Supplementary Results

Proteome statistics

The PeptideAtlas build was constructed using the sequence search results of 108,000 correct MS/MS spectra ($P \geq 0.9$). We identified 16543 unique peptides at a peptide false discovery rate (FDR) of less than 1% [1] which represented 2221 proteins at a protein FDR of less than 1%. Overall, the identified proteins matched to 62% of the predicted gene models and contained 75% (1291 proteins) of the known or characterized proteins, 51% (85) of the proteins with putative function and 49% (867) of the hypothetical proteins. The data was compiled into a publicly accessible instance of PeptideAtlas [2] to facilitate further studies of Leptospirosis employing targeted proteomics. We used Gene Ontology (GO) [3] to group the identified proteins according to their cellular function. The largest GO groups of identified proteins were metabolic enzymes (22.5%; 501 proteins) and proteins that are not associated with a specific cellular process (50%; 1123 proteins). About 12% of the proteins were associated with the functions “transcription”, “translation”, “protein folding” and “protein degradation”, while only 0.5% were associated with the function “stress response” (Supplementary Figure 1). The estimated false discovery rate (FDR) for spectra in the atlas is 0.006, and the combined sensitivity is estimated at 90%. All the data is available for browsing and downloading at http://www.peptideatlas.org/.

Stress-induced changes in the Leptospira proteome

We used inclusion list based to relatively quantify changes that occur in the Leptospira proteome as a response to stress (Figure 2). Overall, this procedure allowed us to identify and quantify ~1000 proteins in each cell state tested, corresponding to ~45% of the observable proteome (Supplementary Table 3).

Starvation state: During starvation, the cytoplasmic concentration of most protein complexes involved in metabolic reactions and protein folding was reduced at least 2-fold (Figure 2). This was associated with significant morphological changes of L. interrogans cells from an elongated shape with a single cytoplasmic membrane and cell wall layer to compact cells with several membrane layers (Figure 2). This to our knowledge so far uncharacterized cell form for this species turned out to be unsuitable for template matching because its larger diameter interfered with electron beam penetration. Some of the proteases, particularly Lon, HtpX, aminopeptidase A and metallopeptidase M20 were up-regulated. The data also verified several previously observed proteomic changes such as the decrease in sporulation stage II anti-antisigma factor SpoIIAA levels [4] and the 2.5 fold increase in Dps, a protein providing DNA protection during starvation. Overall, the observed pattern of proteomic changes is consistent with the transition of the cells into a resting state with a stalled metabolism.

Ciprofloxacin treatment: Ciprofloxacin is a commonly used drug against Leptospirosis and inhibits DNA-gyrase [5] that causes the cell to compensate for the DNA-topo-isomeric stress by an up-regulation of recombinase A [6,7]. After 24h of antibiotic treatment with 5 μg/ml Ciprofloxacin we observed a fifteen-fold increase of recombinase A, whereas the ribosomal concentration decreased by 25%. A fifteen-fold decrease of DnaK-suppressor resulted in a three-fold DnaK abundance increase, whereas DnaJ, clpX and clpP remained unchanged. While the concentration of the unfoldase clpB increased by ~50% the concentration of the Hsp15 proteins decreased by thirty- to forty-fold (Figure 2). Under the chosen conditions antibiotic treatment did not result in significant morphological changes. These changes were accompanied by a massive up-regulation of a cluster of proteins of unknown function that have so far been annotated as hypothetical (Figure 2). Using proteome wide absolute abundance determination we estimate that the fraction of the total cellular proteome represented by the products of these genes increased from less than 1% to 20% upon antibiotic treatment [8]. Also, most of the proteases and cytoplasmic proteins involved cell shape determination and division that were targeted, did not exhibit significant changes (Figure 2). Despite the presence of increased amounts of DnaK-suppressor we were able to detect two transcription factors of the TetR- and ArsR-family that underwent pronounced changes in abundance under these conditions. They might be key regulators for the formidable adjustments of protein expression we observed. Another candidate for the transcriptional control of these processes is the product of gene LIC10526: The heat-inducible transcriptional repressor was below the detection limit in control cells, implying a very low abundance, but seven-fold enriched in heat-shock and antibiotics-stimulated cells as compared to the starved condition. The gene product of LIC20013, a CheY-like response regulator of the chemotaxis system, was strongly induced under heat-shock as well as antibiotics-stimulated conditions. In contrast, an entire set of seven additional CheY-proteins showed no response [9]. Obviously, *L. interrogans* cells undergo substantial adjustments in the proteome when reacting to stress induced by antibiotics.

Heat shock/fever state: After 1h of stimulation at 42°C the concentration of two gene products, Hsp15 and Hsp15-like, increased by more than ten-fold (Figure 2), while most of the other complexes involved in stress response, e.g. the proteins of the clp system and Hsp90, remained unchanged. DnaJ and DnaK were up-regulated by 60-75% (Supplementary Table 3). These changes are consistent with the response to heat induced protein unfolding. In contrast to the starvation state, heat shock treatment did not induce significant morphological changes.

Noise models and generation of Phantom cells

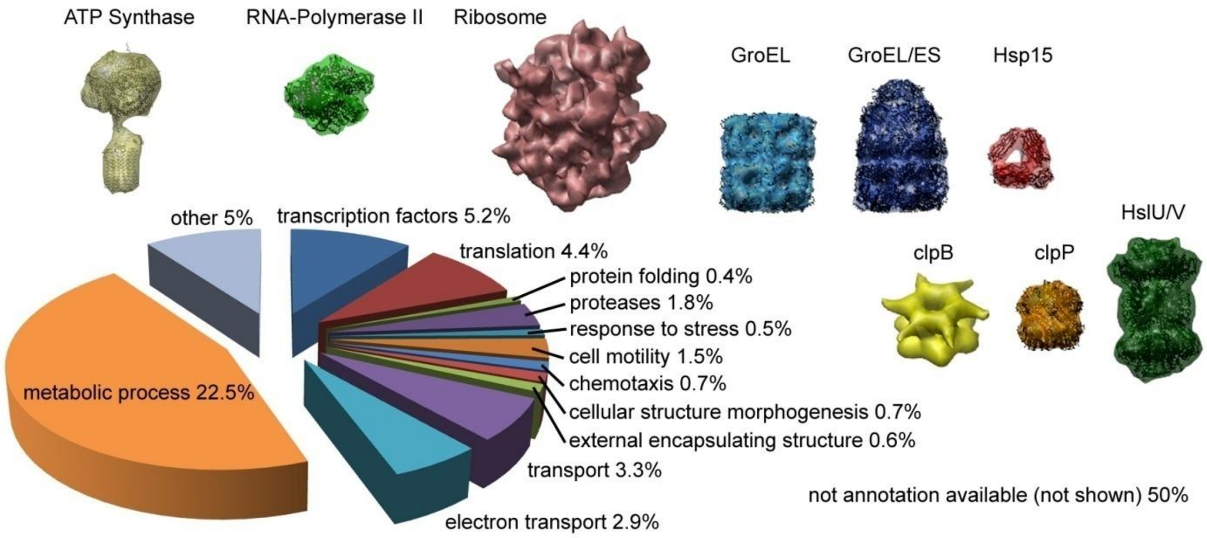
We initially generated test data sets (phantom cells) in silico that contained the selected target protein complexes at the relevant sampling rate, contrast transfer function (CTF), modulation transfer function (MTF) as well as angular coverage of a real tomogram and adjusted the noise level with a kernel corresponding to the distribution of the electron optical density observed within non-occupied regions in real datasets. In such simulations the majority of the chosen template protein complexes were detected with good confidence (not shown). However, a recent detailed analysis of the noise components in single particle cryo electron microscopy has indicated that the noise models used to date and in our experiments mentioned above might not be adequate. It was shown that structural noise (caused by the structural diversity of the macromolecules themselves) is of the same order of magnitude as the other noise components [10]. Since this finding might imply that the structural diversity of the targeted macromolecules could influence the cross-correlation intensity to such an extent that true matches are difficult to discriminate from pure noise correlation, we decided to account for this problem in the test data (see main text).

Detection of ATP-Synthase and Hsp15

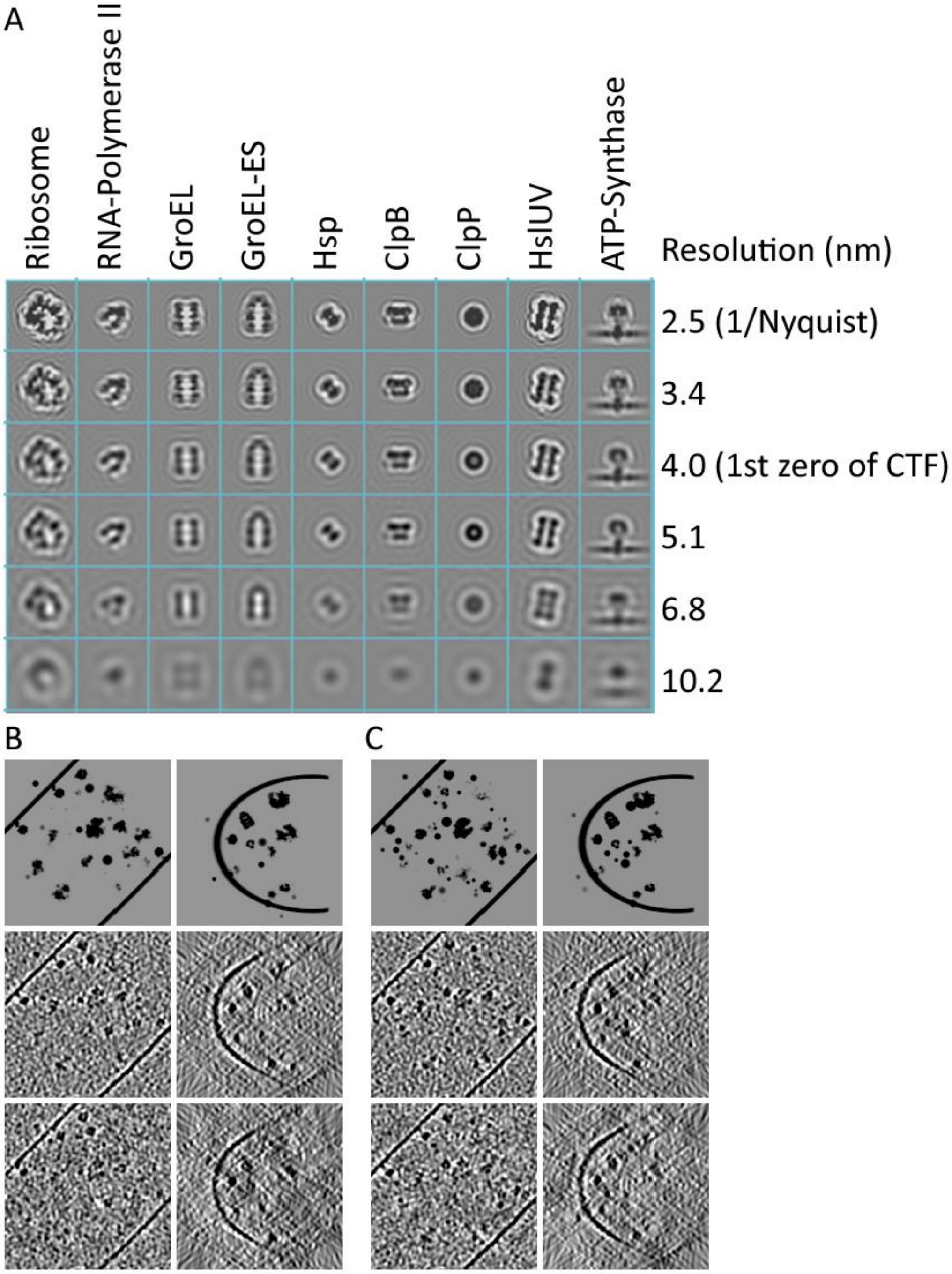
The detection of ATP-Synthase is complicated by an angular bias problem: The cross-correlation intensity is dependent on the spatial orientation. Since membranes are highly entropic structures and the electron optical density is higher inside of the cells than outside false positive hits can match to the membrane domain but still to incorrect positions. This finding illustrates the difficulty of detecting membrane proteins and is further complicated by the ‘missing wedge’ problem that can introduce an angular bias to the detection. By filtering out ‘top and down’ views the performance can be improved up to 60% specificity but on the cost of sensitivity (angular bias correction).

Small heat shock proteins have been shown to form different oligomeric states in vitro in some [11] but not all investigated species [12]. The structure most closely related to Hsp15 (pdb_2BYU) that served as a template in this study forms a dodecameric assembly. We have also matched a tetracosameric form (pdb_1shs) as an alternative, but observed lower cross-correlation intensities. Nevertheless, if a protein complex is not fully assembled or the oligomeric form present in the template database is not the predominant form in the cell, the separation of false from true positives is blurred.

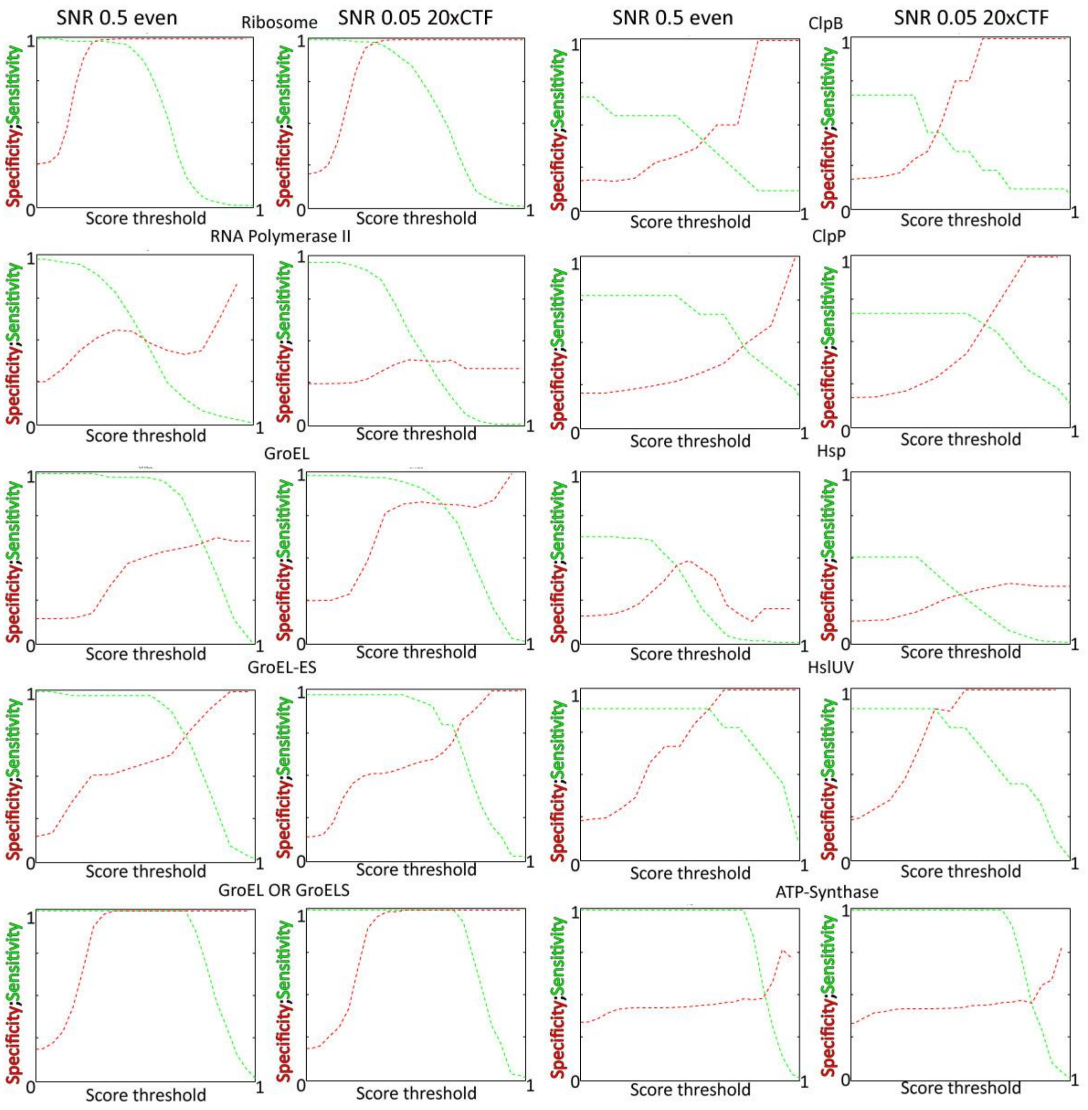
Supplementary Figures



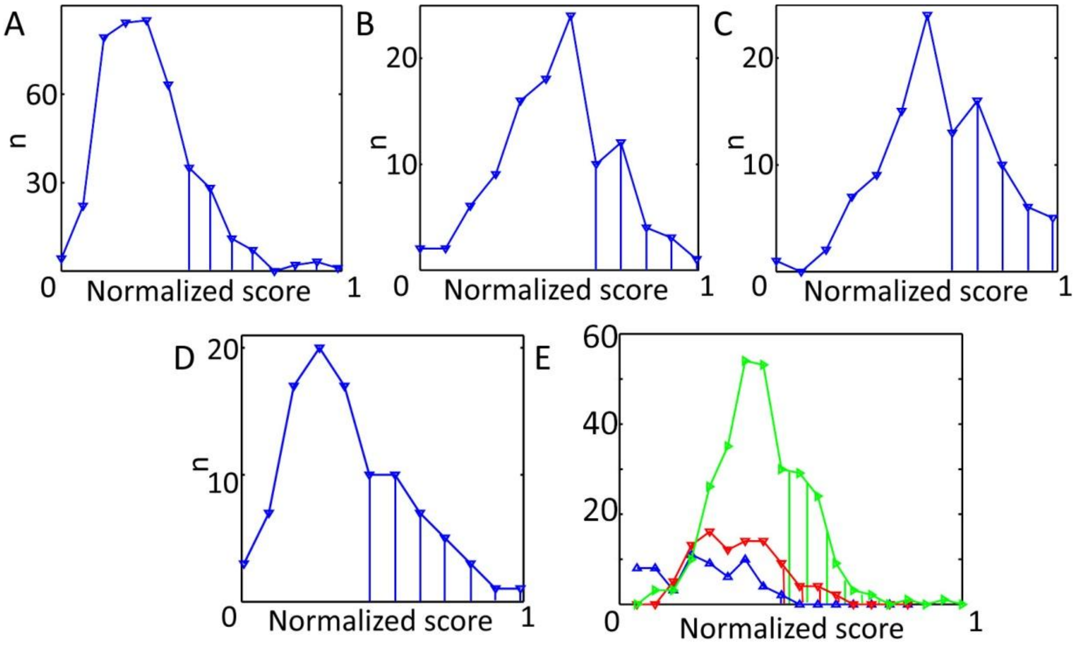
Supplementary Figure 1. Proteome of *Leptospira interrogans* with an emphasis on conserved protein complexes of known structure. 61% of the open reading frames in *Leptospira interrogans* were identified by shotgun proteomics (data available at www.peptideatlas.org). The distribution of the assigned function of the identified proteins (based on GeneOntologies) is shown as a pie chart, where the genes without any annotation available (50%) were omitted. Conserved protein complexes (Table 1) that have been localized in electron tomograms by template matching (see below), are shown as surface rendered views, superimposed with amino acid chain traces (in black, if applicable). These protein complexes are: ATP-Synthase (ATP generation); RNA-Polymerase II (transcription); ribosome (translation); GroEL, GroES, Hsp15 (protein folding) and clpB, clpP, HslU/HslV (protein unfolding and degradation). The templates have been filtered to 4 nm resolution (1st zero of CTF) for template matching (Supplementary Figure 2).



