar biosynthesis protein) (lipopolysacchar		Metabolism of Complex Lipids	11.977	11.844	9.637	12.000	6.89E-01	9.15E-03	-0.13	2.36
lpg1425	orotidine 5'-phosphate decarboxylase PyrF	*pyrF*	Nucleotide Metabolism	11.107	8.988	8.400	10.093	2.55E-02	7.86E-02	-2.12	1.69
lpg1425	orotidine 5'-phosphate decarboxylase PyrF	*pyrF*	Nucleotide Metabolism	11.211	8.880	8.527	10.269	4.98E-03	7.34E-02	-2.33	1.74
lpg1426	hypothetical (serine protease?)	*VpdC*	Protein fate / hydrolases / secretion	10.849	8.239	9.118	7.649	5.55E-05	1.27E-01	-2.61	-1.47
lpg1426	hypothetical (serine protease?)	*VpdC*	Protein fate / hydrolases / secretion	10.607	7.983	8.311	7.244	1.48E-04	3.77E-01	-2.62	-1.07
lpg1427	short chain dehydrogenase (3-oxoacyl [acyl carrier protein] reductase		Lipid Metabolism	12.463	10.061	12.997	10.640	1.10E-04	5.25E-06	-2.40	-2.36
lpg1427	short chain dehydrogenase (3-oxoacyl [acyl carrier protein] reductase		Lipid Metabolism	12.518	10.584	13.013	10.712	4.92E-05	7.33E-06	-1.93	-2.30
lpg1428	competence comG operon protein?, type 4 fimbrial pilin related signa		Named proteins of general function	9.794	7.710	9.551	6.732	6.23E-05	1.49E-03	-2.08	-2.82
lpg1428	competence comG operon protein?, type 4 fimbrial pilin related signa		Named proteins of general function	9.840	8.016	8.453	6.914	5.39E-04	4.76E-01	-1.82	-1.54
lpg1429	ORF		ORFs of unknown function (unique)	10.316	9.429	9.083	9.844	1.60E-01	2.47E-01	-0.89	0.76
lpg1429	ORF		ORFs of unknown function (unique)	10.710	9.744	8.985	10.291	1.07E-01	1.19E-01	-0.97	1.31
lpg1430	4-hydroxybenzoate octaprenyltransferase UbiA		Metabolism of Cofactors and Vitamins	9.470	10.039	9.526	9.598	3.46E-01	9.03E-01	0.57	0.07
lpg1430	4-hydroxybenzoate octaprenyltransferase UbiA		Metabolism of Cofactors and Vitamins	9.525	10.080	9.473	9.856	3.71E-01	4.60E-01	0.56	0.38
lpg1431	outer membrane lipoprotein?		Named proteins of general function	12.700	12.064	12.371	10.815	2.31E-01	1.33E-02	-0.64	-1.56
lpg1431	outer membrane lipoprotein?		Named proteins of general function	12.715	12.295	12.401	11.230	2.50E-01	7.05E-03	-0.42	-1.17
lpg1432	FAD linked oxidase (isoamyl alcohol oxidase) (oxidoreductase, oxyge		Named proteins of general function	9.320	8.733	9.841	7.865	5.42E-01	5.51E-03	-0.59	-1.98
lpg1432	FAD linked oxidase (isoamyl alcohol oxidase) (oxidoreductase, oxyge		Named proteins of general function	9.298	9.150	9.856	8.420	9.09E-01	1.24E-01	-0.15	-1.44
lpg1433	2-deoxyribose-5-phosphate aldolase	*deoC*	Carbohydrate Metabolism	10.342	8.612	8.254	8.151	1.13E-02	9.19E-01	-1.73	-0.10
lpg1433	2-deoxyribose-5-phosphate aldolase	*deoC*	Carbohydrate Metabolism	10.095	7.985	8.580	8.552	1.14E-02	9.70E-01	-2.11	-0.03
lpg1434	xanthosine phosphorylase (purine nucleoside phosphoryl	*xapA*	Nucleotide Metabolism	11.519	10.086	11.463	11.677	5.54E-04	5.79E-01	-1.43	0.21
lpg1434	xanthosine phosphorylase (purine nucleoside phosphoryl	*xapA*	Nucleotide Metabolism	11.150	10.541	11.230	11.994	1.58E-01	3.08E-02	-0.61	0.76
lpg1435	cytidine deaminase (cytidine and deoxycytidine deamina	*cdd*	Nucleotide Metabolism	11.871	10.483	9.881	11.902	3.57E-02	1.46E-02	-1.39	2.02
lpg1435	cytidine deaminase (cytidine and deoxycytidine deamina	*cdd*	Nucleotide Metabolism	11.571	11.040	9.902	12.104	5.99E-01	1.48E-02	-0.53	2.20
lpg1436	ORF		ORFs of unknown function (unique)	10.229	9.624	9.411	9.256	2.49E-01	8.14E-01	-0.60	-0.16
lpg1436	ORF		ORFs of unknown function (unique)	10.283	9.403	9.331	9.192	1.83E-01	8.77E-01	-0.88	-0.14
lpg1437	sensor histidine kinase CpxA (two component sensor)	*cpxA*	Signal transduction / other regulatory f	11.121	10.058	9.970	9.213	1.18E-01	2.73E-01	-1.06	-0.76
lpg1437	sensor histidine kinase CpxA (two component sensor)	*cpxA*	Signal transduction / other regulatory f	11.155	10.191	9.838	9.331	5.40E-02	1.79E-01	-0.96	-0.51
lpg1438	transcriptional regulatory protein CpxR (DNA binding resp	*cpxR*	Transcription factors / DNA binding pro	13.132	10.699	13.080	10.506	1.90E-05	4.67E-06	-2.43	-2.57
lpg1438	transcriptional regulatory protein CpxR (DNA binding resp	*cpxR*	Transcription factors / DNA binding pro	13.171	11.126	13.153	10.904	1.11E-08	3.79E-07	-2.05	-2.25
lpg1439	Mg2+ and Co2+ transporter CorC (metal ion transporter) (hemolysin)		Transport and binding, Toxin productio	13.734	10.798	13.693	9.581	3.53E-03	2.13E-03	-2.94	-4.11
lpg1439	Mg2+ and Co2+ transporter CorC (metal ion transporter) (hemolysin)		Transport and binding, Toxin productio	13.699	11.285	13.622	9.931	9.98E-04	7.19E-04	-2.41	-3.69
lpg1440	metal dependent hydrolase		Protein fate / hydrolases / secretion	12.603	10.503	12.829	11.262	5.87E-07	4.18E-05	-2.10	-1.57
lpg1440	metal dependent hydrolase		Protein fate / hydrolases / secretion	12.470	10.623	12.639	11.374	2.78E-05	4.02E-06	-1.85	-1.26
lpg1441	phosphate starvation-inducible protein PhoH (ATP binding protein)		Detoxification / adaptation, Signal tran	13.856	12.529	14.250	12.106	1.65E-03	8.10E-05	-1.33	-2.14
lpg1441	phosphate starvation-inducible protein PhoH (ATP binding protein)		Detoxification / adaptation, Signal tran	13.854	12.626	14.208	12.543	2.33E-02	4.16E-03	-1.23	-1.66
lpg1442	metal dependent phosphoesterase (PHP family)		Protein fate / hydrolases / secretion	11.579	10.743	9.487	11.620	2.97E-01	3.24E-03	-0.84	2.13
lpg1442	metal dependent phosphoesterase (PHP family)		Protein fate / hydrolases / secretion	11.686	11.285	9.504	11.949	3.13E-01	3.52E-04	-0.40	2.44
lpg1443	translation factor (Sua5/YciO/YrdC/YwlC family protein)		Translation	11.411	10.689	10.224	9.698	7.61E-02	4.56E-01	-0.72	-0.53
lpg1443	translation factor (Sua5/YciO/YrdC/YwlC family protein)		Translation	11.393	10.522	10.112	10.505	6.13E-02	4.38E-01	-0.87	0.39
lpg1444	tryptophanyl tRNA synthetase	*trpS*	Amino Acid Metabolism, Translation	11.943	12.049	11.943	12.052	6.93E-01	7.03E-01	0.11	0.11
lpg1444	tryptophanyl tRNA synthetase	*trpS*	Amino Acid Metabolism, Translation	12.044	12.383	11.923	12.187	2.84E-01	2.58E-01	0.34	0.26
lpg1445	conserved hypothetical protein		Unknown / hypothetical proteins	10.134	9.500	9.069	9.848	1.03E-01	1.41E-01	-0.63	0.78
lpg1445	conserved hypothetical protein		Unknown / hypothetical proteins	10.162	9.960	8.776	9.750	6.75E-01	1.34E-01	-0.20	0.97
lpg1446	hypothetical (transcriptional regulator) TIGR00281		Transcription factors / DNA binding pro	10.313	8.211	10.398	9.129	5.36E-04	6.85E-02	-2.10	-1.27
lpg1446	hypothetical (transcriptional regulator) TIGR00281		Transcription factors / DNA binding pro	10.462	8.276	9.982	9.625	2.05E-02	5.83E-01	-2.19	-0.36
lpg1447	pseudouridine synthase		DNA/RNA degradation / restriction, Tra	12.232	11.468	12.850	12.260	1.06E-03	6.51E-03	-0.76	-0.59
lpg1447	pseudouridine synthase		DNA/RNA degradation / restriction, Tra	12.190	11.535	12.737	12.229	6.56E-04	2.42E-02	-0.66	-0.51
lpg1448	transcription regulator protein, COG2197: response regulator containi		Signal transduction / other regulatory f	9.972	7.428	8.203	8.216	2.26E-02	9.86E-01	-2.54	0.01
lpg1448	transcription regulator protein, COG2197: response regulator containi		Signal transduction / other regulatory f	10.159	9.118	7.283	8.704	3.96E-01	4.58E-01	-1.04	1.42
lpg1449	ORF		ORFs of unknown function (unique)	10.166	10.343	9.893	10.410	4.43E-01	4.05E-02	0.18	0.52
lpg1449	ORF		ORFs of unknown function (unique)	10.101	10.277	9.805	10.475	5.58E-01	2.35E-02	0.18	0.67
lpg1450	iron/ascorbate oxidoreductase family protein, putative		Named proteins of general function	9.702	8.999	8.783	8.586	1.00E-01	8.16E-01	-0.70	-0.20
lpg1450	iron/ascorbate oxidoreductase family protein, putative		Named proteins of general function	9.213	9.710	9.133	9.136	2.76E-01	9.98E-01	0.50	0.00
lpg1451	hypothetical (phosphatidylethanolamine binding protein)		Cell envelope synthesis, Transport and	12.150	13.868	14.485	13.439	7.75E-03	9.18E-02	1.72	-1.05
lpg1451	hypothetical (phosphatidylethanolamine binding protein)		Cell envelope synthesis, Transport and	11.304	13.444	13.572	12.629	5.26E-03	1.90E-01	2.14	-0.94

lpg1452	lipase A? (hydrolase, alpha/beta fold family), kraken-like (serine hydro		Protein fate / hydrolases / secretion	10.072	9.145	9.421	9.497	1.56E-01	9.18E-01	-0.93	0.08
lpg1452	lipase A? (hydrolase, alpha/beta fold family), kraken-like (serine hydro		Protein fate / hydrolases / secretion	10.593	10.210	9.827	10.201	4.67E-01	6.00E-01	-0.38	0.37
lpg1453	ORF		ORFs of unknown function (unique)	12.885	14.680	13.212	13.909	9.30E-07	1.68E-03	1.80	0.70
lpg1453	ORF		ORFs of unknown function (unique)	12.739	14.697	13.151	13.950	5.93E-07	1.51E-03	1.96	0.80
lpg1454	multidrug efflux protein (MFS transporter)		Transport and binding	9.305	8.966	10.438	7.835	6.12E-01	1.11E-02	-0.34	-2.60
lpg1454	multidrug efflux protein (MFS transporter)		Transport and binding	9.245	8.676	10.128	8.935	4.06E-01	9.22E-02	-0.57	-1.19
lpg1455	phospholipase C (phosphatidylcholine hydrolyzing)		Metabolism of Complex Lipids	10.873	9.732	12.782	8.511	3.12E-02	5.98E-05	-1.14	-4.27
lpg1455	phospholipase C (phosphatidylcholine hydrolyzing)		Metabolism of Complex Lipids	10.508	9.725	12.644	8.593	2.03E-01	2.80E-04	-0.78	-4.05
lpg1456	23S rRNA (uracil-5-)methyltransferase RumA (RNA methyltransferase		DNA/RNA degradation / restriction, Tra	8.329	10.475	8.818	9.815	2.75E-02	1.42E-01	2.15	1.00
lpg1456	23S rRNA (uracil-5-)methyltransferase RumA (RNA methyltransferase		DNA/RNA degradation / restriction, Tra	8.637	10.102	8.629	10.332	9.30E-03	1.46E-02	1.47	1.70
lpg1457	GTP pyrophosphokinase ((p)ppGpp synthetase I) stringe	*relA*	Nucleotide Metabolism	12.201	11.959	11.831	11.942	2.90E-01	6.01E-01	-0.24	0.11
lpg1457	GTP pyrophosphokinase ((p)ppGpp synthetase I) stringe	*relA*	Nucleotide Metabolism	12.137	11.955	11.811	11.978	4.45E-01	4.34E-01	-0.18	0.17
lpg1458	hypothetical membrane protein		Unknown / hypothetical proteins	10.794	9.426	9.395	9.211	1.84E-03	7.47E-01	-1.37	-0.18
lpg1458	hypothetical membrane protein		Unknown / hypothetical proteins	10.744	9.533	9.252	9.182	4.35E-03	9.14E-01	-1.21	-0.07
lpg1459	aspartate aminotransferase (aminotransferase, N-succiny	*yfdZ*	Amino Acid Metabolism	11.885	11.688	10.356	11.524	7.59E-01	4.36E-02	-0.20	1.17
lpg1459	aspartate aminotransferase (aminotransferase, N-succiny	*yfdZ*	Amino Acid Metabolism	12.031	11.343	9.625	11.387	1.94E-01	1.50E-02	-0.69	1.76
lpg1460	conserved hypothetical protein		Unknown / hypothetical proteins	11.822	10.865	9.841	11.921	7.85E-02	1.67E-03	-0.96	2.08
lpg1460	conserved hypothetical protein		Unknown / hypothetical proteins	11.865	10.791	9.613	11.980	5.43E-02	1.20E-03	-1.07	2.37
lpg1461	single stranded DNA specific exonuclease RecJ	*recJ*	DNA/RNA degradation / restriction	12.688	11.231	12.412	11.338	2.28E-04	1.19E-04	-1.46	-1.07
lpg1461	single stranded DNA specific exonuclease RecJ	*recJ*	DNA/RNA degradation / restriction	12.664	11.262	12.341	11.281	8.97E-05	9.43E-03	-1.40	-1.06
lpg1462	zinc binding TIM barrel protein, YjbN family (tRNA-dihydrouridine synt		DNA/RNA degradation / restriction, Tra	10.525	10.648	10.276	10.672	7.26E-01	3.26E-01	0.12	0.40
lpg1462	zinc binding TIM barrel protein, YjbN family (tRNA-dihydrouridine synt		DNA/RNA degradation / restriction, Tra	10.491	10.627	10.126	10.578	7.52E-01	4.06E-01	0.14	0.45
lpg1463	preprotein translocase; secretion protein SecA	*secA*	Protein fate / hydrolases / secretion	12.060	11.768	11.908	12.305	3.68E-01	2.81E-01	-0.29	0.40
lpg1463	preprotein translocase; secretion protein SecA	*secA*	Protein fate / hydrolases / secretion	12.096	11.630	11.890	12.324	1.79E-01	1.97E-01	-0.47	0.43
lpg1464	NTP pyrophosphohydrolase (mutator protein MutT) (8-oxo-dGTPase)		DNA/RNA degradation / restriction, Re	11.379	9.360	9.818	9.253	3.94E-03	4.55E-01	-2.02	-0.57
lpg1464	NTP pyrophosphohydrolase (mutator protein MutT) (8-oxo-dGTPase)		DNA/RNA degradation / restriction, Re	11.373	9.714	9.348	9.491	1.60E-02	8.60E-01	-1.66	0.14
lpg1465	ORF		ORFs of unknown function (unique)	9.147	9.167	8.419	7.341	9.67E-01	4.03E-01	0.02	-1.08
lpg1465	ORF		ORFs of unknown function (unique)	9.495	9.623	8.634	8.211	7.90E-01	6.15E-01	0.13	-0.42
lpg1466	conserved hypothetical protein		Unknown / hypothetical proteins	11.116	11.848	10.682	10.097	6.17E-02	1.58E-01	0.73	-0.59
lpg1466	conserved hypothetical protein		Unknown / hypothetical proteins	11.175	11.885	10.659	10.146	4.89E-02	1.68E-01	0.71	-0.51
lpg1467	dephospho-CoA kinase (DNA repair protein?)		Metabolism of Cofactors and Vitamins	10.351	10.224	10.119	9.724	6.53E-01	1.62E-01	-0.13	-0.40
lpg1467	dephospho-CoA kinase (DNA repair protein?)		Metabolism of Cofactors and Vitamins	10.458	10.138	9.941	9.830	2.02E-01	6.98E-01	-0.32	-0.11
lpg1468	small ORF (157aa)		ORFs of unknown function (unique)	11.543	13.598	12.934	11.963	2.05E-05	2.94E-03	2.06	-0.97
lpg1468	small ORF (157aa)		ORFs of unknown function (unique)	11.573	13.579	12.920	11.969	7.35E-05	3.38E-03	2.01	-0.95
lpg1469	Rtn protein (membrane protein involved in resistance to lambda and I		Detoxification / adaptation	9.316	9.187	9.170	6.789	8.53E-01	1.55E-01	-0.13	-2.38
lpg1469	Rtn protein (membrane protein involved in resistance to lambda and I		Detoxification / adaptation	9.273	8.817	9.181	9.068	3.07E-01	9.02E-01	-0.46	-0.11
lpg1470	serine-type D-Ala-D-Ala carboxypeptidase (D-alanyl-D-alanine carbox		Protein fate / hydrolases / secretion	9.884	9.728	9.046	10.060	8.60E-01	8.80E-02	-0.16	1.01
lpg1470	serine-type D-Ala-D-Ala carboxypeptidase (D-alanyl-D-alanine carbox		Protein fate / hydrolases / secretion	10.664	9.884	8.466	10.378	7.76E-02	1.99E-03	-0.78	1.91
lpg1471	adenosylmethionine-8-amino-7-oxononanoate aminotran	*bioA*	Metabolism of Cofactors and Vitamins	9.484	8.059	9.375	7.927	3.62E-02	2.25E-01	-1.42	-1.45
lpg1471	adenosylmethionine-8-amino-7-oxononanoate aminotran	*bioA*	Metabolism of Cofactors and Vitamins	9.826	8.456	8.910	8.734	1.45E-02	7.76E-01	-1.37	-0.18
lpg1472	biotin synthase BioB		Metabolism of Cofactors and Vitamins	9.978	9.651	10.129	9.343	5.90E-01	3.01E-01	-0.33	-0.79
lpg1472	biotin synthase BioB		Metabolism of Cofactors and Vitamins	10.002	9.281	10.216	10.130	3.44E-01	8.52E-01	-0.72	-0.09
lpg1473	8-amino-7-oxononanoate synthase	*bioF*	Metabolism of Cofactors and Vitamins	7.164	7.842	8.973	8.644	4.07E-01	5.11E-01	0.68	-0.33
lpg1473	8-amino-7-oxononanoate synthase	*bioF*	Metabolism of Cofactors and Vitamins	6.883	8.125	8.625	8.761	1.46E-01	8.39E-01	1.24	0.14
lpg1474	biotin biosynthesis protein BioH (hydrolase?)	*bioH*	Metabolism of Cofactors and Vitamins	10.471	10.038	11.199	9.837	1.03E-01	1.69E-04	-0.43	-1.36
lpg1474	biotin biosynthesis protein BioH (hydrolase?)	*bioH*	Metabolism of Cofactors and Vitamins	10.285	9.669	11.056	9.921	1.68E-02	6.83E-05	-0.62	-1.13
lpg1475	dethiobiotin synthetase (cobyrinic acid a,c-diamide synth	*bioD*	Metabolism of Cofactors and Vitamins	10.438	8.763	10.583	9.419	7.63E-06	2.36E-02	-1.67	-1.16
lpg1475	dethiobiotin synthetase (cobyrinic acid a,c-diamide synth	*bioD*	Metabolism of Cofactors and Vitamins	10.406	9.228	10.604	9.696	3.54E-04	7.78E-03	-1.18	-0.91
lpg1476	hypothetical (type I antifreeze protein?) COG2331		Unknown / hypothetical proteins	11.100	12.315	10.462	12.486	6.88E-03	5.15E-04	1.21	2.02
lpg1476	hypothetical (type I antifreeze protein?) COG2331		Unknown / hypothetical proteins	11.057	12.359	10.429	12.502	3.39E-03	1.95E-04	1.30	2.07
lpg1477	transmembrane protein		Unknown / hypothetical proteins	11.995	11.435	10.744	11.286	2.27E-01	2.55E-01	-0.56	0.54
lpg1477	transmembrane protein		Unknown / hypothetical proteins	12.061	11.466	10.582	11.528	2.29E-01	4.76E-02	-0.59	0.95
lpg1478	aspartyl tRNA synthetase		Amino Acid Metabolism, Translation	12.125	10.750	10.135	11.460	2.57E-03	3.62E-02	-1.37	1.33
lpg1478	aspartyl tRNA synthetase		Amino Acid Metabolism, Translation	12.080	10.973	9.814	11.547	7.84E-03	6.03E-02	-1.11	1.73
lpg1479	potassium efflux system KefA (integral membrane protein)		Transport and binding	10.828	9.979	9.522	9.725	9.20E-03	7.09E-01	-0.85	0.20
lpg1479	potassium efflux system KefA (integral membrane protein)		Transport and binding	11.275	10.055	9.989	10.199	4.47E-04	6.47E-01	-1.22	0.21
lpg1480	DNA mismatch repair protein MutH	*mutH*	Replication and Repair	10.385	9.633	10.118	9.199	1.38E-01	1.20E-01	-0.75	-0.92
lpg1480	DNA mismatch repair protein MutH	*mutH*	Replication and Repair	10.664	9.815	9.889	9.882	4.45E-02	9.88E-01	-0.85	-0.01
lpg1481	ORF		ORFs of unknown function (unique)	10.787	10.758	10.163	9.756	9.59E-01	2.47E-01	-0.03	-0.41
lpg1481	ORF		ORFs of unknown function (unique)	11.305	10.635	10.246	9.961	4.50E-02	4.83E-01	-0.67	-0.29
lpg1482	ORF		ORFs of unknown function (unique)	12.766	15.031	12.160	13.155	6.14E-06	1.71E-02	2.27	1.00
lpg1482	ORF		ORFs of unknown function (unique)	12.846	15.022	12.174	13.191	2.39E-06	1.29E-02	2.18	1.02
lpg1483	ovarian-specific serine/threonine-protein kinase	*legK1*	Named proteins of general function	9.928	10.160	10.650	9.819	4.67E-01	9.13E-02	0.23	-0.83
lpg1483	ovarian-specific serine/threonine-protein kinase	*legK1*	Named proteins of general function	10.328	9.485	9.946	9.847	3.45E-01	9.11E-01	-0.84	-0.10

lpg1484	ORF		ORFs of unknown function (unique)	8.401	10.843	9.543	11.594	2.12E-03	2.57E-06	2.44	2.05
lpg1484	ORF		ORFs of unknown function (unique)	8.488	10.352	9.025	11.724	1.03E-02	2.93E-05	1.86	2.70
lpg1485	hypothetical		Unknown / hypothetical proteins	9.238	8.988	13.079	8.400	8.39E-01	6.72E-03	-0.25	-4.68
lpg1485	hypothetical		Unknown / hypothetical proteins	9.258	8.605	12.996	8.490	5.15E-01	1.35E-02	-0.65	-4.51
lpg1486	AsnC family transcription regulator protein (amino acid metabolism)		Transcription factors / DNA binding pr	9.743	8.972	9.570	8.501	2.29E-01	1.55E-01	-0.77	-1.07
lpg1486	AsnC family transcription regulator protein (amino acid metabolism)		Transcription factors / DNA binding pr	9.877	9.260	10.110	9.047	3.05E-01	1.85E-01	-0.62	-1.06
lpg1487	acetyltransferase, GNAT family		Named proteins of general function	8.717	9.079	9.773	8.991	1.97E-01	1.07E-01	0.36	-0.78
lpg1487	acetyltransferase, GNAT family		Named proteins of general function	8.696	10.170	9.840	9.315	7.22E-02	5.90E-01	1.47	-0.52
lpg1488	surface antigen of Plasmodium and Entamoeba	*legC5*	Named proteins of general function	10.461	11.039	9.510	10.679	2.12E-01	1.08E-01	0.58	1.17
lpg1488	surface antigen of Plasmodium and Entamoeba	*legC5*	Named proteins of general function	10.564	11.666	9.681	11.536	2.04E-01	1.07E-01	1.10	1.86
lpg1489	ORF		ORFs of unknown function (unique)	10.368	12.322	10.603	10.655	4.69E-03	8.84E-01	1.95	0.05
lpg1489	ORF		ORFs of unknown function (unique)	10.754	12.498	10.429	10.692	1.42E-03	5.19E-01	1.74	0.26
lpg1490	adenylate cyclase PLUS two component hybrid sensor a	*cyaA*	Nucleotide Metabolism	9.384	8.104	12.508	7.446	2.23E-01	2.04E-03	-1.28	-5.06
lpg1490	adenylate cyclase PLUS two component hybrid sensor a	*cyaA*	Nucleotide Metabolism	9.433	8.561	12.567	8.222	4.32E-01	2.82E-03	-0.87	-4.35
lpg1491	ORF		ORFs of unknown function (unique)	9.983	10.118	13.074	9.966	8.80E-01	3.35E-03	0.14	-3.11
lpg1491	ORF		ORFs of unknown function (unique)	10.014	10.705	13.146	10.858	5.46E-01	3.88E-02	0.69	-2.29
lpg1492	spectinomycin phosphotransferase		Transport and binding	8.080	7.539	8.649	7.096	4.04E-01	2.35E-01	-0.54	-1.55
lpg1492	spectinomycin phosphotransferase		Transport and binding	8.140	6.593	8.792	8.475	2.12E-01	6.65E-01	-1.55	-0.32
lpg1493	small ORF (72aa)?		ORFs of unknown function (unique)	8.135	8.700	9.163	9.285	5.60E-01	9.23E-01	0.57	0.12
lpg1493	small ORF (72aa)?		ORFs of unknown function (unique)	8.517	9.474	9.501	10.086	4.16E-01	6.21E-01	0.96	0.58
lpg1494	small ORF (140aa) hypothetical		Unknown / hypothetical proteins	9.069	9.363	9.349	8.988	5.45E-01	2.08E-01	0.29	-0.36
lpg1494	small ORF (140aa) hypothetical		Unknown / hypothetical proteins	8.976	9.437	9.234	8.964	1.66E-01	5.34E-01	0.46	-0.27
lpg1495	small ORF (97aa)		ORFs of unknown function (unique)	12.233	14.493	13.067	11.032	4.65E-04	9.32E-04	2.26	-2.04
lpg1495	small ORF (97aa)		ORFs of unknown function (unique)	12.065	14.239	12.985	11.110	4.36E-03	9.67E-04	2.17	-1.88
lpg1496	ORF		ORFs of unknown function (unique)	9.249	8.887	13.981	8.336	7.88E-01	9.37E-04	-0.36	-5.65
lpg1496	ORF		ORFs of unknown function (unique)	8.457	8.719	13.356	7.827	8.34E-01	1.69E-04	0.26	-5.53
lpg1497	aminopeptidase N	*pepN*	Metabolism of Other Amino Acids	11.825	10.835	14.125	10.024	1.99E-01	1.10E-04	-0.99	-4.10
lpg1497	aminopeptidase N	*pepN*	Metabolism of Other Amino Acids	11.843	10.462	14.151	10.099	4.76E-02	6.93E-05	-1.38	-4.05
lpg1498	ORF		ORFs of unknown function (unique)	10.708	10.642	10.306	9.708	8.92E-01	3.31E-01	-0.07	-0.60
lpg1498	ORF		ORFs of unknown function (unique)	11.139	10.791	10.312	10.303	2.40E-01	9.85E-01	-0.35	-0.01
lpg1499	ORF		ORFs of unknown function (unique)	11.881	11.025	11.384	9.535	1.63E-02	9.49E-05	-0.86	-1.85
lpg1499	ORF		ORFs of unknown function (unique)	11.754	11.277	11.433	9.885	1.69E-01	1.49E-03	-0.48	-1.55
lpg1500	oxidoreductase, short chain dehydrogenase/reductase (3-oxoacyl-[ac		Lipid Metabolism	10.317	10.759	10.668	9.804	3.71E-01	3.91E-01	0.44	-0.86
lpg1500	oxidoreductase, short chain dehydrogenase/reductase (3-oxoacyl-[ac		Lipid Metabolism	9.977	10.695	9.580	10.065	1.36E-01	3.28E-01	0.72	0.49
lpg1501	GCN5-related N-acetyltransferase (ribosomal protein-alanine acetyltr		Protein fate / hydrolases / secretion	9.736	6.584	9.333	7.342	3.82E-02	5.58E-02	-3.15	-1.99
lpg1501	GCN5-related N-acetyltransferase (ribosomal protein-alanine acetyltr		Protein fate / hydrolases / secretion	9.587	7.439	9.096	7.342	3.93E-03	3.55E-02	-2.15	-1.75
lpg1502	dihydrolipoamide dehydrogenase	*lpdA*	Carbohydrate Metabolism, Amino Acid	13.655	12.026	13.070	12.622	6.43E-07	3.58E-02	-1.63	-0.45
lpg1502	dihydrolipoamide dehydrogenase	*lpdA*	Carbohydrate Metabolism, Amino Acid	13.615	11.948	13.005	12.639	4.97E-06	7.39E-02	-1.67	-0.37
lpg1503	pyruvate dehydrogenase E2 component (dihydrolipoamic	*aceF*	Carbohydrate Metabolism	12.312	11.090	11.722	11.772	7.69E-03	8.99E-01	-1.22	0.05
lpg1503	pyruvate dehydrogenase E2 component (dihydrolipoamic	*aceF*	Carbohydrate Metabolism	12.283	11.191	11.572	11.776	1.77E-02	6.54E-01	-1.09	0.20
lpg1504	pyruvate dehydrogenase E1 component oxidoreductase	*aceE*	Carbohydrate Metabolism, Amino Acid	11.644	11.041	10.997	12.019	2.92E-01	2.06E-01	-0.60	1.02
lpg1504	pyruvate dehydrogenase E1 component oxidoreductase	*aceE*	Carbohydrate Metabolism, Amino Acid	11.588	11.214	10.893	12.601	5.56E-01	1.99E-02	-0.37	1.71
lpg1505	conserved hypothetical protein		Unknown / hypothetical proteins	12.678	12.861	11.902	13.143	3.92E-01	8.15E-04	0.18	1.24
lpg1505	conserved hypothetical protein		Unknown / hypothetical proteins	12.642	12.885	11.788	13.179	2.05E-01	3.92E-04	0.24	1.39
lpg1506	inner membrane protein AmpE (beta lactamase induction?)		Named proteins of general function	10.465	10.998	10.432	10.338	5.76E-01	8.13E-01	0.53	-0.09
lpg1506	inner membrane protein AmpE (beta lactamase induction?)		Named proteins of general function	11.011	10.706	10.211	10.276	5.94E-01	8.82E-01	-0.31	0.07
lpg1507	sodium/hydrogen antiporter (glutathione regulated potassium efflux sy		Transport and binding	11.105	11.203	9.892	11.308	7.81E-01	5.65E-03	0.10	1.42
lpg1507	sodium/hydrogen antiporter (glutathione regulated potassium efflux sy		Transport and binding	11.129	11.019	9.718	11.405	6.80E-01	2.02E-03	-0.11	1.69
lpg1508	rare lipoprotein A		Named proteins of general function	9.895	9.872	9.114	9.829	9.33E-01	5.15E-02	-0.02	0.71
lpg1508	rare lipoprotein A		Named proteins of general function	9.731	9.643	8.495	9.829	8.55E-01	1.55E-01	-0.09	1.33
lpg1509	D-alanyl-D-alanine carboxypeptidase		Protein fate / hydrolases / secretion	13.081	11.907	11.593	12.174	3.27E-02	2.53E-01	-1.17	0.58
lpg1509	D-alanyl-D-alanine carboxypeptidase		Protein fate / hydrolases / secretion	12.999	12.029	11.386	12.127	7.47E-02	1.86E-01	-0.97	0.74
lpg1510	D-alanine-aminotransferase (D-aspartate aminotransferase)		Amino Acid Metabolism, Metabolism o	12.598	9.856	9.961	10.953	5.16E-04	2.26E-01	-2.74	0.99
lpg1510	D-alanine-aminotransferase (D-aspartate aminotransferase)		Amino Acid Metabolism, Metabolism o	12.664	9.756	9.866	11.018	5.42E-04	2.78E-01	-2.91	1.15
lpg1511	lipoate-protein ligase B (lipoate biosynthesis protein B) (type I secreti		Transport and binding, Toxin productio	11.827	10.148	10.699	11.609	1.15E-02	8.42E-02	-1.68	0.91
lpg1511	lipoate-protein ligase B (lipoate biosynthesis protein B) (type I secreti		Transport and binding, Toxin productio	11.824	10.597	10.808	11.733	1.92E-02	4.88E-02	-1.23	0.92
lpg1512	DedA/PAP2 domain protein (integral membrane protein) (type I secre		Transport and binding, Toxin productio	12.017	9.464	11.123	10.496	3.31E-06	1.60E-01	-2.55	-0.63
lpg1512	DedA/PAP2 domain protein (integral membrane protein) (type I secre		Transport and binding, Toxin productio	12.058	9.309	10.882	10.444	1.39E-05	4.10E-01	-2.75	-0.44
lpg1513	type I secretion system LssZ		Transport and binding, Toxin productio	11.774	11.084	11.757	10.075	3.18E-01	1.81E-04	-0.69	-1.68
lpg1513	type I secretion system LssZ		Transport and binding, Toxin productio	11.229	11.356	10.705	9.842	8.10E-01	1.18E-01	0.13	-0.86
lpg1514	lipoprotein (inner membrane protein) (type I secretion system LssA)		Transport and binding, Toxin productio	9.343	9.456	9.392	9.090	8.28E-01	5.12E-01	0.11	-0.30
lpg1514	lipoprotein (inner membrane protein) (type I secretion system LssA)		Transport and binding, Toxin productio	9.696	10.021	9.496	10.310	7.09E-01	2.14E-01	0.32	0.81
lpg1515	toxin secretion ATP binding protein (ABC-type bacteriocin/antibiotic e		Transport and binding, Toxin productio	11.290	9.283	12.389	8.400	7.96E-03	1.53E-05	-2.01	-3.99
lpg1515	toxin secretion ATP binding protein (ABC-type bacteriocin/antibiotic e		Transport and binding, Toxin productio	11.252	9.315	12.352	8.485	7.63E-04	7.73E-05	-1.94	-3.87

lpg1516	ABC transporter, ATP binding/permease fusion protein (toxin secretio		Transport and binding, Toxin productio	11.408	8.686	12.061	9.240	8.94E-05	6.40E-05	-2.72	-2.82
lpg1516	ABC transporter, ATP binding/permease fusion protein (toxin secretio		Transport and binding, Toxin productio	11.458	8.878	12.049	9.689	1.79E-04	2.36E-04	-2.58	-2.36
lpg1517	HlyD family secretion protein (hemolysin) (type I secretion system Ls		Toxin production / other pathogen func	10.344	7.962	10.043	7.312	1.89E-05	6.50E-04	-2.38	-2.73
lpg1517	HlyD family secretion protein (hemolysin) (type I secretion system Ls		Toxin production / other pathogen func	10.235	6.648	10.046	7.733	1.39E-02	9.44E-03	-3.59	-2.31
lpg1518	sensory box protein/GGDEF domain/EAL domain (type I secretion sys		Protein fate / hydrolases / secretion, S	8.632	7.416	9.925	6.152	4.51E-01	1.91E-03	-1.22	-3.77
lpg1518	sensory box protein/GGDEF domain/EAL domain (type I secretion sys		Protein fate / hydrolases / secretion, S	9.634	8.740	10.338	7.319	7.70E-02	9.24E-03	-0.89	-3.02
lpg1519	purine/pyrimidine phosphoribosyltransferase (hypoxanthine phosphor		Nucleotide Metabolism	12.675	10.564	10.496	11.195	1.11E-02	2.62E-01	-2.11	0.70
lpg1519	purine/pyrimidine phosphoribosyltransferase (hypoxanthine phosphor		Nucleotide Metabolism	12.570	11.375	10.052	11.557	2.26E-01	5.47E-02	-1.19	1.50
lpg1520	uncharacterized conserved hypothetical protein COG4517		Unknown / hypothetical proteins	13.774	12.764	11.507	13.224	1.51E-01	1.55E-02	-1.01	1.72
lpg1520	uncharacterized conserved hypothetical protein COG4517		Unknown / hypothetical proteins	13.343	12.781	11.216	13.385	4.65E-01	3.57E-03	-0.56	2.17
lpg1521	generic methyl-transferase		Named proteins of general function	12.238	11.385	10.495	11.488	8.41E-02	8.82E-02	-0.85	0.99
lpg1521	generic methyl-transferase		Named proteins of general function	12.438	11.526	10.556	11.575	1.63E-02	7.47E-02	-0.91	1.02
lpg1522	(type IV) pilus assembly protein PilB	*pilB*	Transport and binding	11.149	9.932	13.363	9.229	2.42E-01	4.00E-04	-1.22	-4.13
lpg1522	(type IV) pilus assembly protein PilB	*pilB*	Transport and binding	10.626	9.613	13.072	9.231	2.08E-01	1.49E-04	-1.01	-3.84
lpg1523	(type IV) pilus assembly protein PilC (bacterial type II sec	*pilC*	Transport and binding, Protein fate / hy	10.286	9.168	12.771	9.249	4.52E-02	2.18E-04	-1.12	-3.52
lpg1523	(type IV) pilus assembly protein PilC (bacterial type II sec	*pilC*	Transport and binding, Protein fate / hy	10.366	9.874	12.757	9.597	4.58E-01	5.10E-04	-0.49	-3.16
lpg1524	type 4 (IV) prepilin-like protein leader peptide processing	*pilD*	Protein fate / hydrolases / secretion	12.169	10.539	12.528	10.261	6.92E-04	1.96E-05	-1.63	-2.27
lpg1524	type 4 (IV) prepilin-like protein leader peptide processing	*pilD*	Protein fate / hydrolases / secretion	12.186	10.473	12.476	10.280	7.14E-04	8.93E-06	-1.71	-2.20
lpg1525	CAAX amino terminal protease family protein		Protein fate / hydrolases / secretion	7.438	6.816	8.808	7.462	4.73E-01	8.12E-02	-0.62	-1.35
lpg1525	CAAX amino terminal protease family protein		Protein fate / hydrolases / secretion	7.633	7.385	8.134	8.257	5.74E-01	9.01E-01	-0.25	0.12
lpg1526	ORF		ORFs of unknown function (unique)	12.314	10.866	13.426	10.780	9.61E-04	1.27E-05	-1.45	-2.65
lpg1526	ORF		ORFs of unknown function (unique)	12.331	10.788	13.427	10.877	1.04E-02	1.06E-05	-1.54	-2.55
lpg1527	small ORF (151aa)		ORFs of unknown function (unique)	11.538	10.582	11.792	9.909	5.27E-02	4.75E-04	-0.96	-1.88
lpg1527	small ORF (151aa)		ORFs of unknown function (unique)	11.510	11.039	11.677	10.352	2.86E-01	5.76E-03	-0.47	-1.33
lpg1528	conserved hypothetical protein		Unknown / hypothetical proteins	11.007	12.397	10.050	11.517	1.10E-02	1.64E-02	1.39	1.47
lpg1528	conserved hypothetical protein		Unknown / hypothetical proteins	11.108	12.492	10.129	11.774	2.47E-03	1.06E-03	1.38	1.65
lpg1529	2-methylcitrate dehydratase PrpD	*prpD*	Carbohydrate Metabolism	10.676	13.387	9.873	12.973	6.59E-05	1.24E-04	2.71	3.10
lpg1529	2-methylcitrate dehydratase PrpD	*prpD*	Carbohydrate Metabolism	10.433	13.358	9.165	12.936	5.07E-04	1.68E-03	2.93	3.77
lpg1530	2-methylcitrate synthase (citrate synthase PrpC)		Carbohydrate Metabolism	13.095	13.641	12.181	11.870	2.69E-02	6.35E-01	0.55	-0.31
lpg1530	2-methylcitrate synthase (citrate synthase PrpC)		Carbohydrate Metabolism	13.097	13.635	12.192	12.445	9.76E-03	2.92E-01	0.54	0.25
lpg1531	phenazine biosynthesis PhzF (oxidoreductase) (PCA synthesis?)		Named proteins of general function	12.015	9.241	12.853	11.124	6.22E-02	3.23E-02	-2.77	-1.73
lpg1531	phenazine biosynthesis PhzF (oxidoreductase) (PCA synthesis?)		Named proteins of general function	12.065	10.835	12.807	11.705	2.76E-05	4.61E-03	-1.23	-1.10
lpg1532	peptidase ? (oxidoreductase, FAD binding) (D-amino acid oxidase far		Protein fate / hydrolases / secretion	10.730	6.893	9.825	8.378	8.53E-03	4.46E-02	-3.84	-1.45
lpg1532	peptidase ? (oxidoreductase, FAD binding) (D-amino acid oxidase far		Protein fate / hydrolases / secretion	10.893	9.072	9.648	9.335	2.76E-02	7.01E-01	-1.82	-0.31
lpg1533	peptide transport protein (POT family) (proton/oligopeptic	*ydgR*	Transport and binding	11.377	9.696	9.007	9.668	3.03E-02	4.35E-01	-1.68	0.66
lpg1533	peptide transport protein (POT family) (proton/oligopeptic	*ydgR*	Transport and binding	11.031	9.778	8.398	9.978	2.14E-01	2.74E-01	-1.25	1.58
lpg1534	glutamate-1-semialdehyde-2,1-aminomutase	*hemL*	Metabolism of Cofactors and Vitamins	11.809	11.186	11.154	11.356	3.62E-01	7.18E-01	-0.62	0.20
lpg1534	glutamate-1-semialdehyde-2,1-aminomutase	*hemL*	Metabolism of Cofactors and Vitamins	12.088	11.523	11.211	11.682	2.10E-01	3.27E-01	-0.56	0.47
lpg1535	rubredoxin (rubredoxin-type Fe(Cys)4 protein)		Energy Metabolism	8.870	8.566	9.266	9.772	7.11E-01	2.40E-01	-0.30	0.51
lpg1535	rubredoxin (rubredoxin-type Fe(Cys)4 protein)		Energy Metabolism	8.590	9.542	9.508	10.220	1.74E-01	3.27E-01	0.95	0.71
lpg1536	transmembrane protein		Unknown / hypothetical proteins	10.281	9.855	8.867	9.252	2.58E-01	5.69E-01	-0.43	0.38
lpg1536	transmembrane protein		Unknown / hypothetical proteins	10.188	9.736	9.307	9.731	2.03E-01	5.76E-01	-0.45	0.42
lpg1537	transport protein		Transport and binding	10.707	10.321	9.815	9.275	7.36E-02	3.60E-01	-0.39	-0.54
lpg1537	transport protein		Transport and binding	10.436	10.522	9.615	9.243	7.92E-01	5.68E-01	0.09	-0.37
lpg1538	poly(A) polymerase I (tRNA nucleotidyltransferase/poly(A	*pcnB*	Transcription	12.398	7.880	9.968	8.979	1.29E-04	1.83E-01	-4.52	-0.99
lpg1538	poly(A) polymerase I (tRNA nucleotidyltransferase/poly(A	*pcnB*	Transcription	12.520	8.067	9.908	8.926	8.02E-05	2.09E-01	-4.45	-0.98
lpg1539	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokin		Metabolism of Cofactors and Vitamins	10.173	10.031	9.918	10.595	6.68E-01	1.97E-01	-0.14	0.68
lpg1539	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokin		Metabolism of Cofactors and Vitamins	10.175	9.852	9.916	10.603	3.91E-01	1.53E-01	-0.32	0.69
lpg1540	universal stress protein A (UspA)		Detoxification / adaptation	10.712	9.559	11.185	9.260	5.75E-03	4.50E-02	-1.15	-1.93
lpg1540	universal stress protein A (UspA)		Detoxification / adaptation	10.810	9.371	11.232	9.458	2.92E-04	7.87E-02	-1.44	-1.77
lpg1541	GTP-binding protein EngA	*engA*	Signal transduction / other regulatory f	11.517	11.511	9.748	12.075	9.86E-01	9.36E-04	-0.01	2.33
lpg1541	GTP-binding protein EngA	*engA*	Signal transduction / other regulatory f	11.439	11.540	9.170	12.108	7.98E-01	2.14E-03	0.10	2.94
lpg1542	PQQ (pyrrolo quinoline) enzyme repeat domain protein (dehydrogena		Named proteins of general function	13.271	12.683	11.850	12.580	1.02E-01	4.95E-02	-0.59	0.73
lpg1542	PQQ (pyrrolo quinoline) enzyme repeat domain protein (dehydrogena		Named proteins of general function	13.215	12.678	11.760	12.577	1.91E-01	2.86E-02	-0.54	0.82
lpg1543	transmembrane protein		Unknown / hypothetical proteins	12.822	12.365	11.918	12.592	2.98E-01	1.49E-01	-0.46	0.67
lpg1543	transmembrane protein		Unknown / hypothetical proteins	12.889	12.299	11.856	12.605	1.93E-01	1.19E-01	-0.59	0.75
lpg1544	histidyl tRNA synthetase	*hisS*	Amino Acid Metabolism, Translation	12.488	12.228	11.958	12.548	3.50E-01	2.41E-02	-0.26	0.59
lpg1544	histidyl tRNA synthetase	*hisS*	Amino Acid Metabolism, Translation	12.459	12.194	11.934	12.563	4.00E-01	3.04E-02	-0.26	0.63
lpg1545	DNA-binding protein, putative		Transcription factors / DNA binding pro	11.504	12.034	10.892	11.167	3.11E-01	6.72E-01	0.53	0.27
lpg1545	DNA-binding protein, putative		Transcription factors / DNA binding pro	11.525	11.716	10.624	11.538	7.39E-01	1.08E-01	0.19	0.91
lpg1546	fimbrial biogenesis and twitching motility protein PilF		Transport and binding, Chemotaxis / m	11.598	11.261	9.896	11.801	3.75E-01	2.38E-02	-0.34	1.91
lpg1546	fimbrial biogenesis and twitching motility protein PilF		Transport and binding, Chemotaxis / m	11.667	11.321	9.736	11.657	3.64E-01	4.69E-02	-0.35	1.92
lpg1547	radical SAM enzyme, Cfr family		Named proteins of general function	12.068	10.527	10.668	11.921	4.86E-03	9.14E-02	-1.54	1.25
lpg1547	radical SAM enzyme, Cfr family		Named proteins of general function	11.923	11.174	10.691	12.016	1.46E-01	8.49E-02	-0.75	1.32

lpg1548	nucleoside diphosphate kinase	*ndk*	Nucleotide Metabolism	12.510	12.320	10.600	14.319	8.10E-01	1.51E-05	-0.19	3.72
lpg1548	nucleoside diphosphate kinase	*ndk*	Nucleotide Metabolism	11.698	12.402	10.608	14.357	6.52E-01	1.07E-05	0.70	3.75
lpg1549	ORF		ORFs of unknown function (unique)	11.933	11.775	12.141	11.632	4.70E-01	1.78E-02	-0.16	-0.51
lpg1549	ORF		ORFs of unknown function (unique)	11.859	11.862	12.015	11.564	9.83E-01	5.19E-02	0.00	-0.45
lpg1550	tRNA-(ms(2)io(6)a)-hydrolase (tRNA hydroxylase)		DNA/RNA degradation / restriction, Tra	11.093	9.922	8.297	10.140	1.77E-03	2.67E-02	-1.17	1.84
lpg1550	tRNA-(ms(2)io(6)a)-hydrolase (tRNA hydroxylase)		DNA/RNA degradation / restriction, Tra	10.607	10.051	8.466	10.386	3.68E-01	7.46E-03	-0.56	1.92
lpg1551	ORF		ORFs of unknown function (unique)	13.326	14.098	14.541	11.642	1.70E-02	4.80E-07	0.77	-2.90
lpg1551	ORF		ORFs of unknown function (unique)	13.342	14.134	14.511	11.699	2.56E-02	5.34E-07	0.79	-2.81
lpg1552	UDP-2,3-diacylglucosamine hydrolase		Metabolism of Complex Carbohydrate	13.151	11.171	10.929	11.377	7.73E-04	4.29E-01	-1.98	0.45
lpg1552	UDP-2,3-diacylglucosamine hydrolase		Metabolism of Complex Carbohydrate	13.127	10.946	10.543	11.365	3.31E-04	2.44E-01	-2.18	0.82
lpg1553	septum site determining protein MinC (FtsZ assembly inh	*minC*	Chemotaxis / motility / cell division, Si	14.051	12.838	12.233	12.925	1.71E-03	1.32E-01	-1.21	0.69
lpg1553	septum site determining protein MinC (FtsZ assembly inh	*minC*	Chemotaxis / motility / cell division, Si	14.033	12.929	12.211	12.954	3.02E-03	1.11E-01	-1.10	0.74
lpg1554	long chain fatty acid-CoA ligase	*fadD-1*	Lipid Metabolism	11.369	11.363	11.357	10.724	9.87E-01	1.52E-01	-0.01	-0.63
lpg1554	long chain fatty acid-CoA ligase	*fadD-1*	Lipid Metabolism	10.086	11.207	10.108	10.884	1.23E-01	1.78E-01	1.12	0.78
lpg1555	arginine 3rd transport system periplasmic binding protein	*artJ*	Transport and binding	9.142	10.459	10.040	9.958	1.41E-01	9.16E-01	1.32	-0.08
lpg1555	arginine 3rd transport system periplasmic binding protein	*artJ*	Transport and binding	9.196	10.535	8.996	10.275	1.62E-01	3.49E-01	1.34	1.28
lpg1556	MutT/nudix family protein (phosphohydrolase)		Named proteins of general function	10.327	9.237	9.206	9.506	3.88E-02	4.47E-01	-1.09	0.30
lpg1556	MutT/nudix family protein (phosphohydrolase)		Named proteins of general function	10.444	9.272	8.685	9.413	9.27E-03	1.82E-01	-1.17	0.73
lpg1557	para-aminobenzoate synthase, component I		Carbohydrate Metabolism, Metabolism	9.983	10.030	8.978	10.258	8.50E-01	1.08E-02	0.05	1.28
lpg1557	para-aminobenzoate synthase, component I		Carbohydrate Metabolism, Metabolism	9.782	9.789	8.883	10.578	9.84E-01	1.77E-03	0.01	1.69
lpg1558	pyruvate dehydrogenase E1 alpha subunit (pyruvate/2-oxoglutarate d		Carbohydrate Metabolism, Amino Acid	11.947	12.026	10.639	11.921	8.45E-01	1.05E-01	0.08	1.28
lpg1558	pyruvate dehydrogenase E1 alpha subunit (pyruvate/2-oxoglutarate d		Carbohydrate Metabolism, Amino Acid	11.863	11.945	10.447	11.985	8.58E-01	6.03E-02	0.08	1.54
lpg1559	pyruvate dehydrogenase E1 beta subunit (pyruvate decarboxylase E		Carbohydrate Metabolism, Amino Acid	13.080	11.891	10.910	12.687	5.77E-02	2.33E-02	-1.19	1.78
lpg1559	pyruvate dehydrogenase E1 beta subunit (pyruvate decarboxylase E		Carbohydrate Metabolism, Amino Acid	13.198	12.030	10.849	12.856	2.83E-02	1.28E-02	-1.17	2.01
lpg1560	dihydrolipoamide acetyltransferase (pyruvate/2-oxoglutarate dehydro		Carbohydrate Metabolism	14.224	13.693	12.208	13.638	2.91E-01	2.00E-02	-0.53	1.43
lpg1560	dihydrolipoamide acetyltransferase (pyruvate/2-oxoglutarate dehydro		Carbohydrate Metabolism	14.344	13.732	12.182	13.624	2.72E-01	1.93E-02	-0.61	1.44
lpg1561	potassium efflux system KefA		Transport and binding	10.166	10.194	8.827	8.985	9.62E-01	8.32E-01	0.03	0.16
lpg1561	potassium efflux system KefA		Transport and binding	9.883	9.804	8.546	9.603	9.14E-01	2.82E-01	-0.08	1.06
lpg1562	mercuric reductase (mercury(II)reductase) (dihydrolipoan	*merA1*	Detoxification / adaptation, Carbohydra	10.432	9.775	10.252	8.968	1.21E-01	2.87E-02	-0.66	-1.28
lpg1562	mercuric reductase (mercury(II)reductase) (dihydrolipoan	*merA1*	Detoxification / adaptation, Carbohydra	10.579	10.008	10.342	9.072	2.71E-01	3.58E-03	-0.57	-1.27
lpg1563	ORF		ORFs of unknown function (unique)	10.132	10.765	10.727	9.932	2.77E-01	6.84E-02	0.63	-0.80
lpg1563	ORF		ORFs of unknown function (unique)	10.083	11.090	10.697	10.305	1.33E-01	2.93E-01	1.01	-0.39
lpg1564	membrane protein (nodulin 21?)		Named proteins of general function	8.791	7.488	9.787	7.145	1.24E-01	2.65E-03	-1.30	-2.64
lpg1564	membrane protein (nodulin 21?)		Named proteins of general function	9.105	8.431	10.105	7.718	6.01E-02	2.87E-03	-0.67	-2.39
lpg1565	thiamine biosynthesis protein NMT-1 (periplasmic ABC tr	*thi3*	Metabolism of Cofactors and Vitamins	9.611	10.730	10.082	10.452	6.78E-03	3.73E-01	1.12	0.37
lpg1565	thiamine biosynthesis protein NMT-1 (periplasmic ABC tr	*thi3*	Metabolism of Cofactors and Vitamins	9.937	10.752	10.111	10.660	3.26E-02	1.56E-01	0.82	0.55
lpg1566	thiamine biosynthesis oxidoreductase ThiO (D-amino acid oxidase fla		Metabolism of Cofactors and Vitamins	9.225	8.127	9.524	8.643	2.77E-01	2.15E-01	-1.10	-0.88
lpg1566	thiamine biosynthesis oxidoreductase ThiO (D-amino acid oxidase fla		Metabolism of Cofactors and Vitamins	9.052	8.542	9.358	8.577	5.82E-01	3.30E-01	-0.51	-0.78
lpg1567	thiamine (thiazole) biosynthesis protein ThiG (hydroxyme	*thiG*	Metabolism of Cofactors and Vitamins	8.572	8.714	8.852	8.492	8.46E-01	6.61E-01	0.14	-0.36
lpg1567	thiamine (thiazole) biosynthesis protein ThiG (hydroxyme	*thiG*	Metabolism of Cofactors and Vitamins	8.617	9.189	8.725	8.411	4.71E-01	8.22E-01	0.57	-0.31
lpg1568	phosphomethylpyrimidine kinase ThiD/thiamin-phosphat	*thiDE*	Metabolism of Cofactors and Vitamins	9.458	9.386	9.321	9.509	8.72E-01	5.10E-01	-0.07	0.19
lpg1568	phosphomethylpyrimidine kinase ThiD/thiamin-phosphat	*thiDE*	Metabolism of Cofactors and Vitamins	9.670	9.711	9.241	9.891	9.12E-01	2.17E-01	0.04	0.65
lpg1569	sulfurylase (ThiF family protein) (molybdopterin biosynthesis protein		Metabolism of Cofactors and Vitamins	8.478	8.451	8.642	8.868	9.79E-01	8.13E-01	-0.03	0.23
lpg1569	sulfurylase (ThiF family protein) (molybdopterin biosynthesis protein		Metabolism of Cofactors and Vitamins	8.300	8.083	8.131	9.057	8.23E-01	4.13E-01	-0.22	0.93
lpg1570	3'-nucleotidase/nuclease (endonuclease)		DNA/RNA degradation / restriction	10.733	9.344	10.144	10.673	8.80E-03	3.01E-01	-1.39	0.53
lpg1570	3'-nucleotidase/nuclease (endonuclease)		DNA/RNA degradation / restriction	10.894	8.899	9.950	10.781	1.53E-02	1.70E-01	-1.99	0.83
lpg1571	TolB colicin import protein	*tolB*	Transport and binding	11.195	10.763	10.577	10.692	3.14E-01	8.88E-01	-0.43	0.12
lpg1571	TolB colicin import protein	*tolB*	Transport and binding	11.133	10.540	10.490	11.104	3.10E-02	2.92E-01	-0.59	0.61
lpg1572	TolA colicin import membrane protein	*tolA*	Transport and binding	11.567	10.744	10.932	11.611	7.14E-04	3.42E-02	-0.82	0.68
lpg1572	TolA colicin import membrane protein	*tolA*	Transport and binding	11.406	10.979	10.772	11.691	2.02E-01	1.57E-02	-0.43	0.92
lpg1573	biopolymer transport protein TolR	*tolR*	Transport and binding	11.173	11.986	10.827	11.758	3.38E-03	2.25E-02	0.81	0.93
lpg1573	biopolymer transport protein TolR	*tolR*	Transport and binding	10.899	12.443	10.708	12.441	3.67E-02	3.53E-02	1.54	1.73
lpg1574	biopolymer transport protein TolQ (colicin import protein)	*tolQ*	Transport and binding	10.931	12.619	11.082	11.749	1.71E-05	6.84E-03	1.69	0.67
lpg1574	biopolymer transport protein TolQ (colicin import protein)	*tolQ*	Transport and binding	11.052	12.792	10.783	11.963	9.55E-07	2.27E-02	1.74	1.18
lpg1575	esterase (4-hydroxybenzoyl-CoA thioesterase family active site)		Biodegradation of Xenobiotics	11.894	12.467	10.958	11.995	1.66E-01	4.36E-03	0.57	1.04
lpg1575	esterase (4-hydroxybenzoyl-CoA thioesterase family active site)		Biodegradation of Xenobiotics	11.911	12.332	10.797	11.862	2.99E-01	1.25E-02	0.42	1.06
lpg1576	Holliday junction DNA helicase RuvB	*ruvB*	Replication and Repair	12.153	11.377	11.123	11.521	1.68E-02	3.28E-01	-0.78	0.40
lpg1576	Holliday junction DNA helicase RuvB	*ruvB*	Replication and Repair	11.962	11.380	11.134	11.568	1.07E-01	1.91E-01	-0.58	0.43
lpg1577	RNA polymerase sigma E factor RpoE (RNA polymerase	*rpoE*	Transcription factors / DNA binding pr	9.930	8.431	12.010	7.084	6.93E-02	3.72E-04	-1.50	-4.93
lpg1577	RNA polymerase sigma E factor RpoE (RNA polymerase	*rpoE*	Transcription factors / DNA binding pr	9.989	8.787	12.044	7.552	1.03E-01	2.03E-03	-1.20	-4.49
lpg1578	small ORF (149aa)		ORFs of unknown function (unique)	10.715	7.934	8.129	7.578	1.41E-04	5.19E-01	-2.78	-0.55
lpg1578	small ORF (149aa)		ORFs of unknown function (unique)	10.505	8.244	8.191	8.531	4.73E-02	7.87E-01	-2.26	0.34
lpg1579	glycine cleavage T protein (aminomethyl transferase)		Metabolism of Cofactors and Vitamins	11.312	10.697	10.641	10.601	1.19E-01	9.42E-01	-0.61	-0.04
lpg1579	glycine cleavage T protein (aminomethyl transferase)		Metabolism of Cofactors and Vitamins	11.285	11.349	10.841	11.633	9.45E-01	4.17E-01	0.06	0.79

lpg1580	cytochrome b-561 transmembrane protein		Energy Metabolism	12.642	10.435	13.052	10.336	1.26E-06	2.46E-06	-2.21	-2.72
lpg1580	cytochrome b-561 transmembrane protein		Energy Metabolism	12.613	10.481	13.019	10.654	6.49E-04	4.85E-05	-2.13	-2.37
lpg1581	NAD-glutamate dehydrogenase		Energy Metabolism, Amino Acid Metab	13.791	13.255	14.217	13.029	6.76E-03	3.46E-06	-0.54	-1.19
lpg1581	NAD-glutamate dehydrogenase		Energy Metabolism, Amino Acid Metab	13.820	13.264	14.203	13.041	8.76E-03	8.73E-06	-0.56	-1.16
lpg1582	hypothetical COG1376		Unknown / hypothetical proteins	11.753	9.964	12.592	10.934	9.80E-02	2.08E-04	-1.79	-1.66
lpg1582	hypothetical COG1376		Unknown / hypothetical proteins	11.763	11.072	12.600	11.282	4.80E-02	7.17E-04	-0.69	-1.32
lpg1583	succinate semialdehyde dehyrogenase (NADP+) (aldehyde dehydrog		Amino Acid Metabolism, Carbohydrate	10.714	10.538	12.802	10.749	8.21E-01	1.57E-02	-0.18	-2.05
lpg1583	succinate semialdehyde dehyrogenase (NADP+) (aldehyde dehydrog		Amino Acid Metabolism, Carbohydrate	10.930	10.687	12.861	11.596	7.07E-01	8.04E-02	-0.24	-1.27
lpg1584	(CDP-alcohol) phosphatidyltransferase (phosphatidylcholine synthase		Amino Acid Metabolism, Metabolism o	11.619	11.797	10.365	11.877	3.90E-01	2.66E-03	0.18	1.51
lpg1584	(CDP-alcohol) phosphatidyltransferase (phosphatidylcholine synthase		Amino Acid Metabolism, Metabolism o	11.539	11.845	10.249	12.055	2.79E-01	3.55E-04	0.31	1.81
lpg1585	small ORF (162aa) conserved domain protein; enhanced entry protei		Toxin production / other pathogen func	11.874	10.342	10.114	10.884	7.47E-03	2.47E-01	-1.53	0.77
lpg1585	small ORF (162aa) conserved domain protein; enhanced entry protei		Toxin production / other pathogen func	11.550	11.194	9.718	11.246	6.22E-01	5.43E-02	-0.36	1.53
lpg1586	small ORF (125aa)		ORFs of unknown function (unique)	12.142	10.072	11.850	9.560	7.15E-06	3.98E-05	-2.07	-2.29
lpg1586	small ORF (125aa)		ORFs of unknown function (unique)	12.080	9.977	11.768	9.672	2.14E-04	1.08E-04	-2.10	-2.10
lpg1587	hypothetical (thioredoxin family?)		Unknown / hypothetical proteins	10.320	8.756	8.114	8.034	8.46E-03	9.57E-01	-1.56	-0.08
lpg1587	hypothetical (thioredoxin family?)		Unknown / hypothetical proteins	10.313	9.206	9.070	9.243	8.42E-03	9.12E-01	-1.11	0.17
lpg1588	ORF	*legC6*	ORFs of unknown function (unique)	12.109	12.842	12.777	10.829	7.20E-02	3.31E-05	0.73	-1.95
lpg1588	ORF	*legC6*	ORFs of unknown function (unique)	12.106	12.681	12.757	11.348	2.02E-01	4.02E-03	0.58	-1.41
lpg1589	50S ribosomal protein L9	*rplI*	Translation	9.755	9.205	9.929	9.547	4.97E-01	6.23E-01	-0.55	-0.38
lpg1589	50S ribosomal protein L9	*rplI*	Translation	10.155	9.449	9.340	9.869	1.96E-01	5.27E-01	-0.71	0.53
lpg1590	membrane protein		Named proteins of general function	14.028	12.158	11.522	12.459	8.60E-04	2.12E-01	-1.87	0.94
lpg1590	membrane protein		Named proteins of general function	14.008	12.173	11.468	12.493	7.09E-04	1.80E-01	-1.84	1.02
lpg1591	30S ribosomal protein S18	*rpsR*	Translation	14.063	13.574	11.444	13.913	4.29E-01	4.63E-03	-0.49	2.47
lpg1591	30S ribosomal protein S18	*rpsR*	Translation	13.943	13.590	11.316	13.961	6.13E-01	5.47E-03	-0.35	2.64
lpg1592	30S ribosomal protein S6	*rpsF*	Translation	14.601	13.987	11.234	14.542	4.43E-01	2.78E-03	-0.61	3.31
lpg1592	30S ribosomal protein S6	*rpsF*	Translation	14.198	14.003	11.129	14.617	8.17E-01	2.00E-03	-0.19	3.49
lpg1593	carbon storage regulator?		Named proteins of general function	13.112	11.499	10.138	11.649	1.62E-02	6.17E-02	-1.61	1.51
lpg1593	carbon storage regulator?		Named proteins of general function	13.035	11.514	9.563	11.689	5.96E-02	4.23E-02	-1.52	2.13
lpg1594	ORF		ORFs of unknown function (unique)	11.466	9.608	10.279	9.800	4.63E-03	5.07E-01	-1.86	-0.48
lpg1594	ORF		ORFs of unknown function (unique)	11.409	9.429	10.093	9.716	4.61E-03	5.44E-01	-1.98	-0.38
lpg1595	hypothetical (LysM domain protein) periplasmic protein, cell wall degr		Named proteins of general function	9.712	8.895	9.696	10.140	4.26E-01	4.26E-01	-0.82	0.44
lpg1595	hypothetical (LysM domain protein) periplasmic protein, cell wall degr		Named proteins of general function	9.484	10.330	9.527	11.330	2.84E-01	1.66E-02	0.85	1.80
lpg1596	enoyl CoA hydratase (alpha subunit of fatty acid oxidatio	*yfcX*	Lipid Metabolism	13.481	14.426	13.989	12.987	2.34E-02	4.31E-02	0.94	-1.00
lpg1596	enoyl CoA hydratase (alpha subunit of fatty acid oxidatio	*yfcX*	Lipid Metabolism	13.573	14.609	13.996	13.208	4.45E-04	7.81E-03	1.04	-0.79
lpg1597	thiolase (beta subunit of fatty acid oxidation complex)		Lipid Metabolism, Amino Acid Metabol	12.970	14.319	13.911	12.881	2.81E-04	2.01E-03	1.35	-1.03
lpg1597	thiolase (beta subunit of fatty acid oxidation complex)		Lipid Metabolism, Amino Acid Metabol	12.972	14.358	13.914	12.937	2.37E-04	1.38E-03	1.39	-0.98
lpg1598	ORF		ORFs of unknown function (unique)	9.273	8.564	8.655	8.417	2.40E-01	8.40E-01	-0.71	-0.24
lpg1598	ORF		ORFs of unknown function (unique)	9.212	8.619	8.605	8.512	4.03E-01	9.26E-01	-0.59	-0.09
lpg1599	small ORF (68aa) hypothetical		Unknown / hypothetical proteins	8.330	8.036	8.762	8.923	6.28E-01	7.33E-01	-0.29	0.16
lpg1599	small ORF (68aa) hypothetical		Unknown / hypothetical proteins	8.966	9.225	9.168	9.867	4.79E-01	1.65E-01	0.26	0.70
lpg1600	tRNA-Ser		tRNA	12.529	12.252	12.776	12.523	7.02E-01	7.15E-01	-0.28	-0.25
lpg1600	tRNA-Ser		tRNA	12.516	12.187	12.760	12.736	6.39E-01	9.55E-01	-0.33	-0.02
lpg1601	tRNA-Arg		tRNA	11.812	9.882	10.535	10.815	2.52E-02	6.51E-01	-1.93	0.28
lpg1601	tRNA-Arg		tRNA	11.678	10.452	9.942	10.928	4.56E-02	2.02E-01	-1.23	0.99
lpg1602	FLJ00180 protein	*legL2*	Unknown / hypothetical proteins	10.279	9.706	9.634	10.011	8.46E-02	3.30E-01	-0.57	0.38
lpg1602	FLJ00180 protein	*legL2*	Unknown / hypothetical proteins	10.338	9.762	9.484	10.326	2.95E-01	1.64E-01	-0.58	0.84
lpg1603	hypothetical		Unknown / hypothetical proteins	10.867	11.086	10.931	10.473	2.60E-01	8.62E-02	0.22	-0.46
lpg1603	hypothetical		Unknown / hypothetical proteins	10.953	11.250	10.677	10.444	9.40E-02	1.96E-01	0.30	-0.23
lpg1604	hypothetical		Unknown / hypothetical proteins	9.771	9.532	10.242	10.073	5.83E-01	3.79E-01	-0.24	-0.17
lpg1604	hypothetical		Unknown / hypothetical proteins	9.990	9.439	9.823	9.698	5.10E-02	7.86E-01	-0.55	-0.13
lpg1605	hypothetical		Unknown / hypothetical proteins	7.476	10.802	9.164	10.209	8.66E-06	5.63E-02	3.33	1.05
lpg1605	hypothetical		Unknown / hypothetical proteins	7.259	10.554	8.857	10.157	3.83E-06	8.06E-02	3.30	1.30
lpg1606	conserved hypothetical protein		Unknown / hypothetical proteins	11.731	10.324	9.801	10.534	3.82E-03	1.75E-01	-1.41	0.73
lpg1606	conserved hypothetical protein		Unknown / hypothetical proteins	11.171	10.338	8.889	11.058	3.17E-01	6.46E-02	-0.83	2.17
lpg1607	phosphoenolpyruvate carboxylase	*capP*	Carbohydrate Metabolism, Energy Me	8.321	8.676	8.164	8.594	3.87E-01	1.97E-01	0.36	0.43
lpg1607	phosphoenolpyruvate carboxylase	*capP*	Carbohydrate Metabolism, Energy Me	8.550	8.869	8.000	9.005	5.78E-01	5.26E-02	0.32	1.01
lpg1608	MutT/nudix family protein		Named proteins of general function	8.332	9.104	9.484	9.077	4.54E-03	2.68E-01	0.77	-0.41
lpg1608	MutT/nudix family protein		Named proteins of general function	8.497	9.175	9.795	9.433	4.62E-02	3.37E-01	0.68	-0.36
lpg1609	gamma-glutamyl phosphate reductase		Amino Acid Metabolism	10.918	10.681	10.101	10.446	6.11E-01	5.11E-01	-0.24	0.34
lpg1609	gamma-glutamyl phosphate reductase		Amino Acid Metabolism	10.968	10.827	9.075	9.675	7.05E-01	7.54E-01	-0.14	0.60
lpg1610	glutamate-5-kinase (gamma-glutamyl kinase)	*proB*	Amino Acid Metabolism	9.052	8.599	8.690	8.051	5.09E-01	4.09E-01	-0.45	-0.64
lpg1610	glutamate-5-kinase (gamma-glutamyl kinase)	*proB*	Amino Acid Metabolism	8.519	8.360	7.884	8.346	8.79E-01	6.27E-01	-0.16	0.46
lpg1611	transcriptional regulator, MerR family (mercury resistance)		Detoxification / adaptation, Transcriptio	9.662	11.119	9.476	10.416	2.15E-04	1.10E-02	1.46	0.94
lpg1611	transcriptional regulator, MerR family (mercury resistance)		Detoxification / adaptation, Transcriptio	9.395	11.082	9.047	10.504	1.27E-04	5.67E-02	1.69	1.46

