Supplementary information: Proteomewide cellular protein concentrations of the human pathogen *Leptospira* interrogans

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Supplement Results

Detailed description of a method for determining absolute protein abundances on a proteome-wide scale

In this study we developed a mass spectrometry based strategy to determine the average number of protein copies per cell in a cell population, for a significant fraction of the proteome in genetically unperturbed cells. The strategy combines three mass spectrometry based proteomic methods and a summary of the workflow is depicted in Figure S1. In a first step, the proteome of the cell sample under study is subjected to extensive mapping via LC-MS/MS experiments, whereby precursor ions selected on the fly by the mass spectrometer (data dependent acquisition, DDA) or by the use of a rolling inclusion list ¹, are subjected to collision activated dissociation (CAD). The resulting fragment ion spectra are then assigned to peptide sequences in a database and the sequence and the number of repeat observations for each peptide is entered into an instance of the PeptideAtlas database ². The result of this first step is a qualitative map of proteins identified by tandem mass spectrometry from the proteome in question. In a second step, the absolute abundance of a limited number of proteins spanning a broad range of protein concentrations is determined by selected reaction monitoring (SRM, also referred to as multiple reaction monitoring, MRM) using stable isotope labeled reference peptides ³. The values from these measurements represent anchor points for the calculation of an absolute abundance scale for a significant fraction of the MS observable proteome. In a third step, the median ion intensities for the signals of the 1-3 most intense precursor ions representing a particular protein are extracted from the LC-MS maps of a trypsinized proteome sample. These values are calibrated by the SRM values to derive absolutely quantified anchor protein values and to generate an absolute abundance scale for a large fraction of the MS observable proteins of the proteome. The combined output from the three mass spectrometry methods results in an extensive map of the MS observable proteome and an estimated absolute abundance scale for a majority of the detected proteins

Proteome coverage statistics

We note that 99.3% of the observed proteins contain minimally two tryptic peptides with favorable properties for mass spectrometry analysis (molecular weight between 0.6 and 5.2 kDa), while the same is true for 98.7% of the unobserved proteins. Therefore these proteins should be detectable by mass spectrometry if expressed above the detection limit. A Codon usage analysis with the CodonW software

⁴ (Figure S2) revealed a difference between the undetected and detected proteins, indicating the lower abundance or absence of the first group under the selected growth conditions.

Absolute protein abundance and cryo-electron tomograms in assembling molecular in vivo models with special emphasis on L. interrogans chemotaxis and motility system

The ability to determine the absolute concentration of a large number of proteins and protein complexes in a specific cell type and to relate this information to the distribution of specific complexes in the cell allowed us to address some open questions in bacterial physiology. We used the proteomewide abundance maps and library of tomograms to characterize the chemotaxis and motility system of *L. interrogans*, which has been recognized as much more complex than in other bacteria ⁵ and plays an important role during pathogenesis.

<u>Chemotaxis:</u> The L. interrogans genome ^{6,7} contains in total 3658 gene models with more than 4% of the protein-coding sequences related to motility and chemotaxis. Due to its mode of living, L. interrogans requires a highly organized motility system that enables movement in dense media as serum and eukaryotic cells as well as skin penetration. As a facultative parasitic organism it also needs the capability to adapt to aqueous surroundings. We extracted the protein copy numbers for the genes assigned to motility and chemotaxis and summarized the cellular protein composition, abundance and structural arrangement of this unusual chemotaxis system in spirochetes (see Figure 1C). The stimulus triggering a signaling cascade that ultimately causes movement is recognized by methyl accepting membrane coupled receptors (MCPs). Thus, a signal needs to travel only a short distance (around 200 nm) to trigger the next (but not the far) motor. Although 12 different genes code for MCPs in L. interrogans, most of them are expressed at low copy numbers of 20-600 per cell (or even below the detection limit), except for a large excess of mcpA (~4000 copies per cell). This protein consequently is the major receptor component ⁸ under the investigated conditions. MCPs regulate autophosphorylation of the sensor histidine kinase CheA, which in turn phosphorylates the response regulator CheY forming CheY-P. The chemo-receptor complex consists of MCP, CheW, and CheA, that were found to occur in ratios of 12:6: 2 per unit cell in vitro ⁹ but sub-stochiometrical in vivo 6.8: 1.6: 2 ¹⁰. Considering all MCPs and three different CheW gene products, the ratio is further reduced in life L. interrogans cells (50:6:2). We can thus confirm the stoichiometric relationship between CheA and CheW (as observed in vitro), whereas the level of MCP to CheA seems to be four times higher in the spirochetes compared to other bacteria. The presence of three different CheW gene products that serve as adaptors for CheA (CheY kinase) implies the existence of different substrates to be phosphorylated. Indeed out of 8 different CheY gene products, 6 were detected in our analysis, 2 of them being very high abundant. Interestingly, the cellular concentration of CheY8 strongly increases during stress induced by antibiotics treatment. Generally, CheY response regulators are present at 20-30 fold excess compared to their kinase CheA and phosphatase CheZ, verifying a large abundance difference between enzyme and substrate indicating that these enzymes work at V_{max} within the cell, as suggested earlier ¹¹. In summary, the components of the *L. interrogans* chemotaxis system have very different abundances forcing the enzymes involved to work at high efficiency. Some components can be adjusted to a changing environment (as in case of Ciprofloxacin exposure), while others are highly ordered and organized around the cell poles, enabling a highly efficient signal transmission in a very concise subvolume of the cell.

Cell shape determination: It is not clear how exactly L. interrogans maintains its spiraled cell shape. The contribution of the peptidoglycan layer, the periplasmic flagella and the cytoplasmic filaments has been discussed ^{5,7} but so far remained elusive. As stated above, the abundance calculations as well as the cryoET data (Figure S3) led us to conclude that the flagellum does not cover the entire cell length. In contrast to B. burgdorferi 12 it is unlikely that the cell shape is determined by the flagellum in L. interrogans. The same arguments can be made for apparent cytoplasmic filaments. These filaments have been visualized using tomography ¹³ and ascribed to MreB. This protein has a longitudinal subunit spacing of 5.1 nm ¹⁴ and occurs in 2500 copies per cell in *Leptospira*, allowing for a maximum of ~13 μm of a single filament. Therefore, a bundle of several filaments stretching throughout most of the cell cannot be explained by MreB alone. Consequently, it is unlikely that the MreB proteins - traditionally denoted as involved in bacterial rod-shape determination 7 - can exclusively determine the cellular shape. They are however predominant in the cytoplasm of subvolumes where cells have been stretched out on the carbon support of the EM-grid (not shown) and therefore speculatively might function in mechanical stress response. Both the periplasmic flagella and cytoplasmic filaments are apparent in most of tomograms, but in many cases do not stretch through the entire subvolume (Figure S3). In tomograms without one or the other structure the cells still display their typical shape, deciphering that none of the two components are critical for maintaining the kinked cellular outline as previously been suggested ^{7,15}. If both structures were present they occurred in a double helical arrangement with the cytoplasmic membrane in between (Figure S3). In contrast, the proteins assigned to the GO term external encapsulating structure ¹⁶ (Table S2), including several peptidoglycan associated membrane

proteins and LipL's, are the most abundant proteins in *L. interrogans*, indicating that the involvement of the peptidoglycan layer might play a more important role than anticipated.

Supplement Figures

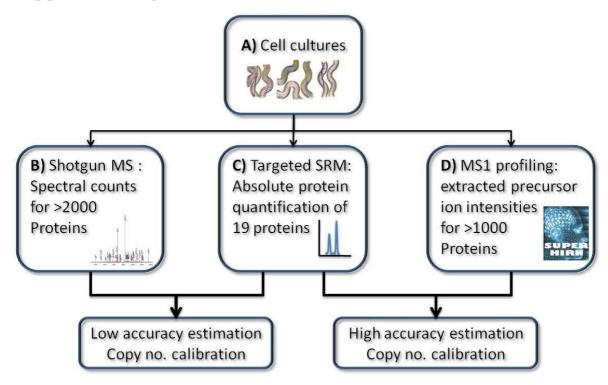


Figure S1. Schematic outline of the mass spectrometry based strategy. A) *L. Interrogans* cells at different states were grown and prepared for MS analysis. B) Generation of a proteome map by peptide separation and inclusion list directed and data dependent tandem mass spectrometry C) Targeted quantitative mass spectrometry measurements by selected reaction monitoring (SRM) using heavy isotope labeled reference peptides and D) label free quantitative mass spectrometry where peptide quantities are estimated from the extracted ion current of the most dominant precursor ions of each protein. The values from the SRM measurements represent anchor points for the calculation of an absolute abundance scale for the proteins with spectral count or extracted precursor ion intensities.

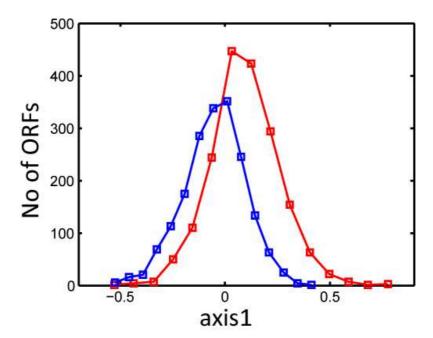


Figure S2. Codon usage analysis of *L. interrogans* genes. The software CodonW was used to identify putative optimal Codons by a correspondence analysis ⁴. Thereby, classification due to the Eigenvalue that corresponds to the major codon usage trend (so called axis1, ⁴) provides a measure for the frequency of optimal Codons of each gene. The distribution of this value is plotted as a histogram separately for the 1864 gene products identified in shotgun MS (blue) and the 1794 proteins not detected (red). The shift between the distributions indicates that the optimal codons were identified correctly and the latter group is low abundant or not expressed under the investigated conditions.

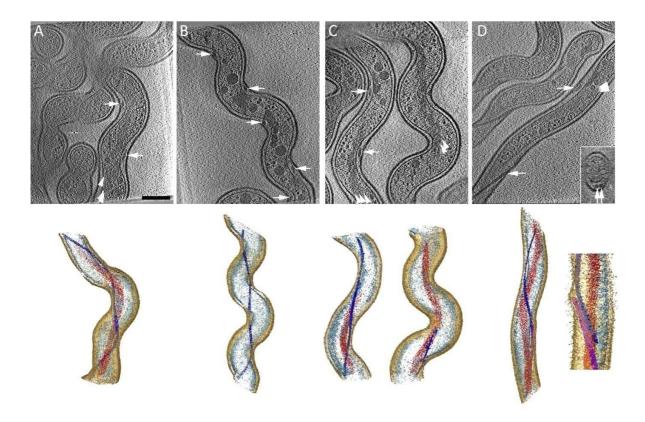


Figure S3. Presence of periplasmic flagella and cytoplasmic filaments *L. interrogans*. Slices through tomographic reconstructions of differently shaped cells are shown in the top panel (arrows: periplasmic flagella; arrowheads: cytoplasmic filaments which might also contribute to cell shape determination ¹³; scalebar: 200 nm). A) Cell with both filaments and flagellum. B) Cell with only flagellum and no filaments discernable. C) Cell with flagellum and partial filaments (left) as well as a cell with trough filaments and flagellar end (right). The lower right cell shown in D is exceptional in the sense that both flagella overlap and displays a straight cell shape (inset shows a cross section). Surface rendered representations are shown in the bottom panel with the encapsulation structure colored in brown, the cytoplasmic membrane in transparent blue, periplasmic flagella in dark blue and filamentous bundles in red. The 2nd flagellum of the cell on the right is colored magenta (inset: rotated and 2-fold magnified view of the alignment region; elongation axis of all cells roughly aligned to the vertical axis). Please note the observed regions without flagella in the middle of the cells. Since both flagella take the shortest path through cells and do not overlap in the middle it is expected be shorter than the average cell length, confirming the estimated protein copy numbers of the proteins involved.

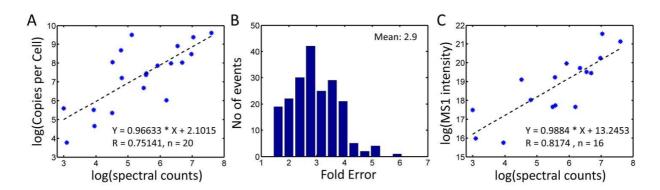


Figure S4. Correlation between spectral counting to SRM absolute abundance data A) The natural logarithm of spectral counts for the selected proteins plotted against the natural logarithm of copies/cell as determined by SRM B) The mean error was estimated to ~3 fold using bootstrap analysis C) Correlation of the natural logarithm of spectral counts with MS1 intensities precursor intensity. Since MS1 intensities were not derived for all the proteins detected by MRM the number of data points is smaller when MS1 intensities are involved.