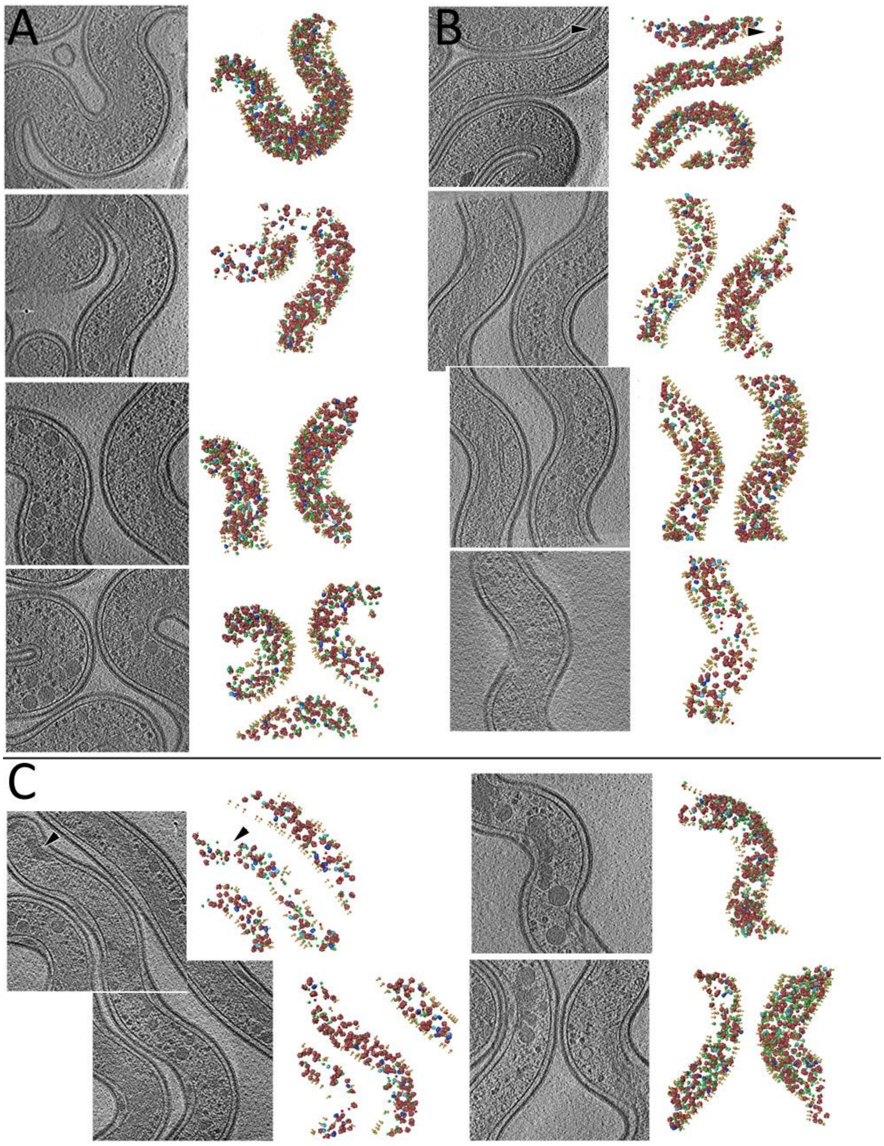
Supplementary Figure 2. CTF-convoluted templates and the effect of molecular crowding. (A) Template library after convolution with CTF, low-pass filtered to the indicated resolution. The chosen templates are distinct up to a resolution of ~5nm. In case of ATP-Synthase a disc shaped density (5 nm radius) was added around the transmembrane domain for template matching. (B-C) Same as Figure 3A and B but for *in silico* test data (phantom cells) in which a moderate (B) or high (C) number of spherical decoys was placed to the periphery of the templates to simulate molecular crowding. Notably, at the given resolution of cryoET this effect has a similar influence as structural noise in single particle electron microscopy: If additional mass (representing other proteins in the local proximity within the cell) is present within the area in which the local cross-correlation is calculated it will cause a decrease in the observed cross-correlation intensity. Although, our chosen template protein complexes comprise for a significant proportion (~25%) of the total cellular protein [8] we have investigated this effect by adding spherical shaped decoys into the proximity of the target proteins complexes in phantom cells in separate test runs: When a moderate number of decoys was added to the empty phantom cell space the discovery rates of all templates decrease slightly. However, if a massive amount of decoys with in part higher electron optical density than the target protein complexes was simulated, the performance was affected to such an extent that only the very large protein complexes (Ribosome, GroEL/GroELS and HslUV) could be discriminated from pure noise correlation. Unprocessed cells are shown on top, cells processed with the conservative noise model (SNR 0.5, even quantum and detector noise contribution) in the middle and cells processed with the optimistic noise model (SNR 0.05, predominate quantum noise contribution) at the bottom.



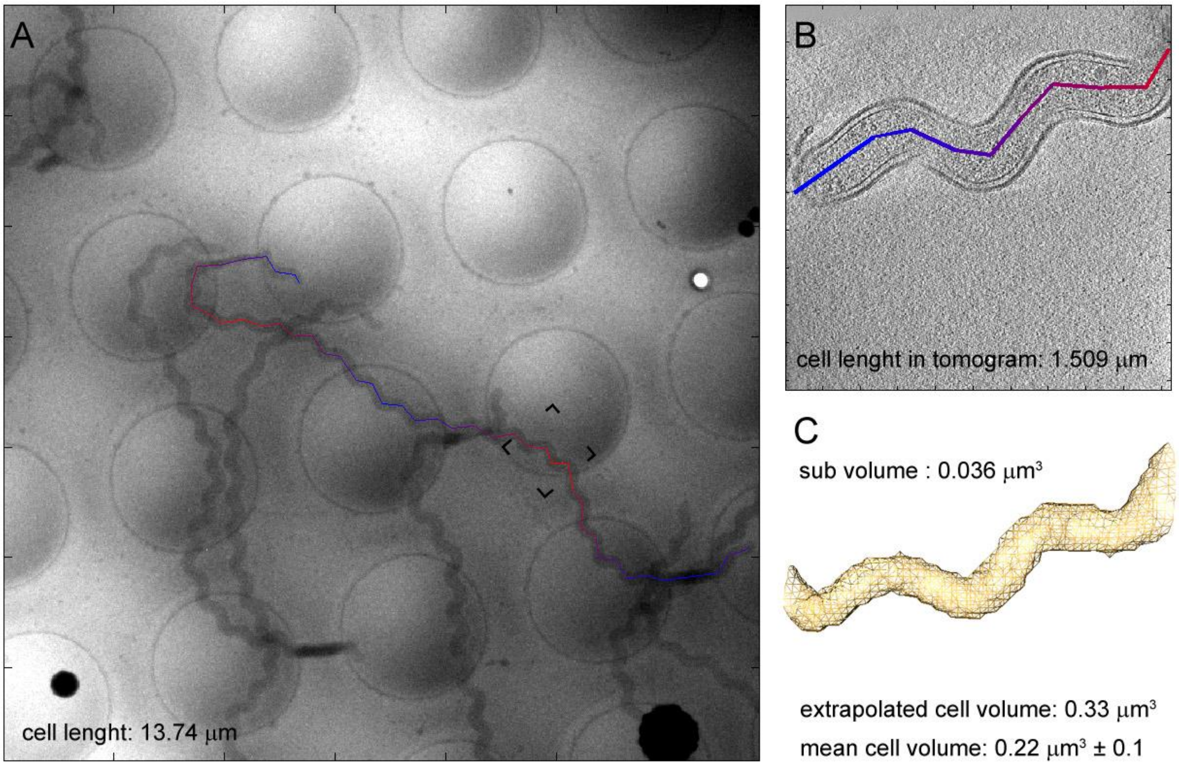
Supplementary Figure 3. Performance of template discovery in *in silico* test data sets (specificity in red, sensitivity in green). Curves for all templates and both noise models discussed in the main text are shown (in case of ATP-Synthase without angular bias correction). In cases in which the red specificity curve goes through an optimum the true from false positive discrimination is poor and the performance will be largely dependent on the template abundance in the cell.



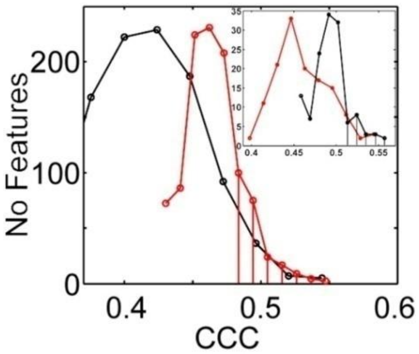
Supplementary Figure 4. Score distributions from selected real data sets of the Ribosome (A), GroEL (B), GroEL-ES (C), ATP-Syntase and Hsp (E) as shown for RNA-Polymerase in Figure 3. The area under the curve marked with vertical lines indicates the absolute abundance of these protein complexes in the respective tomographic volumes as determined by SRM mass spectrometry. In case of GroEL and GroEL-ES the abundance of GroEL alone has been used to fill the area und both distributions due their curve shape, since *Leptospira* cells express GroES in excess to GroEL. In case of Hsp15 the score distribution from tomograms of similar volume of the untreated (blue), heat-shocked (red) and ciprofloxacin-treated state (green). The statistical model improves with the increasing cellular abundance of Hsp.



Supplementary Figure 5. Template matching in tomograms of *Leptospira interrogans* cells of the non-stimulated (A), heat-shocked (B) and antibiotics-treated condition (C). A slice through the three-dimensional reconstruction is shown at the left, the localization of all detected protein complexes on the right (Color-coding according to Supplementary Figure 1). Large sphere-shape homogeneous densities displace protein complexes. The same is true for flagellar motors apparent in two cells tips (arrowheads).



Supplementary Figure 6. Volume determination. (A) The cell length was determined from electron micrographs taken at low magnification that contained the entire cell body. *Leptospira* cells had an average cell length of 11.6 μm with a standard deviation of 3.85 μm. (B) The cell length covered by the individual tomograms was determined in the same way (framed in A). (C) The cytoplasmic subvolume covered by the individual tomograms was determined by semi-automatic segmentation in Amira and summing up the relevant voxels. Afterwards the total cell volume was estimated by extrapolation of the cytoplasmic subvolme to the total cell length. The numbers shown are examples for the depicted cell; the average cytoplasmic volume of all cells was 0.22 μm^3.



Supplementary Figure 7. Distribution of cross correlation coefficients (CCCs) extracted from three tomograms of the antibiotics treated state for Hsp15 (red) and a competing template of similar size (ClpP, black) at the very same coordinates (inset: vice versa). The CCCs were extracted from three tomograms of the antibiotics-treated state that cover ~25% of the average cell volume. The area under the apparent 'shoulder' of ~250 features corresponds roughly to the expected abundance of Hsp15 (~300 complexes in the relevant subvolumes). The CCCs of ClpP, a competing template of similar size, that were extracted from the very same coordinates, have a lower intensity (black) and different curve shape indicating noise correlation. Inset: the distribution of the highest CCCs of ClpP has a 'shoulder' covering ~25 features (inset, black), while ~35 complexes would be expected in a subvolume of this size. Although Hsp15 is 10-fold more abundant than ClpP under these conditions (Table 1), the CCCs for this competing template extracted from the same coordinates have a lower intensity (red).

Supplementary Table 1 Structures of protein complex candidates for template matching

Template	Reference	Oligomeric state	Molecular Mass [kDa]	Complexes per Cell	Method
Ribosome	Pdb_ 2AW7_2AWB	Multicomponent protomer	2200	4500	SRM
RNA Polymerase	pdb_2GHO	Multicomponent protomer	340	3000	SRM
ATP Synthase	pdb_1QO1	6mer	450	1500	SRM
GroEL	pdb_1KP8	14mer	810	1100	SRM
GroELS	pdb_1aon	21mer	870		
Hsp15	pdb_2BYU	12mer	220	40	SRM
clpB	emd_1243	6mer	600	70	SRM
clpP	pdb_1YG6	14mer	304	140	SRM
HslUV	pdb_1G3I	24mer	830	20	SRM
Transaldolase	pdb_1vpx	20mer	520	150	MS1
Bacterioferretin	pdb_1BFR	24mer	450	4	SPC
GTP-Cyclohydrolase	pdb_1GTP	20mer	500	75	MS1
Glutamine Synthase	pdb_2gls	12mer	620	320	SPC
Lumazine Synthase	pdb_1NQU	5mer	420	4	SPC
Acetyl-CoA-Carboxylase	pdb_1vrg	6mer	350	40	SPC
Acetolactate Synthase	pdb_1OZF	4mer	250	10	SPC
Aspartyl-tRNA-Synthase	pdb_1eqr	3mer	200	100	SPC
Carbamoyl Phosphatase	pdb_1bxr	8mer	650	120	SPC
Citrate Synthase	pdb_2h12	6mer	300	220	MS1
Cytosolic Amino-Peptidase	pdb_1gyt	12mer	660	90	MS1
Dihydrolipoamide Acetyl-Transferase	pdb_1dpb	24mer	640	30	MS1
Enolase	pdb_1w6t	8mer	390	100	MS1
LIC11615_UbiD	pdb_2idb	6mer	350	17	SPC
Ornithine Carbamoyltransferase	pdb_1a1s	12mer	420	65	MS1
Phoshoribosyl-Pyrophosphatase	pdb_1dkr	6mer	210	55	MS1
Aspartate Carbamoyltransferase	pdb_1f1b	12mer	300	10	SPC

Supplementary Table 1. List of protein complexes that were initially candidates for template matching. Please not that only the templates 1-9 are discussed in the main text. The absolute abundance was in the cell was measured by SRM or estimated as described [8] based on spectral counts (SPC) or MS1 intensities (MS1).

Supplementary Table 2 Absolute quantification based on SRM [fmol/μl]

gi No and description	peptide sequence	Control	Heat-shocked	Antibiotics-treated	Starved
45657124 ATP synthase A	ILEVPVGPELLGR	20.95	20.36	31.72	22.91
45657124 ATP synthase A	TSIALDTILNQK	27.21	28.24	38.23	24.57
45657126 ATP synthase B	FSQAGSEVSALLGR	15.40	15.09	21.49	14.16
45657869 ClpB	AVDLIDEASSK	1.02	1.00	1.13	0.74
45657869 ClpB	IADIQLEGLR	1.66	1.60	2.54	1.19
45657810 ClpP	IAEVFEELTGSK	8.07	6.66	8.95	6.03
45657810 ClpP	IFLWGPVTDESSK	2.93	2.12	1.71	0.99
45657810 ClpP	LNQILADACGHPISK	5.93	4.64	4.24	2.11
45656498 Fatty acid synthase	TEVITHANLVR	4.37	2.90	2.41	2.08
45659137 Fatty acid synthase	AIAEEVPK	3.48	2.86	1.64	1.312
45659137 Fatty acid synthase	EFFDTSFK	6.82	5.46	3.25	2.53
45657072 flagellar hook protein	VATAVFNNPAGLDK	0.34	0.18	0.28	0.32
45657269 flagellar M-ring protein	GFTPDGPAGTEPNIAPGYK	0.16	0.13	0.15	0.19
45657269 flagellar M-ring protein	IISDFEEDLEK	0.12	0.08	0.09	0.09
45657753 flagellin protein	ANLGAYFNR	47.25	43.70	72.95	94.99
45657753 flagellin protein	VLAIQSSNGIYSAEDR	29.68	27.26	51.44	58.82
45657213 GroEL	AVTAAVESIQK	48.48	56.06	50.17	40.00
45657213 GroEL	VEDALSATR	47.96	53.88	60.18	52.18
45657214 GroES	ESDILAVVK	32.85	31.99	19.50	9.75
45657214 GroES	VGDTVLYGK	53.05	54.33	48.87	22.88
45657473 hslU	HGSGQITGFATSSTLADEEDRK	0.77	0.57	0.47	0.34
45657473 hslU	LLEEVSFEGPDLPESQR	0.95	0.81	1.01	0.83
45658059 HSP15-like	ILELPTEVDSEK	0.79	7.44	26.74	0.31
45658060 HSP15	DVQVQLEK	0.67	7.01	15.51	0.18
45657141 MreB	GIVLTGGGCLLR	11.21	11.86	16.49	12.17
45657141 MreB	TGGDEFDEAIIK	5.70	5.32	8.29	7.02
45657611 recombinase A	IVEIYGPESSGK	2.58	2.30	33.70	2.16
45656646 50s Ribosome L7/12	LTLVEAADLVK	133.05	119.43	107.56	28.39
45657961 30S Ribosome S6	EFLINQNILR	19.13	14.83	11.49	4.57
45658686 30S Ribosome S5	FSFNALSVVGDQR	10.14	8.51	7.22	1.80
45656647 RNA-Polymerase beta	ITNLDYLPNLIQIQK	10.05	10.21	10.59	10.59
45656647 RNA-Polymerase beta	TFDLGEVGR	9.70	9.52	10.35	10.21
45656648 RNA-Polymerase beta	FATSDLNDLYR	9.48	9.10	8.29	8.58

Supplementary Table 2. Absolute quantification based on SRM. The observed values corresponding to the stable isotope labeled reference peptides used are given in [fmol/μl].