lpg1612	transcriptional regulator SkgA (mercury resistance) (transcriptional ac		Detoxification / adaptation, Transcriptio	9.868	9.270	9.215	9.133	2.12E-03	8.48E-01	-0.60	-0.08
lpg1612	transcriptional regulator SkgA (mercury resistance) (transcriptional ac		Detoxification / adaptation, Transcriptio	9.988	9.748	9.095	9.408	5.82E-01	5.57E-01	-0.24	0.31
lpg1613	acetyltransferase, GNAT family		Named proteins of general function	8.903	10.637	8.402	8.594	1.14E-05	7.99E-01	1.73	0.19
lpg1613	acetyltransferase, GNAT family		Named proteins of general function	8.382	10.735	6.923	8.886	1.84E-04	2.03E-02	2.35	1.96
lpg1614	glutamate rich protein GrpB	*yqkA*	Named proteins of general function	8.856	10.557	9.388	8.415	1.21E-02	1.36E-01	1.70	-0.97
lpg1614	glutamate rich protein GrpB	*yqkA*	Named proteins of general function	8.688	10.849	9.323	8.604	2.19E-04	2.12E-01	2.16	-0.72
lpg1615	multidrug resistance ABC transporter ATP binding protein	*abcT3*	Transport and binding	8.505	8.753	9.478	8.924	5.56E-01	1.92E-01	0.25	-0.55
lpg1615	multidrug resistance ABC transporter ATP binding protein	*abcT3*	Transport and binding	8.891	9.087	9.405	9.113	6.02E-01	5.22E-01	0.20	-0.29
lpg1616	ABC transporter ATP-binding protein Uup (erythromycin r	*uup*	Transport and binding	8.213	7.516	8.683	6.143	4.56E-01	3.68E-02	-0.70	-2.54
lpg1616	ABC transporter ATP-binding protein Uup (erythromycin r	*uup*	Transport and binding	8.053	8.437	8.250	8.603	5.78E-01	8.55E-01	0.38	0.35
lpg1617	probable signal peptide protein		Unknown / hypothetical proteins	9.980	8.926	11.110	9.015	5.45E-02	9.48E-03	-1.05	-2.09
lpg1617	probable signal peptide protein		Unknown / hypothetical proteins	9.911	8.871	11.116	9.246	3.84E-03	6.08E-04	-1.04	-1.87
lpg1618	beta-lactamase AmpS (OXA-18) (oxacillin hydrolase)		Detoxification / adaptation, Protein fate	9.810	10.178	10.311	10.410	4.84E-01	6.64E-01	0.37	0.10
lpg1618	beta-lactamase AmpS (OXA-18) (oxacillin hydrolase)		Detoxification / adaptation, Protein fate	9.861	10.216	10.194	10.297	4.36E-01	6.87E-01	0.36	0.10
lpg1619	cell division protein FtsI/penicillin binding protein 2 (stage	*ftsI4*	Cell envelope synthesis, Chemotaxis /	10.079	9.724	10.122	8.136	3.55E-01	1.70E-01	-0.35	-1.99
lpg1619	cell division protein FtsI/penicillin binding protein 2 (stage	*ftsI4*	Cell envelope synthesis, Chemotaxis /	10.022	9.958	10.192	8.634	8.78E-01	2.55E-02	-0.06	-1.56
lpg1620	small ORF (146aa) beta lactamase repressor (transcriptional repress		Transcription factors / DNA binding pro	8.458	9.326	8.087	8.166	1.75E-01	9.55E-01	0.87	0.08
lpg1620	small ORF (146aa) beta lactamase repressor (transcriptional repress		Transcription factors / DNA binding pro	8.956	9.898	8.997	9.255	7.21E-02	6.07E-01	0.94	0.26
lpg1621	ORF	*ceg23*	ORFs of unknown function (unique)	9.854	7.674	9.472	7.061	1.45E-01	2.85E-02	-2.18	-2.41
lpg1621	ORF	*ceg23*	ORFs of unknown function (unique)	9.454	8.863	9.279	8.962	5.01E-01	6.30E-01	-0.59	-0.32
lpg1622	ORF		ORFs of unknown function (unique)	8.909	9.220	10.914	8.614	3.95E-01	1.08E-01	0.31	-2.30
lpg1622	ORF		ORFs of unknown function (unique)	9.267	8.143	10.964	8.833	3.16E-02	6.38E-04	-1.12	-2.13
lpg1623	hydrogenase		Named proteins of general function	10.457	11.800	9.351	12.540	1.71E-03	3.87E-05	1.34	3.19
lpg1623	hydrogenase		Named proteins of general function	10.232	11.810	9.151	12.515	1.05E-03	8.80E-05	1.58	3.36
lpg1624	alpha/beta hydrolase (hydrolase, alpha/beta fold family) (esterase/lipa		Protein fate / hydrolases / secretion	10.552	10.301	10.237	10.390	4.07E-01	4.49E-01	-0.25	0.15
lpg1624	alpha/beta hydrolase (hydrolase, alpha/beta fold family) (esterase/lipa		Protein fate / hydrolases / secretion	10.251	9.816	10.114	10.486	4.28E-01	2.06E-01	-0.44	0.37
lpg1625	small ORF (130aa)		ORFs of unknown function (unique)	9.161	9.436	9.238	9.757	5.72E-01	1.87E-01	0.28	0.52
lpg1625	small ORF (130aa)		ORFs of unknown function (unique)	8.922	9.339	8.741	9.691	2.66E-01	5.77E-02	0.42	0.95
lpg1626	copper efflux ATPase (cation (heavy metal) transport P-type ATPase)		Transport and binding	10.957	10.309	11.898	10.179	6.16E-02	1.11E-03	-0.65	-1.72
lpg1626	copper efflux ATPase (cation (heavy metal) transport P-type ATPase)		Transport and binding	10.990	10.902	11.927	10.512	7.12E-01	5.56E-03	-0.09	-1.42
lpg1627	putative secreted protein		Named proteins of general function	8.895	9.775	9.639	10.540	9.42E-02	1.47E-01	0.88	0.90
lpg1627	putative secreted protein		Named proteins of general function	8.578	9.581	8.904	10.240	7.68E-02	7.12E-02	1.00	1.34
lpg1628	coenzyme F390 synthetase FtsA (related to gramicidin S synthetase I		Named proteins of general function	8.094	8.255	8.413	7.376	8.77E-01	6.58E-02	0.16	-1.04
lpg1628	coenzyme F390 synthetase FtsA (related to gramicidin S synthetase I		Named proteins of general function	8.579	7.226	7.529	8.250	2.47E-01	3.83E-01	-1.35	0.72
lpg1629	Zn-dependent hydrolase GumP		Protein fate / hydrolases / secretion	8.976	7.156	8.015	9.134	3.15E-02	2.08E-01	-1.82	1.12
lpg1629	Zn-dependent hydrolase GumP		Protein fate / hydrolases / secretion	9.096	7.824	7.421	9.059	8.49E-02	2.58E-01	-1.27	1.64
lpg1630	3-beta-hydroxysteroid dehydrogenase/isomerase (DTDP-4-dehydrorh		Lipid Metabolism	9.742	10.788	9.735	9.662	1.04E-02	8.72E-01	1.05	-0.07
lpg1630	3-beta-hydroxysteroid dehydrogenase/isomerase (DTDP-4-dehydrorh		Lipid Metabolism	9.754	10.807	9.399	9.782	3.78E-03	6.14E-01	1.05	0.38
lpg1631	chalcone and stilbene synthases (3-oxoacyl[ACP]synthase II)		Lipid Metabolism	9.703	11.121	10.802	11.051	1.51E-03	3.21E-01	1.42	0.25
lpg1631	chalcone and stilbene synthases (3-oxoacyl[ACP]synthase II)		Lipid Metabolism	9.070	11.423	10.467	11.040	7.33E-05	1.23E-02	2.35	0.57
lpg1632	glycosyltransferase (sulfolipid sulfoquinovosyldiacylglycerol biosynthe		Metabolism of Complex Lipids	10.044	9.948	8.803	8.920	7.59E-01	9.26E-01	-0.10	0.12
lpg1632	glycosyltransferase (sulfolipid sulfoquinovosyldiacylglycerol biosynthe		Metabolism of Complex Lipids	10.058	10.151	8.796	9.830	6.99E-01	4.76E-02	0.09	1.03
lpg1633	ORF		ORFs of unknown function (unique)	8.306	9.133	7.792	8.450	9.24E-02	2.08E-01	0.83	0.66
lpg1633	ORF		ORFs of unknown function (unique)	8.530	9.681	6.550	8.951	2.07E-01	2.06E-02	1.15	2.40
lpg1634	oxidase (FAD binding oxidoreductase)		Named proteins of general function	8.997	9.471	10.027	8.040	2.85E-01	3.30E-03	0.47	-1.99
lpg1634	oxidase (FAD binding oxidoreductase)		Named proteins of general function	9.224	9.112	9.921	8.251	8.30E-01	2.55E-02	-0.11	-1.67
lpg1635	dienelactone hydrolase		Biodegradation of Xenobiotics	9.798	8.157	12.206	7.726	6.77E-02	3.60E-04	-1.64	-4.48
lpg1635	dienelactone hydrolase		Biodegradation of Xenobiotics	9.863	8.472	12.289	8.205	6.86E-02	2.36E-03	-1.39	-4.08
lpg1636	acetyltransferase, GNAT family (GCN5-related N-acetyltransferase) (r		Named proteins of general function	8.954	8.447	11.698	8.192	6.07E-01	3.75E-03	-0.51	-3.51
lpg1636	acetyltransferase, GNAT family (GCN5-related N-acetyltransferase) (r		Named proteins of general function	7.543	9.251	11.602	9.447	2.64E-01	3.89E-02	1.71	-2.15
lpg1637	polysaccharide deacetylase (chitooligosaccharide deacetylase)		Metabolism of Complex Carbohydrates	10.807	11.795	12.911	10.811	4.23E-02	2.46E-03	0.99	-2.10
lpg1637	polysaccharide deacetylase (chitooligosaccharide deacetylase)		Metabolism of Complex Carbohydrates	10.961	11.606	12.967	10.902	1.68E-01	2.75E-03	0.64	-2.07
lpg1638	drug:proton antiporter (integral membrane transport protein) (permeas		Transport and binding	11.475	9.887	10.269	10.022	4.25E-03	6.76E-01	-1.59	-0.25
lpg1638	drug:proton antiporter (integral membrane transport protein) (permeas		Transport and binding	11.314	10.325	9.523	10.472	6.69E-02	1.33E-01	-0.99	0.95
lpg1639	ORF		ORFs of unknown function (unique)	9.768	8.645	12.445	7.732	2.24E-01	7.85E-04	-1.12	-4.71
lpg1639	ORF		ORFs of unknown function (unique)	9.792	8.294	12.448	8.364	1.56E-01	2.64E-03	-1.50	-4.08
lpg1640	transmembrane protein		Unknown / hypothetical proteins	10.278	9.050	9.439	8.855	1.33E-02	4.06E-01	-1.23	-0.58
lpg1640	transmembrane protein		Unknown / hypothetical proteins	10.520	10.040	9.357	10.280	3.68E-01	6.11E-02	-0.48	0.92
lpg1641	acylaminoacyl peptidase (peptidase S9, prolyl oligopeptidase family)		Protein fate / hydrolases / secretion	10.457	9.362	11.998	9.791	1.64E-01	7.58E-03	-1.09	-2.21
lpg1641	acylaminoacyl peptidase (peptidase S9, prolyl oligopeptidase family)		Protein fate / hydrolases / secretion	10.517	9.572	12.062	10.185	1.63E-01	7.39E-03	-0.95	-1.88
lpg1642	SidB, RTX (repeat in toxin) cytotoxin	*sidB*	Toxin production / other pathogen func	9.237	8.647	7.807	7.439	2.93E-01	6.24E-01	-0.59	-0.37
lpg1642	SidB, RTX (repeat in toxin) cytotoxin	*sidB*	Toxin production / other pathogen func	9.486	8.417	7.645	7.525	8.51E-03	8.61E-01	-1.07	-0.12
lpg1643	threonine synthase	*thrC*	Amino Acid Metabolism, Metabolism o	8.688	9.186	10.422	8.379	1.98E-01	1.71E-02	0.50	-2.04
lpg1643	threonine synthase	*thrC*	Amino Acid Metabolism, Metabolism o	8.955	10.014	10.568	9.172	9.70E-02	1.69E-03	1.06	-1.40

lpg1644	ORF		ORFs of unknown function (unique)	9.845	8.824	9.705	7.237	2.31E-03	1.27E-03	-1.02	-2.47
lpg1644	ORF		ORFs of unknown function (unique)	9.744	9.462	9.632	8.526	4.67E-01	2.96E-02	-0.28	-1.11
lpg1645	hypothetical (periplasmic protein?)		Named proteins of general function	8.190	8.685	9.476	7.636	3.43E-01	1.41E-02	0.49	-1.84
lpg1645	hypothetical (periplasmic protein?)		Named proteins of general function	8.088	8.851	9.430	8.071	3.09E-02	1.81E-03	0.76	-1.36
lpg1646	cytochrome b561 transmembrane protein (secretory vesicle-specific		Toxin production / other pathogen func	11.773	11.080	12.803	10.220	2.06E-01	1.41E-04	-0.69	-2.58
lpg1646	cytochrome b561 transmembrane protein (secretory vesicle-specific		Toxin production / other pathogen func	11.770	10.463	12.781	10.432	9.36E-02	1.43E-04	-1.31	-2.35
lpg1647	hypothetical (exported protein)		Unknown / hypothetical proteins	12.006	10.368	12.600	9.215	1.02E-01	6.04E-06	-1.64	-3.39
lpg1647	hypothetical (exported protein)		Unknown / hypothetical proteins	11.086	10.343	12.486	9.128	2.08E-01	5.56E-06	-0.74	-3.36
lpg1648	signal peptide protein (integral membrane or exported protein?)		Named proteins of general function	11.231	10.110	12.331	8.097	1.35E-04	2.22E-04	-1.12	-4.23
lpg1648	signal peptide protein (integral membrane or exported protein?)		Named proteins of general function	11.236	9.810	12.357	8.508	3.20E-04	7.13E-05	-1.43	-3.85
lpg1649	myo-inositol catabolism protein IolE	*iolE*	Carbohydrate Metabolism	8.568	8.667	7.766	7.924	8.75E-01	8.43E-01	0.10	0.16
lpg1649	myo-inositol catabolism protein IolE	*iolE*	Carbohydrate Metabolism	8.572	9.571	8.148	8.902	4.52E-01	5.95E-01	1.00	0.75
lpg1650	myo-inositol catabolism protein IolD (malonic semialdehy	*iolD*	Carbohydrate Metabolism	10.841	9.795	9.781	9.412	2.50E-02	4.63E-01	-1.05	-0.37
lpg1650	myo-inositol catabolism protein IolD (malonic semialdehy	*iolD*	Carbohydrate Metabolism	10.983	10.127	9.733	10.168	1.64E-01	4.75E-01	-0.86	0.44
lpg1651	IolC/IolB transferase kinase protein (5-dehydro-2-deoxyglucokinase)		Carbohydrate Metabolism	10.682	9.022	8.749	8.209	4.44E-04	4.73E-01	-1.66	-0.54
lpg1651	IolC/IolB transferase kinase protein (5-dehydro-2-deoxyglucokinase)		Carbohydrate Metabolism	10.504	9.382	8.932	9.129	6.86E-02	7.98E-01	-1.12	0.20
lpg1652	myo-inositol-2-dehydrogenase (oxidoreductase, NAD binding)		Carbohydrate Metabolism, Metabolism	11.064	10.115	9.575	9.219	2.01E-01	6.97E-01	-0.95	-0.36
lpg1652	myo-inositol-2-dehydrogenase (oxidoreductase, NAD binding)		Carbohydrate Metabolism, Metabolism	10.940	10.189	9.312	10.345	2.25E-01	1.28E-01	-0.75	1.03
lpg1653	D-xylose-proton symporter (galactose-proton symport) (sugar transp		Transport and binding	11.344	9.595	9.482	9.248	1.98E-04	6.64E-01	-1.75	-0.23
lpg1653	D-xylose-proton symporter (galactose-proton symport) (sugar transp		Transport and binding	10.853	9.245	8.601	9.342	1.07E-03	2.83E-01	-1.61	0.74
lpg1654	ORF		ORFs of unknown function (unique)	10.444	11.164	10.061	8.956	1.30E-01	2.76E-02	0.72	-1.11
lpg1654	ORF		ORFs of unknown function (unique)	9.732	11.012	9.379	8.913	6.65E-02	2.85E-01	1.28	-0.47
lpg1655	class 4 metalloprotease (zinc metalloprotease) (virulence	*lasB*	Toxin production / other pathogen func	10.890	9.443	10.836	8.735	1.10E-03	8.64E-04	-1.45	-2.10
lpg1655	class 4 metalloprotease (zinc metalloprotease) (virulence	*lasB*	Toxin production / other pathogen func	10.713	8.919	11.007	9.233	2.76E-03	1.24E-02	-1.79	-1.77
lpg1656	hypothetical		Unknown / hypothetical proteins	9.999	10.367	9.575	10.478	1.63E-01	5.34E-02	0.37	0.90
lpg1656	hypothetical		Unknown / hypothetical proteins	9.969	10.305	9.390	10.468	2.95E-01	3.38E-02	0.34	1.08
lpg1657	NG,NG-dimethylarginine dimethylaminohydrolase		Named proteins of general function	9.974	9.199	8.382	8.802	2.35E-02	5.58E-01	-0.77	0.42
lpg1657	NG,NG-dimethylarginine dimethylaminohydrolase		Named proteins of general function	9.765	9.087	8.133	9.213	1.53E-01	1.99E-01	-0.68	1.08
lpg1658	amino acid antiporter (glutamate/gamma-aminobutyrate antiporter)		Transport and binding	11.005	10.339	10.276	10.463	1.62E-01	7.17E-01	-0.67	0.19
lpg1658	amino acid antiporter (glutamate/gamma-aminobutyrate antiporter)		Transport and binding	11.073	10.210	10.252	10.460	7.16E-02	6.46E-01	-0.86	0.21
lpg1659	membrane protein		Named proteins of general function	10.919	9.717	12.213	9.179	3.78E-02	3.89E-03	-1.20	-3.03
lpg1659	membrane protein		Named proteins of general function	10.821	9.870	12.220	9.358	7.16E-02	3.70E-03	-0.95	-2.86
lpg1660	ORF	*LegL3*	ORFs of unknown function (unique)	8.418	7.577	10.002	7.662	4.07E-01	1.11E-01	-0.84	-2.34
lpg1660	ORF	*LegL3*	ORFs of unknown function (unique)	8.420	7.997	9.673	7.500	6.72E-01	1.97E-01	-0.42	-2.17
lpg1661	hypothetical (expressed protein?)		Unknown / hypothetical proteins	10.077	9.223	9.202	8.916	2.40E-02	4.94E-01	-0.85	-0.29
lpg1661	hypothetical (expressed protein?)		Unknown / hypothetical proteins	10.061	9.213	9.314	9.825	5.15E-03	3.46E-02	-0.85	0.51
lpg1662	putative transport protein		Transport and binding	11.111	10.162	10.511	10.329	9.29E-02	4.77E-01	-0.95	-0.18
lpg1662	putative transport protein		Transport and binding	11.039	10.187	9.829	10.233	9.02E-02	6.46E-01	-0.85	0.40
lpg1663	ORF		ORFs of unknown function (unique)	10.860	12.057	9.965	11.990	6.05E-02	9.16E-03	1.20	2.02
lpg1663	ORF		ORFs of unknown function (unique)	11.177	12.008	9.547	12.021	1.64E-02	2.56E-02	0.83	2.47
lpg1664	penicillin binding protein 1C, peptidoglycan biosynthesis		Cell envelope synthesis, Metabolism	9.943	10.680	8.350	10.781	8.05E-02	5.27E-03	0.74	2.43
lpg1664	penicillin binding protein 1C, peptidoglycan biosynthesis		Cell envelope synthesis, Metabolism	9.182	10.744	8.213	10.719	4.99E-02	4.64E-04	1.56	2.51
lpg1665	hypothetical (lipoprotein)		Named proteins of general function	10.551	9.945	10.626	9.852	2.30E-02	1.73E-02	-0.61	-0.77
lpg1665	hypothetical (lipoprotein)		Named proteins of general function	10.387	9.667	10.608	9.864	1.16E-02	1.19E-02	-0.72	-0.74
lpg1666	ORF		ORFs of unknown function (unique)	9.619	8.692	8.786	9.421	1.42E-02	2.16E-01	-0.93	0.63
lpg1666	ORF		ORFs of unknown function (unique)	9.584	9.006	9.015	10.078	5.39E-02	2.16E-02	-0.58	1.06
lpg1667	conserved hypothetical protein		Unknown / hypothetical proteins	10.106	9.051	11.678	8.757	1.17E-02	2.36E-04	-1.06	-2.92
lpg1667	conserved hypothetical protein		Unknown / hypothetical proteins	10.106	9.099	11.727	8.944	2.92E-02	1.53E-04	-1.01	-2.78
lpg1668	ORF		ORFs of unknown function (unique)	10.225	9.857	10.991	10.165	5.61E-02	2.44E-02	-0.37	-0.83
lpg1668	ORF		ORFs of unknown function (unique)	10.340	10.479	10.828	10.673	8.13E-01	8.23E-01	0.14	-0.16
lpg1669	alpha-amylase, putative		Metabolism of Complex Carbohydrate	9.039	10.308	13.764	8.463	2.70E-01	4.01E-04	1.27	-5.30
lpg1669	alpha-amylase, putative		Metabolism of Complex Carbohydrate	9.249	10.473	13.789	8.673	2.89E-01	2.53E-03	1.22	-5.12
lpg1670	ORF		ORFs of unknown function (unique)	10.641	12.164	12.571	9.357	1.04E-02	9.84E-05	1.52	-3.21
lpg1670	ORF		ORFs of unknown function (unique)	10.332	12.226	12.642	9.522	1.11E-03	1.16E-04	1.89	-3.12
lpg1671	alpha-amylase, putative		Metabolism of Complex Carbohydrate	10.531	10.843	11.377	10.231	5.08E-01	3.41E-03	0.31	-1.15
lpg1671	alpha-amylase, putative		Metabolism of Complex Carbohydrate	10.435	10.645	11.163	10.406	6.19E-01	4.60E-02	0.21	-0.76
lpg1672	phosphoribosylglycinamide formyltransferase (phosphoribosylamine-		Nucleotide Metabolism, Metabolism of	11.303	9.486	11.928	10.176	1.11E-04	6.55E-05	-1.82	-1.75
lpg1672	phosphoribosylglycinamide formyltransferase (phosphoribosylamine-		Nucleotide Metabolism, Metabolism of	11.309	9.172	12.033	10.283	1.39E-03	3.60E-04	-2.14	-1.75
lpg1673	phosphoribosylamine-glycine ligase (GARS) (glycinamide ribonucleot		Nucleotide Metabolism	10.091	8.979	10.976	8.673	2.37E-02	1.36E-04	-1.11	-2.30
lpg1673	phosphoribosylamine-glycine ligase (GARS) (glycinamide ribonucleot		Nucleotide Metabolism	10.237	9.088	11.026	9.117	7.48E-04	3.20E-06	-1.15	-1.91
lpg1674	amidophosphoribosyltransferase (glutamine phosphoribo	*purF*	Nucleotide Metabolism, Amino Acid M	11.622	9.761	12.244	11.021	5.55E-05	2.37E-05	-1.86	-1.22
lpg1674	amidophosphoribosyltransferase (glutamine phosphoribo	*purF*	Nucleotide Metabolism, Amino Acid M	11.724	10.142	12.219	11.027	8.61E-05	4.97E-04	-1.58	-1.19
lpg1675	phosphoribosylimidazole-succinocarboxamide synthase (SAICAR sy		Nucleotide Metabolism	12.691	10.656	12.462	11.284	3.63E-05	2.74E-03	-2.04	-1.18
lpg1675	phosphoribosylimidazole-succinocarboxamide synthase (SAICAR sy		Nucleotide Metabolism	12.675	10.805	12.437	11.653	7.16E-05	6.18E-05	-1.87	-0.78

lpg1676	phosphoribosylformylglycinamidine synthase I (FGAM sy	*purQ*	Nucleotide Metabolism	11.825	10.460	11.210	11.209	3.89E-02	9.98E-01	-1.36	0.00
lpg1676	phosphoribosylformylglycinamidine synthase I (FGAM sy	*purQ*	Nucleotide Metabolism	12.128	10.641	11.438	11.712	6.04E-02	5.86E-01	-1.49	0.27
lpg1677	phosphoribosylformylglycinamidine cyclo ligase (phosph	*purM*	Nucleotide Metabolism	12.328	11.214	11.825	11.239	3.73E-04	1.84E-02	-1.11	-0.59
lpg1677	phosphoribosylformylglycinamidine cyclo ligase (phosph	*purM*	Nucleotide Metabolism	12.179	11.338	11.595	11.401	1.04E-02	4.95E-01	-0.84	-0.19
lpg1678	phosphoribosylformylglycinamidine synthase II (FGAM sy	*purL2*	Nucleotide Metabolism	10.979	10.232	12.074	11.202	5.17E-01	8.82E-02	-0.75	-0.87
lpg1678	phosphoribosylformylglycinamidine synthase II (FGAM sy	*purL2*	Nucleotide Metabolism	11.117	11.378	12.053	11.638	4.34E-01	3.24E-01	0.26	-0.41
lpg1679	hypothetical		Unknown / hypothetical proteins	9.037	9.753	9.447	10.454	4.85E-02	6.62E-02	0.72	1.01
lpg1679	hypothetical		Unknown / hypothetical proteins	8.894	9.842	9.522	10.640	3.36E-02	5.30E-02	0.95	1.12
lpg1680	thiol:disulfide interchange protein DsbD	*dsbD*	Named proteins of general function	10.252	11.224	11.906	9.429	4.50E-02	6.92E-04	0.97	-2.48
lpg1680	thiol:disulfide interchange protein DsbD	*dsbD*	Named proteins of general function	10.234	11.122	11.898	9.498	8.83E-02	7.39E-04	0.89	-2.40
lpg1681	small ORF (105aa)		ORFs of unknown function (unique)	11.449	10.857	8.957	9.451	3.78E-01	6.01E-01	-0.59	0.49
lpg1681	small ORF (105aa)		ORFs of unknown function (unique)	11.119	10.990	8.883	9.981	8.86E-01	2.22E-01	-0.13	1.10
lpg1682	oxidoreductase, short chain dehydrogenase/reductase family		Named proteins of general function	9.769	9.867	8.560	8.685	7.71E-01	8.76E-01	0.10	0.13
lpg1682	oxidoreductase, short chain dehydrogenase/reductase family		Named proteins of general function	9.815	9.726	9.297	9.622	7.72E-01	6.39E-01	-0.09	0.33
lpg1683	ORF		ORFs of unknown function (unique)	9.134	8.959	12.049	9.891	7.28E-01	1.05E-02	-0.17	-2.16
lpg1683	ORF		ORFs of unknown function (unique)	9.571	9.612	12.130	10.579	9.34E-01	1.68E-02	0.04	-1.55
lpg1684	ORF		ORFs of unknown function (unique)	7.859	11.767	10.038	9.084	2.01E-02	2.65E-01	3.91	-0.95
lpg1684	ORF		ORFs of unknown function (unique)	9.122	11.724	10.246	9.542	3.50E-03	2.80E-01	2.60	-0.70
lpg1685	ORF		ORFs of unknown function (unique)	11.109	12.072	12.151	10.493	3.49E-02	6.38E-04	0.96	-1.66
lpg1685	ORF		ORFs of unknown function (unique)	11.075	12.446	12.084	10.637	1.98E-03	5.75E-04	1.37	-1.45
lpg1686	small ORF (105aa)		ORFs of unknown function (unique)	9.921	10.105	12.559	10.410	8.71E-01	5.33E-02	0.18	-2.15
lpg1686	small ORF (105aa)		ORFs of unknown function (unique)	9.691	10.195	12.383	10.589	6.81E-01	2.02E-01	0.50	-1.79
lpg1687	ORF		ORFs of unknown function (unique)	7.923	8.915	10.019	9.287	2.30E-01	1.70E-01	0.99	-0.73
lpg1687	ORF		ORFs of unknown function (unique)	7.704	7.136	9.680	9.041	7.18E-01	3.67E-01	-0.57	-0.64
lpg1688	possible flagellar hook-length control protein		Chemotaxis / motility / cell division, Si	7.471	8.677	10.026	8.077	9.87E-02	1.03E-02	1.21	-1.95
lpg1688	possible flagellar hook-length control protein		Chemotaxis / motility / cell division, Si	7.692	7.628	9.811	8.668	9.53E-01	2.29E-01	-0.06	-1.14
lpg1689	23.7 kDa protein		Named proteins of general function	8.897	8.354	9.393	7.988	2.88E-01	4.23E-02	-0.54	-1.40
lpg1689	23.7 kDa protein		Named proteins of general function	8.736	8.974	9.396	8.611	6.23E-01	2.83E-01	0.24	-0.79
lpg1690	aconitate hydratase (citrate hydro-lyase) (aconitase)	*acnA*	Carbohydrate Metabolism, Energy Me	13.430	14.237	14.875	14.710	3.74E-02	6.33E-01	0.81	-0.17
lpg1690	aconitate hydratase (citrate hydro-lyase) (aconitase)	*acnA*	Carbohydrate Metabolism, Energy Me	13.475	14.250	14.904	14.742	6.39E-02	6.14E-01	0.77	-0.16
lpg1691	amino acid antiporter (glutamate/gamma-aminobutyrate antiporter)		Transport and binding	9.840	9.930	9.531	9.434	8.25E-01	8.36E-01	0.09	-0.10
lpg1691	amino acid antiporter (glutamate/gamma-aminobutyrate antiporter)		Transport and binding	9.745	10.330	9.699	10.131	1.65E-01	4.39E-01	0.58	0.43
lpg1692	ORF		ORFs of unknown function (unique)	11.270	11.547	9.965	11.095	3.24E-01	4.85E-02	0.28	1.13
lpg1692	ORF		ORFs of unknown function (unique)	11.225	11.639	9.916	11.286	9.31E-02	2.03E-02	0.41	1.37
lpg1693	small ORF (92aa)		ORFs of unknown function (unique)	8.334	8.241	9.657	8.589	8.56E-01	4.74E-02	-0.09	-1.07
lpg1693	small ORF (92aa)		ORFs of unknown function (unique)	8.423	8.748	9.433	8.693	6.24E-01	2.47E-01	0.32	-0.74
lpg1694	transposase IS630 family (transposase ISA1083)		Viral functions / Phage / Transposases	8.530	10.251	9.939	9.635	1.10E-02	4.74E-01	1.72	-0.30
lpg1694	transposase IS630 family (transposase ISA1083)		Viral functions / Phage / Transposases	9.992	10.000	10.168	10.257	9.87E-01	8.68E-01	0.01	0.09
lpg1694	transposase IS630 family (transposase ISA1083)		Viral functions / Phage / Transposases	8.522	10.617	9.721	9.855	1.36E-02	6.95E-01	2.09	0.13
lpg1694	transposase IS630 family (transposase ISA1083)		Viral functions / Phage / Transposases	9.857	10.273	10.680	10.820	3.45E-01	5.72E-01	0.42	0.14
lpg1695	transposase IS630 family		Viral functions / Phage / Transposases	11.123	11.040	9.564	11.074	7.52E-01	4.95E-02	-0.08	1.51
lpg1695	transposase IS630 family		Viral functions / Phage / Transposases	10.717	11.918	9.511	12.081	1.03E-02	3.09E-03	1.20	2.57
lpg1696	proline dehydrogenase/delta-1-pyrroline-5-carboxylate de	*putA*	Amino Acid Metabolism	11.182	12.144	11.528	11.758	2.56E-03	4.61E-01	0.96	0.23
lpg1696	proline dehydrogenase/delta-1-pyrroline-5-carboxylate de	*putA*	Amino Acid Metabolism	10.999	12.316	11.451	11.861	5.50E-05	2.19E-01	1.32	0.41
lpg1697	conserved hypothetical protein		Unknown / hypothetical proteins	10.571	11.790	9.973	10.191	2.53E-03	5.03E-01	1.22	0.22
lpg1697	conserved hypothetical protein		Unknown / hypothetical proteins	10.555	11.808	9.835	10.283	4.42E-04	3.69E-01	1.25	0.45
lpg1698	(ProQ, activator of ProP osmoprotectant transporter?)		Detoxification / adaptation, Transcripti	11.384	12.718	9.938	12.122	2.12E-02	1.02E-04	1.33	2.18
lpg1698	(ProQ, activator of ProP osmoprotectant transporter?)		Detoxification / adaptation, Transcripti	11.254	12.707	9.757	12.081	4.02E-02	2.05E-03	1.45	2.32
lpg1699	3-demethylubiquinone-9 3-methyltransferase UbiG	*ubiG*	Metabolism of Cofactors and Vitamins	12.226	12.928	10.822	13.211	6.91E-03	3.12E-04	0.70	2.39
lpg1699	3-demethylubiquinone-9 3-methyltransferase UbiG	*ubiG*	Metabolism of Cofactors and Vitamins	12.119	12.933	10.804	13.230	1.09E-02	2.24E-04	0.81	2.43
lpg1700	uracil DNA glycosylase		Nucleotide Metabolism	10.733	10.866	10.750	10.777	5.28E-01	9.45E-01	0.13	0.03
lpg1700	uracil DNA glycosylase		Nucleotide Metabolism	10.598	10.845	9.537	10.792	3.53E-01	5.93E-02	0.25	1.26
lpg1701	kinectin 1 (kinesin receptor)	*LegC3*	Named proteins of general function	10.880	10.757	10.519	9.771	8.53E-01	3.50E-02	-0.12	-0.75
lpg1701	kinectin 1 (kinesin receptor)	*LegC3*	Named proteins of general function	10.477	11.164	9.132	9.789	7.27E-02	3.44E-01	0.69	0.66
lpg1702	Tpr		Named proteins of general function	12.975	15.026	14.356	12.049	1.53E-03	9.87E-06	2.05	-2.31
lpg1702	Tpr		Named proteins of general function	12.974	15.019	14.334	12.066	1.72E-03	1.64E-05	2.04	-2.27
lpg1703	SOS mutagenesis and repair UmuC protein		Replication and Repair	9.504	10.377	8.899	9.635	1.30E-02	2.75E-02	0.87	0.74
lpg1703	SOS mutagenesis and repair UmuC protein		Replication and Repair	9.533	10.715	9.063	10.067	2.42E-03	2.74E-04	1.18	1.00
lpg1704	SOS (error prone) mutagenesis protein UmuD (RumA)		Replication and Repair	8.703	9.631	9.243	10.005	5.58E-02	1.85E-01	0.93	0.76
lpg1704	SOS (error prone) mutagenesis protein UmuD (RumA)		Replication and Repair	8.881	9.715	9.396	10.232	2.06E-02	1.06E-01	0.83	0.84
lpg1705	carboxypeptidase G2 (peptidase, M20/M25/M40 family)		Protein fate / hydrolases / secretion	10.733	10.432	10.335	10.404	3.70E-01	8.56E-01	-0.30	0.07
lpg1705	carboxypeptidase G2 (peptidase, M20/M25/M40 family)		Protein fate / hydrolases / secretion	10.742	10.271	10.173	10.421	2.26E-01	5.81E-01	-0.47	0.25
lpg1706	arginine/ornithine succinyltransferase (arginine-N-succinyltransferase		Amino Acid Metabolism	10.359	9.828	9.807	10.096	1.96E-01	6.51E-01	-0.53	0.29
lpg1706	arginine/ornithine succinyltransferase (arginine-N-succinyltransferase		Amino Acid Metabolism	10.340	10.005	9.859	10.151	3.85E-01	4.82E-01	-0.33	0.29

lpg1707	succinylglutamic-5-semialdehyde dehydrogenase (aldehy	*aruD*	Amino Acid Metabolism, Biodegradati	10.966	11.759	10.804	12.011	1.34E-02	3.38E-03	0.79	1.21
lpg1707	succinylglutamic-5-semialdehyde dehydrogenase (aldehy	*aruD*	Amino Acid Metabolism, Biodegradati	11.403	12.327	10.880	12.403	1.32E-01	6.20E-03	0.92	1.52
lpg1708	succinylarginine dihydrolase	*astB*	Amino Acid Metabolism, Nucleotide M	11.946	11.875	12.523	11.625	7.88E-01	4.05E-02	-0.07	-0.90
lpg1708	succinylarginine dihydrolase	*astB*	Amino Acid Metabolism, Nucleotide M	11.785	11.954	10.277	11.723	6.80E-01	3.97E-03	0.17	1.45
lpg1709	conserved hypothetical protein		Unknown / hypothetical proteins	10.929	9.493	9.699	9.752	4.61E-02	9.26E-01	-1.44	0.05
lpg1709	conserved hypothetical protein		Unknown / hypothetical proteins	11.090	10.069	9.592	10.164	8.18E-02	2.37E-01	-1.02	0.57
lpg1710	small ORF (121aa)		ORFs of unknown function (unique)	10.630	9.353	9.666	8.862	1.21E-02	2.17E-02	-1.28	-0.80
lpg1710	small ORF (121aa)		ORFs of unknown function (unique)	10.468	9.072	9.823	9.042	1.50E-02	7.61E-02	-1.40	-0.78
lpg1711	ribosome recycling factor (ribosome releasing factor)	*frr*	Translation	12.573	14.088	12.104	12.040	9.37E-04	8.05E-01	1.51	-0.06
lpg1711	ribosome recycling factor (ribosome releasing factor)	*frr*	Translation	12.638	14.346	11.994	12.483	3.85E-04	4.09E-01	1.71	0.49
lpg1712	uridylate kinase (uridine monophosphate kinase)	*pyrH*	Nucleotide Metabolism	12.307	11.965	10.978	12.389	6.75E-01	1.24E-02	-0.34	1.41
lpg1712	uridylate kinase (uridine monophosphate kinase)	*pyrH*	Nucleotide Metabolism	12.298	11.990	10.996	12.520	7.15E-01	7.85E-03	-0.31	1.52
lpg1713	translation elongation factor Ts (EF-Ts) (ubiquitin associa	*tsf*	Translation	12.833	12.585	10.948	13.225	6.44E-01	5.79E-03	-0.25	2.28
lpg1713	translation elongation factor Ts (EF-Ts) (ubiquitin associa	*tsf*	Translation	12.988	12.544	10.749	13.249	4.15E-01	4.83E-03	-0.44	2.50
lpg1714	30S ribosomal protein S2	*rpsB*	Translation	13.720	14.022	11.217	14.768	5.24E-01	4.57E-04	0.30	3.55
lpg1714	30S ribosomal protein S2	*rpsB*	Translation	13.692	14.052	11.197	14.782	5.26E-01	3.71E-04	0.36	3.59
lpg1715	16 kD immunogenic protein		Named proteins of general function	15.054	14.261	14.762	14.039	5.72E-01	5.37E-01	-0.79	-0.72
lpg1715	16 kD immunogenic protein		Named proteins of general function	15.027	14.799	14.755	14.505	7.50E-01	7.08E-01	-0.23	-0.25
lpg1716	small ORF (152aa)		ORFs of unknown function (unique)	13.219	13.122	11.397	11.847	8.60E-01	2.35E-01	-0.10	0.45
lpg1716	small ORF (152aa)		ORFs of unknown function (unique)	13.287	13.081	11.164	11.823	6.90E-01	2.37E-01	-0.21	0.66
lpg1717	hypothetical protein		Unknown / hypothetical proteins	8.777	9.846	9.148	8.909	1.84E-02	6.08E-01	1.07	-0.24
lpg1717	hypothetical protein		Unknown / hypothetical proteins	8.657	9.608	8.746	8.663	5.17E-02	7.75E-01	0.95	-0.08
lpg1718	huntingtin interacting protein B	*LegAS4*	Named proteins of general function	10.821	12.696	11.505	10.348	6.23E-03	1.39E-02	1.88	-1.16
lpg1718	huntingtin interacting protein B	*LegAS4*	Named proteins of general function	10.806	12.969	11.563	10.606	1.05E-03	3.79E-02	2.16	-0.96
lpg1719	methionine aminopeptidase	*map*	Protein fate / hydrolases / secretion	13.118	12.543	11.257	13.071	4.47E-01	7.32E-02	-0.57	1.81
lpg1719	methionine aminopeptidase	*map*	Protein fate / hydrolases / secretion	13.196	12.927	11.044	13.798	5.86E-01	2.41E-04	-0.27	2.75
lpg1720	protein-PII uridylyltransferase	*glnD*	Signal transduction / other regulatory f	10.585	8.841	9.419	9.988	3.39E-03	2.32E-01	-1.74	0.57
lpg1720	protein-PII uridylyltransferase	*glnD*	Signal transduction / other regulatory f	10.722	9.707	8.973	10.187	1.93E-01	1.19E-01	-1.02	1.21
lpg1721	deaminase (zinc binding protein) (zinc binding hydrolase)	*yfhC*	Nucleotide Metabolism	11.211	10.624	12.014	9.878	3.00E-01	2.62E-03	-0.59	-2.14
lpg1721	deaminase (zinc binding protein) (zinc binding hydrolase)	*yfhC*	Nucleotide Metabolism	11.115	10.208	11.862	10.024	6.00E-02	1.10E-02	-0.91	-1.84
lpg1722	GMP synthetase	*guaA*	Nucleotide Metabolism, Amino Acid M	10.973	11.338	10.809	11.356	2.95E-01	1.15E-01	0.37	0.55
lpg1722	GMP synthetase	*guaA*	Nucleotide Metabolism, Amino Acid M	10.977	12.091	10.830	11.989	9.95E-02	6.98E-02	1.11	1.16
lpg1723	inosine-5'-monophosphate dehydrogenase	*guaB*	Nucleotide Metabolism	11.047	12.371	11.532	11.798	9.68E-05	2.54E-01	1.32	0.27
lpg1723	inosine-5'-monophosphate dehydrogenase	*guaB*	Nucleotide Metabolism	11.223	12.340	11.467	11.960	2.93E-04	1.73E-02	1.12	0.49
lpg1724	septum site-determining protein MinD (cell division inhibit	*minD*	Chemotaxis / motility / cell division, Si	13.584	13.805	12.308	12.651	7.53E-01	5.58E-01	0.22	0.34
lpg1724	septum site-determining protein MinD (cell division inhibit	*minD*	Chemotaxis / motility / cell division, Si	13.567	13.889	12.273	13.016	6.21E-01	5.21E-02	0.32	0.74
lpg1725	septum formation (cell division) topological specificity fac	*minE*	Chemotaxis / motility / cell division	12.342	11.949	12.206	10.960	3.84E-01	5.50E-04	-0.39	-1.25
lpg1725	septum formation (cell division) topological specificity fac	*minE*	Chemotaxis / motility / cell division	12.252	11.671	12.042	10.949	2.39E-01	2.33E-03	-0.58	-1.09
lpg1726	oxidoreductase, acyl CoA dehydrogenase family (acyl C	*yafH*	Lipid Metabolism, Metabolism of Com	12.036	11.803	13.613	11.462	8.02E-01	8.50E-04	-0.23	-2.15
lpg1726	oxidoreductase, acyl CoA dehydrogenase family (acyl C	*yafH*	Lipid Metabolism, Metabolism of Com	12.021	12.064	13.624	11.622	9.54E-01	1.63E-03	0.04	-2.00
lpg1727	hydrolase		Protein fate / hydrolases / secretion	12.243	10.891	11.144	11.988	1.37E-03	3.38E-02	-1.35	0.84
lpg1727	hydrolase		Protein fate / hydrolases / secretion	12.387	10.278	11.109	11.966	1.13E-03	2.76E-02	-2.11	0.86
lpg1728	unknown		Unknown / hypothetical proteins	11.969	10.956	11.068	11.772	1.90E-02	3.73E-03	-1.01	0.70
lpg1728	unknown		Unknown / hypothetical proteins	12.049	10.186	11.051	11.762	1.14E-01	5.78E-03	-1.86	0.71
lpg1729	sn-glycerol-3-phosphate transport, ATP binding protein	*ugpC*	Transport and binding	10.857	9.523	10.471	9.585	1.76E-03	1.94E-02	-1.33	-0.89
lpg1729	sn-glycerol-3-phosphate transport, ATP binding protein	*ugpC*	Transport and binding	10.721	9.649	10.417	9.813	6.78E-03	5.02E-02	-1.07	-0.60
lpg1730	sn-glycerol-3-phosphate transmembrane ABC transporte	*ugpE*	Transport and binding	12.043	10.764	11.134	9.478	1.05E-01	3.72E-01	-1.28	-1.66
lpg1730	sn-glycerol-3-phosphate transmembrane ABC transporte	*ugpE*	Transport and binding	12.017	10.221	11.382	10.111	9.75E-07	2.12E-03	-1.80	-1.27
lpg1731	sn-glycerol-3-phosphate transmembrane ABC transporte	*ugpA*	Transport and binding	11.129	10.144	10.450	9.265	9.33E-03	1.73E-03	-0.98	-1.19
lpg1731	sn-glycerol-3-phosphate transmembrane ABC transporte	*ugpA*	Transport and binding	11.084	10.289	10.413	9.639	2.68E-02	1.34E-02	-0.79	-0.77
lpg1732	quinone oxidoreductase (alcohol dehydrogenase, zinc c	*qor*	Named proteins of general function	9.289	10.018	10.234	10.228	7.99E-02	9.84E-01	0.73	-0.01
lpg1732	quinone oxidoreductase (alcohol dehydrogenase, zinc c	*qor*	Named proteins of general function	9.585	10.561	10.215	10.347	4.99E-03	6.63E-01	0.98	0.13
lpg1733	chloride channel protein EriC (voltage gated)		Transport and binding	11.186	9.835	9.324	9.979	8.50E-03	2.62E-01	-1.35	0.65
lpg1733	chloride channel protein EriC (voltage gated)		Transport and binding	11.161	10.380	9.432	10.258	1.26E-02	6.54E-02	-0.78	0.83
lpg1734	anthranilate synthase (glutamine amidotransferase) component I		Amino Acid Metabolism	11.951	12.181	10.890	11.919	6.29E-01	4.85E-02	0.23	1.03
lpg1734	anthranilate synthase (glutamine amidotransferase) component I		Amino Acid Metabolism	11.979	12.181	10.814	12.026	6.78E-01	2.58E-02	0.20	1.21
lpg1735	glutamyl/tRNA (Gln) amidotransferase, C subunit	*gatC*	DNA/RNA degradation / restriction, Tr	9.359	9.926	9.177	9.858	1.50E-01	2.29E-01	0.57	0.68
lpg1735	glutamyl/tRNA (Gln) amidotransferase, C subunit	*gatC*	DNA/RNA degradation / restriction, Tr	9.503	9.787	8.863	9.775	5.23E-01	1.76E-01	0.28	0.91
lpg1736	glutamyl/tRNA (Gln) amidotransferase, A subunit	*gatA*	DNA/RNA degradation / restriction, Tr	10.350	10.877	8.856	10.272	2.57E-01	8.68E-02	0.53	1.42
lpg1736	glutamyl/tRNA (Gln) amidotransferase, A subunit	*gatA*	DNA/RNA degradation / restriction, Tr	10.383	10.718	8.253	10.160	3.91E-01	1.72E-01	0.34	1.91
lpg1737	glutamyl/tRNA (Gln) amidotransferase, B subunit	*gatB*	DNA/RNA degradation / restriction, Tr	11.268	12.873	11.636	12.712	1.67E-04	3.05E-04	1.60	1.08
lpg1737	glutamyl/tRNA (Gln) amidotransferase, B subunit	*gatB*	DNA/RNA degradation / restriction, Tr	11.355	12.699	10.855	12.366	4.49E-04	1.45E-03	1.34	1.51
lpg1738	ORF		ORFs of unknown function (unique)	12.493	12.231	10.360	12.652	5.36E-01	8.31E-04	-0.26	2.29
lpg1738	ORF		ORFs of unknown function (unique)	12.423	11.892	9.601	12.033	3.13E-01	1.90E-02	-0.53	2.43

lpg1739	adenylate/guanylate cyclase transmembrane protein (ade	*gidA*	Nucleotide Metabolism	8.793	7.556	8.964	7.687	2.17E-01	4.52E-02	-1.24	-1.28
lpg1739	adenylate/guanylate cyclase transmembrane protein (ade	*gidA*	Nucleotide Metabolism	9.052	7.634	8.792	8.150	2.80E-01	3.49E-01	-1.42	-0.64
lpg1740	small ORF (154aa)		ORFs of unknown function (unique)	11.865	13.062	11.262	11.633	2.69E-02	1.57E-01	1.20	0.37
lpg1740	small ORF (154aa)		ORFs of unknown function (unique)	11.725	12.950	11.174	11.623	7.86E-02	1.90E-01	1.23	0.45
lpg1741	conserved hypothetical protein		Unknown / hypothetical proteins	9.878	11.267	10.788	11.048	1.61E-02	2.59E-01	1.39	0.26
lpg1741	conserved hypothetical protein		Unknown / hypothetical proteins	9.869	11.518	10.532	11.493	2.51E-02	7.73E-03	1.65	0.96
lpg1742	conserved hypothetical protein		Unknown / hypothetical proteins	10.087	10.877	10.141	10.851	2.83E-01	7.49E-02	0.79	0.71
lpg1742	conserved hypothetical protein		Unknown / hypothetical proteins	10.596	11.008	9.816	10.888	1.69E-01	4.85E-02	0.41	1.07
lpg1743	Fis transcriptional activator (factor for inversion stimulatio	*fis*	Transcription factors / DNA binding pro	10.993	13.543	10.358	11.851	4.76E-04	3.42E-02	2.55	1.49
lpg1743	Fis transcriptional activator (factor for inversion stimulatio	*fis*	Transcription factors / DNA binding pro	11.040	13.569	9.969	11.807	6.01E-04	1.09E-01	2.53	1.84
lpg1744	HesB family protein (iron binding protein IscA) [Fe-S] clus	*ydiC*	Transport and binding	11.587	10.588	11.529	10.989	1.56E-01	8.44E-03	-1.00	-0.54
lpg1744	HesB family protein (iron binding protein IscA) [Fe-S] clus	*ydiC*	Transport and binding	11.966	11.067	11.551	11.692	2.14E-01	8.17E-01	-0.90	0.14
lpg1745	NifU family iron binding protein, [Fe-S] cluster formation/repair protein		Signal transduction / other regulatory f	9.904	10.541	10.227	10.242	4.11E-01	9.74E-01	0.64	0.02
lpg1745	NifU family iron binding protein, [Fe-S] cluster formation/repair protein		Signal transduction / other regulatory f	10.502	10.818	10.105	10.626	4.66E-01	3.05E-01	0.32	0.52
lpg1746	cysteine desulfurase (aminotransferase NifS) (cysteine s	*iscS*	Amino Acid Metabolism	12.579	12.057	11.498	11.716	6.72E-02	4.51E-01	-0.52	0.22
lpg1746	cysteine desulfurase (aminotransferase NifS) (cysteine s	*iscS*	Amino Acid Metabolism	12.574	12.034	11.293	11.810	9.31E-02	2.77E-01	-0.54	0.52
lpg1747	RNA methyltransferase (TrmH family) (SpoU family-rRNA methylase)		DNA/RNA degradation / restriction, Tra	12.014	9.904	10.052	10.983	5.48E-03	1.03E-01	-2.11	0.93
lpg1747	RNA methyltransferase (TrmH family) (SpoU family-rRNA methylase)		DNA/RNA degradation / restriction, Tra	11.911	10.192	9.435	10.882	6.76E-02	1.19E-01	-1.72	1.45
lpg1748	inositol-1-monophosphatase (extragenic suppressor prot	*suhB*	Biosynthesis of Secondary Metabolites	10.134	10.145	10.261	10.168	9.65E-01	8.07E-01	0.01	-0.09
lpg1748	inositol-1-monophosphatase (extragenic suppressor prot	*suhB*	Biosynthesis of Secondary Metabolites	10.315	9.922	10.332	10.280	3.20E-01	7.99E-01	-0.39	-0.05
lpg1749	signal peptide peptidase (peptidase U7 family)	*sppA*	Protein fate / hydrolases / secretion	9.782	9.619	8.657	9.608	8.57E-01	1.73E-01	-0.16	0.95
lpg1749	signal peptide peptidase (peptidase U7 family)	*sppA*	Protein fate / hydrolases / secretion	10.303	10.347	8.532	10.540	9.52E-01	2.39E-02	0.04	2.01
lpg1750	ClpB protein (heat shock protein) Clp ATPase (ATP-depe	*clpB*	Detoxification / adaptation, Protein fate	11.450	11.414	12.389	12.066	9.41E-01	4.21E-01	-0.04	-0.32
lpg1750	ClpB protein (heat shock protein) Clp ATPase (ATP-depe	*clpB*	Detoxification / adaptation, Protein fate	11.305	11.620	12.290	12.056	4.85E-01	5.96E-01	0.31	-0.23
lpg1751	ORF		ORFs of unknown function (unique)	8.742	11.713	9.796	10.402	8.81E-04	3.97E-01	2.97	0.61
lpg1751	ORF		ORFs of unknown function (unique)	8.901	11.952	9.249	10.787	2.92E-05	4.94E-03	3.05	1.54
lpg1752	ORF		ORFs of unknown function (unique)	10.000	11.920	10.781	10.375	1.29E-03	2.10E-01	1.92	-0.41
lpg1752	ORF		ORFs of unknown function (unique)	10.352	12.036	10.635	10.572	3.07E-04	8.36E-01	1.68	-0.06
lpg1753	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-mes	*mpl*	Cell envelope synthesis, Amino Acid M	11.112	11.280	10.669	11.169	7.10E-01	2.79E-02	0.17	0.50
lpg1753	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-mes	*mpl*	Cell envelope synthesis, Amino Acid M	11.018	11.340	10.528	11.195	5.43E-01	2.10E-02	0.32	0.67
lpg1754	ORF		ORFs of unknown function (unique)	8.885	8.619	8.598	8.820	7.56E-01	8.22E-01	-0.27	0.22
lpg1754	ORF		ORFs of unknown function (unique)	8.885	9.399	8.599	8.836	6.02E-01	8.54E-01	0.51	0.24
lpg1755	transmembrane protein (protease?)		Named proteins of general function	10.533	8.135	8.910	9.457	1.19E-03	4.09E-01	-2.40	0.55
lpg1755	transmembrane protein (protease?)		Named proteins of general function	10.560	7.993	8.717	9.471	2.49E-03	3.02E-01	-2.57	0.75
lpg1756	flagellar protein FliJ	*fliJ*	Chemotaxis / motility / cell division	9.951	9.265	9.982	9.536	3.90E-01	2.70E-01	-0.69	-0.45
lpg1756	flagellar protein FliJ	*fliJ*	Chemotaxis / motility / cell division	9.632	9.305	9.613	9.405	6.13E-01	6.35E-01	-0.33	-0.21
lpg1757	nucleotide binding protein FliI (flagellum specific ATP syn	*fliI*	Chemotaxis / motility / cell division, Sig	10.402	10.468	9.627	10.918	7.87E-01	7.23E-03	0.07	1.29
lpg1757	nucleotide binding protein FliI (flagellum specific ATP syn	*fliI*	Chemotaxis / motility / cell division, Sig	10.576	11.991	10.051	12.136	7.34E-02	1.69E-02	1.42	2.08
lpg1758	flagellar assembly protein FliH (export of flagellar protein:	*fliH*	Transport and binding, Chemotaxis / m	10.148	9.680	11.312	10.261	4.27E-01	3.45E-02	-0.47	-1.05
lpg1758	flagellar assembly protein FliH (export of flagellar protein:	*fliH*	Transport and binding, Chemotaxis / m	10.021	10.115	11.213	10.394	7.79E-01	4.57E-02	0.09	-0.82
lpg1759	flagellar motor switch protein FliG	*fliG*	Chemotaxis / motility / cell division	7.900	7.713	9.250	7.844	7.18E-01	1.66E-01	-0.19	-1.41
lpg1759	flagellar motor switch protein FliG	*fliG*	Chemotaxis / motility / cell division	8.109	8.261	9.137	8.723	9.30E-01	7.71E-01	0.15	-0.41
lpg1760	flagellar basal body M-ring protein FliF	*fliF*	Chemotaxis / motility / cell division	11.038	10.197	10.261	9.004	3.46E-02	2.88E-01	-0.84	-1.26
lpg1760	flagellar basal body M-ring protein FliF	*fliF*	Chemotaxis / motility / cell division	10.824	10.012	10.476	9.764	2.00E-01	5.02E-03	-0.81	-0.71
lpg1761	flagellar hook-basal body protein FliE		Chemotaxis / motility / cell division	8.918	10.172	9.241	9.406	8.42E-03	5.02E-01	1.25	0.16
lpg1761	flagellar hook-basal body protein FliE		Chemotaxis / motility / cell division	8.347	10.216	9.251	9.493	9.04E-03	5.46E-01	1.87	0.24
lpg1762	sigma 54-dependent response regulator (two component	*fleR*	Chemotaxis / motility / cell division, Sig	10.705	9.807	10.257	8.852	1.39E-01	5.66E-02	-0.90	-1.40
lpg1762	sigma 54-dependent response regulator (two component	*fleR*	Chemotaxis / motility / cell division, Sig	10.756	9.309	10.293	9.369	1.26E-02	7.25E-02	-1.45	-0.92
lpg1763	sensor kinase HydH (two component sensor) (flagellar re	*flrB*	Chemotaxis / motility / cell division, Sig	9.538	9.586	9.530	8.146	9.38E-01	3.17E-01	0.05	-1.38
lpg1763	sensor kinase HydH (two component sensor) (flagellar re	*flrB*	Chemotaxis / motility / cell division, Sig	9.676	7.954	9.508	8.814	8.58E-03	6.59E-02	-1.72	-0.69
lpg1764	ATPase associated with chromosome architecture (ATPase, AAA fam		DNA/RNA degradation / restriction	11.943	10.752	12.429	11.677	2.06E-03	1.15E-02	-1.19	-0.75
lpg1764	ATPase associated with chromosome architecture (ATPase, AAA fam		DNA/RNA degradation / restriction	11.722	10.695	12.068	11.793	5.30E-02	1.53E-01	-1.03	-0.27
lpg1765	outer membrane lipoprotein carrier protein (periplasmic c	*lolA*	Transport and binding	9.761	9.928	11.771	9.076	8.10E-01	5.00E-03	0.17	-2.69
lpg1765	outer membrane lipoprotein carrier protein (periplasmic c	*lolA*	Transport and binding	10.014	10.383	11.878	9.959	5.83E-01	6.29E-02	0.37	-1.92
lpg1766	cell division protein FtsK (DNA translocase FtsK) (sporula	*ftsK*	Chemotaxis / motility / cell division	12.201	11.941	11.599	12.909	4.64E-01	1.19E-03	-0.26	1.31
lpg1766	cell division protein FtsK (DNA translocase FtsK) (sporula	*ftsK*	Chemotaxis / motility / cell division	12.233	12.176	11.651	13.075	8.22E-01	3.97E-04	-0.06	1.42
lpg1767	thioredoxin reductase	*trxB1*	Nucleotide Metabolism	11.462	13.706	11.060	13.005	8.86E-02	1.20E-02	2.24	1.94
lpg1767	thioredoxin reductase	*trxB1*	Nucleotide Metabolism	11.514	14.005	11.083	13.088	2.27E-02	5.28E-03	2.49	2.00
lpg1768	leucyl/phenylalanyl-tRNA protein transferase	*aat*	DNA/RNA degradation / restriction, Tra	12.356	11.864	10.816	11.905	2.79E-01	1.63E-02	-0.49	1.09
lpg1768	leucyl/phenylalanyl-tRNA protein transferase	*aat*	DNA/RNA degradation / restriction, Tra	12.327	12.240	10.887	12.074	6.10E-01	4.26E-03	-0.09	1.19
lpg1769	rhodanese domain protein		Named proteins of general function	11.726	10.959	11.692	10.815	3.57E-02	6.57E-04	-0.77	-0.88
lpg1769	rhodanese domain protein		Named proteins of general function	11.533	10.688	11.703	10.922	1.19E-01	6.16E-03	-0.85	-0.78
lpg1770	translation initiation factor IF-1	*infA*	Translation	13.834	12.382	10.566	12.771	1.92E-01	2.56E-02	-1.45	2.20
lpg1770	translation initiation factor IF-1	*infA*	Translation	13.483	11.844	9.883	12.288	2.41E-01	6.67E-02	-1.64	2.40

lpg1771	peptide maturation protein PmbA (microcin (peptide antib	*pmbA*	Named proteins of general function	10.267	11.808	9.855	11.036	1.71E-03	1.41E-02	1.54	1.18
lpg1771	peptide maturation protein PmbA (microcin (peptide antib	*pmbA*	Named proteins of general function	10.175	11.768	9.530	11.182	2.29E-04	2.76E-03	1.59	1.65
lpg1772	hypothetical (lipoprotein?)		Unknown / hypothetical proteins	10.859	10.381	7.709	10.380	5.16E-01	2.44E-02	-0.48	2.67
lpg1772	hypothetical (lipoprotein?)		Unknown / hypothetical proteins	11.062	11.466	7.988	10.918	6.37E-01	5.46E-02	0.40	2.93
lpg1773	protein associating with small stress protein PASS1	*Pass1*	Named proteins of general function	10.301	10.674	10.387	9.922	2.26E-01	2.38E-01	0.37	-0.46
lpg1773	protein associating with small stress protein PASS1	*Pass1*	Named proteins of general function	9.940	10.637	10.190	9.937	1.47E-01	5.98E-01	0.70	-0.25
lpg1774	ribonucleoside-diphosphate reductase, alpha subunit (rib	*nrdA*	Nucleotide Metabolism	12.479	12.523	11.994	12.807	8.96E-01	4.13E-03	0.04	0.81
lpg1774	ribonucleoside-diphosphate reductase, alpha subunit (rib	*nrdA*	Nucleotide Metabolism	12.571	12.519	11.921	12.844	8.61E-01	2.42E-04	-0.05	0.92
lpg1775	ribonucleoside-diphosphate reductase, beta subunit (ribo	*nrdB*	Nucleotide Metabolism	10.259	10.809	10.780	10.802	1.54E-01	8.46E-01	0.55	0.02
lpg1775	ribonucleoside-diphosphate reductase, beta subunit (ribo	*nrdB*	Nucleotide Metabolism	10.222	10.688	10.509	10.729	2.10E-01	1.93E-01	0.47	0.22
lpg1776	small ORF (161aa)		ORFs of unknown function (unique)	13.908	13.769	12.592	13.907	7.56E-01	1.27E-02	-0.14	1.32
lpg1776	small ORF (161aa)		ORFs of unknown function (unique)	13.873	14.104	12.486	14.084	6.51E-01	6.69E-03	0.23	1.60
lpg1777	lysine tRNA synthetase, heat inducible	*lysU*	Amino Acid Metabolism, Translation	12.925	12.719	12.406	13.511	3.83E-01	3.35E-04	-0.21	1.10
lpg1777	lysine tRNA synthetase, heat inducible	*lysU*	Amino Acid Metabolism, Translation	13.021	12.829	12.388	13.511	2.71E-01	2.20E-04	-0.19	1.12
lpg1778	peptide chain release factor 2 (RF-2)	*prfB*	Translation	10.799	10.854	10.617	12.282	9.05E-01	1.46E-03	0.06	1.66
lpg1778	peptide chain release factor 2 (RF-2)	*prfB*	Translation	10.630	11.260	10.357	12.752	5.07E-01	3.43E-03	0.63	2.39
lpg1779	hypothetical		Unknown / hypothetical proteins	9.853	8.931	11.478	9.048	3.58E-02	3.90E-05	-0.92	-2.43
lpg1779	hypothetical		Unknown / hypothetical proteins	9.781	9.651	11.502	9.289	5.31E-01	1.82E-04	-0.13	-2.21
lpg1780	flagellar motor protein MotB (probable chemotaxis protei	*motB*	Chemotaxis / motility / cell division	8.513	8.139	9.063	8.439	4.05E-01	2.97E-01	-0.37	-0.62
lpg1780	flagellar motor protein MotB (probable chemotaxis protei	*motB*	Chemotaxis / motility / cell division	8.721	8.290	9.266	8.957	5.74E-01	7.72E-01	-0.43	-0.31
lpg1781	flagellar motor protein MotA (chemotaxis MotA protein)	*motA*	Chemotaxis / motility / cell division	9.602	8.785	11.345	7.019	1.71E-01	5.44E-04	-0.82	-4.33
lpg1781	flagellar motor protein MotA (chemotaxis MotA protein)	*motA*	Chemotaxis / motility / cell division	9.499	7.932	11.416	7.978	7.21E-03	1.78E-06	-1.57	-3.44
lpg1782	flagellar biosynthesis sigma factor FliA (motility sigma fac	*fliA*	Chemotaxis / motility / cell division, Tra	9.420	9.150	12.016	7.067	7.09E-01	2.67E-03	-0.27	-4.95
lpg1782	flagellar biosynthesis sigma factor FliA (motility sigma fac	*fliA*	Chemotaxis / motility / cell division, Tra	9.275	8.745	11.993	8.801	5.14E-01	3.85E-03	-0.53	-3.19
lpg1783	flagellar biosynthesis MinD (septum-site determining protein, cell divis		Chemotaxis / motility / cell division, Tra	10.762	9.958	12.588	9.443	1.61E-01	1.17E-02	-0.80	-3.15
lpg1783	flagellar biosynthesis MinD (septum-site determining protein, cell divis		Chemotaxis / motility / cell division, Tra	10.702	10.401	12.506	10.238	5.78E-01	4.84E-03	-0.30	-2.27
lpg1784	flagellar GTP-binding protein FlhF (flagellar biosynthesis protein FlhF		Chemotaxis / motility / cell division	9.452	9.405	12.121	7.881	9.60E-01	4.78E-04	-0.05	-4.24
lpg1784	flagellar GTP-binding protein FlhF (flagellar biosynthesis protein FlhF		Chemotaxis / motility / cell division	9.323	9.620	12.086	8.247	7.79E-01	3.05E-02	0.30	-3.84
lpg1785	flagellar biosynthetic protein FlhA	*flhA*	Chemotaxis / motility / cell division	9.554	10.866	10.747	10.634	6.03E-02	8.05E-01	1.31	-0.11
lpg1785	flagellar biosynthetic protein FlhA	*flhA*	Chemotaxis / motility / cell division	9.709	11.299	10.782	11.023	5.75E-02	7.03E-01	1.59	0.24
lpg1786	flagellar biosynthetic protein FlhB	*flhB*	Chemotaxis / motility / cell division	8.409	8.015	8.549	8.552	4.89E-01	9.98E-01	-0.39	0.00
lpg1786	flagellar biosynthetic protein FlhB	*flhB*	Chemotaxis / motility / cell division	8.580	8.450	8.131	9.039	8.47E-01	2.92E-01	-0.13	0.91
lpg1787	flagellar biosynthetic protein FliR	*fliR*	Chemotaxis / motility / cell division	9.589	9.204	12.665	9.431	5.50E-01	6.56E-04	-0.38	-3.23
lpg1787	flagellar biosynthetic protein FliR	*fliR*	Chemotaxis / motility / cell division	9.444	9.546	12.614	9.579	8.77E-01	1.47E-03	0.10	-3.03
lpg1788	flagellar biosynthetic protein FliQ	*fliQ*	Chemotaxis / motility / cell division	9.613	8.671	9.671	8.714	5.54E-01	2.80E-01	-0.94	-0.96
lpg1788	flagellar biosynthetic protein FliQ	*fliQ*	Chemotaxis / motility / cell division	9.431	9.637	8.495	9.535	6.37E-01	1.53E-01	0.21	1.04
lpg1789	flagellar biosynthetic protein FliP		Chemotaxis / motility / cell division	9.453	8.457	10.128	7.710	1.87E-01	5.58E-03	-1.00	-2.42
lpg1789	flagellar biosynthetic protein FliP		Chemotaxis / motility / cell division	9.371	8.471	10.245	8.824	2.21E-01	1.56E-02	-0.90	-1.42
lpg1790	flagellar assembly protein FliO	*fliO*	Chemotaxis / motility / cell division	9.176	9.323	9.534	8.937	7.90E-01	3.65E-01	0.15	-0.60
lpg1790	flagellar assembly protein FliO	*fliO*	Chemotaxis / motility / cell division	9.127	9.157	9.505	9.006	9.58E-01	5.12E-01	0.03	-0.50
lpg1791	flagellar motor switch protein FliN		Chemotaxis / motility / cell division	9.471	9.404	9.665	9.549	8.42E-01	7.17E-01	-0.07	-0.12
lpg1791	flagellar motor switch protein FliN		Chemotaxis / motility / cell division	8.893	8.568	9.560	9.516	3.83E-01	9.11E-01	-0.33	-0.04
lpg1792	flagellar protein (flagellar motor switch protein FliM)	*fliM*	Chemotaxis / motility / cell division	10.901	11.055	12.758	11.431	7.45E-01	1.54E-02	0.15	-1.33
lpg1792	flagellar protein (flagellar motor switch protein FliM)	*fliM*	Chemotaxis / motility / cell division	10.964	11.316	12.745	11.486	4.25E-01	2.19E-02	0.35	-1.26
lpg1793	small ORF (84aa)		ORFs of unknown function (unique)	8.184	7.933	10.630	8.379	8.58E-01	1.06E-01	-0.25	-2.25
lpg1793	small ORF (84aa)		ORFs of unknown function (unique)	7.769	7.961	10.622	8.970	8.88E-01	2.42E-01	0.19	-1.65
lpg1794	oxidoreductase (L-gululonolactone oxidase) (FAD/FMN containing de		Named proteins of general function	9.923	9.964	8.638	10.318	9.60E-01	4.00E-03	0.04	1.68
lpg1794	oxidoreductase (L-gululonolactone oxidase) (FAD/FMN containing de		Named proteins of general function	10.789	9.639	8.478	10.268	4.88E-02	5.80E-03	-1.15	1.79
lpg1795	oxidoreductase, short chain dehydrogenase/reductase family, (lipoprc		Named proteins of general function	10.659	10.323	11.186	10.519	7.72E-01	4.66E-01	-0.34	-0.67
lpg1795	oxidoreductase, short chain dehydrogenase/reductase family, (lipoprc		Named proteins of general function	10.063	10.297	10.421	10.568	7.69E-01	8.46E-01	0.23	0.15
lpg1796	transcriptional regulator, LysR family		Transcription factors / DNA binding prc	10.435	8.575	11.403	8.216	2.82E-03	4.03E-03	-1.86	-3.19
lpg1796	transcriptional regulator, LysR family		Transcription factors / DNA binding prc	10.589	9.212	11.509	8.944	5.90E-03	5.34E-04	-1.38	-2.56
lpg1797	ORF		ORFs of unknown function (unique)	9.436	9.540	10.010	8.586	8.33E-01	3.04E-01	0.10	-1.42
lpg1797	ORF		ORFs of unknown function (unique)	9.689	9.878	9.885	9.010	6.27E-01	2.84E-01	0.19	-0.87
lpg1798	ORF		ORFs of unknown function (unique)	9.514	9.938	9.197	9.143	5.41E-01	9.33E-01	0.42	-0.05
lpg1798	ORF		ORFs of unknown function (unique)	9.702	10.236	9.264	9.367	3.76E-01	8.60E-01	0.53	0.10
lpg1799	alanyl tRNA synthetase	*alaS*	Amino Acid Metabolism, Translation	11.481	11.637	10.046	12.176	5.92E-01	3.44E-02	0.16	2.13
lpg1799	alanyl tRNA synthetase	*alaS*	Amino Acid Metabolism, Translation	11.782	11.652	10.035	12.338	4.62E-01	6.66E-03	-0.13	2.30
lpg1800	regulatory protein RecX		Transcription factors / DNA binding prc	12.934	12.841	12.626	12.633	8.40E-01	9.83E-01	-0.09	0.01
lpg1800	regulatory protein RecX		Transcription factors / DNA binding prc	12.988	12.915	12.622	13.010	8.81E-01	8.77E-02	-0.07	0.39
lpg1801	RecA bacterial DNA recombination protein (recombinase	*recA*	Replication and Repair	13.707	13.813	12.531	13.505	7.28E-01	2.45E-02	0.11	0.97
lpg1801	RecA bacterial DNA recombination protein (recombinase	*recA*	Replication and Repair	13.678	13.805	12.509	13.542	6.66E-01	1.93E-02	0.13	1.03
lpg1802	small ORF (106aa)		ORFs of unknown function (unique)	10.861	11.744	10.352	10.113	5.89E-02	6.75E-01	0.88	-0.24
lpg1802	small ORF (106aa)		ORFs of unknown function (unique)	10.818	11.487	10.509	10.271	2.79E-01	7.27E-01	0.67	-0.24