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Acession Number	Protein description	Reference peptide	Control	Ciprofl	Control	Ciproflox
		sequence	(fmol/u	oxacin	(copies	acin
			I)	(fmol/	/cell	(copies/c
				ul)	SRM*)	ell SRM)
sp Q72SY1 ATPA_L EPIC	ATP synthase subunit alpha (EC 3.6.3.14) (ATPase subunit alpha)	ILEVPVGPELLGR	20.95	31.72	7424	11649
LFIC	Subuliit aiplia)	TSIALDTILNQK	27.21	38.23		
sp Q72SX9 ATPB_L	ATP synthase subunit beta (EC 3.6.3.14) (ATPase	FSQAGSEVSALLGR	15.40	21.49	4749	7189
sp Q72QU2 CLPB_	subunit beta) Chaperone clpB	AVDLIDEASSK	1.02	1.13	414	632
LEPIC		IADIQLEGLR	1.66	2.54		
sp Q72R01 CLPP2_	ATP-dependent Clp protease proteolytic subunit 2	IAEVFEELTGSK	8.07	8.95	1741	1681
LEPIC	(EC 3.4.21.92)	IALVILLIUSK	8.07	8.93	1/41	1001
		IFLWGPVTDESSK	2.93	1.71		
		LNQILADACGHPIS	5.93	4.24		
ref YP_000584.1 Y	fatty acid synthase subunit beta	K TEVITHANLVR	4.37	2.41	1348	766
P_000584.1		ALAFEVOK	2.40	1.64	1507	704
		AIAEEVPK EFFDTSFK	3.48 6.82	1.64 3.25	1587	794
ref YP 001158.1 Y	flagellar hook protein	VATAVFNNPAGLD	0.82	0.28	105	82
P_001158.1	nagenar nook protein	K	0.34	0.28	103	82
ref YP_001355.1 Y P 001355.1	flagellar M-ring protein	GFTPDGPAGTEPNI APGYK	0.16	0.15	43	35
_		IISDFEEDLEK	0.12	0.09		
ref YP_001839.1 Y P 001839.1	flagellin protein	ANLGAYFNR	47.25	72.95	11860	18043
_		VLAIQSSNGIYSAE DR	29.68	51.44		
sp P61438 CH60_L EPIC	60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock 58 kDa protein)	AVTAAVESIQK	48.48	50.17	14868	17711
EPIC	(Heat Shock 38 kDa protein)	VEDALSATR	47.96	60.18		
sp P61436 CH10 L	10 kDa chaperonin (Protein Cpn10) (groES protein)	ESDILAVVK	32.85	19.50	13244	11919
EPIC EPIC	(Heat shock 10 kDa protein)				13211	11313
		VGDTVLYGK	53.05	48.87		
sp Q72RY7 HSLU_L EPIC	ATP-dependent hsl protease ATP-binding subunit hslU	HGSGQITGFATSST LADEEDRK	0.77	0.47	266	202
		LLEEVSFEGPDLPES QR	0.95	1.01		
ref YP_002145.1 Y P 002145.1	Hsp15-like protein	ILELPTEVDSEK	0.79	26.74	244	10281
sp Q72QA1 HSP15 LEPIC	Probable 15 kDa heat shock protein	DVQVQLEK	0.67	15.51	208	5964
ref YP_001227.1 Y P 001227.1	MreB	GIVLTGGGCLLR	11.21	16.49	2608	4036
P_001227.1		TGGDEFDEAIIK	5.70	8.29		
sp P62217 RECA_L EPIC	Protein recA (Recombinase A)	IVEIYGPESSGK	2.58	33.70	795	12823
sp Q72QK0 RS6_LE PIC	30S ribosomal protein S6	EFLINQNILR	19.13	11.49	5899	4077
ref YP_002772.1 Y P 002772.1	30S ribosomal protein S5	FSFNALSVVGDQR	10.14	7.22	3126	2643
sp Q72NI8 RPOA_L EPIC	DNA-directed RNA polymerase alpha chain (EC 2.7.7.6)	ITNLDYLPNLIQIQK	10.05	10.59	3100	3264
sp Q72UA7 RPOC_ LEPIC	DNA-directed RNA polymerase beta' chain (EC 2.7.7.6)	TFDLGEVGR	9.70	10.35	2991	3204
	=:::::=;	FATSDLNDLYR	9.48	8.29	2923	2535

• •	nated protein copies per cell for the					
Accession number	Protein description	GO annotation	Control (copies/cell MS1)	Ciprofloxacin 24h (copies/cell MS1)	Control (copies/cell Spectral counts)	
ref YP 003221.1 YP 003221.1	ABC transporter, ATP-binding protein	ABC-transporter	1185	1796	923	
ref YP 002117.1 YP 002117.1	ABC transporter, ATP-binding protein	ABC-transporter	504	443	85	
ref YP 000522.1 YP 000522.1	ABC transporter ATP-binding protein	ABC-transporter	240	394	238	
ref YP 000340.1 YP 000340.1	ABC transporter ATP-binding protein	ABC-transporter		386	281	
ref YP 000502.1 YP 000502.1	ABC transporter, atp-binding protein	ABC-transporter	275	271	75	
ref YP 001503.1 YP 001503.1	ABC transporter, ATP-binding protein	ABC-transporter	227	209	169	
ref YP 000922.1 YP 000922.1	ABC transporter, ATP-binding protein	ABC-transporter	217	184	30	
ref YP 000224.1 YP 000224.1	ABC transporter ATP-binding protein	ABC-transporter	143	179	75	
ref YP_002457.1 YP_002457.1	sulfate ABC transporter periplasmic sulphate-binding protein precursor	ABC-transporter	275	164	403	
ref YP 002606.1 YP 002606.1	ABC transporter ATP-binding protein	ABC-transporter	326		207	
ref YP 003334.1 YP 003334.1	ABC Transporter, ATP-binding protein	ABC-transporter	320		143	
ref YP 003287.1 YP 003287.1	ABC transporter ATP-binding protein	ABC-transporter			47	
ref YP 002245.1 YP 002245.1	ABC transporter ATP-binding protein	ABC-transporter			27	
ref YP_003617.1 YP_003617.1	phosphate ABC transporter periplasmic phosphate-binding protein	ABC-transporter			21	
ref YP_000615.1 YP_000615.1	ABC transporter ATP-binding protein	ABC-transporter			155	
ref YP 001755.1 YP 001755.1	ABC transporter, ATP-binding protein	ABC-transporter			82	
ref YP 001189.1 YP 001189.1	ABC transporter permease protein	ABC-transporter			61	
ref YP_000516.1 YP_000516.1	ABC transporter, ATP-binding protein	ABC-transporter			34	
ref YP_001775.1 YP_001775.1	ABC transporter, ATP-binding protein	ABC-transporter			21	
ref YP 001051.1 YP 001051.1	ABC transporter ATP-binding protein	ABC-transporter			17	
ref YP 002229.1 YP 002229.1	ABC transporter ATP-binding protein	ABC-transporter			14	
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ref YP_002456.1 YP_002456.1	sulfate ABC transport system permease protein	ABC-transporter			14	
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ref YP_002013.1 YP_002013.1	ABC transporter ATP-binding protein	ABC-transporter			5	
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ref YP_002605.1 YP_002605.1	ABC transporter, membrane spanning protein	ABC-transporter				
ref YP_001050.1 YP_001050.1	ABC transporter integral membrane protein	ABC-transporter				
ref YP_001456.1 YP_001456.1	ABC transporter ATP-binding protein	ABC-transporter				
ref YP_001807.1 YP_001807.1	ABC transporter ATP-binding protein	ABC-transporter				
ref YP_003286.1 YP_003286.1	dipeptide ABC transport system permease protein	ABC-transporter				
ref YP_000659.1 YP_000659.1	ABC transporter ATP-binding protein	ABC-transporter				
ref YP_002866.1 YP_002866.1	dipeptide/oligopeptide ABC transport system permease protein	ABC-transporter				
ref YP_000132.1 YP_000132.1	ABC transporter ATP-binding protein	ABC-transporter				
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ref YP_001537.1 YP_001537.1	FtsA	cell cycle	433	533	75	
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ref YP_002882.1 YP_002882.1	cell division protein FtsZ	cell cycle			50	
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ref YP 002381.1 YP 002381.1	hypothetical protein LIC12452	cell cycle	<u> </u>		54
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ref YP_003095.1 YP_003095.1	cell volume regulation protein CvrA	cell cycle			
ref YP_001814.1 YP_001814.1	cell division protein	cell cycle			
ref YP 002287.1 YP 002287.1	cell surface saccharide acetylase protein	cell cycle			
ref YP 002836.1 YP 002836.1	methyl-accepting chemotaxis protein	chemotaxis	4238	6006	391
ref YP 003091.1 YP 003091.1	methyl-accepting chemotaxis-like	chemotaxis	3700	861	615
ref YP 001482.1 YP 001482.1	chemotaxis protein	chemotaxis	628	790	288
ref YP_001185.1 YP_001185.1	methyl-accepting chemotaxis transducer	chemotaxis	263	516	24
	transmembrane protein			525	
ref YP_002175.1 YP_002175.1	chemotaxis protein	chemotaxis	324	454	192
ref YP_001661.1 YP_001661.1	histidine kinase response regulator hybrid	chemotaxis	262	423	766
	protein				
ref YP_002385.1 YP_002385.1	chemotaxis protein	chemotaxis		325	177
ref YP_001820.1 YP_001820.1	chemotaxis protein methyltransferase	chemotaxis	335	296	169
ref YP_001660.1 YP_001660.1	histidine kinase response regulator hybrid	chemotaxis	121	255	347
	protein				
ref YP_003297.1 YP_003297.1	methyl-accepting chemotaxis	chemotaxis	209	214	50
	transmembrane protein				
ref YP_002428.1 YP_002428.1	chemoreceptor (methyl-accepting	chemotaxis		193	118
	chemotaxis) transmembrane protein				
ref YP_000063.1 YP_000063.1	histidine kinase sensor protein	chemotaxis	191	176	47
ref YP_001486.1 YP_001486.1	histidine kinase response regulator hybrid	chemotaxis		137	136
	protein				
ref YP_002311.1 YP_002311.1	histidine kinase sensor protein	chemotaxis	113	127	
ref YP_001969.1 YP_001969.1	histidine kinase sensor protein	chemotaxis	151	120	78
ref YP_002550.1 YP_002550.1	histidine kinase response regulator hybrid	chemotaxis	68	76	147
SIND COMMON ALVEN COMMON A	protein		254	64	120
ref YP_001485.1 YP_001485.1	chemotaxis response regulator	chemotaxis	251	64	129
ref YP_001992.1 YP_001992.1	histidine kinase response regulator hybrid	chemotaxis	135		211
ref YP_001080.1 YP_001080.1	protein histidine kinase response regulator hybrid	chemotaxis	_		261
161119_001080.1119_001080.1	protein	Chemotaxis			201
ref YP_001449.1 YP_001449.1	chemotaxis protein	chemotaxis	+		162
ref YP_001172.1 YP_001172.1	histidine kinase response regulator hybrid	chemotaxis			158
161/11_001172.1/11_001172.1	protein	CHCHIOLUXIS			150
ref YP 003236.1 YP 003236.1	histidine kinase sensor protein	chemotaxis			107
ref YP_001481.1 YP_001481.1	chemotaxis protein	chemotaxis			75
ref YP 001170.1 YP 001170.1	histidine kinase sensor protein	chemotaxis			54
sp P62643 CHEB3_LEPIC	Chemotaxis response regulator protein-	chemotaxis			27
	glutamate methylesterase of group 3				
	operon (EC 3.1.1.61) - Lep				
ref YP_001994.1 YP_001994.1	histidine kinase response regulator hybrid	chemotaxis			21
	protein				
ref YP_002021.1 YP_002021.1	histidine kinase sensor protein	chemotaxis			17
ref YP_001643.1 YP_001643.1	methyl-accepting chemotaxis protein	chemotaxis			14
ref YP_003195.1 YP_003195.1	histidine kinase sensor protein	chemotaxis			
sp P62641 CHEB1_LEPIC	Chemotaxis response regulator protein-	chemotaxis			234
	glutamate methylesterase of group 1				
	operon (EC 3.1.1.61)				
ref YP_001483.1 YP_001483.1	chemotaxis protein histidine kinase	chemotaxis			136
ref YP_001487.1 YP_001487.1	histidine kinase sensor protein	chemotaxis			57
ref YP_001402.1 YP_001402.1	histidine kinase response regulator hybrid	chemotaxis			40
Clyp opacat the pages :	protein				27
ref YP_003631.1 YP_003631.1	histidine kinase sensor protein	chemotaxis	1		37
ref YP_003019.1 YP_003019.1	histidine kinase response regulator hybrid	chemotaxis			34
*** TOTAL TO	protein	ah amaati-			20
ref YP_002994.1 YP_002994.1	histidine kinase response regulator hybrid	chemotaxis			30
ref YP_002031.1 YP_002031.1	histidine kinase sensor protein	chemotavic			30
ref YP_002031.1 YP_002031.1 ref YP_002170.1 YP_002170.1	histidine kinase sensor protein histidine kinase response regulator hybrid	chemotaxis chemotaxis			30 17
161117_002170.1[17_002170.1	protein	CHEIHOLAXIS			1/
ref YP_001507.1 YP_001507.1	histidine kinase sensor protein	chemotaxis			17
ref YP 002999.1 YP 002999.1	histidine kinase sensor protein	chemotaxis			17
101111 _002555.1 [11 _002555.1	madame kindae achadi protein	CHCHIOLAXIS			1,