Supplementary Table 3 Relative quantification based on MS1 intensities

gi No	Annotation	C2H	Std	NF	C2AB	Std	NF	C2S	Std	NF	H2AB	Std	NF	H2S	Std	NF	AB2S	Std	NF
45655586	hypothetical protein LIC20001	1.14	0.5	10	1.02	0.3	10	0.81	0.6	7	0.91	0.4	10	0.75	0.4	8	0.82	0.5	8
45655594	glutamate-1-semialdehyde aminotransferase	0.73	0.5	5	0.47	0.2	4	0.34	0.1	3	0.68	0.3	5	3.09	4.5	3	0.48	0.1	3
45655596	response regulator	8.96	11.0	3	10.28	9.2	2				0.79	0.0	2						
45655609	short-chain dehydrogenase	1.42	0.2	2	1.49	0.3	2	2.48	0.8	2	3.29	4.6	4	6.17	6.4	5	4.98	6.7	4
45655611	NADH dehydrogenase	1.43	0.2	10	1.49	0.4	12	1.77	0.5	12	0.99	0.2	10	1.34	0.2	11	1.21	0.3	12
45655613	hypothetical protein LIC20030	1.19	0.1	2	2.57	0.7	2	2.46	0.4	2	2.19	0.8	2	2.09	0.5	2	1.11	0.3	3
45655615	hypothetical protein LIC20032	0.85	0.2	2	0.57	0.1	2	0.42	0.2	2	0.72	0.3	2	0.54	0.3	2	0.73	0.1	2
45655618	hypothetical protein LIC20035	0.69	0.2	11	0.87	0.1	11	0.60	0.1	9	1.46	0.4	11	0.90	0.3	9	0.73	0.2	10
45655619	hypothetical protein LIC20036	0.93	0.6	2	0.88	0.3	2				1.06	0.4	2						
45655627	heat shock protein 90	0.98	0.2	25	0.62	0.3	26	0.36	0.2	20	0.66	0.3	26	0.31	0.2	19	0.51	0.3	20
45655641	methylmalonyl-CoA mutase	0.88	0.3	10	1.00	0.3	10	0.67	0.5	11	1.19	0.3	9	0.84	0.5	10	0.52	0.2	10
45655645	phosphoribosyl-ATP pyrophosphatase	0.44	0.1	4															
45655647	3-oxoacyl-(acyl-carrier protein) reductase	0.79	0.1	4	0.47	0.1	4	0.08	0.0	4	0.53	0.2	5	0.11	0.0	4	0.18	0.1	4
45655660	polysaccharide deacetylase	1.39	0.8	2	0.37	0.1	3												
45655661	hypothetical protein LIC20078	0.85	0.1	12	0.58	0.3	13	0.17	0.1	10	0.64	0.4	14	0.14	0.1	9	0.30	0.1	10
45655666	S-adenosyl-L-homocysteine hydrolase	0.82	0.1	13	0.46	0.1	13	0.20	0.1	12	0.57	0.2	14	0.20	0.1	11	0.37	0.2	11
45655668	B12-dependent homocysteine-N5-methyltetrahydrofolate transmethylase	1.03	0.1	7	0.45	0.2	6	0.30	0.1	3	0.48	0.2	6	0.37	0.2	3	0.60	0.4	3
45655676	bacterioferritin comigratory protein	0.58	0.0	3	1.32	1.7	4	0.30	0.1	2	0.85	0.7	3	0.50	0.2	2	0.58	0.5	2
45655679	hypothetical protein LIC20096	1.53	0.4	6	1.90	1.1	5	5.72	4.3	6	1.14	0.5	5	3.41	2.0	6	3.71	0.4	4
45655680	short-chain dehydrogenase	1.14	0.2	2	0.86	0.2	2	0.78	0.6	2	0.80	0.4	2	0.76	0.7	2	0.84	0.5	2
45655681	phage-related integrase/recombinase													0.40	0.2	2			
45655683	hypothetical protein LIC20100	0.65	0.1	4	1.10	0.4	5	0.54	0.2	4	1.54	0.4	5	0.80	0.2	4	0.62	0.1	5
45655684	CheD	0.91	0.6	4	1.70	0.7	4				2.10	1.0	4						
45655700	hypothetical protein LIC20118	1.00	0.4	3	2.09	0.7	3	18.11	18.0	3	1.90	0.5	4	14.21	9.1	4	4.79	2.2	4
45655718	hypothetical protein LIC20136				1.39	1.1	2	3.99	2.1	3	0.90	0.1	2	4.84	1.7	3	4.95	1.7	4
45655720	capsular polysaccharide biosynthesis protein	0.95	0.5	2	0.90	0.1	2				1.12	0.7	2						
45655725	HtrA1	0.85	0.1	4	0.66	0.3	5	2.27	0.4	6	0.90	0.3	6	2.74	0.7	4	3.27	0.9	4
45655726	HtrA1-like protein	1.60	1.0	5	0.83	0.6	4	2.14	1.5	5	0.65	0.3	4	1.59	0.4	4	1.63	1.1	5
45655728	hypothetical protein LIC20146																2.40	2.4	2
45655730	heme oxygenase	0.69	0.1	3	0.53	0.0	3	0.28	0.1	3	0.78	0.1	3	0.41	0.0	3	0.53	0.1	3
45655735	hypothetical protein LIC20153	0.70	1.0	4	0.48	0.2	4				2.73	2.1	4						
45655738	hypothetical protein LIC20156	0.45	0.0	2	0.25	0.1	2				0.55	0.1	2						
45655754	lipoprotein	1.05	0.3	4	1.91	0.5	5				1.59	0.3	4						
45655757	dnaK suppressor	0.62	0.2	6	0.07	0.0	2				0.12	0.0	2						
45655767	hypothetical protein LIC20185	1.29	0.3	8	0.49	0.4	8	0.63	0.4	9	0.39	0.4	8	0.50	0.3	8	1.25	1.3	8
45655776	hypothetical protein LIC20196	0.61	0.1	5	1.81	0.1	6	0.57	0.1	5	2.41	0.4	5	0.85	0.2	5	0.33	0.0	5
45655777	cysteine protease	0.63	0.3	9	0.69	0.4	8	0.27	0.1	2	1.09	0.7	9	0.73	0.3	2			
45655785	hypothetical protein LIC20205	1.10	0.1	5	0.58	0.2	4	0.53	0.3	4	0.47	0.2	5	2.53	4.8	7	1.15	0.6	4
45655788	methylmalonyl-COA mutase small subunit	1.07	0.2	4	0.54	0.1	4	0.52	0.1	4	0.49	0.1	5	0.45	0.0	4	1.02	0.2	5
45655789	methylmalonyl-CoA mutase	0.88	0.5	4	0.95	0.4	4	0.38	0.1	3	1.43	1.2	4	0.59	0.5	3	0.35	0.1	3
45655796	ExbB	0.99	0.3	3	1.70	0.5	3	3.30	1.3	3	1.79	0.6	3	3.47	1.6	3	2.17	1.2	3
45655797	ExbD	1.04	0.5	2	1.37	0.3	2				1.54	1.0	2						
45655807	acireductone dioxygenase enzyme ARD and ARD'	0.37	0.1	4	1.05	0.8	4				3.01	2.5	4						
45655814	S-adenosylmethionine decarboxylase like protein	1.01	0.9	3	0.79	1.0	2				0.42	0.5	2						
45655816	hypothetical protein LIC20240				0.88	0.1	2												
45655824	aconitate hydratase	0.77	0.2	19	1.06	0.5	22	0.68	0.3	20	1.40	0.6	19	0.87	0.3	18	0.68	0.3	20
45655825	peptidoglycan-associated cytoplasmic membrane protein	1.48	0.3	4	1.67	0.2	4	0.78	0.5	2	1.16	0.3	4	0.50	0.1	2	0.41	0.2	2

45655829	response regulator										1.17	0.7	2	2.61	0.6	2	2.52	1.0	2
45655841	aspartate-semialdehyde dehydrogenase	0.72	0.1	3	0.55	0.5	2	0.24	0.0	2	0.82	0.8	2	0.33	0.1	2	0.76	0.7	2
45655849	ParA	1.47	0.4	2	1.31	0.2	2				0.91	0.1	2						
45655850	ParB	1.64	0.5	3	1.19	1.0	3	2.01	1.9	3	0.67	0.4	3	1.43	1.7	3	2.43	2.8	3
45655916	DNA polymerase III beta subunit	0.71	0.3	10	1.15	0.2	9	0.96	0.3	10	1.36	0.5	10	1.40	0.5	10	0.88	0.3	10
45655919	DNA gyrase subunit B	1.29	0.4	6	0.87	0.7	6	1.08	0.5	3	0.77	0.3	5	0.73	0.1	3	0.78	0.2	3
45655920	DNA gyrase subunit A	1.31	0.2	15	1.06	0.2	15	1.11	0.5	11	0.86	0.3	15	0.90	0.4	12	1.25	0.7	13
45655923	putative lipoprotein	0.98	0.2	13	1.75	0.5	13	1.06	0.2	11	1.90	0.3	14	1.06	0.4	13	0.57	0.2	12
45655925	LipL21	1.08	0.3	10	1.10	0.2	10	2.32	0.6	10	1.05	0.6	10	2.10	0.9	10	2.14	0.5	10
45655931	hypothetical protein LIC10017				0.37	0.1	2												
45655933	3-oxoacyl-acyl carrier protein reductase	1.10	0.3	2	0.76	0.1	2	0.38	0.3	2	0.73	0.3	2	0.32	0.2	2	0.52	0.4	2
45655942	putative lipoprotein	0.89	0.2	3	0.87	0.1	3	0.84	0.2	3	0.99	0.1	3	0.96	0.2	3	0.97	0.1	3
45655943	inositol monophosphatase	0.65	0.3	2	0.86	0.2	2												
45655945	beta-galactosidase	1.46	0.5	5	1.12	0.1	4	3.09	0.8	4	0.89	0.3	4	3.04	1.5	5	2.72	0.6	5
45655951	GMC oxidoreductase				1.11	0.3	2	1.23	0.2	2							1.17	0.5	2
45655957	Aer	0.93	0.4	2	0.71	0.1	2	1.03	0.2	2	0.83	0.3	2	1.17	0.3	2	1.44	0.1	2
45655959	dTDP-glucose 4-6-dehydratase	1.20	0.2	8	0.90	0.4	7	0.57	0.2	6	0.88	0.4	8	0.47	0.1	6	0.66	0.1	5
45655960	proton-translocating transhydrogenase, subunit alpha part 1	0.89	0.1	16	1.21	0.3	17	1.64	0.5	15	1.28	0.4	18	1.85	0.6	16	1.43	0.5	16
45655968	putative lipoprotein	0.54	0.1	5															
45655974	hypothetical protein LIC10060	1.29	0.3	10	1.55	0.4	10	2.43	1.0	11	1.40	0.6	10	1.96	0.8	11	1.85	0.9	12
45655977	histidine kinase sensor protein	1.27	0.3	2	0.92	0.1	2	0.42	0.1	2	0.73	0.1	2	0.33	0.0	2	0.46	0.0	2
45655978	hypothetical protein LIC10064	0.58	0.3	5	1.07	0.3	4	2.85	4.6	4	2.48	1.2	4	3.58	5.5	4	0.56	0.3	4
45655979	deoxycytidine triphosphate deaminase	0.77	0.0	2	0.93	0.1	2				1.21	0.2	2						
45655980	enoyl-Coa hydratase/isomerase family	1.15	0.5	3	0.99	0.5	4	1.03	0.5	2	0.83	0.6	3	0.71	0.2	2	1.59	0.8	2
45655982	hypothetical protein LIC10068	1.42	0.1	2				1.23	1.5	2				0.90	1.1	2			
45655988	diaminopimelate epimerase	1.78	1.6	2	1.31	0.7	2				0.97	0.5	2						
45656005	long-chain-fatty-acid CoA ligase	1.31	0.5	16	1.31	0.5	16	1.22	0.7	16	1.00	0.5	18	0.77	0.3	17	0.97	0.8	17
45656025	hypothetical protein LIC10115	1.57	0.5	8	1.73	0.5	8	2.94	1.1	9	1.00	0.2	8	1.58	0.5	8	1.66	0.4	9
45656027	hypothetical protein LIC10117	1.13	0.5	8	1.33	0.4	9	3.13	0.9	8	1.25	0.6	9	2.41	1.0	8	2.04	0.5	10
45656033	LipL45-like protein	2.00	0.7	4	1.75	0.5	4	1.21	0.5	3	0.88	0.0	4	0.76	0.5	3	0.85	0.5	3
45656034	hypothetical protein LIC10124	1.05	0.2	4	3.28	3.2	4	4.75	5.9	4	1.68	0.3	4	2.04	0.5	4	1.35	0.4	5
45656035	hypothetical protein LIC10125	1.09	0.3	8	0.56	0.3	5	2.72	3.0	6	0.84	0.3	9	1.90	0.9	9	2.37	1.1	11
45656042	sigma 54 activator	1.16	0.6	3	0.94	0.7	2	0.53	0.1	2	0.72	0.0	2	0.68	0.2	2			
45656051	NADH dehydrogenase I G subunit	1.70	1.0	6	1.32	0.5	5	1.03	0.5	6	0.97	0.2	5	0.93	0.2	5	0.86	0.4	6
45656063	hypothetical protein LIC10157	1.25	0.2	10	1.29	0.5	10	0.83	0.3	10	1.20	0.8	11	0.76	0.5	11	0.62	0.1	11
45656064	hypothetical protein LIC10158	1.93	1.9	2	1.05	0.7	2				0.68	0.3	2						
45656066	malic enzyme										0.72	0.2	2						
45656068	fumarate hydratase	0.72	0.2	4	0.97	0.3	4	0.63	0.1	3	1.37	0.3	4	0.79	0.1	3	0.59	0.1	3
45656072	hypothetical protein LIC10166																0.91	1.2	3
45656080	hypothetical protein LIC10174				132.98	85.8	4												
45656081	hypothetical protein LIC10175	1.08	0.2	6	677.42	467.8	8	2.22	1.0	7	601.17	283.0	7	2.95	1.0	7	0.01	0.0	17
45656082	hypothetical protein LIC10176	1.33	0.8	4	634.23	254.3	4	4.49	1.8	4	600.34	223.0	5	3.99	1.6	4	0.01	0.0	6
45656083	hypothetical protein LIC10177				276.41	281.7	3												
45656092	hypothetical protein LIC10187				1.87	1.0	2												
45656094	hypothetical protein LIC10189																9.04	6.6	2
45656096	peptidoglycan associated cytoplasmic membrane protein	0.87	0.2	15	1.06	0.2	12	1.29	0.5	13	1.18	0.7	16	1.50	0.6	14	1.47	0.9	14
45656113	cytochrome c oxidase polypeptide II	1.39	0.3	14	1.62	0.4	12	2.21	1.0	15	1.17	0.2	11	1.72	0.4	15	1.45	0.5	13
45656114	cytochrome c oxidase polypeptide I	1.37	0.3	4	1.74	1.1	4	3.72	1.9	4	1.21	0.4	4	2.62	0.7	4	2.27	0.6	4
45656116	hypothetical protein LIC10211										23.61	31.2	2	2.73	2.9	2	0.27	0.2	2
45656119	transcriptional regulator (CarD family)	0.95	0.1	9	0.64	0.1	10	1.00	1.8	8	0.68	0.1	9	0.69	0.9	8	1.62	2.1	9
45656120	hypothetical protein LIC10215	1.20	0.3	6	1.47	0.5	7	1.28	0.1	6	1.01	0.1	6	1.02	0.1	6	0.94	0.2	6
45656121	phosphoenolpyruvate carboxykinase	0.81	0.2	34	1.04	0.4	30	0.27	0.1	21	1.23	0.5	30	0.30	0.1	21	0.25	0.1	19
45656124	hypothetical protein LIC10219	1.21	0.2	4	1.80	0.6	5	3.19	0.7	4	1.29	0.3	4	2.67	0.7	4	1.93	0.4	4
45656126	aspartyl/glutamyl-tRNA amidotransferase subunit B	0.78	0.4	5	0.90	0.2	5	0.57	0.3	4	1.01	0.3	4	1.07	1.1	4	0.58	0.2	4
45656129	hypothetical protein LIC10224	1.07	0.3	3	1.50	0.5	3	2.16	0.7	3	1.38	0.3	3	2.02	0.4	3	1.47	0.1	3
45656130	RNA polymerase ECF-type sigma factor	1.02	0.1	2	1.08	0.1	2	0.80	0.0	2	1.05	0.0	2	0.78	0.1	2	0.74	0.1	2
45656131	hypothetical protein LIC10226	0.58	0.2	4	0.47	0.4	4	0.50	0.1	2	0.82	0.8	4	1.00	0.0	2	1.33	1.2	2
45656136	hypothetical protein LIC10231	1.49	0.8	2	1.00	0.1	2				1.28	0.9	3						
45656137	lipoprotein releasing system transmembrane protein	1.90	1.2	3	2.47	1.2	3	5.14	3.9	3	1.38	0.6	3	3.06	2.8	3	2.36	1.1	4

45656138	ABC transporter ATP-binding protein	0.96	0.2	2	1.39	0.3	2				1.44	0.1	2						
45656140	hypothetical protein LIC10235	1.44	0.1	4	0.90	0.3	4	2.17	0.4	5	0.62	0.2	4	1.81	0.1	4	2.76	1.2	4
45656142	cyclic nucleotide binding protein	0.79	0.2	4	0.89	0.4	4	1.12	0.1	3	0.83	0.1	4	1.16	0.2	2	1.21	0.5	3
45656149	hypothetical protein LIC10244	1.40	0.9	2				8.50	3.7	2				6.73	1.9	2			
45656157	exonuclease				3.50	2.1	3												
45656158	alcohol dehydrogenase	0.70	0.2	4	1.11	0.2	4	0.64	0.2	4	1.43	0.1	4	0.89	0.4	4	0.53	0.1	4
45656173	cyclic nucleotide binding protein	5.98	6.6	2	2.91	3.8	2				0.35	0.2	2						
45656176	elongation factor EF-2	1.12	1.3	14	1.11	0.6	14	1.03	2.0	11	1.15	0.8	14	0.53	0.3	11	0.98	1.4	11
45656186	zinc-binding dehydrogenase family	0.87	0.2	4	1.15	0.5	5	1.14	0.7	5	1.32	0.9	5	0.76	0.2	4	0.72	0.3	4
45656190	penicillin G acylase precursor	0.88	0.1	3	0.65	0.2	3	3.95	2.4	3	0.73	0.1	3	4.26	1.9	3	5.86	2.5	3
45656194	H+-translocating transhydrogenase subunit beta	1.38	0.2	4	1.01	0.4	4	0.37	0.0	4	0.72	0.3	4	0.27	0.0	4	0.47	0.3	4
45656197	glycerophosphoryl diester phosphodiesterase	0.75	0.2	4	1.18	0.8	4				1.04	0.3	4						
45656205	putative lipoprotein	0.87	0.4	2	1.57	0.8	2	1.25	0.0	2	1.78	0.1	2	1.61	0.7	2	0.92	0.5	2
45656213	glycine dehydrogenase	0.91	0.2	10	0.45	0.2	7	0.22	0.1	6	0.54	0.2	7	0.23	0.1	5	0.50	0.3	5
45656218	hypothetical protein LIC10314	0.83	0.3	17	1.11	0.3	13	3.07	2.2	17	1.06	0.5	15	3.18	1.6	17	2.62	1.1	15
45656221	ribose 5-phosphate isomerase B	0.68	0.2	3	1.07	0.2	3	0.16	0.1	2	1.59	0.1	3	0.20	0.1	2	0.13	0.1	2
45656229	hemolysin	0.74	0.2	3	1.07	0.2	3	0.74	0.8	2	1.57	0.7	3	1.36	1.6	2	0.62	0.6	2
45656241	hypothetical protein LIC10337	0.98	0.2	4	1.76	0.8	3				1.87	1.3	3						
45656243	hemolysin B	0.92	0.2	6	0.53	0.2	5				0.56	0.1	5						
45656248	anti-sigma factor antagonist	0.53	0.2	4	0.85	0.1	3	0.34	0.1	4	1.35	0.1	3	0.84	0.7	4	0.38	0.1	3
45656252	hypothetical protein LIC10348	0.52	0.2	5	0.28	0.1	4				0.65	0.4	4						
45656254	ABC transporter ATP-binding protein																1.58	0.3	2
45656263	electron transfer flavoprotein alpha-subunit	0.84	0.1	12	1.20	0.4	15	0.37	0.2	14	1.36	0.3	14	0.43	0.2	14	0.29	0.1	12
45656264	electron transport flavoprotein beta subunit	0.77	0.3	14	1.26	0.6	16	0.13	0.0	8	1.50	0.6	14	0.17	0.1	8	0.11	0.0	7
45656266	isovaleryl-CoA dehydrogenase	0.94	0.2	10	1.04	0.3	10	0.57	0.2	10	1.10	0.4	9	0.85	1.0	10	0.62	0.2	9
45656280	hypothetical protein LIC10380	1.34	0.4	8	1.24	0.6	9	2.77	2.2	8	0.81	0.3	8	1.69	1.1	8	1.81	0.5	8
45656282	acyl-CoA dehydrogenase	0.81	0.2	4	0.67	0.3	4				0.65	0.1	4						
45656286	RNA polymerase ECF-type sigma factor	0.81	0.1	2															
45656287	hypothetical protein LIC10387										0.71	0.6	2	2.82	0.8	2	5.35	3.3	2
45656296	acetyl-CoA acetyltransferase	0.79	0.2	11	0.95	0.2	11	0.33	0.1	11	1.17	0.1	10	0.44	0.2	11	0.42	0.2	11
45656303	riboflavin synthase beta chain	1.45	0.1	3	1.64	0.1	3	2.22	1.0	3	1.14	0.1	3	1.59	0.9	3	1.36	0.6	3
45656305	hypothetical protein LIC10405	1.39	1.2	2				2.58	2.7	2	1.24	0.9	2	1.47	0.5	3	1.93	1.9	2
45656309	2-isopropylmalate synthase				17.06	22.6	2				23.36	7.6	2				0.80	0.1	3
45656311	hypothetical protein LIC10411	3.09	4.0	4	6.24	11.7	4	15.33	29.3	4	0.91	1.2	4	2.09	3.0	4	1.88	1.1	4
45656315	hypothetical protein LIC10415	0.60	0.2	3	0.54	0.2	3	0.44	0.3	3	1.00	0.7	3	0.88	0.6	3	1.10	1.1	3
45656325	hypothetical protein LIC10425	0.90	0.5	2	0.53	0.1	2				0.64	0.2	2						
45656327	UDP-N-acetylglucosamine pyrophosphorylase	0.93	0.3	7	0.99	0.1	4	0.23	0.2	4	0.94	0.1	4	0.26	0.2	4	0.25	0.2	3
45656328	phosphoribosyl pyrophosphate synthetase	1.07	0.2	2	8.76	10.5	2	1.62	1.5	2	7.41	8.4	2	1.41	1.2	2	0.29	0.2	2
45656329	50S ribosomal protein L25	0.98	0.1	7	0.69	0.2	7	0.36	0.1	7	0.77	0.1	6	0.34	0.1	6	0.55	0.1	7
45656330	peptidyl-tRNA hydrolase	1.40	0.9	4	1.04	0.5	2				0.93	0.6	2						
45656331	cell division protein	1.14	0.1	14	0.64	0.2	14	0.38	0.1	11	0.56	0.1	14	0.33	0.1	12	0.54	0.2	12
45656338	hypothetical protein LIC10439	0.89	0.3	2	1.54	0.2	2	0.27	0.1	2	1.84	0.8	2	0.34	0.2	2	0.17	0.1	2
45656339	nitrogen regulatory protein pII	0.84	0.1	2	0.38	0.2	2				0.47	0.2	2						
45656343	glucose-1-phosphate thymidylyltransferase										0.66	0.2	2						
45656344	glutamine-fructose-6-phosphate transaminase	1.01	0.2	11	0.90	0.2	11	0.84	0.3	10	0.91	0.2	11	0.73	0.3	11	0.80	0.3	11
45656345	phosphomannomutase	1.62	0.9	5	0.78	0.3	3	0.59	0.1	2	0.35	0.1	2				0.83	0.5	2
45656350	glycosyltransferase	1.29	0.3	14	1.54	0.2	14	3.04	0.7	13	1.25	0.3	15	2.50	1.0	15	1.86	0.9	16
45656362	Ig-like repeat domain protein 3																10.37	2.0	2
45656380	hypothetical protein LIC10482	0.85	0.3	4	0.45	0.1	4	2.06	1.6	4	0.61	0.2	5	1.84	1.1	4	3.17	1.8	4
45656381	hypothetical protein LIC10483	0.91	0.3	13	1.06	0.4	13	1.69	0.5	11	1.14	0.3	13	1.88	0.4	11	1.73	0.3	11
45656382	threonine synthase	0.97	0.2	12	0.84	0.2	12	0.37	0.1	9	0.87	0.1	12	0.35	0.1	9	0.40	0.1	9
45656384	hypothetical protein LIC10486	1.20	0.4	5	1.15	0.4	5	1.12	0.2	5	1.06	0.3	5	1.01	0.3	4	0.77	0.2	4
45656405	putative lipoprotein	1.08	0.3	4	1.11	0.5	4	0.25	0.1	2	1.01	0.4	4	0.20	0.1	2	0.16	0.0	2
45656410	hypothetical protein LIC10512	0.35	0.0	3	0.49	0.3	3				1.36	0.6	3						
45656415	leucyl-tRNA synthetase	2.13	1.9	2	0.85	0.5	2				0.49	0.2	2						
45656416	ABC transporter, atp-binding protein	1.03	0.3	2	0.99	0.1	2				1.00	0.3	2						
45656420	oxidoreductase family	1.10	0.2	5	0.98	0.3	6	0.95	0.2	6	0.95	0.5	6	1.00	0.4	6	0.99	0.2	6
45656421	DnaJ	1.74	0.7	6	1.04	0.4	6	0.63	0.3	4	0.62	0.1	6	0.38	0.1	5	0.55	0.1	5
45656422	DnaK	1.54	0.3	50	2.93	0.8	50	0.49	0.2	39	1.93	0.4	49	0.33	0.1	38	0.17	0.0	37
45656423	GrpE	1.05	0.0	2	1.32	0.4	2				1.23	0.2	4	0.56	0.2	3	0.45	0.2	3