lpg1803	hypothetical		Unknown / hypothetical proteins	8.237	9.700	7.841	9.618	3.85E-02	1.14E-02	1.46	1.78
lpg1803	hypothetical		Unknown / hypothetical proteins	9.008	9.767	7.865	9.934	1.72E-01	1.13E-02	0.76	2.07
lpg1804	hypothetical 17.2kDa protein COG1546 CinA-related protein, compet		Detoxification / adaptation	8.489	8.741	9.450	9.163	6.93E-01	3.68E-01	0.25	-0.29
lpg1804	hypothetical 17.2kDa protein COG1546 CinA-related protein, compet		Detoxification / adaptation	8.743	8.943	9.393	9.654	7.71E-01	5.00E-01	0.20	0.26
lpg1805	DNA mismatch repair protein MutS	*mutS*	Replication and Repair	11.616	11.109	10.781	11.310	1.56E-01	1.08E-01	-0.51	0.53
lpg1805	DNA mismatch repair protein MutS	*mutS*	Replication and Repair	10.721	11.889	10.004	11.930	4.04E-01	3.65E-02	1.17	1.93
lpg1806	outer membrane protein		Named proteins of general function	10.503	9.517	9.475	10.383	3.98E-01	3.36E-01	-0.99	0.91
lpg1806	outer membrane protein		Named proteins of general function	10.548	9.912	9.204	10.974	6.45E-01	1.56E-01	-0.64	1.77
lpg1807	periplasmic protein		Named proteins of general function	10.518	9.000	9.862	8.835	3.17E-02	3.93E-02	-1.52	-1.03
lpg1807	periplasmic protein		Named proteins of general function	10.498	10.207	9.376	9.747	7.59E-01	7.39E-01	-0.29	0.37
lpg1808	porphobilinogen synthase (delta-aminolevulinic acid dehy	*hemB*	Metabolism of Cofactors and Vitamins	10.147	9.406	10.266	10.395	3.81E-02	5.93E-01	-0.74	0.13
lpg1808	porphobilinogen synthase (delta-aminolevulinic acid dehy	*hemB*	Metabolism of Cofactors and Vitamins	10.583	11.278	10.356	10.874	1.28E-01	7.19E-02	0.70	0.52
lpg1809	small ORF (130aa)		ORFs of unknown function (unique)	14.643	14.252	13.307	14.709	7.24E-01	1.79E-01	-0.39	1.40
lpg1809	small ORF (130aa)		ORFs of unknown function (unique)	14.783	14.663	13.326	14.991	8.76E-01	3.83E-02	-0.12	1.67
lpg1810	long chain fatty acid transporter (fatty acid outer membrane porin)		Transport and binding	13.930	14.229	12.582	13.771	5.53E-01	1.95E-02	0.30	1.19
lpg1810	long chain fatty acid transporter (fatty acid outer membrane porin)		Transport and binding	13.786	14.236	12.550	13.882	3.52E-01	1.36E-02	0.45	1.33
lpg1811	aspartokinase (aspartate kinase, lysine sensitive)	*lysC*	Amino Acid Metabolism	10.517	13.110	9.952	12.848	5.90E-03	3.10E-04	2.59	2.90
lpg1811	aspartokinase (aspartate kinase, lysine sensitive)	*lysC*	Amino Acid Metabolism	11.369	13.096	9.335	12.813	8.03E-05	1.05E-03	1.73	3.48
lpg1812	ATP-dependent DNA helicase (UvrD/Rep helicase) (ATP dependent r		Replication and Repair	11.653	9.341	8.668	9.302	2.86E-04	4.95E-01	-2.31	0.63
lpg1812	ATP-dependent DNA helicase (UvrD/Rep helicase) (ATP dependent r		Replication and Repair	11.427	9.436	8.979	9.637	2.67E-03	3.36E-01	-1.99	0.66
lpg1813	ATPase (Mrp), MRP protein, ATP binding protein	*mrp*	Named proteins of general function	10.844	11.646	11.779	12.151	2.04E-02	2.44E-01	0.80	0.37
lpg1813	ATPase (Mrp), MRP protein, ATP binding protein	*mrp*	Named proteins of general function	10.829	11.115	11.489	11.939	3.99E-01	5.37E-02	0.29	0.45
lpg1814	hypothetical protein		Unknown / hypothetical proteins	10.442	8.893	7.501	8.373	7.36E-02	5.84E-01	-1.55	0.87
lpg1814	hypothetical protein		Unknown / hypothetical proteins	10.682	8.695	7.849	8.796	1.67E-01	5.16E-01	-1.99	0.95
lpg1815	hydrogen peroxide-inducible genes activator OxyR (oxida	*oxyR*	Detoxification / adaptation, Transcripti	9.740	8.954	8.724	8.619	1.49E-01	7.97E-01	-0.79	-0.10
lpg1815	hydrogen peroxide-inducible genes activator OxyR (oxida	*oxyR*	Detoxification / adaptation, Transcripti	9.881	8.899	8.897	8.946	1.26E-02	9.30E-01	-0.98	0.05
lpg1816	major facilitator family transporter (multidrug efflux transporter, MFS f		Transport and binding	10.343	8.249	10.600	9.256	3.85E-02	1.54E-02	-2.09	-1.34
lpg1816	major facilitator family transporter (multidrug efflux transporter, MFS f		Transport and binding	10.209	9.733	10.424	9.936	3.00E-01	2.87E-01	-0.48	-0.49
lpg1817	ORF		ORFs of unknown function (unique)	11.417	10.937	11.404	10.474	4.19E-01	2.03E-02	-0.48	-0.93
lpg1817	ORF		ORFs of unknown function (unique)	11.358	10.953	11.292	10.659	4.72E-01	3.85E-02	-0.40	-0.63
lpg1818	tetraacyl disaccharide 4'-kinase		Metabolism of Complex Carbohydrate	10.168	9.238	9.494	8.586	7.71E-02	5.00E-02	-0.93	-0.91
lpg1818	tetraacyl disaccharide 4'-kinase		Metabolism of Complex Carbohydrate	10.214	8.837	9.799	9.457	3.97E-02	5.05E-01	-1.38	-0.34
lpg1819	ABC transporter, ATP binding/permease protein MsbA (multicopy sup		Unknown / hypothetical proteins	11.359	9.081	8.430	9.613	2.33E-04	2.33E-01	-2.28	1.18
lpg1819	ABC transporter, ATP binding/permease protein MsbA (multicopy sup		Unknown / hypothetical proteins	11.107	8.798	8.109	9.541	4.50E-03	1.31E-01	-2.31	1.43
lpg1820	ORF		ORFs of unknown function (unique)	11.393	10.817	12.058	10.866	1.30E-01	5.55E-04	-0.58	-1.19
lpg1820	ORF		ORFs of unknown function (unique)	11.508	11.064	12.108	10.977	5.01E-02	5.35E-03	-0.44	-1.13
lpg1821	dihydroorotate oxidase (dihydroorotate dehydrogenase)	*pyrD*	Nucleotide Metabolism	11.040	10.139	10.001	10.469	6.57E-03	2.47E-01	-0.90	0.47
lpg1821	dihydroorotate oxidase (dihydroorotate dehydrogenase)	*pyrD*	Nucleotide Metabolism	11.091	10.408	9.702	10.590	2.44E-02	7.59E-02	-0.68	0.89
lpg1822	ORF		ORFs of unknown function (unique)	11.322	10.833	11.124	9.894	4.75E-01	2.78E-02	-0.49	-1.23
lpg1822	ORF		ORFs of unknown function (unique)	11.356	11.443	10.893	10.612	7.40E-01	5.52E-01	0.09	-0.28
lpg1823	conserved hypothetical protein		Unknown / hypothetical proteins	12.288	12.782	11.831	12.200	3.92E-01	5.16E-01	0.49	0.37
lpg1823	conserved hypothetical protein		Unknown / hypothetical proteins	12.376	13.472	11.853	12.735	1.31E-03	8.01E-03	1.10	0.88
lpg1824	acyl CoA dehydrogenase (isovaleryl CoA dehydrogenase)		Amino Acid Metabolism	12.780	13.022	11.869	12.874	5.47E-01	2.32E-02	0.24	1.00
lpg1824	acyl CoA dehydrogenase (isovaleryl CoA dehydrogenase)		Amino Acid Metabolism	12.808	13.044	11.884	12.976	5.18E-01	1.46E-02	0.24	1.09
lpg1825	acyl CoA C-acetyltransferase (acetoacetyl CoA thiolase)	*atoB*	Lipid Metabolism, Amino Acid Metabol	13.370	14.432	13.870	13.842	4.35E-05	8.52E-01	1.06	-0.03
lpg1825	acyl CoA C-acetyltransferase (acetoacetyl CoA thiolase)	*atoB*	Lipid Metabolism, Amino Acid Metabol	13.468	14.459	13.895	13.910	3.62E-05	8.98E-01	0.99	0.02
lpg1826	hypothetical		Unknown / hypothetical proteins	13.051	12.761	12.082	12.954	4.46E-01	1.03E-02	-0.29	0.87
lpg1826	hypothetical		Unknown / hypothetical proteins	13.022	12.926	12.041	13.059	6.40E-01	1.80E-03	-0.10	1.02
lpg1827	propionyl CoA carboxylase beta subunit (3-methylcrotonyl CoA carbo		Amino Acid Metabolism, Carbohydrate	11.300	11.274	11.759	11.478	9.64E-01	1.33E-01	-0.03	-0.28
lpg1827	propionyl CoA carboxylase beta subunit (3-methylcrotonyl CoA carbo		Amino Acid Metabolism, Carbohydrate	11.259	11.255	11.674	11.397	9.94E-01	2.55E-01	0.00	-0.28
lpg1828	enoyl CoA hydratase/isomerase (crotonase)		Lipid Metabolism, Amino Acid Metabol	12.050	12.524	11.509	12.485	1.64E-01	3.88E-03	0.47	0.98
lpg1828	enoyl CoA hydratase/isomerase (crotonase)		Lipid Metabolism, Amino Acid Metabol	12.016	12.456	11.466	12.567	1.97E-01	3.93E-03	0.44	1.10
lpg1829	acyl CoA carboxylase subunit alpha subunit (3-methylcrotonyl-CoA ca		Lipid Metabolism	11.494	11.886	10.641	11.462	5.47E-01	2.54E-01	0.39	0.82
lpg1829	acyl CoA carboxylase subunit alpha subunit (3-methylcrotonyl-CoA ca		Lipid Metabolism	11.173	11.582	10.185	11.385	3.74E-01	7.01E-02	0.41	1.20
lpg1830	hydroxymethylglutaryl-CoA lyase (3-hydroxy-3-methylglut	*mvaB*	Lipid Metabolism, Amino Acid Metabol	11.108	10.048	10.748	10.126	1.53E-02	1.10E-01	-1.06	-0.62
lpg1830	hydroxymethylglutaryl-CoA lyase (3-hydroxy-3-methylglut	*mvaB*	Lipid Metabolism, Amino Acid Metabol	11.223	10.215	10.382	10.015	5.19E-03	5.66E-01	-1.01	-0.37
lpg1831	acetoacetyl CoA synthetase		Carbohydrate Metabolism	11.698	11.906	13.444	11.308	5.99E-01	3.69E-02	0.21	-2.14
lpg1831	acetoacetyl CoA synthetase		Carbohydrate Metabolism	11.649	11.605	13.460	11.606	9.47E-01	2.80E-02	-0.04	-1.85
lpg1832	small ORF (138aa) (similar to putative VirA/G regulated VirK gene of		Toxin production / other pathogen func	12.236	11.144	10.068	10.547	1.31E-01	5.24E-01	-1.09	0.48
lpg1832	small ORF (138aa) (similar to putative VirA/G regulated VirK gene of		Toxin production / other pathogen func	12.294	11.215	10.066	10.730	1.20E-01	3.89E-01	-1.08	0.66
lpg1833	D-methionine transport ATP binding protein MetN (ABC t	*metN*	Transport and binding	9.959	9.618	9.312	9.391	3.94E-01	8.85E-01	-0.34	0.08
lpg1833	D-methionine transport ATP binding protein MetN (ABC t	*metN*	Transport and binding	9.766	9.498	8.722	9.756	5.24E-01	9.09E-02	-0.27	1.03
lpg1834	ATP binding protein, permease protein (D-methionine tra	*metI*	Transport and binding	10.672	10.846	10.028	10.431	6.47E-01	2.32E-01	0.17	0.40
lpg1834	ATP binding protein, permease protein (D-methionine tra	*metI*	Transport and binding	10.498	10.715	9.960	10.462	5.50E-01	1.18E-01	0.22	0.50

lpg1835	29 kDa immunogenic protein (L. pneumophila), lipoprotein (ABC trans		Transport and binding	12.453	13.167	11.739	12.300	4.33E-02	1.47E-02	0.71	0.56
lpg1835	29 kDa immunogenic protein (L. pneumophila), lipoprotein (ABC trans		Transport and binding	12.470	13.219	11.793	12.377	1.59E-02	6.34E-03	0.75	0.58
lpg1836	coiled coil domain protein	*ceg25*	Unknown / hypothetical proteins	10.248	12.105	11.102	11.697	8.03E-04	1.32E-01	1.86	0.59
lpg1836	coiled coil domain protein	*ceg25*	Unknown / hypothetical proteins	9.905	12.115	11.020	11.736	9.61E-06	1.10E-01	2.21	0.72
lpg1837	SAM-dependent methyltransferase		Named proteins of general function	11.242	10.049	10.826	10.679	2.36E-03	6.25E-01	-1.19	-0.15
lpg1837	SAM-dependent methyltransferase		Named proteins of general function	11.388	10.229	11.053	10.957	3.72E-04	4.99E-01	-1.16	-0.10
lpg1838	histidinol phosphate phosphatase (histidinol phosphatase)		Amino Acid Metabolism	10.629	10.142	8.793	10.958	3.28E-01	1.02E-01	-0.49	2.16
lpg1838	histidinol phosphate phosphatase (histidinol phosphatase)		Amino Acid Metabolism	10.704	9.737	9.059	11.488	2.69E-01	1.32E-02	-0.97	2.43
lpg1839	glycyl tRNA synthetase, beta subunit	*glyS*	Amino Acid Metabolism, Translation	11.398	10.035	9.731	11.484	2.23E-04	1.14E-02	-1.36	1.75
lpg1839	glycyl tRNA synthetase, beta subunit	*glyS*	Amino Acid Metabolism, Translation	10.967	9.963	9.059	11.606	6.47E-02	1.43E-03	-1.00	2.55
lpg1840	glycyl tRNA synthetase, alpha subunit	*glyQ*	Amino Acid Metabolism, Translation	12.594	11.505	10.724	12.731	1.14E-01	6.00E-03	-1.09	2.01
lpg1840	glycyl tRNA synthetase, alpha subunit	*glyQ*	Amino Acid Metabolism, Translation	11.989	11.612	10.271	12.726	7.21E-01	3.52E-03	-0.38	2.46
lpg1841	27 kDa outer membrane protein	*com1*	Named proteins of general function	14.291	13.285	12.810	12.941	4.31E-01	8.98E-01	-1.01	0.13
lpg1841	27 kDa outer membrane protein	*com1*	Named proteins of general function	14.414	13.778	12.847	13.448	3.49E-01	2.92E-01	-0.64	0.60
lpg1842	DNA dependent ATPase I and helicase II (DNA helicase I	*uvrD*	Replication and Repair	10.749	10.259	11.160	10.551	3.90E-02	1.14E-02	-0.49	-0.61
lpg1842	DNA dependent ATPase I and helicase II (DNA helicase I	*uvrD*	Replication and Repair	10.793	10.326	11.161	10.705	3.19E-01	3.70E-02	-0.47	-0.46
lpg1843	proline iminopeptidase (prolyl aminopeptidase)	*pip*	Amino Acid Metabolism	11.074	11.923	9.436	11.400	1.58E-01	1.99E-02	0.85	1.96
lpg1843	proline iminopeptidase (prolyl aminopeptidase)	*pip*	Amino Acid Metabolism	11.051	11.062	9.059	11.168	9.93E-01	2.44E-02	0.01	2.11
lpg1844	D-tyrosyl-tRNA (Tyr) deacylase	*dtD*	DNA/RNA degradation / restriction, Tra	10.794	10.108	9.080	10.124	3.17E-01	1.04E-01	-0.69	1.04
lpg1844	D-tyrosyl-tRNA (Tyr) deacylase	*dtD*	DNA/RNA degradation / restriction, Tra	11.255	11.266	9.254	10.945	9.90E-01	1.95E-01	0.01	1.69
lpg1845	lipoprotein VacJ, peptidoglycan stabilization, virulence fa	*vacJ*	Cell envelope synthesis, Toxin product	12.078	11.636	9.469	11.307	3.32E-01	2.13E-03	-0.44	1.84
lpg1845	lipoprotein VacJ, peptidoglycan stabilization, virulence fa	*vacJ*	Cell envelope synthesis, Toxin product	11.915	11.644	9.254	11.327	6.08E-01	2.17E-03	-0.27	2.07
lpg1846	glutathione synthetase	*gshB*	Amino Acid Metabolism, Metabolism o	10.116	7.743	8.745	9.377	6.20E-02	1.37E-01	-2.37	0.63
lpg1846	glutathione synthetase	*gshB*	Amino Acid Metabolism, Metabolism o	10.242	8.777	9.123	10.116	1.30E-01	8.63E-02	-1.47	0.99
lpg1847	glutamate-cysteine ligase		Amino Acid Metabolism, Metabolism o	11.508	10.968	11.933	11.436	3.55E-01	4.71E-01	-0.54	-0.50
lpg1847	glutamate-cysteine ligase		Amino Acid Metabolism, Metabolism o	11.339	11.442	12.056	11.726	7.24E-01	1.23E-01	0.10	-0.33
lpg1848	ABC transporter, transmembrane permease?		Transport and binding	10.562	9.938	9.451	9.893	1.15E-01	3.27E-01	-0.62	0.44
lpg1848	ABC transporter, transmembrane permease?		Transport and binding	10.537	10.160	9.545	10.338	3.74E-01	9.63E-02	-0.38	0.79
lpg1849	small ORF (93aa)?		ORFs of unknown function (unique)	12.000	11.804	11.047	10.840	6.30E-01	6.22E-01	-0.20	-0.21
lpg1849	small ORF (93aa)?		ORFs of unknown function (unique)	12.209	11.726	11.123	10.933	5.51E-02	6.67E-01	-0.48	-0.19
lpg1850	rhodanese domain protein (dinucleotide utilizing enzymes involved in		Metabolism of Cofactors and Vitamins	11.338	10.697	11.328	10.148	1.60E-02	1.66E-04	-0.64	-1.18
lpg1850	rhodanese domain protein (dinucleotide utilizing enzymes involved in		Metabolism of Cofactors and Vitamins	11.271	10.771	11.261	10.612	2.33E-01	9.27E-03	-0.50	-0.65
lpg1851	ORF		ORFs of unknown function (unique)	13.656	15.486	13.839	12.489	4.94E-05	2.31E-06	1.83	-1.35
lpg1851	ORF		ORFs of unknown function (unique)	13.615	15.400	13.827	12.542	1.01E-04	7.25E-07	1.78	-1.29
lpg1852	alkaline phosphatase (alkaline phosphomonoesterase) (Ca2+ ATPase		Named proteins of general function	10.119	11.052	9.073	12.495	6.76E-02	3.35E-04	0.93	3.42
lpg1852	alkaline phosphatase (alkaline phosphomonoesterase) (Ca2+ ATPase		Named proteins of general function	9.946	11.389	8.960	13.032	1.76E-02	7.26E-05	1.44	4.07
lpg1853	uridine kinase (uridine/cytidine kinase)	*udk*	Nucleotide Metabolism	11.576	11.040	8.730	12.250	3.87E-01	1.34E-03	-0.54	3.52
lpg1853	uridine kinase (uridine/cytidine kinase)	*udk*	Nucleotide Metabolism	11.740	11.817	7.705	12.247	9.25E-01	1.28E-02	0.08	4.54
lpg1854	enoyl reductase (NADH dependent enoyl ACP reductase	*fabI*	Lipid Metabolism	10.976	10.176	9.646	10.021	1.37E-01	5.44E-01	-0.80	0.37
lpg1854	enoyl reductase (NADH dependent enoyl ACP reductase	*fabI*	Lipid Metabolism	10.042	10.313	9.458	10.116	8.32E-01	2.55E-01	0.27	0.66
lpg1855	peptidyl prolyl cis-trans isomerase D	*ppiD*	Protein fate / hydrolases / secretion	10.148	8.966	8.891	9.537	8.85E-02	4.07E-01	-1.18	0.65
lpg1855	peptidyl prolyl cis-trans isomerase D	*ppiD*	Protein fate / hydrolases / secretion	10.321	9.407	8.227	9.481	1.51E-01	2.28E-01	-0.91	1.25
lpg1856	tRNA-Asp		tRNA	12.525	14.223	12.378	13.782	1.64E-04	5.01E-03	1.70	1.40
lpg1856	tRNA-Asp		tRNA	12.562	14.346	12.338	13.963	6.24E-05	2.35E-03	1.78	1.63
lpg1857	tRNA-Val		tRNA	10.861	12.391	11.149	11.213	1.73E-03	9.53E-01	1.53	0.06
lpg1857	tRNA-Val		tRNA	10.923	12.429	10.923	12.115	1.22E-03	7.75E-02	1.51	1.19
lpg1858	HupB DNA binding protein HU-beta (HU-1)/bending (bac	*hupB*	Transcription factors / DNA binding pro	15.265	15.525	15.042	15.112	3.18E-01	6.55E-01	0.26	0.07
lpg1858	HupB DNA binding protein HU-beta (HU-1)/bending (bac	*hupB*	Transcription factors / DNA binding pro	15.065	15.632	14.914	15.081	4.92E-02	2.62E-01	0.57	0.17
lpg1859	ATP-dependent protease La	*lon*	Protein fate / hydrolases / secretion	12.210	11.852	12.196	11.514	4.24E-01	2.05E-02	-0.36	-0.68
lpg1859	ATP-dependent protease La	*lon*	Protein fate / hydrolases / secretion	12.350	11.746	12.197	11.782	2.80E-01	1.18E-01	-0.60	-0.42
lpg1860	ATP-dependent Clp protease, ATP binding subunit ClpX	*clpX*	Protein fate / hydrolases / secretion	12.522	11.900	11.066	11.898	6.33E-02	1.14E-01	-0.62	0.83
lpg1860	ATP-dependent Clp protease, ATP binding subunit ClpX	*clpX*	Protein fate / hydrolases / secretion	12.198	12.561	11.078	12.561	5.60E-01	4.72E-02	0.36	1.48
lpg1861	ATP-dependent Clp protease, proteolytic subunit ClpP	*clpP*	Detoxification / adaptation, Protein fate	14.377	13.743	13.123	14.818	6.54E-02	1.48E-04	-0.63	1.69
lpg1861	ATP-dependent Clp protease, proteolytic subunit ClpP	*clpP*	Detoxification / adaptation, Protein fate	14.633	13.971	13.143	14.843	1.10E-01	1.29E-04	-0.66	1.70
lpg1862	trigger factor TF (FKBP-type peptidyl prolyl cis-trans ison	*tig*	Toxin production / other pathogen func	13.682	13.141	12.259	14.428	3.21E-01	2.89E-04	-0.54	2.17
lpg1862	trigger factor TF (FKBP-type peptidyl prolyl cis-trans ison	*tig*	Toxin production / other pathogen func	13.552	13.139	12.226	14.429	4.05E-01	2.49E-04	-0.41	2.20
lpg1863	tRNA-Leu		tRNA	12.394	12.774	11.957	13.413	3.57E-01	3.15E-03	0.38	1.46
lpg1863	tRNA-Leu		tRNA	12.313	12.564	11.550	13.433	6.00E-01	3.86E-03	0.25	1.88
lpg1864	tRNA-His		tRNA	12.389	11.254	11.763	12.833	1.41E-01	2.26E-01	-1.13	1.07
lpg1864	tRNA-His		tRNA	12.565	11.467	11.818	13.262	5.18E-02	9.72E-03	-1.10	1.44
lpg1865	tRNA-Arg		tRNA	11.770	8.887	10.085	9.966	9.44E-04	8.82E-01	-2.88	-0.12
lpg1865	tRNA-Arg		tRNA	11.429	9.359	9.947	10.466	1.77E-03	4.75E-01	-2.07	0.52
lpg1866	tRNA-Pro		tRNA	10.623	9.677	9.957	10.698	4.80E-01	1.97E-01	-0.95	0.74
lpg1866	tRNA-Pro		tRNA	11.177	10.302	9.827	10.989	8.91E-02	4.87E-02	-0.88	1.16

lpg1867	site specific recombinase, phage integrase		Viral functions / Phage / Transposases	10.518	10.483	9.437	10.605	9.00E-01	3.66E-04	-0.04	1.17
lpg1867	site specific recombinase, phage integrase		Viral functions / Phage / Transposases	10.131	10.632	8.948	10.563	1.02E-01	7.62E-04	0.50	1.61
lpg1868	ABC transporter, ATP-binding component (ATPase component of ABC		Transport and binding	9.221	8.353	8.765	8.763	4.89E-02	9.96E-01	-0.87	0.00
lpg1868	ABC transporter, ATP-binding component (ATPase component of ABC		Transport and binding	9.553	8.935	8.959	9.232	3.70E-01	6.95E-01	-0.62	0.27
lpg1869	ribonuclease III (dsRNA-specific ribonuclease) (RNAse II	*rnc*	DNA/RNA degradation / restriction	12.688	9.859	11.050	10.585	2.17E-04	2.91E-01	-2.83	-0.46
lpg1869	ribonuclease III (dsRNA-specific ribonuclease) (RNAse II	*rnc*	DNA/RNA degradation / restriction	12.500	10.044	10.985	10.633	1.54E-03	3.96E-01	-2.46	-0.35
lpg1870	transmembrane protein (fimbrial? pilin?)		Named proteins of general function	12.856	12.583	13.016	12.179	1.94E-01	4.08E-03	-0.27	-0.84
lpg1870	transmembrane protein (fimbrial? pilin?)		Named proteins of general function	12.848	12.636	12.979	12.213	3.06E-01	7.51E-03	-0.21	-0.77
lpg1871	signal peptidase I (lepB-1)	*lepB-1*	Protein fate / hydrolases / secretion	11.337	11.563	11.458	12.017	4.04E-01	9.28E-02	0.23	0.56
lpg1871	signal peptidase I (lepB-1)	*lepB-1*	Protein fate / hydrolases / secretion	11.290	11.904	11.205	12.038	1.86E-01	4.26E-02	0.61	0.83
lpg1872	GTP binding elongation factor LepA	*lepA*	Toxin production / other pathogen func	12.485	12.130	11.286	12.555	5.07E-01	1.19E-02	-0.35	1.27
lpg1872	GTP binding elongation factor LepA	*lepA*	Toxin production / other pathogen func	12.464	12.081	11.151	12.592	4.19E-01	6.45E-03	-0.38	1.44
lpg1873	membrane bound lytic murein transglycosylase (peptidoglycan N-ace		Metabolism of Complex Carbohydrates	9.823	10.049	8.878	10.318	6.86E-01	1.98E-02	0.23	1.44
lpg1873	membrane bound lytic murein transglycosylase (peptidoglycan N-ace		Metabolism of Complex Carbohydrates	9.706	10.112	8.778	10.239	5.53E-01	2.63E-01	0.41	1.46
lpg1874	general secretion pathway protein L		Protein fate / hydrolases / secretion	11.436	9.866	9.464	9.326	6.64E-05	7.42E-01	-1.57	-0.14
lpg1874	general secretion pathway protein L		Protein fate / hydrolases / secretion	10.844	10.214	9.081	9.484	3.27E-01	4.90E-01	-0.63	0.40
lpg1875	putative general secretion pathway protein M-type yghD	*yghD*	Protein fate / hydrolases / secretion	9.304	8.522	9.441	8.235	1.17E-01	4.15E-02	-0.78	-1.21
lpg1875	putative general secretion pathway protein M-type yghD	*yghD*	Protein fate / hydrolases / secretion	9.552	9.106	9.501	8.678	1.19E-01	3.83E-02	-0.45	-0.82
lpg1876	ORF		ORFs of unknown function (unique)	9.549	8.730	13.857	8.203	5.26E-01	1.57E-05	-0.82	-5.65
lpg1876	ORF		ORFs of unknown function (unique)	9.843	9.835	12.741	7.935	9.94E-01	5.63E-03	-0.01	-4.81
lpg1877	deoxyguanosinetriphosphate (dGTP) triphosphohydrolase		Signal transduction / other regulatory f	10.494	10.817	10.135	10.804	5.86E-01	8.42E-02	0.32	0.67
lpg1877	deoxyguanosinetriphosphate (dGTP) triphosphohydrolase		Signal transduction / other regulatory f	10.393	11.608	9.747	10.865	1.82E-02	5.32E-03	1.22	1.12
lpg1878	tRNA-Glu		tRNA	11.287	10.466	10.099	10.772	2.86E-01	4.92E-01	-0.82	0.67
lpg1878	tRNA-Glu		tRNA	11.046	10.894	10.165	10.987	8.73E-01	4.28E-01	-0.15	0.82
lpg1880	tRNA-Ala		tRNA	10.576	11.009	10.610	11.397	2.23E-01	1.07E-01	0.43	0.79
lpg1880	tRNA-Ala		tRNA	10.278	10.737	10.322	11.239	4.17E-01	1.39E-01	0.46	0.92
lpg1881	ORF		ORFs of unknown function (unique)	10.066	10.586	10.291	10.107	9.01E-02	4.65E-01	0.52	-0.18
lpg1881	ORF		ORFs of unknown function (unique)	10.259	10.569	10.065	10.514	4.05E-01	9.23E-02	0.31	0.45
lpg1882	lactoylglutathione lyase	*gloA*	Carbohydrate Metabolism	10.812	12.605	11.409	11.875	1.46E-03	4.56E-01	1.79	0.47
lpg1882	lactoylglutathione lyase	*gloA*	Carbohydrate Metabolism	10.772	12.247	11.233	11.772	1.04E-04	2.30E-01	1.48	0.54
lpg1883	transmembrane protein		Unknown / hypothetical proteins	12.037	12.262	11.179	11.517	4.69E-01	5.06E-01	0.22	0.34
lpg1883	transmembrane protein		Unknown / hypothetical proteins	11.990	11.906	11.140	11.656	7.47E-01	1.46E-01	-0.08	0.52
lpg1884	Microtubule binding protein, putative	*legC2 / YlfB*	Named proteins of general function	10.121	8.549	10.658	8.460	5.37E-02	1.46E-03	-1.57	-2.20
lpg1884	Microtubule binding protein, putative	*legC2 / YlfB*	Named proteins of general function	10.154	8.974	10.376	8.658	4.77E-02	9.87E-03	-1.18	-1.72
lpg1885	small ORF (104aa)		ORFs of unknown function (unique)	9.763	10.966	12.211	10.200	1.44E-01	5.67E-02	1.20	-2.01
lpg1885	small ORF (104aa)		ORFs of unknown function (unique)	9.914	11.037	12.199	10.197	1.69E-01	6.94E-02	1.12	-2.00
lpg1886	acylphosphatase		Named proteins of general function	10.531	10.440	11.265	10.084	7.03E-01	2.83E-02	-0.09	-1.18
lpg1886	acylphosphatase		Named proteins of general function	10.723	10.804	11.468	10.453	8.74E-01	9.90E-02	0.08	-1.02
lpg1887	ORF		ORFs of unknown function (unique)	11.732	12.313	14.454	11.359	3.83E-01	2.61E-03	0.58	-3.10
lpg1887	ORF		ORFs of unknown function (unique)	11.809	12.293	14.418	11.504	4.52E-01	3.21E-03	0.48	-2.91
lpg1888	ORF		ORFs of unknown function (unique)	10.324	9.880	10.392	9.879	4.81E-01	3.45E-01	-0.44	-0.51
lpg1888	ORF		ORFs of unknown function (unique)	10.222	10.083	10.310	9.867	7.72E-01	4.22E-01	-0.14	-0.44
lpg1889	lipase (triacyglycerol lipase)		Protein fate / hydrolases / secretion	11.433	11.247	14.692	10.688	8.24E-01	1.13E-03	-0.19	-4.00
lpg1889	lipase (triacyglycerol lipase)		Protein fate / hydrolases / secretion	11.353	11.600	14.565	10.982	7.56E-01	1.64E-03	0.25	-3.58
lpg1890	galA protein 1	*legLC8*	Named proteins of general function	9.819	12.938	10.270	10.511	8.98E-03	6.99E-01	3.12	0.24
lpg1890	galA protein 1	*legLC8*	Named proteins of general function	9.843	13.295	10.447	10.892	8.89E-04	4.80E-01	3.45	0.45
lpg1891	hypothetical protein HI1736		Unknown / hypothetical proteins	11.626	11.499	11.758	9.622	7.35E-01	6.48E-06	-0.13	-2.14
lpg1891	hypothetical protein HI1736		Unknown / hypothetical proteins	11.677	11.627	11.834	9.763	8.77E-01	6.36E-03	-0.05	-2.07
lpg1892	small ORF (127aa)		ORFs of unknown function (unique)	9.797	10.628	8.680	9.472	5.51E-02	1.92E-01	0.83	0.79
lpg1892	small ORF (127aa)		ORFs of unknown function (unique)	10.081	10.458	8.446	9.611	2.01E-01	2.77E-01	0.38	1.17
lpg1893	major facilitator family transporter (multidrug efflux transporter MFS fa		Transport and binding	9.506	9.382	8.751	10.964	7.90E-01	1.32E-05	-0.12	2.21
lpg1893	major facilitator family transporter (multidrug efflux transporter MFS fa		Transport and binding	9.149	9.645	8.430	10.991	2.29E-01	2.19E-04	0.50	2.56
lpg1894	chloride channel protein (voltage gated?)		Transport and binding	9.887	7.983	9.564	9.207	7.52E-02	3.54E-01	-1.90	-0.36
lpg1894	chloride channel protein (voltage gated?)		Transport and binding	9.663	7.754	9.056	8.963	1.32E-01	8.52E-01	-1.91	-0.09
lpg1895	ORF		ORFs of unknown function (unique)	10.607	10.076	14.094	8.894	4.84E-01	2.27E-02	-0.53	-5.20
lpg1895	ORF		ORFs of unknown function (unique)	10.574	10.417	13.917	10.017	8.20E-01	1.36E-02	-0.16	-3.90
lpg1896	COG3012: conserved protein (SEC-C motif domain prote	*ychJ*	Named proteins of general function	9.107	9.252	8.390	9.757	7.43E-01	5.83E-03	0.15	1.37
lpg1896	COG3012: conserved protein (SEC-C motif domain prote	*ychJ*	Named proteins of general function	8.842	9.185	6.376	9.286	5.34E-01	6.42E-03	0.34	2.91
lpg1897	glutathione-regulated potassium efflux system		Transport and binding	10.892	9.190	10.287	10.423	6.66E-02	6.63E-01	-1.70	0.14
lpg1897	glutathione-regulated potassium efflux system		Transport and binding	10.698	9.550	9.755	10.510	1.03E-01	6.18E-02	-1.15	0.75
lpg1898	methanol dehydrogenase regulatory protein (MoxR protein)		Transcription factors / DNA binding pro	9.688	8.920	11.950	8.223	4.04E-01	5.22E-03	-0.77	-3.73
lpg1898	methanol dehydrogenase regulatory protein (MoxR protein)		Transcription factors / DNA binding pro	10.119	8.903	12.017	9.025	1.50E-01	4.22E-03	-1.22	-2.99
lpg1899	transmembrane protein		Unknown / hypothetical proteins	9.250	8.758	11.064	8.038	6.15E-01	1.46E-03	-0.49	-3.03
lpg1899	transmembrane protein		Unknown / hypothetical proteins	9.326	7.696	10.975	8.286	1.58E-01	4.78E-03	-1.63	-2.69

lpg1900	transglutaminase domain protein		Named proteins of general function	9.088	8.681	10.913	9.139	6.05E-01	2.49E-02	-0.41	-1.77
lpg1900	transglutaminase domain protein		Named proteins of general function	8.397	9.384	10.733	9.403	2.56E-01	5.50E-02	0.99	-1.33
lpg1901	conserved hypothetical protein		Unknown / hypothetical proteins	9.146	10.269	8.113	10.126	5.43E-03	9.37E-04	1.12	2.01
lpg1901	conserved hypothetical protein		Unknown / hypothetical proteins	9.278	9.822	7.679	10.048	3.57E-01	1.13E-04	0.54	2.37
lpg1902	ORF DnaJ-like protein DjlA?		Unknown / hypothetical proteins	9.231	9.161	7.358	6.690	8.69E-01	7.67E-01	-0.07	-0.67
lpg1902	ORF DnaJ-like protein DjlA?		Unknown / hypothetical proteins	10.022	9.560	7.824	8.746	2.90E-01	2.44E-01	-0.46	0.92
lpg1903	hydrolase (esterase/lipase/thioesterase)		Protein fate / hydrolases / secretion	9.013	9.751	13.240	8.479	4.82E-01	2.53E-05	0.74	-4.76
lpg1903	hydrolase (esterase/lipase/thioesterase)		Protein fate / hydrolases / secretion	9.293	10.696	13.346	8.722	2.43E-01	6.06E-03	1.40	-4.62
lpg1904	integral membrane protein (transporter, drug/metabolite protein)		Transport and binding	9.069	8.713	9.251	8.301	3.57E-01	6.06E-02	-0.36	-0.95
lpg1904	integral membrane protein (transporter, drug/metabolite protein)		Transport and binding	8.987	8.902	8.665	7.818	8.52E-01	1.36E-01	-0.08	-0.85
lpg1905	ectonucleoside triphosphate diphosphohydrolase I (apyrase) (E-type		Nucleotide Metabolism	10.364	11.168	8.389	11.011	2.00E-01	2.59E-02	0.80	2.62
lpg1905	ectonucleoside triphosphate diphosphohydrolase I (apyrase) (E-type		Nucleotide Metabolism	9.558	11.750	8.804	11.729	1.69E-03	1.19E-02	2.19	2.93
lpg1906	transporting ATPase		Transport and binding	11.720	12.442	11.888	11.938	1.53E-02	8.66E-01	0.72	0.05
lpg1906	transporting ATPase		Transport and binding	11.687	12.338	11.670	11.902	2.44E-02	3.45E-01	0.65	0.23
lpg1907	ORF		ORFs of unknown function (unique)	9.896	11.137	10.412	9.626	1.52E-04	2.40E-02	1.24	-0.79
lpg1907	ORF		ORFs of unknown function (unique)	9.856	10.967	10.177	10.114	1.31E-03	8.85E-01	1.11	-0.06
lpg1908	glutathione S-transferase	*gst*	Detoxification / adaptation, Metabolis	11.642	12.453	12.915	10.786	2.29E-01	3.63E-02	0.81	-2.13
lpg1908	glutathione S-transferase	*gst*	Detoxification / adaptation, Metabolis	11.622	12.581	12.952	10.949	1.90E-01	5.32E-02	0.96	-2.00
lpg1909	ORF		ORFs of unknown function (unique)	9.876	9.025	8.383	8.583	2.97E-02	7.99E-01	-0.85	0.20
lpg1909	ORF		ORFs of unknown function (unique)	9.593	7.845	8.844	9.166	7.41E-02	6.23E-01	-1.75	0.32
lpg1910	D-alanyl-D-alanine carboxypeptidase (DD-peptidase) (beta-lactamas		Protein fate / hydrolases / secretion	10.337	9.374	9.198	9.236	2.98E-01	9.66E-01	-0.96	0.04
lpg1910	D-alanyl-D-alanine carboxypeptidase (DD-peptidase) (beta-lactamas		Protein fate / hydrolases / secretion	9.937	9.230	9.301	9.620	1.33E-01	5.71E-01	-0.71	0.32
lpg1911	glutamate tRNA synthetase catalytic subunit (glutamyl tR	*gltX*	Amino Acid Metabolism, Metabolism o	12.167	11.973	10.111	12.225	7.35E-01	2.56E-03	-0.19	2.11
lpg1911	glutamate tRNA synthetase catalytic subunit (glutamyl tR	*gltX*	Amino Acid Metabolism, Metabolism o	12.219	12.078	9.738	12.268	7.97E-01	1.86E-03	-0.14	2.53
lpg1912	sensory box histidine kinase/response regulator (two component histi		Signal transduction / other regulatory f	9.477	8.943	9.726	8.456	5.99E-02	4.81E-02	-0.53	-1.27
lpg1912	sensory box histidine kinase/response regulator (two component histi		Signal transduction / other regulatory f	8.675	9.356	9.700	8.606	4.11E-01	2.26E-02	0.68	-1.09
lpg1913	6-phosphofructokinase		Carbohydrate Metabolism	11.583	11.218	11.669	10.955	1.11E-01	6.09E-02	-0.36	-0.71
lpg1913	6-phosphofructokinase		Carbohydrate Metabolism	11.523	12.043	11.128	12.240	4.45E-01	1.13E-01	0.52	1.11
lpg1914	fimbrial protein, type IV pilin, PilE	*pilE*	Transport and binding	10.039	9.329	12.441	8.220	2.16E-01	4.08E-04	-0.71	-4.22
lpg1914	fimbrial protein, type IV pilin, PilE	*pilE*	Transport and binding	9.875	9.469	12.428	9.721	5.22E-01	1.05E-03	-0.41	-2.71
lpg1915	Tfp pilus assembly protein, major type IV pilin class A	*pilE*	Transport and binding	12.844	12.681	15.060	11.076	7.86E-01	1.47E-04	-0.16	-3.98
lpg1915	Tfp pilus assembly protein, major type IV pilin class A	*pilE*	Transport and binding	12.789	12.841	15.044	11.151	9.23E-01	2.11E-04	0.05	-3.89
lpg1916	possible regulator of murein genes (BolA protein)	*bolA*	Cell envelope synthesis, Transcription	11.257	9.497	10.441	10.842	6.32E-05	4.48E-01	-1.76	0.40
lpg1916	possible regulator of murein genes (BolA protein)	*bolA*	Cell envelope synthesis, Transcription	10.986	9.560	10.349	11.022	3.11E-02	7.79E-02	-1.43	0.67
lpg1917	amino acid antiporter (glutamate/gamma-aminobutyrate antiporter)		Transport and binding	10.309	10.039	10.366	9.544	4.87E-01	1.66E-02	-0.27	-0.82
lpg1917	amino acid antiporter (glutamate/gamma-aminobutyrate antiporter)		Transport and binding	10.491	10.028	10.473	9.794	1.55E-01	4.13E-02	-0.46	-0.68
lpg1918	ORF		ORFs of unknown function (unique)	11.547	14.140	13.233	12.024	1.14E-04	2.85E-02	2.59	-1.21
lpg1918	ORF		ORFs of unknown function (unique)	11.607	14.161	13.230	12.064	1.27E-04	3.77E-02	2.55	-1.17
lpg1919	3-deoxy-manno-octulosonate cytidylyltransferase (CTP:	*kdsB*	Metabolism of Complex Carbohydrate	11.272	11.308	11.797	10.852	8.41E-01	1.39E-02	0.04	-0.95
lpg1919	3-deoxy-manno-octulosonate cytidylyltransferase (CTP:	*kdsB*	Metabolism of Complex Carbohydrate	11.352	11.171	11.753	10.812	1.53E-01	3.22E-02	-0.18	-0.94
lpg1920	tetraacyldisaccharide-1-P-4'-kinase	*lpxK*	Metabolism of Complex Carbohydrate	11.642	11.230	9.860	11.240	4.60E-01	8.83E-03	-0.41	1.38
lpg1920	tetraacyldisaccharide-1-P-4'-kinase	*lpxK*	Metabolism of Complex Carbohydrate	11.703	11.144	9.504	11.039	3.12E-01	2.02E-02	-0.56	1.53
lpg1921	glycoprotease; metal dependent protease?		Protein fate / hydrolases / secretion	8.457	11.559	8.899	9.916	6.21E-03	8.37E-03	3.10	1.02
lpg1921	glycoprotease; metal dependent protease?		Protein fate / hydrolases / secretion	9.196	9.908	8.914	9.953	9.63E-02	4.27E-03	0.71	1.04
lpg1922	ATP dependent DNA helicase (DEAD box family) Rad3		Replication and Repair	9.631	10.348	8.539	9.854	3.62E-01	5.24E-02	0.72	1.31
lpg1922	ATP dependent DNA helicase (DEAD box family) Rad3		Replication and Repair	10.382	13.020	9.857	11.422	1.76E-04	1.85E-02	2.64	1.57
lpg1923	ferredoxin II (ferredoxin, 4Fe-4S)		Energy Metabolism	12.527	11.977	10.664	11.485	4.10E-01	1.48E-01	-0.55	0.82
lpg1923	ferredoxin II (ferredoxin, 4Fe-4S)		Energy Metabolism	12.204	11.767	10.432	11.688	5.98E-01	3.69E-02	-0.44	1.26
lpg1924	hypothetical protein		Unknown / hypothetical proteins	8.061	9.647	8.339	9.724	4.34E-02	2.07E-02	1.59	1.38
lpg1924	hypothetical protein		Unknown / hypothetical proteins	7.220	10.176	8.123	9.671	1.32E-02	1.03E-01	2.96	1.55
lpg1925	ORF		ORFs of unknown function (unique)	9.756	9.659	10.891	10.196	8.18E-01	1.42E-01	-0.10	-0.70
lpg1925	ORF		ORFs of unknown function (unique)	9.259	9.764	10.821	10.462	2.31E-01	3.59E-01	0.50	-0.36
lpg1926	hypothetical protein		Unknown / hypothetical proteins	9.798	9.399	13.030	8.587	6.31E-01	4.01E-04	-0.40	-4.44
lpg1926	hypothetical protein		Unknown / hypothetical proteins	9.649	9.643	12.940	8.944	9.94E-01	6.72E-04	-0.01	-4.00
lpg1927	conserved hypothetical protein		Unknown / hypothetical proteins	11.452	11.145	12.479	11.525	2.82E-01	3.01E-02	-0.31	-0.95
lpg1927	conserved hypothetical protein		Unknown / hypothetical proteins	11.473	11.613	12.431	11.871	7.56E-01	2.02E-01	0.14	-0.56
lpg1928	enzyme involved in pigment biosynthesis?	*indA*	Toxin production / other pathogen func	9.704	8.670	11.153	9.355	2.17E-01	7.93E-03	-1.03	-1.80
lpg1928	enzyme involved in pigment biosynthesis?	*indA*	Toxin production / other pathogen func	9.287	9.413	10.805	9.750	7.89E-01	1.84E-01	0.13	-1.05
lpg1929	tRNA-Phe		tRNA	10.841	8.291	9.895	10.777	1.19E-01	2.10E-01	-2.55	0.88
lpg1929	tRNA-Phe		tRNA	11.121	9.783	9.568	10.547	1.62E-02	2.05E-01	-1.34	0.98
lpg1930	ORF		ORFs of unknown function (unique)	10.301	10.869	10.482	10.131	6.01E-02	2.15E-01	0.57	-0.35
lpg1930	ORF		ORFs of unknown function (unique)	10.135	10.964	10.577	10.782	2.62E-02	7.19E-01	0.83	0.20
lpg1931	ORF		ORFs of unknown function (unique)	10.053	8.874	8.741	8.110	5.35E-02	4.57E-01	-1.18	-0.63
lpg1931	ORF		ORFs of unknown function (unique)	10.199	9.482	8.272	8.276	3.97E-03	9.96E-01	-0.72	0.00

lpg1932	small ORF (104aa)		ORFs of unknown function (unique)	9.981	9.548	9.811	9.778	3.27E-01	9.52E-01	-0.43	-0.03
lpg1932	small ORF (104aa)		ORFs of unknown function (unique)	9.893	9.299	9.356	9.680	3.75E-02	4.55E-01	-0.59	0.32
lpg1933	ORF		ORFs of unknown function (unique)	8.953	10.091	10.193	9.951	1.98E-02	5.26E-01	1.14	-0.24
lpg1933	ORF		ORFs of unknown function (unique)	9.303	10.143	10.253	10.095	1.77E-01	6.73E-01	0.84	-0.16
lpg1934	hypothetical (HipA transcription factor?) (stringent stress response, ce		Signal transduction / other regulatory f	10.380	10.577	8.985	10.873	5.45E-01	2.21E-03	0.20	1.89
lpg1934	hypothetical (HipA transcription factor?) (stringent stress response, ce		Signal transduction / other regulatory f	10.507	10.574	8.381	10.643	8.47E-01	2.07E-02	0.07	2.26
lpg1935	small ORF (93aa) HTH motif? transcriptional regulator?		Transcription factors / DNA binding pro	8.843	7.886	8.595	7.785	2.61E-01	5.07E-01	-0.96	-0.81
lpg1935	small ORF (93aa) HTH motif? transcriptional regulator?		Transcription factors / DNA binding pro	8.941	9.151	8.376	8.692	8.85E-01	7.99E-01	0.21	0.32
lpg1936	methoxymalonyl CoA synthase (31-O-demethyl-FK506 methyltransfer		Named proteins of general function	10.545	10.345	10.662	10.293	7.40E-01	1.99E-01	-0.20	-0.37
lpg1936	methoxymalonyl CoA synthase (31-O-demethyl-FK506 methyltransfer		Named proteins of general function	10.404	10.526	10.620	10.538	8.38E-01	8.03E-01	0.12	-0.08
lpg1937	pyoverdine biosynthesis regulatory gene (SyrP-like protein)		Named proteins of general function	9.597	9.532	10.440	9.152	6.99E-01	2.30E-03	-0.06	-1.29
lpg1937	pyoverdine biosynthesis regulatory gene (SyrP-like protein)		Named proteins of general function	9.564	9.428	10.102	8.971	5.74E-01	5.34E-03	-0.14	-1.13
lpg1938	coenzyme F390 synthetase (capsular polysaccharide biosynthesis pr		Cell envelope synthesis	9.458	7.360	8.888	6.659	1.74E-02	1.73E-01	-2.10	-2.23
lpg1938	coenzyme F390 synthetase (capsular polysaccharide biosynthesis pr		Cell envelope synthesis	9.551	8.231	8.789	8.238	3.56E-03	7.16E-01	-1.32	-0.55
lpg1939	polyketide synthase, type I		Named proteins of general function	9.862	8.759	11.845	8.589	9.76E-02	1.00E-02	-1.10	-3.26
lpg1939	polyketide synthase, type I		Named proteins of general function	9.828	8.659	11.935	9.164	7.08E-02	6.74E-03	-1.17	-2.77
lpg1940	peptide synthetase (mycosubtilin (iturin antibiotic) synthetase MycC (r		Toxin production / other pathogen func	11.752	10.803	12.677	11.138	4.59E-02	1.69E-03	-0.95	-1.54
lpg1940	peptide synthetase (mycosubtilin (iturin antibiotic) synthetase MycC (r		Toxin production / other pathogen func	11.751	11.043	12.710	11.315	1.03E-01	1.42E-03	-0.71	-1.40
lpg1941	acyl CoA dehydrogenase (butyryl CoA dehydrogenase)		Carbohydrate Metabolism, Biodegrada	10.917	10.769	11.457	10.791	5.55E-01	1.39E-01	-0.15	-0.67
lpg1941	acyl CoA dehydrogenase (butyryl CoA dehydrogenase)		Carbohydrate Metabolism, Biodegrada	10.873	10.890	11.409	10.766	9.31E-01	1.16E-01	0.02	-0.64
lpg1942	3-hydroxyacyl CoA dehydrogenase (beta-hydroxybutyryl CoA dehydro		Biodegradation of Xenobiotics, Carboh	12.411	11.621	12.584	11.917	1.08E-02	5.21E-02	-0.79	-0.67
lpg1942	3-hydroxyacyl CoA dehydrogenase (beta-hydroxybutyryl CoA dehydro		Biodegradation of Xenobiotics, Carboh	12.122	11.678	12.669	12.078	1.72E-01	8.19E-02	-0.44	-0.59
lpg1943	small ORF (85aa) hypothetical		Unknown / hypothetical proteins	13.484	11.998	11.072	11.071	1.69E-02	9.99E-01	-1.49	0.00
lpg1943	small ORF (85aa) hypothetical		Unknown / hypothetical proteins	13.294	11.980	11.085	11.188	8.58E-02	8.25E-01	-1.31	0.10
lpg1944	conserved hypothetical protein		Unknown / hypothetical proteins	9.041	9.115	11.108	8.905	9.23E-01	4.03E-02	0.07	-2.20
lpg1944	conserved hypothetical protein		Unknown / hypothetical proteins	9.517	8.917	10.357	9.087	4.04E-01	3.43E-01	-0.60	-1.27
lpg1945	3',5'-cyclic nucleotide phosphodiesterase		Signal transduction / other regulatory f	13.236	11.541	11.358	13.026	8.97E-04	8.22E-03	-1.69	1.67
lpg1945	3',5'-cyclic nucleotide phosphodiesterase		Signal transduction / other regulatory f	13.227	12.162	11.344	13.226	1.70E-01	4.85E-03	-1.07	1.88
lpg1946	transcriptional regulator LuxR		Transcription factors / DNA binding pro	9.628	9.303	10.380	8.584	3.20E-01	7.22E-03	-0.33	-1.80
lpg1946	transcriptional regulator LuxR		Transcription factors / DNA binding pro	10.072	9.576	10.767	9.195	3.39E-01	2.55E-03	-0.50	-1.57
lpg1947	hypothetical protein		Unknown / hypothetical proteins	8.399	9.730	9.203	9.068	5.34E-02	7.56E-01	1.33	-0.13
lpg1947	hypothetical protein		Unknown / hypothetical proteins	8.518	9.954	9.336	9.325	1.47E-02	9.81E-01	1.44	-0.01
lpg1948	FLJ00180 protein	*legLC4*	Unknown / hypothetical proteins	10.546	13.233	12.020	11.213	5.46E-02	1.73E-01	2.69	-0.81
lpg1948	FLJ00180 protein	*legLC4*	Unknown / hypothetical proteins	10.330	13.623	11.897	11.340	3.46E-03	2.04E-01	3.29	-0.56
lpg1949	hypothetical protein		Unknown / hypothetical proteins	9.338	7.907	11.021	8.168	2.32E-02	1.10E-03	-1.43	-2.85
lpg1949	hypothetical protein		Unknown / hypothetical proteins	9.437	8.345	10.922	8.821	1.04E-01	1.44E-03	-1.09	-2.10
lpg1950	guanine nucleotide exchange protein (RalF) (ADP ribosyl	*RalF*	Toxin production / other pathogen func	10.199	9.913	12.433	9.469	5.87E-01	1.20E-03	-0.29	-2.96
lpg1950	guanine nucleotide exchange protein (RalF) (ADP ribosyl	*RalF*	Toxin production / other pathogen func	10.055	9.786	12.358	9.672	6.97E-01	1.16E-02	-0.27	-2.69
lpg1951	hypothetical		Unknown / hypothetical proteins	9.397	9.147	11.272	9.412	6.70E-01	2.43E-02	-0.25	-1.86
lpg1951	hypothetical		Unknown / hypothetical proteins	9.855	9.468	11.369	9.589	5.27E-01	8.21E-03	-0.39	-1.78
lpg1952	3',5'-cyclic nucleotide phosphodiesterase		Nucleotide Metabolism	9.204	9.313	10.434	9.639	6.87E-01	3.78E-01	0.11	-0.80
lpg1952	3',5'-cyclic nucleotide phosphodiesterase		Nucleotide Metabolism	8.872	8.655	9.233	9.038	7.42E-01	8.46E-01	-0.22	-0.20
lpg1953	ORF	*legC3*	ORFs of unknown function (unique)	9.696	11.059	10.445	10.703	4.58E-04	2.46E-01	1.36	0.26
lpg1953	ORF	*legC3*	ORFs of unknown function (unique)	10.242	10.898	10.601	10.864	1.61E-01	1.94E-01	0.66	0.26
lpg1954	ORF		ORFs of unknown function (unique)	8.360	6.938	8.365	6.703	1.94E-01	1.91E-01	-1.42	-1.66
lpg1954	ORF		ORFs of unknown function (unique)	8.041	7.553	8.823	7.419	4.89E-01	2.25E-01	-0.49	-1.40
lpg1955	hypothetical (gluconate permease?) (transport protein)		Transport and binding	8.816	9.743	9.007	11.626	4.30E-01	3.13E-04	0.93	2.62
lpg1955	hypothetical (gluconate permease?) (transport protein)		Transport and binding	9.754	11.155	9.310	12.243	1.28E-02	9.74E-05	1.40	2.93
lpg1956	chloromuconate cycloisomerase (mandelate racemase/muconate lact		Named proteins of general function	8.938	10.757	8.373	11.015	3.41E-02	5.02E-05	1.82	2.64
lpg1956	chloromuconate cycloisomerase (mandelate racemase/muconate lact		Named proteins of general function	9.589	11.148	8.178	11.608	4.70E-02	4.08E-03	1.56	3.43
lpg1957	ebhA protein		Named proteins of general function	10.539	11.811	9.874	11.740	8.02E-02	6.95E-02	1.27	1.87
lpg1957	ebhA protein		Named proteins of general function	10.959	11.739	9.515	11.817	1.86E-01	1.32E-02	0.78	2.30
lpg1958	FLJ00180 protein	*legL5*	Unknown / hypothetical proteins	9.618	9.895	10.460	9.734	4.53E-01	1.79E-02	0.28	-0.73
lpg1958	FLJ00180 protein	*legL5*	Unknown / hypothetical proteins	9.306	10.210	10.361	10.423	8.07E-02	8.61E-01	0.90	0.06
lpg1959	ORF		ORFs of unknown function (unique)	9.284	8.826	9.285	8.788	2.23E-01	1.65E-01	-0.46	-0.50
lpg1959	ORF		ORFs of unknown function (unique)	9.164	8.667	7.622	9.083	3.07E-01	2.32E-01	-0.50	1.46
lpg1960	ORF		ORFs of unknown function (unique)	11.056	11.965	14.371	10.223	4.09E-01	3.12E-04	0.91	-4.15
lpg1960	ORF		ORFs of unknown function (unique)	11.001	11.841	14.347	10.371	4.62E-01	4.22E-04	0.84	-3.98
lpg1961	ORF		ORFs of unknown function (unique)	9.731	10.928	10.880	10.548	4.54E-02	6.44E-01	1.20	-0.33
lpg1961	ORF		ORFs of unknown function (unique)	9.736	11.482	11.284	11.153	7.99E-02	8.94E-01	1.75	-0.13
lpg1962	peptidyl-prolyl cis-trans isomerase (rotamase)		Toxin production / other pathogen func	10.768	10.733	9.524	10.010	9.40E-01	4.33E-01	-0.04	0.49
lpg1962	peptidyl-prolyl cis-trans isomerase (rotamase)		Toxin production / other pathogen func	10.991	10.696	9.347	11.013	6.17E-01	2.02E-01	-0.29	1.67
lpg1963	hypothetical protein		Unknown / hypothetical proteins	10.345	8.781	13.289	8.066	1.57E-01	1.14E-04	-1.56	-5.22
lpg1963	hypothetical protein		Unknown / hypothetical proteins	10.379	9.085	13.335	8.408	1.53E-01	4.59E-04	-1.29	-4.93

lpg1964	ORF		ORFs of unknown function (unique)	8.987	9.770	9.351	9.172	2.05E-01	8.19E-01	0.78	-0.18
lpg1964	ORF		ORFs of unknown function (unique)	9.309	10.224	9.385	9.868	1.37E-01	3.98E-01	0.91	0.48
lpg1965	hypothetical protein		Unknown / hypothetical proteins	8.558	9.754	9.495	8.304	1.96E-03	5.71E-02	1.20	-1.19
lpg1965	hypothetical protein		Unknown / hypothetical proteins	8.591	10.523	9.633	9.958	5.33E-05	6.67E-01	1.93	0.33
lpg1966	ORF		ORFs of unknown function (unique)	10.251	10.780	9.838	9.743	2.82E-01	9.09E-01	0.53	-0.09
lpg1966	ORF		ORFs of unknown function (unique)	10.223	10.380	9.814	9.722	7.49E-01	9.18E-01	0.16	-0.09
lpg1967	transcriptional regulator, TetR family (tetracyclin resistance)		Transcription factors / DNA binding pr	10.126	9.868	10.870	9.947	4.08E-01	1.06E-01	-0.26	-0.92
lpg1967	transcriptional regulator, TetR family (tetracyclin resistance)		Transcription factors / DNA binding pr	9.994	9.971	11.041	10.213	9.44E-01	1.00E-01	-0.02	-0.83
lpg1968	hypothetical protein		Unknown / hypothetical proteins	7.115	8.899	8.571	9.427	7.19E-02	1.71E-01	1.78	0.86
lpg1968	hypothetical protein		Unknown / hypothetical proteins	7.840	8.633	7.917	9.133	3.95E-01	2.09E-01	0.79	1.22
lpg1969	putative		Unknown / hypothetical proteins	11.025	9.547	11.247	9.571	1.08E-01	1.13E-01	-1.48	-1.68
lpg1969	putative		Unknown / hypothetical proteins	10.217	9.812	11.104	9.790	5.15E-01	2.57E-02	-0.41	-1.31
lpg1970	glutathione S-transferase		Metabolism of Other Amino Acids	11.491	11.303	10.050	11.098	7.30E-01	9.43E-02	-0.19	1.05
lpg1970	glutathione S-transferase		Metabolism of Other Amino Acids	11.688	11.480	9.219	11.420	5.82E-01	7.46E-02	-0.21	2.20
lpg1971	organic hydroperoxide resistance protein, COG1764:predicted redox		Detoxification / adaptation	11.031	10.965	9.736	11.004	8.87E-01	4.50E-02	-0.07	1.27
lpg1971	organic hydroperoxide resistance protein, COG1764:predicted redox		Detoxification / adaptation	10.816	10.817	8.591	11.218	9.99E-01	1.49E-02	0.00	2.63
lpg1972	small ORF (125aa)		ORFs of unknown function (unique)	12.066	15.133	12.523	12.103	4.61E-06	8.05E-02	3.07	-0.42
lpg1972	small ORF (125aa)		ORFs of unknown function (unique)	12.064	15.140	12.481	12.165	2.17E-06	1.22E-01	3.08	-0.32
lpg1973	ORF		ORFs of unknown function (unique)	11.853	12.152	12.303	11.617	3.63E-01	3.84E-04	0.30	-0.69
lpg1973	ORF		ORFs of unknown function (unique)	11.917	11.826	12.374	11.748	6.18E-01	2.50E-03	-0.09	-0.63
lpg1974	major outer membrane protein		Toxin production / other pathogen func	13.406	12.816	12.286	11.688	2.07E-01	1.60E-01	-0.59	-0.60
lpg1974	major outer membrane protein		Toxin production / other pathogen func	13.355	12.825	12.087	11.748	2.83E-01	4.51E-01	-0.53	-0.34
lpg1975	ORF		ORFs of unknown function (unique)	9.971	9.391	9.278	9.777	9.93E-02	1.33E-01	-0.58	0.50
lpg1975	ORF		ORFs of unknown function (unique)	10.005	9.278	9.224	9.847	1.12E-01	3.10E-01	-0.73	0.62
lpg1976	UVB-resistance protein UVR8	*legG1*	Named proteins of general function	7.367	10.401	7.843	7.909	3.53E-04	9.49E-01	3.03	0.07
lpg1976	UVB-resistance protein UVR8	*legG1*	Named proteins of general function	6.781	10.554	7.866	8.294	3.39E-04	6.48E-01	3.77	0.43
lpg1977	intracellular protease (ThiJ/PfpI family)		Protein fate / hydrolases / secretion	9.497	10.892	11.285	10.277	1.17E-01	9.52E-02	1.40	-1.01
lpg1977	intracellular protease (ThiJ/PfpI family)		Protein fate / hydrolases / secretion	9.546	11.130	10.760	10.525	3.32E-02	7.68E-01	1.58	-0.24
lpg1978	hypothetical Teichoic Acid Biosynthesis Protein)		Named proteins of general function	7.135	9.642	8.936	9.401	3.20E-02	2.65E-01	2.51	0.46
lpg1978	hypothetical Teichoic Acid Biosynthesis Protein)		Named proteins of general function	7.610	9.531	8.760	9.454	6.85E-03	1.99E-01	1.92	0.69
lpg1979	ORF		ORFs of unknown function (unique)	7.959	8.637	8.029	8.520	2.89E-01	6.37E-01	0.68	0.49
lpg1979	ORF		ORFs of unknown function (unique)	9.033	8.999	6.863	7.419	9.75E-01	7.65E-01	-0.03	0.56
lpg1980	small ORF (100aa)		ORFs of unknown function (unique)	9.281	8.578	8.944	7.828	1.44E-01	2.92E-01	-0.70	-1.12
lpg1980	small ORF (100aa)		ORFs of unknown function (unique)	9.132	8.723	8.668	8.315	2.54E-01	5.53E-01	-0.41	-0.35
lpg1981	small ORF (98aa)		ORFs of unknown function (unique)	8.133	9.382	8.036	9.114	3.93E-02	3.69E-01	1.25	1.08
lpg1981	small ORF (98aa)		ORFs of unknown function (unique)	8.554	10.605	7.932	10.299	2.47E-03	3.61E-03	2.05	2.37
lpg1982	hypothetical protein		Unknown / hypothetical proteins	8.896	8.664	10.229	7.809	7.53E-01	9.66E-03	-0.23	-2.42
lpg1982	hypothetical protein		Unknown / hypothetical proteins	8.896	8.353	9.853	8.432	4.03E-01	2.63E-02	-0.54	-1.42
lpg1983	protein product; some similarities with 3-hydroxy-3-methylglutaryl coe		Unknown / hypothetical proteins	9.237	9.061	10.184	8.083	7.79E-01	1.83E-01	-0.18	-2.10
lpg1983	protein product; some similarities with 3-hydroxy-3-methylglutaryl coe		Unknown / hypothetical proteins	9.228	9.160	10.157	8.248	9.19E-01	1.36E-01	-0.07	-1.91
lpg1984	hydantoin racemase	*hyuE*	Named proteins of general function	9.011	8.598	10.322	8.324	1.09E-01	1.43E-02	-0.41	-2.00
lpg1984	hydantoin racemase	*hyuE*	Named proteins of general function	9.292	8.927	10.268	8.812	3.29E-01	2.78E-02	-0.37	-1.46
lpg1985	guanine aminohydrolase (guanine deaminase)	*gad*	Nucleotide Metabolism	9.293	9.787	11.454	9.293	5.64E-01	9.67E-03	0.49	-2.16
lpg1985	guanine aminohydrolase (guanine deaminase)	*gad*	Nucleotide Metabolism	9.202	9.610	11.064	9.749	6.98E-01	1.19E-01	0.41	-1.31
lpg1986	ORF		ORFs of unknown function (unique)	8.390	9.266	9.554	9.504	1.48E-01	9.05E-01	0.88	-0.05
lpg1986	ORF		ORFs of unknown function (unique)	9.496	9.644	9.484	10.540	7.66E-01	7.74E-02	0.15	1.06
lpg1987	phosphohistidine phosphatase SixA		Carbohydrate Metabolism, Metabolis	9.095	8.433	10.261	8.241	1.66E-01	5.86E-02	-0.66	-2.02
lpg1987	phosphohistidine phosphatase SixA		Carbohydrate Metabolism, Metabolis	8.592	8.166	10.264	8.579	4.40E-01	6.54E-02	-0.43	-1.69
lpg1988	dihydrofolate reductase		Metabolism of Cofactors and Vitamins	9.911	10.670	8.603	10.088	1.34E-01	5.31E-03	0.76	1.49
lpg1988	dihydrofolate reductase		Metabolism of Cofactors and Vitamins	9.733	10.551	7.616	10.075	5.36E-02	1.92E-03	0.82	2.46
lpg1989	glutathione S-transferase?		Detoxification / adaptation	10.003	8.532	9.432	8.221	2.32E-02	4.90E-02	-1.47	-1.21
lpg1989	glutathione S-transferase?		Detoxification / adaptation	9.857	8.337	9.239	8.122	5.53E-02	2.39E-01	-1.52	-1.12
lpg1990	ORF		ORFs of unknown function (unique)	8.953	7.353	7.178	4.874	1.85E-01	1.71E-01	-1.60	-2.30
lpg1990	ORF		ORFs of unknown function (unique)	8.541	8.304	6.469	4.402	7.17E-01	3.47E-01	-0.24	-2.07
lpg1991	hypothetical conserved protein		Unknown / hypothetical proteins	10.056	9.309	9.733	9.197	1.09E-01	4.38E-01	-0.75	-0.54
lpg1991	hypothetical conserved protein		Unknown / hypothetical proteins	10.029	8.405	9.758	9.299	1.04E-02	4.24E-01	-1.62	-0.46
lpg1992	ORF		ORFs of unknown function (unique)	11.350	11.602	12.315	11.487	6.94E-01	2.31E-01	0.25	-0.83
lpg1992	ORF		ORFs of unknown function (unique)	11.306	11.716	12.236	11.666	4.00E-01	2.14E-01	0.41	-0.57
lpg1993	polysaccharide deacetylase		Metabolism of Complex Carbohydrate	10.217	8.695	12.985	8.852	2.01E-01	1.36E-03	-1.52	-4.13
lpg1993	polysaccharide deacetylase		Metabolism of Complex Carbohydrate	10.313	9.800	12.995	9.015	6.61E-01	4.36E-03	-0.51	-3.98
lpg1994	(outer) membrane bound lytic murein transglycosylase family protein		Metabolism of Complex Carbohydrate	11.638	11.789	10.983	11.701	6.14E-01	6.33E-03	0.15	0.72
lpg1994	(outer) membrane bound lytic murein transglycosylase family protein		Metabolism of Complex Carbohydrate	11.781	11.829	10.948	11.724	7.90E-01	2.24E-03	0.05	0.78
lpg1995	ORF		ORFs of unknown function (unique)	9.332	8.736	8.319	8.712	1.28E-01	6.34E-01	-0.60	0.39
lpg1995	ORF		ORFs of unknown function (unique)	9.652	9.043	8.515	8.923	1.67E-01	6.34E-01	-0.61	0.41