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ref YP_001395.1 YP_001395.1	histidine kinase sensor protein	chemotaxis			14
ref YP_002410.1 YP_002410.1	putative methyl-accepting chemotaxis I	chemotaxis			14
ref YP_000967.1 YP_000967.1	histidine kinase sensor protein	chemotaxis			11
ref YP_001190.1 YP_001190.1	histidine kinase sensor protein	chemotaxis			8
ref YP_000116.1 YP_000116.1	histidine kinase sensor protein	chemotaxis			5
ref YP_003100.1 YP_003100.1	histidine kinase response regulator hybrid	chemotaxis			
	protein				
ref YP_001401.1 YP_001401.1	histidine kinase sensor protein	chemotaxis			
ref YP_003177.1 YP_003177.1	histidine kinase sensor protein	chemotaxis			
ref YP_003404.1 YP_003404.1	histidine kinase sensor protein	chemotaxis			
ref YP_001370.1 YP_001370.1	putative methyl-accepting chemotaxis	chemotaxis			
	transmembrane protein				
ref YP_002845.1 YP_002845.1	chemotaxis motility protein A	chemotaxis			
ref YP_000783.1 YP_000783.1	histidine kinase sensor protein	chemotaxis			
ref YP_000897.1 YP_000897.1	histidine kinase sensor protein	chemotaxis			
ref YP_003304.1 YP_003304.1	methyl-accepting chemotaxis protein	chemotaxis			
ref YP 001996.1 YP 001996.1	chemotaxis protein	chemotaxis			
ref YP 000536.1 YP 000536.1	histidine kinase	chemotaxis			
ref YP 000323.1 YP 000323.1	histidine kinase	chemotaxis			
ref YP 001258.1 YP 001258.1	histidine kinase sensor protein	chemotaxis			
ref YP 003020.1 YP 003020.1	histidine kinase sensor protein	chemotaxis			
ref YP_003613.1 YP_003613.1	histidine kinase sensor protein	chemotaxis			
ref YP 002725.1 YP 002725.1	histidine kinase sensor protein	chemotaxis			
ref YP 000096.1 YP 000096.1	histidine kinase sensor protein	chemotaxis			+
ref YP_000096.1 YP_000096.1	histidine kinase sensor protein	chemotaxis			+
ref YP 001387.1 YP 001387.1	·				
· - · -	histidine kinase sensor protein	chemotaxis			
ref YP_001844.1 YP_001844.1	histidine kinase sensor protein	chemotaxis			
ref YP_002153.1 YP_002153.1	histidine kinase sensor protein	chemotaxis			
ref YP_003574.1 YP_003574.1	histidine kinase sensor protein	chemotaxis			
ref YP_000669.1 YP_000669.1	methyl-accepting chemotaxis transducer	chemotaxis			
Store and the store and the	transmembrane protein				l
ref YP_000167.1 YP_000167.1	hypothetical protein LIC10175	Cipro induced	422	39916	657
		hypothetical			
Store and the store and the		protein			
ref YP_002538.1 YP_002538.1	hypothetical protein LIC12615	Cipro induced	364	31064	682
		hypothetical			
flyn oggest a tlyn oggest	1 11 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	protein	22.1	21122	212
ref YP_000168.1 YP_000168.1	hypothetical protein LIC10176	Cipro induced	224	24432	219
		hypothetical			
Clare and a clare and a		protein			1
ref YP_000169.1 YP_000169.1	hypothetical protein LIC10177	Cipro induced	240	13249	230
		hypothetical			
Store and the store and the		protein			
ref YP_002537.1 YP_002537.1	hypothetical protein LIC12614	Cipro induced	73	9336	472
		hypothetical			
thyp operated the second	L	protein		04.00	20-
ref YP_002539.1 YP_002539.1	hypothetical protein LIC12616	Cipro induced		8186	207
		hypothetical			
Club approximation and the		protein	101	5050	1000
ref YP_000166.1 YP_000166.1	hypothetical protein LIC10174	Cipro induced	131	5860	200
		hypothetical			
thun coarse this seems	L collection of the control of the collection of	protein	445	22.62	60
ref YP_002523.1 YP_002523.1	hypothetical protein LIC12600	Cipro induced	145	2242	68
		hypothetical			
		protein			
ref YP_002526.1 YP_002526.1	hypothetical protein LIC12603	Cipro induced		2050	125
		hypothetical			
		protein			1
ref YP_002536.1 YP_002536.1	hypothetical protein LIC12613	Cipro induced		1784	151
		hypothetical			
Club cooperation cooperation		protein		1700	+_
ref YP_002525.1 YP_002525.1	hypothetical protein LIC12602	Cipro induced		1720	5
		hypothetical			
		protein			

ref YP_002528.1 YP_002528.1	hypothetical protein LIC12605	Cipro induced hypothetical protein		1375	118
ref YP_002524.1 YP_002524.1	hypothetical protein LIC12601	Cipro induced hypothetical protein	69	1258	8
ref YP_000159.1 YP_000159.1	hypothetical protein LIC10167	Cipro induced hypothetical protein		1204	173
ref YP_000177.1 YP_000177.1	hypothetical protein LIC10186	Cipro induced hypothetical protein		1078	14
ref YP_002499.1 YP_002499.1	cytoplasmic membrane protein	cytoplasmic membrane	1064	1141	940
ref YP_003395.1 YP_003395.1	hypothetical protein LIC20001	cytoplasmic membrane	306	327	415
ref YP_001800.1 YP_001800.1	cytoplasmic membrane protein	cytoplasmic membrane		98	82
ref YP_001052.1 YP_001052.1	cytoplasmic membrane protein	cytoplasmic membrane	220		17
ref YP_002679.1 YP_002679.1	cytoplasmic membrane protein	cytoplasmic membrane			226
ref YP_000962.1 YP_000962.1	cytoplasmic membrane protein	cytoplasmic membrane			155
ref YP_000695.1 YP_000695.1	cytoplasmic membrane protein	cytoplasmic membrane			68
ref YP_002333.1 YP_002333.1	cytoplasmic membrane protein	cytoplasmic membrane			24
ref YP_002574.1 YP_002574.1	cytoplasmic membrane protein	cytoplasmic membrane			8
ref YP_001929.1 YP_001929.1	cytoplasmic membrane protein	cytoplasmic membrane			151
ref YP_000926.1 YP_000926.1	cytoplasmic membrane protein	cytoplasmic membrane			54
ref YP_001067.1 YP_001067.1	cytoplasmic membrane protein	cytoplasmic membrane			37
ref YP_003356.1 YP_003356.1	cytoplasmic membrane protein	cytoplasmic membrane			21
ref YP_001146.1 YP_001146.1	cytoplasmic membrane protein	cytoplasmic membrane			17
ref YP_001257.1 YP_001257.1	cytoplasmic membrane protein	cytoplasmic membrane			14
ref YP_001873.1 YP_001873.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_000486.1 YP_000486.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_001982.1 YP_001982.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_002194.1 YP_002194.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_000494.1 YP_000494.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_001150.1 YP_001150.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_001465.1 YP_001465.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_001618.1 YP_001618.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_002407.1 YP_002407.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_002441.1 YP_002441.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_002815.1 YP_002815.1	cytoplasmic membrane protein	cytoplasmic membrane			

ref YP_002854.1 YP_002854.1	cytoplasmic membrane protein	cytoplasmic			
	, ,	membrane			
ref YP_002909.1 YP_002909.1	cytoplasmic membrane protein	cytoplasmic			
		membrane			
ref YP_003386.1 YP_003386.1	cytoplasmic membrane protein	cytoplasmic			
. (LVD, 002505 4 LVD, 002505 4		membrane	_		
ref YP_003595.1 YP_003595.1	cytoplasmic membrane protein	cytoplasmic			
ref YP_003621.1 YP_003621.1	cytoplasmic membrane protein	membrane cytoplasmic			
161[11_003021.1[11_003021.1	cytopiasinic membrane protein	membrane			
ref YP 003622.1 YP 003622.1	cytoplasmic membrane protein	cytoplasmic			
		membrane			
ref YP_002003.1 YP_002003.1	cytoplasmic membrane protein	cytoplasmic			
		membrane			
ref YP_001469.1 YP_001469.1	cytoplasmic membrane protein	cytoplasmic			
Slyp cooper thyp cooper t		membrane	_		
ref YP_002307.1 YP_002307.1	cytoplasmic membrane protein	cytoplasmic membrane			
ref YP_000181.1 YP_000181.1	cytoplasmic membrane protein	cytoplasmic			
101111 _000101.1111 _000101.1	cycopiasinie membrane protein	membrane			
ref YP_000802.1 YP_000802.1	cytoplasmic membrane protein	cytoplasmic			
		membrane			
ref YP_000479.1 YP_000479.1	cytoplasmic membrane protein	cytoplasmic			
		membrane			
ref YP_002472.1 YP_002472.1	DNA binding protein	DNA/RNA	1083	1420	379
		binding			
ref YP_001152.1 YP_001152.1	hypothetical protein LIC11182	DNA/RNA	753	920	44
Long Collins and Collins	5	binding	2010		242
sp Q72Q67 HFQ_LEPIC	Protein hfq	DNA/RNA	2040	450	242
ref YP_000150.1 YP_000150.1	hypothetical protein LIC10158	binding DNA/RNA	369	254	192
161[17_000130.1[17_000130.1	hypothetical protein Lic10138	binding	309	234	192
ref YP_003659.1 YP_003659.1	ParB	DNA/RNA	207	249	316
		binding			
sp Q72S30 Y1156_LEPIC	UPF0109 protein LIC_11556	DNA/RNA			85
	· _	binding			
ref YP_001954.1 YP_001954.1	hypothetical protein LIC12016	DNA/RNA			82
		binding			
ref YP_003387.1 YP_003387.1	ParB	DNA/RNA			40
ref YP_001317.1 YP_001317.1	Down formits markets	binding	_		8
ref[YP_001317.1[YP_001317.1	ParB family protein	DNA/RNA binding			8
ref YP_000905.1 YP_000905.1	type I restriction enzyme	DNA/RNA			21
161[11_000303.1[11_000303.1	type rrestriction enzyme	binding			21
ref YP_003413.1 YP_003413.1	ParB	DNA/RNA			14
		binding			
ref YP_000160.1 YP_000160.1	hypothetical protein LIC10168	DNA/RNA			
		binding			
ref YP_000881.1 YP_000881.1	hypothetical protein LIC10904	DNA/RNA			
Slyp coarse that coarse		binding	-		
ref YP_002583.1 YP_002583.1	DNA binding protein with PIN domain	DNA/RNA			
ref YP 003497.1 YP 003497.1	DNA binding protein	binding DNA/RNA			
161117_003437.1[17_003497.1	PIAN DITIONING PLOTEIN	binding			
ref YP 003496.1 YP 003496.1	DNA binding protein	DNA/RNA			
,		binding			
ref YP_001554.1 YP_001554.1	DNA mismatch repair protein	DNA/RNA			
	·	binding			
ref YP_003292.1 YP_003292.1	DNA mismatch repair protein	DNA/RNA			
dia and an analysis		binding			
ref YP_000157.1 YP_000157.1	hypothetical protein LIC10165	DNA/RNA			
cn D62217 DECA LEDIC	Drotoin roch (Docombinate A)	binding	660	4702	057
sp P62217 RECA_LEPIC	Protein recA (Recombinase A)	DNA/RNA	660	4703	957
l	İ	metabolic	1		