45656424	heat-inducible transcriptional repressor										1.12	0.4	2	7.37	1.1	2	7.24	3.6	2
45656436	ABC transporter ATP-binding protein	1.01	0.1	3	2.42	1.7	3	0.52	0.3	2	2.40	1.7	3	0.53	0.4	2	0.38	0.3	2
45656444	lipase	1.07	0.1	2	1.13	0.6	2	2.02	1.5	2	1.03	0.4	2	1.98	1.6	2	2.49	2.6	2
45656445	putative lipoprotein	1.57	1.0	2	0.81	0.6	2	20.53	24.0	2	0.83	1.0	2	10.31	8.6	2	54.60	73.2	2
45656448	anti-sigma factor antagonist	0.93	0.2	4	0.76	0.1	4	0.95	0.7	4	0.80	0.3	5	1.13	1.0	4	1.15	0.9	4
45656449	hypothetical protein LIC10551	1.25	0.4	12	1.38	0.4	12	1.62	0.4	11	1.01	0.3	12	1.19	0.6	11	1.19	0.3	11
45656452	hypothetical protein LIC10554	0.91	0.3	2	0.91	0.1	2	1.67	1.2	2	1.03	0.2	2	1.72	0.8	2	1.77	1.1	2
45656455	response regulator	0.74	0.2	3	0.87	0.2	3	0.66	0.0	3	1.20	0.2	3	0.94	0.3	3	0.77	0.1	3
45656456	hypothetical protein LIC10558	0.96	0.2	2	2.82	3.8	3	12.15	18.2	3	0.65	0.0	2	1.77	0.2	2	3.33	1.1	3
45656463	enoyl-CoA hydratase	0.76	0.2	2	0.53	0.4	2	0.45	0.2	2	0.65	0.4	2	0.68	0.5	2	1.50	1.6	2
45656469	homoserine dehydrogenase	0.58	0.3	2	1.32	0.8	2	2.23	0.2	2	2.22	0.1	2	4.64	3.0	2	2.13	1.5	2
45656476	hypothetical protein LIC10578	1.06	0.5	7	0.55	0.3	6	0.84	0.2	5	0.63	0.3	6	1.03	0.5	5	1.41	0.3	5
45656480	anthranilate synthase component I	0.83	0.3	2	0.83	0.0	2				1.06	0.4	2						
45656481	acyl-CoA dehydrogenase	0.79	0.0	4	0.74	0.3	6	0.39	0.1	5	0.89	0.4	5	0.46	0.2	5	0.61	0.3	5
45656497	hypothetical protein LIC10599																7.62	0.6	2
45656498	fatty acid synthase subunit beta	1.00	0.6	4	1.55	1.3	4	0.66	0.2	3	1.43	0.3	4	0.93	0.2	3	0.72	0.1	3
45656499	hypothetical protein LIC10601	0.76	0.2	5	0.81	0.2	5	0.78	0.2	4	1.25	0.2	4	1.09	0.2	4	0.87	0.1	4
45656504	DNA-binding stress protein	1.00	0.1	8	0.67	0.4	8	3.10	0.4	8	0.72	0.4	8	3.32	0.5	8	5.78	4.7	9
45656505	aminotransferase	0.86	0.3	11	0.85	0.3	10	0.63	0.4	9	1.14	0.5	11	0.78	0.5	9	0.79	0.4	9
45656506	ATP-dependent protease La	2.11	0.9	4	1.81	0.1	5	4.62	3.0	6	0.76	0.4	5	1.27	0.3	5	2.09	1.2	5
45656520	motility protein A	1.24	0.1	3	0.92	0.1	3	1.60	0.3	3	0.74	0.1	3	1.29	0.2	3	1.70	0.6	4
45656521	flagellar motor protein	1.05	0.6	3	1.43	1.3	3	1.28	1.4	3	1.22	0.3	4	1.02	0.5	4	0.81	0.2	4
45656522	flagellar protein	1.05	0.4	6	0.83	0.3	5	2.18	0.4	5	0.79	0.2	6	2.29	1.0	6	2.50	0.5	6
45656526	putative lipoprotein																3.78	2.7	2
45656553	hypothetical protein LIC10655	0.37	0.1	2	0.56	0.1	2	0.80	0.9	2									
45656560	hypothetical protein LIC10662	0.28	0.1	2	1.18	1.1	2	0.75	0.6	2	3.64	2.3	2	2.42	1.1	2	0.71	0.2	2
45656562	hypothetical protein LIC10664	0.72	0.3	3	0.64	0.1	3	0.32	0.1	3	0.95	0.3	3	0.47	0.1	3	0.50	0.0	3
45656570	hypothetical protein LIC10672	1.18	0.1	6	0.66	0.1	5	1.49	0.2	6	0.50	0.1	6	1.25	0.3	7	2.65	0.3	6
45656579	phosphoribosylformylglycinamidine synthase	1.25	0.6	4	1.46	1.1	4	3.58	4.4	3	1.83	1.8	4	2.21	2.4	3	1.07	0.3	3
45656588	hypothetical protein LIC10690	1.45	0.3	8	1.15	0.4	8	1.12	0.6	8	0.75	0.2	8	0.75	0.3	8	0.96	0.4	8
45656598	3-oxoacyl-[acyl-carrier-protein] reductase oxidoreductase	0.75	0.1	16	0.67	0.2	17	0.26	0.1	14	0.90	0.2	16	0.34	0.1	15	0.34	0.1	15
45656603	hypothetical protein LIC10705				0.49	0.1	2												
45656610	hypothetical protein LIC10712	0.16	0.0	2	0.37	0.1	3				2.60	0.4	2						
45656612	outer membrane receptor protein	1.31	0.5	11	0.65	0.3	11	1.32	0.8	9	0.54	0.2	10	1.12	0.5	10	2.02	0.9	10
45656617	polyphosphate kinase	0.94	0.1	4	0.75	0.3	5	0.64	0.3	5	0.75	0.3	5	0.71	0.1	4	0.84	0.3	5
45656628	bacterioferritin comigratory protein	0.91	0.2	3	1.03	0.4	3				0.81	0.5	5						
45656629	cytosol aminopeptidase protein	1.42	0.3	9	1.38	0.2	8	3.35	0.7	10	0.86	0.2	9	2.35	0.5	8	2.49	0.5	11
45656634	ATP-dependent RNA helicase	1.25	1.6	2							0.64	0.1	2						
45656642	transcription antitermination protein	0.75	0.1	5	0.95	0.2	6	0.09	0.1	3	1.28	0.4	5	0.12	0.1	3	0.10	0.1	3
45656643	50S ribosomal protein L11	0.81	0.2	9	0.73	0.3	9	0.24	0.1	5	0.78	0.1	10	0.33	0.2	6	0.28	0.2	5
45656644	50S ribosomal protein L1	1.10	0.2	8	0.66	0.5	9	0.33	0.3	7	0.59	0.2	8	0.32	0.3	7	0.78	0.7	7
45656645	50S ribosomal protein L10	0.89	0.2	4	1.09	1.5	5	0.90	1.2	2	0.49	0.2	4				7.84	10.4	4
45656646	50s ribosomal protein L7/L12	0.48	0.1	8	0.10	0.0	7	0.01	0.0	5	0.23	0.1	8	0.02	0.0	4	0.10	0.0	4
45656647	DNA-directed RNA polymerase beta subunit	1.14	0.2	47	0.83	0.3	47	1.16	0.4	44	0.80	0.3	50	1.04	0.5	45	1.38	0.5	44
45656648	DNA-directed RNA polymerase beta' subunit	1.18	0.3	66	0.80	0.2	64	1.37	0.4	64	0.70	0.2	71	1.21	0.5	69	1.69	0.5	66
45656649	30S ribosomal protein S12	1.10	0.0	3	0.56	0.2	3	0.31	0.2	3	0.77	0.5	4	0.51	0.5	4	0.61	0.2	4
45656650	30S ribosomal protein S7	0.93	0.1	11	0.27	0.0	12	0.31	0.1	11	0.28	0.1	13	0.33	0.1	11	1.06	0.4	10
45656654	hypothetical protein LIC10760	0.61	0.2	4	1.10	0.4	3	1.37	1.3	3	2.12	0.4	3	1.90	1.1	3	0.60	0.2	2
45656655	50S ribosomal protein L13	0.97	0.1	7	0.51	0.2	7	0.05	0.0	2	0.47	0.2	6	0.05	0.0	2	0.09	0.0	2
45656656	30S ribosomal protein S9	0.93	0.0	2	0.34	0.0	2				0.36	0.0	2						
45656657	alanyl-tRNA synthetase	1.00	0.3	6	1.28	0.4	6	0.53	0.2	3	1.16	0.2	7	0.59	0.2	4	0.50	0.2	4
45656658	hypothetical protein LIC10764	0.60	0.2	3	0.97	0.1	2	0.11	0.0	2	1.39	0.0	2	0.16	0.0	2	0.12	0.0	2
45656659	hypothetical protein LIC10765	0.88	0.6	2															
45656662	metalloprotease	0.69	0.1	2	0.95	0.1	3	0.61	0.1	2	1.37	0.3	2				0.66	0.0	2
45656663	processing metalloprotease	0.96	0.5	4	0.99	0.1	3	0.59	0.2	5	1.78	1.3	3	0.96	0.7	4	0.64	0.2	3
45656666	hypothetical protein LIC10772	0.83	0.1	5	0.36	0.1	4	0.34	0.1	3	0.45	0.1	4	0.76	0.6	3	1.15	0.4	3
45656680	flagellar filament sheath protein	1.25	0.4	13	0.90	0.2	12	1.83	0.8	12	0.69	0.2	13	1.37	0.8	13	2.30	0.8	12
45656681	flagellar filament sheath protein	1.31	0.5	18	1.02	0.6	16	2.89	1.9	18	0.88	0.3	16	2.05	0.6	16	2.24	1.2	19
45656682	transcript cleavage factor/unknown domain fusion protein	1.09	0.2	31	0.83	0.3	33	0.41	0.2	26	0.74	0.2	35	0.39	0.2	29	0.50	0.2	29
45656686	surface antigen	2.15	2.8	3	0.21	0.0	2	1.35	1.3	2	0.70	0.5	3	0.63	0.3	2			
45656729	glyoxalase	0.84	0.3	4	0.36	0.1	3	0.66	0.4	4	0.40	0.2	3	0.63	0.5	4	2.54	1.7	3

45656733	dihydrodipicolinate synthase	0.79	0.1	5	1.54	0.4	5	1.01	0.3	6	1.72	0.2	5	1.03	0.1	5	0.70	0.2	5
45656738	hypothetical protein LIC10847	0.39	0.2	2															
45656739	hypothetical protein LIC10848	1.06	0.4	3	1.55	0.5	3				1.46	0.0	3						
45656741	30S ribosomal protein S2	0.80	0.1	6	0.57	0.1	7	0.32	0.0	4	0.64	0.2	5	0.39	0.1	4	0.63	0.1	4
45656742	elongation factor Ts	0.63	0.1	7	0.77	0.0	5	0.17	0.0	7	1.16	0.2	6	0.29	0.1	7	0.20	0.1	5
45656743	uridylate kinase	1.13	0.6	6	0.70	0.3	5	2.95	4.7	3	0.65	0.1	5	1.43	1.9	3	1.81	2.7	3
45656744	ribosome recycling factor	0.76	0.1	3				0.23	0.1	2				0.31	0.1	2			
45656748	integral membrane zinc metalloprotease	1.56	0.2	10	1.48	0.6	12	6.23	4.5	12	0.90	0.3	11	3.46	2.8	11	4.05	3.7	12
45656749	prolyl-tRNA synthetase	1.25	0.4	5	0.74	0.1	4	0.63	0.1	4	0.53	0.1	4	0.49	0.2	4	0.85	0.1	4
45656750	tryptophan synthase subunit beta	1.39	0.3	4	1.36	0.7	5	2.56	1.9	4	0.88	0.5	4	1.88	1.5	4	2.23	2.2	4
45656753	adenylate/guanylate cyclase	1.34	0.3	16	1.35	0.5	19	2.79	1.7	19	1.02	0.2	17	2.01	0.7	18	2.18	0.9	17
45656764	hypothetical protein LIC10873	0.97	0.2	5	1.52	0.3	6	2.33	0.4	5	1.49	0.3	8	2.61	0.6	8	1.64	0.2	7
45656765	molybdopterin oxidoreductase	1.40	0.4	36	1.31	0.5	35	3.02	1.3	35	1.02	0.5	37	2.28	1.0	36	2.27	0.8	37
45656766	molybdopterin oxidoredutase membrane subunit																5.34	4.9	2
45656767	hypothetical protein LIC10876	1.31	0.4	6	1.25	0.2	6	4.40	2.7	6	1.00	0.4	7	2.77	1.0	6	2.88	1.1	6
45656768	hypothetical protein LIC10877	1.13	0.3	10	1.18	0.5	10	3.95	2.1	10	0.94	0.5	12	3.02	1.2	11	4.48	4.2	12
45656769	hypothetical protein LIC10878	1.68	0.4	3	1.11	0.3	3	3.61	1.4	2	0.65	0.1	3	2.37	0.5	2	3.87	0.9	2
45656770	putative lipoprotein	1.35	0.3	6	1.01	0.3	4	3.42	0.8	5	0.76	0.2	4	2.44	0.6	4	2.80	0.3	4
45656791	adenylate/guanylate cyclase	1.30	0.4	2	0.66	0.5	2	2.07	2.2	2	0.46	0.3	2	1.40	1.3	2	3.86	1.4	6
45656807	hypothetical protein LIC10918				1.13	0.3	3	0.44	0.2	3							0.41	0.2	3
45656816	putative lipoprotein	0.90	0.2	6	1.05	0.2	7	0.38	0.2	6	1.23	0.4	6	0.52	0.2	5	0.34	0.1	6
45656836	ABC transporter, ATP-binding protein	1.43	0.3	2	0.85	0.5	2	0.95	0.4	2	0.57	0.2	2	0.65	0.1	2	1.21	0.3	2
45656843	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	1.00	0.1	3	0.55	0.1	3	0.49	0.1	2	0.56	0.2	3	0.55	0.1	3	0.92	0.5	2
45656846	alcohol dehydrogenase	0.65	0.4	4	0.99	0.5	4	0.84	0.2	3	1.94	1.4	4	1.33	0.8	3	0.82	0.4	3
45656847	monooxygenase	1.43	0.2	7	1.20	0.3	7	4.38	0.7	6	0.87	0.3	6	3.27	0.8	6	2.92	1.1	7
45656854	hypothetical protein LIC10966																1.76	0.1	2
45656858	acyl-CoA dehydrogenase	1.02	0.3	16	0.67	0.2	15	0.70	0.4	17	0.65	0.3	17	0.58	0.3	17	0.90	0.3	16
45656861	outer membrane protein	1.19	0.1	8	0.91	0.2	7	4.17	1.3	8	0.65	0.1	7	3.40	1.1	8	4.34	1.2	7
45656862	acetyl-CoA acetyltransferase	0.60	0.2	7	0.56	0.2	7	0.29	0.1	5	0.88	0.3	6	0.34	0.1	5	0.55	0.1	5
45656873	hypothetical protein LIC10985	1.30	0.2	5	0.63	0.4	5	0.53	0.3	4	0.45	0.3	5	0.51	0.2	5	1.47	1.6	4
45656890	LipL71	1.09	0.1	29	1.14	0.2	30	0.88	0.3	25	1.02	0.1	27	0.80	0.3	25	0.81	0.3	28
45656891	anti-sigma factor antagonist	0.57	0.2	6	0.92	0.3	7	0.50	0.1	4	1.53	0.3	6	0.72	0.2	4	0.48	0.1	4
45656893	transcriptional regulator (FUR family)				1.32	0.3	2	0.78	0.2	2							0.63	0.3	2
45656896	hypothetical protein LIC11009	0.54	0.2	15	0.57	0.1	15	0.21	0.1	12	1.21	0.6	16	0.38	0.2	12	0.36	0.1	12
45656899	OppA	1.50	0.5	11	1.16	0.3	9	2.06	0.4	11	0.82	0.1	10	1.57	0.4	12	1.92	0.7	11
45656902	adenylosuccinate lyase	0.83	0.1	2	0.76	0.5	2				0.89	0.4	2						
45656912	hypothetical protein LIC11028	1.21	0.9	2				1.45	0.5	2				1.41	0.6	2			
45656919	hypothetical protein LIC11035	0.48	0.0	2															
45656920	hypothetical protein LIC11036	0.56	0.3	2										0.82	0.2	2			
45656935	hypothetical protein LIC11051	0.55	0.2	2	0.53	0.0	2				1.01	0.4	2						
45656942	putative lipoprotein										5.80	0.0	2						
45656943	hypothetical protein LIC11059				6.22	6.1	2												
45656947	prolipoprotein diacylglycerol transferase	1.19	0.0	2	1.25	0.5	2	3.03	1.0	2	1.04	0.4	2	2.54	0.8	2	2.46	0.2	2
45656949	poly A polymerase	1.57	0.6	5	1.31	0.9	5	3.72	1.1	6	0.45	0.3	4	2.21	1.0	6	3.32	1.9	4
45656958	hypothetical protein LIC11074	0.76	0.3	7	1.53	0.4	7	0.38	0.2	6	2.17	0.4	8	0.48	0.1	6	0.24	0.1	6
45656966	cytoplasmic membrane protein	0.59	0.0	2															
45656973	hypothetical protein LIC11089	1.16	0.2	4	0.59	0.1	4				0.51	0.1	4						
45656979	adenylate/guanylate cyclase	1.10	0.2	10	1.02	0.2	10	0.93	0.3	10	1.00	0.2	11	0.78	0.2	11	0.83	0.2	10
45656980	hypothetical protein LIC11096	0.87	0.1	2	1.67	1.2	2	2.16	2.0	2	2.37	1.2	3	2.69	1.5	3	1.10	0.3	3
45656985	dihydroxy-acid dehydratase	0.95	0.2	3	1.07	0.1	3	0.42	0.1	3	1.15	0.2	3	0.45	0.1	3	0.40	0.1	3
45656999	thiosulfate sulfurtransferase	0.80	0.1	11	0.87	0.1	12	0.41	0.1	7	1.03	0.1	11	0.57	0.2	8	0.48	0.1	8
45657016	pyruvate kinase	2.05	0.1	2	1.30	0.2	2	0.97	0.3	2	0.63	0.1	2	0.48	0.2	2	0.78	0.4	2
45657024	alpha-galactosidase	2.02	1.2	4	0.89	0.7	3	1.11	0.5	3	0.52	0.3	3	0.78	0.5	3	2.90	1.9	3
45657025	ribonuclease D	0.94	0.1	5	1.26	0.4	5	0.79	0.4	5	1.32	0.4	5	0.83	0.4	5	0.67	0.4	6
45657046	hypothetical protein LIC11162	1.24	0.3	2	0.94	0.3	2	0.48	0.5	2	0.75	0.1	2	0.35	0.3	2	0.45	0.4	2
45657066	hypothetical protein LIC11182	1.60	0.4	2	1.36	0.1	2	2.13	0.5	2	0.87	0.2	2	1.33	0.0	2	1.55	0.3	2
45657067	hypothetical protein LIC11183	0.18	0.1	5	1.08	0.7	7	0.12	0.1	2	5.18	3.0	5	0.84	0.7	2	0.13	0.1	2
45657072	flagellar hook protein	1.03	0.1	4	0.92	0.3	4	3.20	0.9	4	0.90	0.3	4	3.11	0.8	4	3.54	1.0	4
45657078	putative citrate lyase	0.81	0.1	14	0.87	0.2	13	0.55	0.2	13	1.11	0.3	14	0.65	0.2	13	0.72	0.5	14
45657080	hypothetical protein LIC11196	0.59	0.1	4	1.02	0.3	4				1.74	0.5	4						
45657081	hypothetical protein LIC11197	0.81	0.1	2	1.42	0.1	2	1.04	1.2	2	1.77	0.2	2	1.44	1.7	2	0.75	0.9	2
45657082	adenylate/guanylate cyclase	0.81	0.3	4	1.23	0.3	4	0.92	0.3	4	1.86	1.4	4	1.19	0.3	4	0.83	0.5	4