lpg1996	ORF (PilW?)		Unknown / hypothetical proteins	11.048	8.617	9.118	7.926	5.86E-02	3.25E-01	-2.43	-1.19
lpg1996	ORF (PilW?)		Unknown / hypothetical proteins	10.056	8.549	7.861	8.424	2.19E-02	5.26E-01	-1.51	0.56
lpg1997	small ORF (104aa)		ORFs of unknown function (unique)	11.629	10.780	8.875	11.411	5.54E-02	4.18E-03	-0.85	2.54
lpg1997	small ORF (104aa)		ORFs of unknown function (unique)	11.393	10.757	8.203	11.169	3.26E-01	2.15E-02	-0.64	2.97
lpg1998	histidinol phosphate aminotransferase	*hisC2*	Amino Acid Metabolism	10.837	10.594	8.118	10.699	4.54E-01	1.79E-02	-0.24	2.58
lpg1998	histidinol phosphate aminotransferase	*hisC2*	Amino Acid Metabolism	10.465	10.468	8.119	10.805	9.97E-01	9.26E-03	0.00	2.69
lpg1999	pterin 4 alpha carbinolamine dehydratase COG2154		Named proteins of general function	13.306	11.774	11.063	11.518	2.25E-01	4.25E-01	-1.53	0.45
lpg1999	pterin 4 alpha carbinolamine dehydratase COG2154		Named proteins of general function	13.950	11.708	10.907	11.639	6.07E-03	2.28E-01	-2.24	0.73
lpg2000	protein export protein SecF (preprotein translocase subu	*secF*	Protein fate / hydrolases / secretion	11.220	9.883	9.957	11.237	1.05E-01	2.81E-02	-1.34	1.28
lpg2000	protein export protein SecF (preprotein translocase subu	*secF*	Protein fate / hydrolases / secretion	11.351	9.977	9.520	11.386	5.38E-02	2.57E-02	-1.37	1.87
lpg2001	protein export protein SecD (preprotein translocase subu	*secD*	Protein fate / hydrolases / secretion	12.985	12.310	10.593	13.928	5.08E-01	6.38E-04	-0.67	3.33
lpg2001	protein export protein SecD (preprotein translocase subu	*secD*	Protein fate / hydrolases / secretion	13.116	12.338	9.658	13.938	3.17E-01	5.71E-03	-0.78	4.28
lpg2002	transmembrane protein YajC, preprotein translocase sub	*yajC*	Protein fate / hydrolases / secretion	11.830	11.333	10.658	12.677	3.51E-01	1.03E-03	-0.50	2.02
lpg2002	transmembrane protein YajC, preprotein translocase sub	*yajC*	Protein fate / hydrolases / secretion	11.708	11.486	10.604	12.691	7.13E-01	4.38E-04	-0.22	2.09
lpg2003	queuine tRNA-ribosyltransferase	*tgt*	DNA/RNA degradation / restriction, Tra	10.462	9.647	8.904	9.136	7.16E-02	8.50E-01	-0.82	0.23
lpg2003	queuine tRNA-ribosyltransferase	*tgt*	DNA/RNA degradation / restriction, Tra	10.650	10.314	9.025	10.072	5.51E-01	2.02E-01	-0.34	1.05
lpg2004	S-adenosylmethionine:tRNA ribosyltransferase-isomeras	*queA*	DNA/RNA degradation / restriction, Tra	9.488	11.006	10.517	11.028	1.14E-01	4.91E-01	1.52	0.51
lpg2004	S-adenosylmethionine:tRNA ribosyltransferase-isomeras	*queA*	DNA/RNA degradation / restriction, Tra	10.178	11.244	10.508	11.236	1.21E-01	1.94E-01	1.07	0.73
lpg2005	small ORF (137aa)		ORFs of unknown function (unique)	11.345	10.876	10.894	9.138	2.80E-01	3.58E-01	-0.47	-1.76
lpg2005	small ORF (137aa)		ORFs of unknown function (unique)	11.270	10.991	11.129	10.948	5.35E-01	6.35E-01	-0.28	-0.18
lpg2006	ABC transporter ATP binding protein	*uup-A*	Transport and binding	9.887	10.465	9.349	11.114	2.30E-01	7.72E-03	0.58	1.76
lpg2006	ABC transporter ATP binding protein	*uup-A*	Transport and binding	9.956	10.602	9.289	11.355	1.21E-01	4.82E-03	0.65	2.07
lpg2007	aspartyl protease		Protein fate / hydrolases / secretion	11.839	10.156	11.175	12.753	1.95E-02	2.59E-03	-1.68	1.58
lpg2007	aspartyl protease		Protein fate / hydrolases / secretion	11.715	10.981	11.094	12.890	2.09E-01	1.07E-03	-0.73	1.80
lpg2008	endoribonuclease L-PSP (translation initiation inhibitor)		DNA/RNA degradation / restriction, Sig	11.403	10.732	11.203	12.855	4.91E-02	6.95E-04	-0.67	1.65
lpg2008	endoribonuclease L-PSP (translation initiation inhibitor)		DNA/RNA degradation / restriction, Sig	11.394	10.695	11.036	12.890	7.70E-02	2.69E-04	-0.70	1.85
lpg2009	guanosine-3,5-bis(diphosphate)-3-pyrophosphohydrolas	*spoT*	Nucleotide Metabolism	11.081	10.096	11.274	10.924	6.92E-02	2.44E-01	-0.98	-0.35
lpg2009	guanosine-3,5-bis(diphosphate)-3-pyrophosphohydrolas	*spoT*	Nucleotide Metabolism	11.028	11.149	11.329	11.682	8.46E-01	4.82E-01	0.12	0.35
lpg2010	guanylate kinase	*gmk*	Nucleotide Metabolism	12.330	11.348	12.473	12.250	3.69E-03	1.40E-01	-0.98	-0.22
lpg2010	guanylate kinase	*gmk*	Nucleotide Metabolism	12.329	11.458	12.483	12.275	2.73E-02	1.77E-01	-0.87	-0.21
lpg2011	stress-induced protein		Detoxification / adaptation	11.153	11.172	11.040	12.393	9.32E-01	1.25E-02	0.02	1.35
lpg2011	stress-induced protein		Detoxification / adaptation	10.986	11.192	10.798	12.336	4.52E-01	1.65E-02	0.21	1.54
lpg2012	ribonuclease PH (RNAse PH)	*rph*	DNA/RNA degradation / restriction, Tra	11.947	12.560	10.959	13.042	8.98E-02	8.41E-06	0.61	2.08
lpg2012	ribonuclease PH (RNAse PH)	*rph*	DNA/RNA degradation / restriction, Tra	11.829	12.585	10.797	13.024	7.69E-02	1.73E-05	0.76	2.23
lpg2013	twitching motility protein (pilin biogenesis protein PilT)	*pilT*	Transport and binding	11.770	12.160	11.921	11.906	6.20E-02	9.60E-01	0.39	-0.02
lpg2013	twitching motility protein (pilin biogenesis protein PilT)	*pilT*	Transport and binding	11.912	12.044	11.923	11.978	6.10E-01	8.58E-01	0.13	0.06
lpg2014	pyridoxal-5'-phosphate dependent enzyme family (may have various		Named proteins of general function	10.293	10.943	9.690	10.946	1.55E-01	1.13E-01	0.65	1.26
lpg2014	pyridoxal-5'-phosphate dependent enzyme family (may have various		Named proteins of general function	9.868	11.174	9.842	11.180	5.22E-02	2.67E-02	1.31	1.34
lpg2015	pyrroline-5-carboxylate reductase (delta-1-pyrroline-5-ca	*proC*	Amino Acid Metabolism	9.543	10.827	9.676	10.400	8.59E-03	1.67E-02	1.28	0.72
lpg2015	pyrroline-5-carboxylate reductase (delta-1-pyrroline-5-ca	*proC*	Amino Acid Metabolism	9.822	10.956	9.482	10.653	4.97E-02	5.34E-02	1.13	1.17
lpg2016	hypothetical (YGGT family protein) (transmembrane protein)		Named proteins of general function	12.262	12.697	10.523	12.651	4.66E-02	2.74E-04	0.43	2.13
lpg2016	hypothetical (YGGT family protein) (transmembrane protein)		Named proteins of general function	12.329	12.848	10.194	12.736	1.57E-02	3.23E-03	0.52	2.54
lpg2017	ORF		ORFs of unknown function (unique)	9.347	9.168	11.582	9.323	7.67E-01	1.82E-04	-0.18	-2.26
lpg2017	ORF		ORFs of unknown function (unique)	9.102	9.153	11.116	8.948	8.53E-01	9.60E-04	0.05	-2.17
lpg2018	hypothetical protein		Unknown / hypothetical proteins	12.432	10.842	13.214	11.071	7.65E-04	3.98E-05	-1.59	-2.14
lpg2018	hypothetical protein		Unknown / hypothetical proteins	12.429	10.972	13.136	11.565	1.37E-03	1.12E-04	-1.46	-1.57
lpg2019	serine metalloprotease (alkaline?) (acidic protease?)		Protein fate / hydrolases / secretion	11.292	12.830	11.328	11.371	5.24E-06	8.01E-01	1.54	0.04
lpg2019	serine metalloprotease (alkaline?) (acidic protease?)		Protein fate / hydrolases / secretion	11.207	12.902	11.261	11.454	2.65E-05	3.06E-01	1.69	0.19
lpg2020	transcriptional regulator OruR, AraC family	*oruR*	Transcription factors / DNA binding pro	10.404	9.089	9.646	8.637	1.54E-02	1.84E-02	-1.32	-1.01
lpg2020	transcriptional regulator OruR, AraC family	*oruR*	Transcription factors / DNA binding pro	10.481	8.626	9.556	8.852	3.46E-02	3.38E-01	-1.85	-0.70
lpg2021	adenosylhomocysteinase	*ahcY*	Amino Acid Metabolism, Metabolism o	12.601	11.313	12.368	11.545	9.73E-04	3.94E-04	-1.29	-0.82
lpg2021	adenosylhomocysteinase	*ahcY*	Amino Acid Metabolism, Metabolism o	12.579	11.932	12.372	12.080	3.54E-01	6.86E-01	-0.65	-0.29
lpg2022	S-adenosylmethionine synthetase	*metK*	Amino Acid Metabolism, Metabolism o	12.963	12.436	11.610	12.976	2.47E-01	2.25E-02	-0.53	1.37
lpg2022	S-adenosylmethionine synthetase	*metK*	Amino Acid Metabolism, Metabolism o	12.889	12.401	11.631	12.998	3.47E-01	1.93E-02	-0.49	1.37
lpg2023	carbamoyl phosphate synthase, small subunit		Nucleotide Metabolism, Amino Acid Me	12.547	12.433	10.931	12.117	7.09E-01	2.79E-01	-0.11	1.19
lpg2023	carbamoyl phosphate synthase, small subunit		Nucleotide Metabolism, Amino Acid Me	12.491	12.269	10.828	13.004	5.59E-01	9.49E-03	-0.22	2.18
lpg2024	heat shock protein DnaJ, chaperone protein	*dnaJ*	Detoxification / adaptation, Protein fate	10.004	10.786	10.196	10.747	3.97E-02	1.94E-01	0.78	0.55
lpg2024	heat shock protein DnaJ, chaperone protein	*dnaJ*	Detoxification / adaptation, Protein fate	9.581	11.524	10.275	11.536	8.97E-03	4.28E-02	1.94	1.26
lpg2025	chaperone protein DnaK, heat shock protein Hsp70	*dnaK*	Detoxification / adaptation, Protein fate	11.782	11.164	12.578	11.862	2.02E-01	2.43E-01	-0.62	-0.72
lpg2025	chaperone protein DnaK, heat shock protein Hsp70	*dnaK*	Detoxification / adaptation, Protein fate	11.811	11.439	12.569	12.097	3.34E-01	2.91E-01	-0.37	-0.47
lpg2026	heat shock protein GrpE	*grpE*	Detoxification / adaptation, Protein fate	11.704	11.800	11.894	12.876	8.51E-01	1.21E-02	0.10	0.98
lpg2026	heat shock protein GrpE	*grpE*	Detoxification / adaptation, Protein fate	11.656	11.320	11.844	12.884	5.14E-01	1.18E-02	-0.34	1.04
lpg2027	2-keto-3-deoxy-D-arabino-heptulosonate 7-phosphate sy	*dhs1*	Amino Acid Metabolism	12.757	12.757	11.931	12.966	9.99E-01	5.78E-04	0.00	1.03
lpg2027	2-keto-3-deoxy-D-arabino-heptulosonate 7-phosphate sy	*dhs1*	Amino Acid Metabolism	12.798	12.835	11.864	12.956	8.29E-01	1.45E-03	0.04	1.09

lpg2028	uroporphyrinogen decarboxylase	*hemE*	Metabolism of Cofactors and Vitamins	11.290	11.487	11.384	12.091	5.33E-01	5.21E-02	0.20	0.71
lpg2028	uroporphyrinogen decarboxylase	*hemE*	Metabolism of Cofactors and Vitamins	11.084	11.467	11.194	12.140	2.84E-01	1.21E-02	0.38	0.95
lpg2029	dihydroneopterin aldolase FolB, kinase? COG1539		Metabolism of Cofactors and Vitamins	8.740	10.766	8.838	9.766	1.81E-03	1.30E-02	2.03	0.93
lpg2029	dihydroneopterin aldolase FolB, kinase? COG1539		Metabolism of Cofactors and Vitamins	9.298	9.983	6.676	8.694	1.97E-01	2.00E-01	0.69	2.02
lpg2030	conserved hypothetical protein		Unknown / hypothetical proteins	11.307	12.606	11.591	11.263	4.19E-03	2.32E-02	1.30	-0.33
lpg2030	conserved hypothetical protein		Unknown / hypothetical proteins	11.192	12.850	11.584	11.265	2.65E-03	1.06E-01	1.66	-0.32
lpg2031	arginyl tRNA synthetase	*argS*	Amino Acid Metabolism, Translation	11.617	12.226	10.382	12.583	1.13E-01	5.85E-04	0.61	2.20
lpg2031	arginyl tRNA synthetase	*argS*	Amino Acid Metabolism, Translation	11.352	12.257	9.805	12.641	9.66E-02	3.02E-04	0.91	2.84
lpg2032	transporter, permease (integral membrane protein)		Transport and binding	11.026	10.684	10.399	10.320	8.31E-01	8.75E-01	-0.34	-0.08
lpg2032	transporter, permease (integral membrane protein)		Transport and binding	11.284	11.998	10.270	10.300	1.07E-01	9.45E-01	0.71	0.03
lpg2033	ATP dependent DNA helicase RecG	*recG*	Replication and Repair	10.467	8.670	9.148	9.253	5.34E-03	8.54E-01	-1.80	0.11
lpg2033	ATP dependent DNA helicase RecG	*recG*	Replication and Repair	10.028	8.727	8.142	9.262	7.44E-02	3.44E-01	-1.30	1.12
lpg2034	cation efflux family protein (cobalt-zinc-cadmium resistance protein C		Transport and binding	10.069	9.470	9.190	9.759	3.56E-01	4.26E-01	-0.60	0.57
lpg2034	cation efflux family protein (cobalt-zinc-cadmium resistance protein C		Transport and binding	9.648	9.351	8.184	10.489	7.98E-01	3.78E-02	-0.30	2.30
lpg2035	transporter, Zip family (solute carrier; Fe(II) transporter)		Transport and binding	10.621	10.274	9.788	10.370	4.49E-01	1.10E-01	-0.35	0.58
lpg2035	transporter, Zip family (solute carrier; Fe(II) transporter)		Transport and binding	10.961	10.506	9.523	10.643	2.59E-01	2.23E-02	-0.45	1.12
lpg2036	Maf-like protein (septum formation) (nucleotide binding protein)		Chemotaxis / motility / cell division, Tra	11.580	9.035	9.438	9.399	3.07E-04	9.75E-01	-2.55	-0.04
lpg2036	Maf-like protein (septum formation) (nucleotide binding protein)		Chemotaxis / motility / cell division, Tra	11.626	8.601	9.041	9.594	8.65E-05	5.97E-01	-3.02	0.55
lpg2037	enolase	*eno*	Carbohydrate Metabolism, Amino Acid	11.438	10.345	9.763	10.845	5.64E-02	3.86E-02	-1.09	1.08
lpg2037	enolase	*eno*	Carbohydrate Metabolism, Amino Acid	11.479	10.450	9.437	10.627	4.31E-02	1.37E-01	-1.03	1.19
lpg2038	transmembrane protein (septum formation initiator?)		Chemotaxis / motility / cell division	10.222	10.476	10.784	9.564	5.87E-01	4.11E-02	0.25	-1.22
lpg2038	transmembrane protein (septum formation initiator?)		Chemotaxis / motility / cell division	10.244	10.196	10.626	9.889	9.35E-01	1.59E-01	-0.05	-0.74
lpg2039	putative mevalonate kinase		Lipid Metabolism	11.591	10.258	11.662	11.356	7.75E-03	1.41E-01	-1.33	-0.31
lpg2039	putative mevalonate kinase		Lipid Metabolism	11.314	10.706	11.678	11.427	1.85E-01	2.27E-01	-0.61	-0.25
lpg2040	mevalonate diphosphate decarboxylase (diphosphomevalonate deca		Lipid Metabolism	12.559	11.373	11.995	11.957	3.46E-04	8.13E-01	-1.19	-0.04
lpg2040	mevalonate diphosphate decarboxylase (diphosphomevalonate deca		Lipid Metabolism	12.227	11.311	11.905	11.941	1.50E-02	8.51E-01	-0.92	0.04
lpg2041	radical activating enzyme (radical SAM domain protein)		Named proteins of general function	12.420	11.183	10.479	11.691	1.76E-03	3.48E-02	-1.24	1.21
lpg2041	radical activating enzyme (radical SAM domain protein)		Named proteins of general function	12.411	11.142	10.412	11.718	7.47E-04	2.14E-02	-1.27	1.31
lpg2042	outer membrane protein (34 kDa), TPR repeat		Toxin production / other pathogen func	13.308	13.818	11.691	13.385	3.61E-01	3.39E-03	0.51	1.69
lpg2042	outer membrane protein (34 kDa), TPR repeat		Toxin production / other pathogen func	13.383	13.781	11.549	13.399	4.42E-01	1.60E-03	0.40	1.85
lpg2043	peptidoglycan associated lipoprotein		Named proteins of general function	13.879	14.832	12.500	14.037	1.25E-01	6.53E-03	0.95	1.54
lpg2043	peptidoglycan associated lipoprotein		Named proteins of general function	13.926	14.941	12.514	14.108	1.30E-01	6.53E-03	1.02	1.59
lpg2044	conserved domain protein		Unknown / hypothetical proteins	11.131	10.685	11.582	11.067	4.38E-01	2.37E-01	-0.45	-0.51
lpg2044	conserved domain protein		Unknown / hypothetical proteins	11.003	11.447	11.934	11.815	8.03E-02	6.60E-01	0.44	-0.12
lpg2045	ABC transport system periplasmic substrate binding protein		Transport and binding	12.199	12.117	11.259	11.990	7.09E-01	1.05E-02	-0.08	0.73
lpg2045	ABC transport system periplasmic substrate binding protein		Transport and binding	12.175	12.173	11.235	11.999	9.92E-01	3.04E-03	0.00	0.76
lpg2046	ABC transporter, ATP binding protein		Transport and binding	11.855	12.052	10.510	12.565	4.54E-01	4.34E-06	0.20	2.06
lpg2046	ABC transporter, ATP binding protein		Transport and binding	11.786	12.395	10.437	12.576	1.76E-01	2.06E-05	0.61	2.14
lpg2047	ABC transporter, permease		Transport and binding	11.545	11.229	10.278	11.266	3.12E-01	3.77E-03	-0.32	0.99
lpg2047	ABC transporter, permease		Transport and binding	11.435	11.188	9.796	11.078	4.73E-01	4.21E-03	-0.25	1.28
lpg2048	ORF		ORFs of unknown function (unique)	9.716	9.465	10.929	10.323	5.97E-01	1.91E-01	-0.25	-0.61
lpg2048	ORF		ORFs of unknown function (unique)	9.832	9.315	10.787	10.379	3.87E-01	2.05E-01	-0.52	-0.41
lpg2049	small ORF (99aa)		ORFs of unknown function (unique)	8.593	7.989	10.971	8.584	5.70E-01	8.68E-03	-0.60	-2.39
lpg2049	small ORF (99aa)		ORFs of unknown function (unique)	9.615	9.238	11.062	9.917	7.22E-01	2.12E-01	-0.38	-1.15
lpg2050	ORF		ORFs of unknown function (unique)	9.657	10.414	8.820	8.554	4.87E-03	7.29E-01	0.76	-0.27
lpg2050	ORF		ORFs of unknown function (unique)	9.307	9.911	8.978	9.103	2.11E-01	7.81E-01	0.60	0.12
lpg2051	isopentenyl-diphosphate delta-isomerase (IPP isomerase) (carotenoi		Lipid Metabolism, Biosynthesis of Sec	11.040	11.511	8.989	11.589	2.83E-01	9.97E-04	0.47	2.60
lpg2051	isopentenyl-diphosphate delta-isomerase (IPP isomerase) (carotenoi		Lipid Metabolism, Biosynthesis of Sec	10.839	11.751	9.313	12.017	4.56E-02	1.64E-04	0.91	2.70
lpg2052	hydroxymethylglutaryl CoA reductase (3-hydroxy-3-methylglutaryl--co		Lipid Metabolism	12.014	11.677	10.561	11.700	3.24E-01	1.42E-02	-0.34	1.14
lpg2052	hydroxymethylglutaryl CoA reductase (3-hydroxy-3-methylglutaryl--co		Lipid Metabolism	12.076	11.671	10.382	11.523	2.32E-01	1.79E-02	-0.40	1.14
lpg2053	ORF		ORFs of unknown function (unique)	9.878	8.992	9.403	9.916	1.17E-02	1.47E-01	-0.89	0.51
lpg2053	ORF		ORFs of unknown function (unique)	10.237	9.357	9.495	10.209	8.53E-02	3.87E-02	-0.88	0.71
lpg2054	tRNA-Lys		tRNA	13.099	12.944	12.357	14.825	7.93E-01	7.41E-05	-0.16	2.47
lpg2054	tRNA-Lys		tRNA	13.085	12.934	12.323	14.842	7.92E-01	1.37E-04	-0.15	2.52
lpg2056	tRNA-Arg		tRNA	8.843	8.120	8.528	7.388	2.90E-01	3.16E-01	-0.72	-1.14
lpg2056	tRNA-Arg		tRNA	8.035	7.984	8.105	8.599	9.64E-01	5.69E-01	-0.05	0.49
lpg2057	Prophage dlp12 integrase (prophage qsr' integrase)	*intD*	Viral functions / Phage / Transposases	9.921	9.011	11.671	9.546	8.29E-02	1.90E-04	-0.91	-2.12
lpg2057	Prophage dlp12 integrase (prophage qsr' integrase)	*intD*	Viral functions / Phage / Transposases	9.865	8.868	11.564	9.842	4.19E-02	4.10E-04	-1.00	-1.72
lpg2058	hypothetical		Unknown / hypothetical proteins	6.784	7.329	7.032	6.887	5.48E-01	8.60E-01	0.55	-0.15
lpg2058	hypothetical		Unknown / hypothetical proteins	8.091	9.528	7.595	10.109	1.80E-01	7.03E-02	1.44	2.51
lpg2059	hypothetical (phage repressor) (putative regulator)		Transcription factors / DNA binding pro	9.030	9.235	10.466	8.674	4.16E-01	1.66E-02	0.21	-1.79
lpg2059	hypothetical (phage repressor) (putative regulator)		Transcription factors / DNA binding pro	9.139	9.042	10.431	9.257	7.35E-01	9.30E-03	-0.10	-1.17
lpg2060	ORF		ORFs of unknown function (unique)	7.961	8.683	9.784	7.969	4.30E-01	6.47E-02	0.72	-1.81
lpg2060	ORF		ORFs of unknown function (unique)	8.023	7.993	8.973	7.974	9.80E-01	3.71E-01	-0.03	-1.00

lpg2061	major facilitator family transporter		Transport and binding	8.209	8.441	9.179	8.738	8.08E-01	6.23E-01	0.23	-0.44
lpg2061	major facilitator family transporter		Transport and binding	7.680	9.473	9.122	9.218	1.22E-01	8.87E-01	1.79	0.10
lpg2062	methylase		Named proteins of general function	8.141	7.932	9.170	8.109	8.53E-01	2.69E-01	-0.21	-1.06
lpg2062	methylase		Named proteins of general function	7.607	7.840	9.049	8.998	8.40E-01	9.66E-01	0.23	-0.05
lpg2063	ABC transporter, ATP binding transmembrane protein		Transport and binding	9.767	7.486	7.284	5.437	3.57E-01	1.66E-01	-2.28	-1.85
lpg2063	ABC transporter, ATP binding transmembrane protein		Transport and binding		6.574	7.649	6.568		1.33E-01		-1.08
lpg2064	ATP-binding transmembrane ABC transporter (ABC transporter ATP b		Transport and binding	7.881	7.639	8.082	6.890	8.90E-01	2.50E-01	-0.24	-1.19
lpg2064	ATP-binding transmembrane ABC transporter (ABC transporter ATP b		Transport and binding	7.268	7.353	8.709	7.699	9.51E-01	1.49E-01	0.09	-1.01
lpg2065	D-xylose reductase III (aldo/keto reudctase family) (2,5-diketo-D-gluc		Carbohydrate Metabolism, Lipid Metab	7.640	7.201	9.202	7.285	5.45E-01	3.79E-02	-0.44	-1.92
lpg2065	D-xylose reductase III (aldo/keto reudctase family) (2,5-diketo-D-gluc		Carbohydrate Metabolism, Lipid Metab	7.874	8.421	8.567	7.609	2.23E-01	3.58E-01	0.55	-0.96
lpg2066	acetyltransferase, GNAT family COG1670		Named proteins of general function	7.235	3.572	9.006	7.629	4.52E-01	5.80E-01	-3.66	-1.38
lpg2066	acetyltransferase, GNAT family COG1670		Named proteins of general function	7.187	10.375	7.313	8.217	1.52E-01	6.48E-01	3.19	0.90
lpg2067	ORF hypothetical		Unknown / hypothetical proteins	8.478	7.943	9.302	7.634	4.18E-01	1.70E-02	-0.54	-1.67
lpg2067	ORF hypothetical		Unknown / hypothetical proteins	8.525	7.175	9.200	8.333	4.65E-02	1.18E-01	-1.35	-0.87
lpg2068	MazG (nucleoside triphosphate pyrophosphohydrolase)		Named proteins of general function	7.608	7.514	10.234	8.294	9.34E-01	1.17E-02	-0.09	-1.94
lpg2068	MazG (nucleoside triphosphate pyrophosphohydrolase)		Named proteins of general function	6.701	7.046	8.774	9.280	8.57E-01	6.38E-01	0.35	0.51
lpg2069	transposase Tn5		Viral functions / Phage / Transposases	7.011	7.508	7.066	5.987	7.46E-01	6.27E-01	0.50	-1.08
lpg2069	transposase Tn5		Viral functions / Phage / Transposases	7.255	6.151	7.430	6.405	3.60E-01	5.10E-01	-1.10	-1.02
lpg2070	reverse transcriptase		Viral functions / Phage / Transposases	7.651	7.876	7.753	8.041	8.16E-01	8.37E-01	0.23	0.29
lpg2070	reverse transcriptase		Viral functions / Phage / Transposases	6.640	7.798	8.070	8.564	4.54E-01	5.76E-01	1.16	0.49
lpg2071	hypothetical		Unknown / hypothetical proteins	8.665	8.976	10.152	7.143	4.01E-01	3.98E-02	0.31	-3.01
lpg2071	hypothetical		Unknown / hypothetical proteins	8.583	8.680	9.878	7.945	8.68E-01	1.43E-01	0.10	-1.93
lpg2072	hypothetical		Unknown / hypothetical proteins	6.568	8.356	7.768	7.451	8.27E-02	7.27E-01	1.79	-0.32
lpg2072	hypothetical		Unknown / hypothetical proteins	6.814	9.414	8.343	9.041	6.89E-02	3.85E-01	2.60	0.70
lpg2073	ORF		ORFs of unknown function (unique)	6.635	7.474	6.841	7.459	3.14E-01	7.04E-01	0.84	0.62
lpg2073	ORF		ORFs of unknown function (unique)	5.696	8.200	7.016	10.084	2.76E-01	7.91E-02	2.50	3.07
lpg2074	hypothetical (DNA adenine methylase?)		Unknown / hypothetical proteins	6.326	8.397	7.677	7.530	4.88E-01	9.31E-01	2.07	-0.15
lpg2074	hypothetical (DNA adenine methylase?)		Unknown / hypothetical proteins	6.782	5.637	7.253	8.458	4.65E-01	4.95E-01	-1.15	1.20
lpg2075	DNA adenine methylase	*dam*	DNA/RNA degradation / restriction	7.447	7.890	7.356	7.258	7.26E-01	9.40E-01	0.44	-0.10
lpg2075	DNA adenine methylase	*dam*	DNA/RNA degradation / restriction	6.519	7.608	6.895	7.905	3.47E-01	4.47E-01	1.09	1.01
lpg2076	hypothetical		Unknown / hypothetical proteins	8.406	8.296	7.541	7.652	8.55E-01	9.33E-01	-0.11	0.11
lpg2076	hypothetical		Unknown / hypothetical proteins	7.924	8.525	7.421	7.904	3.39E-01	7.39E-01	0.60	0.48
lpg2077	TraI (mobilization protein, DNA helicase) (TrwC)		Transport and binding, DNA/RNA degr	10.014	8.390	8.917	7.506	6.01E-02	2.74E-01	-1.62	-1.41
lpg2077	TraI (mobilization protein, DNA helicase) (TrwC)		Transport and binding, DNA/RNA degr	9.909	8.870	9.219	8.895	3.71E-02	7.07E-01	-1.04	-0.32
lpg2078	TraD (conjugal DNA metabolism) (bacterial conjugative coupling prote		Transport and binding	9.634	9.404	9.347	8.913	5.17E-01	5.33E-01	-0.23	-0.43
lpg2078	TraD (conjugal DNA metabolism) (bacterial conjugative coupling prote		Transport and binding	9.851	9.752	9.426	9.140	8.19E-01	7.23E-01	-0.10	-0.29
lpg2079	TraG (mating pair stabilization and pilus assembly protein	*traG*	Transport and binding	9.547	5.772	9.856	7.752	4.89E-02	1.51E-02	-3.77	-2.10
lpg2079	TraG (mating pair stabilization and pilus assembly protein	*traG*	Transport and binding	8.519	7.972	9.670	7.916	9.04E-02	6.33E-03	-0.55	-1.75
lpg2080	TraH (pilus assembly protein) (conjugative transfer: asse	*traH*	Transport and binding	6.876	8.896	7.261	8.525	1.45E-01	1.84E-01	2.02	1.26
lpg2080	TraH (pilus assembly protein) (conjugative transfer: asse	*traH*	Transport and binding	5.464	7.749	6.897	8.264	3.79E-01	1.89E-01	2.28	1.37
lpg2081	sex pilus assembly TraF (conjugative transfer: assembly)	*traF*	Transport and binding, Viral functions /	8.270	8.401	9.428	8.066	8.47E-01	8.15E-02	0.13	-1.36
lpg2081	sex pilus assembly TraF (conjugative transfer: assembly)	*traF*	Transport and binding, Viral functions /	9.236	9.201	10.309	9.201	9.33E-01	3.05E-02	-0.03	-1.11
lpg2082	small ORF (57aa) sex pilus assembly TraF (conjugative t	*traF*	Transport and binding	9.301	8.401	10.647	9.366	4.01E-01	1.40E-02	-0.90	-1.28
lpg2082	small ORF (57aa) sex pilus assembly TraF (conjugative t	*traF*	Transport and binding	8.920	9.928	10.512	9.436	7.76E-04	2.32E-02	1.01	-1.08
lpg2083	TraN (mating pair stablization protein) (conjugative transf	*traN*	Transport and binding	7.132	8.430	7.479	7.824	1.49E-01	8.49E-01	1.30	0.35
lpg2083	TraN (mating pair stablization protein) (conjugative transf	*traN*	Transport and binding	5.985	8.914	6.705	8.371	2.96E-02	2.59E-01	2.93	1.67
lpg2084	putative conjugative transfer protein TrbC		Transport and binding	8.395	7.800	8.155	8.030	2.03E-01	9.31E-01	-0.60	-0.12
lpg2084	putative conjugative transfer protein TrbC		Transport and binding	8.694	7.881	7.742	8.425	4.50E-01	5.59E-01	-0.81	0.68
lpg2085	TraU (sex pilus assembly and synthesis protein) (conjuga	*traU*	Transport and binding	9.438	8.619	10.010	9.305	2.67E-01	3.45E-01	-0.82	-0.70
lpg2085	TraU (sex pilus assembly and synthesis protein) (conjuga	*traU*	Transport and binding	9.382	9.558	9.319	9.986	8.89E-01	6.02E-01	0.18	0.67
lpg2086	TraW (sex pilus assembly and synthesis protein)		Transport and binding	7.120	7.614	7.724	8.451	5.31E-01	2.56E-01	0.49	0.73
lpg2086	TraW (sex pilus assembly and synthesis protein)		Transport and binding	7.758	6.837	6.605	8.371	5.58E-01	1.54E-01	-0.92	1.77
lpg2087	TraC (sex pilus assembly and synthesis protein) (conjuga	*traC*	Transport and binding	7.281	7.535	6.759	7.234	7.17E-01	7.33E-01	0.25	0.48
lpg2087	TraC (sex pilus assembly and synthesis protein) (conjuga	*traC*	Transport and binding	6.316	8.258	7.550	9.863	3.91E-01	2.02E-01	1.94	2.31
lpg2088	conjugative transfer: assembly	*traV*	Transport and binding	8.783	8.387	10.073	9.430	4.80E-01	5.37E-02	-0.40	-0.64
lpg2088	conjugative transfer: assembly	*traV*	Transport and binding	9.324	9.370	9.976	10.532	9.32E-01	3.27E-01	0.05	0.56
lpg2089	putative conjugative transfer protein TraB		Transport and binding, Replication anc	8.643	9.879	9.163	9.244	1.02E-02	8.29E-01	1.24	0.08
lpg2089	putative conjugative transfer protein TraB		Transport and binding, Replication anc	8.594	8.971	9.141	9.310	5.75E-01	6.99E-01	0.38	0.17
lpg2090	putative conjugative transfer protein TraK		Transport and binding	7.788	5.949	7.010	6.888	1.10E-01	8.97E-01	-1.84	-0.12
lpg2090	putative conjugative transfer protein TraK		Transport and binding	6.286	7.997	4.554	9.066	5.80E-01	1.74E-01	1.71	4.51
lpg2091	putative conjugative transfer protein TraE		Transport and binding	7.272	8.593	8.954	7.889	3.96E-01	4.57E-01	1.32	-1.07
lpg2091	putative conjugative transfer protein TraE		Transport and binding	9.308	10.637	8.856	8.545	4.09E-01	7.40E-01	1.33	-0.31
lpg2092	ORF (sex pilus assembly protein??)		Unknown / hypothetical proteins	8.007	7.480	8.813	8.418	8.30E-01	6.35E-01	-0.53	-0.40
lpg2092	ORF (sex pilus assembly protein??)		Unknown / hypothetical proteins	8.276	6.326	7.548	8.071	3.98E-01	6.85E-01	-1.95	0.52

lpg2093	ORF (fimbrial protein precursor?)		Unknown / hypothetical proteins	6.774	6.420	8.307	7.813	8.88E-01	8.76E-01	-0.35	-0.49
lpg2093	ORF (fimbrial protein precursor?)		Unknown / hypothetical proteins	5.829	8.960	6.821	6.927	3.33E-01	9.75E-01	3.13	0.11
lpg2094	carbon storage regulator RsmA (controls glycogen synthe	*csrA*	Signal transduction / other regulatory f	8.937	8.871	9.803	8.406	9.09E-01	1.97E-02	-0.07	-1.40
lpg2094	carbon storage regulator RsmA (controls glycogen synthe	*csrA*	Signal transduction / other regulatory f	8.764	10.469	9.729	8.815	1.17E-02	2.11E-01	1.71	-0.91
lpg2095	LvrA	*lvrA*	Transport and binding, Protein fate / hy	7.331	7.264	6.727	5.282	9.51E-01	4.34E-01	-0.07	-1.45
lpg2095	LvrA	*lvrA*	Transport and binding, Protein fate / hy	6.778	8.305	6.365	7.363	2.81E-01	5.51E-01	1.53	1.00
lpg2096	hypothetical (prophage repressor CI?)		Unknown / hypothetical proteins	9.828	9.475	10.998	9.124	3.37E-01	2.36E-02	-0.35	-1.87
lpg2096	hypothetical (prophage repressor CI?)		Unknown / hypothetical proteins	9.551	9.013	10.835	9.499	8.35E-02	9.97E-02	-0.54	-1.34
lpg2097	hypothetical protein		Unknown / hypothetical proteins	9.516	9.320	8.780	8.896	8.02E-01	8.95E-01	-0.20	0.12
lpg2097	hypothetical protein		Unknown / hypothetical proteins	9.732	9.200	8.431	8.580	3.39E-01	8.59E-01	-0.53	0.15
lpg2098	MsrA3 - peptide methionine sulfoxide reductase		Detoxification / adaptation	9.042	7.724	7.871	7.734	4.29E-03	9.08E-01	-1.32	-0.14
lpg2098	MsrA3 - peptide methionine sulfoxide reductase		Detoxification / adaptation	9.241	7.727	8.286	8.450	1.25E-02	8.68E-01	-1.51	0.16
lpg2099	MsrA2 - peptide methionine sulfoxide reductase		Detoxification / adaptation	7.673	6.498	7.206	6.712	3.47E-01	6.71E-01	-1.18	-0.49
lpg2099	MsrA2 - peptide methionine sulfoxide reductase		Detoxification / adaptation	7.699	7.087	7.376	7.388	5.53E-01	9.90E-01	-0.61	0.01
lpg2100	phosphatidoglycerophosphate synthase?		Metabolism of Complex Lipids	12.207	11.909	13.345	12.370	5.98E-01	6.95E-02	-0.30	-0.98
lpg2100	phosphatidoglycerophosphate synthase?		Metabolism of Complex Lipids	12.163	12.008	13.233	12.299	7.16E-01	5.59E-02	-0.16	-0.93
lpg2101	mercuric reductase (dihydrolipoamide dehydrogenase/glu	*merA1*	Detoxification / adaptation	10.341	9.522	10.849	8.539	1.51E-01	7.26E-02	-0.82	-2.31
lpg2101	mercuric reductase (dihydrolipoamide dehydrogenase/glu	*merA1*	Detoxification / adaptation	10.277	9.576	10.757	9.100	2.10E-01	1.32E-02	-0.70	-1.66
lpg2102	sterol desaturase		Lipid Metabolism	7.079	7.794	8.205	8.033	6.31E-01	9.04E-01	0.72	-0.17
lpg2102	sterol desaturase		Lipid Metabolism	7.864	8.326	8.266	8.146	6.66E-01	9.21E-01	0.46	-0.12
lpg2103	small ORF (48aa) integrase/recombinase?		Viral functions / Phage / Transposases	7.279	8.665	6.740	6.690	2.72E-01	9.79E-01	1.39	-0.05
lpg2103	small ORF (48aa) integrase/recombinase?		Viral functions / Phage / Transposases	7.783	8.433	7.630	8.065	5.43E-01	7.74E-01	0.65	0.43
lpg2104	glutathione S-transferase?		Detoxification / adaptation	7.606	7.633	8.562	8.096	9.85E-01	6.02E-01	0.03	-0.47
lpg2104	glutathione S-transferase?		Detoxification / adaptation	7.420	6.493	8.172	8.252	6.22E-01	9.40E-01	-0.93	0.08
lpg2105	transmembrane protein? COG2259		Unknown / hypothetical proteins	7.309	6.995	9.302	6.985	8.29E-01	9.60E-02	-0.31	-2.32
lpg2105	transmembrane protein? COG2259		Unknown / hypothetical proteins	8.446	9.073	9.173	7.984	5.81E-01	3.73E-01	0.63	-1.19
lpg2106	conserved hypothetical protein		Unknown / hypothetical proteins	9.095	7.785	8.241	7.982	1.59E-01	8.00E-01	-1.31	-0.26
lpg2106	conserved hypothetical protein		Unknown / hypothetical proteins	9.563	6.749	7.880	8.619	1.47E-05	3.82E-01	-2.81	0.74
lpg2107	hypothetical protein		Unknown / hypothetical proteins	5.843	8.293	6.620	7.257	5.84E-02	8.07E-01	2.45	0.64
lpg2107	hypothetical protein		Unknown / hypothetical proteins	5.375	7.432	6.620	8.226	2.20E-01	2.94E-01	2.06	1.61
lpg2108	ORF (integral membrane protein?)		Unknown / hypothetical proteins	6.729	7.090	8.651	7.960	8.19E-01	3.71E-01	0.36	-0.69
lpg2108	ORF (integral membrane protein?)		Unknown / hypothetical proteins	6.849	7.667	8.189	8.298	5.66E-01	9.39E-01	0.82	0.11
lpg2109	ORF		ORFs of unknown function (unique)	8.037	9.894	9.483	9.356	2.04E-01	9.04E-01	1.86	-0.13
lpg2109	ORF		ORFs of unknown function (unique)	8.228	10.509	9.338	9.681	3.98E-02	6.24E-01	2.28	0.34
lpg2110	hypothetical protein		Unknown / hypothetical proteins	9.773	9.026	10.573	9.743	2.58E-01	2.14E-01	-0.75	-0.83
lpg2110	hypothetical protein		Unknown / hypothetical proteins	9.694	9.566	10.510	9.732	7.29E-01	2.52E-01	-0.13	-0.78
lpg2111	peptide methionine sulfoxide reductase		Detoxification / adaptation	6.702	8.242	7.178	6.069	2.44E-02	5.85E-01	1.54	-1.11
lpg2111	peptide methionine sulfoxide reductase		Detoxification / adaptation	6.621	7.236	7.223	6.925	6.01E-01	7.79E-01	0.61	-0.30
lpg2112	24 kDa macrophage-induced major protein (alkylhydroperoxidase Ahp		Toxin production / other pathogen func	7.391	7.350	6.161	6.416	9.66E-01	9.08E-01	-0.04	0.26
lpg2112	24 kDa macrophage-induced major protein (alkylhydroperoxidase Ahp		Toxin production / other pathogen func	7.687	7.687	7.426	8.525	9.99E-01	2.10E-01	0.00	1.10
lpg2113	ATP dependent DNA helicase?	*recG*	DNA/RNA degradation / restriction, Tra	7.952	7.382	9.011	6.137	2.99E-01	3.17E-03	-0.57	-2.87
lpg2113	ATP dependent DNA helicase?	*recG*	DNA/RNA degradation / restriction, Tra	7.210	7.125	8.828	7.251	9.47E-01	4.52E-02	-0.09	-1.58
lpg2114	transposase		Viral functions / Phage / Transposases	7.653	7.380	4.718	6.412	8.92E-01	4.16E-01	-0.27	1.69
lpg2114	transposase		Viral functions / Phage / Transposases	7.254	7.045	4.809	7.739	9.54E-01	6.98E-02	-0.21	2.93
lpg2115	hypothetical (phage AbiD protein)		Viral functions / Phage / Transposases	9.447	9.900	11.135	9.299	3.15E-01	1.75E-03	0.45	-1.84
lpg2115	hypothetical (phage AbiD protein)		Viral functions / Phage / Transposases	10.125	9.653	9.841	9.712	5.39E-01	8.34E-01	-0.47	-0.13
lpg2119	transposase (ISmav2) COG2801		Viral functions / Phage / Transposases	8.281	8.810	9.047	7.707	3.02E-01	8.12E-02	0.53	-1.34
lpg2119	transposase (ISmav2) COG2801		Viral functions / Phage / Transposases	8.406	9.007	9.373	8.107	4.02E-01	6.46E-02	0.60	-1.27
lpg2120	transposase, IS4 family (Tn5, TnpA)		Viral functions / Phage / Transposases	8.662	7.743	9.161	8.706	3.78E-01	5.75E-01	-0.92	-0.46
lpg2120	transposase, IS4 family (Tn5, TnpA)		Viral functions / Phage / Transposases	8.736	8.810	9.105	9.229	8.59E-01	8.55E-01	0.07	0.12
lpg2121	cold shock DNA binding domain protein (cold shock transcriptional reg		Detoxification / adaptation, Transcriptio	14.468	9.547	12.309	10.001	2.88E-05	2.55E-03	-4.92	-2.31
lpg2121	cold shock DNA binding domain protein (cold shock transcriptional reg		Detoxification / adaptation, Transcriptio	14.303	9.611	12.282	10.252	5.10E-05	5.82E-03	-4.69	-2.03
lpg2122	ATP dependent RNA helicase DeaD	*dbpA*	DNA/RNA degradation / restriction, Tra	11.862	11.374	9.782	10.749	1.83E-01	1.49E-01	-0.49	0.97
lpg2122	ATP dependent RNA helicase DeaD	*dbpA*	DNA/RNA degradation / restriction, Tra	11.999	11.303	9.864	10.923	3.17E-02	1.31E-01	-0.70	1.06
lpg2123	cobalt zinc cadmium cation transporter (membrane protein)		Transport and binding	11.158	9.966	12.367	9.568	1.10E-01	6.61E-04	-1.19	-2.80
lpg2123	cobalt zinc cadmium cation transporter (membrane protein)		Transport and binding	11.123	10.029	12.392	10.094	1.25E-01	2.00E-04	-1.09	-2.30
lpg2124	small ORF (57aa)		ORFs of unknown function (unique)	8.185	9.263	8.597	8.841	4.56E-01	7.63E-01	1.08	0.24
lpg2124	small ORF (57aa)		ORFs of unknown function (unique)	8.745	8.862	8.404	8.925	9.35E-01	5.22E-01	0.12	0.52
lpg2125	small ORF (153aa) transmembrane transport protein? cAMP depende		Transport and binding	10.658	10.408	12.444	10.309	5.55E-01	4.78E-04	-0.25	-2.13
lpg2125	small ORF (153aa) transmembrane transport protein? cAMP depende		Transport and binding	10.710	10.768	12.236	10.613	8.17E-01	1.14E-03	0.06	-1.62
lpg2126	Kup system potassium uptake protein	*kup2*	Transport and binding	9.266	8.961	10.540	8.074	6.01E-01	5.55E-03	-0.31	-2.47
lpg2126	Kup system potassium uptake protein	*kup2*	Transport and binding	9.499	9.101	10.537	8.177	5.53E-01	4.01E-02	-0.40	-2.36
lpg2127	hypothetical COG3034		Unknown / hypothetical proteins	9.180	11.871	10.443	8.665	3.28E-05	6.53E-03	2.69	-1.78
lpg2127	hypothetical COG3034		Unknown / hypothetical proteins	9.467	12.035	10.166	8.839	6.80E-05	8.66E-03	2.57	-1.33

lpg2128	ORF		ORFs of unknown function (unique)	9.925	10.323	8.297	11.101	2.56E-01	2.57E-04	0.40	2.80
lpg2128	ORF		ORFs of unknown function (unique)	9.675	10.231	7.329	11.174	3.11E-01	2.88E-03	0.56	3.85
lpg2129	small ORF (98aa)?		ORFs of unknown function (unique)	6.987	5.852	8.264	6.538	1.54E-01	3.89E-02	-1.13	-1.73
lpg2129	small ORF (98aa)?		ORFs of unknown function (unique)	6.569	7.080	8.087	7.517	7.71E-01	6.98E-01	0.51	-0.57
lpg2130	small ORF (89aa)?		ORFs of unknown function (unique)	9.111	9.504	9.314	8.485	5.24E-01	4.47E-01	0.39	-0.83
lpg2130	small ORF (89aa)?		ORFs of unknown function (unique)	9.442	8.754	10.105	9.378	6.09E-01	2.91E-01	-0.69	-0.73
lpg2131	ankyrin 3, node of Ranvier (ankyrin G)	*legA6*	Named proteins of general function	8.817	10.125	9.983	10.204	5.43E-02	7.10E-01	1.31	0.22
lpg2131	ankyrin 3, node of Ranvier (ankyrin G)	*legA6*	Named proteins of general function	9.631	11.544	10.134	11.726	2.21E-04	1.84E-03	1.91	1.59
lpg2132	sensory box/GGDEF family protein (regulatory components of sensor		Signal transduction / other regulatory f	9.626	9.696	11.759	7.994	8.96E-01	6.57E-03	0.07	-3.77
lpg2132	sensory box/GGDEF family protein (regulatory components of sensor		Signal transduction / other regulatory f	9.801	8.885	11.479	8.410	3.48E-01	5.08E-02	-0.92	-3.07
lpg2133	proline/glycine betaine transporter (major facilitator family transporter)		Transport and binding	10.079	10.040	10.814	10.681	9.53E-01	8.23E-01	-0.04	-0.13
lpg2133	proline/glycine betaine transporter (major facilitator family transporter)		Transport and binding	9.981	10.166	10.611	10.717	7.57E-01	8.44E-01	0.18	0.11
lpg2134	chemiosmotic efflux system protein A (heavy metal efflux pump CzcA)		Transport and binding	9.788	8.773	10.409	8.517	1.31E-01	1.41E-02	-1.02	-1.89
lpg2134	chemiosmotic efflux system protein A (heavy metal efflux pump CzcA)		Transport and binding	9.972	9.453	10.404	9.211	4.50E-01	1.27E-01	-0.52	-1.19
lpg2135	chemiosmotic efflux system protein B (cation efflux system)		Transport and binding	10.583	8.838	10.310	9.758	9.11E-03	3.19E-01	-1.75	-0.55
lpg2135	chemiosmotic efflux system protein B (cation efflux system)		Transport and binding	10.487	8.841	9.373	9.298	1.57E-03	9.46E-01	-1.65	-0.08
lpg2136	chemiosmotic efflux system protein C (cobalt-zinc-cadmium resistanc		Transport and binding	11.969	10.572	10.237	11.555	2.75E-04	5.49E-03	-1.40	1.32
lpg2136	chemiosmotic efflux system protein C (cobalt-zinc-cadmium resistanc		Transport and binding	11.871	10.473	10.055	11.481	2.58E-04	3.79E-03	-1.40	1.43
lpg2137	calmodulin-dependent protein kinase	*legK2*	Signal transduction / other regulatory f	10.161	9.769	11.727	9.983	3.49E-01	5.24E-03	-0.39	-1.74
lpg2137	calmodulin-dependent protein kinase	*legK2*	Signal transduction / other regulatory f	10.279	10.247	11.735	10.831	9.47E-01	6.74E-02	-0.03	-0.90
lpg2138	transcriptional regulator, LysR family		Transcription factors / DNA binding pro	9.183	8.776	11.134	8.381	4.72E-01	2.84E-03	-0.41	-2.75
lpg2138	transcriptional regulator, LysR family		Transcription factors / DNA binding pro	9.095	9.399	11.145	8.739	6.06E-01	2.02E-02	0.30	-2.41
lpg2139	pyridoxamine 5'-phosphate oxidase		Metabolism of Cofactors and Vitamins	10.695	10.649	11.436	11.519	8.25E-01	7.30E-01	-0.05	0.08
lpg2139	pyridoxamine 5'-phosphate oxidase		Metabolism of Cofactors and Vitamins	10.762	10.825	11.237	11.571	7.24E-01	1.59E-01	0.06	0.33
lpg2140	small ORF (126aa) transcriptional regulator, MarR family		Transcription factors / DNA binding pro	10.315	10.057	10.942	10.367	5.85E-01	4.49E-01	-0.26	-0.58
lpg2140	small ORF (126aa) transcriptional regulator, MarR family		Transcription factors / DNA binding pro	10.134	9.200	10.338	10.178	4.99E-01	5.98E-01	-0.93	-0.16
lpg2141	glucose-1-dehydrogenase, (3-oxoacyl-(acyl carrier protein) reductase		Named proteins of general function	9.723	11.483	9.730	11.552	5.47E-02	8.85E-02	1.76	1.82
lpg2141	glucose-1-dehydrogenase, (3-oxoacyl-(acyl carrier protein) reductase		Named proteins of general function	9.508	10.475	9.033	10.883	2.75E-01	7.42E-02	0.97	1.85
lpg2142	small ORF (86aa)?		ORFs of unknown function (unique)	8.329	8.531	8.559	8.192	6.94E-01	5.69E-01	0.20	-0.37
lpg2142	small ORF (86aa)?		ORFs of unknown function (unique)	8.156	9.693	9.157	9.154	2.68E-02	9.95E-01	1.54	0.00
lpg2143	ORF		ORFs of unknown function (unique)	8.797	7.989	10.543	7.619	1.41E-01	1.30E-03	-0.81	-2.92
lpg2143	ORF		ORFs of unknown function (unique)	8.851	8.242	10.336	8.888	4.19E-01	1.19E-01	-0.61	-1.45
lpg2144	F-box protein?	*legAU13*	Named proteins of general function	8.333	8.863	10.267	7.159	1.73E-01	2.95E-03	0.53	-3.11
lpg2144	F-box protein?	*legAU13*	Named proteins of general function	9.085	9.991	10.313	9.380	1.51E-01	2.35E-02	0.91	-0.93
lpg2145	two component response regulator, CheY homologous receiver doma		Signal transduction / other regulatory f	9.228	9.554	11.169	7.616	6.47E-01	3.02E-02	0.33	-3.55
lpg2145	two component response regulator, CheY homologous receiver doma		Signal transduction / other regulatory f	9.451	9.169	11.384	9.279	7.18E-01	2.92E-02	-0.28	-2.11
lpg2146	response regulator TutC (two component hybrid sensor and regulator		Signal transduction / other regulatory f	8.424	7.359	9.635	6.748	1.72E-01	9.51E-02	-1.06	-2.89
lpg2146	response regulator TutC (two component hybrid sensor and regulator		Signal transduction / other regulatory f	8.112	6.962	9.710	7.324	4.04E-01	1.39E-01	-1.15	-2.39
lpg2147	ORF		ORFs of unknown function (unique)	11.471	10.790	14.376	10.813	3.82E-01	2.39E-03	-0.68	-3.56
lpg2147	ORF		ORFs of unknown function (unique)	11.723	10.882	14.402	10.918	2.50E-01	2.78E-03	-0.84	-3.48
lpg2148	ORF		ORFs of unknown function (unique)	9.353	10.602	10.582	8.681	5.53E-02	6.65E-03	1.25	-1.90
lpg2148	ORF		ORFs of unknown function (unique)	9.543	10.816	10.504	9.003	1.34E-02	4.07E-02	1.27	-1.50
lpg2149	ORF		ORFs of unknown function (unique)	11.674	12.995	13.768	10.925	4.12E-02	8.85E-04	1.32	-2.84
lpg2149	ORF		ORFs of unknown function (unique)	11.715	12.987	13.790	10.980	5.35E-02	6.32E-04	1.27	-2.81
lpg2150	ORF		ORFs of unknown function (unique)	10.954	10.869	10.129	11.232	7.52E-01	1.87E-02	-0.09	1.10
lpg2150	ORF		ORFs of unknown function (unique)	10.884	11.011	9.570	11.224	6.97E-01	2.51E-02	0.13	1.65
lpg2151	aminoglycoside 6-adenylyltransferase (streptomycin aminoglycoside (		Detoxification / adaptation	10.701	9.443	9.663	9.286	8.52E-02	7.29E-01	-1.26	-0.38
lpg2151	aminoglycoside 6-adenylyltransferase (streptomycin aminoglycoside (		Detoxification / adaptation	10.531	9.957	9.098	10.394	2.19E-01	1.69E-01	-0.57	1.30
lpg2152	multidrug resistance ABC transporter ATP-binding proteir	*abcT3*	Transport and binding	11.103	10.007	11.225	10.073	2.26E-04	2.28E-04	-1.10	-1.15
lpg2152	multidrug resistance ABC transporter ATP-binding proteir	*abcT3*	Transport and binding	10.985	10.122	11.071	10.013	1.60E-02	2.20E-04	-0.86	-1.06
lpg2153	SdeC, SdeB, AliA, SdeA, SdeD homology	*sdeC*	Toxin production / other pathogen func	10.477	11.240	13.723	10.821	3.74E-01	3.09E-03	0.76	-2.90
lpg2153	SdeC, SdeB, AliA, SdeA, SdeD homology	*sdeC*	Toxin production / other pathogen func	10.571	11.170	13.778	11.206	4.43E-01	1.15E-02	0.60	-2.57
lpg2154	SdeC, SdeB, AliA, SdeA, SdeD homology		Toxin production / other pathogen func	10.351	14.832	11.920	12.369	1.85E-07	4.05E-01	4.48	0.45
lpg2154	SdeC, SdeB, AliA, SdeA, SdeD homology		Toxin production / other pathogen func	10.481	14.849	11.804	12.427	5.43E-07	2.94E-01	4.37	0.62
lpg2155	ORF	*sidJ*	ORFs of unknown function (unique)	11.699	10.897	12.991	10.151	4.10E-01	6.87E-06	-0.80	-2.84
lpg2155	ORF	*sidJ*	ORFs of unknown function (unique)	11.137	11.131	12.586	10.243	9.87E-01	2.00E-04	-0.01	-2.34
lpg2156	SdeC, SdeB, SdeA, SidE, SdeD, AliA homology, C. elega	*sdeB*	Toxin production / other pathogen func	9.967	9.408	10.040	8.682	5.25E-01	3.93E-01	-0.56	-1.36
lpg2156	SdeC, SdeB, SdeA, SidE, SdeD, AliA homology, C. elega	*sdeB*	Toxin production / other pathogen func	7.973	8.453	9.500	8.289	5.25E-01	7.88E-02	0.48	-1.21
lpg2157	SdeA, IMH1; Encodes a protein implicated in protein tran	*sdeA*	Transport and binding, Detoxification /	10.642	10.811	13.761	10.486	7.62E-01	3.40E-04	0.17	-3.27
lpg2157	SdeA, IMH1; Encodes a protein implicated in protein tran	*sdeA*	Transport and binding, Detoxification /	10.846	10.969	13.697	11.121	8.19E-01	1.14E-03	0.12	-2.58
lpg2158	phosphatidylethanolamine N-methyltransferase	*pmtA*	Amino Acid Metabolism	12.742	11.923	11.560	11.438	2.73E-04	8.34E-01	-0.82	-0.12
lpg2158	phosphatidylethanolamine N-methyltransferase	*pmtA*	Amino Acid Metabolism	12.537	11.834	11.317	11.402	6.75E-05	8.86E-01	-0.70	0.08
lpg2159	CrtF (enzyme methylating tetracycline) (hydroxyneurosporene (C20) r		Toxin production / other pathogen func	8.654	7.565	9.310	8.224	2.69E-01	1.61E-01	-1.09	-1.09
lpg2159	CrtF (enzyme methylating tetracycline) (hydroxyneurosporene (C20) r		Toxin production / other pathogen func	8.896	8.729	9.332	8.471	7.20E-01	2.31E-01	-0.17	-0.86

lpg2160	ORF		ORFs of unknown function (unique)	9.989	12.196	9.539	11.719	4.87E-04	8.67E-05	2.21	2.18
lpg2160	ORF		ORFs of unknown function (unique)	9.880	12.159	9.353	11.789	2.86E-04	4.27E-06	2.28	2.44
lpg2161	conserved hypothetical protein		Unknown / hypothetical proteins	8.318	9.306	9.982	8.848	4.23E-02	1.54E-01	0.99	-1.13
lpg2161	conserved hypothetical protein		Unknown / hypothetical proteins	8.666	10.158	9.529	9.898	3.00E-02	6.26E-01	1.49	0.37
lpg2162	ORF		ORFs of unknown function (unique)	8.049	7.386	8.842	9.845	5.25E-01	1.01E-02	-0.66	1.00
lpg2162	ORF		ORFs of unknown function (unique)	8.170	8.667	8.134	9.298	3.43E-01	1.00E-01	0.50	1.16
lpg2163	(AraC family) transcriptional regulator		Transcription factors / DNA binding pro	10.344	10.579	10.886	10.592	4.83E-01	1.07E-01	0.23	-0.29
lpg2163	(AraC family) transcriptional regulator		Transcription factors / DNA binding pro	10.473	11.269	10.755	10.478	3.10E-01	2.63E-01	0.80	-0.28
lpg2164	hypothetical protein		Unknown / hypothetical proteins	12.359	11.813	11.776	11.603	3.34E-02	5.10E-01	-0.55	-0.17
lpg2164	hypothetical protein		Unknown / hypothetical proteins	12.335	11.988	11.459	11.731	3.67E-01	6.39E-01	-0.35	0.27
lpg2165	small ORF (170 aa)		ORFs of unknown function (unique)	9.243	9.004	7.090	7.655	5.15E-01	4.87E-01	-0.24	0.56
lpg2165	small ORF (170 aa)		ORFs of unknown function (unique)	9.035	9.368	6.811	8.429	5.00E-01	8.62E-02	0.33	1.62
lpg2166	hypothetical protein		Unknown / hypothetical proteins	11.184	11.682	9.566	11.425	3.52E-01	2.46E-01	0.50	1.86
lpg2166	hypothetical protein		Unknown / hypothetical proteins	9.939	11.610	7.917	11.390	4.81E-02	1.60E-03	1.67	3.47
lpg2167	transcription regulator protein, DeoR family		Transcription factors / DNA binding pro	9.416	9.794	9.555	9.908	3.62E-01	3.78E-01	0.38	0.35
lpg2167	transcription regulator protein, DeoR family		Transcription factors / DNA binding pro	9.531	10.179	9.144	9.964	7.54E-02	1.53E-01	0.65	0.82
lpg2168	acetyltransferase, GNAT family		Named proteins of general function	11.953	11.357	11.270	10.742	3.34E-01	3.99E-01	-0.60	-0.53
lpg2168	acetyltransferase, GNAT family		Named proteins of general function	11.861	11.492	11.155	11.126	3.83E-01	9.39E-01	-0.37	-0.03
lpg2169	hypothetical		Unknown / hypothetical proteins	9.532	9.483	10.521	9.510	9.39E-01	2.94E-02	-0.05	-1.01
lpg2169	hypothetical		Unknown / hypothetical proteins	9.385	9.667	10.551	10.298	6.50E-01	7.26E-01	0.28	-0.25
lpg2170	ORF		ORFs of unknown function (unique)	10.588	10.389	10.602	9.940	6.59E-01	2.67E-01	-0.20	-0.66
lpg2170	ORF		ORFs of unknown function (unique)	10.578	10.220	10.809	10.251	5.36E-01	1.80E-01	-0.36	-0.56
lpg2171	hypothetical conserved protein		Unknown / hypothetical proteins	9.101	11.037	10.051	10.869	1.05E-02	4.61E-01	1.94	0.82
lpg2171	hypothetical conserved protein		Unknown / hypothetical proteins	9.599	12.309	10.644	12.010	7.46E-04	7.05E-02	2.71	1.37
lpg2172	adenosylhomocysteinase		Amino Acid Metabolism, Metabolism o	11.211	11.459	12.389	12.092	6.29E-01	6.63E-01	0.25	-0.30
lpg2172	adenosylhomocysteinase		Amino Acid Metabolism, Metabolism o	10.845	10.871	11.749	11.814	9.66E-01	9.26E-01	0.03	0.06
lpg2174	tRNA-Lys		tRNA	10.895	11.833	10.279	13.445	1.55E-01	4.84E-03	0.94	3.17
lpg2174	tRNA-Lys		tRNA	10.801	12.394	10.313	13.917	1.33E-02	1.40E-05	1.59	3.60
lpg2175	(2-pyrone-4,6-)dicarboxylic acid hydrolase		Protein fate / hydrolases / secretion	11.233	11.317	13.299	10.327	9.08E-01	2.39E-03	0.08	-2.97
lpg2175	(2-pyrone-4,6-)dicarboxylic acid hydrolase		Protein fate / hydrolases / secretion	11.256	11.723	13.349	10.455	4.85E-01	3.03E-03	0.47	-2.89
lpg2176	sphingosine-1-phosphate lyase I (group II decarboxylase	*legS2*	Amino Acid Metabolism, Metabolism o	10.303	8.943	8.526	11.515	4.07E-02	2.76E-03	-1.36	2.99
lpg2176	sphingosine-1-phosphate lyase I (group II decarboxylase	*legS2*	Amino Acid Metabolism, Metabolism o	10.384	9.208	7.661	11.431	2.64E-03	2.76E-03	-1.18	3.77
lpg2177	HlyD family secretion protein (RND multidfug efflux membrane fusion		Transport and binding	10.350	9.418	12.140	8.996	1.03E-01	7.27E-05	-0.93	-3.14
lpg2177	HlyD family secretion protein (RND multidfug efflux membrane fusion		Transport and binding	10.434	9.645	12.205	9.867	1.43E-01	1.97E-03	-0.79	-2.34
lpg2178	probable multidrug-efflux system transmembrane protein	*mexF2*	Transport and binding	9.711	9.424	10.298	9.082	5.78E-01	1.60E-01	-0.29	-1.22
lpg2178	probable multidrug-efflux system transmembrane protein	*mexF2*	Transport and binding	9.271	9.213	9.179	9.037	9.31E-01	8.87E-01	-0.06	-0.14
lpg2179	peptide synthetase (non-ribosomal) (microcystin synthetase) (similar		Toxin production / other pathogen func	9.275	10.310	9.686	8.367	1.38E-01	2.52E-02	1.03	-1.32
lpg2179	peptide synthetase (non-ribosomal) (microcystin synthetase) (similar		Toxin production / other pathogen func	9.296	10.224	9.672	8.594	1.91E-01	1.28E-02	0.93	-1.08
lpg2180	sensory box histidine kinase/response regulator (aerobic respiration c		Signal transduction / other regulatory f	10.179	9.535	11.699	8.495	2.71E-01	1.38E-03	-0.64	-3.20
lpg2180	sensory box histidine kinase/response regulator (aerobic respiration c		Signal transduction / other regulatory f	10.212	8.651	11.487	8.589	8.36E-02	1.84E-03	-1.56	-2.90
lpg2181	sensory box sensor histidine kinase/response regulator, putative		Signal transduction / other regulatory f	10.447	10.592	14.069	8.468	8.98E-01	3.00E-03	0.15	-5.60
lpg2181	sensory box sensor histidine kinase/response regulator, putative		Signal transduction / other regulatory f	9.770	10.345	14.037	8.928	6.40E-01	3.03E-03	0.58	-5.11
lpg2182	BG:DS09218.5 gene product		Unknown / hypothetical proteins	12.951	11.186	13.811	12.385	1.56E-01	1.96E-01	-1.76	-1.43
lpg2182	BG:DS09218.5 gene product		Unknown / hypothetical proteins	12.990	12.512	13.816	12.887	3.50E-01	3.75E-01	-0.48	-0.93
lpg2183	regulatory protein, SyrP-like (antibiotic production)		Toxin production / other pathogen func	9.481	9.624	10.331	10.121	7.66E-01	6.76E-01	0.14	-0.21
lpg2183	regulatory protein, SyrP-like (antibiotic production)		Toxin production / other pathogen func	9.573	9.330	9.508	9.515	6.53E-01	9.89E-01	-0.24	0.01
lpg2185	small ORF (102aa)		ORFs of unknown function (unique)	11.918	13.945	13.281	14.261	5.54E-04	6.23E-02	2.03	0.98
lpg2185	small ORF (102aa)		ORFs of unknown function (unique)	11.944	14.108	13.252	14.392	2.93E-04	2.65E-02	2.16	1.14
lpg2186	polyketide synthase, type I	*pksJ*	Named proteins of general function	10.341	11.258	10.603	11.412	3.91E-02	5.44E-02	0.92	0.81
lpg2186	polyketide synthase, type I	*pksJ*	Named proteins of general function	10.236	11.285	10.547	11.546	9.37E-02	1.83E-02	1.05	1.00
lpg2187	small ORF (133aa)		ORFs of unknown function (unique)	10.793	10.710	13.890	10.451	9.00E-01	9.91E-04	-0.08	-3.44
lpg2187	small ORF (133aa)		ORFs of unknown function (unique)	10.588	10.972	13.830	10.597	5.95E-01	1.74E-03	0.38	-3.23
lpg2188	small ORF (50aa)		ORFs of unknown function (unique)	9.030	9.759	10.231	10.791	6.46E-01	5.24E-01	0.73	0.56
lpg2188	small ORF (50aa)		ORFs of unknown function (unique)	7.133	10.032	8.794	10.071	2.29E-01	2.65E-01	2.90	1.28
lpg2189	drug efflux protein (transport protein) (resistance protein)	*ygjT*	Transport and binding	11.124	10.196	11.325	9.641	4.59E-02	5.17E-04	-0.93	-1.68
lpg2189	drug efflux protein (transport protein) (resistance protein)	*ygjT*	Transport and binding	10.880	10.046	11.299	9.778	5.67E-02	8.51E-04	-0.83	-1.52
lpg2190	IcmL homolog		Transport and binding, Toxin productio	9.147	10.126	9.794	10.227	3.60E-02	1.78E-01	0.98	0.43
lpg2190	IcmL homolog		Transport and binding, Toxin productio	9.301	10.946	10.078	11.118	6.85E-04	1.60E-02	1.64	1.04
lpg2191	global stress protein GspA (heat shock protein 16 kDa, h	*ib*	Detoxification / adaptation	12.829	13.138	14.968	12.459	5.39E-01	5.59E-04	0.31	-2.51
lpg2191	global stress protein GspA (heat shock protein 16 kDa, h	*ib*	Detoxification / adaptation	12.902	13.305	14.982	12.697	3.85E-01	1.97E-04	0.40	-2.29
lpg2192	small HspC2 heat shock protein (16.9 kDa)		Detoxification / adaptation	11.486	12.525	13.560	12.689	5.50E-02	6.97E-02	1.04	-0.87
lpg2192	small HspC2 heat shock protein (16.9 kDa)		Detoxification / adaptation	11.565	12.712	13.588	12.947	1.87E-02	1.39E-01	1.15	-0.64
lpg2193	sulfate transporter		Transport and binding	9.931	10.626	10.488	10.595	2.39E-02	7.68E-01	0.70	0.11
lpg2193	sulfate transporter		Transport and binding	9.832	9.704	10.418	10.560	8.50E-01	6.78E-01	-0.13	0.14

lpg2194	(beta)-carbonic anhydrase		Energy Metabolism	13.506	12.582	13.011	12.144	3.12E-01	2.16E-01	-0.92	-0.87
lpg2194	(beta)-carbonic anhydrase		Energy Metabolism	13.480	13.012	12.974	12.452	3.50E-01	2.42E-01	-0.47	-0.52
lpg2195	small ORF (98aa)		ORFs of unknown function (unique)	9.158	9.316	10.703	9.421	8.96E-01	9.31E-02	0.16	-1.28
lpg2195	small ORF (98aa)		ORFs of unknown function (unique)	8.895	9.740	10.107	9.338	4.22E-01	3.55E-01	0.85	-0.77
lpg2196	ornithine cyclodeaminase (mu-crystallin family)		Amino Acid Metabolism	12.232	12.227	13.808	11.759	9.93E-01	6.79E-03	-0.01	-2.05
lpg2196	ornithine cyclodeaminase (mu-crystallin family)		Amino Acid Metabolism	12.179	12.230	13.775	11.942	9.35E-01	2.60E-03	0.05	-1.83
lpg2197	COG4319 ketosteroid isomerase		Lipid Metabolism	11.399	11.815	14.275	11.711	6.04E-01	9.60E-03	0.42	-2.56
lpg2197	COG4319 ketosteroid isomerase		Lipid Metabolism	11.412	11.826	14.247	11.692	5.97E-01	1.01E-02	0.41	-2.56
lpg2198	peptide transport (POT family) (proton/(oligo)peptide symporter, putat		Transport and binding	9.437	11.130	9.920	10.695	1.07E-02	2.88E-01	1.69	0.78
lpg2198	peptide transport (POT family) (proton/(oligo)peptide symporter, putat		Transport and binding	9.650	10.933	9.283	10.470	8.42E-05	3.69E-02	1.28	1.19
lpg2199	ORF		ORFs of unknown function (unique)	10.188	12.469	10.464	9.684	2.19E-04	7.13E-02	2.28	-0.78
lpg2199	ORF		ORFs of unknown function (unique)	10.100	12.816	8.628	9.662	2.64E-03	5.19E-01	2.72	1.03
lpg2200	ORF	*cegC4*	ORFs of unknown function (unique)	11.053	12.832	12.303	10.756	3.88E-04	3.05E-04	1.78	-1.55
lpg2200	ORF	*cegC4*	ORFs of unknown function (unique)	10.996	12.850	12.310	10.963	3.94E-04	1.82E-03	1.85	-1.35
lpg2201	replication factor C subunit (activator I)		Signal transduction / other regulatory f	10.756	10.335	12.535	10.041	4.00E-01	1.37E-03	-0.42	-2.49
lpg2201	replication factor C subunit (activator I)		Signal transduction / other regulatory f	10.747	10.640	12.460	10.453	8.81E-01	4.46E-03	-0.11	-2.01
lpg2202	uncharacterized conserved hypothetical protein COG1371		Unknown / hypothetical proteins	9.983	9.660	9.841	10.019	7.01E-01	7.77E-01	-0.32	0.18
lpg2202	uncharacterized conserved hypothetical protein COG1371		Unknown / hypothetical proteins	10.157	9.395	9.386	9.643	4.02E-01	8.26E-01	-0.76	0.26
lpg2203	(alginate O-acetylation protein?)		Cell envelope synthesis	11.100	10.012	10.072	10.558	1.34E-03	3.36E-01	-1.09	0.49
lpg2203	(alginate O-acetylation protein?)		Cell envelope synthesis	10.975	9.996	9.414	10.644	6.10E-03	1.66E-01	-0.98	1.23
lpg2204	alginate O-acetylation protein (cellulose acetylase)		Cell envelope synthesis	10.072	10.117	10.066	11.758	9.45E-01	3.72E-03	0.04	1.69
lpg2204	alginate O-acetylation protein (cellulose acetylase)		Cell envelope synthesis	9.960	10.063	10.079	11.801	8.83E-01	2.50E-03	0.10	1.72
lpg2205	ORF		ORFs of unknown function (unique)	10.517	11.260	11.922	10.131	3.48E-01	1.64E-02	0.74	-1.79
lpg2205	ORF		ORFs of unknown function (unique)	10.528	11.152	11.791	10.483	3.09E-01	1.32E-02	0.62	-1.31
lpg2206	ORF	*wipB*	ORFs of unknown function (unique)	9.815	9.891	9.765	8.928	7.67E-01	1.68E-01	0.08	-0.84
lpg2206	ORF	*wipB*	ORFs of unknown function (unique)	9.711	9.840	9.489	9.657	6.75E-01	7.28E-01	0.13	0.17
lpg2207	conserved hypothetical protein		Unknown / hypothetical proteins	9.339	9.116	11.114	8.792	7.39E-01	2.24E-02	-0.22	-2.32
lpg2207	conserved hypothetical protein		Unknown / hypothetical proteins	9.534	9.072	10.879	8.942	4.88E-01	4.89E-02	-0.46	-1.94
lpg2208	zinc binding dehydrogenase (zinc binding oxidoreductase) (quinone c		Carbohydrate Metabolism, Lipid Metat	12.041	13.221	11.218	12.738	2.34E-02	1.53E-03	1.18	1.52
lpg2208	zinc binding dehydrogenase (zinc binding oxidoreductase) (quinone c		Carbohydrate Metabolism, Lipid Metat	12.174	13.309	11.096	12.832	2.35E-02	8.50E-04	1.14	1.74
lpg2209	hypothetical (phosphatidylethanolamine-binding protein?)		Transport and binding	9.574	8.505	11.532	6.013	3.66E-01	1.09E-03	-1.07	-5.52
lpg2209	hypothetical (phosphatidylethanolamine-binding protein?)		Transport and binding	8.686	8.239	10.916		7.57E-01		-0.45	
lpg2210	hypothetical		Unknown / hypothetical proteins	9.723	9.579	10.629	10.271	7.24E-01	6.37E-01	-0.14	-0.36
lpg2210	hypothetical		Unknown / hypothetical proteins	9.687	9.575	10.636	10.747	8.27E-01	8.10E-01	-0.11	0.11
lpg2211	uncharacterized conserved hypothetical protein COG0432		Unknown / hypothetical proteins	11.524	12.654	11.319	12.836	1.32E-02	1.20E-03	1.13	1.52
lpg2211	uncharacterized conserved hypothetical protein COG0432		Unknown / hypothetical proteins	11.527	12.652	11.316	12.863	1.93E-02	6.10E-04	1.12	1.55
lpg2212	acetylpolyamine aminohydolase	*bcp*	Protein fate / hydrolases / secretion	8.982	8.908	10.037	8.153	8.93E-01	3.52E-03	-0.07	-1.88
lpg2212	acetylpolyamine aminohydolase	*bcp*	Protein fate / hydrolases / secretion	8.487	8.423	9.796	8.906	8.98E-01	3.49E-02	-0.06	-0.89
lpg2213	hemin binding protein Hbp		Transport and binding	14.726	15.414	12.668	15.507	2.89E-01	9.37E-04	0.69	2.84
lpg2213	hemin binding protein Hbp		Transport and binding	14.594	15.383	12.698	15.545	2.12E-01	3.82E-04	0.79	2.85
lpg2214	nucleoside-diphosphate sugar epimerase (cell division inhibitor)		Chemotaxis / motility / cell division, Sig	12.445	12.519	12.664	12.269	5.26E-01	3.84E-03	0.07	-0.39
lpg2214	nucleoside-diphosphate sugar epimerase (cell division inhibitor)		Chemotaxis / motility / cell division, Sig	12.453	12.397	12.594	12.256	7.11E-01	1.44E-02	-0.06	-0.34
lpg2215	RIKEN cDNA G431002C21 gene	*legA2*	Unknown / hypothetical proteins	9.894	9.255	9.921	9.416	1.74E-01	2.78E-01	-0.64	-0.50
lpg2215	RIKEN cDNA G431002C21 gene	*legA2*	Unknown / hypothetical proteins	9.423	9.608	10.349	9.847	5.57E-01	2.90E-01	0.19	-0.50
lpg2216	purine NTPase, putative		Nucleotide Metabolism	10.907	11.110	11.568	9.184	4.66E-01	9.06E-06	0.20	-2.38
lpg2216	purine NTPase, putative		Nucleotide Metabolism	10.850	11.237	11.496	9.479	9.08E-02	6.61E-04	0.39	-2.02
lpg2217	chitinase domain (two component system sensor kinase) (sugar hydr		Signal transduction / other regulatory f	9.966	11.183	11.572	9.741	5.81E-03	5.86E-04	1.22	-1.83
lpg2217	chitinase domain (two component system sensor kinase) (sugar hydr		Signal transduction / other regulatory f	9.923	10.997	11.526	9.909	1.19E-02	9.98E-04	1.07	-1.62
lpg2218	choline monooxygenase (benzene 1,2-dioxygenase a subunit)		Biodegradation of Xenobiotics	11.045	12.211	11.369	11.620	1.31E-03	3.81E-01	1.17	0.25
lpg2218	choline monooxygenase (benzene 1,2-dioxygenase a subunit)		Biodegradation of Xenobiotics	11.029	12.853	11.439	12.125	7.38E-03	2.98E-01	1.82	0.69
lpg2219	conserved hypothetical protein		Unknown / hypothetical proteins	11.086	11.387	10.373	10.129	3.07E-01	3.70E-01	0.30	-0.24
lpg2219	conserved hypothetical protein		Unknown / hypothetical proteins	11.164	11.472	10.279	10.175	2.92E-01	6.38E-01	0.31	-0.10
lpg2220	ORF		ORFs of unknown function (unique)	11.152	11.164	10.884	10.123	9.82E-01	1.89E-01	0.01	-0.76
lpg2220	ORF		ORFs of unknown function (unique)	10.985	11.150	10.692	10.152	7.02E-01	2.72E-01	0.17	-0.54
lpg2221	ORF		ORFs of unknown function (unique)	11.683	11.844	12.179	11.341	7.67E-01	3.52E-01	0.16	-0.84
lpg2221	ORF		ORFs of unknown function (unique)	11.595	11.987	12.185	11.650	4.88E-01	4.41E-01	0.39	-0.54
lpg2222	TPR repeat protein, protein-protein interaction		Signal transduction / other regulatory f	11.747	14.028	14.989	11.014	1.09E-02	1.92E-04	2.28	-3.97
lpg2222	TPR repeat protein, protein-protein interaction		Signal transduction / other regulatory f	11.728	14.004	14.824	10.970	1.09E-02	5.32E-04	2.28	-3.85
lpg2223	ORF		ORFs of unknown function (unique)	11.420	12.360	12.187	11.674	3.95E-02	1.71E-01	0.94	-0.51
lpg2223	ORF		ORFs of unknown function (unique)	11.418	12.339	12.177	11.708	7.03E-02	1.97E-01	0.92	-0.47
lpg2224	UVB-resistance protein UVR8		Named proteins of general function	9.544	9.848	9.941	9.222	4.69E-01	2.52E-01	0.30	-0.72
lpg2224	UVB-resistance protein UVR8		Named proteins of general function	9.745	10.889	9.703	10.802	2.42E-01	2.74E-01	1.14	1.10
lpg2225	expressed protein (GH3 homolog) (auxin-regulated protein)		Named proteins of general function	10.296	10.427	10.933	10.848	3.32E-01	7.14E-01	0.13	-0.08
lpg2225	expressed protein (GH3 homolog) (auxin-regulated protein)		Named proteins of general function	10.650	11.915	11.347	12.555	9.63E-03	2.51E-02	1.27	1.21