		process			
ref YP_002622.1 YP_002622.1	polynucleotide phosphorylase	DNA/RNA	1821	1796	2354
		metabolic			
		process			
ref YP_001743.1 YP_001743.1	ATP-dependent DNA helicase	DNA/RNA	1382	1174	611
	7111 dependent 21111 menede	metabolic	1502		011
		process			
ref YP_002046.1 YP_002046.1	single-stranded DNA binding protein	DNA/RNA	1339	1030	447
161[11_002040.1[11_002040.1	Single-stranded blvA binding protein	metabolic	1333	1030	447
		process			
ref YP_003253.1 YP_003253.1	DNA gyrase subunit B	DNA/RNA	879	775	363
161117_003233.1117_003233.1	DIVA gyrase suburiit b	metabolic	8/9	773	303
LOTOCOOLNED LIEUC	100 - 1 - B42 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	process	420	500	260
sp Q72S00 NRDJ_LEPIC	Vitamin B12-dependent ribonucleotide	DNA/RNA	438	598	269
	reductase (EC 1.17.4.1) (Ribonucleoside-	metabolic			
	diphosphate reductase)	process			
ref YP_003252.1 YP_003252.1	DNA gyrase subunit A	DNA/RNA	590	594	395
		metabolic			
		process			
ref YP_000006.1 YP_000006.1	DNA gyrase subunit A	DNA/RNA	536	537	230
		metabolic			
		process			
ref YP_001639.1 YP_001639.1	endonuclease	DNA/RNA	256	443	558
		metabolic			
		process			
ref YP_000005.1 YP_000005.1	DNA gyrase subunit B	DNA/RNA	571	420	242
161[17_000003.1[17_000003.1	DIVA gyrase suburiit b	metabolic	3/1	420	242
Clyp codddd dlyp codddd	"	process	216	251	200
ref YP_001111.1 YP_001111.1	ribonuclease D	DNA/RNA	316	361	223
		metabolic			
		process			
ref YP_000243.1 YP_000243.1	exonuclease	DNA/RNA	196	357	114
		metabolic			
		process			
sp Q72RM8 UVRA_LEPIC	UvrABC system protein A (UvrA protein)	DNA/RNA	377	342	200
–	(Excinuclease ABC subunit A)	metabolic			
	,	process			
ref YP_003170.1 YP_003170.1	ribonuclease D	DNA/RNA	200	172	75
		metabolic			
		process			
sp P62038 Y2886_LEPIC	UPF0082 protein LIC 12886	DNA/RNA	149	62	103
301102030112000_LLF1C	OFFO082 protein LiC_12880	metabolic	149	02	103
SIVE COACAA ALVE COACAA A	h	process			204
ref YP_001911.1 YP_001911.1	hypothetical protein LIC11971	DNA/RNA			281
		metabolic			
		process			
sp Q72N95 UVRB_LEPIC	UvrABC system protein B (Protein uvrB)	DNA/RNA			132
	(Excinuclease ABC subunit B)	metabolic			
		process			
sp Q72SA5 XERD_LEPIC	Tyrosine recombinase xerD	DNA/RNA			71
		metabolic			
		process			
ref YP_003490.1 YP_003490.1	phage-related integrase/recombinase	DNA/RNA			68
	,	metabolic			
		process			
ref YP_002343.1 YP_002343.1	chromosome segregation protein	DNA/RNA			54
	I I I I I I I I I I I I I I I I I I I	metabolic			
		process			
rofIVD 002442 1 IVD 002442 4	DNA mismatch renair protein	<u> </u>			40
ref YP_002442.1 YP_002442.1	DNA mismatch repair protein	DNA/RNA			40
		metabolic			
Character and the state of the		process	_		
ref YP_003189.1 YP_003189.1	NAD dependent DNA ligase	DNA/RNA			226
		metabolic			
	1	process			
ref YP_002043.1 YP_002043.1	replicative DNA helicase	DNA/RNA			82

		metabolic	
		process	
ref YP_001112.1 YP_001112.1	RadA	DNA/RNA	78
		metabolic	
		process	
ref YP_001118.1 YP_001118.1	DNA helicase subunit A	DNA/RNA	61
		metabolic	
		process	
sp P61669 MUTS_LEPIC	DNA mismatch repair protein mutS	DNA/RNA	61
		metabolic	
		process	
sp Q72PL7 SCPA_LEPIC	Segregation and condensation protein A	DNA/RNA	54
		metabolic	
		process	
sp P61534 RUVB_LEPIC	Holliday junction ATP	DNA/RNA	50
		metabolic	
		process	
sp Q72LS5 RECR_LEPIC	Recombination protein recR	DNA/RNA	50
	·	metabolic	
		process	
sp Q72RZ8 EX7S_LEPIC	Probable exodeoxyribonuclease VII small	DNA/RNA	40
11	subunit (EC 3.1.11.6) (Exonuclease VII	metabolic	"
	small subunit)	process	
ref YP_001036.1 YP_001036.1	single-stranded DNA exonuclease	DNA/RNA	30
161111_001030.1 11_001030.1	Single-strailueu Diva exultutiease	metabolic	30
flyp 004502 4 lyp 004502 4	ATD days and ant DNA halfares	process DNA/RNA	24
ref YP_001582.1 YP_001582.1	ATP-dependent DNA helicase	•	24
		metabolic	
		process	
ref YP_001413.1 YP_001413.1	exodeoxyribonuclease	DNA/RNA	24
		metabolic	
		process	
sp Q72RZ7 EX7L_LEPIC	Probable exodeoxyribonuclease VII large	DNA/RNA	21
	subunit (EC 3.1.11.6) (Exonuclease VII	metabolic	
	large subunit)	process	
ref YP_001684.1 YP_001684.1	atp-dependent DNA helicase	DNA/RNA	17
		metabolic	
		process	
ref YP_000903.1 YP_000903.1	type I restriction enzyme	DNA/RNA	17
		metabolic	
		process	
ref YP_002610.1 YP_002610.1	ATP-dependent DNA helicase	DNA/RNA	11
		metabolic	
		process	
ref YP_002512.1 YP_002512.1	ATP-dependent DNA helicase	DNA/RNA	8
		metabolic	
		process	
ref YP_001711.1 YP_001711.1	endonuclease III	DNA/RNA	8
· – · -		metabolic	
		process	
ref YP_000652.1 YP_000652.1	Mrr	DNA/RNA	8
		metabolic	
		process	
ref YP_001295.1 YP_001295.1	ribonuclease BN transmembrane protein	DNA/RNA	8
		metabolic	
		process	
ref YP_001226.1 YP_001226.1	exopolyphosphatase	DNA/RNA	
161111-001220.1 11-001220.1	елорогурнозрнагазе	metabolic	
colO7FFWELDNC LEDIC	Dihanuslassa III /FC 2 4 2C 2) /DN III)	process	
sp Q75FW5 RNC_LEPIC	Ribonuclease III (EC 3.1.26.3) (RNase III)	DNA/RNA	
		metabolic	
		process	
rotive 003607 11VD 003607 1	exodeoxyribonuclease v alpha chain	DNA/RNA	I
ref YP_002607.1 YP_002607.1	CXOGCOXYTIDOTIGCICGSC V dipila citatii	· ·	
161 17_002007.1 17_002007.1	exodeoxymboliucieuse v uipila chuin	metabolic process	

ref YP_002585.1 YP_002585.1	IS1500 transposase	DNA/RNA			
101111 _002303.1111 _002303.1	is 1500 transposase	metabolic			
		process			
ref YP_003279.1 YP_003279.1	IS1500 transposase	DNA/RNA			
101711 _003273.1711 _003273.1	151500 (14115)05430	metabolic			
		process			
ref YP_000229.1 YP_000229.1	3-methyladenine DNA glycosylase	DNA/RNA			
161 17_000229.1 17_000229.1	3-methylademine DNA glycosylase	metabolic			
flyp 002204 4 lyp 002204 4	2 mathedadasiaa DNA abaasadasa	process			
ref YP_002294.1 YP_002294.1	3-methyladenine DNA glycosylase	DNA/RNA			
		metabolic			
		process			
ref YP_002976.1 YP_002976.1	3-methyl-adenine DNA glycosylase I	DNA/RNA			
		metabolic			
		process			
sp Q72WD6 DNAA_LEPIC	Chromosomal replication initiator protein	DNA/RNA			
	dnaA	metabolic			
		process			
ref YP_000406.1 YP_000406.1	DNA helicase II	DNA/RNA			
		metabolic			
		process			
ref YP_002608.1 YP_002608.1	exodeoxyribonuclease V beta chain	DNA/RNA			
	,	metabolic			
		process			
ref YP_002609.1 YP_002609.1	exodeoxyribonuclease v gamma chain	DNA/RNA			
101111 _002003.1111 _002003.1	cxodcoxyriborideicuse v gariiria eriairi	metabolic			
(1) (D. 002005 4 LVD. 002005 4		process			
ref YP_003085.1 YP_003085.1	exonuclease	DNA/RNA			
		metabolic			
		process			
ref YP_001991.1 YP_001991.1	IS1500 transposase	DNA/RNA			
		metabolic			
		process			
ref YP_002642.1 YP_002642.1	IS1533 transposase	DNA/RNA			
		metabolic			
		process			
ref YP_000557.1 YP_000557.1	IS1533 transposase	DNA/RNA			
	·	metabolic			
		process			
ref YP_000975.1 YP_000975.1	IS1533 transposase	DNA/RNA			
- 1 =		metabolic			
		process			
ref YP_002641.1 YP_002641.1	IS1533 transposase	DNA/RNA			
	.52555 (runsposase	metabolic			
rofIVD 001535 4 IVD 001535 4	Ma cholataco cubunit chil	process			
ref YP_001525.1 YP_001525.1	Mg chelatase subunit chll	DNA/RNA			
		metabolic			
LIVE COAFICATIVE COLOR		process		-	
ref YP_001510.1 YP_001510.1	primosomal protein N'	DNA/RNA			
		metabolic			
		process			
ref YP_002801.1 YP_002801.1	putative holliday junction	DNA/RNA			
	endodeoxyribonuclease protein	metabolic			
		process			
ref YP_000954.1 YP_000954.1	transposase, IS1501	DNA/RNA	<u> </u>		
_		metabolic			
		process			
ref YP_000763.1 YP_000763.1	transposase, IS1501	DNA/RNA			
,	,	metabolic			
		process			
ref YP_000764.1 YP_000764.1	transposase, IS1501	DNA/RNA			
10.111_000704.111F_000704.1	1 ansposase, 151501				
		metabolic			
**************************************	+rangnasasa 164.504	process			
ref YP_001311.1 YP_001311.1	transposase, IS1501	DNA/RNA			
İ		metabolic			