45657087	response regulator	1.53	0.8	2	2.49	1.5	3	2.05	0.0	2	0.89	0.4	3	1.51	0.6	3	2.08	1.2	3
45657092	hypothetical protein LIC11209	0.76	0.5	5	0.92	0.5	4	1.20	0.2	4	0.95	0.4	4	1.25	0.2	4	1.54	0.8	4
45657099	methyl-accepting chemotaxis transducer transmembrane protein	1.26	0.4	6	2.02	0.7	5	3.98	1.3	5	2.11	1.1	7	3.50	1.4	5	1.38	0.4	5
45657102	peroxiredoxin	0.81	0.2	15	2.12	0.7	16	0.49	0.3	14	2.71	0.6	16	0.59	0.3	14	0.19	0.1	14
45657107	hypothetical protein LIC11224	0.71	0.1	11	1.59	0.4	12	1.49	0.3	12	2.02	0.4	10	1.90	0.5	10	0.89	0.3	12
45657116	signal peptidase I	1.74	0.2	2	1.87	0.5	2				1.07	0.2	2						
45657120	ATP synthase A chain	2.20	1.1	2	2.11	1.4	2	4.90	3.0	2	1.08	0.3	3	2.35	0.4	3	2.21	0.2	3
45657122	ATP synthase B chain	0.74	0.0	7	0.39	0.2	7	1.46	0.2	7	0.52	0.2	7	1.94	0.2	7	3.69	1.3	6
45657123	ATP synthase delta chain	0.73	0.1	2	1.25	1.0	2	1.51	1.4	2							1.11	0.2	2
45657124	ATP synthase subunit A	1.33	0.3	24	0.93	0.3	23	1.38	0.5	23	0.76	0.3	24	1.17	0.6	25	1.43	0.4	22
45657125	ATP synthase gamma chain	1.27	0.2	4	1.42	0.6	4	3.26	1.4	4	1.12	0.4	4	2.07	1.1	6	2.69	1.9	4
45657126	ATP synthase subunit B	1.27	0.2	18	0.96	0.4	19	1.21	0.3	18	0.77	0.3	19	1.03	0.3	18	1.27	0.4	19
45657141	MreB	1.07	0.1	20	1.20	0.3	20	1.19	0.4	21	1.21	0.3	22	1.19	0.4	22	0.96	0.2	21
45657142	MreC	1.31	0.7	6	1.17	0.7	6	2.65	1.2	6	0.95	0.5	6	2.12	0.5	6	1.94	0.4	5
45657155	hypothetical protein LIC11273	0.98	0.3	5	0.94	0.1	5	0.43	0.2	4	1.08	0.3	6	0.51	0.2	5	0.49	0.2	5
45657156	hypothetical protein LIC11274	1.03	0.5	7	1.18	0.4	5	2.46	0.9	7	1.61	1.3	6	2.36	1.6	7	2.01	0.5	5
45657162	peptide chain release factor 3	0.69	0.2	2															
45657174	hypothetical protein LIC11294	1.38	0.4	20	1.31	0.5	21	2.53	0.9	18	0.83	0.3	19	2.03	0.7	18	2.32	1.0	21
45657179	putative lipoprotein	0.76	0.0	2	0.80	0.2	2	0.51	0.1	2	1.07	0.3	2	0.68	0.1	2	0.67	0.3	2
45657190	bacterioferritin	0.32	0.1	2	0.98	0.0	2	2.77	0.8	2	3.42	1.5	2	10.45	7.4	2	3.22	0.9	3
45657193	aminopeptidase P	0.66	0.4	2	1.15	0.1	2				2.18	1.3	2						
45657200	hypothetical protein LIC11320	1.20	0.7	3															
45657207	flagellar P-ring protein precursor	0.77	0.1	2				2.51	0.0	2				3.26	0.2	2			
45657212	hypothetical protein LIC11334	0.58	0.3	3	0.89	0.2	3	1.26	0.2	3	1.84	0.9	3	2.92	2.2	3	1.45	0.4	3
45657213	GroEL	1.40	0.2	30	1.01	0.2	30	1.29	0.4	30	0.73	0.1	33	0.92	0.3	30	1.29	0.4	32
45657214	GroES	0.91	0.1	11	0.19	0.0	10	0.09	0.0	9	0.20	0.0	10	0.10	0.0	10	0.46	0.2	10
45657230	LipL32	0.82	0.1	24	0.50	0.2	24	0.14	0.0	18	0.62	0.2	24	0.17	0.0	17	0.29	0.1	19
45657232	S-adenosylmethionine synthetase	0.77	0.2	20	0.92	0.2	20	0.45	0.1	15	1.07	0.2	21	0.57	0.1	16	0.52	0.1	15
45657233	transketolase	1.87	1.5	3	2.08	1.8	3	0.49	0.4	2	1.05	0.1	3	0.43	0.2	2	0.42	0.2	2
45657237	MaoC	0.77	0.2	14	0.97	0.2	15	0.33	0.2	13	1.22	0.3	15	0.38	0.2	12	0.30	0.1	12
45657240	hypothetical protein LIC11362	0.48	0.0	2															
45657242	short-chain dehydrogenase	1.18	0.3	10	1.27	0.4	10	0.85	0.7	11	1.32	0.5	10	0.70	0.3	10	0.50	0.3	11
45657248	flagellar motor switch protein	1.01	0.0	4	0.68	0.1	4	0.65	0.1	4	0.82	0.2	4	0.65	0.1	4	0.81	0.2	4
45657256	septum site-determining protein	3.23	3.6	2	0.82	0.5	2				0.47	0.4	2						
45657258	sigma factor WhiG	0.87	0.1	8	0.62	0.1	8	0.35	0.2	9	0.75	0.1	7	0.45	0.2	9	0.62	0.3	9
45657269	flagellar M-ring protein	1.10	0.1	4	0.95	0.1	5	2.87	0.4	4	0.88	0.1	4	2.29	0.5	4	3.04	0.5	4
45657282	hypothetical protein LIC11405	1.23	0.4	10	1.08	0.3	9	1.56	1.0	9	0.85	0.3	10	0.92	0.4	7	1.36	0.6	8
45657285	hypothetical protein LIC11408	0.72	0.2	9	0.74	0.2	6	0.52	0.1	7	1.03	0.3	7	0.83	0.4	8	0.77	0.3	7
45657286	acetolactate synthase large subunit	0.86	0.4	11	1.07	0.7	11	1.80	2.6	8	1.07	0.5	12	1.73	1.5	8	1.98	1.5	9
45657290	glycosyl hydrolase	1.16	0.2	11	1.42	0.8	10	1.08	0.2	7	1.29	0.6	10	1.13	0.4	7	0.64	0.2	7
45657292	FKBP-type peptidyl-prolyl cis-trans isomerase	0.87	0.1	12	0.99	0.2	12	0.10	0.0	4	1.18	0.2	12	0.11	0.1	4	0.10	0.1	4
45657293	ATP-dependent Clp protease, proteolytic subunit	0.81	0.1	5	0.94	0.2	6	0.65	0.5	5	1.13	0.1	5	0.44	0.3	4	0.62	0.4	5
45657294	ATP-dependent protease ATP-binding subunit	0.94	0.2	10	0.82	0.2	7	0.70	0.4	8	0.84	0.2	7	0.70	0.4	8	0.57	0.3	5
45657297	phosphate sodium symporter	1.47	0.6	7	1.49	0.4	5	4.12	2.3	6	1.61	0.5	8	3.78	1.1	8	2.22	0.6	7
45657299	glycine rich RNA-binding protein	0.79	0.0	2	0.07	0.0	2				0.09	0.0	2						
45657300	peptidyl-prolyl cis-trans isomerase	0.50	0.1	2	1.23	0.2	2				2.62	1.1	2						
45657307	cyclic nucleotide binding protein	0.66	0.4	3	1.14	0.4	3				2.97	3.3	3						
45657312	hypothetical protein LIC11436	0.96	0.1	2	0.51	0.0	2				0.53	0.0	2						
45657313	adenylate/guanylate cyclase	1.07	0.1	8	0.59	0.2	8	1.37	0.7	9	0.56	0.1	8	1.26	0.5	9	2.06	0.4	7
45657314	peptidyl-prolyl cis-trans isomerase	1.29	1.0	3	1.32	0.6	3	0.13	0.1	2	1.16	0.3	3	0.18	0.1	2	0.13	0.1	2
45657318	hypothetical protein LIC11442	0.64	0.1	2				4.10	4.9	2				7.58	5.6	3			
45657320	response regulator	1.19	0.2	5	1.39	0.2	3	1.77	0.8	5	1.20	0.1	3	1.48	0.7	5	1.46	0.5	3
45657331	LipL31	1.00	0.2	8	1.02	0.1	9	1.36	0.4	9	0.94	0.4	9	1.28	0.2	8	1.24	0.5	9
45657333	outer membrane protein, porin superfamily	0.94	0.2	2	0.61	0.1	2	2.11	0.6	2	0.68	0.2	2	2.23	0.2	2	3.52	1.4	2
45657335	glutamyl-tRNA(Gln) amidotransferase subunit C	1.03	0.6	2															
45657336	glutamyl-tRNA(Gln) amidotransferase subunit A	0.97	0.1	2	0.63	0.2	4				0.78	0.1	2						
45657343	hypothetical protein LIC11468	1.14	0.4	4	1.66	0.7	3				1.24	0.3	3						
45657345	thioredoxin reductase	0.76	0.5	5	1.04	0.4	6	0.35	0.0	4	1.14	0.5	4	2.70	4.4	4	0.44	0.1	4
45657364	hypothetical protein LIC11489	1.04	0.2	18	1.09	0.2	15	0.86	0.5	16	1.06	0.3	15	0.76	0.4	16	0.72	0.2	14
45657373	hypothetical protein LIC11498	1.21	0.1	2	1.14	0.1	2	2.49	0.4	2	0.95	0.1	2	2.08	0.5	2	2.18	0.2	2

45657374	hypothetical protein LIC11499	0.36	0.0	3	0.06	0.0	3	0.04	0.0	2	0.18	0.0	3	0.11	0.0	2	0.70	0.2	2
45657385	putative polypeptide deformylase protein	0.64	0.2	4	0.46	0.2	4	0.35	0.1	3	0.79	0.5	4	0.57	0.3	3	0.91	0.5	3
45657387	hypothetical protein LIC11514	0.48	0.2	4	0.60	0.5	4	0.34	0.3	3	1.64	2.0	4	0.94	1.1	3	0.42	0.2	3
45657390	acetyl-CoA carboxylase alpha subunit	0.92	0.2	9	0.90	0.2	11	0.83	0.2	9	0.92	0.1	9	0.83	0.2	9	0.92	0.2	9
45657391	biotin carboxylase subunit of acetyl CoA carboxylase	1.19	0.4	8	0.99	0.2	7	0.84	0.2	6	0.79	0.3	10	0.73	0.2	6	0.86	0.2	6
45657396	chemotaxis protein	1.72	0.4	26	1.12	0.5	25	0.98	0.7	19	0.63	0.2	23	0.50	0.3	19	0.87	0.6	18
45657399	chemotaxis response regulator	1.03	0.5	4	0.18	0.0	2				0.18	0.0	2						
45657400	histidine kinase response regulator hybrid protein										1.02	0.4	2	1.65	0.4	3	1.48	0.2	2
45657402	penicillin tolerance protein	0.70	0.3	3	0.74	0.1	3				1.13	0.3	3	0.42	0.2	2			
45657404	flagellin protein	0.81	0.5	5	0.95	0.2	5	6.16	3.5	6	0.81	0.2	5	4.10	0.9	5	5.38	2.0	5
45657405	flagellin protein	1.32	0.3	6	1.61	0.1	4	5.63	2.1	7	1.21	0.3	4	3.41	0.8	6	2.93	0.9	6
45657414	2-dehydro-3-deoxyphosphooctonate aldolase	0.97	0.1	4	1.81	0.5	4	0.61	0.3	3	1.87	0.5	4	0.62	0.4	3	0.42	0.3	3
45657417	ABC transporter, ATP-binding protein	1.12	0.3	2	1.12	0.2	2	1.38	0.1	2	0.82	0.3	3	1.24	0.2	3	1.71	0.8	3
45657426	serine/threonine kinase	1.31	0.4	2	0.93	0.7	2				0.66	0.4	2						
45657428	30S ribosomal protein S16	0.89	0.5	8	0.01	0.0	2				0.02	0.0	2						
45657432	50S ribosomal protein L19	1.09	0.1	6	0.70	0.1	6	0.42	0.1	5	0.67	0.1	5	0.38	0.1	5	0.60	0.2	5
45657443	general secretory pathway protein D	1.29	0.4	7	1.01	0.2	7	2.04	1.0	8	0.76	0.3	8	1.76	1.1	9	2.40	0.5	7
45657446	general secretory pathway protein G	0.99	0.2	6	1.03	0.2	6	0.26	0.1	5	1.10	0.2	7	0.26	0.1	6	0.23	0.1	6
45657451	FtsA	1.40	0.5	6	1.34	0.3	5	2.00	1.5	5	0.97	0.3	5	2.26	2.0	6	2.04	2.1	5
45657460	ribonucleotide-diphosphate reductase alpha subunit	1.27	0.3	10	1.26	0.5	12	0.43	0.2	6	1.50	1.1	13	0.75	0.5	7	0.47	0.3	7
45657469	2-isopropylmalate synthase 2	0.99	0.4	2	0.81	0.9	2				0.69	0.7	2						
45657473	ATP-dependent protease ATP-binding subunit	1.17	0.0	3	0.98	0.1	2				0.83	0.1	2						
45657474	hypothetical protein LIC11602	1.28	0.3	4	2.35	1.8	6	4.92	2.8	5	0.84	0.0	4	2.74	0.9	5	3.23	1.7	6
45657485	GTP-binding protein	1.11	0.6	2	0.96	0.7	2				0.82	0.2	2						
45657489	transcriptional regulator (ArsR family)	0.87	0.2	17	0.11	0.0	12	0.16	0.0	12	0.13	0.0	12	0.19	0.0	12	1.45	0.2	12
45657490	3-ketoacyl-(acyl-carrier-protein) reductase	0.72	0.2	6	1.01	0.9	7	1.00	1.3	4	0.96	0.2	6	0.64	0.5	4	0.62	0.3	4
45657491	hypothetical protein LIC11619										0.59	0.3	2	0.69	0.0	2	1.35	0.7	2
45657493	biopolymer transport protein	0.59	0.1	3	0.85	0.3	3	1.17	0.2	3	1.72	0.7	4	1.97	0.7	4	1.30	0.7	4
45657494	biopolymer transport exbd-related transmembrane protein	1.55	0.2	2	1.07	0.3	3				0.78	0.0	2						
45657497	hypothetical protein LIC11625	0.92	0.2	4	0.29	0.1	4	1.32	0.5	4	0.32	0.1	4	1.46	0.5	4	4.67	1.4	4
45657502	long-chain-fatty-acid CoA ligase	1.16	0.2	10	1.23	0.3	10	1.48	0.5	8	0.95	0.2	9	1.10	0.3	7	1.00	0.2	8
45657508	hypothetical protein LIC11636	1.45	0.3	3	1.29	0.3	3	1.96	0.2	3	0.89	0.0	3	1.38	0.2	3	1.55	0.2	3
45657509	hypothetical protein LIC11637	1.78	0.4	4	0.95	0.1	3	2.97	2.0	2	0.58	0.2	3	1.65	0.5	2	2.92	1.7	2
45657514	hypothetical protein LIC11642										1.29	0.6	2						
45657515	LipL45	1.28	0.9	19	1.94	1.7	18	2.46	3.1	18	1.44	0.9	18	1.27	0.6	18	0.83	0.2	15
45657522	transaldolase	0.92	0.3	8	1.13	0.4	7	0.78	0.2	7	1.29	0.4	8	0.84	0.3	6	0.71	0.2	7
45657523	hypothetical protein LIC11653																3.55	0.9	2
45657525	PurH	1.17	0.1	3	0.68	0.2	3	0.95	0.0	2	0.59	0.2	3	0.85	0.2	2	1.19	0.2	2
45657536	hypothetical protein LIC11668	1.90	0.0	2	1.11	0.0	2				0.59	0.0	2						
45657542	alkylglycerone-phosphate synthase	1.06	0.7	2	1.61	0.6	2	0.91	0.1	2	1.88	1.7	3	1.05	0.7	3	0.62	0.1	3
45657551	hypothetical protein LIC11685	0.59	0.1	2															
45657553	endonuclease	1.80	0.9	2	3.16	0.8	2	5.87	0.1	2	2.15	1.5	2	3.79	1.4	3	3.36	2.5	3
45657559	hypothetical protein LIC11693	0.66	0.4	3	1.31	0.0	3	0.66	0.2	2	3.21	1.8	4	7.72	10.1	3	1.75	2.1	3
45657565	glycerol-3-phosphate dehydrogenase	1.10	0.6	2	0.85	0.5	2				0.78	0.0	2						
45657567	RNA polymerase sigma-70 factor	1.03	0.2	12	0.67	0.2	11	0.79	0.2	11	0.63	0.1	11	0.68	0.1	11	1.08	0.4	12
45657569	hypothetical protein LIC11703	0.63	0.0	4	0.49	0.1	4				0.78	0.3	6						
45657570	30S ribosomal protein S21	0.68	0.1	2															
45657574	histidine kinase response regulator hybrid protein	1.32	0.4	6	2.15	1.1	7	7.06	3.0	7	1.22	0.1	8	5.59	1.5	8	3.70	1.0	9
45657575	histidine kinase response regulator hybrid protein	1.69	0.8	15	1.79	1.2	13	5.34	3.4	12	1.01	0.3	13	3.03	1.2	12	4.01	0.8	11
45657579	motility protein B	0.93	0.1	2	0.84	0.3	3	2.37	0.5	3	0.75	0.3	2	1.94	0.8	4	2.96	0.6	3
45657583	nucleotide excision repair subunit A UVRABC	1.02	0.3	3	0.88	0.1	3	0.28	0.2	2	0.89	0.2	3	0.30	0.2	2	0.35	0.3	2
45657592	2-isopropylmalate synthase	0.98	0.1	5	0.65	0.3	4	0.46	0.1	2	0.67	0.3	4	0.48	0.1	2	1.11	1.0	2
45657595	2,4-dienoyl-coa reductase	0.85	0.2	3	1.35	0.4	4	2.66	0.9	4	1.52	0.4	3	2.77	0.7	3	1.74	0.5	4
45657597	FKBP-type peptidyl-prolyl cis-trans isomerase	1.57	1.1	3	2.40	0.2	3	0.71	0.4	3	1.91	0.9	3	0.49	0.2	3	0.29	0.1	3
45657605	hypothetical protein LIC11739	0.81	0.3	2				0.31	0.2	2				0.36	0.1	2			
45657606	PmbA	0.91	0.3	4	0.95	0.5	4	0.58	0.3	3	1.14	0.7	4	0.65	0.3	3	0.49	0.2	3
45657607	TldD	0.94	0.2	3	0.69	0.5	3				0.79	0.5	4	0.70	0.4	2	0.71	0.6	2
45657611	recombinase A	0.89	0.2	7	13.19	7.9	8	0.63	0.7	4	13.58	8.4	8	0.50	0.2	4	0.22	0.4	4
45657612	N-acetyl-gamma-glutamyl-phosphate reductase	1.07	0.6	4	1.74	0.8	4	0.83	0.5	4	2.10	1.1	4	0.95	0.5	4	0.46	0.1	4