lpg2226	isovaleryl CoA dehydrogenase (non-ribosomal peptide synthase) (acy		Amino Acid Metabolism	10.096	9.596	10.500	10.502	2.01E-01	9.96E-01	-0.50	0.00
lpg2226	isovaleryl CoA dehydrogenase (non-ribosomal peptide synthase) (acy		Amino Acid Metabolism	9.944	9.241	10.242	10.441	1.07E-01	6.06E-01	-0.70	0.20
lpg2227	acetyl CoA carboxylase alpha subunit (propionyl CoA carboxylase bet		Amino Acid Metabolism, Carbohydrate	10.402	11.263	11.340	11.645	4.72E-02	5.80E-01	0.86	0.31
lpg2227	acetyl CoA carboxylase alpha subunit (propionyl CoA carboxylase bet		Amino Acid Metabolism, Carbohydrate	10.403	11.224	11.297	11.663	5.79E-02	4.94E-01	0.82	0.37
lpg2228	3-oxoacyl (acyl carrier protein) synthase III		Lipid Metabolism	9.926	10.203	10.739	10.132	1.90E-01	3.31E-01	0.28	-0.61
lpg2228	3-oxoacyl (acyl carrier protein) synthase III		Lipid Metabolism	9.870	9.859	10.887	10.301	9.68E-01	2.69E-01	-0.01	-0.59
lpg2229	saframycin Mx1 synthetase B (acyl CoA synthase) (nonribosomal pep		Biosynthesis of Secondary Metabolite	9.771	11.479	10.973	11.827	8.01E-03	9.86E-02	1.71	0.85
lpg2229	saframycin Mx1 synthetase B (acyl CoA synthase) (nonribosomal pep		Biosynthesis of Secondary Metabolite	10.425	12.817	11.656	12.898	7.29E-03	9.47E-02	2.39	1.24
lpg2230	acyl CoA ligase (long chain fatty acid CoA ligase) (O succinyl benzoic		Lipid Metabolism	10.320	10.649	11.840	11.145	3.30E-01	9.81E-02	0.33	-0.69
lpg2230	acyl CoA ligase (long chain fatty acid CoA ligase) (O succinyl benzoic		Lipid Metabolism	10.722	11.295	11.976	11.816	1.47E-01	7.08E-01	0.57	-0.16
lpg2231	3-oxoacyl reductase (short chain dehydrogenase/reducta	*fabG*	Lipid Metabolism	10.615	9.956	11.921	11.041	3.17E-02	3.05E-03	-0.66	-0.88
lpg2231	3-oxoacyl reductase (short chain dehydrogenase/reducta	*fabG*	Lipid Metabolism	10.667	9.892	11.934	11.142	3.33E-02	1.81E-02	-0.78	-0.79
lpg2232	3-oxoacyl-(acyl carrier protein) synthase III (FabH)	*fabH*	Lipid Metabolism	9.980	10.304	10.828	10.705	3.14E-01	7.47E-01	0.32	-0.12
lpg2232	3-oxoacyl-(acyl carrier protein) synthase III (FabH)	*fabH*	Lipid Metabolism	9.906	10.502	10.663	10.797	6.86E-02	7.19E-01	0.60	0.13
lpg2233	acyl carrier protein		Named proteins of general function	11.942	12.374	10.532	12.338	1.64E-01	8.78E-03	0.43	1.81
lpg2233	acyl carrier protein		Named proteins of general function	11.927	12.354	10.408	12.505	8.90E-02	2.24E-03	0.43	2.10
lpg2234	multidrug resistance protein D (drug resistance transporter Bcr/CflA fa		Transport and binding	10.834	10.620	10.327	10.918	7.39E-01	2.37E-01	-0.21	0.59
lpg2234	multidrug resistance protein D (drug resistance transporter Bcr/CflA fa		Transport and binding	10.815	10.426	10.229	10.973	3.72E-01	1.19E-01	-0.39	0.74
lpg2235	sterol desaturase		Lipid Metabolism	9.923	9.800	9.160	9.720	6.51E-01	1.98E-01	-0.12	0.56
lpg2235	sterol desaturase		Lipid Metabolism	10.005	9.785	9.006	9.675	1.65E-01	3.27E-01	-0.22	0.67
lpg2236	nitric oxide reductase, (subunit B)		Energy Metabolism	10.057	9.732	11.218	9.906	6.71E-01	1.58E-01	-0.32	-1.31
lpg2236	nitric oxide reductase, (subunit B)		Energy Metabolism	10.109	9.731	10.952	9.654	4.77E-01	2.51E-01	-0.38	-1.30
lpg2237	multidrug resistance ABC transporter ATP-binding protei	*abcT3*	Transport and binding	12.226	11.239	12.952	11.186	4.86E-02	4.31E-03	-0.99	-1.77
lpg2237	multidrug resistance ABC transporter ATP-binding protei	*abcT3*	Transport and binding	12.316	12.126	12.926	11.905	7.14E-01	3.34E-02	-0.19	-1.02
lpg2238	transmembrane protein		Unknown / hypothetical proteins	11.775	10.683	11.041	10.588	4.95E-02	3.68E-01	-1.09	-0.45
lpg2238	transmembrane protein		Unknown / hypothetical proteins	12.329	10.713	10.990	10.658	4.21E-03	4.13E-01	-1.62	-0.33
lpg2239	ORF		ORFs of unknown function (unique)	8.516	5.799	11.866	7.588	8.69E-02	6.03E-04	-2.72	-4.28
lpg2239	ORF		ORFs of unknown function (unique)	8.330	8.253	11.707	8.032	9.50E-01	5.86E-03	-0.08	-3.67
lpg2240	dipeptidyl aminopeptidase/acylaminoacyl peptidase		Protein fate / hydrolases / secretion	11.063	12.263	10.943	12.208	6.60E-03	2.43E-03	1.20	1.26
lpg2240	dipeptidyl aminopeptidase/acylaminoacyl peptidase		Protein fate / hydrolases / secretion	11.273	12.304	10.892	12.161	3.63E-04	1.43E-03	1.03	1.27
lpg2241	GTP cyclohydrolase II; riboflavin biosynthesis		Metabolism of Cofactors and Vitamins	9.751	10.846	10.915	9.554	3.01E-02	8.83E-04	1.09	-1.36
lpg2241	GTP cyclohydrolase II; riboflavin biosynthesis		Metabolism of Cofactors and Vitamins	10.134	10.604	11.068	9.919	3.62E-01	1.73E-03	0.47	-1.15
lpg2242	hypothetical		Unknown / hypothetical proteins	9.885	10.274	10.037	10.076	1.91E-01	9.16E-01	0.39	0.04
lpg2242	hypothetical		Unknown / hypothetical proteins	10.725	10.271	9.922	10.086	6.27E-01	7.75E-01	-0.45	0.16
lpg2243	uracil phosphoribosyltransferase (UMP pyrophosphorylase)		Nucleotide Metabolism	10.517	10.509	10.362	9.937	9.85E-01	3.84E-01	-0.01	-0.43
lpg2243	uracil phosphoribosyltransferase (UMP pyrophosphorylase)		Nucleotide Metabolism	10.667	11.192	10.309	10.799	4.73E-01	5.78E-01	0.52	0.49
lpg2244	ORF		ORFs of unknown function (unique)	9.122	9.459	10.255	8.425	4.65E-01	1.48E-02	0.34	-1.83
lpg2244	ORF		ORFs of unknown function (unique)	8.809	9.107	9.995	8.555	5.48E-01	1.87E-02	0.30	-1.44
lpg2245	C4-dicarboxylate transport protein (Na+/H+ dicarboxylat	*dctA*	Transport and binding	10.507	12.359	11.912	10.278	1.03E-02	8.16E-03	1.85	-1.63
lpg2245	C4-dicarboxylate transport protein (Na+/H+ dicarboxylat	*dctA*	Transport and binding	10.508	12.773	11.868	10.584	1.49E-03	2.57E-02	2.27	-1.28
lpg2246	ORF		ORFs of unknown function (unique)	9.284	11.748	13.710	8.749	2.95E-02	9.15E-04	2.46	-4.96
lpg2246	ORF		ORFs of unknown function (unique)	10.157	11.740	13.858	9.203	8.80E-02	3.66E-04	1.58	-4.65
lpg2247	DedA family protein (integral membrane protein)		Named proteins of general function	10.262	9.530	9.351	7.944	8.86E-02	2.43E-01	-0.73	-1.41
lpg2247	DedA family protein (integral membrane protein)		Named proteins of general function	10.484	9.097	9.078	8.167	5.22E-03	1.41E-01	-1.39	-0.91
lpg2248	ORF		ORFs of unknown function (unique)	11.173	13.505	12.657	11.502	1.10E-02	2.43E-02	2.33	-1.16
lpg2248	ORF		ORFs of unknown function (unique)	11.138	13.503	12.670	11.775	8.68E-03	8.64E-03	2.37	-0.89
lpg2249	glutamine amidotransferase, class I (glutamine synthetase)		Nucleotide Metabolism	10.623	10.666	9.796	10.364	8.80E-01	4.01E-01	0.04	0.57
lpg2249	glutamine amidotransferase, class I (glutamine synthetase)		Nucleotide Metabolism	10.548	11.049	10.062	11.116	6.95E-02	7.66E-02	0.50	1.05
lpg2250	alcohol dehydrogenase, iron containing (NAD dependent 4-hydroxybu		Carbohydrate Metabolism, Lipid Metab	9.228	9.998	9.216	10.242	6.90E-02	1.00E-01	0.77	1.03
lpg2250	alcohol dehydrogenase, iron containing (NAD dependent 4-hydroxybu		Carbohydrate Metabolism, Lipid Metab	8.744	9.882	9.320	10.380	2.24E-02	5.54E-02	1.14	1.06
lpg2251	succinate semialdehyde dehydrogenase (aldehyde dehydrogenase)		Carbohydrate Metabolism, Amino Acid	9.114	8.365	8.425	9.020	1.99E-01	3.35E-01	-0.75	0.59
lpg2251	succinate semialdehyde dehydrogenase (aldehyde dehydrogenase)		Carbohydrate Metabolism, Amino Acid	8.934	8.900	8.491	9.574	9.56E-01	1.07E-01	-0.03	1.08
lpg2252	glutamine synthetase		Energy Metabolism, Amino Acid Metab	10.721	9.041	10.014	9.782	9.25E-04	5.91E-01	-1.68	-0.23
lpg2252	glutamine synthetase		Energy Metabolism, Amino Acid Metab	10.550	9.762	9.641	10.208	2.90E-01	4.04E-01	-0.79	0.57
lpg2253	hypothetical		Unknown / hypothetical proteins	11.787	11.974	12.707	12.512	7.49E-01	6.98E-01	0.19	-0.20
lpg2253	hypothetical		Unknown / hypothetical proteins	11.358	11.839	11.213	12.371	3.48E-01	4.20E-02	0.48	1.16
lpg2254	conserved hypothetical protein		Unknown / hypothetical proteins	12.298	10.866	10.264	11.365	6.61E-02	5.39E-02	-1.43	1.10
lpg2254	conserved hypothetical protein		Unknown / hypothetical proteins	12.469	10.909	10.075	11.226	1.69E-02	7.27E-02	-1.56	1.15
lpg2255	ORF		ORFs of unknown function (unique)	14.822	14.483	14.900	12.100	4.23E-01	4.05E-06	-0.34	-2.80
lpg2255	ORF		ORFs of unknown function (unique)	14.975	14.455	14.936	12.148	2.43E-01	5.02E-06	-0.52	-2.79
lpg2256	metallo-beta-lactamase superfamily protein (cleavage and polyadeny		DNA/RNA degradation / restriction, Tra	10.440	10.252	11.551	10.595	5.68E-01	4.46E-03	-0.19	-0.96
lpg2256	metallo-beta-lactamase superfamily protein (cleavage and polyadeny		DNA/RNA degradation / restriction, Tra	10.532	10.606	11.647	10.717	7.28E-01	9.50E-03	0.07	-0.93
lpg2257	ORF		ORFs of unknown function (unique)	10.367	9.994	13.043	9.625	6.97E-01	8.54E-03	-0.37	-3.42
lpg2257	ORF		ORFs of unknown function (unique)	10.291	9.702	13.076	9.867	5.33E-01	1.00E-02	-0.59	-3.21

lpg2258	small ORF (96aa) hypothetical		Unknown / hypothetical proteins	10.268	9.909	12.698	9.903	5.75E-01	5.62E-03	-0.36	-2.79
lpg2258	small ORF (96aa) hypothetical		Unknown / hypothetical proteins	10.333	9.460	12.693	10.031	2.17E-01	4.52E-03	-0.87	-2.66
lpg2259	periplasmic, osmotically inducible protein?	*osmY*	Detoxification / adaptation	13.230	12.705	12.411	12.280	1.52E-01	7.05E-01	-0.52	-0.13
lpg2259	periplasmic, osmotically inducible protein?	*osmY*	Detoxification / adaptation	13.140	12.818	12.325	12.352	3.46E-01	9.30E-01	-0.32	0.03
lpg2260	PHA synthase (polyhydroxyalkanoic synthase) (poly-3-hy	*phbC*	Named proteins of general function	11.455	11.830	12.034	11.858	4.14E-01	6.03E-01	0.37	-0.18
lpg2260	PHA synthase (polyhydroxyalkanoic synthase) (poly-3-hy	*phbC*	Named proteins of general function	11.047	11.805	11.860	11.759	1.31E-01	7.79E-01	0.76	-0.10
lpg2261	phosphate acetyl/butyryltransferase family protein) includes: (de)hydr		Carbohydrate Metabolism	11.203	11.485	12.404	11.129	5.20E-01	8.19E-03	0.28	-1.27
lpg2261	phosphate acetyl/butyryltransferase family protein) includes: (de)hydr		Carbohydrate Metabolism	11.135	11.472	12.370	11.117	4.32E-01	1.57E-02	0.34	-1.25
lpg2262	acetate kinase (acetokinase) (acetate and butyrate kinas	*ackA2*	Metabolism of Other Amino Acids, Car	10.689	10.788	11.576	10.417	8.53E-01	1.07E-02	0.10	-1.16
lpg2262	acetate kinase (acetokinase) (acetate and butyrate kinas	*ackA2*	Metabolism of Other Amino Acids, Car	10.640	11.269	11.590	10.979	2.00E-01	1.65E-01	0.63	-0.61
lpg2263	curved DNA binding protein (DnaJ N-terminal domain:Dn	*cbpA*	Protein fate / hydrolases / secretion, Tı	8.549	9.970	8.898	9.753	6.31E-02	3.13E-02	1.42	0.85
lpg2263	curved DNA binding protein (DnaJ N-terminal domain:Dn	*cbpA*	Protein fate / hydrolases / secretion, Tı	7.102	9.103	8.740	9.595	7.50E-02	1.33E-01	2.00	0.86
lpg2264	small ORF (104aa) hypothetical (MerR family bacterial regulator? trar		Transcription factors / DNA binding prc	8.171	8.501	9.821	8.338	7.19E-01	1.74E-01	0.33	-1.48
lpg2264	small ORF (104aa) hypothetical (MerR family bacterial regulator? trar		Transcription factors / DNA binding prc	9.069	8.931	9.669	8.706	8.84E-01	2.30E-01	-0.14	-0.96
lpg2265	acyltransferase		Named proteins of general function	9.211	10.196	9.673	10.022	1.56E-04	2.89E-01	0.98	0.35
lpg2265	acyltransferase		Named proteins of general function	9.006	10.471	9.708	10.429	1.24E-02	1.71E-01	1.46	0.72
lpg2266	conserved hypothetical protein		Unknown / hypothetical proteins	8.751	9.003	9.375	9.321	7.85E-01	8.94E-01	0.25	-0.05
lpg2266	conserved hypothetical protein		Unknown / hypothetical proteins	9.047	9.392	9.318	9.608	4.89E-01	4.95E-01	0.34	0.29
lpg2267	prolidase (aryldialkylphosphatase) (Xaa-pro dipeptidase)		Protein fate / hydrolases / secretion	8.344	8.808	9.180	8.201	4.17E-01	1.24E-01	0.46	-0.98
lpg2267	prolidase (aryldialkylphosphatase) (Xaa-pro dipeptidase)		Protein fate / hydrolases / secretion	8.080	8.611	8.815	8.340	2.87E-01	6.13E-01	0.53	-0.47
lpg2268	ORF		ORFs of unknown function (unique)	9.954	9.365	13.061	9.071	5.27E-01	8.70E-04	-0.59	-3.99
lpg2268	ORF		ORFs of unknown function (unique)	10.176	9.346	13.068	9.353	3.50E-01	1.06E-03	-0.83	-3.72
lpg2269	hypothetical (includes LidB and unknown) ?		Named proteins of general function	11.691	11.149	12.269	11.783	2.53E-02	7.39E-02	-0.54	-0.49
lpg2269	hypothetical (includes LidB and unknown) ?		Named proteins of general function	11.678	11.015	12.181	11.729	2.67E-02	1.01E-01	-0.66	-0.45
lpg2270	oxidoreductase (NAD-dependent epimerase/dehydratase)		Named proteins of general function	11.117	10.498	11.491	11.141	4.42E-01	6.85E-01	-0.62	-0.35
lpg2270	oxidoreductase (NAD-dependent epimerase/dehydratase)		Named proteins of general function	10.132	10.070	10.877	10.864	8.87E-01	9.56E-01	-0.06	-0.01
lpg2271	ORF		ORFs of unknown function (unique)	11.412	11.793	10.142	11.181	7.00E-01	1.32E-01	0.38	1.04
lpg2271	ORF		ORFs of unknown function (unique)	11.614	12.511	10.167	11.384	3.70E-02	2.27E-02	0.90	1.22
lpg2272	transmembrane protein		Unknown / hypothetical proteins	11.368	10.635	11.640	10.305	2.01E-01	5.88E-02	-0.73	-1.34
lpg2272	transmembrane protein		Unknown / hypothetical proteins	10.698	11.200	11.154	11.143	2.15E-01	9.87E-01	0.50	-0.01
lpg2273	glycerol-3-phosphate binding periplasmic protein (sn-glyc	*ugpB*	Transport and binding	10.411	10.786	9.808	10.721	5.64E-01	2.66E-02	0.37	0.91
lpg2273	glycerol-3-phosphate binding periplasmic protein (sn-glyc	*ugpB*	Transport and binding	10.610	10.153	9.202	10.592	1.74E-01	4.74E-02	-0.46	1.39
lpg2274	glycerophosphoryl diester esterase (glycerophosphoryldi	*ugpQ*	Metabolism of Complex Lipids	10.754	11.053	9.803	11.113	5.95E-01	8.06E-02	0.30	1.31
lpg2274	glycerophosphoryl diester esterase (glycerophosphoryldi	*ugpQ*	Metabolism of Complex Lipids	10.850	11.305	9.322	11.282	4.46E-01	9.70E-02	0.46	1.96
lpg2275	hypothetical		Unknown / hypothetical proteins	11.543	11.533	11.674	11.642	9.90E-01	8.41E-01	-0.01	-0.03
lpg2275	hypothetical		Unknown / hypothetical proteins	11.472	11.867	11.598	11.572	4.59E-01	8.79E-01	0.40	-0.03
lpg2276	Glu/Leu/Phe/Val dehydrogenase (leucine dehydrogenase)		Amino Acid Metabolism	13.666	13.719	12.109	13.395	9.50E-01	2.79E-01	0.05	1.29
lpg2276	Glu/Leu/Phe/Val dehydrogenase (leucine dehydrogenase)		Amino Acid Metabolism	13.638	13.549	12.130	13.730	9.29E-01	7.38E-02	-0.09	1.60
lpg2277	O-methyltransferase, SAM-dependent		Metabolism of Cofactors and Vitamins	12.149	12.863	10.962	13.036	1.81E-01	1.11E-03	0.71	2.07
lpg2277	O-methyltransferase, SAM-dependent		Metabolism of Cofactors and Vitamins	12.038	12.934	10.898	13.113	1.63E-01	1.14E-03	0.90	2.22
lpg2278	4-hydroxyphenylpyruvate dioxygenase (legiolysin) oxidor	*hpd*	Amino Acid Metabolism	13.072	13.519	11.835	13.118	5.09E-01	1.98E-01	0.45	1.28
lpg2278	4-hydroxyphenylpyruvate dioxygenase (legiolysin) oxidor	*hpd*	Amino Acid Metabolism	13.270	13.824	11.863	13.487	1.72E-01	2.88E-02	0.55	1.62
lpg2279	fumarylacetoacetate hydrolase (aromatic amino acid degradation prot		Amino Acid Metabolism	12.663	13.319	11.782	13.348	6.15E-02	2.06E-02	0.66	1.57
lpg2279	fumarylacetoacetate hydrolase (aromatic amino acid degradation prot		Amino Acid Metabolism	12.426	13.046	11.337	13.089	9.36E-02	6.07E-03	0.62	1.75
lpg2280	glutathione S-transferase		Amino Acid Metabolism, Biodegradatic	11.554	10.506	9.863	10.668	1.76E-02	6.21E-02	-1.05	0.80
lpg2280	glutathione S-transferase		Amino Acid Metabolism, Biodegradatic	11.571	10.977	9.870	10.931	3.28E-01	6.66E-02	-0.59	1.06
lpg2281	ORF		ORFs of unknown function (unique)	9.468	10.221	9.879	10.195	6.04E-02	4.09E-01	0.75	0.32
lpg2281	ORF		ORFs of unknown function (unique)	9.607	10.330	9.904	10.317	6.52E-03	2.60E-01	0.72	0.41
lpg2282	asparaginyl tRNA synthetase	*asnS*	Amino Acid Metabolism, Translation	12.262	12.281	10.191	12.835	9.62E-01	5.98E-04	0.02	2.64
lpg2282	asparaginyl tRNA synthetase	*asnS*	Amino Acid Metabolism, Translation	12.342	12.254	9.653	12.814	7.73E-01	7.22E-04	-0.09	3.16
lpg2283	small ORF (132aa)		ORFs of unknown function (unique)	13.121	13.948	12.816	13.166	3.72E-04	7.54E-02	0.83	0.35
lpg2283	small ORF (132aa)		ORFs of unknown function (unique)	13.171	13.949	12.700	13.219	3.62E-04	1.80E-02	0.78	0.52
lpg2284	ABC transporter, ATP binding protein (lipoprotein releasing system)		Transport and binding	11.638	12.631	9.601	12.341	4.90E-03	7.12E-05	0.99	2.74
lpg2284	ABC transporter, ATP binding protein (lipoprotein releasing system)		Transport and binding	11.275	12.647	9.107	12.406	2.34E-02	3.09E-04	1.37	3.30
lpg2285	lipoprotein ABC transporter (permease) (lipoprotein releasing system)		Transport and binding	9.925	11.067	8.921	11.697	1.54E-02	9.73E-04	1.14	2.78
lpg2285	lipoprotein ABC transporter (permease) (lipoprotein releasing system)		Transport and binding	10.196	11.084	8.022	11.841	1.97E-02	1.36E-02	0.89	3.82
lpg2286	pirin (chromosome condensation) protein		Signal transduction / other regulatory f	9.950	9.828	10.468	9.894	8.33E-01	2.80E-02	-0.12	-0.57
lpg2286	pirin (chromosome condensation) protein		Signal transduction / other regulatory f	10.104	10.651	10.337	10.532	1.13E-01	7.62E-01	0.55	0.19
lpg2287	[acyl carrier protein] phosphodiesterase	*acpD*	Metabolism of Cofactors and Vitamins	10.725	10.903	11.260	10.453	6.30E-01	6.82E-02	0.18	-0.81
lpg2287	[acyl carrier protein] phosphodiesterase	*acpD*	Metabolism of Cofactors and Vitamins	10.747	11.096	11.208	10.692	4.56E-01	2.30E-01	0.35	-0.52
lpg2288	transcriptional regulator, LysR family		Transcription factors / DNA binding prc	8.989	10.265	9.944	9.582	7.39E-03	3.65E-01	1.28	-0.36
lpg2288	transcriptional regulator, LysR family		Transcription factors / DNA binding prc	9.023	9.635	9.691	9.892	2.54E-01	6.45E-01	0.61	0.20
lpg2289	ORF		ORFs of unknown function (unique)	12.422	10.382	9.829	11.028	2.02E-02	3.07E-01	-2.04	1.20
lpg2289	ORF		ORFs of unknown function (unique)	12.213	10.159	9.198	10.633	5.05E-02	2.51E-01	-2.05	1.43

lpg2290	tRNA-Leu		tRNA	12.152	10.250	11.319	10.822	7.56E-04	3.71E-01	-1.90	-0.50
lpg2290	tRNA-Leu		tRNA	12.187	10.195	11.092	10.883	4.60E-04	6.85E-01	-1.99	-0.21
lpg2291	tRNA-Cys		tRNA	12.307	11.025	11.457	11.552	1.10E-01	8.43E-01	-1.28	0.09
lpg2291	tRNA-Cys		tRNA	12.640	11.811	11.613	12.448	2.00E-01	1.06E-01	-0.83	0.83
lpg2292	tRNA-Gly		tRNA	12.824	10.093	10.789	10.534	1.12E-03	7.30E-01	-2.73	-0.25
lpg2292	tRNA-Gly		tRNA	12.664	9.926	10.775	10.858	9.22E-03	9.05E-01	-2.74	0.08
lpg2293	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidy	*pgsA*	Metabolism of Complex Lipids	12.253	12.024	12.967	11.135	5.83E-01	1.83E-01	-0.23	-1.83
lpg2293	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidy	*pgsA*	Metabolism of Complex Lipids	12.043	11.701	12.808	11.879	6.15E-01	1.36E-01	-0.34	-0.93
lpg2294	hydrolase (haloacid dehalogenase family) (phosphoglycolate phospha		Carbohydrate Metabolism	11.808	11.316	11.553	11.122	3.08E-01	1.16E-01	-0.49	-0.43
lpg2294	hydrolase (haloacid dehalogenase family) (phosphoglycolate phospha		Carbohydrate Metabolism	11.376	11.429	11.544	11.191	8.35E-01	1.70E-01	0.05	-0.35
lpg2295	ribosomal large subunit (23S rRNA) pseudouridine synth	*rluC*	DNA/RNA degradation / restriction, Tra	13.170	13.462	13.725	13.814	2.14E-01	6.83E-01	0.29	0.09
lpg2295	ribosomal large subunit (23S rRNA) pseudouridine synth	*rluC*	DNA/RNA degradation / restriction, Tra	13.183	13.466	13.709	13.829	2.25E-01	6.15E-01	0.28	0.12
lpg2296	ORF		ORFs of unknown function (unique)	12.715	10.534	9.125	12.000	4.91E-05	4.25E-03	-2.18	2.87
lpg2296	ORF		ORFs of unknown function (unique)	12.727	10.198	8.930	12.006	3.61E-04	4.71E-03	-2.53	3.08
lpg2297	ribonuclease E	*rne*	Metabolism of Complex Carbohydrate	11.513	13.598	11.589	11.587	1.33E-06	9.95E-01	2.09	0.00
lpg2297	ribonuclease E	*rne*	Metabolism of Complex Carbohydrate	11.223	13.543	11.427	11.481	1.78E-05	8.91E-01	2.32	0.05
lpg2298	inclusion membrane protein A	*legC7/YifA*	Named proteins of general function	11.232	10.144	9.612	12.250	1.46E-01	7.00E-03	-1.09	2.64
lpg2298	inclusion membrane protein A	*legC7/YifA*	Named proteins of general function	11.343	10.839	9.475	12.473	4.06E-01	6.80E-04	-0.50	3.00
lpg2299	ATP-dependent RNA helicase (RNA polymerase associat	*hepA*	Signal transduction / other regulatory f	9.419	9.073	8.964	9.711	4.99E-01	1.60E-01	-0.35	0.75
lpg2299	ATP-dependent RNA helicase (RNA polymerase associat	*hepA*	Signal transduction / other regulatory f	9.310	9.247	8.043	9.504	8.99E-01	2.29E-01	-0.06	1.46
lpg2300	ankyrin repeat domain protein	*legA3*	Named proteins of general function	10.874	11.447	12.874	11.668	4.08E-01	6.25E-03	0.57	-1.21
lpg2300	ankyrin repeat domain protein	*legA3*	Named proteins of general function	11.155	11.645	12.993	12.150	4.34E-01	8.92E-02	0.49	-0.84
lpg2301	hypothetical (Smr domain protein)		Named proteins of general function	11.778	11.433	13.626	11.754	4.90E-01	4.78E-03	-0.35	-1.87
lpg2301	hypothetical (Smr domain protein)		Named proteins of general function	11.827	11.624	13.649	11.848	6.73E-01	4.93E-03	-0.20	-1.80
lpg2302	aspartate semialdehyde dehydrogenase	*asd*	Amino Acid Metabolism	10.255	12.632	11.340	12.426	4.02E-06	1.11E-02	2.38	1.09
lpg2302	aspartate semialdehyde dehydrogenase	*asd*	Amino Acid Metabolism	10.219	12.112	11.179	12.353	3.39E-03	5.14E-02	1.89	1.17
lpg2303	chorismate synthase AroC		Amino Acid Metabolism	10.459	9.755	11.806	9.691	2.29E-01	9.70E-03	-0.70	-2.12
lpg2303	chorismate synthase AroC		Amino Acid Metabolism	10.166	10.131	11.188	10.186	9.18E-01	3.27E-02	-0.03	-1.00
lpg2304	adenine specific methylase		Signal transduction / other regulatory f	10.816	12.359	9.445	12.669	4.81E-03	3.59E-05	1.54	3.22
lpg2304	adenine specific methylase		Signal transduction / other regulatory f	10.693	12.429	9.126	12.669	6.54E-03	3.95E-05	1.74	3.54
lpg2305	Smr domain protein, ATP binding/mismatch repair?		Replication and Repair	10.940	10.412	12.095	10.233	4.86E-01	2.98E-02	-0.53	-1.86
lpg2305	Smr domain protein, ATP binding/mismatch repair?		Replication and Repair	10.956	10.501	12.193	10.836	4.54E-01	2.20E-03	-0.45	-1.36
lpg2306	rhodanese domain protein		Named proteins of general function	11.360	11.136	10.273	11.842	6.39E-01	7.64E-02	-0.22	1.57
lpg2306	rhodanese domain protein		Named proteins of general function	11.394	11.423	10.319	12.068	9.20E-01	1.21E-02	0.03	1.75
lpg2307	glutaredoxin 3	*grxC*	Detoxification / adaptation	10.342	10.903	9.743	11.022	4.23E-01	8.66E-02	0.56	1.28
lpg2307	glutaredoxin 3	*grxC*	Detoxification / adaptation	10.605	10.674	10.039	11.497	8.36E-01	9.78E-03	0.07	1.46
lpg2308	protein export protein SecB (preprotein translocase)	*secB*	Protein fate / hydrolases / secretion	11.949	12.227	10.942	12.735	7.13E-01	2.13E-02	0.28	1.79
lpg2308	protein export protein SecB (preprotein translocase)	*secB*	Protein fate / hydrolases / secretion	11.987	12.261	10.792	12.708	7.15E-01	2.88E-02	0.27	1.92
lpg2309	glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P	*gpsA*	Metabolism of Complex Lipids	10.993	9.525	10.301	11.268	3.61E-02	1.53E-02	-1.47	0.97
lpg2309	glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P	*gpsA*	Metabolism of Complex Lipids	10.837	9.250	10.160	11.288	4.94E-03	1.49E-02	-1.59	1.13
lpg2310	glutamate racemase	*murI*	Amino Acid Metabolism, Metabolism o	10.072	9.642	12.600	9.273	5.45E-01	3.48E-04	-0.43	-3.33
lpg2310	glutamate racemase	*murI*	Amino Acid Metabolism, Metabolism o	10.030	11.160	12.569	10.354	1.45E-01	5.26E-03	1.13	-2.21
lpg2311	interaptin		Named proteins of general function	8.267	9.690	9.577	8.959	1.62E-02	6.41E-01	1.42	-0.62
lpg2311	interaptin		Named proteins of general function	8.380	9.273	9.621	9.211	2.01E-01	7.00E-01	0.89	-0.41
lpg2312	small ORF (100aa)		ORFs of unknown function (unique)	8.541	9.538	12.072	8.575	2.79E-01	3.01E-03	1.00	-3.50
lpg2312	small ORF (100aa)		ORFs of unknown function (unique)	8.754	9.058	11.646	8.565	7.76E-01	2.36E-02	0.30	-3.08
lpg2313	hypothetical		Unknown / hypothetical proteins	13.182	13.475	13.725	13.258	4.49E-01	4.85E-01	0.29	-0.47
lpg2313	hypothetical		Unknown / hypothetical proteins	13.022	13.440	13.717	13.332	1.88E-01	4.95E-01	0.42	-0.39
lpg2314	dihydropicolinate synthase		Amino Acid Metabolism	12.449	12.886	11.870	12.617	4.17E-03	2.43E-03	0.44	0.75
lpg2314	dihydropicolinate synthase		Amino Acid Metabolism	12.170	12.771	11.706	12.670	2.74E-02	1.20E-03	0.60	0.96
lpg2315	ORF (COG2885 outer membrane protein and related peptidoglycan a		Named proteins of general function	12.848	13.512	14.444	13.778	3.64E-01	4.39E-01	0.66	-0.67
lpg2315	ORF (COG2885 outer membrane protein and related peptidoglycan a		Named proteins of general function	12.637	13.567	14.256	13.882	1.16E-01	6.78E-01	0.93	-0.37
lpg2316	3-hydroxybutyrate dehydrogenase (D-beta hydroxybutyr	*bdhA*	Lipid Metabolism, Carbohydrate Meta	11.833	11.845	14.774	11.334	9.86E-01	3.53E-04	0.01	-3.44
lpg2316	3-hydroxybutyrate dehydrogenase (D-beta hydroxybutyr	*bdhA*	Lipid Metabolism, Carbohydrate Meta	11.766	11.759	14.747	11.377	9.93E-01	3.66E-04	-0.01	-3.37
lpg2317	transmembrane protein		Unknown / hypothetical proteins	10.083	9.644	12.555	8.664	4.65E-01	2.26E-03	-0.44	-3.89
lpg2317	transmembrane protein		Unknown / hypothetical proteins	10.309	9.645	12.690	9.826	2.43E-01	1.01E-02	-0.66	-2.86
lpg2318	chemotaxis (motility protein A) transmembrane (proton c	*motA*	Chemotaxis / motility / cell division	11.379	9.516	13.069	9.871	4.35E-02	5.28E-04	-1.86	-3.20
lpg2318	chemotaxis (motility protein A) transmembrane (proton c	*motA*	Chemotaxis / motility / cell division	11.276	10.252	12.982	10.363	1.82E-01	2.78E-03	-1.02	-2.62
lpg2319	chemotaxis (motility protein B) transmembrane (flagellar	*motB*	Chemotaxis / motility / cell division	9.568	8.983	10.783	9.257	3.11E-02	1.07E-03	-0.59	-1.53
lpg2319	chemotaxis (motility protein B) transmembrane (flagellar	*motB*	Chemotaxis / motility / cell division	9.763	8.527	10.807	9.655	3.35E-02	1.20E-02	-1.24	-1.15
lpg2320	small ORF (157aa)		ORFs of unknown function (unique)	11.699	13.180	10.294	12.196	3.89E-04	1.70E-03	1.48	1.90
lpg2320	small ORF (157aa)		ORFs of unknown function (unique)	11.603	13.174	9.970	12.134	6.65E-04	9.57E-03	1.57	2.16
lpg2321	serine transporter	*sdaC*	Transport and binding	12.543	14.444	11.342	13.560	5.48E-04	1.37E-04	1.90	2.22
lpg2321	serine transporter	*sdaC*	Transport and binding	12.515	14.478	11.363	13.623	7.39E-04	7.75E-05	1.96	2.26

lpg2322	cardiac ankyrin repeat protein	*legA5*	Named proteins of general function	8.876	10.061	9.998	9.097	8.45E-02	1.30E-01	1.18	-0.90
lpg2322	cardiac ankyrin repeat protein	*legA5*	Named proteins of general function	8.877	10.539	10.144	9.495	2.02E-02	2.91E-01	1.66	-0.65
lpg2323	type II secretion system protein (twitching motility protein	*uptC*	Protein fate / hydrolases / secretion, C	9.153	9.085	11.936	7.559	9.52E-01	3.35E-04	-0.07	-4.38
lpg2323	type II secretion system protein (twitching motility protein	*uptC*	Protein fate / hydrolases / secretion, C	9.097	9.342	11.965	8.701	7.41E-01	1.72E-03	0.25	-3.26
lpg2324	L-gulono-gamma-lactone oxidase	*Gulo*	Carbohydrate Metabolism	9.756	10.251	10.811	8.297	3.48E-01	1.33E-02	0.50	-2.51
lpg2324	L-gulono-gamma-lactone oxidase	*Gulo*	Carbohydrate Metabolism	9.688	10.747	10.968	9.211	2.91E-01	2.18E-01	1.06	-1.76
lpg2325	hypothetical (SnoK protein?)		Unknown / hypothetical proteins	9.462	10.352	9.243	10.015	1.20E-02	3.84E-02	0.89	0.77
lpg2325	hypothetical (SnoK protein?)		Unknown / hypothetical proteins	9.419	10.395	9.395	10.208	5.30E-03	1.61E-03	0.98	0.81
lpg2326	DNA repair protein RadA	*radA*	Replication and Repair	10.032	11.327	10.190	11.225	8.34E-04	1.12E-03	1.30	1.03
lpg2326	DNA repair protein RadA	*radA*	Replication and Repair	10.150	11.709	10.262	11.968	4.71E-02	4.06E-02	1.56	1.71
lpg2327	CG18304 gene product		Unknown / hypothetical proteins	11.226	12.756	12.766	8.410	1.99E-02	4.95E-05	1.53	-4.36
lpg2327	CG18304 gene product		Unknown / hypothetical proteins	11.262	12.819	12.801	8.692	1.41E-02	5.01E-05	1.56	-4.11
lpg2328	small ORF (127aa)		ORFs of unknown function (unique)	12.559	12.678	11.844	12.456	5.74E-01	8.50E-02	0.12	0.61
lpg2328	small ORF (127aa)		ORFs of unknown function (unique)	12.424	12.714	11.786	12.533	4.14E-01	4.15E-02	0.29	0.75
lpg2329	exodeoxyribonuclease VII small subunit (exonuclease VI	*xseB*	DNA/RNA degradation / restriction	11.812	12.941	13.086	13.480	1.16E-02	5.04E-01	1.13	0.39
lpg2329	exodeoxyribonuclease VII small subunit (exonuclease VI	*xseB*	DNA/RNA degradation / restriction	10.025	10.126	10.678	11.715	8.97E-01	4.16E-02	0.10	1.04
lpg2330	geranyltranstransferase (farnesyl-diphosphate synthase)	*ispA*	Lipid Metabolism, Biosynthesis of Sec	10.064	8.372	9.350	11.475	2.34E-03	8.88E-04	-1.69	2.13
lpg2330	geranyltranstransferase (farnesyl-diphosphate synthase)	*ispA*	Lipid Metabolism, Biosynthesis of Sec	9.670	9.271	8.581	11.851	7.89E-01	4.69E-03	-0.40	3.27
lpg2331	biotin synthase BioC (SAM (and some other nucleotide)	*bioC*	Metabolism of Cofactors and Vitamins	9.460	10.250	8.793	10.228	1.58E-01	1.05E-02	0.79	1.44
lpg2331	biotin synthase BioC (SAM (and some other nucleotide)	*bioC*	Metabolism of Cofactors and Vitamins	9.776	10.377	8.432	10.305	9.68E-02	1.73E-02	0.60	1.87
lpg2332	competence protein ComF (phosphoribosyltransferase)		Transport and binding	8.949	8.957	9.129	8.165	9.89E-01	2.19E-01	0.01	-0.96
lpg2332	competence protein ComF (phosphoribosyltransferase)		Transport and binding	8.397	9.404	9.165	8.982	2.73E-02	7.04E-01	1.01	-0.18
lpg2333	membrane associated zinc metalloprotease		Protein fate / hydrolases / secretion	10.312	10.032	11.306	9.649	6.21E-01	2.86E-02	-0.28	-1.66
lpg2333	membrane associated zinc metalloprotease		Protein fate / hydrolases / secretion	10.443	9.861	11.310	10.035	2.62E-01	2.92E-02	-0.58	-1.28
lpg2334	ORF		ORFs of unknown function (unique)	9.678	9.382	12.745	8.934	6.77E-01	6.02E-04	-0.30	-3.81
lpg2334	ORF		ORFs of unknown function (unique)	9.690	8.891	12.708	9.120	3.34E-01	5.30E-04	-0.80	-3.59
lpg2335	glutamyl tRNA reductase	*hemA*	Metabolism of Cofactors and Vitamins	11.272	11.423	10.685	10.899	7.07E-01	8.18E-01	0.15	0.21
lpg2335	glutamyl tRNA reductase	*hemA*	Metabolism of Cofactors and Vitamins	11.287	11.463	10.719	11.398	6.72E-01	1.38E-01	0.18	0.68
lpg2336	peptide chain release factor 1 (RF-1)	*prfA*	Translation	11.310	10.356	10.735	11.479	1.04E-01	5.23E-02	-0.95	0.74
lpg2336	peptide chain release factor 1 (RF-1)	*prfA*	Translation	11.222	10.440	10.446	11.380	7.72E-02	3.88E-02	-0.78	0.93
lpg2337	protein methyltransferase HemK (modification methylase)		Protein fate / hydrolases / secretion	8.877	10.264	9.924	9.943	6.35E-02	9.77E-01	1.39	0.02
lpg2337	protein methyltransferase HemK (modification methylase)		Protein fate / hydrolases / secretion	7.722	10.210	9.956	10.354	1.18E-02	2.85E-01	2.49	0.40
lpg2338	DnaK suppressor protein	*dksA*	Transcription factors / DNA binding pro	14.039	12.656	13.386	13.692	2.26E-05	1.15E-01	-1.38	0.31
lpg2338	DnaK suppressor protein	*dksA*	Transcription factors / DNA binding pro	14.052	12.685	13.352	13.713	3.44E-05	7.12E-02	-1.37	0.36
lpg2339	ORF		ORFs of unknown function (unique)	11.366	8.827	10.205	10.374	1.86E-04	7.52E-01	-2.54	0.17
lpg2339	ORF		ORFs of unknown function (unique)	11.417	9.160	10.256	10.816	4.75E-04	2.05E-01	-2.26	0.56
lpg2340	3-deoxy-D-manno-oct-2-ulosonic acid transferase (Kdo tr	*kdtA*	Metabolism of Complex Carbohydrate	9.118	8.360	8.880	7.787	2.10E-01	1.43E-01	-0.76	-1.09
lpg2340	3-deoxy-D-manno-oct-2-ulosonic acid transferase (Kdo tr	*kdtA*	Metabolism of Complex Carbohydrate	9.415	8.462	8.722	8.629	9.77E-03	8.90E-01	-0.95	-0.09
lpg2341	DNA binding protein DnaJ, heat shock protein		Detoxification / adaptation, Transcripti	8.624	8.880	8.689	7.138	6.64E-01	1.75E-01	0.26	-1.55
lpg2341	DNA binding protein DnaJ, heat shock protein		Detoxification / adaptation, Transcripti	8.110	8.069	9.157	8.597	9.04E-01	4.26E-01	-0.04	-0.56
lpg2342	ORF		ORFs of unknown function (unique)	10.172	9.188	9.471	9.489	2.10E-01	9.82E-01	-0.98	0.02
lpg2342	ORF		ORFs of unknown function (unique)	10.077	10.108	9.727	10.314	8.92E-01	3.94E-02	0.03	0.59
lpg2343	lysophospholipase A (glycerophospholipid-cholesterol ac	*sseJ*	Toxin production / other pathogen func	12.716	13.209	12.780	13.909	2.12E-03	4.52E-03	0.49	1.13
lpg2343	lysophospholipase A (glycerophospholipid-cholesterol ac	*sseJ*	Toxin production / other pathogen func	12.726	13.258	12.788	13.940	2.78E-03	1.86E-03	0.53	1.15
lpg2344	ORF		ORFs of unknown function (unique)	9.877	13.876	7.886	14.269	1.36E-04	1.28E-06	4.00	6.38
lpg2344	ORF		ORFs of unknown function (unique)	9.834	13.835	7.389	14.167	2.04E-04	1.81E-05	4.00	6.78
lpg2345	ATP-dependent RNA helicase (cold shock DEAD box pro	*deaD*	Detoxification / adaptation	10.516	11.466	10.214	11.844	1.64E-02	1.10E-03	0.95	1.63
lpg2345	ATP-dependent RNA helicase (cold shock DEAD box pro	*deaD*	Detoxification / adaptation	10.505	11.573	9.997	11.908	3.99E-03	1.37E-04	1.07	1.91
lpg2346	transcriptional regulator (diacylglycerol kinase catalytic domain?) sphi		Transcription factors / DNA binding pro	11.047	10.227	9.642	9.974	4.43E-02	4.08E-01	-0.82	0.33
lpg2346	transcriptional regulator (diacylglycerol kinase catalytic domain?) sphi		Transcription factors / DNA binding pro	11.054	10.519	10.121	10.728	4.64E-01	5.12E-01	-0.54	0.61
lpg2347	2,4-dienoyl-CoA reductase FadH1 (NADPH dehydrogena	*fadH*	Metabolism of Cofactors and Vitamins	10.571	11.487	11.152	11.351	2.70E-05	4.32E-01	0.92	0.20
lpg2347	2,4-dienoyl-CoA reductase FadH1 (NADPH dehydrogena	*fadH*	Metabolism of Cofactors and Vitamins	10.518	11.512	11.095	11.409	5.96E-05	6.65E-02	0.99	0.31
lpg2348	superoxide dismutase (copper-zinc)	*sodC*	Detoxification / adaptation	11.713	11.571	13.707	10.848	7.54E-01	3.90E-04	-0.14	-2.86
lpg2348	superoxide dismutase (copper-zinc)	*sodC*	Detoxification / adaptation	11.751	11.443	13.694	10.891	5.98E-01	3.81E-04	-0.31	-2.80
lpg2349	alkylhydroperoxidase AhpD family core domain protein		Detoxification / adaptation	10.545	10.962	11.825	10.909	1.32E-01	1.65E-01	0.42	-0.92
lpg2349	alkylhydroperoxidase AhpD family core domain protein		Detoxification / adaptation	10.700	10.938	11.805	11.048	4.76E-01	2.51E-01	0.24	-0.76
lpg2350	alkylhydroperoxide reductase (antioxidant protein, AhpC/TSA family)		Detoxification / adaptation	11.773	11.937	11.911	10.631	5.36E-01	2.96E-05	0.16	-1.28
lpg2350	alkylhydroperoxide reductase (antioxidant protein, AhpC/TSA family)		Detoxification / adaptation	11.622	11.958	11.841	10.709	3.48E-01	2.25E-04	0.34	-1.13
lpg2351	ORF		ORFs of unknown function (unique)	10.291	9.357	13.144	8.911	1.75E-01	1.59E-03	-0.93	-4.23
lpg2351	ORF		ORFs of unknown function (unique)	10.220	9.376	13.221	9.075	1.78E-01	1.66E-03	-0.84	-4.15
lpg2352	malate dehydrogenase	*mdh*	Carbohydrate Metabolism, Energy Me	13.684	13.619	14.306	13.721	7.99E-01	8.76E-02	-0.06	-0.59
lpg2352	malate dehydrogenase	*mdh*	Carbohydrate Metabolism, Energy Me	13.596	13.538	14.204	13.660	8.65E-01	1.83E-01	-0.06	-0.54
lpg2353	NUDIX hydrolase (MutT/nudix family protein) (nucleoside	*yrfE*	Metabolism of Complex Carbohydrate	11.655	11.495	11.694	11.480	7.35E-01	3.17E-01	-0.16	-0.21
lpg2353	NUDIX hydrolase (MutT/nudix family protein) (nucleoside	*yrfE*	Metabolism of Complex Carbohydrate	11.277	12.442	11.923	12.789	7.03E-04	4.00E-03	1.16	0.87

lpg2354	(oxygen-independent) coproporphyrinogen III oxidase		Metabolism of Cofactors and Vitamins	9.382	7.995	8.547	9.697	1.66E-01	5.85E-02	-1.39	1.15
lpg2354	(oxygen-independent) coproporphyrinogen III oxidase		Metabolism of Cofactors and Vitamins	9.212	8.866	8.116	9.623	3.00E-01	1.66E-01	-0.35	1.51
lpg2355	amidase (enantiomer selective) (glu-tRNA amidotransferase subunit A		Amino Acid Metabolism, Metabolism o	9.334	9.680	8.950	9.364	2.20E-01	4.75E-01	0.35	0.41
lpg2355	amidase (enantiomer selective) (glu-tRNA amidotransferase subunit A		Amino Acid Metabolism, Metabolism o	9.329	9.973	8.429	9.598	2.70E-02	5.51E-02	0.64	1.17
lpg2356	transmembrane protein		Unknown / hypothetical proteins	12.056	12.090	11.521	11.892	8.59E-01	1.44E-01	0.03	0.37
lpg2356	transmembrane protein		Unknown / hypothetical proteins	12.147	12.070	11.317	11.817	6.84E-01	6.83E-02	-0.08	0.50
lpg2357	O-sialoglycoprotein endopeptidase	*gcp*	Protein fate / hydrolases / secretion	12.199	11.170	11.044	11.799	1.44E-03	2.65E-02	-1.03	0.76
lpg2357	O-sialoglycoprotein endopeptidase	*gcp*	Protein fate / hydrolases / secretion	12.251	11.152	10.920	11.734	4.46E-04	1.37E-02	-1.10	0.81
lpg2358	30S ribosomal protein S21	*rpsU*	Translation	10.658	10.844	9.250	12.570	8.50E-01	2.23E-04	0.19	3.32
lpg2358	30S ribosomal protein S21	*rpsU*	Translation	11.117	10.347	9.183	12.862	6.18E-02	4.63E-05	-0.77	3.68
lpg2359	conserved hypothetical protein		Unknown / hypothetical proteins	11.386	10.005	8.986	11.533	7.51E-04	3.92E-02	-1.38	2.55
lpg2359	conserved hypothetical protein		Unknown / hypothetical proteins	10.989	10.308	9.399	12.142	3.19E-01	8.45E-04	-0.68	2.74
lpg2360	DNA primase DnaG		Replication and Repair	9.109	8.037	9.160	9.267	9.81E-02	8.98E-01	-1.07	0.11
lpg2360	DNA primase DnaG		Replication and Repair	9.637	7.863	8.563	9.283	6.28E-05	3.56E-01	-1.77	0.72
lpg2361	RNA polymerase sigma 70 factor (sigma factor RpoD)	*rpoD*	Transcription factors / DNA binding prc	13.049	13.412	12.764	13.649	1.51E-01	1.50E-03	0.36	0.88
lpg2361	RNA polymerase sigma 70 factor (sigma factor RpoD)	*rpoD*	Transcription factors / DNA binding prc	13.035	13.417	12.707	13.657	1.11E-01	8.10E-04	0.38	0.95
lpg2362	tRNA-Met		tRNA	7.334	8.579	7.870	8.050	1.07E-01	8.26E-01	1.24	0.18
lpg2362	tRNA-Met		tRNA	7.382	8.280	7.476	8.345	3.79E-01	2.89E-01	0.90	0.87
lpg2363	transposase (IS652)		Viral functions / Phage / Transposases	8.827	10.888	9.804	10.338	5.38E-03	3.23E-01	2.06	0.53
lpg2363	transposase (IS652)		Viral functions / Phage / Transposases	9.130	10.560	9.297	10.150	2.47E-02	1.36E-01	1.43	0.85
lpg2364	small ORF (121aa)		ORFs of unknown function (unique)	9.525	7.734	12.308	7.654	3.90E-03	6.49E-03	-1.79	-4.65
lpg2364	small ORF (121aa)		ORFs of unknown function (unique)	9.583	8.067	12.160	8.281	3.79E-02	2.09E-02	-1.52	-3.88
lpg2365	TraK		Transport and binding, Protein fate / hy	10.873	11.078	9.738	10.998	4.13E-01	6.21E-04	0.20	1.26
lpg2365	TraK		Transport and binding, Protein fate / hy	10.796	10.938	9.258	11.317	7.65E-01	8.31E-03	0.14	2.06
lpg2366	inner membrane protein		Named proteins of general function	8.615	9.956	10.214	9.467	2.59E-02	1.28E-01	1.34	-0.75
lpg2366	inner membrane protein		Named proteins of general function	8.752	10.087	10.145	10.271	9.79E-03	7.85E-01	1.33	0.13
lpg2367	ORF		ORFs of unknown function (unique)	9.858	10.255	9.750	9.647	3.36E-01	7.47E-01	0.40	-0.10
lpg2367	ORF		ORFs of unknown function (unique)	9.564	11.177	9.197	10.352	3.13E-02	4.90E-02	1.61	1.16
lpg2368	transcriptional regulator? phage repressor?		Transcription factors / DNA binding prc	9.205	8.409	8.987	9.237	1.63E-01	3.49E-01	-0.80	0.25
lpg2368	transcriptional regulator? phage repressor?		Transcription factors / DNA binding prc	8.800	8.119	8.278	9.406	1.49E-01	5.10E-02	-0.68	1.13
lpg2369	HipA (persistence to inhibition of murein or DNA biosynthesis, DNA bi		Cell envelope synthesis, Signal transd	9.461	9.241	10.067	9.365	5.58E-01	1.48E-01	-0.22	-0.70
lpg2369	HipA (persistence to inhibition of murein or DNA biosynthesis, DNA bi		Cell envelope synthesis, Signal transd	9.380	9.553	10.033	9.389	5.15E-01	3.49E-01	0.17	-0.64
lpg2370	conserved hypothetical protein		Unknown / hypothetical proteins	9.645	8.607	10.996	8.674	1.68E-01	1.67E-02	-1.04	-2.32
lpg2370	conserved hypothetical protein		Unknown / hypothetical proteins	9.668	7.177	7.741	7.543	1.10E-01	8.83E-01	-2.49	-0.20
lpg2371	ORF		ORFs of unknown function (unique)	6.506	6.277	8.006	6.819	8.24E-01	1.80E-01	-0.23	-1.19
lpg2371	ORF		ORFs of unknown function (unique)	6.340	7.421	6.681	8.047	4.60E-01	2.70E-01	1.08	1.37
lpg2372	ORF		ORFs of unknown function (unique)	9.229	10.618	10.298	9.532	6.89E-04	2.19E-01	1.39	-0.77
lpg2372	ORF		ORFs of unknown function (unique)	8.903	10.601	10.255	10.113	5.54E-05	7.29E-01	1.70	-0.14
lpg2373	hypothetical protein		Unknown / hypothetical proteins	8.357	7.746	7.898	7.677	3.50E-01	8.31E-01	-0.61	-0.22
lpg2373	hypothetical protein		Unknown / hypothetical proteins	8.191	8.479	7.359	8.720	6.54E-01	2.48E-01	0.29	1.36
lpg2374	mannose-6-phosphate isomerase		Carbohydrate Metabolism	10.385	9.971	10.201	10.377	2.99E-01	7.47E-01	-0.41	0.18
lpg2374	mannose-6-phosphate isomerase		Carbohydrate Metabolism	10.355	9.838	9.951	10.475	3.87E-01	3.87E-01	-0.52	0.52
lpg2375	small ORF (157aa)		ORFs of unknown function (unique)	9.869	9.643	10.314	9.564	3.52E-01	1.72E-01	-0.23	-0.75
lpg2375	small ORF (157aa)		ORFs of unknown function (unique)	9.871	9.390	10.272	10.134	1.14E-01	6.90E-01	-0.48	-0.14
lpg2376	transcriptional regulator, LysR family		Transcription factors / DNA binding prc	9.566	8.804	10.628	7.606	1.02E-01	2.80E-03	-0.76	-3.02
lpg2376	transcriptional regulator, LysR family		Transcription factors / DNA binding prc	9.554	8.882	10.593	8.473	3.69E-01	9.24E-03	-0.67	-2.12
lpg2377	small ORF (75aa) transcriptional regulator?		Transcription factors / DNA binding prc	9.142	9.209	10.195	9.278	9.25E-01	2.45E-01	0.07	-0.92
lpg2377	small ORF (75aa) transcriptional regulator?		Transcription factors / DNA binding prc	9.064	9.035	9.836	9.399	9.70E-01	5.40E-01	-0.03	-0.44
lpg2378	small ORF (57aa) hypothetical?		Unknown / hypothetical proteins	8.967	8.952	9.112	8.357	9.75E-01	3.49E-01	-0.01	-0.76
lpg2378	small ORF (57aa) hypothetical?		Unknown / hypothetical proteins	9.484	8.938	8.974	8.819	2.15E-01	8.38E-01	-0.55	-0.15
lpg2379	hypothetical protein HI0665		Unknown / hypothetical proteins	9.869	10.430	11.003	11.014	4.28E-01	9.83E-01	0.56	0.01
lpg2379	hypothetical protein HI0665		Unknown / hypothetical proteins	9.937	11.412	11.067	11.442	1.73E-03	1.69E-01	1.47	0.37
lpg2380	conserved hypothetical protein		Unknown / hypothetical proteins	8.700	8.076	8.715	7.839	4.17E-01	2.56E-01	-0.62	-0.88
lpg2380	conserved hypothetical protein		Unknown / hypothetical proteins	8.761	8.045	8.761	8.778	3.70E-01	9.83E-01	-0.72	0.02
lpg2381	magnesium-transporting ATPase, P-type	*mgt*	Transport and binding	8.321	9.076	9.609	9.810	3.86E-01	8.56E-01	0.76	0.20
lpg2381	magnesium-transporting ATPase, P-type	*mgt*	Transport and binding	8.564	9.050	9.723	10.007	5.74E-01	7.56E-01	0.49	0.28
lpg2382	ORF		ORFs of unknown function (unique)	9.765	8.953	10.701	8.697	2.46E-01	6.85E-02	-0.81	-2.00
lpg2382	ORF		ORFs of unknown function (unique)	10.250	8.950	10.989	9.152	9.94E-02	7.76E-02	-1.30	-1.84
lpg2383	transcriptional regulator, LysR family		Transcription factors / DNA binding prc	8.305	7.952	10.188	7.139	8.49E-01	1.08E-01	-0.35	-3.05
lpg2383	transcriptional regulator, LysR family		Transcription factors / DNA binding prc	7.744	6.874	10.019	7.352	5.55E-01	1.21E-01	-0.87	-2.67
lpg2384	Kup system potassium uptake protein	*kup*	Transport and binding	10.716	10.155	10.940	10.858	2.60E-01	8.18E-01	-0.56	-0.08
lpg2384	Kup system potassium uptake protein	*kup*	Transport and binding	10.758	10.080	10.886	10.856	2.01E-01	9.24E-01	-0.68	-0.03
lpg2385	hypothetical protein		Unknown / hypothetical proteins	9.560	8.319	11.639	8.399	1.70E-01	5.80E-03	-1.24	-3.24
lpg2385	hypothetical protein		Unknown / hypothetical proteins	9.548	9.354	11.626	8.499	7.40E-01	1.08E-03	-0.19	-3.13

lpg2386	ORF		ORFs of unknown function (unique)	11.744	12.180	10.749	12.164	2.54E-01	1.60E-03	0.44	1.42
lpg2386	ORF		ORFs of unknown function (unique)	11.765	12.290	10.614	12.249	6.52E-02	1.60E-04	0.52	1.63
lpg2387	plasminogen activator (coagulase/fibrinolysin) (outer mer	*pla*	Protein fate / hydrolases / secretion	10.301	11.958	10.547	9.350	8.46E-04	4.34E-02	1.66	-1.20
lpg2387	plasminogen activator (coagulase/fibrinolysin) (outer mer	*pla*	Protein fate / hydrolases / secretion	10.217	11.894	10.654	9.665	1.31E-04	6.35E-02	1.68	-0.99
lpg2388	amino acid permease (transporter) (L-asparagine permease)		Transport and binding	10.194	9.530	10.223	9.181	1.85E-01	1.35E-01	-0.66	-1.04
lpg2388	amino acid permease (transporter) (L-asparagine permease)		Transport and binding	10.183	9.803	10.093	9.961	4.24E-01	8.24E-01	-0.38	-0.13
lpg2389	catalase-peroxidase KatB		Amino Acid Metabolism, Energy Metab	10.257	11.696	10.170	10.946	1.55E-04	3.39E-02	1.44	0.78
lpg2389	catalase-peroxidase KatB		Amino Acid Metabolism, Energy Metab	10.152	11.682	10.002	11.094	1.15E-03	2.40E-02	1.53	1.09
lpg2390	proline/betaine transporter (major facilitator family transp	*proP1*	Transport and binding	8.932	7.341	8.091	7.053	8.55E-02	1.00E-01	-1.59	-1.04
lpg2390	proline/betaine transporter (major facilitator family transp	*proP1*	Transport and binding	8.632	7.793	8.525	7.680	1.54E-01	2.42E-02	-0.84	-0.84
lpg2391	sdbC	*sdbC*	Named proteins of general function	10.828	12.401	11.549	10.765	3.56E-06	1.04E-03	1.57	-0.78
lpg2391	sdbC	*sdbC*	Named proteins of general function	10.789	12.426	11.588	10.881	7.34E-06	1.25E-03	1.64	-0.71
lpg2392	leucine rich repeat protein family	*legL6*	Named proteins of general function	9.669	10.257	9.602	9.688	1.13E-01	9.06E-01	0.59	0.09
lpg2392	leucine rich repeat protein family	*legL6*	Named proteins of general function	9.787	10.073	9.208	9.602	4.26E-01	6.46E-01	0.29	0.39
lpg2393	bacterioferritin (cytochrome b1)		Energy Metabolism	11.384	9.837	13.388	9.601	2.04E-02	4.51E-05	-1.55	-3.79
lpg2393	bacterioferritin (cytochrome b1)		Energy Metabolism	11.354	9.980	13.381	9.745	9.08E-02	9.28E-05	-1.37	-3.64
lpg2394	small ORF (77aa)		ORFs of unknown function (unique)	8.381	7.913	9.760	7.669	4.57E-01	3.25E-02	-0.47	-2.09
lpg2394	small ORF (77aa)		ORFs of unknown function (unique)	7.628	6.772	9.176	7.716	5.25E-01	2.39E-01	-0.86	-1.46
lpg2395	ORF		ORFs of unknown function (unique)	9.980	12.338	14.309	9.358	7.01E-02	2.08E-04	2.36	-4.95
lpg2395	ORF		ORFs of unknown function (unique)	9.998	13.384	14.364	10.202	8.85E-03	8.13E-03	3.39	-4.16
lpg2396	transcriptional regulator		Transcription factors / DNA binding pro	8.813	9.387	11.064	9.684	3.61E-01	8.17E-03	0.57	-1.38
lpg2396	transcriptional regulator		Transcription factors / DNA binding pro	8.013	9.457	10.810	9.627	4.85E-02	1.45E-02	1.44	-1.18
lpg2397	secreted peptidase (cell wall endopeptidase)		Protein fate / hydrolases / secretion	10.079	9.496	10.954	10.306	1.39E-01	2.40E-01	-0.58	-0.65
lpg2397	secreted peptidase (cell wall endopeptidase)		Protein fate / hydrolases / secretion	10.122	9.618	10.975	10.434	7.11E-02	3.15E-01	-0.50	-0.54
lpg2398	aminoglycoside 6'-N-acetyltransferase		Named proteins of general function	10.332	8.150	10.833	8.313	1.30E-03	1.03E-03	-2.18	-2.52
lpg2398	aminoglycoside 6'-N-acetyltransferase		Named proteins of general function	10.113	7.721	10.503	8.493	1.58E-02	1.20E-02	-2.39	-2.01
lpg2399	unknown virulence protein		Toxin production / other pathogen func	8.687	8.075	12.770	8.259	4.60E-01	5.19E-05	-0.61	-4.51
lpg2399	unknown virulence protein		Toxin production / other pathogen func	8.920	7.940	12.745	8.487	3.20E-01	2.31E-04	-0.98	-4.26
lpg2400	unnamed protein product	*legL7*	Unknown / hypothetical proteins	9.791	10.078	9.624	9.037	5.62E-01	6.27E-01	0.29	-0.59
lpg2400	unnamed protein product	*legL7*	Unknown / hypothetical proteins	9.889	9.972	9.778	9.336	7.26E-01	5.96E-01	0.08	-0.44
lpg2401	putative secreted esterase		Named proteins of general function	9.429	10.372	9.708	9.663	3.96E-02	9.22E-01	0.94	-0.05
lpg2401	putative secreted esterase		Named proteins of general function	9.407	10.867	9.794	9.828	1.57E-03	9.50E-01	1.46	0.03
lpg2402	regulatory protein (transcriptional regulator, LysR)		Transcription factors / DNA binding pro	10.960	12.491	13.311	12.363	3.38E-02	3.02E-01	1.53	-0.95
lpg2402	regulatory protein (transcriptional regulator, LysR)		Transcription factors / DNA binding pro	10.901	12.513	13.174	12.453	2.91E-02	4.42E-01	1.61	-0.72
lpg2403	ORF		ORFs of unknown function (unique)	10.089	10.632	10.893	9.696	2.40E-01	2.07E-02	0.54	-1.20
lpg2403	ORF		ORFs of unknown function (unique)	10.067	10.703	10.445	9.952	1.39E-01	2.12E-01	0.64	-0.49
lpg2404	ORF		ORFs of unknown function (unique)	9.022	8.895	9.727	8.444	8.70E-01	2.68E-02	-0.13	-1.28
lpg2404	ORF		ORFs of unknown function (unique)	9.052	9.689	9.389	8.363	2.98E-01	1.94E-01	0.64	-1.03
lpg2405	mutator mutT protein	*mutT*	DNA/RNA degradation / restriction	9.147	9.276	10.223	8.703	4.93E-01	9.55E-02	0.13	-1.52
lpg2405	mutator mutT protein	*mutT*	DNA/RNA degradation / restriction	9.283	10.132	10.096	9.678	4.34E-01	6.37E-01	0.85	-0.42
lpg2406	ORF		ORFs of unknown function (unique)	11.368	11.210	13.347	11.680	8.51E-01	6.94E-03	-0.16	-1.67
lpg2406	ORF		ORFs of unknown function (unique)	11.482	11.907	13.392	12.187	6.00E-01	8.10E-02	0.43	-1.21
lpg2407	small ORF (101aa)		ORFs of unknown function (unique)	8.162	8.706	8.713	7.407	3.20E-01	2.11E-01	0.54	-1.31
lpg2407	small ORF (101aa)		ORFs of unknown function (unique)	7.543	9.205	8.785	8.764	6.87E-02	9.87E-01	1.66	-0.02
lpg2408	hypothetical protein		Unknown / hypothetical proteins	9.186	10.062	10.601	9.472	1.65E-01	8.02E-02	0.88	-1.13
lpg2408	hypothetical protein		Unknown / hypothetical proteins	8.992	9.051	9.416	8.314	9.02E-01	1.55E-01	0.06	-1.10
lpg2409	ORF	*ceg29*	ORFs of unknown function (unique)	10.352	12.935	10.196	11.393	2.06E-04	1.37E-01	2.58	1.20
lpg2409	ORF	*ceg29*	ORFs of unknown function (unique)	9.910	12.905	10.145	11.520	1.51E-03	6.04E-02	2.99	1.38
lpg2410	hypothetical (serine protease?) (membrane spanning pro	*VpdA*	Named proteins of general function	9.882	11.325	11.655	8.947	9.55E-02	2.30E-02	1.44	-2.71
lpg2410	hypothetical (serine protease?) (membrane spanning pro	*VpdA*	Named proteins of general function	10.137	11.894	12.166	9.840	4.51E-02	3.48E-03	1.76	-2.33
lpg2411	ORF		ORFs of unknown function (unique)	8.600	11.538	8.592	10.581	1.72E-03	8.90E-02	2.94	1.99
lpg2411	ORF		ORFs of unknown function (unique)	8.183	11.697	7.540	10.304	1.94E-03	8.52E-04	3.51	2.76
lpg2412	AMPC cephalosporinase (AmpC beta-lactamase) (penici	*ampC*	Cell envelope synthesis, Detoxificatior	8.807	9.369	8.993	9.912	3.87E-01	6.25E-02	0.56	0.92
lpg2412	AMPC cephalosporinase (AmpC beta-lactamase) (penici	*ampC*	Cell envelope synthesis, Detoxificatior	9.382	9.166	8.967	10.291	4.77E-01	3.02E-02	-0.22	1.32
lpg2413	small ORF (145aa)		ORFs of unknown function (unique)	11.656	12.856	13.174	10.274	2.59E-02	7.87E-05	1.20	-2.90
lpg2413	small ORF (145aa)		ORFs of unknown function (unique)	11.760	12.914	13.236	10.410	2.33E-02	6.73E-05	1.15	-2.83
lpg2414	small ORF (97aa)		ORFs of unknown function (unique)	10.768	10.415	11.009	10.436	4.73E-01	1.61E-01	-0.35	-0.57
lpg2414	small ORF (97aa)		ORFs of unknown function (unique)	11.004	10.529	11.046	10.877	4.62E-01	8.29E-01	-0.47	-0.17
lpg2415	transmembrane protein		Unknown / hypothetical proteins	9.954	9.548	12.924	8.709	6.72E-01	2.09E-03	-0.41	-4.21
lpg2415	transmembrane protein		Unknown / hypothetical proteins	9.674	10.754	12.940	9.121	4.31E-01	6.41E-03	1.08	-3.82
lpg2416	ankyrin repeat containing protein?	*legA1*	Named proteins of general function	8.681	8.097	9.104	6.999	2.31E-01	1.46E-07	-0.58	-2.11
lpg2416	ankyrin repeat containing protein?	*legA1*	Named proteins of general function	8.705	8.088	9.126	7.403	2.39E-01	2.14E-02	-0.62	-1.72
lpg2417	ORF		ORFs of unknown function (unique)	11.483	8.401	9.524	10.687	2.94E-03	6.50E-02	-3.08	1.16
lpg2417	ORF		ORFs of unknown function (unique)	11.622	8.994	9.342	10.729	3.93E-05	4.90E-02	-2.63	1.39