ref YP_003281.1 YP_003281.1			process	
metabolic process meta	reflyP_001310.11yP_001310.1	transposase, IS1501		
Process Proc				
metabolic process Proc				
Process	ref YP_003281.1 YP_003281.1	transposase, IS1501	DNA/RNA	
ref yP_000487.1 YP_000487.1 transposase, IS3			metabolic	
metabolic process proc			process	
Process	ref YP_000497.1 YP_000497.1	transposase, IS3	DNA/RNA	
Per Per			metabolic	
metabolic process			process	
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ref YP_002974.1 YP_002974.1	transposase, ISlin1	DNA/RNA			
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ref YP_002980.1 YP_002980.1	transposase, ISlin1	DNA/RNA			
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ref YP_003025.1 YP_003025.1	transposase, ISlin1	DNA/RNA			
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ref YP_001519.1 YP_001519.1	ribonuclease HII	DNA/RNA			
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ref YP_000350.1 YP_000350.1	electron transport flavoprotein beta	process electron carrier	4506	45.47	2272
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ref YP_003420.1 YP_003420.1	NADH dehydrogenase	electron carrier	702	823	192
		activity			
ref YP_002666.1 YP_002666.1	NADH dehydrogenase I F subunit	electron carrier	798	589	488
		activity			
ref YP_003164.1 YP_003164.1	NADH oxidoreductase	activity electron carrier	479	441	226
		activity electron carrier activity	479		
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sp Q72VZ9 NUOI_LEPIC	NADH-quinone oxidoreductase subunit I (EC 1.6.99.5) (NADH dehydrogenase I subunit I) (NDH-1 subunit	electron carrier activity			14
ref YP_002794.1 YP_002794.1	hypothetical protein LIC12878	electron carrier activity			316
sp Q72RB6 QUEF_LEPIC	NADPH-dependent 7-cyano-7- deazaguanine reductase (EC 1.7.1) (NADPH-dependent nitrile oxidoreductas	electron carrier activity			114
ref YP_003524.1 YP_003524.1	ferredoxin-like protein	electron carrier activity			50
ref YP_002662.1 YP_002662.1	NADH dehydrogenase I B subunit	electron carrier activity			27
ref YP_003327.1 YP_003327.1	hydrogenase subunit	electron carrier activity			8
ref YP_002669.1 YP_002669.1	NADH dehydrogenase I K subunit	electron carrier activity			8
ref YP_002672.1 YP_002672.1	NADH dehydrogenase I N subunit	electron carrier activity			
ref YP_002671.1 YP_002671.1	NADH dehydrogenase I M subunit	electron carrier activity			
sp Q72NT2 NUOH_LEPIC	NADH-quinone oxidoreductase subunit H (EC 1.6.99.5) (NADH dehydrogenase I subunit H) (NDH-1 subunit	electron carrier activity			
ref YP_003129.1 YP_003129.1	Fe-S oxidoreductase	electron carrier activity			
ref YP_002670.1 YP_002670.1	NADH dehydrogenase I L subunit	electron carrier			
ref YP_003476.1 YP_003476.1	ferredoxin	electron carrier activity			
ref YP_003237.1 YP_003237.1	ferredoxin	electron carrier activity			
ref YP_003526.1 YP_003526.1	ferredoxin	electron carrier activity			
ref YP_003323.1 YP_003323.1	hydrogenase subunit	electron carrier activity			
ref YP_003322.1 YP_003322.1	hydrogenase subunit	electron carrier activity			
ref YP_003325.1 YP_003325.1	hydrogenase subunit	electron carrier activity			
ref YP_002661.1 YP_002661.1	NADH dehydrogenase I A subunit	electron carrier			
ref YP_002668.1 YP_002668.1	NADH dehydrogenase I J subunit	electron carrier activity			
ref YP_001316.1 YP_001316.1	LipL32	external encapsulating structure	38050	32190	3793
ref YP_000182.1 YP_000182.1	peptidoglycan associated cytoplasmic membrane protein	external encapsulating structure	30389	28606	992
ref YP_002879.1 YP_002879.1	LipL41	external encapsulating structure	10531	12297	3999
ref YP_000011.1 YP_000011.1	LipL21	external encapsulating structure	8830	8893	804
ref YP_002972.1 YP_002972.1	LipL36	external encapsulating structure	14100	8789	1335
ref YP_000976.1 YP_000976.1	LipL71	external encapsulating structure	6913	7060	464
ref YP_001601.1 YP_001601.1	LipL45	external encapsulating structure	3506	4544	1606

ref YP_001417.1 YP_001417.1	LipL31	external	1422	1412	292
		encapsulating			
ref YP_000119.1 YP_000119.1	LipL45-like protein	structure external	455	604	339
161117-000119.1117-000119.1	Lipt45-like protein	encapsulating	455	604	339
		structure			
ref YP_003634.1 YP_003634.1	peptidoglycan-associated cytoplasmic	external	231	339	37
' - ' -	membrane protein	encapsulating			
	·	structure			
ref YP_000772.1 YP_000772.1	surface antigen	external	147	105	85
		encapsulating			
		structure			
ref YP_003506.1 YP_003506.1	LipL45 homologue	external			177
		encapsulating			
flyn cooperative cooperat		structure	-		160
ref YP_000050.1 YP_000050.1	peptidoglycan-associated cytoplasmic	external			162
	membrane protein	encapsulating			
ref YP_000576.1 YP_000576.1	peptidoglycan-associated cytoplasmic	structure external			118
161 17_000370.1 17_000370.1	peptidoglycan-associated cytoplasmic membrane protein	encapsulating			110
	membrane protein	structure			
ref YP_002865.1 YP_002865.1	S-layer-like protein	external			
		encapsulating			
		structure	1		
ref YP_003317.1 YP_003317.1	LipL45-like protein	external			
		encapsulating			
		structure			
ref YP_000875.1 YP_000875.1	LipL48	external			
		encapsulating			
		structure			
ref YP_002891.1 YP_002891.1	peptide methionine sulfoxide reductase 2	external			
		encapsulating			
ref YP_000521.1 YP_000521.1	peptidoglycan associated periplasmic	structure external			
Tel TP_000521.1 TP_000521.1	peptidoglycan associated periplasmic protein	encapsulating			
	protein	structure			
ref YP_003380.1 YP_003380.1	peptidoglycan-associated cytoplasmic	external			
	membrane protein	encapsulating			
	·	structure			
ref YP_001839.1 YP_001839.1	flagellin protein	flagellum	14041	12240	5087
ref YP_000767.1 YP_000767.1	flagellar filament sheath protein	flagellum	4328	3719	1929
ref YP_000766.1 YP_000766.1	flagellar filament sheath protein	flagellum	3520	3424	774
ref YP_001490.1 YP_001490.1	flagellin protein	flagellum	3482	3115	2248
sp Q72R59 FLAB_LEPIC	Flagellar filament 35 kDa core protein	flagellum	2038	1683	1156
	(Flagellin class B)				
ref YP_001228.1 YP_001228.1	MreC	flagellum	575	836	27
ref YP_001290.1 YP_001290.1	FIgG	flagellum	831	794	224
ref YP_001334.1 YP_001334.1	flagellar motor switch protein	flagellum	493	415	234
ref YP_001491.1 YP_001491.1	flagellin protein	flagellum	289	408	591
ref YP_000608.1 YP_000608.1	flagellar protein flagellar motor protein	flagellum	458	326	89 44
ref YP_000607.1 YP_000607.1 ref YP_001355.1 YP_001355.1	flagellar M-ring protein	flagellum flagellum	274	276 226	71
ref YP_001355.1 YP_001355.1	motility protein A	flagellum	193	190	57
ref YP_003352.1 YP_003352.1	hypothetical protein LIC13449	flagellum	248	178	89
ref YP_001665.1 YP_001665.1	motility protein B	flagellum	159	124	230
ref YP_003354.1 YP_003354.1	flagellar hook-associated protein	flagellum	1	117	44
ref YP 001613.1 YP 001613.1	FliS	flagellum	249		37
sp Q72SP8 FLGI_LEPIC	Flagellar P-ring protein precursor (Basal	flagellum	122		155
	body P-ring protein)				
ref YP_001341.1 YP_001341.1	flagellar GTP-binding protein	flagellum			44
ref YP_003244.1 YP_003244.1	MotB	flagellum			
ref YP_000288.1 YP_000288.1	flagellar basal body rod protein	flagellum			
ref YP_001158.1 YP_001158.1	flagellar hook protein	flagellum			181
ref YP_000605.1 YP_000605.1	flagellar protein	flagellum			166

ref YP_001785.1 YP_001785.1	flagellar motor switch protein	flagellum			96
ref YP 001357.1 YP 001357.1	flagellar assembly protein	flagellum			71
ref YP_001356.1 YP_001356.1	FliG	flagellum			47
ref YP_003353.1 YP_003353.1	flagellar hook-associated protein	flagellum			44
ref YP_000707.1 YP_000707.1	flagellar hook-associated protein	flagellum			30
ref YP_002968.1 YP_002968.1	flagellar motor protein	flagellum			24
ref YP_001848.1 YP_001848.1	FliG	flagellum			24
ref YP_001353.1 YP_001353.1	FliJ	flagellum			24
ref YP 001354.1 YP 001354.1	FliI	flagellum			17
ref YP_001795.1 YP_001795.1	flagellar motor switch protein	flagellum			14
ref YP_000023.1 YP_000023.1	flagellar motor protein	flagellum			11
ref YP_001352.1 YP_001352.1	flagellar protein B	flagellum			11
ref YP_001335.1 YP_001335.1	FliO	flagellum			11
ref YP_001973.1 YP_001973.1	hook protein	flagellum			5
ref YP_001292.1 YP_001292.1	flagellar L-ring protein precursor	flagellum			
ref YP_001340.1 YP_001340.1	flagellar biosynthesis transmembrane	flagellum			
Tel[1P_001540.1[1P_001540.1	protein	nagenum			
ref YP_000289.1 YP_000289.1	flagellar basal-body rod protein	flagellum			
ref YP_001338.1 YP_001338.1	flagellar biosynthetic protein	flagellum			
ref YP_001337.1 YP_001337.1	flagellar biosynthetic protein fliQ	flagellum			
ref YP_001521.1 YP_001521.1	flagellar biosynthetic transmembrane protein	flagellum			
ref YP_001157.1 YP_001157.1	flagellar hook assembly scaffolding protein	flagellum			
sp Q72VK0 FLIE_LEPIC	Flagellar hook-basal body complex protein fliE	flagellum			
ref YP_001339.1 YP_001339.1	flagellar protein	flagellum			
ref YP_001336.1 YP_001336.1	flagellar protein export system	flagellum			
ref YP 002861.1 YP 002861.1	flagellin protein	flagellum			
ref YP_001294.1 YP_001294.1	flagellum-specific muramidase	flagellum			
ref YP 003255.1 YP 003255.1	FlgG	flagellum			
ref YP 003561.1 YP 003561.1	MotA/ToIQ/ExbB proton channel family	flagellum			
sp Q72NF9 EFTU_LEPIC	Elongation factor Tu (EF-Tu)	hydrolase activity	14424	16925	7996
sp Q72SX9 ATPB_LEPIC	ATP synthase subunit beta (EC 3.6.3.14) (ATPase subunit beta) (ATP synthase F1 sector subunit beta)	hydrolase activity	5229	5434	4785
ref YP_002962.1 YP_002962.1	hypothetical protein LIC13050	hydrolase activity	5022	2720	1624
sp Q72SY1 ATPA_LEPIC	ATP synthase subunit alpha (EC 3.6.3.14)	hydrolase	2852	2347	3018
3P[Q/2311]ATTA_EETTO	(ATPase subunit alpha) (ATP synthase F1 sector subunit alph	activity	2032	2347	3018
sp Q72VM5 EFG_LEPIC	Elongation factor G (EF-G)	hydrolase activity	2204	2051	2752
sp Q75FU8 SAHH_LEPIC	Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)	hydrolase activity	2977	1803	1530
sp Q72NX3 IF2_LEPIC	Translation initiation factor IF-2	hydrolase activity	1386	1287	603
ref YP_001376.1 YP_001376.1	glycosyl hydrolase	hydrolase activity	879	995	452
ref YP_001153.1 YP_001153.1	hypothetical protein LIC11183	hydrolase activity	807	746	169
sp Q72SY0 ATPG_LEPIC	ATP synthase gamma chain (EC 3.6.3.14) (ATP synthase F1 sector gamma subunit)	hydrolase activity	423	570	332
ref YP_000060.1 YP_000060.1	hypothetical protein LIC10060	hydrolase activity	565	539	147
ref YP_001208.1 YP_001208.1	ATP synthase B chain	hydrolase activity	818	527	54
sp Q75FT0 CHED2_LEPIC	Probable chemoreceptor glutamine deamidase cheD 2 (EC 3.5.1.44) - Leptospira interrogans serogroup I	hydrolase activity	266	407	411
ref YP_002289.1 YP_002289.1	elongation factor EF-G	hydrolase activity	998	370	504