45657616	hypothetical protein LIC11750	0.36	0.2	4	1.00	0.4	7	0.81	0.5	2	2.12	0.6	5				0.94	0.5	2
45657617	lipopolysaccharide core biosynthesis protein	1.53	1.3	3	1.25	1.9	3	6.63	8.7	2	0.50	0.6	3	2.36	2.7	2	2.80	1.3	2
45657618	glycosyl transferase	1.77	0.5	4	2.54	0.5	3	4.67	1.7	4	1.36	0.1	4	2.93	0.3	5	2.13	0.2	4
45657626	50S ribosomal protein L28	0.96	0.3	5	0.18	0.0	2	0.21	0.2	2	0.22	0.0	2	0.18	0.2	2			
45657633	N-acetylornithine aminotransferase	1.07	0.3	6	1.06	0.5	6	0.59	0.2	6	0.76	0.2	5	0.52	0.2	6	0.56	0.1	5
45657634	3-isopropylmalate dehydrogenase	0.77	0.1	5	0.72	0.2	6	0.31	0.1	2	0.96	0.2	5	0.41	0.1	2	0.37	0.1	2
45657635	response regulator	0.68	0.1	6	0.48	0.1	6	0.19	0.0	5	0.70	0.1	6	0.28	0.1	5	0.46	0.1	5
45657647	malate dehydrogenase	0.71	0.1	15	1.10	0.2	13	0.55	0.2	15	1.38	0.3	14	0.78	0.2	15	0.51	0.1	15
45657648	hypothetical protein LIC11782	0.79	0.1	10	1.11	0.1	10	0.09	0.0	6	1.35	0.2	10	0.10	0.0	6	0.09	0.1	7
45657656	aspartate aminotransferase	0.68	0.1	5	0.77	0.1	5	0.35	0.1	5	1.16	0.2	5	0.57	0.2	5	0.65	0.4	5
45657657	ATP-dependent DNA helicase	0.92	0.3	11	0.94	0.7	10	0.86	0.7	11	0.82	0.2	11	0.62	0.3	11	0.71	0.2	10
45657659	endopeptidase IV	1.20	0.2	11	0.95	0.2	12	1.27	0.5	12	0.86	0.1	12	1.03	0.3	11	1.40	0.6	12
45657665	glycerol kinase	1.11	0.2	7	1.55	0.3	6	1.97	1.2	8	1.34	0.3	7	1.94	0.8	8	1.52	0.3	7
45657676	hypothetical protein LIC11811	1.08	0.2	2				0.98	0.5	2				0.89	0.3	2			
45657685	cysteine synthase	1.22	0.5	4	3.29	3.1	3	0.67	0.1	2	2.35	2.2	3	0.49	0.1	2	0.45	0.1	2
45657686	3-isopropylmalate dehydratase small subunit	0.74	0.1	7	0.97	0.3	7	0.30	0.1	3	1.28	0.3	8	0.41	0.1	3	0.44	0.1	3
45657687	isopropylmalate isomerase large subunit	0.76	0.1	7	0.99	0.2	7	0.46	0.3	6	1.25	0.2	6	0.62	0.5	6	0.55	0.5	6
45657697	putative lipoprotein	0.97	0.2	7	0.69	0.6	7	1.06	0.8	6	0.71	0.7	7	1.14	0.8	6	4.84	4.5	6
45657702	peptidyl-prolyl cis-trans isomerase	1.11	0.2	6	1.27	0.3	6	1.50	0.5	6	1.14	0.2	7	1.26	0.2	6	1.17	0.2	6
45657707	hypothetical protein LIC11844	1.32	0.8	5	2.41	2.3	6	6.75	2.9	7	1.35	0.7	6	3.42	1.6	5	2.89	1.0	7
45657708	hypothetical protein LIC11845	1.24	0.2	11	1.32	0.2	13	3.85	1.3	11	0.98	0.5	14	2.88	2.0	12	3.51	1.3	13
45657711	hypothetical protein LIC11848	0.99	0.2	20	0.56	0.2	20	3.41	1.2	19	0.53	0.1	18	3.45	1.5	21	5.48	2.0	20
45657714	cytoplasmic membrane protein										0.72	0.4	2	3.05	0.1	2	4.97	2.6	2
45657715	O-acetylhomoserine (thiol) lyase	1.12	0.3	7	1.90	1.7	7	0.58	0.3	6	1.30	0.9	8	0.65	0.3	7	0.61	0.4	8
45657727	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase										1.23	1.4	2	1.28	0.7	3	1.57	1.4	2
45657734	chemotaxis protein methyltransferase	1.23	0.3	4	1.35	0.7	4	1.24	0.2	4	0.95	0.5	4	1.02	0.4	4	1.44	0.7	3
45657748	putative lipoprotein	1.09	0.1	23	1.16	0.3	24	1.68	1.0	25	1.05	0.3	24	1.52	0.5	25	1.44	0.7	24
45657752	flagellin protein	1.04	0.1	11	0.78	0.2	10	3.46	0.9	11	0.74	0.1	10	3.43	0.7	11	5.18	1.7	10
45657753	flagellin protein	1.17	0.1	8	0.89	0.1	9	4.63	0.6	8	0.80	0.1	10	4.03	0.6	8	4.87	1.3	10
45657760	pyruvate dehydrogenase alpha2 subunit protein	1.15	0.2	4	1.03	0.1	4	0.54	0.4	3	0.93	0.2	4	0.47	0.3	3	0.48	0.3	3
45657761	dihydrolipoamide acetyltransferase	0.95	0.3	6	1.43	0.3	6	1.04	0.3	6	1.43	0.4	5	1.17	0.1	5	0.73	0.2	6
45657773	lysyl-tRNA synthetase																0.54	0.1	2
45657774	udp-n-acetyl-d-mannosamine transferase																0.53	0.2	2
45657779	IMP dehydrogenase	1.04	0.5	5	1.02	0.3	5	1.44	0.6	5	1.09	0.1	4	1.39	0.1	5	1.30	0.1	4
45657788	FAD-binding oxidoreductase	1.09	0.4	2	2.23	1.5	2	1.54	0.4	2	2.44	2.3	2	1.58	0.9	2	0.82	0.4	2
45657789	short-chain dehydrogenase	0.95	0.4	5	0.96	0.4	6	1.10	0.1	5	0.90	0.3	6	0.90	0.2	5	1.20	0.4	6
45657794	hypothetical protein LIC11935													16.60	2.1	2			
45657799	heavy metal efflux pump	0.62	0.4	5	0.75	0.1	4	0.58	0.3	3	2.92	3.2	4	1.32	1.0	3	0.53	0.3	3
45657803	translocase	1.26	0.2	15	0.90	0.3	16	0.44	0.1	13	0.72	0.2	16	0.34	0.1	13	0.49	0.1	14
45657805	hypothetical protein LIC11946	0.89	0.5	2	2.58	1.1	2												
45657810	ATP-dependent CLP protease-like, proteolytic subunit	0.91	0.1	15	1.08	0.2	14	0.42	0.2	16	1.35	0.3	18	0.48	0.2	17	0.39	0.1	15
45657813	enolase	1.04	0.3	14	2.25	1.8	15	1.81	1.7	12	2.32	2.6	14	2.01	2.8	12	0.72	0.2	11
45657814	hypothetical protein LIC11955	1.04	0.3	2	0.17	0.0	2	0.75	0.3	2	0.17	0.1	2	0.79	0.5	2	4.30	1.4	2
45657816	response regulator	0.66	0.4	4	1.26	0.9	3	1.09	0.1	2	2.06	0.3	3	1.57	0.7	2	0.83	0.5	2
45657822	hypothetical protein LIC11966	1.08	0.4	13	0.54	0.1	11	1.13	0.6	13	0.68	0.2	12	0.96	0.3	13	1.53	0.5	13
45657829	acyl-CoA dehydrogenase	0.87	0.2	7	0.80	0.2	7	0.53	0.1	5	0.95	0.3	6	0.71	0.2	5	0.61	0.2	6
45657830	cyclic nucleotide binding protein	0.88	0.1	15	0.95	0.4	20	0.53	0.3	15	1.10	0.7	18	0.56	0.2	13	0.56	0.2	16
45657831	thioredoxin													4.44	6.0	2			
45657835	hypothetical protein LIC11982	1.85	0.8	4	1.94	1.0	4	3.91	2.4	4	1.18	0.6	4	2.29	1.3	4	2.11	1.4	4
45657838	RNA-binding protein	0.65	0.0	7	0.52	0.2	7	0.04	0.0	6	0.84	0.2	7	0.06	0.0	5	0.08	0.0	5
45657841	hypothetical protein LIC11988										0.97	0.1	2	1.56	0.1	2	1.60	0.0	2
45657845	D-3-phosphoglycerate dehydrogenase	0.99	0.4	4	1.56	1.7	3	1.90	1.8	2	1.27	0.9	3	1.43	1.0	2	0.88	0.1	2
45657855	succinate dehydrogenase	1.14	0.2	18	1.59	0.4	19	2.32	0.6	17	1.61	0.6	21	1.99	0.4	16	1.35	0.3	16
45657856	succinate dehydrogenase	0.94	0.2	5	2.09	0.4	4	2.62	1.0	6	1.85	0.6	4	2.55	0.8	6	1.64	0.5	5
45657861	hypothetical protein LIC12008	1.00	0.2	4	1.29	1.1	4	2.09	0.8	5	1.98	2.4	4	1.81	0.4	4	3.39	2.7	3
45657863	GTP-binding protein LepA	1.03	0.1	3	0.87	0.1	3				1.42	1.1	4						
45657869	ATP-dependent protease	1.22	0.2	13	0.72	0.2	14	2.43	1.5	15	0.62	0.1	13	1.62	1.0	14	2.80	1.9	17
45657874	hypothetical protein LIC12022	1.43	0.5	2	0.87	0.1	2				0.66	0.3	2						
45657877	asparaginyl-tRNA synthetase	1.36	0.9	3	1.69	1.2	4				1.28	0.3	4						
45657879	hypothetical protein LIC12027	1.99	1.4	3	1.20	0.9	3				0.60	0.2	3						
45657883	histidine kinase sensor protein	1.09	0.2	3	0.72	0.2	3	1.33	0.5	2	0.71	0.4	3	1.40	0.9	2	1.64	0.2	2

45657884	catalase	0.95	0.3	15	1.24	0.4	14	1.44	0.6	14	1.24	0.4	13	1.61	0.7	15	1.15	0.4	14
45657886	transcriptional regulator (FUR family)	0.63	0.0	2															
45657906	histidine kinase response regulator hybrid protein	0.96	0.0	2															
45657918	hypothetical protein LIC12070	1.09	0.2	5	0.54	0.1	3	0.28	0.1	2	0.50	0.0	3	0.27	0.1	2	0.53	0.3	2
45657919	hypothetical protein LIC12071	1.55	0.9	3	1.71	1.4	3	2.70	1.9	2	0.91	0.3	4	1.23	0.3	3	1.43	0.4	3
45657923	hypothetical protein LIC12075	1.17	0.1	7	1.06	0.2	7	2.69	0.5	7	0.97	0.2	7	2.81	0.6	7	2.45	0.7	7
45657930	cysteine synthase	0.89	0.2	18	0.90	0.5	19	1.00	0.3	16	0.87	0.4	18	1.13	0.4	16	1.24	0.4	17
45657938	glyceraldehyde-3-phosphate dehydrogenase	0.80	0.3	8	1.24	0.2	8	0.21	0.1	7	1.71	0.5	8	0.24	0.2	8	0.15	0.1	8
45657939	phosphoglycerate kinase	1.13	0.4	8	0.91	0.1	7	0.43	0.1	5	0.83	0.3	9	1.15	1.8	6	0.50	0.1	5
45657942	triosephosphate isomerase	0.75	0.2	7	0.95	0.1	6	0.47	0.1	5	1.49	0.1	5	0.68	0.2	6	0.43	0.1	5
45657950	arginyl-tRNA synthetase	1.05	0.4	2															
45657954	hypothetical protein LIC12106	1.20	0.2	2				3.80	0.8	2				3.23	1.0	2			
45657956	aspartyl-tRNA synthetase	1.23	0.2	5	0.81	0.2	5				0.68	0.1	4						
45657958	50S ribosomal protein L9	0.84	0.1	14	0.58	0.1	13	0.03	0.0	3	0.69	0.1	14	0.04	0.0	3	0.05	0.0	3
45657960	single-stranded DNA binding protein	0.87	0.2	7	0.47	0.3	7	0.09	0.0	3	0.69	0.3	7	0.10	0.0	3	0.13	0.0	3
45657961	30S ribosomal protein S6	0.59	0.1	6	0.50	0.1	6	0.26	0.1	3	0.95	0.2	6	0.45	0.2	3	0.48	0.2	3
45657971	glucose-1-phosphate thymidylyltransferase	0.66	0.1	4	0.55	0.2	4				0.84	0.3	4						
45657972	dTDP-glucose 4,6-dehydratase	1.03	0.2	3	1.19	1.4	4	2.02	2.1	3	0.33	0.3	2	0.76	0.2	2	3.38	4.1	4
45657974	dTDP-4-dehydrorhamnose 3,5-epimerase	0.92	0.3	2	0.52	0.2	2	1.18	0.5	2	0.78	0.4	3	1.75	0.9	3	2.33	1.3	3
45657986	colanic acid biosynthesis glycosyl-transferase										0.41	0.1	2						
45657989	UDP-glucose 4-epimerase	1.01	0.3	3	0.86	0.2	3				1.16	0.6	4	1.14	0.4	2	1.02	0.4	2
45657999	cdp-glucose 4,6-dehydratase	0.68	0.1	4	0.62	0.3	4	1.44	0.6	4	0.93	0.4	4	2.09	0.7	4	2.68	1.5	4
45658002	D-3-phosphoglycerate dehydrogenase	0.96	0.1	4	0.79	0.2	5	0.66	0.2	3	0.82	0.4	6	0.72	0.3	3	0.85	0.2	3
45658014	putative molybdenum cofactor biosynthesis protein	1.10	0.3	8	1.01	0.5	7	1.36	0.8	6	0.96	0.2	7	0.98	0.2	6	1.03	0.2	6
45658015	alcohol dehydrogenase	0.86	0.3	6	1.14	0.4	7	0.39	0.2	5	1.13	0.4	6	0.47	0.3	5	0.35	0.2	5
45658017	aspartate aminotransferase	0.76	0.1	4	0.61	0.2	5	0.26	0.2	4	0.59	0.1	5	0.37	0.4	4	0.38	0.3	4
45658018	sialic acid synthase	1.11	0.1	7	0.70	0.3	6	0.91	0.1	3	0.64	0.3	6	0.94	0.4	4	0.85	0.1	3
45658020	nucleoside-diphosphate-sugar pyrophosphorylase	1.09	0.1	2	0.70	0.0	2	1.51	0.1	2	0.64	0.0	2	1.38	0.0	2	2.16	0.1	2
45658021	putative UDP-N-acetylglucosamine-2-epimerase	0.88	0.2	3	0.61	0.3	3				0.70	0.2	3						
45658023	acetyl transferase													0.76	0.3	2			
45658025	UDP-glucose 4-epimerase	0.77	0.1	2	0.53	0.2	2				0.68	0.1	2						
45658027	hypothetical protein LIC12178										1.40	0.7	2	2.91	0.5	2	2.27	0.8	2
45658028	sugar transferase																2.33	0.0	2
45658029	methyltransferase	1.45	0.3	3	0.95	0.4	3	1.80	0.5	3	0.69	0.4	3	1.24	0.5	4	2.12	1.1	3
45658031	ABC transporter, ATP-binding protein	1.00	0.1	4	1.03	0.7	2	0.51	0.2	4	1.11	0.7	2	0.52	0.2	4	0.45	0.0	2
45658036	perosamine synthetase	0.90	0.3	3	0.68	0.1	3	0.84	0.4	2	0.67	0.1	2	0.93	0.0	2			
45658037	hypothetical protein LIC12188	0.81	0.2	8	0.79	0.3	7	0.58	0.2	7	0.90	0.3	7	0.55	0.3	7	0.55	0.3	6
45658038	hypothetical protein LIC12189	0.86	0.2	4	0.94	0.3	4	0.53	0.4	4	1.18	0.6	4	0.71	0.7	4	0.55	0.2	4
45658042	hypothetical protein LIC12193	1.00	0.6	3	1.03	0.6	4	1.32	0.9	3	1.46	0.9	3	1.56	1.0	3	1.05	0.2	3
45658043	transketolase beta subunit	0.98	0.3	5	0.99	0.6	4	1.23	0.6	3	0.94	0.3	4	1.45	1.1	3	1.16	1.3	4
45658046	aminotransferase	0.67	0.2	5	0.51	0.2	5	0.73	0.8	5	0.81	0.4	5	0.53	0.2	4	0.79	0.3	5
45658047	aminotransferase	0.88	0.3	16	0.85	0.3	16	0.89	0.3	16	0.90	0.4	17	0.96	0.3	15	1.14	0.4	15
45658048	UDP-glucose 4-epimerase	0.85	0.3	5	1.15	0.3	7	1.36	0.8	6	1.07	0.3	5	1.66	0.6	6	1.15	0.5	6
45658049	ADP-heptose synthetase	1.01	0.3	11	0.96	0.2	9	1.26	0.5	9	0.98	0.1	8	1.23	0.5	9	1.27	0.3	6
45658050	mannose-1-phosphate guanyltransferase	1.38	0.0	2	1.08	0.3	2				0.78	0.2	2						
45658051	UDP-glucose 4-epimerase	1.09	0.2	7	0.87	0.2	9	0.46	0.3	9	0.89	0.2	8	0.38	0.1	8	0.54	0.3	9
45658054	gdp-l-fucose synthetase	1.75	0.9	3				3.27	2.4	3				1.64	0.7	3			
45658056	hypothetical protein LIC12207	1.02	0.4	7	0.57	0.2	7	0.26	0.1	4	0.70	0.4	6	0.26	0.1	4	0.46	0.2	5
45658059	Hsp15-like protein	43.36	20.5	3	51.80	24.4	3				1.27	0.2	9	0.01	0.0	2	0.01	0.0	2
45658060	Hsp15	9.67	14.5	3				3.00	3.0	3	1.18	0.7	11	0.72	0.4	3	5.69	7.3	3
45658066	putative lipoprotein	1.22	0.6	4	1.67	0.9	4	1.93	0.6	3	1.32	0.3	4	1.72	0.6	4	1.03	0.3	4
45658076	hypothetical protein LIC12227	0.05	0.0	2															
45658080	hypothetical protein LIC12231	1.04	0.1	2	0.96	0.1	2	1.49	0.2	2	0.92	0.1	2	1.43	0.1	2	1.55	0.0	2
45658081	thymidylate synthase				3.25	3.4	2	3.32	4.0	2							0.84	0.4	2
45658082	fructose-bisphosphate aldolase	0.88	0.2	8	1.07	0.4	9	0.81	0.4	9	1.16	0.5	8	0.87	0.5	8	0.88	0.3	8
45658089	chemotaxis protein	1.17	0.3	3	1.68	0.6	3	1.39	0.7	3	1.42	0.2	3	1.16	0.4	3	0.79	0.2	3
45658094	host factor-1	0.80	0.3	8	0.17	0.1	5	2.08	0.7	8	0.23	0.1	5	2.45	0.4	7	11.94	2.6	5
45658096	hypothetical protein LIC12247	0.86	0.3	2															
45658099	carboxy-terminal processing protease	0.68	0.2	23	1.05	0.3	21	0.30	0.1	19	1.71	0.7	23	0.53	0.4	19	0.34	0.3	20
45658112	hypothetical protein LIC12263	0.92	0.3	6	0.57	0.1	4	0.84	0.3	5	0.79	0.3	6	1.26	0.4	6	1.54	0.1	6