lpg2418	penicillin-binding protein AmpH, putative		Toxin production / other pathogen func	11.490	9.532	9.498	10.661	4.81E-02	1.55E-01	-1.96	1.16
lpg2418	penicillin-binding protein AmpH, putative		Toxin production / other pathogen func	10.720	9.852	8.805	10.719	6.13E-03	3.69E-03	-0.87	1.91
lpg2419	ORF		ORFs of unknown function (unique)	10.191	9.915	9.735	11.002	7.17E-01	1.10E-01	-0.28	1.27
lpg2419	ORF		ORFs of unknown function (unique)	10.421	9.816	9.755	11.067	4.56E-01	1.73E-01	-0.60	1.31
lpg2420	ORF		ORFs of unknown function (unique)	10.970	10.932	10.446	12.368	9.32E-01	1.66E-05	-0.04	1.92
lpg2420	ORF		ORFs of unknown function (unique)	10.581	10.860	10.266	12.296	7.29E-01	1.35E-06	0.28	2.03
lpg2422	hypothetical protein		Unknown / hypothetical proteins	6.779	8.310	11.115	7.791	3.13E-01	4.78E-02	1.53	-3.32
lpg2422	hypothetical protein		Unknown / hypothetical proteins	7.240	7.459	11.623	8.549	8.68E-01	8.08E-03	0.22	-3.07
lpg2423	hypothetical protein-transmembrane region and signal peptide predict		Named proteins of general function	9.720	10.325	10.378	9.606	2.10E-01	2.23E-02	0.61	-0.77
lpg2423	hypothetical protein-transmembrane region and signal peptide predict		Named proteins of general function	9.560	11.190	10.367	10.252	9.10E-02	8.77E-01	1.63	-0.12
lpg2424	ORF		ORFs of unknown function (unique)	10.338	11.987	11.535	9.106	1.07E-03	1.12E-03	1.65	-2.43
lpg2424	ORF		ORFs of unknown function (unique)	9.945	12.226	10.507	10.570	9.31E-04	9.21E-01	2.28	0.06
lpg2425	ORF		ORFs of unknown function (unique)	11.084	11.993	11.053	11.310	9.62E-04	4.01E-01	0.91	0.26
lpg2425	ORF		ORFs of unknown function (unique)	10.756	11.797	10.434	11.065	3.38E-02	1.09E-02	1.04	0.63
lpg2426	malonate decarboxylase alpha subunit	*mdcA*	Energy Metabolism	9.685	9.221	11.492	8.358	5.32E-01	1.13E-02	-0.46	-3.13
lpg2426	malonate decarboxylase alpha subunit	*mdcA*	Energy Metabolism	9.419	9.311	11.529	8.878	8.65E-01	2.71E-02	-0.11	-2.65
lpg2427	acetyl coenzyme A carboxylase, carboxyltransferase sub	*mdcB*	Energy Metabolism	9.226	8.615	11.637	8.511	3.96E-01	1.47E-04	-0.61	-3.13
lpg2427	acetyl coenzyme A carboxylase, carboxyltransferase sub	*mdcB*	Energy Metabolism	9.249	8.999	11.553	8.484	6.55E-01	1.95E-04	-0.25	-3.07
lpg2428	malonate decarboxylase gamma subunit	*mdcC*	Energy Metabolism	8.885	7.843	12.086	7.875	3.08E-01	3.69E-03	-1.04	-4.21
lpg2428	malonate decarboxylase gamma subunit	*mdcC*	Energy Metabolism	8.843	8.119	12.099	8.042	4.20E-01	1.81E-02	-0.72	-4.06
lpg2429	ORF (MdcE? malonate decarboxylase?)	*mdcG*	Energy Metabolism	8.302	8.189	10.737	6.758	9.25E-01	3.49E-04	-0.11	-3.98
lpg2429	ORF (MdcE? malonate decarboxylase?)	*mdcG*	Energy Metabolism	8.929	7.946	10.745	7.072	2.12E-01	6.51E-03	-0.98	-3.67
lpg2430	2-(5-triphosphoribosyl)-3'-dephosphocoenzyme A syntha	*mdcB*	Signal transduction / other regulatory f	9.745	7.224	10.550	7.562	3.74E-04	1.15E-04	-2.52	-2.99
lpg2430	2-(5-triphosphoribosyl)-3'-dephosphocoenzyme A syntha	*mdcB*	Signal transduction / other regulatory f	9.884	8.024	10.543	8.195	1.07E-04	8.80E-05	-1.86	-2.35
lpg2431	putative malonyl-CoA acyl-carrier-protein transacylase		Lipid Metabolism	8.747	8.984	9.835	9.474	8.04E-01	5.33E-01	0.24	-0.36
lpg2431	putative malonyl-CoA acyl-carrier-protein transacylase		Lipid Metabolism	9.085	9.647	9.504	9.879	4.35E-01	6.00E-01	0.56	0.37
lpg2432	alkaline phosphatase	*phoA*	Named proteins of general function	7.624	8.294	7.956	7.162	5.09E-01	6.04E-01	0.67	-0.79
lpg2432	alkaline phosphatase	*phoA*	Named proteins of general function	7.476	8.688	7.317	8.595	2.09E-01	1.30E-01	1.21	1.28
lpg2433	ORF		ORFs of unknown function (unique)	8.541	9.228	9.569	9.100	2.72E-01	5.21E-01	0.69	-0.47
lpg2433	ORF		ORFs of unknown function (unique)	8.166	9.553	9.397	9.699	7.05E-02	5.68E-01	1.39	0.30
lpg2434	conserved hypothetical protein		Unknown / hypothetical proteins	9.624	10.820	10.810	9.599	4.56E-03	9.40E-02	1.20	-1.21
lpg2434	conserved hypothetical protein		Unknown / hypothetical proteins	9.763	10.705	11.061	9.862	5.08E-02	5.90E-02	0.94	-1.20
lpg2435	ORF		ORFs of unknown function (unique)	10.493	9.687	11.785	9.370	1.01E-01	4.02E-03	-0.81	-2.41
lpg2435	ORF		ORFs of unknown function (unique)	10.655	9.795	11.816	9.555	8.38E-02	5.70E-03	-0.86	-2.26
lpg2436	small ORF (126aa)		ORFs of unknown function (unique)	10.175	8.595	10.546	8.473	4.62E-02	1.66E-04	-1.58	-2.07
lpg2436	small ORF (126aa)		ORFs of unknown function (unique)	10.489	9.704	10.594	8.755	3.55E-01	1.34E-03	-0.79	-1.84
lpg2437	small ORF (62aa)		ORFs of unknown function (unique)	7.797	7.980	9.599	7.993	7.93E-01	5.43E-03	0.18	-1.61
lpg2437	small ORF (62aa)		ORFs of unknown function (unique)	8.062	8.047	9.111	8.542	9.85E-01	1.93E-01	-0.02	-0.57
lpg2438	florfenicol efflux pump (multidrug resistance transporter, drug resistan		Transport and binding, Toxin productio	9.610	10.312	10.185	10.191	2.28E-01	9.91E-01	0.70	0.01
lpg2438	florfenicol efflux pump (multidrug resistance transporter, drug resistan		Transport and binding, Toxin productio	9.569	10.349	9.926	10.114	2.01E-01	6.81E-01	0.78	0.19
lpg2439	NADPH-dependent FMN reductase domain protein (chromate reduct		Metabolism of Cofactors and Vitamins	11.133	12.181	11.882	12.067	1.87E-05	3.95E-01	1.05	0.18
lpg2439	NADPH-dependent FMN reductase domain protein (chromate reduct		Metabolism of Cofactors and Vitamins	11.126	12.162	11.844	12.061	1.65E-05	3.07E-01	1.04	0.22
lpg2440	glutathione S-transferase		Detoxification / adaptation	11.262	11.144	12.090	11.028	5.32E-01	1.47E-03	-0.12	-1.06
lpg2440	glutathione S-transferase		Detoxification / adaptation	11.269	11.243	12.090	11.407	9.03E-01	1.98E-02	-0.03	-0.68
lpg2441	DNA binding protein (3-demethylubiquinone-9 3-methyltransferase)		Transcription factors / DNA binding pr	9.631	8.458	11.175	8.615	3.66E-02	5.56E-04	-1.17	-2.56
lpg2441	DNA binding protein (3-demethylubiquinone-9 3-methyltransferase)		Transcription factors / DNA binding pr	9.767	8.710	11.120	9.332	1.21E-01	2.72E-02	-1.06	-1.79
lpg2442	PhnB protein		Named proteins of general function	10.543	10.686	12.538	10.443	8.17E-01	5.14E-03	0.14	-2.10
lpg2442	PhnB protein		Named proteins of general function	10.642	10.699	12.636	10.846	9.24E-01	3.03E-03	0.06	-1.79
lpg2443	ORF		ORFs of unknown function (unique)	11.763	13.069	11.390	11.437	4.71E-05	8.43E-01	1.31	0.05
lpg2443	ORF		ORFs of unknown function (unique)	11.609	13.070	11.247	11.343	4.75E-05	7.43E-01	1.46	0.10
lpg2444	ORF		ORFs of unknown function (unique)	9.244	11.242	11.033	7.202	1.84E-03	1.30E-04	2.00	-3.83
lpg2444	ORF		ORFs of unknown function (unique)	9.329	11.435	10.914	7.869	1.67E-03	2.29E-03	2.11	-3.05
lpg2445	161aa ORF (serpentine receptor Sre?)		Unknown / hypothetical proteins	10.259	8.565	8.800	8.214	2.04E-02	4.00E-01	-1.69	-0.59
lpg2445	161aa ORF (serpentine receptor Sre?)		Unknown / hypothetical proteins	10.373	8.024	7.534	7.697	1.73E-05	9.03E-01	-2.35	0.16
lpg2446	small ORF (92aa)		ORFs of unknown function (unique)	9.894	10.007	9.943	8.965	7.36E-01	4.59E-03	0.11	-0.98
lpg2446	small ORF (92aa)		ORFs of unknown function (unique)	9.673	9.602	9.408	9.003	7.43E-01	4.40E-01	-0.07	-0.40
lpg2447	endonuclease containing URI domain, putative pseudogene		Viral functions / Phage / Transposases	9.792	9.642	8.946	9.397	5.86E-01	3.19E-01	-0.15	0.45
lpg2447	endonuclease containing URI domain, putative pseudogene		Viral functions / Phage / Transposases	9.777	10.048	8.638	10.012	6.21E-01	2.88E-02	0.27	1.37
lpg2449	D-alanyl-D-alanine dipeptidase		Protein fate / hydrolases / secretion	9.369	9.086	9.911	9.700	2.14E-01	3.84E-01	-0.28	-0.21
lpg2449	D-alanyl-D-alanine dipeptidase		Protein fate / hydrolases / secretion	9.303	9.506	9.726	9.777	3.50E-01	8.39E-01	0.20	0.05
lpg2450	integral membrane protein (zinc uptake?)		Named proteins of general function	9.721	10.316	9.961	10.417	3.61E-01	5.01E-01	0.59	0.46
lpg2450	integral membrane protein (zinc uptake?)		Named proteins of general function	9.645	10.224	9.645	10.192	3.78E-01	4.15E-01	0.58	0.55
lpg2451	putative N-hydroxyarylamine O-acetyltransferase		Named proteins of general function	11.868	13.666	10.893	12.590	1.42E-04	5.81E-04	1.80	1.70
lpg2451	putative N-hydroxyarylamine O-acetyltransferase		Named proteins of general function	11.719	13.951	10.962	12.962	6.40E-08	6.29E-07	2.23	2.00

lpg2452	hypothetical protein	*legA14*	Unknown / hypothetical proteins	10.194	9.484	9.579	10.157	1.03E-01	5.94E-02	-0.71	0.58
lpg2452	hypothetical protein	*legA14*	Unknown / hypothetical proteins	9.958	9.612	9.427	10.031	1.34E-01	3.86E-01	-0.35	0.60
lpg2453	small ORF (149aa)		ORFs of unknown function (unique)	11.769	11.884	10.891	11.556	8.39E-01	1.33E-01	0.11	0.66
lpg2453	small ORF (149aa)		ORFs of unknown function (unique)	11.664	11.382	10.553	11.264	7.87E-01	3.97E-01	-0.28	0.71
lpg2454	acetyltransferase, GNAT family, ElaA-like protein		Named proteins of general function	10.727	11.151	11.449	10.428	3.24E-01	7.89E-02	0.42	-1.02
lpg2454	acetyltransferase, GNAT family, ElaA-like protein		Named proteins of general function	10.860	11.146	11.284	10.528	5.10E-01	1.91E-01	0.29	-0.76
lpg2455	ORF		ORFs of unknown function (unique)	12.553	13.513	12.174	13.726	4.46E-01	9.49E-02	0.96	1.55
lpg2455	ORF		ORFs of unknown function (unique)	12.590	14.670	12.098	14.465	5.15E-10	2.34E-07	2.08	2.37
lpg2456	ORF	*legA15*	ORFs of unknown function (unique)	11.812	11.965	13.327	12.051	5.00E-01	3.19E-03	0.15	-1.28
lpg2456	ORF	*legA15*	ORFs of unknown function (unique)	11.757	12.065	13.294	12.228	2.81E-01	1.15E-02	0.31	-1.07
lpg2457	two component response regulator (response regulator receiver)		Signal transduction / other regulatory f	9.103	9.886	10.893	9.366	1.66E-01	6.85E-02	0.78	-1.53
lpg2457	two component response regulator (response regulator receiver)		Signal transduction / other regulatory f	8.982	9.986	10.803	9.770	9.44E-03	2.05E-01	1.00	-1.03
lpg2458	sensory box histidine kinase (two-component sensor histidine kinase,		Signal transduction / other regulatory f	8.509	8.313	10.094	7.980	6.03E-01	2.43E-03	-0.20	-2.11
lpg2458	sensory box histidine kinase (two-component sensor histidine kinase,		Signal transduction / other regulatory f	8.349	8.758	10.109	8.618	6.86E-01	4.32E-02	0.41	-1.49
lpg2459	guanylate cyclase		Signal transduction / other regulatory f	8.083	8.051	11.118	5.688	9.78E-01	2.11E-02	-0.03	-5.43
lpg2459	guanylate cyclase		Signal transduction / other regulatory f	8.425	8.374	11.144	8.016	9.59E-01	5.26E-02	-0.05	-3.13
lpg2460	hypothetical		Unknown / hypothetical proteins	9.020	11.469	8.918	8.532	3.57E-06	5.79E-01	2.45	-0.39
lpg2460	hypothetical		Unknown / hypothetical proteins	9.251	11.549	8.517	9.156	3.43E-04	3.47E-01	2.30	0.64
lpg2461	ORF		ORFs of unknown function (unique)	8.626	9.918	9.358	8.627	3.76E-02	5.38E-01	1.29	-0.73
lpg2461	ORF		ORFs of unknown function (unique)	8.077	9.663	8.348	8.366	7.21E-02	9.92E-01	1.59	0.02
lpg2462	exported protein		Named proteins of general function	11.396	10.900	10.029	11.301	3.12E-01	3.40E-02	-0.50	1.27
lpg2462	exported protein		Named proteins of general function	11.496	11.033	9.746	11.482	7.42E-02	1.06E-02	-0.46	1.74
lpg2463	peptide aspartate b-dioxygenase (lipid synthesis)		Named proteins of general function	11.905	12.629	10.998	12.489	9.09E-03	6.86E-03	0.72	1.49
lpg2463	peptide aspartate b-dioxygenase (lipid synthesis)		Named proteins of general function	11.927	12.899	10.740	12.559	3.41E-02	2.99E-03	0.97	1.82
lpg2464	ORF	*sidM/drrA*	ORFs of unknown function (unique)	11.336	13.004	12.883	10.461	1.20E-02	2.01E-04	1.67	-2.42
lpg2464	ORF	*sidM/drrA*	ORFs of unknown function (unique)	11.427	13.125	12.868	10.491	2.01E-02	6.30E-04	1.70	-2.38
lpg2465	SidD	*sidD*	Toxin production / other pathogen func	11.865	15.476	13.056	12.584	5.59E-06	3.72E-01	3.61	-0.47
lpg2465	SidD	*sidD*	Toxin production / other pathogen func	11.876	15.425	13.106	12.636	2.53E-05	3.69E-01	3.55	-0.47
lpg2466	hydrogenase expression/formation protein (F420-nonred	*vhtD*	Named proteins of general function	10.742	10.017	10.899	8.066	2.24E-01	2.51E-03	-0.72	-2.83
lpg2466	hydrogenase expression/formation protein (F420-nonred	*vhtD*	Named proteins of general function	10.762	10.707	10.832	9.154	9.02E-01	1.90E-03	-0.05	-1.68
lpg2467	cytochrome c3 hydrogenase alpha chain (hydrogenase/s	*hydA*	Energy Metabolism	6.800	8.547	8.630	6.318	5.14E-02	7.89E-02	1.75	-2.31
lpg2467	cytochrome c3 hydrogenase alpha chain (hydrogenase/s	*hydA*	Energy Metabolism	7.888	8.486	8.538	6.596	3.24E-01	1.76E-01	0.60	-1.94
lpg2468	sulfhydrogenase delta subunit (cytochrome c3 hydrogenase delta sub		Energy Metabolism	10.528	10.271	10.699	10.686	5.07E-01	9.55E-01	-0.26	-0.01
lpg2468	sulfhydrogenase delta subunit (cytochrome c3 hydrogenase delta sub		Energy Metabolism	10.425	10.916	10.624	10.863	2.57E-01	3.67E-01	0.49	0.24
lpg2469	hydrogenase/sulfur reductase gamma subunit (cytochron	*hydG-2*	Energy Metabolism	12.915	13.841	13.700	14.084	6.61E-02	3.91E-01	0.93	0.38
lpg2469	hydrogenase/sulfur reductase gamma subunit (cytochron	*hydG-2*	Energy Metabolism	12.946	13.854	13.722	14.112	7.72E-02	3.77E-01	0.91	0.39
lpg2470	cytochrome c3 hydrogenase alpha (or beta) chain (sulfhydrogenase)		Energy Metabolism	9.540	9.004	9.605	9.450	1.99E-01	7.55E-01	-0.54	-0.16
lpg2470	cytochrome c3 hydrogenase alpha (or beta) chain (sulfhydrogenase)		Energy Metabolism	9.340	8.429	9.402	9.613	3.35E-01	7.23E-01	-0.91	0.21
lpg2471	hydrogenase expression/formation protein HypE	*hypE*	Transport and binding	10.709	9.317	10.288	10.074	2.08E-04	4.52E-01	-1.39	-0.21
lpg2471	hydrogenase expression/formation protein HypE	*hypE*	Transport and binding	10.651	9.624	9.922	10.177	3.10E-02	4.93E-01	-1.03	0.25
lpg2472	hydrogenase expression/formation protein HypD	*hypD*	Transport and binding	10.325	8.133	8.733	10.239	2.11E-04	2.43E-02	-2.19	1.51
lpg2472	hydrogenase expression/formation protein HypD	*hypD*	Transport and binding	10.159	7.968	7.511	10.232	1.15E-03	9.06E-03	-2.19	2.72
lpg2473	hydrogenase expression/formation protein HypC	*hypC*	Transport and binding	10.039	9.799	8.675	10.242	6.51E-01	2.57E-03	-0.24	1.57
lpg2473	hydrogenase expression/formation protein HypC	*hypC*	Transport and binding	9.957	9.670	8.206	9.909	6.22E-01	1.77E-02	-0.29	1.70
lpg2474	hydrogenase maturation protein HypF	*hypF*	Transport and binding	9.902	9.419	9.211	8.713	2.57E-01	7.76E-01	-0.48	-0.50
lpg2474	hydrogenase maturation protein HypF	*hypF*	Transport and binding	10.057	8.965	9.448	9.051	3.26E-01	6.56E-01	-1.09	-0.40
lpg2475	hydrogenase expression/formation protein (hydrogenase	*hypB*	Transport and binding	10.493	10.004	9.116	10.741	1.58E-01	1.00E-02	-0.49	1.62
lpg2475	hydrogenase expression/formation protein (hydrogenase	*hypB*	Transport and binding	10.377	10.149	9.056	10.930	5.64E-01	1.04E-02	-0.23	1.87
lpg2476	hydrogenase nickel incorporation protein HypA	*hypA*	Transport and binding	10.580	10.951	10.128	11.241	3.98E-01	4.69E-02	0.37	1.11
lpg2476	hydrogenase nickel incorporation protein HypA	*hypA*	Transport and binding	10.258	11.058	8.922	11.502	3.16E-01	4.44E-03	0.80	2.58
lpg2477	high affinity nickel transport protein		Transport and binding	10.696	10.755	9.629	10.861	8.21E-01	1.62E-02	0.06	1.23
lpg2477	high affinity nickel transport protein		Transport and binding	10.972	11.103	9.720	11.090	7.71E-01	3.00E-02	0.13	1.37
lpg2478	glycosyltransferase, group 2 family protein (glycan biosynthesis)		Metabolism of Complex Carbohydrates	8.472	9.487	8.749	10.176	8.54E-03	1.37E-02	1.02	1.43
lpg2478	glycosyltransferase, group 2 family protein (glycan biosynthesis)		Metabolism of Complex Carbohydrates	8.631	9.053	8.729	10.163	3.19E-01	1.35E-03	0.42	1.43
lpg2479	membrane protein?		Unknown / hypothetical proteins	9.755	9.649	9.843	9.399	8.60E-01	5.37E-01	-0.11	-0.44
lpg2479	membrane protein?		Unknown / hypothetical proteins	9.522	9.426	9.107	9.398	8.71E-01	7.97E-01	-0.10	0.29
lpg2480	cellobiose phosphorylase?		Named proteins of general function	10.723	10.195	10.950	11.528	5.22E-02	5.28E-03	-0.53	0.58
lpg2480	cellobiose phosphorylase?		Named proteins of general function	10.760	10.136	10.901	11.565	3.70E-02	1.57E-03	-0.62	0.66
lpg2481	integral membrane protein (permease) (amino acid metabolite efflux)		Transport and binding	12.263	11.824	12.237	12.423	1.00E-01	2.32E-01	-0.44	0.19
lpg2481	integral membrane protein (permease) (amino acid metabolite efflux)		Transport and binding	12.324	11.788	12.198	12.476	7.32E-02	9.58E-02	-0.54	0.28
lpg2482	SdbC	*sdbC*	Named proteins of general function	8.404	9.460	9.621	9.251	1.80E-02	5.31E-01	1.06	-0.37
lpg2482	SdbC	*sdbC*	Named proteins of general function	8.167	10.795	9.658	11.161	5.02E-03	5.79E-02	2.63	1.50
lpg2483	hypothetical		Unknown / hypothetical proteins	10.725	10.621	10.772	10.126	8.05E-01	1.82E-01	-0.10	-0.65
lpg2483	hypothetical		Unknown / hypothetical proteins	10.766	10.569	9.981	9.782	6.29E-01	7.13E-01	-0.20	-0.20

lpg2484	ribosomal protein HAM1 (xanthosine triphosphate pyrophosphatase)		Nucleotide Metabolism, Translation	10.110	10.067	9.888	11.190	9.53E-01	7.80E-03	-0.04	1.30
lpg2484	ribosomal protein HAM1 (xanthosine triphosphate pyrophosphatase)		Nucleotide Metabolism, Translation	9.847	10.566	9.748	11.314	3.13E-01	2.88E-02	0.72	1.57
lpg2485	TPR domain protein (glycosyltransferase) (O-linked N-acetylglucosan		Metabolism of Complex Carbohydrates	9.879	9.651	10.773	10.916	2.45E-01	6.80E-01	-0.23	0.14
lpg2485	TPR domain protein (glycosyltransferase) (O-linked N-acetylglucosan		Metabolism of Complex Carbohydrates	10.019	9.066	10.819	10.978	1.15E-02	6.22E-01	-0.95	0.16
lpg2486	phosphomannomutase		Carbohydrate Metabolism	12.496	12.141	9.572	13.536	3.85E-01	1.57E-03	-0.35	3.96
lpg2486	phosphomannomutase		Carbohydrate Metabolism	12.484	12.045	9.255	13.555	3.26E-01	8.47E-03	-0.44	4.30
lpg2487	deoxyuridinetriphosphatase (deoxyuridine 5'-triphosphate	*dut*	Nucleotide Metabolism	10.530	11.194	10.338	12.101	1.41E-01	1.26E-03	0.66	1.76
lpg2487	deoxyuridinetriphosphatase (deoxyuridine 5'-triphosphate	*dut*	Nucleotide Metabolism	10.544	11.053	10.194	12.124	2.88E-01	9.93E-04	0.51	1.93
lpg2488	phosphopantothenoylcysteine decarboxylase/phosphopantothenate-c		Metabolism of Cofactors and Vitamins	9.917	11.954	9.865	11.588	8.69E-05	7.51E-05	2.04	1.72
lpg2488	phosphopantothenoylcysteine decarboxylase/phosphopantothenate-c		Metabolism of Cofactors and Vitamins	10.180	11.915	9.729	11.665	8.43E-07	2.48E-06	1.74	1.94
lpg2489	DNA repair protein RadC		Replication and Repair	9.369	9.935	9.235	9.707	4.56E-02	5.33E-01	0.57	0.47
lpg2489	DNA repair protein RadC		Replication and Repair	9.442	9.749	7.983	10.091	1.54E-01	1.42E-01	0.31	2.11
lpg2490	LepB, non-muscle myosin heavy chain B (endosomal pro	*lepB*	Toxin production / other pathogen func	10.921	11.495	9.931	12.320	9.12E-02	7.22E-06	0.57	2.39
lpg2490	LepB, non-muscle myosin heavy chain B (endosomal pro	*lepB*	Toxin production / other pathogen func	10.813	11.568	10.022	12.413	4.63E-02	1.48E-05	0.76	2.39
lpg2491	conserved hypothetical protein		Unknown / hypothetical proteins	8.490	7.889	9.770	8.703	5.35E-01	9.94E-02	-0.60	-1.07
lpg2491	conserved hypothetical protein		Unknown / hypothetical proteins	8.648	8.062	9.517	8.820	3.04E-01	2.50E-01	-0.59	-0.70
lpg2492	alcohol dehydrogenase		Carbohydrate Metabolism, Lipid Metab	10.654	9.176	12.490	9.183	1.83E-01	3.43E-05	-1.48	-3.31
lpg2492	alcohol dehydrogenase		Carbohydrate Metabolism, Lipid Metab	10.287	9.560	12.194	9.379	1.68E-01	6.63E-04	-0.73	-2.81
lpg2493	small heat shock protein HspC2 (molecular chaperone)		Detoxification / adaptation, Protein fate	10.965	11.301	14.724	8.194	7.31E-01	2.67E-04	0.34	-6.53
lpg2493	small heat shock protein HspC2 (molecular chaperone)		Detoxification / adaptation, Protein fate	10.957	11.642	14.730	8.435	4.24E-01	8.55E-05	0.68	-6.30
lpg2494	conserved hypothetical protein		Unknown / hypothetical proteins	9.546	10.308	8.985	10.321	3.62E-01	1.56E-01	0.76	1.34
lpg2494	conserved hypothetical protein		Unknown / hypothetical proteins	10.012	10.453	8.792	10.390	1.21E-01	6.74E-02	0.44	1.60
lpg2495	homospermidine synthase	*hss*	Named proteins of general function	11.996	11.589	12.993	11.085	3.70E-01	7.66E-04	-0.41	-1.91
lpg2495	homospermidine synthase	*hss*	Named proteins of general function	12.020	11.815	12.961	11.700	5.82E-01	2.08E-03	-0.20	-1.26
lpg2496	RNA methyltransferase TrmH family, group 2 (rRNA methylase) (tRNA		DNA/RNA degradation / restriction, Tra	10.704	10.224	10.309	10.793	1.58E-01	1.77E-01	-0.48	0.48
lpg2496	RNA methyltransferase TrmH family, group 2 (rRNA methylase) (tRNA		DNA/RNA degradation / restriction, Tra	10.546	10.351	10.227	10.858	4.10E-01	1.39E-01	-0.20	0.63
lpg2497	conserved hypothetical protein		Unknown / hypothetical proteins	10.763	9.853	11.026	9.971	1.05E-01	2.81E-02	-0.91	-1.05
lpg2497	conserved hypothetical protein		Unknown / hypothetical proteins	10.809	9.933	11.054	10.136	5.94E-02	3.65E-02	-0.88	-0.92
lpg2498	ORF		ORFs of unknown function (unique)	11.411	13.320	10.913	11.946	1.76E-05	5.63E-02	1.91	1.03
lpg2498	ORF		ORFs of unknown function (unique)	11.952	13.461	10.851	11.930	6.11E-02	2.53E-02	1.51	1.08
lpg2499	lysine decarboxylase		Amino Acid Metabolism	11.828	10.847	12.343	10.211	9.70E-04	1.57E-04	-0.98	-2.13
lpg2499	lysine decarboxylase		Amino Acid Metabolism	11.785	10.949	12.431	10.381	1.29E-02	1.74E-04	-0.84	-2.05
lpg2500	carbonic anhydrase Mig5		Detoxification / adaptation	11.087	11.266	13.580	9.989	7.58E-01	8.79E-05	0.18	-3.59
lpg2500	carbonic anhydrase Mig5		Detoxification / adaptation	10.892	11.121	13.387	10.048	7.49E-01	1.17E-04	0.23	-3.34
lpg2501	multidrug resistance protein D (permease of the major facilitator supe		Transport and binding	11.021	10.555	10.067	10.748	2.45E-01	1.07E-01	-0.47	0.68
lpg2501	multidrug resistance protein D (permease of the major facilitator supe		Transport and binding	10.870	10.854	9.802	11.508	9.88E-01	7.29E-02	-0.02	1.71
lpg2502	small ORF (82aa)		ORFs of unknown function (unique)	10.624	10.113	10.128	9.233	2.77E-01	1.68E-01	-0.51	-0.89
lpg2502	small ORF (82aa)		ORFs of unknown function (unique)	10.592	10.220	10.212	9.479	3.53E-01	1.39E-01	-0.37	-0.73
lpg2503	small ORF (106aa)		ORFs of unknown function (unique)	8.783	9.450	9.772	8.475	6.48E-02	4.59E-02	0.67	-1.30
lpg2503	small ORF (106aa)		ORFs of unknown function (unique)	8.751	9.303	9.854	8.584	1.03E-01	2.10E-02	0.55	-1.27
lpg2504	ORF		ORFs of unknown function (unique)	9.893	8.223	9.640	8.008	9.60E-03	1.91E-02	-1.67	-1.63
lpg2504	ORF		ORFs of unknown function (unique)	10.124	10.009	9.805	9.583	9.15E-01	8.28E-01	-0.11	-0.22
lpg2505	ORF		ORFs of unknown function (unique)	11.534	10.624	11.308	10.061	8.53E-02	1.12E-02	-0.91	-1.25
lpg2505	ORF		ORFs of unknown function (unique)	12.038	10.896	11.086	10.266	1.37E-01	1.98E-01	-1.14	-0.82
lpg2506	sensor histidine kinase/response regulator LuxN		Signal transduction / other regulatory f	11.140	10.142	9.782	10.142	6.46E-02	5.86E-01	-1.00	0.36
lpg2506	sensor histidine kinase/response regulator LuxN		Signal transduction / other regulatory f	11.157	10.267	9.577	10.175	8.86E-02	3.66E-01	-0.89	0.60
lpg2507	ORF		ORFs of unknown function (unique)	10.041	10.113	9.188	10.093	9.38E-01	5.06E-01	0.07	0.91
lpg2507	ORF		ORFs of unknown function (unique)	9.534	10.194	8.322	10.698	5.97E-01	1.98E-01	0.66	2.38
lpg2508	ORF	*sdjA*	ORFs of unknown function (unique)	10.067	12.939	11.663	9.826	7.86E-05	6.21E-05	2.87	-1.84
lpg2508	ORF	*sdjA*	ORFs of unknown function (unique)	9.890	12.998	11.616	10.537	6.03E-05	1.09E-03	3.11	-1.08
lpg2509	SdeD	*sdeD*	Toxin production / other pathogen func	10.212	14.154	12.143	11.418	5.18E-03	3.94E-01	3.94	-0.73
lpg2509	SdeD	*sdeD*	Toxin production / other pathogen func	10.194	15.143	12.062	11.819	1.57E-04	7.66E-01	4.95	-0.24
lpg2510	SdcA	*sdcA*	Named proteins of general function	10.806	12.269	13.765	10.634	8.11E-02	4.62E-04	1.46	-3.13
lpg2510	SdcA	*sdcA*	Named proteins of general function	10.844	12.673	13.746	10.693	1.23E-02	7.91E-04	1.83	-3.05
lpg2511	SidC, interaptin	*sidC*	Toxin production / other pathogen func	11.194	13.491	14.353	9.840	1.02E-02	8.10E-05	2.30	-4.51
lpg2511	SidC, interaptin	*sidC*	Toxin production / other pathogen func	11.184	13.566	14.335	9.934	9.12E-03	6.96E-05	2.38	-4.40
lpg2512	RND multidrug efflux transporter MexF (cation efflux) (AcrB/AcrD/Acr		Transport and binding	10.957	10.183	10.859	9.340	6.69E-03	5.55E-02	-0.77	-1.52
lpg2512	RND multidrug efflux transporter MexF (cation efflux) (AcrB/AcrD/Acr		Transport and binding	10.885	10.777	10.132	9.848	8.32E-01	6.23E-01	-0.11	-0.28
lpg2513	RND multidrug efflux membrane fusion protein		Transport and binding	11.359	11.780	10.209	11.852	2.50E-01	4.65E-02	0.42	1.64
lpg2513	RND multidrug efflux membrane fusion protein		Transport and binding	11.259	11.783	10.021	11.937	2.13E-01	1.93E-03	0.52	1.92
lpg2514	outer membrane efflux protein (RND multidrug efflux)		Transport and binding	10.578	10.686	10.509	10.616	6.68E-01	7.95E-01	0.11	0.11
lpg2514	outer membrane efflux protein (RND multidrug efflux)		Transport and binding	9.563	10.468	9.472	9.985	9.81E-02	2.51E-01	0.90	0.51
lpg2515	structural toxin protein (hemagglutinin/hemolysin) RtxA		Toxin production / other pathogen func	10.268	10.602	11.130	10.508	2.66E-01	6.27E-02	0.33	-0.62
lpg2515	structural toxin protein (hemagglutinin/hemolysin) RtxA		Toxin production / other pathogen func	10.413	10.960	11.198	10.958	1.08E-01	5.53E-01	0.55	-0.24

lpg2516	major facilitator family transporter (sugar transport, multidrug efflux)		Transport and binding	9.970	12.105	9.830	10.907	3.12E-04	1.33E-03	2.14	1.08
lpg2516	major facilitator family transporter (sugar transport, multidrug efflux)		Transport and binding	9.806	12.067	9.716	10.997	1.56E-04	1.78E-04	2.26	1.28
lpg2517	transcriptional regulator (AsnC family)		Transcription factors / DNA binding pr	9.425	9.067	9.439	9.967	1.93E-01	9.37E-02	-0.36	0.53
lpg2517	transcriptional regulator (AsnC family)		Transcription factors / DNA binding pr	9.499	9.349	9.269	10.352	6.79E-01	8.93E-03	-0.15	1.08
lpg2518	small ORF (113aa)		ORFs of unknown function (unique)	9.617	11.061	9.782	9.428	3.37E-04	2.22E-01	1.44	-0.35
lpg2518	small ORF (113aa)		ORFs of unknown function (unique)	9.631	11.229	9.443	9.387	1.54E-04	8.98E-01	1.60	-0.06
lpg2519	ORF		ORFs of unknown function (unique)	11.854	12.712	11.037	11.512	1.58E-02	3.40E-01	0.86	0.47
lpg2519	ORF		ORFs of unknown function (unique)	11.847	12.623	10.863	11.538	7.73E-02	2.03E-01	0.78	0.68
lpg2520	small ORF (122aa)		ORFs of unknown function (unique)	9.069	9.538	11.283	8.232	4.68E-01	8.68E-03	0.47	-3.05
lpg2520	small ORF (122aa)		ORFs of unknown function (unique)	9.048	9.223	11.068	9.138	8.16E-01	1.71E-02	0.17	-1.93
lpg2521	transmembrane protein		Unknown / hypothetical proteins	12.286	11.137	13.002	12.145	1.44E-03	2.93E-02	-1.15	-0.86
lpg2521	transmembrane protein		Unknown / hypothetical proteins	12.277	11.088	13.012	12.253	1.66E-03	4.08E-02	-1.19	-0.76
lpg2522	metal-activated pyridoxal enzyme (low specificity D-threonine aldolas		Amino Acid Metabolism	10.907	9.527	10.461	10.970	1.82E-01	5.02E-01	-1.38	0.51
lpg2522	metal-activated pyridoxal enzyme (low specificity D-threonine aldolas		Amino Acid Metabolism	10.945	10.117	10.602	11.223	4.75E-02	2.64E-01	-0.83	0.62
lpg2523	ORF		ORFs of unknown function (unique)	9.579	9.658	9.295	9.587	9.21E-01	7.11E-01	0.08	0.29
lpg2523	ORF		ORFs of unknown function (unique)	9.984	8.758	9.114	9.724	2.19E-02	4.20E-01	-1.23	0.61
lpg2524	transcriptional regulator, LuxR family		Transcription factors / DNA binding pr	8.042	8.952	11.655	8.541	4.54E-01	1.75E-02	0.91	-3.11
lpg2524	transcriptional regulator, LuxR family		Transcription factors / DNA binding pr	8.657	7.765	11.575	8.753	2.93E-01	1.63E-02	-0.89	-2.82
lpg2525	ORF		ORFs of unknown function (unique)	12.301	10.245	10.657	9.300	4.41E-04	1.02E-01	-2.06	-1.36
lpg2525	ORF		ORFs of unknown function (unique)	12.204	10.122	10.502	9.585	4.63E-04	1.33E-01	-2.08	-0.92
lpg2526	ORF		ORFs of unknown function (unique)	11.903	13.857	12.934	12.915	1.10E-03	9.59E-01	1.95	-0.02
lpg2526	ORF		ORFs of unknown function (unique)	11.825	14.190	12.946	13.016	2.44E-05	8.39E-01	2.36	0.07
lpg2527	contains coiled coil domain		Unknown / hypothetical proteins	8.100	8.655	11.551	6.483	6.99E-01	1.02E-03	0.56	-5.07
lpg2527	contains coiled coil domain		Unknown / hypothetical proteins	7.127	10.180	11.473	7.861	2.12E-01	9.73E-02	3.05	-3.61
lpg2528	alpha-amylase, putative		Named proteins of general function	8.887	9.588	11.976	9.029	3.07E-01	1.42E-04	0.70	-2.95
lpg2528	alpha-amylase, putative		Named proteins of general function	9.315	10.144	12.018	10.055	1.84E-01	2.18E-02	0.83	-1.96
lpg2529	ORF		ORFs of unknown function (unique)	13.814	15.578	13.646	12.778	3.43E-02	1.31E-01	1.76	-0.87
lpg2529	ORF		ORFs of unknown function (unique)	13.809	15.600	13.632	12.816	1.86E-02	1.56E-01	1.79	-0.82
lpg2530	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) s	*aroF*	Amino Acid Metabolism	8.240	12.240	8.708	9.874	2.17E-05	5.27E-04	4.00	1.17
lpg2530	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) s	*aroF*	Amino Acid Metabolism	8.983	12.240	8.903	10.405	3.16E-06	2.48E-02	3.26	1.50
lpg2531	chorismate mutase/prephenate dehydratase (P-protein)		Amino Acid Metabolism	8.258	12.815	7.849	8.652	5.70E-10	3.39E-01	4.56	0.80
lpg2531	chorismate mutase/prephenate dehydratase (P-protein)		Amino Acid Metabolism	7.966	12.966	7.923	9.213	6.28E-07	3.59E-01	5.00	1.29
lpg2532	aspartate aminotransferase (PLP-dependent aminotransferase)		Amino Acid Metabolism, Energy Meta	7.267	11.801	8.957	8.536	2.04E-07	3.04E-01	4.53	-0.42
lpg2532	aspartate aminotransferase (PLP-dependent aminotransferase)		Amino Acid Metabolism, Energy Meta	7.264	12.369	8.131	9.850	3.15E-05	2.20E-01	5.11	1.72
lpg2533	tellurite resistance protein (hemagglutinin)	*tehB*	Transport and binding, Toxin productio	9.196	10.638	9.126	10.561	5.46E-03	5.02E-02	1.44	1.43
lpg2533	tellurite resistance protein (hemagglutinin)	*tehB*	Transport and binding, Toxin productio	8.916	10.843	8.828	10.379	5.80E-04	1.07E-02	1.93	1.55
lpg2534	hypothetical (iron regulator, rhizobial) (transcriptional regulator?) CO		Transcription factors / DNA binding pr	7.647	8.597	8.851	8.361	5.43E-02	2.58E-01	0.95	-0.49
lpg2534	hypothetical (iron regulator, rhizobial) (transcriptional regulator?) CO		Transcription factors / DNA binding pr	7.120	8.761	7.907	8.085	9.17E-02	6.26E-01	1.64	0.18
lpg2535	limited homology to myoglobin (hemoglobin, cyanoglobin)		Unknown / hypothetical proteins	9.008	7.909	8.817	8.666	1.43E-01	6.54E-01	-1.10	-0.15
lpg2535	limited homology to myoglobin (hemoglobin, cyanoglobin)		Unknown / hypothetical proteins	8.825	8.432	8.542	8.707	2.38E-01	4.42E-01	-0.39	0.17
lpg2536	ferredoxin reductase (NAD(P)H-flavin reductase) (iron-sulfur cluster b		Metabolism of Cofactors and Vitamins	8.664	8.504	9.793	8.721	6.59E-01	7.83E-02	-0.16	-1.07
lpg2536	ferredoxin reductase (NAD(P)H-flavin reductase) (iron-sulfur cluster b		Metabolism of Cofactors and Vitamins	7.929	8.429	8.606	9.057	6.77E-01	7.03E-01	0.50	0.45
lpg2537	5-carboxyvanillate decarboxylase (2-amino-3-carboxylmuconate-6-se		Named proteins of general function	9.472	9.386	11.899	9.447	8.81E-01	1.54E-05	-0.09	-2.45
lpg2537	5-carboxyvanillate decarboxylase (2-amino-3-carboxylmuconate-6-se		Named proteins of general function	9.388	9.954	11.773	9.873	2.53E-01	2.98E-04	0.57	-1.90
lpg2538	ORF		ORFs of unknown function (unique)	10.580	10.701	9.546	11.591	8.35E-01	3.84E-04	0.12	2.04
lpg2538	ORF		ORFs of unknown function (unique)	10.890	10.787	9.473	11.535	6.85E-01	1.92E-03	-0.10	2.06
lpg2539	small ORF (135aa)		ORFs of unknown function (unique)	9.788	8.079	8.867	7.503	5.11E-02	3.55E-01	-1.71	-1.36
lpg2539	small ORF (135aa)		ORFs of unknown function (unique)	9.874	7.524	8.982	7.815	8.20E-02	2.04E-01	-2.35	-1.17
lpg2540	large conductance mechanosensitive channel	*mscL*	Energy Metabolism	11.246	11.435	10.022	11.148	5.30E-01	2.62E-02	0.19	1.13
lpg2540	large conductance mechanosensitive channel	*mscL*	Energy Metabolism	10.927	11.357	9.834	11.223	4.58E-01	2.18E-02	0.43	1.39
lpg2541	ORF		ORFs of unknown function (unique)	10.364	9.984	8.868	10.506	4.57E-01	5.32E-02	-0.38	1.64
lpg2541	ORF		ORFs of unknown function (unique)	10.416	9.473	8.727	10.393	1.72E-01	2.87E-02	-0.94	1.67
lpg2542	small ORF (163aa)		ORFs of unknown function (unique)	10.931	10.490	10.532	10.417	3.04E-01	9.20E-01	-0.44	-0.12
lpg2542	small ORF (163aa)		ORFs of unknown function (unique)	11.120	10.347	9.532	10.837	1.48E-01	4.76E-02	-0.77	1.30
lpg2543	ORF		ORFs of unknown function (unique)	9.076	9.824	9.608	9.499	1.70E-01	9.25E-01	0.75	-0.11
lpg2543	ORF		ORFs of unknown function (unique)	8.659	9.577	9.569	9.778	5.43E-02	6.94E-01	0.92	0.21
lpg2544	membrane-bound lytic murein transglycosylase A	*mltA*	Cell envelope synthesis, Metabolism o	9.217	8.331	9.390	7.214	1.85E-02	1.46E-01	-0.89	-2.18
lpg2544	membrane-bound lytic murein transglycosylase A	*mltA*	Cell envelope synthesis, Metabolism o	8.469	9.722	9.116	9.765	3.45E-01	5.74E-01	1.25	0.65
lpg2545	small ORF (96aa)		ORFs of unknown function (unique)	10.589	9.479	11.376	9.009	3.65E-03	1.11E-04	-1.11	-2.37
lpg2545	small ORF (96aa)		ORFs of unknown function (unique)	10.569	9.688	11.400	9.399	3.02E-02	1.25E-03	-0.88	-2.00
lpg2546	hypothetical protein		Unknown / hypothetical proteins	10.135	10.198	10.426	9.046	9.06E-01	1.33E-02	0.06	-1.38
lpg2546	hypothetical protein		Unknown / hypothetical proteins	10.051	10.559	10.229	9.167	3.27E-01	5.14E-02	0.51	-1.06
lpg2547	chaperonin CsaA (protein secretion chaperonin)	*csaA*	Protein fate / hydrolases / secretion	10.650	11.143	10.717	10.109	1.83E-02	4.18E-02	0.49	-0.61
lpg2547	chaperonin CsaA (protein secretion chaperonin)	*csaA*	Protein fate / hydrolases / secretion	10.554	11.269	10.731	10.283	7.27E-04	7.65E-02	0.72	-0.45

lpg2548	transmembrane protein (transporter, drug metabolite exporter family?		Transport and binding	11.086	10.906	10.013	10.448	6.93E-01	1.35E-01	-0.18	0.43
lpg2548	transmembrane protein (transporter, drug metabolite exporter family?		Transport and binding	11.057	11.078	9.454	10.910	9.37E-01	4.26E-02	0.02	1.46
lpg2549	transcriptional regulator (AraC-family) (enhancer)		Transcription factors / DNA binding prc	10.213	9.027	9.182	9.120	1.33E-02	9.03E-01	-1.19	-0.06
lpg2549	transcriptional regulator (AraC-family) (enhancer)		Transcription factors / DNA binding prc	9.953	9.167	9.137	9.393	3.55E-01	6.20E-01	-0.79	0.26
lpg2550	ORF		ORFs of unknown function (unique)	10.288	9.016	10.335	8.899	1.50E-02	3.39E-02	-1.27	-1.44
lpg2550	ORF		ORFs of unknown function (unique)	10.219	9.427	10.516	9.131	8.07E-02	5.03E-02	-0.79	-1.39
lpg2551	hypothetical		Unknown / hypothetical proteins	9.598	9.243	9.082	9.372	5.86E-02	6.21E-01	-0.36	0.29
lpg2551	hypothetical		Unknown / hypothetical proteins	9.395	9.461	9.536	9.843	8.94E-01	4.00E-01	0.07	0.31
lpg2552	ORF		ORFs of unknown function (unique)	12.194	12.082	10.706	12.877	8.50E-01	2.54E-03	-0.11	2.17
lpg2552	ORF		ORFs of unknown function (unique)	11.231	10.192	9.306	11.640	5.19E-03	3.16E-02	-1.04	2.33
lpg2553	hexosephosphate transport (sugar phosphate sensor pro	*uhpC*	Transport and binding	11.634	10.927	11.585	11.378	2.96E-02	7.52E-01	-0.71	-0.21
lpg2553	hexosephosphate transport (sugar phosphate sensor pro	*uhpC*	Transport and binding	11.682	10.936	11.642	11.838	2.10E-03	3.12E-01	-0.75	0.20
lpg2554	rare lipoprotein A		Named proteins of general function	11.797	11.815	9.941	11.402	9.83E-01	5.23E-02	0.02	1.46
lpg2554	rare lipoprotein A		Named proteins of general function	11.566	11.765	9.891	11.517	8.41E-01	2.48E-02	0.20	1.63
lpg2555	ORF		ORFs of unknown function (unique)	10.318	8.758	9.956	8.735	3.84E-02	2.94E-02	-1.56	-1.22
lpg2555	ORF		ORFs of unknown function (unique)	10.003	9.226	9.671	8.645	1.55E-01	1.19E-01	-0.78	-1.03
lpg2556	putative protein kinase	*legK3*	Viral functions / Phage / Transposases	10.751	9.984	10.396	10.616	1.13E-01	5.15E-01	-0.77	0.22
lpg2556	putative protein kinase	*legK3*	Viral functions / Phage / Transposases	10.867	10.231	10.329	10.651	2.72E-02	2.84E-01	-0.64	0.32
lpg2557	protein product; similar to probable transcriptional regulator		Unknown / hypothetical proteins	7.529	8.997	9.391	8.321	2.09E-01	3.52E-01	1.47	-1.07
lpg2557	protein product; similar to probable transcriptional regulator		Unknown / hypothetical proteins	8.352	8.083	8.002	8.297	8.80E-01	7.91E-01	-0.27	0.29
lpg2558	integrase of prophage CP-933C		Viral functions / Phage / Transposases	8.606	8.084	8.645	8.115	7.50E-01	6.25E-01	-0.52	-0.53
lpg2558	integrase of prophage CP-933C		Viral functions / Phage / Transposases	9.935	9.808	9.365	9.949	8.83E-01	6.29E-01	-0.13	0.58
lpg2559	ATP-dependent DNA helicase	*recG*	Replication and Repair	10.418	7.946	9.463	8.862	8.68E-04	1.98E-01	-2.47	-0.60
lpg2559	ATP-dependent DNA helicase	*recG*	Replication and Repair	10.528	8.124	9.349	9.209	3.08E-02	8.67E-01	-2.40	-0.14
lpg2560	unknown protein		Unknown / hypothetical proteins	11.334	11.160	11.532	10.652	5.60E-01	9.70E-03	-0.17	-0.88
lpg2560	unknown protein		Unknown / hypothetical proteins	11.357	11.628	11.514	11.071	5.69E-01	2.55E-01	0.27	-0.44
lpg2561	hypothetical protein		Unknown / hypothetical proteins	9.663	9.018	10.836	9.220	1.77E-01	2.18E-02	-0.64	-1.62
lpg2561	hypothetical protein		Unknown / hypothetical proteins	9.643	7.943	10.785	9.220	6.36E-02	3.76E-02	-1.70	-1.57
lpg2562	phage repressor		Transcription factors / DNA binding prc	8.894	9.162	8.318	7.860	6.63E-01	3.58E-01	0.27	-0.46
lpg2562	phage repressor		Transcription factors / DNA binding prc	9.249	8.692	8.060	8.869	4.41E-01	1.54E-01	-0.56	0.81
lpg2563	prophage regulatory protein?		Viral functions / Phage / Transposases	11.086	9.867	10.164	11.737	7.19E-02	1.51E-03	-1.22	1.57
lpg2563	prophage regulatory protein?		Viral functions / Phage / Transposases	10.771	10.426	10.185	12.010	6.90E-01	1.24E-03	-0.35	1.83
lpg2564	LvrA		Transport and binding, Toxin productio	8.592	10.357	8.685	8.958	2.34E-03	7.95E-01	1.77	0.27
lpg2564	LvrA		Transport and binding, Toxin productio	8.538	9.880	8.600	9.173	2.14E-02	4.76E-01	1.34	0.57
lpg2565	transposase ORF-A (IS-type)		Viral functions / Phage / Transposases	9.729	11.243	9.818	11.304	9.15E-04	7.37E-04	1.51	1.49
lpg2565	transposase ORF-A (IS-type)		Viral functions / Phage / Transposases	9.046	11.148	9.633	11.352	7.81E-03	7.00E-03	2.10	1.72
lpg2566	ISxcC1 transposase		Viral functions / Phage / Transposases	10.980	11.039	11.990	10.896	9.31E-01	3.39E-02	0.06	-1.09
lpg2566	ISxcC1 transposase		Viral functions / Phage / Transposases	10.933	11.500	11.803	11.536	2.46E-02	3.25E-01	0.57	-0.27
lpg2567	ISI400 transposase B		Viral functions / Phage / Transposases	8.753	8.996	8.593	9.205	3.23E-01	1.78E-01	0.24	0.61
lpg2567	ISI400 transposase B		Viral functions / Phage / Transposases	8.058	8.010	8.213	9.052	9.64E-01	1.29E-01	-0.05	0.84
lpg2568	hypothetical		Unknown / hypothetical proteins	10.100	10.875	11.227	9.140	1.02E-01	3.90E-03	0.77	-2.09
lpg2568	hypothetical		Unknown / hypothetical proteins	10.116	10.799	11.344	9.332	1.03E-01	3.62E-03	0.68	-2.01
lpg2569	ORF transcription regulator? fatty acid phospholipid synthesis protein		Unknown / hypothetical proteins	8.917	10.381	10.392	8.115	2.41E-02	1.76E-02	1.46	-2.28
lpg2569	ORF transcription regulator? fatty acid phospholipid synthesis protein		Unknown / hypothetical proteins	9.180	10.402	10.500	8.745	6.48E-02	2.04E-02	1.22	-1.76
lpg2570	transposase (invertase, resolvase) COG1961, putative pseudogene		Viral functions / Phage / Transposases	9.074	8.308	9.371	8.135	5.25E-03	3.08E-02	-0.77	-1.24
lpg2570	transposase (invertase, resolvase) COG1961, putative pseudogene		Viral functions / Phage / Transposases	9.006	9.405	9.324	8.538	3.85E-01	1.23E-01	0.40	-0.79
lpg2571	ORF		ORFs of unknown function (unique)	11.205	10.762	9.880	10.451	1.18E-01	3.11E-01	-0.44	0.57
lpg2571	ORF		ORFs of unknown function (unique)	11.263	10.457	9.520	10.513	2.13E-02	1.62E-01	-0.81	0.99
lpg2572	ORF		ORFs of unknown function (unique)	9.872	7.736	9.660	6.699	3.19E-02	2.88E-03	-2.14	-2.96
lpg2572	ORF		ORFs of unknown function (unique)	9.818	7.564	9.796	7.892	7.62E-03	9.30E-03	-2.25	-1.90
lpg2573	transposase (resolvase, DNA invertase) (resolvase/integrase)		Viral functions / Phage / Transposases	10.620	8.988	9.651	7.601	1.70E-01	8.62E-02	-1.63	-2.05
lpg2573	transposase (resolvase, DNA invertase) (resolvase/integrase)		Viral functions / Phage / Transposases	9.458	8.473	8.802	7.209	1.25E-01	3.48E-02	-0.99	-1.59
lpg2574	conserved hypothetical protein		Unknown / hypothetical proteins	9.035	9.449	8.029	7.683	4.42E-01	8.79E-01	0.41	-0.35
lpg2574	conserved hypothetical protein		Unknown / hypothetical proteins	8.445	9.157	6.429	8.579	4.63E-01	1.29E-01	0.71	2.15
lpg2575	tRNA-Pro		tRNA	11.629	10.354	11.611	10.206	1.90E-03	1.37E-02	-1.28	-1.40
lpg2575	tRNA-Pro		tRNA	11.584	10.605	11.612	10.379	1.42E-02	4.91E-02	-0.98	-1.23
lpg2576	uroporphyrin-III C-methyltransferase?		Named proteins of general function	11.968	9.737	11.398	10.203	2.46E-03	2.34E-02	-2.23	-1.20
lpg2576	uroporphyrin-III C-methyltransferase?		Named proteins of general function	12.086	9.754	11.560	10.423	2.65E-03	1.56E-02	-2.33	-1.14
lpg2577	ORF		ORFs of unknown function (unique)	14.363	14.132	13.276	14.278	7.80E-01	3.74E-01	-0.23	1.00
lpg2577	ORF		ORFs of unknown function (unique)	14.497	14.880	13.273	15.234	2.48E-01	4.70E-04	0.38	1.96
lpg2578	hypothetical? (84aa ORF)		Unknown / hypothetical proteins	12.606	11.547	13.729	11.319	3.27E-03	7.21E-06	-1.06	-2.41
lpg2578	hypothetical? (84aa ORF)		Unknown / hypothetical proteins	12.601	11.473	13.712	11.596	2.44E-03	1.45E-05	-1.13	-2.12
lpg2579	small ORF (137aa)		ORFs of unknown function (unique)	8.758	9.605	9.323	8.117	1.25E-01	3.92E-02	0.85	-1.21
lpg2579	small ORF (137aa)		ORFs of unknown function (unique)	9.465	9.869	9.479	9.015	1.96E-01	1.52E-01	0.40	-0.46

lpg2580	glutaryl CoA dehydrogenase	*gcdH*	Lipid Metabolism, Amino Acid Metabol	13.568	12.861	11.229	12.080	4.51E-01	1.22E-01	-0.71	0.85
lpg2580	glutaryl CoA dehydrogenase	*gcdH*	Lipid Metabolism, Amino Acid Metabol	13.759	12.912	11.146	12.048	1.73E-01	1.18E-01	-0.85	0.90
lpg2581	2-oxoisovalerate dehydrogenase, E1 component, alpha and beta fusi		Amino Acid Metabolism	11.375	11.491	10.592	11.426	7.62E-01	9.15E-02	0.12	0.83
lpg2581	2-oxoisovalerate dehydrogenase, E1 component, alpha and beta fusi		Amino Acid Metabolism	11.294	11.582	10.308	11.532	4.50E-01	4.63E-02	0.29	1.22
lpg2582	conserved hypothetical protein		Unknown / hypothetical proteins	9.013	7.792	10.787	8.488	1.50E-01	3.56E-03	-1.22	-2.30
lpg2582	conserved hypothetical protein		Unknown / hypothetical proteins	10.208	12.142	10.805	12.182	7.33E-02	1.74E-01	1.93	1.38
lpg2583	flagellar protein FlhB		Chemotaxis / motility / cell division	7.865	9.022	11.502	8.534	3.33E-01	3.73E-02	1.16	-2.97
lpg2583	flagellar protein FlhB		Chemotaxis / motility / cell division	8.050	8.687	11.425	8.658	4.53E-01	1.34E-02	0.64	-2.77
lpg2584	SidF, inhibitor of growth family, member 3	*sidF*	Chemotaxis / motility / cell division, Sig	10.304	9.678	12.230	10.738	3.37E-01	1.62E-02	-0.63	-1.49
lpg2584	SidF, inhibitor of growth family, member 3	*sidF*	Chemotaxis / motility / cell division, Sig	10.283	9.676	12.123	10.902	3.47E-01	2.17E-02	-0.61	-1.22
lpg2585	D-alanyl-D-alanine dipeptidase	*pcgL*	Protein fate / hydrolases / secretion	9.554	7.670	8.846	8.313	9.67E-02	1.64E-01	-1.88	-0.53
lpg2585	D-alanyl-D-alanine dipeptidase	*pcgL*	Protein fate / hydrolases / secretion	9.665	8.808	8.931	8.638	3.49E-02	4.30E-01	-0.86	-0.29
lpg2586	cysteine protease (papain C1 family)		Protein fate / hydrolases / secretion	9.809	12.206	11.207	10.917	2.04E-07	4.84E-01	2.40	-0.29
lpg2586	cysteine protease (papain C1 family)		Protein fate / hydrolases / secretion	9.810	12.190	11.224	10.996	1.53E-08	5.26E-01	2.38	-0.23
lpg2587	probable thermolabile hemolysin		Toxin production / other pathogen func	9.937	10.985	12.143	9.002	7.86E-02	2.42E-05	1.05	-3.14
lpg2587	probable thermolabile hemolysin		Toxin production / other pathogen func	10.141	11.126	12.156	9.157	4.43E-02	6.10E-05	0.98	-3.00
lpg2588	acid sphingomyelinase-like phosphodiesterase	*legS1*	DNA/RNA degradation / restriction	11.526	11.223	12.286	10.829	3.40E-01	5.26E-03	-0.30	-1.46
lpg2588	acid sphingomyelinase-like phosphodiesterase	*legS1*	DNA/RNA degradation / restriction	11.637	11.265	12.138	10.857	2.53E-01	2.55E-03	-0.37	-1.28
lpg2589	D-alanyl-D-alanine carboxypeptidase, fraction B; penicilli	*dacB*	Cell envelope synthesis, Protein fate /	11.228	10.507	10.305	11.391	3.16E-01	2.47E-01	-0.72	1.09
lpg2589	D-alanyl-D-alanine carboxypeptidase, fraction B; penicilli	*dacB*	Cell envelope synthesis, Protein fate /	11.103	11.034	9.674	12.130	8.80E-01	1.13E-03	-0.07	2.46
lpg2590	chromosome partitioning protein ParB (Spo0J)	*spoOJ*	Chemotaxis / motility / cell division	9.260	9.607	9.175	9.446	6.47E-01	8.51E-01	0.35	0.27
lpg2590	chromosome partitioning protein ParB (Spo0J)	*spoOJ*	Chemotaxis / motility / cell division	9.033	8.659	8.417	9.633	3.37E-01	1.14E-01	-0.37	1.22
lpg2591	small ORF (165aa)	*ceg33*	ORFs of unknown function (unique)	10.063	9.535	10.543	9.195	2.08E-01	2.39E-02	-0.53	-1.35
lpg2591	small ORF (165aa)	*ceg33*	ORFs of unknown function (unique)	9.990	9.454	10.252	8.914	2.60E-01	5.30E-03	-0.54	-1.34
lpg2592	conserved hypothetical protein		Unknown / hypothetical proteins	11.812	10.660	12.314	10.742	1.97E-03	3.27E-02	-1.15	-1.57
lpg2592	conserved hypothetical protein		Unknown / hypothetical proteins	11.872	10.814	12.442	11.109	3.23E-04	2.19E-03	-1.06	-1.33
lpg2593	rRNA methyltransferase (SUN protein)		DNA/RNA degradation / restriction, Tra	11.339	9.052	10.542	10.659	1.03E-03	7.62E-01	-2.29	0.12
lpg2593	rRNA methyltransferase (SUN protein)		DNA/RNA degradation / restriction, Tra	11.404	9.619	10.449	10.967	1.94E-06	3.52E-01	-1.79	0.52
lpg2594	methionyl tRNA formyltransferase	*fmt*	Amino Acid Metabolism, Metabolism o	11.164	10.565	9.441	11.277	2.54E-01	8.71E-02	-0.60	1.84
lpg2594	methionyl tRNA formyltransferase	*fmt*	Amino Acid Metabolism, Metabolism o	11.597	10.184	9.489	11.946	4.22E-03	4.38E-03	-1.41	2.46
lpg2595	peptide deformylase (polypeptide deformylase)	*def*	Protein fate / hydrolases / secretion, Tr	12.197	12.042	11.109	12.769	7.38E-01	3.62E-04	-0.16	1.66
lpg2595	peptide deformylase (polypeptide deformylase)	*def*	Protein fate / hydrolases / secretion, Tr	12.275	12.271	11.174	12.990	9.93E-01	3.62E-05	0.00	1.82
lpg2596	signal peptide protein (LysM domain protein)		Named proteins of general function	9.844	10.347	9.679	10.840	2.75E-01	1.37E-02	0.50	1.16
lpg2596	signal peptide protein (LysM domain protein)		Named proteins of general function	9.726	10.569	9.638	10.911	4.34E-02	2.09E-03	0.84	1.27
lpg2597	DNA processing enzyme DprA (SMF family) (Rossman fold nucleotide		DNA/RNA degradation / restriction	10.312	9.092	11.430	8.930	1.49E-03	6.38E-04	-1.22	-2.50
lpg2597	DNA processing enzyme DprA (SMF family) (Rossman fold nucleotide		DNA/RNA degradation / restriction	10.117	9.035	11.516	9.591	2.12E-03	3.29E-04	-1.08	-1.92
lpg2598	small ORF (138aa)		ORFs of unknown function (unique)	11.387	11.478	10.369	12.728	8.64E-01	3.71E-03	0.09	2.36
lpg2598	small ORF (138aa)		ORFs of unknown function (unique)	11.220	11.440	10.321	12.871	7.17E-01	1.70E-04	0.22	2.55
lpg2599	DNA topoisomerase I	*topA*	Transcription, Replication and Repair	10.752	9.867	11.106	12.015	1.54E-03	7.43E-03	-0.88	0.91
lpg2599	DNA topoisomerase I	*topA*	Transcription, Replication and Repair	10.868	9.847	11.043	11.972	4.39E-04	1.13E-02	-1.02	0.93
lpg2600	acyltransferase (O-antigen acetylase, lipopolysaccharide biosynthesis		Toxin production / other pathogen func	9.790	9.276	8.639	8.748	3.20E-01	8.42E-01	-0.51	0.11
lpg2600	acyltransferase (O-antigen acetylase, lipopolysaccharide biosynthesis		Toxin production / other pathogen func	9.723	8.943	8.396	9.239	2.18E-01	5.51E-02	-0.78	0.84
lpg2601	conserved hypothetical protein		Unknown / hypothetical proteins	13.233	12.805	12.399	12.243	1.83E-01	5.69E-01	-0.43	-0.16
lpg2601	conserved hypothetical protein		Unknown / hypothetical proteins	13.261	12.756	12.318	12.258	1.61E-01	8.35E-01	-0.50	-0.06
lpg2602	conserved domain protein		Unknown / hypothetical proteins	10.406	10.061	11.078	9.652	4.70E-01	4.14E-03	-0.34	-1.43
lpg2602	conserved domain protein		Unknown / hypothetical proteins	10.241	9.620	10.672	9.722	2.09E-01	8.53E-02	-0.62	-0.95
lpg2603	ORF		ORFs of unknown function (unique)	10.192	11.167	13.635	9.229	2.45E-01	2.79E-04	0.98	-4.41
lpg2603	ORF		ORFs of unknown function (unique)	10.136	11.201	13.586	9.615	2.01E-01	9.50E-04	1.07	-3.97
lpg2604	hypothetical (membrane protein) (temperature sensitive suppressor o		Named proteins of general function	10.444	10.384	11.055	10.588	8.76E-01	8.26E-02	-0.06	-0.47
lpg2604	hypothetical (membrane protein) (temperature sensitive suppressor o		Named proteins of general function	10.504	10.641	11.042	10.895	7.31E-01	6.17E-01	0.14	-0.15
lpg2605	conserved hypothetical protein		Unknown / hypothetical proteins	10.533	9.361	11.087	8.812	9.39E-03	3.32E-03	-1.17	-2.27
lpg2605	conserved hypothetical protein		Unknown / hypothetical proteins	10.463	9.258	11.069	9.240	5.39E-03	3.61E-03	-1.20	-1.83
lpg2606	glutamine amidotransferase		Amino Acid Metabolism	10.479	10.224	12.079	9.842	7.22E-01	5.60E-04	-0.25	-2.24
lpg2606	glutamine amidotransferase		Amino Acid Metabolism	10.406	9.727	12.037	10.072	3.74E-01	2.07E-03	-0.68	-1.97
lpg2607	metallopeptidase PepO, peptidase, M13 family (endothel	*pepO*	Protein fate / hydrolases / secretion	10.027	10.155	11.362	9.830	7.73E-01	3.29E-03	0.13	-1.53
lpg2607	metallopeptidase PepO, peptidase, M13 family (endothel	*pepO*	Protein fate / hydrolases / secretion	10.223	10.769	11.429	10.567	2.24E-01	1.04E-01	0.55	-0.86
lpg2608	UDP-3-O-acyl-N-acetylglucosamine deacetylase	*lpxC*	Metabolism of Complex Carbohydrates	13.449	12.033	11.730	12.410	8.06E-03	1.11E-01	-1.42	0.68
lpg2608	UDP-3-O-acyl-N-acetylglucosamine deacetylase	*lpxC*	Metabolism of Complex Carbohydrates	13.480	12.023	11.697	12.425	3.66E-03	8.80E-02	-1.46	0.73
lpg2609	cell division protein FtsZ	*ftsZ*	Chemotaxis / motility / cell division	13.473	14.393	13.410	13.820	1.02E-02	5.21E-02	0.92	0.41
lpg2609	cell division protein FtsZ	*ftsZ*	Chemotaxis / motility / cell division	13.106	14.526	13.081	14.040	2.25E-02	6.73E-02	1.42	0.96
lpg2610	cell division protein FtsA	*ftsA*	Chemotaxis / motility / cell division	13.215	12.715	12.193	12.784	3.32E-02	2.70E-02	-0.50	0.59
lpg2610	cell division protein FtsA	*ftsA*	Chemotaxis / motility / cell division	13.087	12.712	12.166	12.791	1.61E-01	1.05E-02	-0.37	0.62
lpg2611	cell division protein FtsQ	*ftsQ*	Chemotaxis / motility / cell division	12.584	11.509	12.155	11.071	1.77E-03	4.23E-05	-1.08	-1.08
lpg2611	cell division protein FtsQ	*ftsQ*	Chemotaxis / motility / cell division	12.628	11.357	12.254	11.872	5.45E-05	1.29E-01	-1.27	-0.38