ref YP_003055.1 YP_003055.1	hypothetical protein LIC13147	hydrolase activity	301	322	92
ref YP_003388.1 YP_003388.1	ParA	hydrolase activity		293	57
ref YP_000029.1 YP_000029.1	inositol monophosphatase	hydrolase activity	375	285	500
ref YP_002352.1 YP_002352.1	hypothetical protein LIC12421	hydrolase activity	314	283	162
ref YP_001209.1 YP_001209.1	ATP synthase delta chain	hydrolase activity	221	237	359
ref YP_001110.1 YP_001110.1	alpha-galactosidase	hydrolase activity	298	234	89
ref YP_000283.1 YP_000283.1	glycerophosphoryl diester phosphodiesterase	hydrolase activity	256	216	71
sp Q72QU8 LEPA_LEPIC	GTP-binding protein lepA - Leptospira interrogans serogroup lcterohaemorrhagiae serovar copenhageni	hydrolase activity	234	212	185
ref YP_002462.1 YP_002462.1	GTP cyclohydrolase 2	hydrolase activity	220	210	500
sp Q72RY7 HSLU_LEPIC	ATP-dependent hsl protease ATP-binding subunit hslU - Leptospira interrogans serogroup lcterohaemorr	hydrolase activity	217	198	64
ref YP_002213.1 YP_002213.1	haloacid dehalogenase-like hydrolase	hydrolase activity		177	30
ref YP_003275.1 YP_003275.1	sulfate adenylyltransferase subunit 1	hydrolase activity	293	167	219
ref YP_001342.1 YP_001342.1	septum site-determining protein	hydrolase activity	226	159	75
ref YP_001965.1 YP_001965.1	hypothetical protein LIC12027	hydrolase activity	139	138	242
ref YP_000940.1 YP_000940.1	hypothetical protein LIC10966	hydrolase activity		133	57
ref YP_001819.1 YP_001819.1	hydrolase	hydrolase activity		129	37
ref YP_003469.1 YP_003469.1	polysaccharide deacetylase	hydrolase activity	283	118	211
sp P62347 HIS2_LEPIC	Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH) - Leptospira interrogans serogroup Icteroh	hydrolase activity	327		100
ref YP_003429.1 YP_003429.1	methanol dehydrogenase regulator	hydrolase activity			351
sp Q72MU5 SURE_LEPIC	5'-nucleotidase surE (EC 3.1.3.5) (Nucleoside 5'-monophosphate phosphohydrolase) - Leptospira interr	hydrolase activity			269
ref YP_001659.1 YP_001659.1	fructose-1,6-bisphosphatase	hydrolase activity			265
sp Q72LY8 GCH1_LEPIC	GTP cyclohydrolase I (EC 3.5.4.16) (GTP-CH-I) - Leptospira interrogans serogroup lcterohaemorrhagiae	hydrolase activity			230
ref YP_001964.1 YP_001964.1	methylenetetrahydrofolate dehydrogenase	hydrolase activity			196
sp Q72SX8 ATPE_LEPIC	ATP synthase epsilon chain (EC 3.6.3.14) (ATP synthase F1 sector epsilon subunit) - Leptospira inter	hydrolase activity			118
ref YP_002328.1 YP_002328.1	hypothetical protein LIC12396	hydrolase activity			118
sp Q72P44 PHL1_LEPIC	Sphingomyelinase C 1 precursor (EC 3.1.4.12) (Sphingomyelin phosphodiesterase 1) (SMase 1) - Leptosp	hydrolase activity			110
ref YP_000211.1 YP_000211.1	ParA	hydrolase activity			96
ref YP_001408.1 YP_001408.1	hydrolase	hydrolase activity			75

ref YP_000339.1 YP_000339.1 hypothetical protein LIC10350 hydrolase activity ref YP_001672.1 YP_001672.1 hypothetical protein LIC11720 hydrolase activity ref YP_002324.1 YP_002324.1 G-aminohexanoate-cyclic-dimer hydrolase hydrolase activity ref YP_000134.1 YP_000134.1 HD-GYP hydrolase domain protein hydrolase activity ref YP_001752.1 YP_001752.1 hypothetical protein LIC11800 hydrolase activity ref YP_001752.1 YP_001752.1 hypothetical protein LIC11800 hydrolase activity ref YP_000260.1 YP_000260.1 chlorohydrolase family protein hydrolase activity ref YP_001076.1 YP_001076.1 acyltransferase hydrolase activity ref YP_000558.1 YP_000558.1 dihydroorotase hydrolase activity ref YP_003088.1 YP_003088.1 (Di)nucleoside polyphosphate hydrolase hydrolase activity ref YP_000189.1 YP_000189.1 inositol monophosphatase hydrolase activity ref YP_000123.1 YP_000123.1 hypothetical protein LIC10127 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity	
ref YP_001672.1 YP_001672.1hypothetical protein LIC11720hydrolase activityref YP_002324.1 YP_002324.16-aminohexanoate-cyclic-dimer hydrolase hydrolase activityref YP_000134.1 YP_000134.1HD-GYP hydrolase domain proteinhydrolase activityref YP_001752.1 YP_001752.1hypothetical protein LIC11800hydrolase activityref YP_000260.1 YP_000260.1chlorohydrolase family proteinhydrolase activityref YP_001076.1 YP_001076.1acyltransferasehydrolase activityref YP_000558.1 YP_000558.1dihydroorotasehydrolase activityref YP_003088.1 YP_003088.1(Di)nucleoside polyphosphate hydrolase activity151ref YP_000189.1 YP_000123.1inositol monophosphatasehydrolase activityref YP_000123.1 YP_000123.1hypothetical protein LIC10127hydrolase activityref YP_001689.1 YP_001689.1hypothetical protein LIC10127hydrolase activityref YP_001689.1 YP_001689.1hypothetical protein LIC10127hydrolase activity	
ref YP_002324.1 YP_002324.1 6-aminohexanoate-cyclic-dimer hydrolase hydrolase activity ref YP_000134.1 YP_000134.1 HD-GYP hydrolase domain protein hydrolase activity ref YP_001752.1 YP_001752.1 hypothetical protein LIC11800 hydrolase activity ref YP_000260.1 YP_000260.1 chlorohydrolase family protein hydrolase activity ref YP_001076.1 YP_001076.1 acyltransferase hydrolase activity ref YP_000558.1 YP_000558.1 dihydroorotase hydrolase hydrolase activity ref YP_003088.1 YP_003088.1 (Di)nucleoside polyphosphate hydrolase hydrolase activity ref YP_000189.1 YP_000189.1 hypothetical protein LIC10127 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity	
ref YP_000134.1 YP_000134.1 HD-GYP hydrolase domain protein hydrolase activity ref YP_001752.1 YP_001752.1 hypothetical protein LIC11800 hydrolase activity ref YP_000260.1 YP_000260.1 chlorohydrolase family protein hydrolase activity ref YP_001076.1 YP_001076.1 acyltransferase hydrolase activity ref YP_00058.1 YP_00058.1 dihydroorotase hydrolase activity ref YP_003088.1 YP_003088.1 (Di)nucleoside polyphosphate hydrolase activity ref YP_000189.1 YP_000189.1 inositol monophosphatase hydrolase activity ref YP_000123.1 YP_000123.1 hypothetical protein LIC10127 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity	
ref YP_000134.1 YP_000134.1HD-GYP hydrolase domain proteinhydrolase activityref YP_001752.1 YP_001752.1hypothetical protein LIC11800hydrolase activityref YP_000260.1 YP_000260.1chlorohydrolase family proteinhydrolase activityref YP_001076.1 YP_001076.1acyltransferasehydrolase activityref YP_000558.1 YP_000558.1dihydroorotasehydrolase activityref YP_003088.1 YP_003088.1(Di)nucleoside polyphosphate hydrolase hydrolase activityhydrolase activityref YP_000189.1 YP_000189.1inositol monophosphatasehydrolase activityref YP_000123.1 YP_000123.1hypothetical protein LIC10127hydrolase activityref YP_001689.1 YP_001689.1hypothetical protein LIC11737hydrolase activity	
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ref YP_001076.1 YP_001076.1 acyltransferase hydrolase activity ref YP_000558.1 YP_000558.1 dihydroorotase hydrolase activity ref YP_003088.1 YP_003088.1 (Di)nucleoside polyphosphate hydrolase hydrolase activity ref YP_000189.1 YP_000189.1 inositol monophosphatase hydrolase activity ref YP_000123.1 YP_000123.1 hypothetical protein LIC10127 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity	
ref YP_000558.1 YP_000558.1dihydroorotasehydrolase activity158ref YP_003088.1 YP_003088.1(Di)nucleoside polyphosphate hydrolase activityhydrolase activity151ref YP_000189.1 YP_000189.1inositol monophosphatasehydrolase activity147ref YP_000123.1 YP_000123.1hypothetical protein LIC10127hydrolase activity110ref YP_001689.1 YP_001689.1hypothetical protein LIC11737hydrolase activity96	
ref YP_003088.1 YP_003088.1 (Di)nucleoside polyphosphate hydrolase activity hydrolase activity ref YP_000189.1 YP_000189.1 inositol monophosphatase hydrolase activity ref YP_000123.1 YP_000123.1 hypothetical protein LIC10127 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity activity 96	
ref YP_000189.1 YP_000189.1 inositol monophosphatase hydrolase activity ref YP_000123.1 YP_000123.1 hypothetical protein LIC10127 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity 96	
ref YP_000123.1 YP_000123.1 hypothetical protein LIC10127 hydrolase activity ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase hydrolase activity	
ref YP_001689.1 YP_001689.1 hypothetical protein LIC11737 hydrolase activity 96	
ref YP_002406.1 YP_002406.1 hypothetical protein LIC12478 hydrolase 96	
activity	
sp Q72MG4 IPYR_LEPIC Inorganic pyrophosphatase (EC 3.6.1.1) hydrolase 96 (Pyrophosphate phospho-hydrolase) activity (PPase) - Leptospira interr	
ref YP_002253.1 YP_002253.1 protein phosphatase hydrolase activity 96	
ref YP_001284.1 YP_001284.1 N-acyl-L-amino acid amidohydrolase hydrolase activity 82	
ref YP_002080.1 YP_002080.1 polysaccharide deacetylase family protein hydrolase activity 78	
ref YP_002513.1 YP_002513.1 hypothetical protein LIC12589 hydrolase activity 75	
sp P61909 DUT_LEPIC Deoxyuridine 5'-triphosphate hydrolase nucleotidohydrolase (EC 3.6.1.23) activity (dUTPase) (dUTP pyrophosphatase) - Le	
ref YP_003086.1 YP_003086.1 acylphosphatase hydrolase activity 57	
ref YP_001928.1 YP_001928.1 hypothetical protein LIC11989 hydrolase activity 57	
ref YP_003419.1 YP_003419.1 phosphotyrosine protein phosphatase hydrolase activity 57	
ref YP_002989.1 YP_002989.1 hypothetical protein LIC13077 hydrolase activity 54	
ref YP_003582.1 YP_003582.1 hypothetical protein LIC20191 hydrolase activity 54	
ref YP_001680.1 YP_001680.1 N-acetylmuramoyl-L-alanine amidase hydrolase activity 54	
ref YP_002842.1 YP_002842.1 beta-lactamase related protein hydrolase activity 47	
ref YP_000117.1 YP_000117.1 hypothetical protein LIC10121 hydrolase activity 47	
ref YP_003412.1 YP_003412.1 ParA hydrolase 47	
activity ref YP_000651.1 YP_000651.1 thioesterase hydrolase 47	
activity ref YP_002126.1 YP_002126.1 mutator protein hydrolase activity 44	

ref YP_003471.1 YP_003471.1	haloacid dehalogenase-like protein	hydrolase activity	40
ref YP_002247.1 YP_002247.1	HIT family hydrolase	hydrolase activity	40
sp Q72MK0 ENGC LEPIC	Probable GTPase engC (EC 3.6.1) -	hydrolase	40
SPIQ/ZIVIKO/LIVOC_ELFIC	Leptospira interrogans serogroup lcterohaemorrhagiae serovar cop	activity	40
ref YP_002800.1 YP_002800.1	arylsulfatase	hydrolase activity	34
ref YP_000184.1 YP_000184.1	hypothetical protein LIC10193	hydrolase activity	34
ref YP_001937.1 YP_001937.1	hydrolase	hydrolase activity	30
ref YP_002936.1 YP_002936.1	hypothetical protein LIC13023	hydrolase activity	30
sp P62392 HIS3_LEPIC	Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH) - Leptospira interrogans serogroup lcteroha	hydrolase activity	30
ref YP_001727.1 YP_001727.1	phosphoserine phosphatase	hydrolase activity	30
ref YP_001435.1 YP_001435.1	hypothetical protein LIC11474	hydrolase activity	21
ref YP_002096.1 YP_002096.1	6-phosphogluconolactonase/glucosamine-	hydrolase	17
	6-phosphate isomerase/deaminase	activity]
ref YP_001740.1 YP_001740.1	alpha/beta hydrolase	hydrolase activity	17
ref YP_000753.1 YP_000753.1	hypothetical protein LIC10773	hydrolase	17
		activity	
ref YP_000900.1 YP_000900.1	metallo-beta-lactamase	hydrolase activity	17
sp Q72M35 COBT_LEPIC	Nicotinate-nucleotide	hydrolase	17
	dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21) (NN:DBI PRT) (N	activity	
ref YP_001120.1 YP_001120.1	nonspecific acid phosphatase precursor	hydrolase activity	17
sp Q72VK9 QUEC_LEPIC	Queuosine biosynthesis protein queC (EC 3.5) - Leptospira interrogans serogroup lcterohaemorrhag	hydrolase activity	17
ref YP_001426.1 YP_001426.1	hypothetical protein LIC11465	hydrolase activity	14
ref YP_002818.1 YP_002818.1	hypothetical protein LIC12902	hydrolase activity	14
sp Q72PP0 LOLD_LEPIC	Lipoprotein-releasing system ATP-binding protein lolD - Leptospira interrogans serogroup Icterohaemo	hydrolase activity	14
ref YP_003026.1 YP_003026.1	metallo-beta-lactamase superfamily hydrolase	hydrolase activity	14
ref YP_003022.1 YP_003022.1	acyltransferase	hydrolase activity	11
ref YP_001997.1 YP_001997.1	acyltransferase	hydrolase activity	11
sp Q75FQ8 COBB_LEPIC	Cobyrinic acid A,C-diamide synthase - Leptospira interrogans serogroup Icterohaemorrhagiae serovar c	hydrolase activity	11
sp Q72UV8 HAM1_LEPIC	HAM1 protein homolog - Leptospira interrogans serogroup lcterohaemorrhagiae serovar copenhageni	hydrolase activity	11
ref YP_002364.1 YP_002364.1	phosphoglycerol transferase	hydrolase activity	11
ref YP_001957.1 YP_001957.1	ATP-dependent helicase	hydrolase activity	8
ref YP_002077.1 YP_002077.1	integral membrane protein	hydrolase	8