45658122	GGDEF family protein	0.69	0.3	2	0.50	0.1	2	1.59	0.3	2	0.74	0.1	2	2.64	1.6	2	3.42	1.6	2
45658125	hypothetical protein LIC12277	0.90	0.5	2	0.75	0.4	2	0.49	0.3	2	0.86	0.1	2	0.53	0.0	2	0.62	0.1	2
45658127	haloacid dehalogenase-like hydrolase										1.57	0.0	2	0.90	0.6	2	0.58	0.4	2
45658133	H+-translocating pyrophosphatase	1.08	0.2	5	1.39	0.3	5	1.69	0.5	5	0.96	0.3	7	1.22	0.8	7	1.01	0.5	6
45658135	putative lipoprotein	1.22	0.2	5	0.71	0.1	4	0.16	0.1	5	0.54	0.1	5	0.16	0.0	4	0.30	0.1	4
45658142	udp-glucose dehydrogenase	1.24	0.2	5	0.90	0.1	5	1.26	0.5	4	0.63	0.2	7	1.46	0.3	4	1.24	0.6	5
45658165	beta-ketoacyl synthase				1.16	0.5	3	11.17	6.1	3	0.59	0.1	2	8.66	7.8	2	9.55	2.1	4
45658166	hypothetical protein LIC12318																14.95	18.7	2
45658168	3-oxoacyl-[acyl-carrier protein] reductase	0.98	0.1	2				1.38	0.9	2				1.38	0.8	2			
45658171	type III beta-ketoacyl synthase-like protein	0.86	0.4	4	1.22	0.2	5	1.99	0.7	5	1.58	0.5	4	2.95	1.6	4	1.97	1.0	6
45658172	serine/threonine kinase with GAF domain	1.40	0.3	13	1.03	0.2	12	1.78	1.0	13	0.73	0.2	14	1.32	0.8	15	2.11	1.1	15
45658173	hypothetical protein LIC12325	1.00	0.5	2	1.45	0.6	2	3.92	0.4	2	1.47	0.1	2	4.52	2.6	2	3.05	1.6	2
45658175	adenylate/guanylate cyclase	1.42	0.7	2	0.81	0.3	2	4.10	2.1	2	0.59	0.1	2	2.84	0.2	2	4.92	0.9	2
45658176	putative lactoylglutathione lyase	0.56	0.2	4	0.77	0.2	4				1.37	0.2	4						
45658181	serine hydroxymethyltransferase	0.92	0.2	7	1.11	0.6	7	1.37	2.1	4	1.29	0.3	6	2.39	3.9	4	0.48	0.3	4
45658187	hypothetical protein LIC12341	0.77	0.1	2	0.51	0.3	2				0.70	0.5	2						
45658192	ribokinase	0.99	0.2	2	0.38	0.4	2				0.43	0.5	2						
45658195	hypothetical protein LIC12349	1.30	0.2	2	0.93	0.1	2				0.72	0.0	2						
45658196	glycyl-tRNA synthetase	0.94	0.5	3	1.32	0.6	3				1.56	0.8	3						
45658203	elongation factor EF-G	0.90	0.2	7	0.60	0.4	7	0.37	0.1	4	0.74	0.5	7	0.47	0.1	4	0.55	0.2	4
45658214	hypothetical protein LIC12368	1.24	1.0	4	2.84	2.1	4	1.48	0.7	4	2.36	0.5	4	1.55	1.0	4	0.63	0.3	4
45658225	histidine kinase sensor protein	1.55	0.3	4	0.84	0.5	4	4.03	0.4	4	0.57	0.3	5	2.44	0.7	5	3.75	1.7	5
45658243	hypothetical protein LIC12397	1.04	0.3	7	1.04	0.3	7	0.63	0.2	5	1.09	0.2	7	0.57	0.2	6	0.42	0.1	4
45658245	hypothetical protein LIC12399	1.19	0.4	3	1.37	0.5	3	2.35	0.0	3	1.30	0.8	3	2.13	0.6	3	1.86	0.6	3
45658246	isoleucyl-tRNA synthetase	1.04	0.3	9	0.74	0.2	9	0.59	0.4	4	0.84	0.2	8	0.50	0.2	4	0.92	0.9	4
45658248	phosphoribosylformylglycinamide synthetase	1.00	0.4	4	0.90	0.5	3	0.85	0.1	2	0.93	0.5	3	0.91	0.4	2	1.40	0.2	2
45658253	putative glutamine synthetase protein	0.92	0.3	19	1.10	0.3	20	1.07	0.4	20	1.01	0.3	20	1.07	0.5	20	1.01	0.3	20
45658259	hypothetical protein LIC12414	1.48	0.9	6	0.21	0.2	2	2.92	2.0	7	0.16	0.1	2	2.17	1.6	7	2.80	0.6	2
45658266	hypothetical protein LIC12421	0.92	0.3	3	0.82	0.1	3	0.67	0.6	2	0.92	0.2	3	0.61	0.4	2	0.74	0.6	2
45658267	aspartate aminotransferase a	0.97	0.2	3	0.76	0.1	4	0.86	0.3	4	0.78	0.1	3	0.76	0.3	3	1.11	0.4	4
45658283	transcriptional regulator	0.89	0.2	7	0.29	0.1	5	0.27	0.1	6	0.47	0.1	5	0.29	0.2	6	0.84	0.5	4
45658290	hypothetical protein LIC12446	0.78	0.1	7	0.97	0.1	6	0.68	0.2	6	1.17	0.3	6	0.90	0.1	5	0.71	0.2	4
45658291	30S ribosomal protein S1	1.02	0.5	21	0.86	0.5	20	0.21	0.1	9	0.87	0.3	20	0.24	0.1	9	0.30	0.2	9
45658297	response regulator	0.57	0.1	8	0.93	0.1	9	0.22	0.1	7	1.70	0.6	9	0.41	0.1	7	0.21	0.1	6
45658299	chemotaxis protein										1.83	0.7	4	4.24	1.8	4	2.28	0.3	4
45658302	hypothetical protein LIC12460	1.04	0.2	8	0.78	0.2	8	2.32	0.2	7	0.78	0.1	7	1.98	0.7	8	2.74	1.0	8
45658304	50S ribosomal protein L35	0.68	0.0	2	0.06	0.0	2				0.09	0.0	2						
45658305	translation initiation factor protein	1.81	0.7	4	1.09	0.5	4	1.60	1.1	3	0.68	0.4	4	0.72	0.4	3	1.97	1.7	3
45658307	threonyl-tRNA synthetase	0.95	0.2	10	0.94	0.4	10	0.30	0.2	8	1.04	0.3	10	0.37	0.2	9	0.39	0.2	10
45658308	carbamoyl-phosphate synthase small subunit	1.55	0.5	2	1.75	1.2	2				1.05	0.4	2						
45658316	oxoglutarate dehydrogenase	1.22	0.3	14	0.64	0.1	16	1.35	0.6	16	0.52	0.1	15	1.04	0.5	15	2.10	0.9	16
45658317	dihydrolipoamide dehydrogenase	1.25	0.4	7	0.83	0.1	6	0.90	0.3	7	0.67	0.1	6	0.66	0.1	6	0.96	0.1	6
45658318	dihydrolipoamide succinyltransferase	1.47	0.4	9	1.05	0.5	7	2.32	1.8	7	0.69	0.1	7	1.89	1.3	8	2.61	2.4	6
45658319	Pbp1A	1.84	0.5	4	1.80	0.9	5	2.62	2.2	6	0.78	0.2	4	0.64	0.3	4	1.10	0.5	6
45658326	DNA binding protein	1.14	0.4	3	0.91	0.3	3	1.99	1.4	3	0.81	0.2	3	1.73	0.9	3	2.32	1.4	3
45658329	hypothetical protein LIC12487	1.56	0.2	2	0.84	0.5	2	0.85	0.2	2	0.52	0.3	2	0.54	0.0	2	1.19	0.6	2
45658331	hypothetical protein LIC12489	0.37	0.0	4	0.42	0.2	3				1.12	0.5	3						
45658337	3-hydroxybutyryl-CoA dehydratase	0.74	0.1	7	0.79	0.1	7	0.19	0.0	6	1.22	0.3	8	0.23	0.0	5	0.23	0.1	6
45658368	ABC transporter, ATP-binding protein	1.62	0.5	2	0.90	0.1	2	1.20	0.4	2	0.59	0.2	2	0.74	0.0	2	1.36	0.5	2
45658371	sulfate ABC transporter periplasmic sulphate-binding protein precursor	1.45	0.1	2	0.65	0.3	2	1.79	1.5	2	0.45	0.2	2	1.26	1.1	2	2.47	1.3	2
45658376	GTP cyclohydrolase 2	1.09	0.2	2	0.94	0.0	2				0.88	0.2	2						
45658380	SecD	1.27	0.5	20	1.24	0.3	19	2.61	1.2	20	1.00	0.3	19	2.09	0.9	20	2.20	0.6	20
45658382	YajC	1.36	0.2	6	2.10	0.7	6	8.91	13.3	6	1.82	0.6	5	9.95	10.6	6	1.71	0.7	6
45658383	anthranilate phophoribosyl transferase	0.83	0.1	2	0.82	0.1	2	0.47	0.1	2	0.99	0.0	2	0.57	0.0	2	0.58	0.0	2
45658384	phosphatidylglycerophosphate synthase													3.59	3.7	2			
45658385	hypothetical protein LIC12543													1.74	1.0	2			
45658386	DNA binding protein	1.50	0.5	9	1.58	0.5	9	1.24	0.5	10	1.09	0.3	12	1.02	0.7	12	0.87	0.4	12
45658387	outer membrane lipoprotein carrier protein	0.92	0.4	4	1.34	0.6	3	0.59	0.4	3	1.39	0.2	3	0.69	0.6	3	0.30	0.2	2
45658392	acyl-CoA dehydrogenase	0.77	0.1	2	1.04	0.0	2	0.61	0.1	2				0.79	0.1	2			
45658404	glycerol-3-phosphate dehydrogenase	1.03	0.3	9	0.95	0.3	7	0.45	0.3	6	0.77	0.3	8	0.39	0.1	6	0.62	0.5	5

45658406	adenylosuccinate synthetase	0.87	0.3	6	0.81	0.3	6	0.51	0.4	4	0.81	0.2	5	0.56	0.4	4	0.51	0.2	4
45658407	hypothetical protein LIC12568	1.04	0.3	4	1.05	0.5	4	0.71	0.2	4	1.01	0.3	4	0.70	0.2	4	0.70	0.1	4
45658411	succinyl-CoA synthetase beta subunit	0.81	0.1	20	0.93	0.3	24	0.12	0.0	17	1.26	0.3	22	0.16	0.0	16	0.12	0.0	17
45658412	succinyl-CoA synthetase alpha subunit	0.81	0.2	14	2.15	3.8	14	0.14	0.1	6	1.75	1.5	14	0.18	0.1	6	0.14	0.1	6
45658413	cytoplasmic membrane protein	1.00	0.2	9	1.07	0.1	7	1.85	0.3	8	1.04	0.1	8	1.74	0.2	7	1.58	0.4	8
45658414	hypothetical protein LIC12576	1.32	0.1	2	0.82	0.3	2				0.63	0.3	2						
45658429	aminopeptidase N	0.95	0.2	6	0.63	0.2	6	0.35	0.1	4	0.81	0.4	6	0.37	0.1	4	0.47	0.2	4
45658437	hypothetical protein LIC12600				47.01	66.1	2				0.34	0.0	2						
45658438	hypothetical protein LIC12601	1.99	1.8	2	5.01	0.4	2				4.16	3.6	2						
45658440	hypothetical protein LIC12603										100.87	134.0	2	4.05	5.2	2	0.05	0.0	2
45658447	hypothetical protein LIC12610	1.16	0.2	2	6.18	1.7	2	0.62	0.2	2	5.57	2.5	2	0.53	0.1	2	0.11	0.1	2
45658448	hypothetical protein LIC12611	1.34	0.3	3	1.31	1.7	3	0.32	0.1	2	0.86	1.0	3	0.27	0.1	2	1.04	0.5	4
45658451	hypothetical protein LIC12614				728.13	247.3	2										0.00	0.0	2
45658452	hypothetical protein LIC12615	1.25	0.3	6	403.47	211.4	9	3.87	1.0	8	408.39	271.3	10	4.20	0.8	9	0.01	0.0	13
45658455	diaminopimelate decarboxylase	0.82	0.3	6	1.04	0.2	8	0.64	0.2	4	1.15	0.3	6	0.90	0.3	5	0.58	0.1	4
45658458	hypothetical protein LIC12621	1.05	0.1	10	1.08	0.2	10	3.49	0.7	9	0.97	0.1	10	3.30	0.5	9	3.28	0.6	10
45658464	histidine kinase response regulator hybrid protein	1.20	0.3	2	1.18	0.3	2	2.89	0.0	2	1.05	0.5	2	2.48	0.6	2	2.55	0.7	2
45658473	transcription termination factor Rho	1.11	0.2	14	0.99	0.2	14	0.43	0.3	14	0.98	0.2	15	0.42	0.3	13	0.37	0.3	12
45658515	thiamine biosynthesis protein ThiC	0.73	0.3	4	0.59	0.2	3	1.00	0.9	3	1.20	1.0	3	1.53	1.2	3	1.59	1.8	2
45658520	ABC transporter ATP-binding protein	1.16	0.5	2															
45658526	hypothetical protein LIC12691	1.37	0.5	5	1.35	0.5	5	0.81	0.2	4	1.06	0.1	4	0.77	0.2	5	0.77	0.2	5
45658528	hypothetical protein LIC12693	0.94	0.2	3				2.03	1.2	3	0.98	0.3	2	2.06	0.8	3			
45658529	glutamate synthase (NADPH) alpha chain precursor	1.04	0.3	20	0.71	0.3	19	0.70	0.4	17	0.70	0.2	20	0.62	0.3	17	0.89	0.4	17
45658536	polynucleotide phosphorylase	1.07	0.2	21	0.92	0.4	22	0.57	0.2	21	0.87	0.4	21	0.53	0.2	20	0.72	0.3	19
45658537	30S ribosomal protein S15	0.80	0.2	3	0.45	0.3	2				0.52	0.1	2						
45658540	translation initiation factor IF-2	0.74	0.2	8	0.87	0.1	8	0.19	0.1	6	1.02	0.2	8	0.28	0.2	7	0.23	0.2	6
45658541	transcription elongation factor NusA	0.84	0.4	16	0.76	0.3	16	0.32	0.2	13	0.93	0.4	16	0.36	0.1	14	0.38	0.1	12
45658559	3-hydroxybutyryl-CoA dehydratase	0.85	0.1	5	0.62	0.2	4	0.60	0.4	4	0.87	0.1	4	0.57	0.3	4	0.69	0.2	4
45658564	hypothetical protein LIC12730	1.56	0.5	4	1.14	0.4	4	1.54	0.5	2	0.75	0.2	4	0.94	0.1	2	1.12	0.1	3
45658571	site-specific modification DNA-methyltransferase	1.52	0.8	4	0.70	0.5	4	1.49	0.1	3	0.59	0.4	5	1.20	0.5	4	4.55	6.1	4
45658573	MaoC family protein	0.72	0.1	4	0.87	0.2	4	0.24	0.1	4	1.21	0.3	4	0.33	0.1	4	0.27	0.1	4
45658574	hypothetical protein LIC12740	1.09	0.2	2	0.80	0.0	2				0.75	0.1	2						
45658577	NADH dehydrogenase I subunit C	1.23	0.3	2	0.99	0.2	2	0.66	0.0	2	0.80	0.0	2	0.56	0.2	2	0.69	0.2	2
45658578	NADH dehydrogenase I D subunit	1.41	0.4	3															
45658580	NADH dehydrogenase I F subunit	0.91	0.3	5	0.62	0.2	5	0.69	0.3	5	0.74	0.3	5	0.81	0.4	5	1.14	0.4	5
45658595	aldehyde dehydrogenase	1.19	0.1	4	0.83	0.1	4	0.68	0.3	4	0.71	0.1	4	0.63	0.2	4	0.71	0.4	4
45658599	thiol peroxidase	0.59	0.2	8	1.25	0.2	8	0.09	0.0	6	1.49	0.9	8	0.17	0.0	7	0.22	0.4	6
45658600	anti-sigma factor antagonist	1.03	0.5	3	1.26	0.3	3	0.48	0.2	2	1.46	0.7	3	0.64	0.1	2	0.35	0.0	2
45658604	gamma-glutamyl phosphate reductase	0.94	0.4	4	3.72	4.8	3	1.28	1.0	2	3.97	4.9	4	1.55	1.5	3	0.96	0.5	3
45658607	50S ribosomal protein L27	1.13	0.3	3	0.31	0.1	3	0.65	0.1	2	0.27	0.0	3	0.51	0.1	2	1.95	0.0	2
45658609	50S ribosomal protein L21	0.86	0.1	5	0.54	0.2	6	0.06	0.0	5	0.47	0.1	5	0.06	0.0	5	0.13	0.0	5
45658626	acetyl-CoA acetyltransferase	0.81	0.1	9	0.77	0.2	10	0.54	0.2	11	1.10	0.2	8	0.76	0.2	9	0.66	0.4	10
45658632	hypothetical protein LIC12801	1.15	0.4	3	1.64	0.7	3	3.80	0.6	3	1.43	0.4	3	3.42	0.6	3	2.53	0.8	3
45658636	hypothetical protein LIC12805	1.18	0.3	2	1.51	0.8	2	3.97	3.7	2	1.23	0.4	2	3.05	2.3	2	2.31	1.2	2
45658643	serine protease MucD precursor	0.76	0.3	11	0.95	0.3	11	1.06	2.4	9	1.30	0.4	11	0.41	0.2	9	0.28	0.1	9
45658651	hypothetical protein LIC12821	0.92	0.3	6	1.61	0.3	4	2.84	0.4	5	1.56	1.1	5	2.67	0.5	5	1.78	0.4	4
45658659	citrate synthase	0.99	0.3	13	0.91	0.3	13	1.10	0.5	13	0.98	0.2	12	0.99	0.4	12	1.18	0.2	12
45658671	aspartate aminotransferase	0.81	0.1	9	0.77	0.2	8	0.30	0.1	7	1.12	0.4	9	0.39	0.1	7	0.41	0.1	6
45658675	50S ribosomal protein L17	1.14	0.1	4	0.60	0.2	4	0.87	0.1	4	0.52	0.1	4	0.88	0.4	6	1.30	0.3	4
45658676	DNA-directed RNA polymerase alpha subunit	1.02	0.2	11	0.80	0.2	11	0.86	0.4	11	0.80	0.2	11	0.91	0.5	11	1.11	0.5	11
45658677	30S ribosomal protein S4	1.00	0.1	5	0.45	0.1	5	0.51	0.2	5	0.52	0.1	6	0.51	0.2	5	0.89	0.1	4
45658678	30S ribosomal protein S11	1.01	0.0	3	0.84	0.1	3	0.53	0.1	3	0.83	0.1	3	0.52	0.0	3	0.63	0.1	3
45658679	30S ribosomal protein S13	0.97	0.1	6	0.33	0.1	6	2.33	3.9	4	0.31	0.1	5	2.27	3.8	4	6.71	10.8	4
45658682	adenylate kinase	0.58	0.1	5	0.49	0.3	7				0.99	0.7	6						
45658683	preprotein translocase SecY	0.86	0.4	3	0.92	0.1	2	1.62	0.9	3	0.85	0.1	2	2.39	1.9	3	1.54	1.2	2
45658684	50S ribosomal protein L15	0.88	0.1	9	0.15	0.1	7	0.06	0.0	5	0.18	0.0	6	0.06	0.0	5	0.50	0.3	6
45658686	30S ribosomal protein S5	0.95	0.2	8	0.57	0.1	8	0.07	0.0	6	0.65	0.1	8	0.07	0.1	6	0.10	0.1	6
45658688	50S ribosomal protein L6	1.21	0.1	8	0.73	0.2	8	0.80	0.2	7	0.59	0.1	7	0.68	0.2	7	0.99	0.4	7
45658689	30S ribosomal protein S8	1.06	0.2	6	0.53	0.2	5	0.19	0.1	2	0.49	0.1	5	0.16	0.1	2	0.23	0.2	2
45658690	30S ribosomal protein S14	0.73	0.0	2	0.13	0.1	2				0.18	0.1	2						
45658691	50S ribosomal protein L5	1.30	0.1	3	0.72	0.0	3	0.33	0.1	2	0.55	0.1	3	0.26	0.1	2	0.45	0.1	2