lpg2612	D-alanine-D-alanine ligase A (DdlA)	*ddlA*	Metabolism of Other Amino Acids, Met	11.425	11.033	11.713	10.806	1.76E-01	1.53E-03	-0.39	-0.91
lpg2612	D-alanine-D-alanine ligase A (DdlA)	*ddlA*	Metabolism of Other Amino Acids, Met	11.786	11.117	11.705	10.852	2.38E-01	2.78E-05	-0.67	-0.85
lpg2613	UDP-N-acetylenolpyruvoylglucosamine reductase	*murB*	Metabolism of Complex Carbohydrate	11.694	10.918	12.445	11.344	9.19E-04	1.33E-04	-0.78	-1.10
lpg2613	UDP-N-acetylenolpyruvoylglucosamine reductase	*murB*	Metabolism of Complex Carbohydrate	11.597	11.498	12.445	11.554	8.76E-01	1.30E-01	-0.10	-0.89
lpg2614	UDP-N-acetylmuramate:L-alanine ligase MurC (L-alanine	*murC*	Metabolism of Other Amino Acids, Met	10.996	11.859	10.065	11.604	2.69E-01	8.95E-03	0.86	1.54
lpg2614	UDP-N-acetylmuramate:L-alanine ligase MurC (L-alanine	*murC*	Metabolism of Other Amino Acids, Met	11.481	11.754	10.084	11.668	5.87E-01	8.98E-03	0.27	1.58
lpg2615	cell division protein FtsW	*ftsW*	Chemotaxis / motility / cell division	11.858	11.179	11.996	11.624	6.69E-04	4.69E-02	-0.68	-0.37
lpg2615	cell division protein FtsW	*ftsW*	Chemotaxis / motility / cell division	11.743	11.168	11.902	11.532	5.08E-03	2.38E-01	-0.58	-0.37
lpg2616	UDP-N-muramoylalanine-D-glutamate ligase	*murD*	Metabolism of Other Amino Acids, Met	10.681	10.283	11.605	10.447	4.79E-01	7.22E-02	-0.40	-1.16
lpg2616	UDP-N-muramoylalanine-D-glutamate ligase	*murD*	Metabolism of Other Amino Acids, Met	10.735	10.967	11.665	11.491	4.91E-01	5.42E-01	0.23	-0.17
lpg2617	phospho-N-acetylmuramoyl-pentapeptide transferase	*mraY*	Metabolism of Complex Carbohydrate	11.445	11.157	10.787	11.140	3.38E-01	2.71E-01	-0.29	0.35
lpg2617	phospho-N-acetylmuramoyl-pentapeptide transferase	*mraY*	Metabolism of Complex Carbohydrate	11.239	11.078	10.399	11.192	7.50E-01	7.23E-02	-0.16	0.79
lpg2618	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopir	*murF*	Amino Acid Metabolism, Metabolism o	11.934	11.633	10.697	12.417	2.87E-01	1.60E-03	-0.30	1.72
lpg2618	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopir	*murF*	Amino Acid Metabolism, Metabolism o	11.695	11.975	10.267	12.914	6.92E-01	2.18E-03	0.28	2.65
lpg2619	cell division protein ZipA		Chemotaxis / motility / cell division	12.235	11.033	11.877	11.041	1.20E-01	2.42E-01	-1.20	-0.84
lpg2619	cell division protein ZipA		Chemotaxis / motility / cell division	12.254	11.418	11.945	11.770	3.98E-02	2.24E-01	-0.84	-0.18
lpg2620	chromosome segregation SMC protein (chromosome partition protein		Chemotaxis / motility / cell division	11.055	9.425	9.119	10.347	3.27E-02	1.09E-01	-1.63	1.23
lpg2620	chromosome segregation SMC protein (chromosome partition protein		Chemotaxis / motility / cell division	10.937	9.930	9.466	11.098	1.81E-01	3.85E-02	-1.01	1.63
lpg2621	acid phosphatase, class B (vegetative storage protein)		Toxin production / other pathogen func	10.118	12.403	8.887	11.184	3.12E-04	8.29E-03	2.29	2.30
lpg2621	acid phosphatase, class B (vegetative storage protein)		Toxin production / other pathogen func	10.277	12.254	8.990	11.579	3.16E-05	2.30E-03	1.98	2.59
lpg2622	hypothetical protein		Unknown / hypothetical proteins	11.063	11.834	11.998	10.717	5.54E-02	2.39E-03	0.77	-1.28
lpg2622	hypothetical protein		Unknown / hypothetical proteins	11.142	12.117	11.956	10.712	1.43E-03	2.89E-04	0.97	-1.24
lpg2623	transmembrane protein		Unknown / hypothetical proteins	8.911	9.715	9.200	10.082	1.59E-01	5.05E-02	0.80	0.88
lpg2623	transmembrane protein		Unknown / hypothetical proteins	9.218	11.145	9.757	11.252	5.76E-02	5.15E-02	1.93	1.50
lpg2624	transcription elongation factor GreA	*greA*	Transcription	12.875	12.653	12.502	11.938	6.91E-01	7.23E-01	-0.22	-0.56
lpg2624	transcription elongation factor GreA	*greA*	Transcription	12.699	12.638	12.336	12.525	9.13E-01	8.46E-01	-0.06	0.19
lpg2625	carbamoyl phosphate synthase, large subunit	*carB*	Nucleotide Metabolism, Amino Acid M	11.479	10.359	10.958	9.883	2.32E-01	1.78E-01	-1.12	-1.07
lpg2625	carbamoyl phosphate synthase, large subunit	*carB*	Nucleotide Metabolism, Amino Acid M	10.588	10.145	10.386	9.838	2.04E-01	1.71E-01	-0.44	-0.55
lpg2626	ORF		ORFs of unknown function (unique)	10.271	9.788	12.097	9.071	3.26E-01	1.82E-03	-0.48	-3.03
lpg2626	ORF		ORFs of unknown function (unique)	10.039	9.847	12.018	9.708	6.18E-01	2.30E-04	-0.19	-2.31
lpg2627	hypothetical (periplasmic flavoprotein)		Named proteins of general function	8.236	8.521	8.590	8.842	5.36E-01	5.47E-01	0.29	0.25
lpg2627	hypothetical (periplasmic flavoprotein)		Named proteins of general function	8.219	8.222	8.091	8.372	9.96E-01	5.52E-01	0.00	0.28
lpg2628	membrane protein		Named proteins of general function	10.336	9.062	9.231	9.556	2.75E-03	6.60E-01	-1.27	0.32
lpg2628	membrane protein		Named proteins of general function	10.285	8.443	8.954	9.671	2.40E-02	3.23E-01	-1.84	0.72
lpg2629	permease		Transport and binding	10.279	8.668	9.346	9.354	3.54E-03	9.84E-01	-1.61	0.01
lpg2629	permease		Transport and binding	9.877	8.832	8.410	9.293	2.91E-01	4.25E-01	-1.05	0.88
lpg2630	permease		Transport and binding	11.616	10.785	9.878	10.571	2.44E-01	5.68E-01	-0.83	0.69
lpg2630	permease		Transport and binding	11.339	10.873	9.638	10.973	5.64E-01	1.35E-01	-0.47	1.33
lpg2631	aminopeptidase A/I (leucine aminopeptidase)	*pepA*	Protein fate / hydrolases / secretion	11.016	11.148	9.030	12.076	7.18E-01	1.73E-03	0.13	3.05
lpg2631	aminopeptidase A/I (leucine aminopeptidase)	*pepA*	Protein fate / hydrolases / secretion	11.012	11.306	8.711	12.119	3.90E-01	1.54E-03	0.29	3.41
lpg2632	DNA polymerase III, chi subunit	*holC*	Replication and Repair	8.134	9.299	7.983	9.218	2.71E-01	3.36E-03	1.16	1.23
lpg2632	DNA polymerase III, chi subunit	*holC*	Replication and Repair	8.944	9.851	7.583	8.952	1.08E-01	2.93E-02	0.91	1.37
lpg2633	hypothetical protein		Unknown / hypothetical proteins	10.356	11.850	9.592	11.974	4.35E-04	3.30E-03	1.49	2.38
lpg2633	hypothetical protein		Unknown / hypothetical proteins	10.395	12.157	8.685	12.402	5.47E-03	5.59E-03	1.76	3.72
lpg2634	leucine aminopeptidase (cytosol aminopeptidase)		Protein fate / hydrolases / secretion	9.839	10.687	9.461	11.288	3.44E-01	3.27E-04	0.85	1.83
lpg2634	leucine aminopeptidase (cytosol aminopeptidase)		Protein fate / hydrolases / secretion	10.299	10.869	9.209	11.086	2.53E-02	9.58E-05	0.57	1.88
lpg2635	integral membrane protein (putative virulence factor) Mvi	*mviN*	Toxin production / other pathogen func	10.691	9.895	10.415	8.892	1.52E-01	6.83E-02	-0.80	-1.52
lpg2635	integral membrane protein (putative virulence factor) Mvi	*mviN*	Toxin production / other pathogen func	10.811	10.275	10.616	9.460	2.45E-01	4.93E-02	-0.54	-1.16
lpg2636	30S ribosomal protein S20	*rpsT*	Translation	11.882	11.457	10.301	12.155	6.47E-01	1.24E-02	-0.42	1.85
lpg2636	30S ribosomal protein S20	*rpsT*	Translation	12.358	11.677	10.319	12.186	1.37E-01	8.43E-03	-0.68	1.87
lpg2637	ORF		ORFs of unknown function (unique)	14.054	14.770	12.274	14.804	1.61E-01	4.63E-04	0.72	2.53
lpg2637	ORF		ORFs of unknown function (unique)	13.850	14.807	12.212	14.812	6.77E-03	5.64E-04	0.96	2.60
lpg2638	ORF		ORFs of unknown function (unique)	11.369	12.605	11.426	12.372	1.16E-03	4.70E-04	1.24	0.95
lpg2638	ORF		ORFs of unknown function (unique)	10.721	12.705	11.015	12.461	9.02E-03	5.31E-04	1.98	1.45
lpg2639	enhanced entry protein EnhC	*enhC*	Toxin production / other pathogen func	12.357	12.641	14.453	11.782	4.91E-01	1.42E-04	0.28	-2.67
lpg2639	enhanced entry protein EnhC	*enhC*	Toxin production / other pathogen func	12.311	12.734	14.434	11.843	3.10E-01	2.35E-04	0.42	-2.59
lpg2640	enhanced entry protein EnhB	*enhB*	Toxin production / other pathogen func	10.627	11.367	13.188	9.671	1.93E-01	1.94E-03	0.74	-3.52
lpg2640	enhanced entry protein EnhB	*enhB*	Toxin production / other pathogen func	10.617	11.379	13.163	9.801	2.13E-01	1.74E-03	0.76	-3.36
lpg2641	enhanced entry protein EnhA	*enhA*	Toxin production / other pathogen func	9.885	10.550	12.680	9.611	3.19E-01	1.43E-03	0.67	-3.07
lpg2641	enhanced entry protein EnhA	*enhA*	Toxin production / other pathogen func	9.880	10.578	12.728	9.996	3.12E-01	5.62E-03	0.70	-2.73
lpg2642	sensory box/GGDEF family protein		Signal transduction / other regulatory f	9.796	9.373	11.505	9.507	2.98E-01	2.60E-04	-0.42	-2.00
lpg2642	sensory box/GGDEF family protein		Signal transduction / other regulatory f	9.901	9.133	11.553	9.573	4.94E-02	6.48E-04	-0.77	-1.98
lpg2643	ORF		ORFs of unknown function (unique)	10.830	10.832	10.156	10.829	9.94E-01	1.85E-01	0.00	0.67
lpg2643	ORF		ORFs of unknown function (unique)	10.940	10.613	10.119	11.030	3.90E-01	4.94E-02	-0.33	0.91

lpg2644	tail fiber protein (collagen-like protein SclB)	*sclB*	Named proteins of general function	11.342	11.699	10.779	13.174	2.90E-01	2.97E-04	0.36	2.39
lpg2644	tail fiber protein (collagen-like protein SclB)	*sclB*	Named proteins of general function	11.136	11.703	10.698	13.192	2.80E-01	1.86E-04	0.57	2.49
lpg2645	excinuclease ABC subunit	*uvrC*	DNA/RNA degradation / restriction	11.410	9.850	10.793	10.545	2.98E-02	4.36E-01	-1.56	-0.25
lpg2645	excinuclease ABC subunit	*uvrC*	DNA/RNA degradation / restriction	11.500	9.375	10.576	10.469	3.23E-03	7.93E-01	-2.12	-0.11
lpg2646	response regulator GacA (global activator)/transcription a	*gacA*	Signal transduction / other regulatory f	13.965	13.401	12.760	13.366	3.02E-01	4.50E-02	-0.56	0.61
lpg2646	response regulator GacA (global activator)/transcription a	*gacA*	Signal transduction / other regulatory f	13.943	13.381	12.712	13.347	2.49E-01	4.02E-02	-0.56	0.64
lpg2647	phenylalanine-4-hydroxylase (PAH) (Phe-4-monooxygena	*phhA*	Amino Acid Metabolism	12.761	12.289	12.643	12.582	9.12E-02	7.75E-01	-0.47	-0.06
lpg2647	phenylalanine-4-hydroxylase (PAH) (Phe-4-monooxygena	*phhA*	Amino Acid Metabolism	12.768	12.256	12.609	12.573	3.42E-02	8.41E-01	-0.51	-0.04
lpg2648	competence damage inducible protein CinA (predicted nu	*cinA*	Toxin production / other pathogen func	8.908	9.238	9.504	8.815	5.71E-01	1.28E-01	0.33	-0.69
lpg2648	competence damage inducible protein CinA (predicted nu	*cinA*	Toxin production / other pathogen func	9.126	9.962	9.292	9.583	8.50E-02	6.06E-01	0.84	0.29
lpg2649	GTP-binding protein, GTP1/Obg family		Signal transduction / other regulatory f	9.545	9.128	9.536	10.163	3.67E-01	3.08E-01	-0.42	0.63
lpg2649	GTP-binding protein, GTP1/Obg family		Signal transduction / other regulatory f	9.460	9.884	9.960	11.576	5.88E-01	1.65E-01	0.42	1.62
lpg2650	50S ribosomal protein L27	*rpmA*	Translation	13.641	13.330	11.928	14.387	6.88E-01	2.97E-02	-0.31	2.46
lpg2650	50S ribosomal protein L27	*rpmA*	Translation	13.590	13.908	12.026	15.206	6.86E-01	2.01E-04	0.32	3.18
lpg2651	50S ribosomal protein L21	*rplU*	Translation	13.089	12.583	10.015	14.430	6.47E-01	1.43E-03	-0.51	4.42
lpg2651	50S ribosomal protein L21	*rplU*	Translation	13.181	13.404	10.006	14.654	8.21E-01	5.20E-04	0.22	4.65
lpg2652	50S ribosomal protein L25, ribosomal 5S rRNA E-loop binding protein		Translation	12.453	11.133	10.520	12.817	2.01E-01	3.50E-02	-1.32	2.30
lpg2652	50S ribosomal protein L25, ribosomal 5S rRNA E-loop binding protein		Translation	12.720	11.615	10.396	13.375	1.02E-01	5.43E-03	-1.11	2.98
lpg2653	peptidyl tRNA hydrolase	*pth*	DNA/RNA degradation / restriction, Pr	12.730	11.340	11.189	12.271	7.17E-03	2.49E-01	-1.39	1.08
lpg2653	peptidyl tRNA hydrolase	*pth*	DNA/RNA degradation / restriction, Pr	12.849	11.292	10.732	12.274	7.45E-03	1.55E-01	-1.56	1.54
lpg2654	GTP binding protein		Signal transduction / other regulatory f	11.114	10.708	10.182	11.735	5.36E-01	1.66E-02	-0.41	1.55
lpg2654	GTP binding protein		Signal transduction / other regulatory f	11.407	10.695	10.091	11.750	1.01E-01	2.35E-02	-0.71	1.66
lpg2655	sensory box protein (cGMP turnover?)		Signal transduction / other regulatory f	10.392	9.725	12.392	10.136	5.60E-01	3.11E-04	-0.67	-2.26
lpg2655	sensory box protein (cGMP turnover?)		Signal transduction / other regulatory f	9.801	10.237	11.661	9.875	4.75E-01	2.06E-03	0.44	-1.79
lpg2656	octaprenyl diphosphate synthase IspB (polyprenyl synthetase)		Named proteins of general function	13.545	12.828	11.215	12.660	2.55E-01	3.01E-02	-0.72	1.44
lpg2656	octaprenyl diphosphate synthase IspB (polyprenyl synthetase)		Named proteins of general function	13.001	12.892	10.674	12.687	9.12E-01	2.14E-02	-0.11	2.01
lpg2657	ferrous iron transporter B	*feoB*	Transport and binding	10.335	7.710	8.689	7.883	6.12E-02	6.64E-01	-2.63	-0.81
lpg2657	ferrous iron transporter B	*feoB*	Transport and binding	10.243	8.456	9.912	9.708	3.78E-04	5.94E-01	-1.79	-0.20
lpg2658	ferrous iron transporter A	*feoA*	Transport and binding	11.064	10.462	10.619	11.017	1.13E-02	1.71E-02	-0.60	0.40
lpg2658	ferrous iron transporter A	*feoA*	Transport and binding	11.086	10.157	10.574	11.071	3.51E-02	9.68E-03	-0.93	0.50
lpg2659	ATPase N2B (nucleotide (GTP) binding protein), COG1485		Signal transduction / other regulatory f	10.639	10.806	9.670	11.726	8.70E-01	1.00E-03	0.17	2.06
lpg2659	ATPase N2B (nucleotide (GTP) binding protein), COG1485		Signal transduction / other regulatory f	11.163	10.717	9.187	11.546	3.44E-01	1.19E-02	-0.45	2.36
lpg2660	transmembrane protein (esterase/lipase/thioesterase family active site		Named proteins of general function	11.421	11.331	11.975	12.138	6.71E-01	1.69E-01	-0.09	0.16
lpg2660	transmembrane protein (esterase/lipase/thioesterase family active site		Named proteins of general function	11.268	11.248	11.600	12.047	9.25E-01	1.29E-02	-0.02	0.45
lpg2661	3-methyl-2-oxobutanoate hydroxymethyltransferase (keto	*panB*	Metabolism of Cofactors and Vitamins	14.168	13.298	12.092	14.697	7.02E-02	2.04E-04	-0.87	2.60
lpg2661	3-methyl-2-oxobutanoate hydroxymethyltransferase (keto	*panB*	Metabolism of Cofactors and Vitamins	14.026	13.216	11.818	14.653	5.14E-02	2.41E-04	-0.81	2.84
lpg2662	pantoate-beta-alanine ligase (pantothenate synthetase)	*panC*	Metabolism of Other Amino Acids, Met	11.204	11.357	9.585	12.416	7.96E-01	1.43E-04	0.15	2.83
lpg2662	pantoate-beta-alanine ligase (pantothenate synthetase)	*panC*	Metabolism of Other Amino Acids, Met	11.148	10.573	9.171	12.247	2.39E-01	1.78E-04	-0.58	3.08
lpg2663	hypothetical protein		Unknown / hypothetical proteins	10.563	8.975	9.773	9.036	2.81E-03	1.27E-01	-1.59	-0.74
lpg2663	hypothetical protein		Unknown / hypothetical proteins	10.679	8.721	9.984	9.308	2.36E-04	1.58E-01	-1.96	-0.68
lpg2664	acetyl-CoA carboxylase, biotin carboxylase subunit (pyruvate carboxy		Carbohydrate Metabolism, Amino Acid	12.133	11.840	12.517	12.226	2.21E-01	1.21E-01	-0.29	-0.29
lpg2664	acetyl-CoA carboxylase, biotin carboxylase subunit (pyruvate carboxy		Carbohydrate Metabolism, Amino Acid	12.132	11.706	12.453	12.251	9.70E-02	2.68E-01	-0.43	-0.20
lpg2665	dienelactone hydrolase family protein		Named proteins of general function	12.163	12.079	12.231	12.752	7.65E-01	9.29E-02	-0.08	0.52
lpg2665	dienelactone hydrolase family protein		Named proteins of general function	12.032	12.070	11.792	12.770	9.14E-01	4.00E-02	0.04	0.98
lpg2666	probable hydrolase		Protein fate / hydrolases / secretion	10.699	11.021	13.354	10.240	7.13E-01	1.31E-03	0.32	-3.11
lpg2666	probable hydrolase		Protein fate / hydrolases / secretion	10.728	11.106	13.357	10.405	6.79E-01	2.44E-03	0.38	-2.95
lpg2667	RNA polymerase sigma-32 factor (sigma factor RpoH)	*rpoH*	Transcription factors / DNA binding pro	12.540	11.474	11.284	11.137	9.42E-02	7.89E-01	-1.07	-0.15
lpg2667	RNA polymerase sigma-32 factor (sigma factor RpoH)	*rpoH*	Transcription factors / DNA binding pro	12.504	11.420	11.269	11.253	8.94E-02	9.73E-01	-1.08	-0.02
lpg2668	cell division ATP transporter (permease protein) FtsX	*ftsX*	Transport and binding, Chemotaxis / m	9.887	10.169	9.627	10.231	4.59E-01	5.55E-02	0.28	0.60
lpg2668	cell division ATP transporter (permease protein) FtsX	*ftsX*	Transport and binding, Chemotaxis / m	10.016	10.083	9.235	10.133	8.46E-01	5.29E-02	0.07	0.90
lpg2669	cell division ATP transporter (ATP binding protein) FtsE	*ftsE*	Chemotaxis / motility / cell division	10.878	9.541	9.448	10.065	2.91E-05	1.48E-01	-1.34	0.62
lpg2669	cell division ATP transporter (ATP binding protein) FtsE	*ftsE*	Chemotaxis / motility / cell division	11.018	9.411	9.453	10.310	8.83E-04	1.04E-01	-1.61	0.86
lpg2670	cell division membrane protein FtsY (signal recognition p	*ftsY*	Protein fate / hydrolases / secretion, C	10.463	10.925	10.435	11.716	2.86E-01	2.52E-02	0.46	1.28
lpg2670	cell division membrane protein FtsY (signal recognition p	*ftsY*	Protein fate / hydrolases / secretion, C	10.622	10.716	10.298	11.682	8.78E-01	8.75E-03	0.09	1.38
lpg2671	zinc protease (peptidase, M16 family)		Protein fate / hydrolases / secretion	11.497	11.448	10.943	10.667	9.54E-01	5.36E-01	-0.05	-0.28
lpg2671	zinc protease (peptidase, M16 family)		Protein fate / hydrolases / secretion	10.539	11.353	10.502	10.687	2.74E-02	5.90E-01	0.81	0.18
lpg2672	zinc protease (peptidase, M16 family)		Protein fate / hydrolases / secretion	11.167	12.322	11.341	11.196	2.24E-03	6.94E-01	1.16	-0.15
lpg2672	zinc protease (peptidase, M16 family)		Protein fate / hydrolases / secretion	11.151	12.288	11.153	11.193	2.63E-03	9.04E-01	1.14	0.04
lpg2673	N6-adenine specific methylase (DNA methylase)		Metabolism of Cofactors and Vitamins	9.920	10.502	10.160	10.445	3.51E-01	6.73E-01	0.58	0.28
lpg2673	N6-adenine specific methylase (DNA methylase)		Metabolism of Cofactors and Vitamins	10.059	10.380	10.294	10.925	6.03E-01	1.96E-01	0.32	0.63
lpg2674	DotD (TraH)	*dotD*	Transport and binding, Toxin productio	13.072	12.543	11.716	12.916	2.31E-01	7.69E-03	-0.53	1.20
lpg2674	DotD (TraH)	*dotD*	Transport and binding, Toxin productio	13.035	12.478	11.689	12.963	2.16E-01	4.91E-03	-0.56	1.27
lpg2675	DotC (TraI)	*dotC*	Transport and binding, Toxin productio	12.501	11.066	11.194	11.940	1.42E-02	1.58E-01	-1.43	0.75
lpg2675	DotC (TraI)	*dotC*	Transport and binding, Toxin productio	12.576	11.213	11.200	11.957	2.94E-02	1.63E-01	-1.36	0.76

lpg2676	DotB (TraJ) (type IV pilus biogenesis protein)	*dotB*	Transport and binding, Toxin productio	13.825	12.635	13.546	14.032	8.51E-04	5.91E-02	-1.19	0.49
lpg2676	DotB (TraJ) (type IV pilus biogenesis protein)	*dotB*	Transport and binding, Toxin productio	13.833	12.800	13.513	14.136	2.19E-03	4.28E-03	-1.03	0.62
lpg2677	5'-nucleotidase		Metabolism of Cofactors and Vitamins	11.466	9.445	11.062	10.194	9.51E-04	2.91E-02	-2.02	-0.87
lpg2677	5'-nucleotidase		Metabolism of Cofactors and Vitamins	11.550	9.584	10.889	10.133	1.25E-04	9.65E-02	-1.97	-0.76
lpg2678	similar to unknown proteins		Unknown / hypothetical proteins	11.391	10.727	10.463	10.495	1.13E-01	9.50E-01	-0.66	0.03
lpg2678	similar to unknown proteins		Unknown / hypothetical proteins	11.381	10.780	10.305	10.792	1.72E-01	3.55E-01	-0.60	0.49
lpg2679	D-isomer specific 2-hydroxyacid dehydrogenase (glycerate dehydroge		Named proteins of general function	10.922	11.264	9.221	11.169	6.12E-01	2.93E-02	0.34	1.95
lpg2679	D-isomer specific 2-hydroxyacid dehydrogenase (glycerate dehydroge		Named proteins of general function	11.327	11.380	8.629	11.053	9.10E-01	1.34E-02	0.05	2.42
lpg2680	UDP-N-acetylmuramyl tripeptide synthase (cyanophycin	*murE3*	Amino Acid Metabolism, Metabolism o	10.324	10.144	9.603	10.007	7.56E-01	3.90E-01	-0.18	0.40
lpg2680	UDP-N-acetylmuramyl tripeptide synthase (cyanophycin	*murE3*	Amino Acid Metabolism, Metabolism o	10.005	9.619	9.523	10.226	4.46E-01	1.61E-01	-0.39	0.70
lpg2681	4-hydroxy-2-oxovalerate aldolase (aldolase/synthase)		Carbohydrate Metabolism, Metabolism	11.533	11.283	12.661	11.310	6.98E-01	1.40E-02	-0.25	-1.35
lpg2681	4-hydroxy-2-oxovalerate aldolase (aldolase/synthase)		Carbohydrate Metabolism, Metabolism	11.511	11.423	12.697	11.500	8.79E-01	1.22E-02	-0.09	-1.20
lpg2682	protein product; unknown protein with two candidate membrane-span		Unknown / hypothetical proteins	9.985	9.478	10.744	9.395	2.91E-01	1.13E-02	-0.51	-1.35
lpg2682	protein product; unknown protein with two candidate membrane-span		Unknown / hypothetical proteins	9.648	9.087	10.325	9.417	2.29E-01	3.85E-02	-0.56	-0.91
lpg2683	DlpA protein (isocitrate/3-isopropylmalate dehydrogenase) TWO ORF		Amino Acid Metabolism	9.237	8.868	10.056	8.622	1.27E-01	2.52E-02	-0.37	-1.43
lpg2683	DlpA protein (isocitrate/3-isopropylmalate dehydrogenase) TWO ORF		Amino Acid Metabolism	9.510	9.045	9.962	9.157	1.61E-01	1.15E-02	-0.47	-0.81
lpg2684	hypothetical		Unknown / hypothetical proteins	9.521	9.171	10.001	9.270	5.98E-01	2.15E-01	-0.35	-0.73
lpg2684	hypothetical		Unknown / hypothetical proteins	9.416	9.761	9.995	9.317	6.91E-01	3.58E-01	0.34	-0.68
lpg2685	dienelactone hydrolase family protein (L. pneumophila small basic pro		Biodegradation of Xenobiotics	10.299	9.880	11.626	9.933	3.88E-01	3.01E-03	-0.42	-1.69
lpg2685	dienelactone hydrolase family protein (L. pneumophila small basic pro		Biodegradation of Xenobiotics	10.308	10.154	11.583	10.194	7.80E-01	8.10E-03	-0.15	-1.39
lpg2686	DotA	*dotA*	Transport and binding, Toxin productio	11.914	11.590	12.720	11.288	5.70E-01	1.56E-01	-0.32	-1.43
lpg2686	DotA	*dotA*	Transport and binding, Toxin productio	12.119	11.819	12.710	11.487	3.59E-01	1.09E-01	-0.30	-1.22
lpg2687	IcmV	*icmV*	Transport and binding, Toxin productio	11.484	12.098	11.427	10.761	2.38E-01	3.46E-01	0.61	-0.67
lpg2687	IcmV	*icmV*	Transport and binding, Toxin productio	11.603	11.879	11.667	11.040	6.26E-01	2.68E-01	0.28	-0.63
lpg2688	IcmW	*icmW*	Transport and binding, Toxin productio	11.358	11.637	11.585	11.173	5.63E-01	2.24E-01	0.28	-0.41
lpg2688	IcmW	*icmW*	Transport and binding, Toxin productio	11.369	11.851	11.538	11.657	3.68E-01	7.19E-01	0.48	0.12
lpg2689	IcmX ((IcmY))	*icmX*	Transport and binding, Toxin productio	12.770	12.383	13.111	12.583	6.08E-01	5.81E-01	-0.39	-0.53
lpg2689	IcmX ((IcmY))	*icmX*	Transport and binding, Toxin productio	12.253	12.772	12.603	12.729	2.45E-01	8.80E-01	0.52	0.13
lpg2690	LphB	*lphB*	Named proteins of general function	9.928	10.200	9.102	10.312	3.68E-01	6.37E-03	0.27	1.21
lpg2690	LphB	*lphB*	Named proteins of general function	9.794	9.421	8.937	10.573	5.96E-01	1.62E-04	-0.37	1.64
lpg2691	cation transporting ATPase PacS (heavy-metal transporting P-type AT		Transport and binding	10.231	11.728	10.232	11.532	4.11E-04	1.28E-02	1.50	1.30
lpg2691	cation transporting ATPase PacS (heavy-metal transporting P-type AT		Transport and binding	10.484	11.772	10.059	11.503	4.28E-03	8.67E-03	1.29	1.44
lpg2692	ORF		ORFs of unknown function (unique)	10.376	12.030	10.559	11.169	8.87E-03	1.48E-01	1.65	0.61
lpg2692	ORF		ORFs of unknown function (unique)	10.455	11.943	9.845	10.952	5.31E-03	4.78E-02	1.49	1.11
lpg2693	hypothetical (SmtA SAM-dependent methyltransferase?)		Unknown / hypothetical proteins	11.200	9.752	12.325	10.021	7.19E-03	6.25E-04	-1.45	-2.30
lpg2693	hypothetical (SmtA SAM-dependent methyltransferase?)		Unknown / hypothetical proteins	11.110	9.764	12.232	10.171	1.99E-03	1.05E-03	-1.35	-2.06
lpg2694	hypothetical (SnoK?) (eukaryotic proteins (PhyH (bacteria	*legD1*	Biosynthesis of Secondary Metabolites	9.423	8.709	9.368	9.078	3.67E-01	7.03E-01	-0.71	-0.29
lpg2694	hypothetical (SnoK?) (eukaryotic proteins (PhyH (bacteria	*legD1*	Biosynthesis of Secondary Metabolites	9.581	9.257	9.027	9.611	6.97E-01	4.06E-01	-0.32	0.58
lpg2695	heptosyl transferase, glycosyltransferase family 9 protein (saccharide		Cell envelope synthesis, Metabolism o	11.415	9.374	10.680	9.749	1.16E-02	9.20E-02	-2.04	-0.93
lpg2695	heptosyl transferase, glycosyltransferase family 9 protein (saccharide		Cell envelope synthesis, Metabolism o	11.128	9.475	10.034	9.338	3.24E-02	3.03E-01	-1.65	-0.70
lpg2696	tRNA delta(2)-isopentenylpyrophosphate transferase (del	*miaA*	DNA/RNA degradation / restriction, Tra	11.582	11.223	11.225	11.757	1.85E-01	6.86E-02	-0.36	0.53
lpg2696	tRNA delta(2)-isopentenylpyrophosphate transferase (del	*miaA*	DNA/RNA degradation / restriction, Tra	11.632	11.327	10.835	11.845	7.94E-02	2.12E-02	-0.31	1.01
lpg2697	DNA mismatch repair protein MutL	*mutL*	Replication and Repair	10.173	9.811	9.559	9.023	5.32E-02	6.13E-01	-0.36	-0.54
lpg2697	DNA mismatch repair protein MutL	*mutL*	Replication and Repair	9.724	10.378	9.881	10.441	3.82E-01	3.99E-01	0.65	0.56
lpg2698	N-acetylmuramoyl-L-alanine amidase	*amiB*	Metabolism of Complex Carbohydrates	10.578	10.765	10.262	10.009	4.97E-01	6.58E-01	0.19	-0.25
lpg2698	N-acetylmuramoyl-L-alanine amidase	*amiB*	Metabolism of Complex Carbohydrates	10.473	10.663	9.995	9.795	4.95E-01	6.81E-01	0.19	-0.20
lpg2699	COG0802 ATPase or kinase		Named proteins of general function	10.015	9.205	9.491	9.750	2.71E-01	6.95E-01	-0.81	0.26
lpg2699	COG0802 ATPase or kinase		Named proteins of general function	10.167	9.317	9.501	9.872	2.28E-01	5.41E-01	-0.85	0.37
lpg2700	sugar kinase		Named proteins of general function	10.950	10.337	10.337	10.968	3.75E-01	2.19E-01	-0.61	0.63
lpg2700	sugar kinase		Named proteins of general function	10.942	10.651	10.263	11.623	7.10E-01	1.05E-01	-0.29	1.36
lpg2701	stringent starvation protein B COG2969	*sspB*	Toxin production / other pathogen func	13.680	13.478	11.724	14.419	4.69E-01	4.38E-04	-0.20	2.69
lpg2701	stringent starvation protein B COG2969	*sspB*	Toxin production / other pathogen func	13.731	13.489	11.620	14.437	3.76E-01	7.33E-04	-0.24	2.82
lpg2702	stringent starvation protein A (transcription activator)	*sspA*	Toxin production / other pathogen func	11.550	10.494	9.307	12.238	4.48E-01	2.50E-02	-1.06	2.93
lpg2702	stringent starvation protein A (transcription activator)	*sspA*	Toxin production / other pathogen func	11.069	11.844	8.865	12.603	3.48E-01	2.35E-03	0.77	3.74
lpg2703	ubiquinol-cytochrome c reductase, cytochrome c1		Energy Metabolism	11.228	9.309	9.438	8.180	8.74E-04	1.04E-01	-1.92	-1.26
lpg2703	ubiquinol-cytochrome c reductase, cytochrome c1		Energy Metabolism	11.547	9.561	9.546	8.323	4.22E-04	6.71E-02	-1.99	-1.22
lpg2704	ubiquinol-cytochrome c reductase, cytochrome b	*petB*	Energy Metabolism	10.992	10.309	10.441	10.414	2.48E-01	9.24E-01	-0.68	-0.03
lpg2704	ubiquinol-cytochrome c reductase, cytochrome b	*petB*	Energy Metabolism	11.071	10.536	9.927	10.258	2.37E-01	3.45E-01	-0.53	0.33
lpg2705	ubiquinol-cytochrome c reductase, iron-sulfur subunit (Ri	*petA*	Energy Metabolism	12.853	12.686	11.751	12.334	6.74E-01	8.59E-02	-0.17	0.58
lpg2705	ubiquinol-cytochrome c reductase, iron-sulfur subunit (Ri	*petA*	Energy Metabolism	12.728	12.729	11.712	12.372	9.98E-01	5.47E-02	0.00	0.66
lpg2706	30S ribosomal protein S9		Translation	14.825	13.255	12.894	14.032	4.26E-03	2.19E-02	-1.57	1.14
lpg2706	30S ribosomal protein S9		Translation	14.577	13.171	12.823	13.974	4.90E-03	1.85E-02	-1.41	1.15
lpg2707	50S ribosomal protein L13	*rplM*	Translation	12.990	12.139	11.507	13.205	2.15E-01	2.43E-03	-0.85	1.70
lpg2707	50S ribosomal protein L13	*rplM*	Translation	13.171	12.097	11.410	13.194	9.82E-02	2.42E-03	-1.07	1.78

lpg2708	ferredoxin 2Fe-2S protein		Energy Metabolism	13.205	11.940	13.399	12.033	1.42E-01	7.27E-02	-1.27	-1.37
lpg2708	ferredoxin 2Fe-2S protein		Energy Metabolism	13.117	12.143	13.307	12.455	1.73E-02	1.19E-02	-0.97	-0.85
lpg2709	integration host factor (IHF) alpha subunit - recombinatio	*ihfA*	Transcription, Replication and Repair	11.518	10.046	12.770	10.147	1.47E-02	5.45E-03	-1.47	-2.62
lpg2709	integration host factor (IHF) alpha subunit - recombinatio	*ihfA*	Transcription, Replication and Repair	11.466	10.434	12.745	11.067	2.02E-02	5.08E-06	-1.03	-1.68
lpg2710	phenylalanyl tRNA synthetase, beta subunit	*pheT*	Amino Acid Metabolism, Translation	11.314	10.406	9.663	11.285	2.25E-01	9.44E-02	-0.91	1.62
lpg2710	phenylalanyl tRNA synthetase, beta subunit	*pheT*	Amino Acid Metabolism, Translation	11.331	11.054	9.954	11.857	5.49E-01	5.56E-03	-0.28	1.90
lpg2711	phenylalanyl tRNA synthetase, alpha subunit	*pheS*	Amino Acid Metabolism, Translation	11.291	11.428	9.150	11.952	8.19E-01	2.44E-02	0.14	2.80
lpg2711	phenylalanyl tRNA synthetase, alpha subunit	*pheS*	Amino Acid Metabolism, Translation	11.304	11.641	9.391	12.408	5.47E-01	9.65E-03	0.34	3.02
lpg2712	50S ribosomal protein L20	*rplT*	Translation	14.759	13.980	12.976	14.154	5.34E-01	3.05E-01	-0.78	1.18
lpg2712	50S ribosomal protein L20	*rplT*	Translation	14.327	14.434	12.577	14.521	8.83E-01	2.25E-02	0.11	1.94
lpg2713	translational initiation factor IF-3	*infC*	Translation	14.664	15.135	13.157	15.429	2.02E-01	3.05E-03	0.47	2.27
lpg2713	translational initiation factor IF-3	*infC*	Translation	14.746	15.109	13.163	15.448	3.94E-01	2.45E-03	0.36	2.28
lpg2714	threonyl tRNA synthase	*thrS*	Amino Acid Metabolism, Translation	11.936	11.723	11.733	11.543	4.16E-01	6.10E-01	-0.21	-0.19
lpg2714	threonyl tRNA synthase	*thrS*	Amino Acid Metabolism, Translation	11.966	11.605	11.674	11.744	2.64E-01	8.49E-01	-0.36	0.07
lpg2715	tRNA-Val		tRNA	10.962	7.855	9.512	8.786	3.21E-03	3.77E-01	-3.11	-0.73
lpg2715	tRNA-Val		tRNA	10.150	8.629	8.313	9.058	3.31E-01	6.29E-01	-1.52	0.74
lpg2716	small ORF (95aa) hypothetical		Unknown / hypothetical proteins	9.299	9.329	9.587	9.606	9.50E-01	9.62E-01	0.03	0.02
lpg2716	small ORF (95aa) hypothetical		Unknown / hypothetical proteins	9.518	10.055	9.173	10.104	4.32E-01	1.25E-01	0.54	0.93
lpg2717	small ORF (161aa)		ORFs of unknown function (unique)	9.452	8.928	8.702	9.597	3.21E-01	9.85E-02	-0.52	0.89
lpg2717	small ORF (161aa)		ORFs of unknown function (unique)	9.328	9.202	8.557	10.090	8.27E-01	4.28E-02	-0.13	1.53
lpg2718	ORF	*wipA*	ORFs of unknown function (unique)	10.649	9.355	9.024	8.901	4.16E-05	8.39E-01	-1.29	-0.12
lpg2718	ORF	*wipA*	ORFs of unknown function (unique)	10.342	8.739	8.330	8.614	7.23E-02	7.81E-01	-1.60	0.28
lpg2719	conserved hypothetical protein		Unknown / hypothetical proteins	9.031	8.027	12.062	8.175	1.57E-01	1.82E-03	-1.00	-3.89
lpg2719	conserved hypothetical protein		Unknown / hypothetical proteins	8.900	8.654	12.097	9.089	7.00E-01	1.62E-02	-0.25	-3.01
lpg2720	hypothetical protein		Unknown / hypothetical proteins	8.487	7.311	12.084	5.922	3.34E-01	2.07E-03	-1.18	-6.16
lpg2720	hypothetical protein		Unknown / hypothetical proteins	7.693	7.952	11.947	6.905	8.42E-01	1.39E-05	0.26	-5.04
lpg2721	glutamine amidotransferase		Amino Acid Metabolism, Nucleotide M	9.378	9.798	11.160	9.737	2.41E-01	8.27E-02	0.42	-1.42
lpg2721	glutamine amidotransferase		Amino Acid Metabolism, Nucleotide M	9.401	9.774	11.162	10.465	4.71E-01	2.42E-01	0.37	-0.70
lpg2722	NADH-dependent flavin oxidoreductase, Oye family (N-ethylmaleimid		Metabolism of Cofactors and Vitamins	12.274	13.205	11.931	13.861	4.14E-03	1.41E-06	0.93	1.93
lpg2722	NADH-dependent flavin oxidoreductase, Oye family (N-ethylmaleimid		Metabolism of Cofactors and Vitamins	12.274	13.166	11.856	13.849	6.99E-03	5.35E-06	0.89	1.99
lpg2723	transcriptional regulator (ArsR family)		Transcription factors / DNA binding pr	12.231	10.142	11.087	10.162	1.75E-02	5.35E-03	-2.09	-0.92
lpg2723	transcriptional regulator (ArsR family)		Transcription factors / DNA binding pr	12.515	10.064	10.893	10.188	5.03E-04	4.45E-02	-2.45	-0.71
lpg2724	small ORF (114aa)		ORFs of unknown function (unique)	10.118	10.427	11.277	10.243	3.95E-01	6.23E-02	0.31	-1.03
lpg2724	small ORF (114aa)		ORFs of unknown function (unique)	10.144	10.396	11.246	10.216	4.92E-01	7.93E-02	0.25	-1.03
lpg2725	inner membrane protein		Named proteins of general function	8.159	10.986	8.973	10.382	2.75E-03	1.78E-01	2.83	1.41
lpg2725	inner membrane protein		Named proteins of general function	7.923	11.563	8.821	11.659	1.67E-03	3.61E-02	3.64	2.84
lpg2726	peptidylprolyl cis-trans isomerase B (cyclophilin-type) Lc	*ppiB*	Cell envelope synthesis, Toxin product	12.298	10.059	11.959	11.515	1.91E-04	4.66E-02	-2.24	-0.44
lpg2726	peptidylprolyl cis-trans isomerase B (cyclophilin-type) Lc	*ppiB*	Cell envelope synthesis, Toxin product	12.230	9.821	12.017	11.587	1.01E-04	4.61E-02	-2.41	-0.43
lpg2727	queuine/archaeosine tRNA-ribosyltransferase (tRNA-gua	*tgt*	DNA/RNA degradation / restriction, Tr	11.271	10.068	10.079	11.726	2.02E-02	2.49E-02	-1.20	1.65
lpg2727	queuine/archaeosine tRNA-ribosyltransferase (tRNA-gua	*tgt*	DNA/RNA degradation / restriction, Tr	11.223	9.649	10.013	11.705	2.43E-02	4.64E-03	-1.57	1.69
lpg2728	ORF		ORFs of unknown function (unique)	11.762	10.424	11.831	10.486	2.67E-05	1.39E-02	-1.34	-1.34
lpg2728	ORF		ORFs of unknown function (unique)	11.783	10.426	11.749	10.438	4.48E-04	8.20E-03	-1.36	-1.31
lpg2729	protein-disulfide oxidoreductase (disulfide bond formatio	*dsbH*	Protein fate / hydrolases / secretion	11.577	11.310	10.238	11.202	3.52E-01	1.02E-01	-0.27	0.96
lpg2729	protein-disulfide oxidoreductase (disulfide bond formatio	*dsbH*	Protein fate / hydrolases / secretion	11.509	11.764	9.460	11.430	6.65E-01	2.45E-03	0.25	1.97
lpg2730	cytochrome c5	*cycB*	Energy Metabolism	12.845	13.377	12.543	13.670	9.22E-02	3.50E-04	0.53	1.13
lpg2730	cytochrome c5	*cycB*	Energy Metabolism	12.853	13.401	12.584	13.790	8.65E-02	2.84E-04	0.55	1.21
lpg2731	aminotransferase class II (8-amino-7-oxononanoate synthetase) (gly		Amino Acid Metabolism	9.907	9.897	10.362	9.470	9.82E-01	4.23E-01	-0.01	-0.89
lpg2731	aminotransferase class II (8-amino-7-oxononanoate synthetase) (gly		Amino Acid Metabolism	10.045	10.122	10.350	9.487	8.78E-01	3.73E-01	0.08	-0.86
lpg2732	(two component) response regulator		Signal transduction / other regulatory f	12.361	11.894	12.729	12.143	7.24E-02	3.63E-02	-0.47	-0.59
lpg2732	(two component) response regulator		Signal transduction / other regulatory f	12.409	11.855	12.784	12.218	8.64E-02	2.75E-02	-0.55	-0.57
lpg2733	hypothetical (transmembrane protein)		Named proteins of general function	10.804	11.109	13.161	10.748	5.18E-01	2.74E-03	0.30	-2.41
lpg2733	hypothetical (transmembrane protein)		Named proteins of general function	10.976	11.780	13.224	11.424	3.27E-02	6.36E-03	0.80	-1.80
lpg2734	sensor protein LuxN (transmembrane sensor histidine kinase/transcri		Signal transduction / other regulatory f	12.475	11.488	12.785	11.155	5.12E-03	1.07E-03	-0.99	-1.63
lpg2734	sensor protein LuxN (transmembrane sensor histidine kinase/transcri		Signal transduction / other regulatory f	12.455	11.639	12.720	11.319	1.12E-02	1.07E-03	-0.82	-1.40
lpg2735	porphobilinogen deaminase (hydroxymethylbilane synthesis)		Metabolism of Cofactors and Vitamins	10.931	11.280	9.816	11.200	4.71E-01	2.33E-02	0.35	1.38
lpg2735	porphobilinogen deaminase (hydroxymethylbilane synthesis)		Metabolism of Cofactors and Vitamins	10.780	11.236	9.248	11.345	4.21E-01	2.32E-03	0.46	2.10
lpg2736	uroporphyrinogen III methylase (uroporphyrinogen-III synthase)		Metabolism of Cofactors and Vitamins	11.643	10.555	11.630	11.587	1.12E-01	8.75E-01	-1.09	-0.04
lpg2736	uroporphyrinogen III methylase (uroporphyrinogen-III synthase)		Metabolism of Cofactors and Vitamins	11.691	10.972	11.428	11.611	7.58E-02	6.12E-01	-0.72	0.18
lpg2737	uroporphyrinogen III methylase (uroporphyrin-III C-methyltransferase		Metabolism of Cofactors and Vitamins	11.177	10.651	11.568	10.035	4.16E-01	7.41E-05	-0.53	-1.53
lpg2737	uroporphyrinogen III methylase (uroporphyrin-III C-methyltransferase		Metabolism of Cofactors and Vitamins	11.365	10.123	11.685	10.188	2.57E-04	4.77E-05	-1.24	-1.50
lpg2738	protoheme IX synthesis HemY	*hemY*	Metabolism of Cofactors and Vitamins	11.260	10.561	11.545	10.088	8.92E-02	7.06E-02	-0.70	-1.46
lpg2738	protoheme IX synthesis HemY	*hemY*	Metabolism of Cofactors and Vitamins	11.224	11.163	11.539	10.968	9.10E-01	4.88E-02	-0.06	-0.57
lpg2739	cation efflux system protein (cobalt zinc cadmium resistance protein		Transport and binding	11.679	10.206	11.886	10.457	4.21E-06	7.17E-05	-1.47	-1.43
lpg2739	cation efflux system protein (cobalt zinc cadmium resistance protein		Transport and binding	11.634	10.223	11.751	10.480	1.43E-05	2.60E-04	-1.41	-1.27

lpg2740	hypothetical (DNA integration/recombination/reversion protein?)		Viral functions / Phage / Transposases	13.186	11.825	13.148	12.664	1.93E-02	3.00E-02	-1.36	-0.48
lpg2740	hypothetical (DNA integration/recombination/reversion protein?)		Viral functions / Phage / Transposases	12.731	11.749	13.139	12.721	2.72E-03	4.44E-02	-0.98	-0.42
lpg2741	oligoribonuclease	*orn*	DNA/RNA degradation / restriction	11.411	9.367	12.085	10.988	8.26E-02	8.74E-02	-2.04	-1.10
lpg2741	oligoribonuclease	*orn*	DNA/RNA degradation / restriction	11.348	10.005	11.301	10.411	8.91E-03	2.35E-01	-1.34	-0.89
lpg2742	tRNA nucleotidyltransferase		Translation	10.233	9.076	11.033	9.495	8.81E-02	4.74E-03	-1.16	-1.54
lpg2742	tRNA nucleotidyltransferase		Translation	10.179	8.560	11.094	9.677	4.48E-02	3.46E-02	-1.62	-1.42
lpg2743	EngC GTPase (cell wall endoglucanase related?)		Cell envelope synthesis, Signal transd	11.178	11.030	11.602	11.182	5.52E-01	1.14E-01	-0.15	-0.42
lpg2743	EngC GTPase (cell wall endoglucanase related?)		Cell envelope synthesis, Signal transd	11.196	11.015	11.257	10.975	5.80E-01	2.18E-01	-0.18	-0.28
lpg2744	ORF		ORFs of unknown function (unique)	8.539	8.673	9.667	8.820	7.27E-01	5.92E-03	0.13	-0.85
lpg2744	ORF		ORFs of unknown function (unique)	7.582	9.531	9.415	9.527	2.01E-02	8.30E-01	1.95	0.11
lpg2745	ORF		ORFs of unknown function (unique)	9.618	8.684	7.948	8.994	1.27E-01	3.75E-01	-0.93	1.05
lpg2745	ORF		ORFs of unknown function (unique)	9.316	9.287	6.177	7.595	9.74E-01	3.80E-01	-0.03	1.42
lpg2752	tRNA-Ile		tRNA	11.583	11.727	10.975	12.220	8.01E-01	1.36E-02	0.14	1.24
lpg2752	tRNA-Ile		tRNA	11.564	11.758	10.898	12.239	7.65E-01	2.02E-02	0.19	1.34
lpg2753	16S rRNA		rRNA	15.476	15.607	15.627	15.617	5.61E-01	9.60E-01	0.13	-0.01
lpg2753	16S rRNA		rRNA	15.393	15.490	15.705	15.706	6.59E-01	9.96E-01	0.10	0.00
lpg2754	DNA polymerase III subunits gamma and tau	*dnaZX*	Nucleotide Metabolism, Replication an	12.705	12.852	12.485	13.653	4.90E-01	5.65E-06	0.15	1.17
lpg2754	DNA polymerase III subunits gamma and tau	*dnaZX*	Nucleotide Metabolism, Replication an	12.695	12.873	12.462	13.646	3.20E-01	2.72E-06	0.18	1.18
lpg2755	hypothetical (transcription regulatory protein TIGR00103?)		Transcription factors / DNA binding pro	13.166	12.390	12.889	12.438	4.50E-02	1.17E-01	-0.78	-0.45
lpg2755	hypothetical (transcription regulatory protein TIGR00103?)		Transcription factors / DNA binding pro	13.221	12.316	12.887	12.461	8.51E-03	1.60E-01	-0.90	-0.43
lpg2756	recombinational DNA repair protein RecR	*recR*	Replication and Repair	11.921	10.751	10.776	11.098	9.20E-03	5.84E-01	-1.17	0.32
lpg2756	recombinational DNA repair protein RecR	*recR*	Replication and Repair	11.887	10.664	10.602	11.224	7.13E-03	4.54E-01	-1.22	0.62
lpg2757	hypothetical protein		Unknown / hypothetical proteins	9.139	9.330	9.819	9.305	7.24E-01	8.12E-02	0.19	-0.51
lpg2757	hypothetical protein		Unknown / hypothetical proteins	8.633	9.191	9.538	9.450	2.26E-01	8.10E-01	0.56	-0.09
lpg2758	hypothetical protein		Unknown / hypothetical proteins	8.772	8.209	8.676	7.623	3.32E-01	2.93E-01	-0.56	-1.05
lpg2758	hypothetical protein		Unknown / hypothetical proteins	9.334	8.377	5.837	8.551	1.25E-01	8.48E-02	-0.96	2.71
lpg2759	ORF		ORFs of unknown function (unique)	8.680	9.412	8.619	8.435	6.88E-02	6.13E-01	0.73	-0.18
lpg2759	ORF		ORFs of unknown function (unique)	7.470	8.837	8.827	8.953	7.36E-02	7.78E-01	1.37	0.13
lpg2760	DNA-binding response regulator (two component response regulator)		Signal transduction / other regulatory f	11.749	11.957	11.101	10.529	4.48E-01	2.26E-01	0.21	-0.57
lpg2760	DNA-binding response regulator (two component response regulator)		Signal transduction / other regulatory f	11.739	12.035	11.192	10.706	2.36E-01	1.66E-01	0.30	-0.49
lpg2761	ORF		ORFs of unknown function (unique)	11.674	14.606	14.025	10.892	5.60E-03	6.87E-03	2.93	-3.13
lpg2761	ORF		ORFs of unknown function (unique)	11.820	14.556	13.681	11.258	7.11E-03	2.93E-02	2.74	-2.42
lpg2762	ORF		ORFs of unknown function (unique)	9.359	9.977	9.162	7.870	2.07E-02	1.92E-01	0.62	-1.29
lpg2762	ORF		ORFs of unknown function (unique)	9.584	10.119	9.170	8.187	1.65E-01	1.50E-01	0.53	-0.98
lpg2763	Mg2+ and Co2+ transporter CorB, hemolysin		Transport and binding, Toxin productio	11.339	11.325	12.455	11.530	9.61E-01	5.45E-03	-0.01	-0.92
lpg2763	Mg2+ and Co2+ transporter CorB, hemolysin		Transport and binding, Toxin productio	10.622	10.803	11.719	11.253	5.61E-01	2.04E-01	0.18	-0.47
lpg2764	inorganic pyrophosphatase	*ppa*	Named proteins of general function	12.403	12.922	9.396	12.440	5.22E-01	4.82E-03	0.52	3.04
lpg2764	inorganic pyrophosphatase	*ppa*	Named proteins of general function	12.641	12.977	9.149	12.457	5.42E-01	1.03E-02	0.34	3.31
lpg2765	HIT family hydrolase (e.g., diadenosine tetraphosphate h	*hit*	Protein fate / hydrolases / secretion, T	12.489	12.643	10.330	13.540	6.27E-01	1.42E-04	0.15	3.21
lpg2765	HIT family hydrolase (e.g., diadenosine tetraphosphate h	*hit*	Protein fate / hydrolases / secretion, T	12.297	12.566	10.213	13.480	5.19E-01	2.35E-04	0.27	3.27
lpg2766	GTP cyclohydrolase I	*folE2*	Metabolism of Cofactors and Vitamins	11.267	11.644	9.715	11.962	6.48E-01	1.20E-02	0.38	2.25
lpg2766	GTP cyclohydrolase I	*folE2*	Metabolism of Cofactors and Vitamins	11.682	11.628	9.723	12.366	9.13E-01	1.24E-02	-0.05	2.64
lpg2767	L-sorbosone dehydrogenase (membrane bound dehydrogenase oxid		Carbohydrate Metabolism, Lipid Metab	9.571	9.009	9.454	9.035	1.50E-01	4.71E-01	-0.56	-0.42
lpg2767	L-sorbosone dehydrogenase (membrane bound dehydrogenase oxid		Carbohydrate Metabolism, Lipid Metab	9.816	9.151	8.809	9.150	9.88E-02	7.07E-01	-0.67	0.34
lpg2768	polyribonucleotide nucleotidyltransferase (polynucleotide	*PNP*	Nucleotide Metabolism	13.287	11.053	10.194	13.933	2.49E-02	1.14E-03	-2.23	3.74
lpg2768	polyribonucleotide nucleotidyltransferase (polynucleotide	*PNP*	Nucleotide Metabolism	13.187	11.106	9.987	13.851	2.30E-02	9.81E-04	-2.08	3.86
lpg2769	30S ribosomal protein S15 (S15/S13E)	*rpsO*	Translation	13.509	11.369	10.157	12.961	3.13E-02	4.59E-02	-2.14	2.80
lpg2769	30S ribosomal protein S15 (S15/S13E)	*rpsO*	Translation	13.689	11.426	8.839	13.351	3.07E-02	2.03E-02	-2.26	4.51
lpg2770	tRNA pseudouridine synthase B		DNA/RNA degradation / restriction, Tra	10.694	9.135	10.780	9.859	3.34E-04	1.28E-01	-1.56	-0.92
lpg2770	tRNA pseudouridine synthase B		DNA/RNA degradation / restriction, Tra	10.834	8.690	9.908	10.310	1.22E-03	3.26E-01	-2.14	0.40
lpg2771	ribosome binding factor A	*rbfA*	Translation	12.482	9.662	8.689	11.740	1.02E-02	1.94E-02	-2.82	3.05
lpg2771	ribosome binding factor A	*rbfA*	Translation	12.339	9.958	8.860	11.927	3.25E-02	1.15E-02	-2.38	3.07
lpg2772	initiation factor IF2-beta (IF-2 gamma, IF-2 alpha)	*infB*	Translation	12.537	11.361	12.281	12.144	2.36E-02	5.16E-01	-1.18	-0.14
lpg2772	initiation factor IF2-beta (IF-2 gamma, IF-2 alpha)	*infB*	Translation	12.727	11.298	12.248	12.229	4.85E-04	9.20E-01	-1.43	-0.02
lpg2773	N utilization substance protein A (transcription pausing L	*nusA*	Protein fate / hydrolases / secretion, T	11.536	11.320	9.563	11.628	8.21E-01	1.96E-02	-0.22	2.06
lpg2773	N utilization substance protein A (transcription pausing L	*nusA*	Protein fate / hydrolases / secretion, T	11.624	11.499	9.409	11.507	8.74E-01	1.13E-02	-0.12	2.10
lpg2774	hypothetical COG 0779		Unknown / hypothetical proteins	12.842	11.078	10.995	12.899	1.77E-03	7.04E-03	-1.76	1.90
lpg2774	hypothetical COG 0779		Unknown / hypothetical proteins	12.664	10.918	10.954	12.880	1.78E-02	5.25E-03	-1.75	1.93
lpg2775	tRNA-Met		tRNA	11.295	9.306	11.266	9.751	5.01E-02	1.42E-02	-1.99	-1.52
lpg2775	tRNA-Met		tRNA	11.561	9.817	11.372	11.053	4.08E-02	7.63E-01	-1.74	-0.32
lpg2776	NADH dehydrogenase I, N subunit	*nuoN*	Metabolism of Cofactors and Vitamins	12.459	10.601	10.843	11.879	1.45E-02	3.98E-02	-1.86	1.04
lpg2776	NADH dehydrogenase I, N subunit	*nuoN*	Metabolism of Cofactors and Vitamins	12.476	10.776	10.854	11.968	1.76E-02	3.34E-02	-1.70	1.11
lpg2777	NADH dehydrogenase I, M subunit	*nuoM*	Metabolism of Cofactors and Vitamins	13.193	11.750	11.731	12.484	3.78E-05	6.50E-02	-1.44	0.75
lpg2777	NADH dehydrogenase I, M subunit	*nuoM*	Metabolism of Cofactors and Vitamins	13.179	11.763	11.742	12.543	3.35E-04	6.91E-02	-1.42	0.80

lpg2778	NADH dehydrogenase I, L subunit (NADH-ubiquinone ox	*nuoL*	Metabolism of Cofactors and Vitamins	12.621	10.952	10.101	10.856	6.60E-04	5.69E-01	-1.67	0.76
lpg2778	NADH dehydrogenase I, L subunit (NADH-ubiquinone ox	*nuoL*	Metabolism of Cofactors and Vitamins	12.683	10.673	10.526	11.590	3.33E-03	2.69E-01	-2.01	1.06
lpg2779	NADH dehydrogenase I, K subunit (NADH-ubiquinone o	*nuoK*	Metabolism of Cofactors and Vitamins	11.941	9.587	10.346	10.788	1.07E-02	4.64E-01	-2.35	0.44
lpg2779	NADH dehydrogenase I, K subunit (NADH-ubiquinone o	*nuoK*	Metabolism of Cofactors and Vitamins	11.869	9.642	9.955	10.859	1.49E-02	2.10E-01	-2.23	0.90
lpg2780	NADH dehydrogenase I, J subunit (NADH-ubiquinone/pl	*nuoJ+G563*	Metabolism of Cofactors and Vitamins	12.080	10.546	10.543	10.969	7.56E-02	5.29E-01	-1.53	0.43
lpg2780	NADH dehydrogenase I, J subunit (NADH-ubiquinone/pl	*nuoJ+G563*	Metabolism of Cofactors and Vitamins	12.074	11.224	10.532	11.790	1.03E-01	2.89E-02	-0.85	1.26
lpg2781	NADH dehydrogenase I, I subunit (NADH-ubiquinone oxi	*nuoI*	Metabolism of Cofactors and Vitamins	12.178	10.217	10.444	10.862	2.31E-03	4.41E-01	-1.96	0.42
lpg2781	NADH dehydrogenase I, I subunit (NADH-ubiquinone oxi	*nuoI*	Metabolism of Cofactors and Vitamins	11.924	10.644	10.040	11.428	6.07E-02	4.65E-02	-1.28	1.39
lpg2782	NADH dehydrogenase I, H subunit (NADH-ubiquinone o	*nuoH*	Metabolism of Cofactors and Vitamins	12.966	11.869	10.661	12.261	4.37E-02	2.91E-02	-1.10	1.60
lpg2782	NADH dehydrogenase I, H subunit (NADH-ubiquinone o	*nuoH*	Metabolism of Cofactors and Vitamins	12.636	11.788	10.492	12.211	2.73E-01	2.13E-02	-0.85	1.72
lpg2783	NADH dehydrogenase I, G subunit (ferredoxin:prokaryoti	*nuoG*	Metabolism of Cofactors and Vitamins	13.864	12.888	12.080	12.932	1.83E-01	4.28E-01	-0.98	0.85
lpg2783	NADH dehydrogenase I, G subunit (ferredoxin:prokaryoti	*nuoG*	Metabolism of Cofactors and Vitamins	13.858	12.749	12.132	13.289	1.83E-01	1.20E-01	-1.11	1.16
lpg2784	NADH dehydrogenase I, F subunit (respiratory chain NA	*nuoF*	Metabolism of Cofactors and Vitamins	13.606	12.912	13.544	13.322	5.32E-02	2.77E-01	-0.69	-0.22
lpg2784	NADH dehydrogenase I, F subunit (respiratory chain NA	*nuoF*	Metabolism of Cofactors and Vitamins	13.594	12.844	13.487	13.302	5.38E-02	3.67E-01	-0.75	-0.18
lpg2785	NADH dehydrogenase I, E subunit (ubiquinone) flavoprotein 2, 24 kD		Metabolism of Cofactors and Vitamins	12.190	10.776	10.341	10.972	1.09E-02	5.24E-01	-1.41	0.63
lpg2785	NADH dehydrogenase I, E subunit (ubiquinone) flavoprotein 2, 24 kD		Metabolism of Cofactors and Vitamins	12.118	10.847	10.236	11.175	2.82E-02	2.66E-01	-1.27	0.94
lpg2786	NADH dehydrogenase I, D subunit (NADH-ubiquinone o	*nuoD*	Metabolism of Cofactors and Vitamins	13.466	12.857	10.732	13.038	2.85E-01	2.19E-03	-0.61	2.31
lpg2786	NADH dehydrogenase I, D subunit (NADH-ubiquinone o	*nuoD*	Metabolism of Cofactors and Vitamins	13.478	12.824	10.590	13.037	2.29E-01	1.84E-03	-0.65	2.45
lpg2787	NADH dehydrogenase I, C subunit (NADH-ubiquinone o	*nuoC*	Metabolism of Cofactors and Vitamins	13.756	12.260	12.420	11.892	9.83E-02	7.01E-01	-1.50	-0.53
lpg2787	NADH dehydrogenase I, C subunit (NADH-ubiquinone o	*nuoC*	Metabolism of Cofactors and Vitamins	13.808	12.505	12.423	12.225	7.48E-02	8.40E-01	-1.30	-0.20
lpg2788	NADH dehydrogenase I, B subunit (NADH-ubiquinone o	*nuoB2*	Metabolism of Cofactors and Vitamins	13.564	13.106	12.008	13.144	1.74E-01	4.42E-02	-0.46	1.14
lpg2788	NADH dehydrogenase I, B subunit (NADH-ubiquinone o	*nuoB2*	Metabolism of Cofactors and Vitamins	13.424	13.011	11.897	13.106	3.02E-01	4.10E-02	-0.41	1.21
lpg2789	NADH dehydrogenase I, A subunit (NADH-ubiquinone/pl	*nuoA*	Metabolism of Cofactors and Vitamins	11.734	11.387	9.978	11.355	3.63E-01	1.02E-02	-0.35	1.38
lpg2789	NADH dehydrogenase I, A subunit (NADH-ubiquinone/pl	*nuoA*	Metabolism of Cofactors and Vitamins	11.721	11.328	10.017	11.448	3.87E-01	8.43E-03	-0.39	1.43
lpg2790	tRNA-Leu		tRNA	10.988	10.670	11.728	10.804	6.16E-01	3.59E-02	-0.32	-0.92
lpg2790	tRNA-Leu		tRNA	11.333	10.662	11.607	10.783	1.63E-01	5.17E-02	-0.67	-0.82
lpg2791	preprotein translocase, SecG subunit	*secG*	Protein fate / hydrolases / secretion	12.823	12.477	11.157	12.654	6.06E-01	4.91E-03	-0.35	1.50
lpg2791	preprotein translocase, SecG subunit	*secG*	Protein fate / hydrolases / secretion	12.071	12.378	11.036	12.639	8.33E-01	4.36E-03	0.31	1.60
lpg2792	triosephosphate isomerase (TIM)	*tpiA*	Carbohydrate Metabolism, Metabolis	11.972	13.017	9.817	13.385	1.18E-01	6.30E-05	1.04	3.57
lpg2792	triosephosphate isomerase (TIM)	*tpiA*	Carbohydrate Metabolism, Metabolis	12.587	13.001	9.495	13.390	5.88E-02	1.37E-04	0.41	3.90
lpg2793	LepA, interaptin	*lepA*	Named proteins of general function	12.566	14.607	13.155	12.349	2.35E-05	5.29E-03	2.04	-0.81
lpg2793	LepA, interaptin	*lepA*	Named proteins of general function	12.588	14.687	13.203	12.457	1.68E-05	3.42E-03	2.10	-0.75
lpg2794	phosphoglucomutase/phosphomannomutase MrsA	*mrsA*	Carbohydrate Metabolism, Biosynthes	12.867	11.510	12.985	12.703	2.15E-04	4.74E-02	-1.36	-0.28
lpg2794	phosphoglucomutase/phosphomannomutase MrsA	*mrsA*	Carbohydrate Metabolism, Biosynthes	12.867	11.529	12.989	12.730	2.68E-04	8.62E-02	-1.34	-0.26
lpg2795	7,8-dihydropteroate synthase		Metabolism of Cofactors and Vitamins	11.888	9.384	10.312	10.092	2.58E-02	7.88E-01	-2.50	-0.22
lpg2795	7,8-dihydropteroate synthase		Metabolism of Cofactors and Vitamins	11.762	9.115	10.083	9.883	2.87E-04	7.08E-01	-2.65	-0.20
lpg2796	cell division protein FtsH (ATP dependent zinc protease)	*ftsH*	Protein fate / hydrolases / secretion, C	12.421	11.732	12.712	12.043	7.48E-03	1.05E-02	-0.69	-0.67
lpg2796	cell division protein FtsH (ATP dependent zinc protease)	*ftsH*	Protein fate / hydrolases / secretion, C	12.429	11.819	12.701	12.077	2.85E-02	1.38E-02	-0.61	-0.62
lpg2797	ribosomal RNA large subunit methyltransferase J (cell division protein		Protein fate / hydrolases / secretion, C	9.522	10.854	9.451	10.629	6.41E-04	9.61E-04	1.33	1.18
lpg2797	ribosomal RNA large subunit methyltransferase J (cell division protein		Protein fate / hydrolases / secretion, C	10.299	11.689	9.927	11.959	4.06E-02	1.87E-02	1.39	2.03
lpg2798	RNA-binding protein containing KH domain COG1534, putative pseu		Named proteins of general function	9.978	9.281	8.143	9.706	3.48E-01	1.28E-01	-0.70	1.56
lpg2798	RNA-binding protein containing KH domain COG1534, putative pseu		Named proteins of general function	10.119	10.300	8.487	10.185	7.17E-01	3.98E-02	0.18	1.70
lpg2799	O-acetyltransferase (O-antigen acetylase) (lipopolysaccharide modifi		Metabolism of Complex Lipids	10.141	8.812	9.387	9.960	1.38E-02	4.42E-01	-1.33	0.57
lpg2799	O-acetyltransferase (O-antigen acetylase) (lipopolysaccharide modifi		Metabolism of Complex Lipids	10.189	9.121	9.150	9.935	4.96E-02	2.78E-01	-1.07	0.78
lpg2800	FrgA (siderophore biosynthetic protein, iron repressed ge	*frgA*	Toxin production / other pathogen func	10.062	9.929	10.206	10.444	8.35E-01	5.04E-01	-0.13	0.24
lpg2800	FrgA (siderophore biosynthetic protein, iron repressed ge	*frgA*	Toxin production / other pathogen func	10.230	10.262	10.148	10.527	9.58E-01	4.00E-01	0.03	0.38
lpg2801	phosphatidylglycerophosphate synthase (CDP-diacylglycerol-glycerol		Metabolism of Complex Lipids	11.191	10.458	11.127	11.077	2.18E-01	7.99E-01	-0.73	-0.05
lpg2801	phosphatidylglycerophosphate synthase (CDP-diacylglycerol-glycerol		Metabolism of Complex Lipids	10.826	10.635	10.163	10.938	6.62E-01	2.05E-01	-0.19	0.78
lpg2802	DnaA-like family protein (chromosomal replication initiation)		Replication and Repair	11.217	10.176	9.666	11.219	1.25E-02	5.07E-03	-1.04	1.55
lpg2802	DnaA-like family protein (chromosomal replication initiation)		Replication and Repair	11.204	10.234	9.484	11.124	3.85E-02	1.47E-02	-0.97	1.64
lpg2803	ORF		ORFs of unknown function (unique)	10.474	8.854	13.763	8.627	1.42E-01	2.57E-03	-1.62	-5.14
lpg2803	ORF		ORFs of unknown function (unique)	10.403	7.894	13.750	9.216	9.03E-02	1.93E-03	-2.51	-4.53
lpg2804	ORF		ORFs of unknown function (unique)	11.431	10.999	12.321	10.805	3.85E-01	1.85E-02	-0.43	-1.52
lpg2804	ORF		ORFs of unknown function (unique)	11.380	11.257	12.314	10.866	7.62E-01	1.43E-02	-0.12	-1.45
lpg2805	peptide transport protein (proton dependent peptide trans	*yhiP*	Transport and binding	13.069	12.266	11.849	10.814	1.06E-02	2.49E-03	-0.80	-1.04
lpg2805	peptide transport protein (proton dependent peptide trans	*yhiP*	Transport and binding	13.054	12.247	11.849	10.888	1.13E-02	4.30E-04	-0.81	-0.96
lpg2806	ORF		ORFs of unknown function (unique)	9.475	10.239	10.510	9.810	3.23E-01	4.76E-01	0.76	-0.70
lpg2806	ORF		ORFs of unknown function (unique)	9.249	10.002	10.150	9.592	3.57E-01	6.25E-01	0.75	-0.56
lpg2807	patatin family protein (lipid acyl hydrolase?)		Protein fate / hydrolases / secretion	12.257	11.605	12.991	11.984	1.42E-02	4.16E-03	-0.65	-1.01
lpg2807	patatin family protein (lipid acyl hydrolase?)		Protein fate / hydrolases / secretion	12.242	11.361	13.010	12.079	2.54E-02	1.99E-03	-0.88	-0.93
lpg2808	shikimate-5-dehydrogenase	*aroE*	Amino Acid Metabolism	12.081	11.886	13.030	11.984	7.35E-01	1.03E-01	-0.19	-1.05
lpg2808	shikimate-5-dehydrogenase	*aroE*	Amino Acid Metabolism	11.925	11.997	13.023	12.122	8.91E-01	1.44E-01	0.07	-0.90
lpg2809	aminopeptidase N	*pepN*	Metabolism of Other Amino Acids	11.938	12.729	11.119	12.998	5.04E-04	7.64E-05	0.79	1.88
lpg2809	aminopeptidase N	*pepN*	Metabolism of Other Amino Acids	11.703	12.780	10.813	13.033	2.59E-03	9.70E-05	1.08	2.22