		activity		
ref YP_000721.1 YP_000721.1	N-acetylmuramoyl-L-alanine amidase	hydrolase		8
,		activity		
ref YP_000337.1 YP_000337.1	paraoxonase	hydrolase		8
		activity		
ref YP 000587.1 YP 000587.1	sulfatase family protein	hydrolase		8
	, ,	activity		
ref YP_001151.1 YP_001151.1	hypothetical protein LIC11181	hydrolase		8
	7,71	activity		
ref YP_003459.1 YP_003459.1	MutT-like protein	hydrolase		8
, ,		activity		
ref YP_000072.1 YP_000072.1	hypothetical protein LIC10072	hydrolase		5
	, ,	activity		
ref YP_001564.1 YP_001564.1	hypothetical protein LIC11606	hydrolase		5
	7,71	activity		
ref YP_002416.1 YP_002416.1	hypothetical protein LIC12488	hydrolase		5
	, ,	activity		
ref YP_003090.1 YP_003090.1	glycerophosphoryl diester	hydrolase		
- 1 =	phosphodiesterase	activity		
ref YP_001474.1 YP_001474.1	hypothetical protein LIC11515	hydrolase		
1 = 1	7,71	activity		
ref YP_003171.1 YP_003171.1	MutT nudix family protein	hydrolase		
1 ====	,,,	activity		
ref YP_001856.1 YP_001856.1	polysaccharide deacetylase	hydrolase		
- 1 =	, , , , , , , , , , , , , , , , , , , ,	activity		
ref YP_000713.1 YP_000713.1	putative lipoprotein	hydrolase		
	patative iipoproteiii	activity		
ref YP_001303.1 YP_001303.1	deoxyribodipyrimidine photolyase	hydrolase		
.6.166136311166136311	aconymical princes, acc	activity		
ref YP_003398.1 YP_003398.1	haloacid dehalogenase-like protein	hydrolase		
.6.166683611166683611	marada dendregendoe mie protein	activity		
ref YP_001584.1 YP_001584.1	inositol monophosphatase family	hydrolase		
	,	activity		
ref YP_000489.1 YP_000489.1	nuclease-like protein	hydrolase		
		activity		
ref YP_003058.1 YP_003058.1	ATP-dependent DNA helicase protein	hydrolase		
, ,		activity		
ref YP_002449.1 YP_002449.1	serine/threonine kinase	hydrolase		
	,	activity		
ref YP_001113.1 YP_001113.1	metal dependent phosphohydrolase	hydrolase		
		activity		
ref YP_003512.1 YP_003512.1	histidinol-phosphate aminotransferase	hydrolase		
	and cobyric acid synthase	activity		
ref YP_002522.1 YP_002522.1	alpha/beta hydrolase superfamily	hydrolase		
· -		activity		
ref YP_001392.1 YP_001392.1	alpha/beta hydrolase superfamily	hydrolase		
	·	activity		
ref YP_001073.1 YP_001073.1	alpha/beta hydrolase superfamily	hydrolase		
		activity		
ref YP_001207.1 YP_001207.1	ATP synthase C chain	hydrolase		
		activity		
ref YP_002155.1 YP_002155.1	beta-lactamase regulatory protein 1	hydrolase		
		activity		
sp Q72RS7 DGTL1_LEPIC	Deoxyguanosinetriphosphate	hydrolase		
	triphosphohydrolase-like protein -	activity		
	Leptospira interrogans serogroup Icter			
ref YP_000377.1 YP_000377.1	hypothetical protein LIC10391	hydrolase		
		activity		
ref YP_000577.1 YP_000577.1	hypothetical protein LIC10593	hydrolase		
		activity		
ref YP_000582.1 YP_000582.1	hypothetical protein LIC10598	hydrolase		
		activity		
ref YP_001283.1 YP_001283.1	hypothetical protein LIC11317	hydrolase		
		activity	1	

ref YP_002414.1 YP_002414.1	integral membrane protein	hydrolase			
ref YP_002078.1 YP_002078.1	integral membrane protein	activity hydrolase			
161 17_002078.1 17_002078.1	integral membrane protein	activity			
ref YP_000089.1 YP_000089.1	metallo-beta-lactamase	hydrolase activity			
sp Q72S65 CHED1_LEPIC	Probable chemoreceptor glutamine	hydrolase			
357Q, 25057GHEDI_EEITE	deamidase cheD 1 (EC 3.5.1.44) - Leptospira interrogans serogroup I	activity			
ref YP_000963.1 YP_000963.1	serine/threonine kinase with GAF domain	hydrolase			
ref YP_001649.1 YP_001649.1	xylanase/chitin deacetylase family protein	activity hydrolase activity			
ref YP_003074.1 YP_003074.1	hypothetical protein LIC13166	hypothetical	8021	7203	2478
ref YP_002544.1 YP_002544.1	hypothetical protein LIC12621	protein hypothetical	3115	3033	1486
ref YP_001797.1 YP_001797.1	hypothetical protein LIC11848	hypothetical	4271	2740	2368
ref YP_001908.1 YP_001908.1	hypothetical protein LIC11966	protein hypothetical	4330	2380	136
ref YP_003427.1 YP_003427.1	hypothetical protein LIC20035	hypothetical	2008	1828	423
ref YP_002123.1 YP_002123.1	hypothetical protein LIC12188	protein hypothetical	1864	1777	649
ref YP_000982.1 YP_000982.1	hypothetical protein LIC11009	protein hypothetical	2566	1777	732
ref YP_003219.1 YP_003219.1	hypothetical protein LIC13314	protein hypothetical	1382	1743	320
ref YP_000535.1 YP_000535.1	hypothetical protein LIC10551	protein hypothetical	1629	1723	196
ref YP_000206.1 YP_000206.1	hypothetical protein LIC10215	protein hypothetical	1209	1715	147
ref YP_002737.1 YP_002737.1	hypothetical protein LIC12821	protein hypothetical	1474	1595	1287
ref YP_002009.1 YP_002009.1	hypothetical protein LIC12075	protein hypothetical	1354	1576	1086
ref YP_002388.1 YP_002388.1	hypothetical protein LIC12460	protein hypothetical	1558	1573	541
		protein	1502	4526	C44
ref YP_001242.1 YP_001242.1	hypothetical protein LIC11274	hypothetical protein	1693	1526	611
ref YP_003470.1 YP_003470.1	hypothetical protein LIC20078	hypothetical protein	4127	1471	257
ref YP_000304.1 YP_000304.1	hypothetical protein LIC10314	hypothetical protein	1292	1464	423
ref YP_000178.1 YP_000178.1	hypothetical protein LIC10187	hypothetical protein	178	1363	17
ref YP_000656.1 YP_000656.1	hypothetical protein LIC10672	hypothetical protein	1870	1271	699
ref YP_003576.1 YP_003576.1	hypothetical protein LIC20185	hypothetical protein	2178	1252	632
ref YP_000064.1 YP_000064.1	hypothetical protein LIC10064	hypothetical protein	1088	1223	335
ref YP_001178.1 YP_001178.1	hypothetical protein LIC11209	hypothetical protein	1165	1213	249
ref YP_003585.1 YP_003585.1	hypothetical protein LIC20196	hypothetical protein	756	1166	488
ref YP_001044.1 YP_001044.1	hypothetical protein LIC11074	hypothetical protein	907	1140	89
ref YP_001193.1 YP_001193.1	hypothetical protein LIC11224	hypothetical protein	748	1136	82
ref YP_001459.1 YP_001459.1	hypothetical protein LIC11498	hypothetical protein	1023	1125	162
ref YP_001450.1 YP_001450.1	hypothetical protein LIC11489	hypothetical	1065	1104	324

		protein			
ref YP_001794.1 YP_001794.1	hypothetical protein LIC11845	hypothetical protein	778	1073	169
ref YP_000853.1 YP_000853.1	hypothetical protein LIC10876	hypothetical protein	813	1031	75
ref YP_002612.1 YP_002612.1	hypothetical protein LIC12691	hypothetical protein	708	1025	44
ref YP_000180.1 YP_000180.1	hypothetical protein LIC10189	hypothetical protein		1001	
ref YP_000155.1 YP_000155.1	hypothetical protein LIC10163	hypothetical protein		991	47
ref YP_003544.1 YP_003544.1	hypothetical protein LIC20153	hypothetical protein	1462	979	200
ref YP_003256.1 YP_003256.1	hypothetical protein LIC13351	hypothetical protein	945	937	177
ref YP_001059.1 YP_001059.1	hypothetical protein LIC11089	hypothetical protein	1344	934	107
ref YP_000646.1 YP_000646.1	hypothetical protein LIC10662	hypothetical protein	828	927	114
ref YP_001166.1 YP_001166.1	hypothetical protein LIC11196	hypothetical protein	954	864	504
ref YP_003488.1 YP_003488.1	hypothetical protein LIC20096	hypothetical protein	815	863	288
ref YP_001368.1 YP_001368.1	hypothetical protein LIC11405	hypothetical protein	977	831	281
ref YP_002166.1 YP_002166.1	hypothetical protein LIC12231	hypothetical protein	801	815	47
ref YP_000113.1 YP_000113.1	hypothetical protein LIC10117	hypothetical protein	618	796	82
ref YP_002198.1 YP_002198.1	hypothetical protein LIC12263	hypothetical protein	924	791	889
ref YP_003625.1 YP_003625.1	hypothetical protein LIC20240	hypothetical protein	893	765	328
ref YP_002329.1 YP_002329.1	hypothetical protein LIC12397	hypothetical protein	745	740	147
ref YP_000467.1 YP_000467.1	hypothetical protein LIC10483	hypothetical protein	717	736	665
ref YP_001793.1 YP_001793.1	hypothetical protein LIC11844	hypothetical protein	333	735	82
ref YP_003337.1 YP_003337.1	hypothetical protein LIC13434	hypothetical protein	621	698	162
ref YP_002871.1 YP_002871.1	hypothetical protein LIC12958	hypothetical protein	1098	683	192
ref YP_000202.1 YP_000202.1	hypothetical protein LIC10211	hypothetical protein		681	30
ref YP_000674.1 YP_000674.1	hypothetical protein LIC10690	hypothetical protein	650	678	96
ref YP_000585.1 YP_000585.1	hypothetical protein LIC10601	hypothetical protein	815	658	699
ref YP_000366.1 YP_000366.1	hypothetical protein LIC10380	hypothetical protein	406	637	107
ref YP_001645.1 YP_001645.1	hypothetical protein LIC11693	hypothetical protein	486	627	54
ref YP_002532.1 YP_002532.1	hypothetical protein LIC12609	hypothetical protein		621	
ref YP_000470.1 YP_000470.1	hypothetical protein LIC10486	hypothetical protein	565	621	125
ref YP_002530.1 YP_002530.1	hypothetical protein LIC12607	hypothetical protein		610	11
ref YP_002531.1 YP_002531.1	hypothetical protein LIC12608	hypothetical protein		605	
ref YP_000740.1 YP_000740.1	hypothetical protein LIC10760	hypothetical protein	652	603	419
ref YP_000175.1 YP_000175.1	hypothetical protein LIC10184	hypothetical		596	