45658692	50S ribosomal protein L24	0.92	0.1	4	0.48	0.2	4				0.51	0.2	4						
45658693	50S ribosomal protein L14	0.97	0.1	4	0.59	0.1	4	0.20	0.2	3	0.62	0.1	4	0.30	0.3	3	0.26	0.2	3
45658694	30S ribosomal protein S17	1.23	0.3	2				0.54	0.1	2				0.44	0.0	2			
45658695	50S ribosomal protein L29	0.54	0.2	7															
45658696	50S ribosomal protein L16	1.01	0.4	8	0.88	0.2	7	0.12	0.1	4	0.64	0.1	7	0.19	0.2	4	0.11	0.1	3
45658697	30S ribosomal protein S3	1.20	0.2	5	0.79	0.2	7	0.55	0.2	7	0.61	0.2	7	0.45	0.2	7	0.71	0.2	8
45658698	50S ribosomal protein L22	1.22	0.2	5	1.02	0.1	5	0.32	0.1	3	0.81	0.2	5	0.25	0.1	3	0.32	0.1	3
45658700	50S ribosomal protein L2	1.17	0.2	12	0.83	0.2	11	0.37	0.2	11	0.72	0.1	12	0.27	0.1	10	0.40	0.2	11
45658701	50S ribosomal protein L23	0.82	0.0	3	0.47	0.0	3	0.16	0.1	3	0.57	0.1	3	0.20	0.1	3	0.36	0.1	3
45658702	50S ribosomal protein L4	1.18	0.1	7	0.74	0.2	7	0.33	0.2	6	0.63	0.2	7	0.33	0.2	7	0.40	0.1	6
45658703	50S ribosomal protein L3	0.97	0.2	6	0.77	0.1	6	0.16	0.0	5	0.68	0.1	6	0.16	0.1	5	0.21	0.0	5
45658704	30S ribosomal protein S10	0.65	0.1	6	0.12	0.0	4				0.17	0.0	4						
45658705	elongation factor Tu	0.87	0.2	25	1.14	0.3	27	0.71	0.4	29	1.35	0.4	26	0.76	0.3	25	0.68	0.5	29
45658713	carbamoyl-phosphate synthase large chain	1.00	0.2	7	0.68	0.2	7	0.41	0.1	7	0.72	0.2	7	0.37	0.1	6	0.56	0.1	5
45658716	hypothetical protein LIC12886	0.74	0.2	3	0.39	0.2	3				0.56	0.3	3						
45658725	putative lipoprotein	1.44	0.4	2	1.31	0.1	2	0.57	0.0	2	0.95	0.3	2	0.41	0.1	2	0.44	0.0	2
45658739	aspartokinase	0.66	0.1	5	0.83	0.3	6	0.78	0.8	2	1.00	0.2	5	0.66	0.4	2	0.72	0.5	2
45658750	methyl-accepting chemotaxis protein	1.19	0.2	36	1.74	0.5	35	7.13	3.0	38	1.48	0.5	37	5.62	2.2	39	3.96	1.3	38
45658753	citrate synthase													2.37	2.9	2			
45658764	hypothetical protein LIC12936	1.33	0.7	5	0.87	0.4	5	2.28	0.6	4	0.72	0.3	5	2.46	1.0	5	3.65	1.3	5
45658765	anti-sigma factor antagonist	0.64	0.0	2	0.96	0.0	2				1.51	0.0	2						
45658772	30S ribosomal protein S1				0.70	0.3	2												
45658785	hypothetical protein LIC12958	1.10	0.2	6	0.50	0.1	5	1.03	0.3	5	0.44	0.1	5	0.90	0.2	5	2.06	1.1	6
45658793	LipL41	0.96	0.5	25	1.22	0.7	26	1.56	0.5	25	1.34	0.6	25	1.73	0.4	22	1.43	0.4	22
45658806	hypothetical protein LIC12979	1.75	0.4	4	1.60	0.5	4	5.71	2.8	5	1.28	0.3	4	4.34	1.0	4	3.06	1.5	5
45658819	sulfate Permease										0.99	0.7	2	3.61	1.5	2	4.14	1.4	2
45658836	acyl-CoA dehydrogenase	0.97	0.1	7	1.28	0.4	7	0.86	0.3	6	1.21	0.3	7	0.74	0.2	6	0.67	0.3	7
45658844	acriflavine resistance	1.36	0.3	15	1.44	0.3	12	3.18	1.0	16	1.13	0.3	13	2.42	0.7	15	2.08	0.3	11
45658872	UDP glucosamine N-acyltransferase	0.95	0.2	4	0.85	0.1	4	0.33	0.1	3	0.93	0.2	4	0.41	0.2	3	0.40	0.1	3
45658876	hypothetical protein LIC13050	0.34	0.1	16	0.60	0.3	16				1.78	0.9	16						
45658885	putative lipoprotein	0.61	0.3	4	1.59	0.3	4				2.90	1.2	4						
45658886	LipL36	0.51	0.2	17	0.57	0.2	17	0.01	0.0	3	1.35	0.9	18	0.19	0.3	3	0.02	0.0	3
45658897	hypothetical protein LIC13071	0.54	0.2	5	0.77	0.9	3	1.22	0.1	5	0.47	0.1	3	1.97	1.2	6	3.15	2.2	3
45658899	transcriptional regulator (TetR family)	2.29	1.5	3	2.60	1.2	3	11.83	4.7	3	1.34	0.4	4	5.39	3.4	4	3.91	1.6	4
45658900	acriflavin resistance	0.51	0.1	7	0.62	0.2	8				1.44	1.1	8						
45658915	hypothetical protein LIC13089	1.65	0.3	4	1.19	0.3	4	2.76	1.1	3	0.94	0.3	4	1.85	0.9	3	2.76	0.6	3
45658916	acriflavin resistance	1.28	0.7	3	1.64	1.0	2				1.09	0.1	2						
45658918	PfaP	1.20	0.4	6	1.18	0.2	5	0.71	0.4	4	0.87	0.3	6	0.50	0.2	4	0.58	0.2	4
45658945	hypothetical protein LIC13122	0.88	0.4	4	0.62	0.2	4				0.79	0.3	4						
45658946	hypothetical protein LIC13123	0.94	0.3	5	1.02	0.5	5	2.89	1.7	5	0.92	0.2	5	3.10	1.3	5	3.01	1.1	6
45658951	methionyl-tRNA synthetase	0.84	0.5	2	1.01	0.5	2	0.35	0.3	2	1.31	0.2	3	0.38	0.1	2	0.32	0.1	2
45658958	acyl-CoA dehydrogenase	1.08	0.5	4	0.75	0.2	4	1.23	0.2	3	0.78	0.3	4	1.32	0.6	3	1.23	0.6	4
45658969	hypothetical protein LIC13147	0.84	0.2	2	1.20	0.6	2				1.38	0.4	2						
45658976	UDP-N-acetylglucosamine acyltransferase	1.12	0.4	8	0.93	0.5	7	1.05	0.5	7	1.11	0.3	7	0.80	0.4	6	1.00	0.8	6
45658984	phospho-2-dehydro-3-deoxyheptonate aldolase Chorismate mutase	0.84	0.1	10	0.69	0.4	6	0.46	0.2	8	1.01	0.6	7	0.56	0.1	8	0.54	0.0	4
45658988	hypothetical protein LIC13166	0.92	0.2	19	0.70	0.1	21	2.66	0.9	22	0.74	0.2	18	2.72	0.8	21	3.70	1.1	20
45658990	GDP-mannose 4,6-dehydratase	1.96	1.1	6	1.88	1.1	4	5.24	3.3	3	0.86	0.6	4	1.77	1.1	3	3.13	1.5	3
45658998	Tas	1.56	0.7	5	0.86	0.2	3				0.62	0.2	3				0.60	0.5	2
45659005	methyl-accepting chemotaxis-like	0.58	0.1	12	0.15	0.0	8	0.24	0.1	10	0.22	0.0	8	0.39	0.1	10	1.62	0.5	8
45659016	cholesterol oxidase	1.41	0.4	6	1.43	0.4	5	1.62	0.2	6	0.84	0.5	6	1.19	0.4	7	1.27	0.5	7
45659018	putative O-methyl transferase	1.05	0.2	6	0.82	0.4	2	1.91	0.5	5	0.85	0.3	2	1.70	0.8	6	2.32	0.5	2
45659023	adenylate/guanylate cyclase	1.53	0.9	4	0.64	0.1	4	0.26	0.1	3	0.58	0.2	3	0.25	0.1	3	0.42	0.1	3
45659034	hypothetical protein LIC13212										1.23	0.0	2	2.53	0.0	2	2.06	0.1	2
45659041	phenylalanyl-tRNA synthetase beta chain	0.83	0.3	2				1.21	1.1	2				1.30	0.9	2			
45659044	lauroyl/myristoyl acyltransferase	1.31	0.0	2	1.11	0.5	2	0.79	0.6	2	0.85	0.4	2	0.60	0.4	2	0.66	0.2	2
45659052	ATP-dependent RNA helicase	1.48	0.4	5	1.02	0.5	5	0.93	0.1	4	0.83	0.3	5	0.53	0.1	4	0.74	0.2	4
45659065	isocitrate dehydrogenase	0.85	0.1	11	0.72	0.2	11	0.46	0.2	9	0.85	0.2	10	0.59	0.3	9	0.71	0.3	9
45659071	apolipoprotein n-acyltransferase	1.15	0.1	6	1.09	0.1	6	1.40	0.3	5	0.90	0.1	8	1.38	0.3	7	1.37	0.3	6
45659078	NADH oxidoreductase	1.48	0.3	4	1.08	0.3	4	1.56	0.3	4	0.73	0.2	4	1.10	0.3	4	1.55	0.5	4
45659084	ribonuclease D	1.12	0.2	3	1.08	0.5	3				0.94	0.3	3						
45659096	hypothetical protein LIC13275	0.66	0.3	2	0.53	0.2	2				0.81	0.0	2						

45659114	hypothetical protein LIC13293	0.51	0.0	2	0.71	0.3	3				1.08	0.5	2						
45659118	hypothetical protein LIC13297	0.94	0.1	2															
45659119	3-hydroxyacyl-CoA dehydrogenase	0.88	0.1	9	0.89	0.2	8	0.27	0.2	8	0.98	0.2	7	0.35	0.2	7	0.33	0.2	8
45659120	acetyl-CoA acetyltransferase	0.92	0.0	8	0.78	0.3	8	0.30	0.1	7	0.83	0.3	9	0.33	0.2	7	0.29	0.1	7
45659129	phenylalanyl-tRNA synthetase alpha chain	1.43	0.6	3	1.00	0.0	2	0.36	0.2	2	0.65	0.3	2	0.35	0.2	2			
45659132	hypothetical protein LIC13313	1.13	0.2	7	1.18	0.3	7	1.75	0.4	6	1.01	0.2	7	1.41	0.4	6	1.32	0.4	6
45659133	hypothetical protein LIC13314	1.47	0.2	15	1.54	0.9	17	0.99	0.5	16	1.04	0.2	17	0.68	0.2	13	0.68	0.4	16
45659135	ABC transporter, ATP-binding protein	1.09	0.3	11	1.29	0.4	12	1.12	0.6	11	1.19	0.3	10	0.92	0.6	10	0.83	0.4	12
45659137	fatty acid synthase subunit beta	0.58	0.1	11	0.61	0.2	10	0.31	0.1	9	1.01	0.2	11	0.47	0.2	9	0.38	0.1	9
45659145	nucleoside diphosphate kinase	0.65	0.1	4	0.81	0.1	4	0.14	0.1	3	1.26	0.3	4	0.24	0.2	3	0.18	0.1	3
45659147	isocitrate dehydrogenase	1.05	0.1	2	0.75	0.1	2	1.01	0.3	2	0.71	0.1	2	0.97	0.3	2	1.39	0.6	2
45659160	putative lipoprotein	1.85	1.0	3	2.52	0.7	2	2.01	1.3	2	1.21	0.3	2	1.63	1.2	2			
45659166	DNA gyrase subunit A	1.11	0.4	10	1.10	0.4	10	1.07	0.5	9	1.11	0.5	9	0.88	0.4	7	1.06	0.5	9
45659167	DNA gyrase subunit B	0.95	0.2	13	0.84	0.2	13	1.10	0.4	13	0.90	0.2	14	1.20	0.4	13	1.36	0.5	14
45659170	hypothetical protein LIC13351	0.71	0.1	8	1.01	0.3	8	0.27	0.1	7	1.52	0.5	8	0.40	0.1	7	0.27	0.1	6
45659172	L-amino acid oxidase	0.33	0.1	2				0.55	0.1	2	0.88	0.6	2	1.74	0.6	2	1.18	0.2	2
45659186	sulfite reductase	0.98	0.1	9	0.67	0.2	11	0.32	0.1	8	0.71	0.1	8	0.40	0.1	7	0.49	0.1	8
45659189	sulfate adenylyltransferase subunit 1	1.07	0.2	3	0.32	0.1	2	0.27	0.1	2	0.34	0.1	2	0.28	0.1	2	0.89	0.5	2
45659209	polysaccharide deacetylase	0.46	0.0	3	0.56	0.2	4	2.01	0.7	2	0.95	0.1	3				3.62	2.8	2
45659210	ketol-acid reductoisomerase	1.00	0.5	11	0.80	0.3	11	0.72	0.2	10	0.84	0.4	11	0.79	0.2	10	0.90	0.3	10
45659211	methyl-accepting chemotaxis transmembrane protein	2.23	1.8	3	1.57	1.3	3	2.93	3.1	3	0.68	0.1	3	1.13	0.3	3	1.65	0.4	3
45659221	acetyl-CoA synthase	1.01	0.4	10	1.13	0.6	10	5.43	8.7	9	1.16	0.8	10	2.36	2.0	8	2.22	2.4	8
45659227	hypothetical protein LIC13410	1.08	0.1	3	0.60	0.2	3	2.21	1.2	3	0.56	0.2	3	2.01	1.0	3	4.58	4.2	3
45659230	5'-phosphoribosylglycinamide transformylase	1.30	0.6	5	0.91	0.6	4				0.78	0.4	4						
45659251	hypothetical protein LIC13434	1.15	0.5	6	0.53	0.4	5				0.78	0.6	7	0.09	0.0	2	0.11	0.1	2
45659259	glutathione peroxidase	1.02	0.3	3	0.89	0.6	4				0.89	0.3	4						
45659260	hypothetical protein LIC13443	1.15	0.2	3															
45659266	hypothetical protein LIC13449				0.78	0.3	2												
45659268	flagellar hook-associated protein																4.84	0.5	2
45659286	ferredoxin--NADP reductase	0.68	0.1	5	1.06	0.2	5	0.49	0.1	5	1.60	0.4	5	0.74	0.2	5	0.46	0.0	5
45659289	DNA polymerase III gamma subunit	1.42	1.0	5	1.34	0.5	6	0.41	0.1	3	0.85	0.4	6	0.29	0.1	2	0.45	0.1	2
45659295	seryl-tRNA synthetase	1.13	0.5	4	1.23	0.6	4	0.94	0.2	2	1.06	0.2	4	0.83	0.3	2	0.90	0.5	2
45659297	hypothetical protein LIC13482	0.43	0.0	2				1.14	1.2	3				1.11	0.1	2			
45659304	metallopeptidase	1.25	0.4	7	1.63	0.5	6	3.49	1.1	6	1.05	0.5	6	2.14	1.0	6	2.78	1.7	8
45659307	branched-chain amino acid aminotransferase	0.78	0.1	2	0.97	0.2	2	0.64	0.2	2	1.24	0.1	2	0.81	0.2	2	0.65	0.1	2

Supplementary Table 3. Relative quantification based on MS1 intensities. From an original data set containing 1081 proteins, 747 were quantified with high confidence: At least 2 independent proteotypic peptides were observed, whereby semi-tryptic peptides were exclude from the analysis. For each state the ratios (e.g. C2H for Control to Heat-shocked ratio), standard deviations (Std) and number of observed proteotypic features (NF) is given. Abbreviations: C: control, H: heat-shocked, AB: antibiotics-treated, S: starved.

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