lpg2810	serine protein kinase	*prkA*	Amino Acid Metabolism	12.575	13.415	14.000	12.866	6.47E-04	7.17E-03	0.84	-1.13
lpg2810	serine protein kinase	*prkA*	Amino Acid Metabolism	12.606	13.407	13.979	12.889	1.74E-03	8.57E-03	0.80	-1.09
lpg2811	hypothetical (glycosyltransferase?)		Unknown / hypothetical proteins	11.601	10.727	12.073	10.909	1.89E-03	1.65E-04	-0.87	-1.16
lpg2811	hypothetical (glycosyltransferase?)		Unknown / hypothetical proteins	11.715	10.835	11.993	11.037	7.22E-03	2.37E-04	-0.88	-0.96
lpg2812	sporulation protein (stage V sporulation protein, SpoVR like family prc		Chemotaxis / motility / cell division	11.756	10.791	12.826	11.267	2.11E-02	2.11E-05	-0.97	-1.56
lpg2812	sporulation protein (stage V sporulation protein, SpoVR like family prc		Chemotaxis / motility / cell division	11.840	10.865	12.845	11.332	3.69E-02	1.15E-05	-0.97	-1.51
lpg2813	ORF	*vipE*	ORFs of unknown function (unique)	10.109	10.610	12.447	10.735	5.87E-01	9.09E-02	0.50	-1.71
lpg2813	ORF	*vipE*	ORFs of unknown function (unique)	9.976	10.727	12.048	10.803	4.28E-01	3.21E-01	0.75	-1.25
lpg2814	aminopeptidase (leucine aminopeptidase)		Amino Acid Metabolism	13.456	12.496	11.515	11.911	2.22E-01	6.54E-01	-0.96	0.40
lpg2814	aminopeptidase (leucine aminopeptidase)		Amino Acid Metabolism	13.530	13.148	11.493	12.587	2.81E-01	1.40E-02	-0.38	1.09
lpg2815	ORF		ORFs of unknown function (unique)	9.909	10.692	9.082	11.312	1.64E-02	7.51E-04	0.78	2.23
lpg2815	ORF		ORFs of unknown function (unique)	10.138	10.796	8.706	11.376	1.24E-02	4.80E-03	0.66	2.67
lpg2816	ATP-dependent DNA helicase Rep	*rep*	Replication and Repair	10.451	10.197	11.733	9.938	7.57E-01	3.50E-03	-0.25	-1.79
lpg2816	ATP-dependent DNA helicase Rep	*rep*	Replication and Repair	10.629	9.252	10.192	10.384	9.64E-02	8.54E-01	-1.38	0.19
lpg2817	heat shock protein 33, redox regulated chaperonin	*yrfI*	Detoxification / adaptation, Protein fate	10.315	9.542	10.527	8.644	8.84E-02	7.43E-02	-0.77	-1.88
lpg2817	heat shock protein 33, redox regulated chaperonin	*yrfI*	Detoxification / adaptation, Protein fate	10.291	9.215	10.428	9.238	7.75E-03	1.17E-01	-1.08	-1.19
lpg2818	conserved hypothetical protein		Unknown / hypothetical proteins	11.975	11.592	13.446	10.671	6.10E-01	9.38E-04	-0.38	-2.78
lpg2818	conserved hypothetical protein		Unknown / hypothetical proteins	11.929	12.235	13.448	11.514	2.24E-01	2.98E-03	0.31	-1.93
lpg2819	tyrosine phosphatase II superfamily protein (myo-inositol hexaphosph		Amino Acid Metabolism, Metabolism o	8.440	8.210	8.685	9.374	7.22E-01	2.19E-01	-0.23	0.69
lpg2819	tyrosine phosphatase II superfamily protein (myo-inositol hexaphosph		Amino Acid Metabolism, Metabolism o	8.662	8.457	8.774	9.654	6.68E-01	1.93E-01	-0.21	0.88
lpg2820	aldo/keto reductase (oxidoreductase)		Named proteins of general function	10.063	9.351	11.927	8.652	1.76E-01	6.10E-03	-0.71	-3.27
lpg2820	aldo/keto reductase (oxidoreductase)		Named proteins of general function	9.659	9.561	11.892	9.808	8.71E-01	2.39E-03	-0.10	-2.08
lpg2821	sugar kinase		Named proteins of general function	8.313	9.174	9.609	7.715	1.55E-01	1.65E-01	0.86	-1.89
lpg2821	sugar kinase		Named proteins of general function	7.954	8.738	8.689	8.114	2.34E-01	3.83E-01	0.78	-0.58
lpg2822	virulence regulator BipA (GTP binding protein type A) me	*bipA*	Toxin production / other pathogen func	11.245	11.768	10.628	12.601	1.04E-02	6.60E-05	0.52	1.97
lpg2822	virulence regulator BipA (GTP binding protein type A) me	*bipA*	Toxin production / other pathogen func	11.175	11.736	10.547	12.569	1.96E-02	3.71E-05	0.56	2.02
lpg2823	sugar kinase (inorganic polyphosphate/ATP-NAD kinase)		Metabolism of Cofactors and Vitamins	10.788	10.754	9.160	11.561	9.26E-01	2.78E-03	-0.03	2.40
lpg2823	sugar kinase (inorganic polyphosphate/ATP-NAD kinase)		Metabolism of Cofactors and Vitamins	10.981	10.682	9.102	11.630	5.53E-01	4.10E-03	-0.30	2.53
lpg2824	DNA repair protein RecN	*recN*	Replication and Repair	11.205	10.440	10.238	10.373	7.47E-02	7.76E-01	-0.76	0.13
lpg2824	DNA repair protein RecN	*recN*	Replication and Repair	11.115	9.801	10.226	10.591	9.15E-04	4.33E-01	-1.31	0.37
lpg2825	cold shock protein CspE		Detoxification / adaptation	13.687	12.029	12.052	11.462	5.51E-03	1.01E-01	-1.66	-0.59
lpg2825	cold shock protein CspE		Detoxification / adaptation	13.758	12.057	11.908	11.450	3.00E-03	2.15E-01	-1.70	-0.46
lpg2826	unknown		Unknown / hypothetical proteins	8.515	9.048	9.784	9.142	3.30E-01	5.36E-02	0.53	-0.64
lpg2826	unknown		Unknown / hypothetical proteins	8.688	9.360	9.413	9.125	1.05E-01	5.22E-01	0.67	-0.29
lpg2827	conserved hypothetical protein		Unknown / hypothetical proteins	10.560	9.782	11.634	9.126	2.12E-01	1.12E-02	-0.78	-2.51
lpg2827	conserved hypothetical protein		Unknown / hypothetical proteins	10.578	10.521	11.575	10.282	9.24E-01	2.63E-02	-0.06	-1.29
lpg2828	ORF		ORFs of unknown function (unique)	11.223	12.612	11.318	9.520	3.89E-02	5.74E-02	1.39	-1.80
lpg2828	ORF		ORFs of unknown function (unique)	11.027	12.456	11.235	10.291	3.49E-02	2.29E-04	1.43	-0.94
lpg2829	SidH (myosin-like protein)	*sidH*	Named proteins of general function	9.702	6.627	12.322	7.165	2.50E-02	4.51E-03	-3.07	-5.16
lpg2829	SidH (myosin-like protein)	*sidH*	Named proteins of general function	10.403	9.390	12.298	9.375	3.75E-01	2.19E-02	-1.01	-2.92
lpg2830	ORF	*legU2*	ORFs of unknown function (unique)	10.382	11.307	10.951	10.367	2.29E-02	1.12E-01	0.93	-0.58
lpg2830	ORF	*legU2*	ORFs of unknown function (unique)	10.438	11.351	10.964	10.432	3.18E-02	1.75E-01	0.91	-0.53
lpg2831	unknown	*vipD*	Unknown / hypothetical proteins	9.881	10.387	13.048	10.656	4.99E-01	6.37E-03	0.51	-2.39
lpg2831	unknown	*vipD*	Unknown / hypothetical proteins	9.816	10.127	12.933	10.626	6.95E-01	8.35E-03	0.31	-2.31
lpg2832	hypothetical		Unknown / hypothetical proteins	12.345	9.448	10.864	9.264	1.94E-02	3.72E-01	-2.90	-1.60
lpg2832	hypothetical		Unknown / hypothetical proteins	12.256	8.696	10.708	9.941	1.29E-03	3.30E-01	-3.56	-0.77
lpg2833	acyl-CoA thioester hydrolase	*yciA*	Protein fate / hydrolases / secretion	12.774	12.249	12.415	12.574	4.68E-02	4.56E-01	-0.53	0.16
lpg2833	acyl-CoA thioester hydrolase	*yciA*	Protein fate / hydrolases / secretion	12.696	12.199	12.297	12.576	8.45E-02	3.24E-01	-0.50	0.28
lpg2834	transcription accessory protein (S1 RNA binding domain)		Transcription	12.577	12.177	12.723	13.317	2.07E-01	4.05E-02	-0.40	0.59
lpg2834	transcription accessory protein (S1 RNA binding domain)		Transcription	12.565	12.266	12.700	13.497	2.52E-01	7.52E-03	-0.30	0.80
lpg2835	thiopurine S-methyltransferase	*tpm*	Nucleotide Metabolism	13.230	12.988	13.284	13.157	3.42E-01	4.39E-01	-0.24	-0.13
lpg2835	thiopurine S-methyltransferase	*tpm*	Nucleotide Metabolism	13.186	12.968	13.222	13.168	3.81E-01	7.21E-01	-0.22	-0.05
lpg2836	glucosamine-fructose-6-phosphate aminotransferase, isc	*glmS*	Amino Acid Metabolism, Metabolism o	12.846	13.009	12.944	13.153	3.10E-01	1.64E-01	0.16	0.21
lpg2836	glucosamine-fructose-6-phosphate aminotransferase, isc	*glmS*	Amino Acid Metabolism, Metabolism o	12.830	12.970	12.882	13.142	3.43E-01	6.25E-02	0.14	0.26
lpg2837	lysophospholipase A (GDSL-motif lipase/hydrolase?)		Protein fate / hydrolases / secretion	12.788	11.657	13.348	9.857	9.63E-04	3.21E-07	-1.13	-3.49
lpg2837	lysophospholipase A (GDSL-motif lipase/hydrolase?)		Protein fate / hydrolases / secretion	12.757	11.651	13.354	10.179	2.25E-03	3.13E-07	-1.11	-3.18
lpg2838	rhodanese domain protein (sulfuryltransferase), ubiquitin C-terminal h		Protein fate / hydrolases / secretion	12.713	12.119	10.666	12.451	2.95E-01	4.25E-03	-0.59	1.79
lpg2838	rhodanese domain protein (sulfuryltransferase), ubiquitin C-terminal h		Protein fate / hydrolases / secretion	12.643	12.110	10.363	12.431	4.15E-01	6.01E-03	-0.53	2.07
lpg2839	SsrA (tmRNA) binding protein (small protein B), protein q	*smpB*	Protein fate / hydrolases / secretion, S	10.886	9.866	9.049	11.452	1.45E-01	6.62E-04	-1.02	2.40
lpg2839	SsrA (tmRNA) binding protein (small protein B), protein q	*smpB*	Protein fate / hydrolases / secretion, S	11.087	10.165	8.815	11.501	5.45E-02	5.46E-04	-0.92	2.69
lpg2840	AhpC/TSA family protein (bacterioferritin comigratory protein), antioxi		Detoxification / adaptation	12.550	12.742	11.002	13.031	7.40E-01	3.79E-03	0.19	2.03
lpg2840	AhpC/TSA family protein (bacterioferritin comigratory protein), antioxi		Detoxification / adaptation	12.615	13.231	9.980	13.494	3.90E-01	1.09E-02	0.62	3.51
lpg2841	major facilitator superfamily (multi-drug resistance translocator, bicycl		Transport and binding, Toxin productio	9.249	8.924	8.185	8.410	6.17E-01	8.29E-01	-0.33	0.22
lpg2841	major facilitator superfamily (multi-drug resistance translocator, bicycl		Transport and binding, Toxin productio	9.589	9.041	7.751	8.904	5.13E-02	1.43E-01	-0.55	1.15

lpg2842	PhoH protein (ATPase) (phosphate starvation inducible protein)		Detoxification / adaptation	11.911	11.731	11.794	12.017	6.22E-01	3.61E-01	-0.18	0.22
lpg2842	PhoH protein (ATPase) (phosphate starvation inducible protein)		Detoxification / adaptation	11.957	11.695	11.659	11.956	4.22E-01	2.30E-01	-0.26	0.30
lpg2843	inosine 5'-monophosphate dehydrogenase (guanosine monophospha		Nucleotide Metabolism	6.052	6.627	8.348	7.570	8.37E-01	6.81E-01	0.57	-0.78
lpg2843	inosine 5'-monophosphate dehydrogenase (guanosine monophospha		Nucleotide Metabolism	7.620	9.219	6.536	10.285	2.17E-01	1.82E-02	1.60	3.75
lpg2844	proteophosphoglycan, membrane associated (mucin?)		Named proteins of general function	12.622	12.817	15.086	12.787	8.93E-01	3.44E-03	0.20	-2.30
lpg2844	proteophosphoglycan, membrane associated (mucin?)		Named proteins of general function	12.574	14.089	15.205	12.933	2.29E-02	1.19E-03	1.52	-2.27
lpg2845	esterase		ORFs of unknown function (unique)	11.293	11.968	11.950	12.701	7.08E-02	2.33E-02	0.68	0.75
lpg2845	esterase		ORFs of unknown function (unique)	11.231	11.955	11.851	12.649	5.50E-02	3.28E-02	0.72	0.80
lpg2846	small ORF (77aa)		ORFs of unknown function (unique)	11.529	10.622	12.280	10.804	7.38E-02	1.19E-03	-0.91	-1.48
lpg2846	small ORF (77aa)		ORFs of unknown function (unique)	11.393	10.708	12.190	10.891	1.89E-01	2.74E-03	-0.69	-1.30
lpg2847	hypothetical protein		Unknown / hypothetical proteins	11.880	12.459	11.762	12.214	1.38E-02	5.40E-02	0.58	0.45
lpg2847	hypothetical protein		Unknown / hypothetical proteins	11.881	12.670	11.693	12.371	1.72E-04	1.08E-03	0.79	0.68
lpg2848	ribonuclease (T2 family)		DNA/RNA degradation / restriction	11.493	10.835	11.086	9.948	2.20E-01	2.99E-04	-0.66	-1.14
lpg2848	ribonuclease (T2 family)		DNA/RNA degradation / restriction	11.510	10.888	11.075	9.992	1.99E-01	1.23E-04	-0.62	-1.08
lpg2849	hypothetical (bacteriophage glycoprotein?)		Viral functions / Phage / Transposases	9.761	9.006	11.210	8.760	3.05E-02	4.36E-04	-0.76	-2.45
lpg2849	hypothetical (bacteriophage glycoprotein?)		Viral functions / Phage / Transposases	9.693	9.044	11.136	8.922	9.67E-02	7.47E-04	-0.65	-2.21
lpg2850	cold shock transcriptional regulator CspA		Detoxification / adaptation, Transcriptio	12.020	11.248	12.696	10.968	9.73E-02	1.17E-06	-0.77	-1.73
lpg2850	cold shock transcriptional regulator CspA		Detoxification / adaptation, Transcriptio	11.931	10.637	12.624	10.985	1.35E-03	8.38E-06	-1.29	-1.64
lpg2851	protoporphyrinogen oxidase	*hemG*	Named proteins of general function	9.237	7.677	9.417	8.116	1.93E-01	6.57E-02	-1.56	-1.30
lpg2851	protoporphyrinogen oxidase	*hemG*	Named proteins of general function	9.248	7.311	9.228	8.077	1.45E-02	2.64E-01	-1.94	-1.15
lpg2852	amidase (6-aminohexanoate-cyclic dimer hydrolase)	*amic*	Amino Acid Metabolism, Metabolism o	10.526	9.200	11.474	8.998	4.57E-02	7.93E-04	-1.33	-2.48
lpg2852	amidase (6-aminohexanoate-cyclic dimer hydrolase)	*amic*	Amino Acid Metabolism, Metabolism o	10.428	9.123	11.031	8.882	6.16E-02	1.10E-03	-1.31	-2.15
lpg2853	hypothetical protein		Unknown / hypothetical proteins	11.084	10.231	10.121	10.117	1.59E-01	9.93E-01	-0.85	0.00
lpg2853	hypothetical protein		Unknown / hypothetical proteins	11.304	11.333	10.354	11.349	9.25E-01	1.31E-01	0.03	1.00
lpg2854	hypothetical (major royal jelly protein 3-like), KQDN repeats		Signal transduction / other regulatory f	8.845	8.330	9.153	8.785	7.15E-01	5.75E-01	-0.51	-0.37
lpg2854	hypothetical (major royal jelly protein 3-like), KQDN repeats		Signal transduction / other regulatory f	9.038	8.829	8.384	8.841	6.65E-01	3.59E-01	-0.21	0.46
lpg2855	TPR (repeat) domain protein, protein-protein interactions		Signal transduction / other regulatory f	10.910	8.870	9.073	9.329	9.02E-04	6.91E-01	-2.04	0.26
lpg2855	TPR (repeat) domain protein, protein-protein interactions		Signal transduction / other regulatory f	10.935	9.932	9.298	9.836	2.67E-01	4.68E-01	-1.00	0.54
lpg2856	hypothetical (von Willebrand factor type A domain protein), regulatory		Signal transduction / other regulatory f	10.777	10.045	9.949	11.006	5.05E-02	3.45E-02	-0.73	1.06
lpg2856	hypothetical (von Willebrand factor type A domain protein), regulatory		Signal transduction / other regulatory f	10.072	9.961	10.001	11.227	9.09E-01	7.52E-03	-0.11	1.23
lpg2857	small ORF (130aa) hypothetical		Unknown / hypothetical proteins	10.474	8.893	9.637	9.747	3.70E-03	8.14E-01	-1.58	0.11
lpg2857	small ORF (130aa) hypothetical		Unknown / hypothetical proteins	10.484	9.318	9.519	10.228	7.52E-04	2.69E-01	-1.17	0.71
lpg2858	conserved hypothetical protein		Unknown / hypothetical proteins	12.748	10.014	10.489	11.263	1.15E-01	4.84E-01	-2.73	0.77
lpg2858	conserved hypothetical protein		Unknown / hypothetical proteins	12.036	10.995	10.324	11.383	1.16E-01	5.31E-02	-1.04	1.06
lpg2859	MoxR protein (ATPase) methanol dehydrogenase regulatory protein		Signal transduction / other regulatory f	7.417	8.370	8.446	6.879	5.21E-01	2.71E-02	0.95	-1.57
lpg2859	MoxR protein (ATPase) methanol dehydrogenase regulatory protein		Signal transduction / other regulatory f	6.836	7.353	8.526	7.823	7.67E-01	3.92E-01	0.52	-0.70
lpg2860	small ORF (158aa)		ORFs of unknown function (unique)	11.661	10.759	10.551	11.260	8.53E-02	1.66E-01	-0.90	0.71
lpg2860	small ORF (158aa)		ORFs of unknown function (unique)	11.498	11.468	10.645	11.471	9.71E-01	1.01E-01	-0.03	0.83
lpg2861	nitrogen regulation protein (transcriptional regulator involved in nitroge		Transcription factors / DNA binding pro	11.506	10.529	11.151	10.989	1.84E-02	6.19E-01	-0.98	-0.16
lpg2861	nitrogen regulation protein (transcriptional regulator involved in nitroge		Transcription factors / DNA binding pro	11.426	10.472	11.019	10.891	3.82E-03	6.64E-01	-0.95	-0.13
lpg2862	ORF	*legC8*	ORFs of unknown function (unique)	9.987	11.124	13.835	8.204	2.80E-01	3.44E-03	1.14	-5.63
lpg2862	ORF	*legC8*	ORFs of unknown function (unique)	10.100	10.888	13.890	9.679	4.38E-01	5.00E-03	0.79	-4.21
lpg2863	pteridine reductase 1 (short chain dehydrogenase/reductase) (glucose		Named proteins of general function	9.922	9.135	9.710	9.715	3.35E-02	9.83E-01	-0.79	0.00
lpg2863	pteridine reductase 1 (short chain dehydrogenase/reductase) (glucose		Named proteins of general function	9.920	8.499	8.574	9.637	1.61E-02	2.69E-01	-1.42	1.06
lpg2864	conserved hypothetical protein		Unknown / hypothetical proteins	11.069	11.035	10.190	12.471	9.19E-01	3.02E-03	-0.03	2.28
lpg2864	conserved hypothetical protein		Unknown / hypothetical proteins	11.164	10.898	9.848	12.485	4.15E-01	4.62E-03	-0.27	2.64
lpg2865	6-pyruvoyl tetrahydropterin synthase, putative		Metabolism of Cofactors and Vitamins	11.916	11.395	10.628	12.129	1.66E-01	1.22E-01	-0.52	1.50
lpg2865	6-pyruvoyl tetrahydropterin synthase, putative		Metabolism of Cofactors and Vitamins	11.760	11.398	10.495	12.158	3.85E-01	8.74E-02	-0.36	1.66
lpg2866	primosomal protein N' (primosomal protein replication factor)		Replication and Repair	13.219	14.588	14.200	14.709	7.44E-03	1.78E-01	1.37	0.51
lpg2866	primosomal protein N' (primosomal protein replication factor)		Replication and Repair	13.215	14.587	14.175	14.722	7.43E-03	1.45E-01	1.37	0.55
lpg2867	COG0824 thioesterase (4-hydroxybenzoyl-CoA-thioesterase)		Biodegradation of Xenobiotics	12.395	11.761	11.486	11.238	2.63E-02	6.03E-01	-0.63	-0.25
lpg2867	COG0824 thioesterase (4-hydroxybenzoyl-CoA-thioesterase)		Biodegradation of Xenobiotics	12.390	11.991	11.659	11.557	7.60E-02	7.27E-01	-0.40	-0.10
lpg2868	thymidylate synthase (TS) (TSase)	*thyA*	Nucleotide Metabolism, Metabolism of	11.009	11.073	10.810	12.353	8.99E-01	1.44E-04	0.06	1.54
lpg2868	thymidylate synthase (TS) (TSase)	*thyA*	Nucleotide Metabolism, Metabolism of	11.116	11.204	10.694	12.333	8.60E-01	2.35E-03	0.09	1.64
lpg2869	prolipoprotein diacylglyceryl transferase	*lgt*	Metabolism of Complex Lipids	9.968	8.617	9.324	9.273	1.22E-01	8.89E-01	-1.35	-0.05
lpg2869	prolipoprotein diacylglyceryl transferase	*lgt*	Metabolism of Complex Lipids	9.808	8.764	9.370	10.222	4.22E-01	4.68E-01	-1.04	0.85
lpg2870	hypothetical (integral membrane protein?)		Unknown / hypothetical proteins	10.086	8.484	8.748	9.210	6.56E-02	5.80E-01	-1.60	0.46
lpg2870	hypothetical (integral membrane protein?)		Unknown / hypothetical proteins	10.587	10.164	7.589	10.849	6.74E-01	2.84E-02	-0.42	3.26
lpg2871	phosphoenolpyruvate protein phosphotransferase PtsP	*ptsP*	Transport and binding	10.314	10.337	10.056	9.760	9.63E-01	5.72E-01	0.02	-0.30
lpg2871	phosphoenolpyruvate protein phosphotransferase PtsP	*ptsP*	Transport and binding	10.432	10.085	9.868	10.240	4.19E-01	4.36E-01	-0.35	0.37
lpg2872	(di)nucleoside polyphosphate hydrolase (MutT/nudix family protein)		Metabolism of Complex Carbohydrate	12.953	12.785	11.903	12.841	7.23E-01	9.70E-02	-0.17	0.94
lpg2872	(di)nucleoside polyphosphate hydrolase (MutT/nudix family protein)		Metabolism of Complex Carbohydrate	12.917	13.200	11.787	13.329	1.98E-01	1.32E-05	0.28	1.54
lpg2873	L-asparaginase I (cytoplasmic)		Amino Acid Metabolism, Metabolism o	7.937	8.160	9.040	7.981	8.26E-01	2.45E-01	0.22	-1.06
lpg2873	L-asparaginase I (cytoplasmic)		Amino Acid Metabolism, Metabolism o	7.803	7.719	8.665	7.729	9.01E-01	4.69E-01	-0.08	-0.94

lpg2874	ORF		ORFs of unknown function (unique)	13.439	14.035	13.319	12.419	4.74E-01	1.24E-01	0.60	-0.90
lpg2874	ORF		ORFs of unknown function (unique)	13.404	13.888	13.315	12.422	5.98E-01	8.73E-02	0.48	-0.89
lpg2875	UDP-N-acetylglucosamine pyrophosphorylase	*glmU*	Amino Acid Metabolism, Metabolism o	11.771	12.286	11.074	12.343	6.59E-02	4.69E-03	0.52	1.27
lpg2875	UDP-N-acetylglucosamine pyrophosphorylase	*glmU*	Amino Acid Metabolism, Metabolism o	11.498	12.241	10.906	12.242	1.19E-01	2.13E-03	0.74	1.34
lpg2876	arsenite efflux protein (arsenite permease, arsenite transporter (ArsB)		Transport and binding	9.667	9.640	7.916	10.289	9.73E-01	5.95E-03	-0.03	2.37
lpg2876	arsenite efflux protein (arsenite permease, arsenite transporter (ArsB)		Transport and binding	9.937	9.970	7.941	10.416	9.44E-01	4.95E-03	0.03	2.47
lpg2877	hypothetical		Unknown / hypothetical proteins	9.745	9.279	7.974	9.135	2.90E-01	2.40E-01	-0.47	1.16
lpg2877	hypothetical		Unknown / hypothetical proteins	9.716	9.304	7.535	8.914	4.03E-01	1.95E-01	-0.41	1.38
lpg2878	cobalt/magnesium uptake transporter	*corA*	Transport and binding	11.165	11.384	11.061	11.691	2.02E-01	7.97E-02	0.22	0.63
lpg2878	cobalt/magnesium uptake transporter	*corA*	Transport and binding	11.116	11.342	11.027	11.720	2.05E-01	4.16E-03	0.23	0.69
lpg2879	ORF		ORFs of unknown function (unique)	12.177	13.918	12.402	11.685	8.57E-07	9.32E-04	1.74	-0.72
lpg2879	ORF		ORFs of unknown function (unique)	12.170	13.920	12.369	11.656	1.73E-06	3.17E-03	1.75	-0.71
lpg2880	endonuclease III (DNA (-apurinic or -apyrimidinic site) lya	*nth*	DNA/RNA degradation / restriction	9.937	9.336	10.563	9.661	1.01E-02	2.26E-02	-0.60	-0.90
lpg2880	endonuclease III (DNA (-apurinic or -apyrimidinic site) lya	*nth*	DNA/RNA degradation / restriction	9.815	9.280	10.572	9.782	2.73E-01	5.04E-02	-0.53	-0.79
lpg2881	iron-sulfur cluster binding protein (4Fe-4S binding domain protein) (el		Energy Metabolism	12.235	11.146	11.991	12.297	1.03E-04	2.87E-02	-1.09	0.31
lpg2881	iron-sulfur cluster binding protein (4Fe-4S binding domain protein) (el		Energy Metabolism	12.313	11.423	12.086	12.419	9.14E-04	1.08E-01	-0.89	0.33
lpg2882	methionyl tRNA synthetase	*metG_1*	Amino Acid Metabolism, Metabolism o	11.358	10.730	10.105	12.253	2.26E-01	6.84E-04	-0.63	2.15
lpg2882	methionyl tRNA synthetase	*metG_1*	Amino Acid Metabolism, Metabolism o	11.731	10.843	9.611	12.335	8.73E-03	1.22E-03	-0.89	2.72
lpg2883	3-octaprenyl-4-hydroxybenzoate carboxy-lyase (aromatic acid decarb		Metabolism of Cofactors and Vitamins	11.211	11.241	11.632	11.571	9.17E-01	7.61E-01	0.03	-0.06
lpg2883	3-octaprenyl-4-hydroxybenzoate carboxy-lyase (aromatic acid decarb		Metabolism of Cofactors and Vitamins	11.172	11.413	11.597	11.674	2.79E-01	5.06E-01	0.24	0.08
lpg2884	ORF		ORFs of unknown function (unique)	13.808	13.154	12.083	12.051	2.53E-01	9.58E-01	-0.65	-0.03
lpg2884	ORF		ORFs of unknown function (unique)	13.689	13.370	12.067	12.327	6.22E-01	6.70E-01	-0.32	0.26
lpg2885	ORF		ORFs of unknown function (unique)	9.508	10.363	8.880	9.768	1.28E-01	9.86E-02	0.86	0.89
lpg2885	ORF		ORFs of unknown function (unique)	9.406	10.659	8.147	9.909	3.19E-02	4.71E-02	1.25	1.76
lpg2886	ExsB protein (transcriptional or post-transcriptional regulator), COG06		Signal transduction / other regulatory f	11.589	12.110	11.157	11.773	9.30E-02	9.20E-02	0.52	0.62
lpg2886	ExsB protein (transcriptional or post-transcriptional regulator), COG06		Signal transduction / other regulatory f	11.685	11.970	11.101	11.800	1.46E-01	7.18E-02	0.28	0.70
lpg2887	phosphomannose isomerase GDP mannose pyrophosph	*rfbA*	Carbohydrate Metabolism	9.638	9.151	9.145	9.108	6.36E-02	8.76E-01	-0.49	-0.04
lpg2887	phosphomannose isomerase GDP mannose pyrophosph	*rfbA*	Carbohydrate Metabolism	9.729	9.138	8.939	8.967	1.13E-02	9.23E-01	-0.59	0.03
lpg2888	ORF		ORFs of unknown function (unique)	10.173	11.250	11.685	9.174	4.13E-02	3.11E-04	1.08	-2.51
lpg2888	ORF		ORFs of unknown function (unique)	10.231	11.345	11.573	9.464	4.23E-02	1.85E-03	1.11	-2.11
lpg2889	glucose inhibited division protein A	*gidA*	Chemotaxis / motility / cell division	10.354	9.886	10.092	10.341	2.91E-01	6.80E-01	-0.47	0.25
lpg2889	glucose inhibited division protein A	*gidA*	Chemotaxis / motility / cell division	10.277	11.210	10.337	10.610	1.14E-02	2.56E-01	0.93	0.27
lpg2890	glucose inhibited division protein B	*gidB*	Chemotaxis / motility / cell division	12.046	12.352	10.808	12.474	5.25E-01	2.05E-03	0.31	1.67
lpg2890	glucose inhibited division protein B	*gidB*	Chemotaxis / motility / cell division	11.910	12.351	10.702	12.582	4.50E-01	6.73E-04	0.44	1.88
lpg2891	sporulation initiation inhibitor protein Soj, chromosome pa	*soj*	Chemotaxis / motility / cell division	11.150	11.255	10.608	11.570	7.98E-01	8.68E-02	0.10	0.96
lpg2891	sporulation initiation inhibitor protein Soj, chromosome pa	*soj*	Chemotaxis / motility / cell division	11.482	11.226	10.369	11.671	3.54E-01	1.20E-02	-0.26	1.30
lpg2892	chromosome partitioning protein ParB		Chemotaxis / motility / cell division, Me	10.452	9.845	8.592	10.489	7.24E-02	5.86E-03	-0.61	1.90
lpg2892	chromosome partitioning protein ParB		Chemotaxis / motility / cell division, Me	10.536	10.030	8.562	10.883	7.00E-02	7.72E-03	-0.51	2.32
lpg2893	ORF		ORFs of unknown function (unique)	9.121	9.999	9.917	9.209	2.23E-01	3.67E-01	0.88	-0.71
lpg2893	ORF		ORFs of unknown function (unique)	9.222	9.499	9.712	9.195	7.00E-01	5.95E-01	0.28	-0.52
lpg2894	cytochrome c oxidase, subunit III		Energy Metabolism	7.313	6.899	8.239	7.354	5.14E-01	1.38E-01	-0.41	-0.88
lpg2894	cytochrome c oxidase, subunit III		Energy Metabolism	5.492	7.569	6.590	8.843	1.62E-01	7.50E-02	2.08	2.25
lpg2895	cytochrome c oxidase, assembly transmembrane protein	*coxG*	Energy Metabolism	11.920	12.098	11.245	12.120	7.22E-01	4.33E-02	0.18	0.87
lpg2895	cytochrome c oxidase, assembly transmembrane protein	*coxG*	Energy Metabolism	11.931	12.108	11.135	12.170	7.23E-01	2.03E-02	0.18	1.03
lpg2896	cytochrome c oxidase, subunit I		Energy Metabolism	12.880	13.205	12.099	13.411	6.13E-01	2.99E-02	0.33	1.31
lpg2896	cytochrome c oxidase, subunit I		Energy Metabolism	12.913	13.890	12.036	13.942	1.56E-04	9.34E-06	0.98	1.91
lpg2897	cytochrome c oxidase, subunit II		Energy Metabolism	8.468	8.410	9.828	7.796	9.52E-01	1.55E-01	-0.06	-2.03
lpg2897	cytochrome c oxidase, subunit II		Energy Metabolism	7.829	8.358	8.527	8.421	2.70E-01	7.80E-01	0.53	-0.11
lpg2898	cytochrome c (alcohol dehydrogenase cytochrome c)		Energy Metabolism	6.769	9.121	8.450	8.179	1.31E-01	8.21E-01	2.35	-0.27
lpg2898	cytochrome c (alcohol dehydrogenase cytochrome c)		Energy Metabolism	7.086	9.709	7.634	8.659	7.59E-02	2.66E-01	2.62	1.03
lpg2899	ferredoxin component COG2146, putative pseudogene		Named proteins of general function	10.789	10.949	10.966	12.218	4.82E-01	1.39E-02	0.16	1.25
lpg2899	ferredoxin component COG2146, putative pseudogene		Named proteins of general function	11.166	10.651	10.787	12.185	3.75E-01	3.46E-02	-0.51	1.40
lpg2900	CapM protein, capsular polysaccharide biosynthesis (glyc	*capM2*	Cell envelope synthesis, Metabolism c	10.872	9.893	9.996	11.978	9.23E-02	1.45E-02	-0.98	1.98
lpg2900	CapM protein, capsular polysaccharide biosynthesis (glyc	*capM2*	Cell envelope synthesis, Metabolism c	10.696	10.460	9.563	12.383	6.23E-01	2.71E-04	-0.24	2.82
lpg2901	transporter, LysE family (amino acid transport protein)		Transport and binding	9.052	9.637	9.452	9.052	8.67E-02	4.87E-01	0.59	-0.40
lpg2901	transporter, LysE family (amino acid transport protein)		Transport and binding	9.061	9.834	9.263	9.205	3.52E-03	9.19E-01	0.77	-0.06
lpg2902	conserved hypothetical protein		Unknown / hypothetical proteins	9.539	10.003	11.173	10.019	7.96E-02	1.46E-02	0.46	-1.15
lpg2902	conserved hypothetical protein		Unknown / hypothetical proteins	9.425	10.002	11.152	10.248	8.20E-02	3.10E-02	0.58	-0.90
lpg2903	ubiquinone/menaquinone biosynthesis methyltransferase UbiE		Metabolism of Cofactors and Vitamins	10.913	10.591	9.269	10.804	5.72E-01	4.67E-02	-0.32	1.53
lpg2903	ubiquinone/menaquinone biosynthesis methyltransferase UbiE		Metabolism of Cofactors and Vitamins	10.824	10.706	9.345	10.991	8.68E-01	2.76E-02	-0.12	1.65
lpg2904	conserved hypothetical protein		Unknown / hypothetical proteins	11.213	10.675	9.682	11.027	2.99E-01	3.47E-03	-0.54	1.34
lpg2904	conserved hypothetical protein		Unknown / hypothetical proteins	11.097	11.079	9.589	11.008	9.71E-01	6.24E-04	-0.02	1.42
lpg2905	ubiquinone biosynthesis AarF		Metabolism of Cofactors and Vitamins	9.265	10.273	9.819	10.623	2.46E-01	1.07E-01	1.01	0.80
lpg2905	ubiquinone biosynthesis AarF		Metabolism of Cofactors and Vitamins	8.981	10.192	9.589	10.404	9.27E-02	2.55E-01	1.21	0.81

lpg2906	sec-independent protein translocase TatB	*tatB*	Protein fate / hydrolases / secretion	11.685	10.340	11.082	10.624	2.97E-03	2.78E-02	-1.35	-0.46
lpg2906	sec-independent protein translocase TatB	*tatB*	Protein fate / hydrolases / secretion	11.721	10.675	11.124	10.803	4.70E-04	7.88E-02	-1.05	-0.32
lpg2907	ORF		ORFs of unknown function (unique)	9.277	10.806	11.352	9.287	4.50E-04	4.53E-03	1.53	-2.06
lpg2907	ORF		ORFs of unknown function (unique)	9.423	10.722	11.344	9.752	2.02E-05	2.25E-03	1.30	-1.59
lpg2908	peptide methionine sulfoxide reductase (protein methioni	*msrA*	Detoxification / adaptation	11.733	12.213	13.341	11.946	3.71E-01	2.16E-02	0.48	-1.40
lpg2908	peptide methionine sulfoxide reductase (protein methioni	*msrA*	Detoxification / adaptation	11.648	12.171	13.354	12.054	3.69E-01	3.22E-02	0.52	-1.30
lpg2909	62aa ORF hypothetical		Unknown / hypothetical proteins	9.686	9.593	10.924	9.322	6.71E-01	3.21E-03	-0.09	-1.60
lpg2909	62aa ORF hypothetical		Unknown / hypothetical proteins	9.426	9.555	10.389	9.578	7.26E-01	1.47E-02	0.13	-0.81
lpg2910	histamine oxidase (copper amine oxidase (phenylethylan	*tynA*	Amino Acid Metabolism, Metabolism o	8.871	9.379	9.340	9.835	1.85E-01	2.69E-01	0.51	0.50
lpg2910	histamine oxidase (copper amine oxidase (phenylethylan	*tynA*	Amino Acid Metabolism, Metabolism o	8.475	10.122	9.376	9.897	2.66E-04	2.40E-01	1.65	0.52
lpg2911	serine carboxypeptidase (protective protein for beta-galactosidase)		Detoxification / adaptation, Protein fate	9.377	9.333	9.533	8.164	8.98E-01	3.15E-01	-0.04	-1.37
lpg2911	serine carboxypeptidase (protective protein for beta-galactosidase)		Detoxification / adaptation, Protein fate	9.660	9.007	9.791	10.023	1.67E-01	7.43E-01	-0.65	0.23
lpg2912	ORF		ORFs of unknown function (unique)	14.169	13.514	11.256	13.302	3.70E-01	8.88E-03	-0.65	2.05
lpg2912	ORF		ORFs of unknown function (unique)	14.097	13.549	11.069	13.335	3.91E-01	9.23E-03	-0.55	2.27
lpg2913	hypothetical (DEXX-box ATPase?)		Unknown / hypothetical proteins	8.933	9.186	8.354	8.655	5.51E-01	6.77E-01	0.25	0.30
lpg2913	hypothetical (DEXX-box ATPase?)		Unknown / hypothetical proteins	8.497	8.671	8.647	9.029	8.48E-01	4.93E-01	0.17	0.38
lpg2914	hypothetical (transcriptional regulator cro/cI family), bacterial regulato		Transcription factors / DNA binding pro	10.315	11.198	10.687	10.085	1.90E-02	2.92E-01	0.88	-0.60
lpg2914	hypothetical (transcriptional regulator cro/cI family), bacterial regulato		Transcription factors / DNA binding pro	10.533	11.340	10.702	10.600	5.07E-02	8.12E-01	0.81	-0.10
lpg2915	protein product; similar to unknown protein		Unknown / hypothetical proteins	10.882	9.425	11.234	8.360	4.52E-06	2.02E-02	-1.46	-2.87
lpg2915	protein product; similar to unknown protein		Unknown / hypothetical proteins	10.921	9.989	11.076	9.373	2.01E-01	1.59E-01	-0.93	-1.70
lpg2916	ORF		ORFs of unknown function (unique)	9.924	8.474	9.690	8.499	5.74E-03	1.43E-02	-1.45	-1.19
lpg2916	ORF		ORFs of unknown function (unique)	9.072	7.963	9.374	8.493	1.70E-01	1.44E-01	-1.11	-0.88
lpg2917	hypothetical		Unknown / hypothetical proteins	10.551	10.739	12.166	11.360	7.48E-01	9.57E-02	0.19	-0.81
lpg2917	hypothetical		Unknown / hypothetical proteins	10.419	11.444	11.994	11.509	2.50E-02	2.93E-01	1.02	-0.48
lpg2918	lytic murein transglycosylase (membrane bound)		Cell envelope synthesis	10.594	11.567	12.944	10.844	1.78E-02	1.53E-03	0.97	-2.10
lpg2918	lytic murein transglycosylase (membrane bound)		Cell envelope synthesis	10.612	11.698	12.913	10.956	1.48E-02	2.88E-03	1.09	-1.96
lpg2919	(serine-type) D-alanyl-D-alanine carboxypeptidase (D-stereospecific		Cell envelope synthesis, Protein fate /	10.264	9.495	12.823	9.065	3.61E-01	1.02E-03	-0.77	-3.76
lpg2919	(serine-type) D-alanyl-D-alanine carboxypeptidase (D-stereospecific		Cell envelope synthesis, Protein fate /	10.298	9.411	12.898	9.273	2.62E-01	9.70E-04	-0.89	-3.63
lpg2920	hypothetical (nucleotidyltransferase?)		Unknown / hypothetical proteins	10.281	10.190	10.648	9.994	8.07E-01	1.39E-01	-0.09	-0.65
lpg2920	hypothetical (nucleotidyltransferase?)		Unknown / hypothetical proteins	9.997	10.100	10.447	10.130	8.48E-01	5.40E-01	0.10	-0.32
lpg2921	hypothetical (nucleotidyltransferase?)		Unknown / hypothetical proteins	9.981	8.681	9.667	9.465	1.40E-02	6.61E-01	-1.30	-0.20
lpg2921	hypothetical (nucleotidyltransferase?)		Unknown / hypothetical proteins	9.751	8.783	9.661	9.464	1.59E-01	7.44E-01	-0.97	-0.20
lpg2922	ABC transporter, permease		Transport and binding	8.013	8.547	8.441	9.606	4.87E-01	1.77E-01	0.53	1.17
lpg2922	ABC transporter, permease		Transport and binding	8.139	7.747	6.552	7.912	6.40E-01	1.03E-01	-0.39	1.36
lpg2923	ABC transporter, ATP binding protein		Transport and binding	9.851	10.139	10.741	10.070	4.29E-01	9.88E-02	0.29	-0.67
lpg2923	ABC transporter, ATP binding protein		Transport and binding	9.562	9.290	10.439	9.897	5.14E-01	1.02E-01	-0.27	-0.54
lpg2924	lipoprotein (RND efflux membrane fusion protein?)		Transport and binding	9.174	9.480	10.194	10.385	5.10E-01	6.46E-01	0.31	0.19
lpg2924	lipoprotein (RND efflux membrane fusion protein?)		Transport and binding	9.066	10.541	10.326	10.840	1.66E-01	4.91E-01	1.48	0.51
lpg2925	outer membrane efflux protein		Transport and binding	7.808	9.668	9.405	9.203	2.39E-03	4.24E-01	1.86	-0.20
lpg2925	outer membrane efflux protein		Transport and binding	7.044	10.083	8.673	9.356	2.26E-02	3.05E-01	3.04	0.68
lpg2926	bis(5'-nucleosyl)tetraphosphatase, symmetrical (diadeno	*apaH*	Nucleotide Metabolism	8.062	7.868	8.481	8.451	7.70E-01	9.46E-01	-0.19	-0.03
lpg2926	bis(5'-nucleosyl)tetraphosphatase, symmetrical (diadeno	*apaH*	Nucleotide Metabolism	7.827	7.808	7.674	9.015	9.85E-01	2.08E-01	-0.02	1.34
lpg2927	conserved hypothetical protein		Unknown / hypothetical proteins	11.143	10.996	11.635	11.725	5.36E-01	6.80E-01	-0.15	0.09
lpg2927	conserved hypothetical protein		Unknown / hypothetical proteins	11.102	11.450	11.668	11.995	4.91E-01	3.00E-01	0.35	0.33
lpg2928	dimethyladenosine transferase (S-adenosylmethionine-6	*ksgA*	DNA/RNA degradation / restriction	12.101	11.686	10.837	11.818	1.80E-01	3.32E-02	-0.42	0.98
lpg2928	dimethyladenosine transferase (S-adenosylmethionine-6	*ksgA*	DNA/RNA degradation / restriction	11.982	11.820	11.024	12.057	6.03E-01	1.43E-04	-0.16	1.03
lpg2929	aspartate-1-decarboxylase (L-aspartate-alpha-decarboxy	*panD*	Amino Acid Metabolism, Metabolism o	11.109	12.988	9.991	12.125	5.36E-04	2.62E-03	1.88	2.13
lpg2929	aspartate-1-decarboxylase (L-aspartate-alpha-decarboxy	*panD*	Amino Acid Metabolism, Metabolism o	11.287	12.918	9.611	12.109	2.62E-06	4.20E-03	1.63	2.50
lpg2930	sec-independent (periplasmic) protein translocase protei	*tatC*	Protein fate / hydrolases / secretion	12.154	10.006	10.804	10.274	7.43E-04	8.45E-02	-2.15	-0.53
lpg2930	sec-independent (periplasmic) protein translocase protei	*tatC*	Protein fate / hydrolases / secretion	11.977	9.855	10.635	10.232	7.91E-03	2.53E-01	-2.12	-0.40
lpg2931	conserved hypothetical protein, COG3785		Unknown / hypothetical proteins	9.322	9.375	11.956	9.090	9.41E-01	3.77E-03	0.05	-2.87
lpg2931	conserved hypothetical protein, COG3785		Unknown / hypothetical proteins	9.231	8.922	11.904	9.528	6.12E-01	1.11E-02	-0.31	-2.38
lpg2932	CDP-6-deoxy-3,4-glucoseen reductase (NAD(P)H-flavin	*ubiB*	Metabolism of Cofactors and Vitamins	10.566	8.855	10.056	10.229	6.75E-02	8.98E-01	-1.71	0.17
lpg2932	CDP-6-deoxy-3,4-glucoseen reductase (NAD(P)H-flavin	*ubiB*	Metabolism of Cofactors and Vitamins	10.247	9.559	9.771	10.649	3.09E-01	7.77E-02	-0.69	0.88
lpg2933	oxidoreductase; 3-octaprenyl-4-hydroxybenzoate carbox	*yigC*	Metabolism of Cofactors and Vitamins	12.044	12.773	13.339	13.016	1.22E-02	2.21E-01	0.73	-0.32
lpg2933	oxidoreductase; 3-octaprenyl-4-hydroxybenzoate carbox	*yigC*	Metabolism of Cofactors and Vitamins	12.055	12.843	13.280	13.465	2.02E-02	6.57E-01	0.79	0.19
lpg2934	transcription termination factor rho		Transcription	12.660	12.188	11.755	13.494	2.10E-01	1.65E-03	-0.47	1.74
lpg2934	transcription termination factor rho		Transcription	12.273	12.206	11.311	13.406	8.90E-01	7.88E-04	-0.07	2.09
lpg2935	RSc1188; probable thioredoxin 1 (redox factor) protein	*trxA*	Energy Metabolism	13.312	12.246	11.860	12.386	9.92E-02	3.48E-01	-1.07	0.53
lpg2935	RSc1188; probable thioredoxin 1 (redox factor) protein	*trxA*	Energy Metabolism	13.120	12.389	11.578	12.587	3.33E-01	9.08E-02	-0.73	1.01
lpg2936	hypothetical		Unknown / hypothetical proteins	10.834	11.341	10.368	11.565	1.05E-01	6.78E-03	0.51	1.20
lpg2936	hypothetical		Unknown / hypothetical proteins	10.630	11.233	10.133	11.490	8.89E-03	2.52E-03	0.60	1.36
lpg2937	fumarate hydratase (fumarase)	*fum*	Carbohydrate Metabolism, Energy Me	11.319	11.642	11.730	12.344	2.88E-01	2.54E-03	0.32	0.61
lpg2937	fumarate hydratase (fumarase)	*fum*	Carbohydrate Metabolism, Energy Me	11.524	11.804	11.658	12.374	2.02E-01	2.97E-04	0.28	0.72

lpg2938	ORF		ORFs of unknown function (unique)	9.181	8.022	7.516	7.471	1.21E-02	9.66E-01	-1.16	-0.04
lpg2938	ORF		ORFs of unknown function (unique)	8.964	8.473	8.406	8.992	1.79E-01	9.76E-02	-0.49	0.59
lpg2939	hypothetical (BNR/Asp box repeat protein)		Named proteins of general function	10.109	9.297	9.268	9.567	1.29E-01	4.72E-01	-0.81	0.30
lpg2939	hypothetical (BNR/Asp box repeat protein)		Named proteins of general function	10.406	9.042	8.258	9.569	7.14E-04	1.50E-01	-1.36	1.31
lpg2940	lipid A lauroyl acyltransferase (may be fused with prior O	*waaM*	Cell envelope synthesis, Lipid Metabol	9.802	9.864	9.642	10.128	8.06E-01	4.16E-01	0.06	0.49
lpg2940	lipid A lauroyl acyltransferase (may be fused with prior O	*waaM*	Cell envelope synthesis, Lipid Metabol	9.753	9.279	8.896	10.248	3.57E-01	1.71E-01	-0.47	1.35
lpg2941	hypothetical (lipid A biosynthesis lauroyl acyltransferase)	*waaM*	Cell envelope synthesis, Lipid Metabol	10.429	8.979	9.075	9.439	2.14E-02	6.65E-01	-1.45	0.36
lpg2941	hypothetical (lipid A biosynthesis lauroyl acyltransferase)	*waaM*	Cell envelope synthesis, Lipid Metabol	10.578	9.826	8.570	9.887	3.40E-01	2.49E-01	-0.75	1.32
lpg2942	ORF		ORFs of unknown function (unique)	13.419	13.434	12.103	13.146	9.73E-01	6.46E-02	0.02	1.04
lpg2942	ORF		ORFs of unknown function (unique)	13.300	13.416	12.111	13.276	8.35E-01	1.49E-02	0.12	1.16
lpg2943	UDP-N-acetylglucosamine acyltransferase, acyl-[acyl carrier protein]-		Metabolism of Complex Carbohydrate	10.883	11.089	8.067	11.496	7.14E-01	3.41E-03	0.21	3.43
lpg2943	UDP-N-acetylglucosamine acyltransferase, acyl-[acyl carrier protein]-		Metabolism of Complex Carbohydrate	10.931	11.290	8.182	12.029	5.53E-01	1.03E-02	0.36	3.85
lpg2944	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransfe	*lpxD*	Metabolism of Complex Carbohydrate	11.244	10.559	11.033	10.735	8.84E-03	4.61E-01	-0.69	-0.30
lpg2944	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransfe	*lpxD*	Metabolism of Complex Carbohydrate	11.256	10.839	11.211	11.184	3.63E-01	9.66E-01	-0.42	-0.03
lpg2945	lipid A-disaccharide synthase	*lpxB*	Metabolism of Complex Carbohydrate	9.589	9.323	8.762	10.196	2.69E-01	6.55E-03	-0.27	1.43
lpg2945	lipid A-disaccharide synthase	*lpxB*	Metabolism of Complex Carbohydrate	9.576	9.548	8.688	10.198	9.41E-01	6.85E-03	-0.03	1.51
lpg2946	unknown protein		Unknown / hypothetical proteins	9.635	8.536	8.292	8.911	2.38E-02	3.26E-01	-1.10	0.62
lpg2946	unknown protein		Unknown / hypothetical proteins	9.682	8.324	7.228	8.900	1.62E-02	9.00E-02	-1.36	1.67
lpg2947	ABC transporter, ATP binding protein		Transport and binding	8.379	7.715	8.195	9.261	6.62E-01	5.10E-01	-0.66	1.07
lpg2947	ABC transporter, ATP binding protein		Transport and binding	9.282	8.530	6.971	8.647	1.72E-01	2.02E-01	-0.75	1.68
lpg2948	hypothetical protein		Unknown / hypothetical proteins	11.430	10.337	9.964	10.925	5.70E-02	1.16E-01	-1.09	0.96
lpg2948	hypothetical protein		Unknown / hypothetical proteins	11.484	10.363	9.659	10.992	2.39E-02	7.34E-02	-1.12	1.33
lpg2949	asparagine synthetase (B) (glutamine hydrolyzing)	*wbmI*	Amino Acid Metabolism	10.284	9.782	10.181	10.982	3.74E-01	1.63E-01	-0.50	0.80
lpg2949	asparagine synthetase (B) (glutamine hydrolyzing)	*wbmI*	Amino Acid Metabolism	10.838	11.208	10.109	13.059	6.24E-01	5.45E-05	0.37	2.95
lpg2950	hypothetical protein		Unknown / hypothetical proteins	11.021	9.095	10.497	9.922	3.30E-03	1.59E-01	-1.93	-0.58
lpg2950	hypothetical protein		Unknown / hypothetical proteins	11.243	8.709	10.254	10.029	8.82E-04	6.82E-01	-2.53	-0.23
lpg2951	cystathionine beta synthase (cysteine synthase)		Amino Acid Metabolism, Metabolism o	10.587	11.666	10.373	11.323	4.46E-02	3.86E-02	1.08	0.95
lpg2951	cystathionine beta synthase (cysteine synthase)		Amino Acid Metabolism, Metabolism o	10.684	11.655	10.314	11.353	3.25E-02	5.15E-02	0.97	1.04
lpg2952	ORF		ORFs of unknown function (unique)	9.615	9.352	10.432	8.978	3.26E-01	1.54E-03	-0.26	-1.45
lpg2952	ORF		ORFs of unknown function (unique)	9.492	8.857	10.323	9.104	1.01E-02	8.40E-03	-0.64	-1.22
lpg2953	ORF		ORFs of unknown function (unique)	11.853	10.991	12.711	9.986	8.52E-02	9.70E-04	-0.86	-2.73
lpg2953	ORF		ORFs of unknown function (unique)	10.911	10.956	11.924	9.952	9.41E-01	1.18E-02	0.04	-1.97
lpg2954	Hypothetical protein		Unknown / hypothetical proteins	12.313	13.246	13.560	13.151	2.35E-01	7.12E-01	0.93	-0.41
lpg2954	Hypothetical protein		Unknown / hypothetical proteins	12.274	13.380	13.559	13.530	1.51E-01	9.76E-01	1.11	-0.03
lpg2955	integration host factor beta subunit (bacterial nucleoid D	*hipB*	Transcription	10.476	12.173	13.154	11.142	1.45E-02	1.18E-02	1.70	-2.01
lpg2955	integration host factor beta subunit (bacterial nucleoid D	*hipB*	Transcription	10.483	12.195	13.217	11.285	1.57E-02	1.19E-02	1.71	-1.93
lpg2956	deoxycytidine triphosphate deaminase	*dcd*	Nucleotide Metabolism	14.562	14.554	12.922	15.648	9.82E-01	6.37E-06	-0.01	2.73
lpg2956	deoxycytidine triphosphate deaminase	*dcd*	Nucleotide Metabolism	14.417	14.535	12.914	15.720	6.66E-01	1.76E-06	0.12	2.81
lpg2957	stomatin like transmembrane protein		Named proteins of general function	9.841	10.256	13.281	10.068	6.04E-01	8.35E-04	0.41	-3.21
lpg2957	stomatin like transmembrane protein		Named proteins of general function	9.961	10.459	13.357	10.399	5.29E-01	1.24E-03	0.50	-2.96
lpg2958	transmembrane protein (nodulation competitiveness protein)		Chemotaxis / motility / cell division	9.007	8.424	11.687	8.860	4.89E-01	6.53E-03	-0.58	-2.83
lpg2958	transmembrane protein (nodulation competitiveness protein)		Chemotaxis / motility / cell division	9.190	8.816	11.776	9.194	6.01E-01	4.25E-03	-0.37	-2.58
lpg2959	conserved hypothetical protein		Unknown / hypothetical proteins	11.449	12.558	9.724	12.243	8.39E-04	3.05E-04	1.11	2.52
lpg2959	conserved hypothetical protein		Unknown / hypothetical proteins	11.156	12.516	9.534	12.203	8.52E-03	1.03E-03	1.36	2.67
lpg2960	major outer membrane protein		Toxin production / other pathogen func	12.099	11.283	10.586	11.448	1.94E-01	1.81E-01	-0.82	0.86
lpg2960	major outer membrane protein		Toxin production / other pathogen func	11.934	11.614	9.949	11.606	6.36E-01	4.56E-02	-0.32	1.66
lpg2961	major outer membrane protein		Toxin production / other pathogen func	14.769	14.373	14.512	14.568	7.63E-01	9.54E-01	-0.40	0.06
lpg2961	major outer membrane protein		Toxin production / other pathogen func	14.558	14.713	14.603	14.837	8.81E-01	7.68E-01	0.15	0.23
lpg2962	sodium-type flagellar protein (lateral flagellar MotY-like protein)		Chemotaxis / motility / cell division	8.700	9.820	12.445	8.805	1.86E-01	3.18E-05	1.12	-3.64
lpg2962	sodium-type flagellar protein (lateral flagellar MotY-like protein)		Chemotaxis / motility / cell division	9.266	9.717	11.602	8.970	5.75E-01	2.26E-02	0.45	-2.63
lpg2963	dihydroorotase, homodimeric type	*pyrC*	Nucleotide Metabolism	10.743	10.942	9.294	10.357	5.93E-01	6.24E-02	0.20	1.06
lpg2963	dihydroorotase, homodimeric type	*pyrC*	Nucleotide Metabolism	10.840	9.536	9.038	10.379	4.17E-01	2.92E-02	-1.30	1.34
lpg2964	ribonuclease T	*rnt*	DNA/RNA degradation / restriction	11.022	11.346	10.762	10.983	3.56E-01	5.30E-01	0.32	0.22
lpg2964	ribonuclease T	*rnt*	DNA/RNA degradation / restriction	10.911	11.115	10.154	10.968	4.82E-01	1.12E-01	0.20	0.81
lpg2965	peroxynitrite reductase; alkylhydrogen peroxide reductase, AhpC/Tsa		Detoxification / adaptation	12.374	12.700	12.028	12.482	1.83E-01	2.00E-02	0.33	0.45
lpg2965	peroxynitrite reductase; alkylhydrogen peroxide reductase, AhpC/Tsa		Detoxification / adaptation	12.258	12.678	12.013	12.554	1.86E-01	3.40E-02	0.42	0.54
lpg2966	glutaredoxin-related protein		Detoxification / adaptation	14.279	14.312	13.778	14.189	8.99E-01	1.17E-01	0.03	0.41
lpg2966	glutaredoxin-related protein		Detoxification / adaptation	14.232	14.338	13.788	14.217	6.48E-01	1.04E-01	0.11	0.43
lpg2967	superoxide dismutase	*sodB*	Detoxification / adaptation	12.077	13.540	11.214	13.702	1.21E-02	2.24E-05	1.46	2.49
lpg2967	superoxide dismutase	*sodB*	Detoxification / adaptation	11.968	13.586	11.186	13.739	1.52E-02	3.59E-06	1.62	2.55
lpg2968	N-acetylornithine aminotransferase ArgD	*argD*	Amino Acid Metabolism	12.840	13.827	10.992	13.945	2.75E-02	3.84E-05	0.99	2.95
lpg2968	N-acetylornithine aminotransferase ArgD	*argD*	Amino Acid Metabolism	12.811	13.888	11.006	14.026	1.96E-02	3.56E-05	1.08	3.02
lpg2969	hypothetical (arylsulfatase?, metal dependent hydrolase?)		Unknown / hypothetical proteins	7.850	8.081	9.298	7.377	7.41E-01	2.68E-01	0.23	-1.92
lpg2969	hypothetical (arylsulfatase?, metal dependent hydrolase?)		Unknown / hypothetical proteins	7.992	8.187	8.772	7.925	6.69E-01	6.16E-01	0.19	-0.85

lpg2970	glycerophosphoryl diester phosphodiesterase		Metabolism of Complex Lipids	10.940	11.266	11.408	10.185	3.00E-01	5.30E-02	0.33	-1.22
lpg2970	glycerophosphoryl diester phosphodiesterase		Metabolism of Complex Lipids	11.038	11.360	11.385	10.366	1.37E-01	1.20E-01	0.32	-1.02
lpg2971	malate dehydrogenase (NAD-linked), malic enzyme (NA	*maeA*	Carbohydrate Metabolism	12.239	14.042	14.853	13.156	3.03E-02	5.92E-02	1.80	-1.70
lpg2971	malate dehydrogenase (NAD-linked), malic enzyme (NA	*maeA*	Carbohydrate Metabolism	12.233	14.103	14.959	13.394	2.59E-02	5.17E-02	1.87	-1.56
lpg2972	SUA5/yciO/yrdC family:Sua5/YciO/YrdC/YwlC protein family (translat		Translation	10.480	9.639	12.011	10.398	2.57E-01	3.17E-03	-0.84	-1.61
lpg2972	SUA5/yciO/yrdC family:Sua5/YciO/YrdC/YwlC protein family (translat		Translation	10.498	10.162	12.022	10.721	4.59E-01	1.49E-03	-0.34	-1.30
lpg2973	tRNA-Met		tRNA	9.534	10.380	9.259	10.393	5.40E-02	1.17E-02	0.85	1.13
lpg2973	tRNA-Met		tRNA	9.330	10.346	8.991	10.486	4.63E-03	1.10E-02	1.02	1.49
lpg2974	phosphatidylserine decarboxylase	*psd*	Amino Acid Metabolism, Metabolism o	11.638	11.925	10.397	12.200	4.29E-01	6.62E-03	0.29	1.80
lpg2974	phosphatidylserine decarboxylase	*psd*	Amino Acid Metabolism, Metabolism o	11.719	11.705	10.364	12.185	9.59E-01	4.04E-03	-0.01	1.82
lpg2975	ORF		ORFs of unknown function (unique)	12.003	11.748	11.898	11.939	5.05E-01	9.25E-01	-0.26	0.04
lpg2975	ORF		ORFs of unknown function (unique)	11.850	12.045	11.845	12.179	5.03E-01	1.85E-01	0.19	0.33
lpg2976	ORF		ORFs of unknown function (unique)	9.785	11.657	11.245	10.222	5.89E-03	9.70E-02	1.87	-1.02
lpg2976	ORF		ORFs of unknown function (unique)	9.823	11.797	11.161	10.495	3.61E-03	2.16E-01	1.97	-0.67
lpg2977	zinc metalloprotease (virulence metalloprotease, hemagglutinin/prote		Toxin production / other pathogen func	11.082	11.992	12.277	11.259	3.05E-02	6.43E-02	0.91	-1.02
lpg2977	zinc metalloprotease (virulence metalloprotease, hemagglutinin/prote		Toxin production / other pathogen func	11.078	12.035	12.333	11.394	1.34E-02	4.48E-02	0.96	-0.94
lpg2978	small ORF (119aa)		ORFs of unknown function (unique)	8.979	8.873	8.828	8.124	8.95E-01	4.49E-01	-0.11	-0.70
lpg2978	small ORF (119aa)		ORFs of unknown function (unique)	8.788	8.588	9.214	8.691	7.46E-01	1.98E-01	-0.20	-0.52
lpg2979	conserved hypothetical protein		Unknown / hypothetical proteins	11.312	10.435	12.333	10.356	4.02E-01	1.07E-01	-0.88	-1.98
lpg2979	conserved hypothetical protein		Unknown / hypothetical proteins	10.642	11.611	11.944	11.591	1.92E-01	6.63E-01	0.97	-0.35
lpg2980	DNA topoisomerase IV subunit A	*parC*	Replication and Repair	9.673	10.930	8.699	10.636	1.39E-01	2.23E-02	1.26	1.94
lpg2980	DNA topoisomerase IV subunit A	*parC*	Replication and Repair	9.673	10.965	8.432	10.638	1.46E-01	2.73E-02	1.29	2.21
lpg2981	ATP synthase epsilon chain, ATP synthase F1 epsilon su	*atpC*	Energy Metabolism	13.466	12.018	11.448	12.953	9.34E-02	8.80E-02	-1.45	1.51
lpg2981	ATP synthase epsilon chain, ATP synthase F1 epsilon su	*atpC*	Energy Metabolism	13.229	11.949	11.331	13.432	2.53E-01	3.68E-03	-1.28	2.10
lpg2982	H+-transporting two-sector ATPase, ATP synthase F1 su	*atpD*	Energy Metabolism	12.547	11.866	9.968	13.525	5.32E-01	1.13E-03	-0.68	3.56
lpg2982	H+-transporting two-sector ATPase, ATP synthase F1 su	*atpD*	Energy Metabolism	13.021	11.757	9.997	13.578	1.29E-01	8.95E-04	-1.26	3.58
lpg2983	ATP synthase gamma chain, ATP synthase F1 gamma c	*atpG*	Energy Metabolism	12.552	11.820	9.911	13.628	3.59E-01	2.72E-03	-0.73	3.72
lpg2983	ATP synthase gamma chain, ATP synthase F1 gamma c	*atpG*	Energy Metabolism	12.609	11.017	9.494	13.519	1.53E-01	4.33E-03	-1.59	4.03
lpg2984	F0F1-ATPase subunit alpha, ATP synthase alpha chain		Energy Metabolism	13.853	12.337	11.854	14.156	9.42E-02	8.06E-02	-1.52	2.30
lpg2984	F0F1-ATPase subunit alpha, ATP synthase alpha chain		Energy Metabolism	13.879	12.861	11.894	15.064	1.21E-01	2.34E-04	-1.02	3.17
lpg2985	ATP synthase F1, delta subunit (F0F1 ATPase subunit de	*atpH*	Energy Metabolism	13.057	10.928	11.039	13.258	2.96E-04	2.52E-03	-2.13	2.22
lpg2985	ATP synthase F1, delta subunit (F0F1 ATPase subunit de	*atpH*	Energy Metabolism	13.071	10.923	10.877	13.265	1.98E-04	3.01E-03	-2.15	2.39
lpg2986	ATP synthase F0, B subunit	*atpF*	Energy Metabolism	12.298	11.512	10.708	13.123	2.66E-01	2.70E-03	-0.79	2.42
lpg2986	ATP synthase F0, B subunit	*atpF*	Energy Metabolism	12.368	11.595	10.388	13.190	1.62E-01	1.91E-03	-0.77	2.80
lpg2987	ATP synthase F0, C subunit	*atpE*	Energy Metabolism	14.187	13.586	12.566	13.392	4.13E-01	6.34E-01	-0.60	0.83
lpg2987	ATP synthase F0, C subunit	*atpE*	Energy Metabolism	13.830	13.733	12.388	14.620	8.39E-01	9.92E-04	-0.10	2.23
lpg2988	ATP synthase F0, A subunit (ATP synthase A chain)	*atpB*	Energy Metabolism	12.609	11.707	11.486	12.942	4.12E-02	4.05E-03	-0.90	1.46
lpg2988	ATP synthase F0, A subunit (ATP synthase A chain)	*atpB*	Energy Metabolism	12.673	11.754	11.180	13.058	2.19E-02	3.74E-03	-0.92	1.88
lpg2989	ATP synthase protein I (ATP synthase F0, I subunit)	*atpI*	Energy Metabolism	12.414	11.910	10.647	13.853	4.69E-01	8.53E-04	-0.50	3.21
lpg2989	ATP synthase protein I (ATP synthase F0, I subunit)	*atpI*	Energy Metabolism	12.523	11.886	10.672	13.916	2.69E-01	7.15E-04	-0.64	3.24
lpg2990	ORF		ORFs of unknown function (unique)	12.278	10.284	10.989	12.160	4.72E-08	1.84E-02	-1.99	1.17
lpg2990	ORF		ORFs of unknown function (unique)	12.148	9.390	10.527	12.110	4.68E-05	1.87E-02	-2.76	1.58
lpg2991	hemolysin, lipoprotein		Toxin production / other pathogen func	10.729	8.429	9.316	8.013	1.91E-02	3.21E-01	-2.30	-1.30
lpg2991	hemolysin, lipoprotein		Toxin production / other pathogen func	10.742	10.567	10.001	9.954	8.78E-01	9.59E-01	-0.18	-0.05
lpg2992	periplasmic protein (lipoprotein, hemolysin)		Named proteins of general function	15.178	15.598	15.503	15.769	2.26E-02	1.15E-01	0.42	0.27
lpg2992	periplasmic protein (lipoprotein, hemolysin)		Named proteins of general function	15.173	15.623	15.456	15.742	5.50E-03	1.11E-01	0.45	0.29
lpg2993	phosphoheptose isomerase	*gmhA*	Metabolism of Complex Carbohydrate	10.841	9.848	9.620	11.263	2.93E-02	1.66E-03	-0.99	1.64
lpg2993	phosphoheptose isomerase	*gmhA*	Metabolism of Complex Carbohydrate	10.669	9.991	8.537	11.242	2.93E-01	4.48E-02	-0.68	2.71
lpg2994	hypothetical (endonuclease?) uncharacterised protein family UPF010		Unknown / hypothetical proteins	9.235	8.914	7.932	8.878	4.15E-01	2.87E-01	-0.32	0.95
lpg2994	hypothetical (endonuclease?) uncharacterised protein family UPF010		Unknown / hypothetical proteins	9.246	9.258	7.796	8.746	9.83E-01	2.56E-01	0.01	0.95
lpg2995	lipoprotein (exported protein)		Named proteins of general function	10.228	10.113	9.353	11.958	6.62E-01	1.67E-04	-0.11	2.61
lpg2995	lipoprotein (exported protein)		Named proteins of general function	9.311	9.963	9.293	11.945	5.32E-01	1.58E-04	0.65	2.65
lpg2996	tetrapyrrole (corrin/porphyrin) methylase (hypothetical protein HI1654		Metabolism of Cofactors and Vitamins	9.477	10.753	10.050	10.101	4.85E-02	9.22E-01	1.28	0.05
lpg2996	tetrapyrrole (corrin/porphyrin) methylase (hypothetical protein HI1654		Metabolism of Cofactors and Vitamins	9.378	10.326	9.729	9.905	1.14E-01	7.39E-01	0.95	0.18
lpg2997	alkane-1-monooxygenase (alkane hydroxylase)		Named proteins of general function	9.577	10.141	9.863	9.586	4.33E-01	6.38E-01	0.56	-0.28
lpg2997	alkane-1-monooxygenase (alkane hydroxylase)		Named proteins of general function	9.249	10.616	8.599	10.277	1.08E-01	2.11E-01	1.37	1.68
lpg2998	sulfate transporter (sulfate permease)		Transport and binding	10.577	9.645	10.594	9.838	1.24E-02	1.72E-01	-0.93	-0.76
lpg2998	sulfate transporter (sulfate permease)		Transport and binding	10.764	9.864	10.763	10.446	1.26E-02	4.82E-01	-0.90	-0.32
lpg2999	CG6763 gene product (eukaryotic homologs?)	*legP*	Unknown / hypothetical proteins	12.569	13.184	12.291	13.214	3.31E-01	3.11E-02	0.61	0.92
lpg2999	CG6763 gene product (eukaryotic homologs?)	*legP*	Unknown / hypothetical proteins	12.638	13.571	12.483	13.678	2.21E-01	4.90E-02	0.93	1.20
lpg3000	ORF		ORFs of unknown function (unique)	11.798	14.605	11.445	13.177	4.13E-08	3.32E-07	2.81	1.73
lpg3000	ORF		ORFs of unknown function (unique)	11.763	14.588	11.451	13.183	2.86E-08	3.87E-07	2.83	1.73
lpg3001	GTP binding protein in thiophene and furan oxidation (G	*thdF*	Named proteins of general function	10.392	7.242	8.600	7.902	6.93E-03	5.63E-01	-3.15	-0.70
lpg3001	GTP binding protein in thiophene and furan oxidation (G	*thdF*	Named proteins of general function	10.197	7.780	8.106	7.708	3.28E-02	7.20E-01	-2.42	-0.40

lpg3002	inner membrane protein, 60 kDa		Named proteins of general function	13.025	11.792	10.395	12.838	6.88E-02	6.91E-03	-1.23	2.44
lpg3002	inner membrane protein, 60 kDa		Named proteins of general function	13.042	11.832	10.060	12.863	7.35E-02	6.35E-03	-1.21	2.80
lpg3003	conserved hypothetical protein TIGR00278, COG0759		Unknown / hypothetical proteins	13.325	10.593	9.455	11.957	1.18E-03	3.39E-02	-2.73	2.50
lpg3003	conserved hypothetical protein TIGR00278, COG0759		Unknown / hypothetical proteins	13.142	11.145	9.927	12.798	4.37E-02	1.55E-02	-2.00	2.87
lpg3004	ribonuclease P protein component	*rnpA*	DNA/RNA degradation / restriction, Tra	13.307	10.272	8.859	11.770	3.61E-03	1.66E-02	-3.03	2.91
lpg3004	ribonuclease P protein component	*rnpA*	DNA/RNA degradation / restriction, Tra	13.431	10.131	8.547	11.575	1.53E-03	3.78E-02	-3.30	3.03
lpg3005	50S ribosomal protein L34	*rpmH*	Translation	12.338	10.980	9.537	12.268	4.92E-01	7.65E-03	-1.36	2.73
lpg3005	50S ribosomal protein L34	*rpmH*	Translation	12.643	10.814	9.144	12.316	2.77E-01	5.23E-03	-1.83	3.17

† $\log_2$ of all replicates averaged

* $\log_2$