		protein			
ref YP_000158.1 YP_000158.1	hypothetical protein LIC10166	hypothetical protein		583	27
ref YP_002211.1 YP_002211.1	hypothetical protein LIC12277	hypothetical protein	611	580	14
ref YP_002142.1 YP_002142.1	hypothetical protein LIC12207	hypothetical protein	740	577	118
ref YP_000223.1 YP_000223.1	lipoprotein releasing system transmembrane protein	hypothetical protein	286	558	37
ref YP_002376.1 YP_002376.1	hypothetical protein LIC12446	hypothetical protein	597	527	50
ref YP_000893.1 YP_000893.1	hypothetical protein LIC10918	hypothetical protein	462	525	351
ref YP_000226.1 YP_000226.1	hypothetical protein LIC10235	hypothetical protein	737	516	129
ref YP_001241.1 YP_001241.1	hypothetical protein LIC11273	hypothetical protein	479	512	61
ref YP_003218.1 YP_003218.1	hypothetical protein LIC13313	hypothetical protein	438	490	89
ref YP_002331.1 YP_002331.1	hypothetical protein LIC12399	hypothetical protein	404	484	40
ref YP_001655.1 YP_001655.1	hypothetical protein LIC11703	hypothetical protein	743	479	136
ref YP_000648.1 YP_000648.1	hypothetical protein LIC10664	hypothetical protein	726	476	226
ref YP_000120.1 YP_000120.1	hypothetical protein LIC10124	hypothetical protein	246	474	399
ref YP_002259.1 YP_002259.1	hypothetical protein LIC12325	hypothetical protein	441	473	312
ref YP_002124.1 YP_002124.1	hypothetical protein LIC12189	hypothetical protein	535	452	96
ref YP_000172.1 YP_000172.1	hypothetical protein LIC10181	hypothetical protein		450	
ref YP_000825.1 YP_000825.1	hypothetical protein LIC10848	hypothetical protein	345	450	211
ref YP_001595.1 YP_001595.1	hypothetical protein LIC11637	hypothetical protein	657	448	443
ref YP_001583.1 YP_001583.1	hypothetical protein LIC11625	hypothetical protein	1221	435	188
ref YP_001429.1 YP_001429.1	hypothetical protein LIC11468	hypothetical protein	312	395	40
ref YP_003422.1 YP_003422.1	hypothetical protein LIC20030	hypothetical protein	258	392	8
ref YP_001609.1 YP_001609.1	hypothetical protein LIC11653	hypothetical protein		381	103
ref YP_001702.1 YP_001702.1	hypothetical protein LIC11750	hypothetical protein	433	371	395
ref YP_000210.1 YP_000210.1	hypothetical protein LIC10219	hypothetical protein	224	363	
ref YP_002128.1 YP_002128.1	hypothetical protein LIC12193	hypothetical protein	323	362	403
ref YP_000769.1 YP_000769.1	hypothetical protein LIC10790	hypothetical protein		359	44
ref YP_003428.1 YP_003428.1	hypothetical protein LIC20036	hypothetical protein	384	355	17
ref YP_002533.1 YP_002533.1	hypothetical protein LIC12610	hypothetical protein	91	350	37
ref YP_000855.1 YP_000855.1	hypothetical protein LIC10878	hypothetical protein	337	347	30
ref YP_003313.1 YP_003313.1	hypothetical protein LIC13410	hypothetical protein	465	341	8
ref YP_000542.1 YP_000542.1	hypothetical protein LIC10558	hypothetical protein	341	325	75
ref YP_000401.1 YP_000401.1	hypothetical protein LIC10415	hypothetical	516	325	196

		protein			
ref YP_002113.1 YP_002113.1	hypothetical protein LIC12178	hypothetical protein		317	34
ref YP_000217.1 YP_000217.1	hypothetical protein LIC10226	hypothetical protein	462	316	541
ref YP_002983.1 YP_002983.1	hypothetical protein LIC13071	hypothetical protein	1602	302	1283
ref YP_002345.1 YP_002345.1	hypothetical protein LIC12414	hypothetical protein	1144	299	246
ref YP_000959.1 YP_000959.1	hypothetical protein LIC10985	hypothetical protein	518	298	103
ref YP_003001.1 YP_003001.1	hypothetical protein LIC13089	hypothetical protein	287	298	68
ref YP_002300.1 YP_002300.1	hypothetical protein LIC12368	hypothetical protein	191	294	17
ref YP_001577.1 YP_001577.1	hypothetical protein LIC11619	hypothetical protein		291	166
ref YP_002718.1 YP_002718.1	hypothetical protein LIC12801	hypothetical protein	216	290	21
ref YP_000538.1 YP_000538.1	hypothetical protein LIC10554	hypothetical protein	309	288	85
ref YP_001029.1 YP_001029.1	hypothetical protein LIC11059	hypothetical protein	78	283	21
ref YP_002850.1 YP_002850.1	hypothetical protein LIC12936	hypothetical protein	319	281	447
ref YP_002493.1 YP_002493.1	hypothetical protein LIC12568	hypothetical protein	320	279	246
ref YP_001132.1 YP_001132.1	hypothetical protein LIC11162	hypothetical protein	314	278	265
ref YP_000689.1 YP_000689.1	hypothetical protein LIC10705	hypothetical protein	394	275	24
ref YP_000165.1 YP_000165.1	hypothetical protein LIC10173	hypothetical protein		272	11
ref YP_000424.1 YP_000424.1	hypothetical protein LIC10439	hypothetical protein	187	256	11
ref YP_001921.1 YP_001921.1	hypothetical protein LIC11982	hypothetical protein	189	251	30
ref YP_001960.1 YP_001960.1	hypothetical protein LIC12022	hypothetical protein	275	247	
ref YP_001298.1 YP_001298.1	hypothetical protein LIC11334	hypothetical protein	264	237	110
ref YP_000338.1 YP_000338.1	hypothetical protein LIC10348	hypothetical protein	608	236	347
ref YP_002281.1 YP_002281.1	hypothetical protein LIC12349	hypothetical protein	246	231	11
ref YP_000752.1 YP_000752.1	hypothetical protein LIC10772	hypothetical protein	714	223	492
ref YP_003120.1 YP_003120.1	hypothetical protein LIC13212	hypothetical protein		221	300
ref YP_001066.1 YP_001066.1	hypothetical protein LIC11096	hypothetical protein	167	214	82
ref YP_001900.1 YP_001900.1	hypothetical protein LIC11955	hypothetical protein	793	212	200
ref YP_002660.1 YP_002660.1	hypothetical protein LIC12740	hypothetical protein	237	202	24
ref YP_002417.1 YP_002417.1	hypothetical protein LIC12489	hypothetical protein	477	200	40
ref YP_002722.1 YP_002722.1	hypothetical protein LIC12805	hypothetical protein	175	198	54
ref YP_000496.1 YP_000496.1	hypothetical protein LIC10512	hypothetical protein	331	196	177
ref YP_001594.1 YP_001594.1	hypothetical protein LIC11636	hypothetical protein	165	194	125
ref YP_002005.1 YP_002005.1	hypothetical protein LIC12071	hypothetical	171	189	14

		protein			
ref YP_002273.1 YP_002273.1	hypothetical protein LIC12341	hypothetical protein	318	185	82
ref YP_001927.1 YP_001927.1	hypothetical protein LIC11988	hypothetical protein		178	11
ref YP_001622.1 YP_001622.1	hypothetical protein LIC11668	hypothetical protein	162	176	21
ref YP_000173.1 YP_000173.1	hypothetical protein LIC10182	hypothetical protein		174	11
ref YP_003424.1 YP_003424.1	hypothetical protein LIC20032	hypothetical protein	255	170	219
ref YP_000466.1 YP_000466.1	hypothetical protein LIC10482	hypothetical protein	246	169	68
ref YP_002500.1 YP_002500.1	hypothetical protein LIC12576	hypothetical protein	186	155	78
ref YP_002004.1 YP_002004.1	hypothetical protein LIC12070	hypothetical protein	249	150	273
ref YP_001495.1 YP_001495.1	hypothetical protein LIC11536	hypothetical protein		147	151
ref YP_000222.1 YP_000222.1	hypothetical protein LIC10231	hypothetical protein	129	146	17
ref YP_003547.1 YP_003547.1	hypothetical protein LIC20156	hypothetical protein	368	142	40
ref YP_001460.1 YP_001460.1	hypothetical protein LIC11499	hypothetical protein	1069	141	439
ref YP_003537.1 YP_003537.1	hypothetical protein LIC20146	hypothetical protein		132	21
ref YP_003527.1 YP_003527.1	hypothetical protein LIC20136	hypothetical protein	105	132	11
ref YP_000373.1 YP_000373.1	hypothetical protein LIC10387	hypothetical protein		129	96
ref YP_002252.1 YP_002252.1	hypothetical protein LIC12318	hypothetical protein		126	92
ref YP_002179.1 YP_002179.1	hypothetical protein LIC12244	hypothetical protein		120	34
ref YP_000694.1 YP_000694.1	hypothetical protein LIC10710	hypothetical protein		111	34
ref YP_001398.1 YP_001398.1	hypothetical protein LIC11436	hypothetical protein	166	101	30
ref YP_000411.1 YP_000411.1	hypothetical protein LIC10425	hypothetical protein	157	101	54
ref YP_000448.1 YP_000448.1	Ig-like repeat domain protein 3	hypothetical protein		91	914
ref YP_000017.1 YP_000017.1	hypothetical protein LIC10017	hypothetical protein	177	88	92
ref YP_000583.1 YP_000583.1	hypothetical protein LIC10599	hypothetical protein		77	44
ref YP_000639.1 YP_000639.1	hypothetical protein LIC10655	hypothetical protein	168	32	34
ref YP_001326.1 YP_001326.1	hypothetical protein LIC11362	hypothetical protein	445		92
ref YP_002182.1 YP_002182.1	hypothetical protein LIC12247	hypothetical protein	421		
ref YP_003204.1 YP_003204.1	hypothetical protein LIC13297	hypothetical protein	382		21
ref YP_000068.1 YP_000068.1	hypothetical protein LIC10068	hypothetical protein	364		75
ref YP_000745.1 YP_000745.1	hypothetical protein LIC10765	hypothetical protein	294		118
ref YP_001006.1 YP_001006.1	hypothetical protein LIC11036	hypothetical protein	267		40
ref YP_003346.1 YP_003346.1	hypothetical protein LIC13443	hypothetical protein	234		92
ref YP_001005.1 YP_001005.1	hypothetical protein LIC11035	hypothetical	215		8

		protein		
ref YP_001286.1 YP_001286.1	hypothetical protein LIC11320	hypothetical protein	186	5
ref YP_000235.1 YP_000235.1	hypothetical protein LIC10244	hypothetical protein	75	147
ref YP_000449.1 YP_000449.1	lg-like repeat domain protein 1	hypothetical protein		553
ref YP_001975.1 YP_001975.1	hypothetical protein LIC12040	hypothetical protein		443
ref YP_001016.1 YP_001016.1	hypothetical protein LIC11046	hypothetical protein		277
ref YP_002260.1 YP_002260.1	hypothetical protein LIC12326	hypothetical protein		261
ref YP_000647.1 YP_000647.1	hypothetical protein LIC10663	hypothetical protein		226
ref YP_000308.1 YP_000308.1	hypothetical protein LIC10318	hypothetical		211
ref YP_003036.1 YP_003036.1	hypothetical protein LIC13128	protein hypothetical		203
ref YP_001037.1 YP_001037.1	hypothetical protein LIC11067	protein hypothetical protein		177
ref YP_000624.1 YP_000624.1	hypothetical protein LIC10640	hypothetical		132
ref YP_002018.1 YP_002018.1	hypothetical protein LIC12084	hypothetical protein		132
ref YP_000505.1 YP_000505.1	hypothetical protein LIC10521	hypothetical protein		129
ref YP_000921.1 YP_000921.1	hypothetical protein LIC10947	hypothetical protein		121
ref YP_000961.1 YP_000961.1	hypothetical protein LIC10987	hypothetical protein		121
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ref YP_000654.1 YP_000654.1	hypothetical protein LIC10670	protein hypothetical	
161 17_000654.1 17_000654.1	hypothetical protein Lic10670	protein	
ref YP 001430.1 YP 001430.1	hypothetical protein LIC11469	hypothetical	
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ref YP_003048.1 YP_003048.1	hypothetical protein LIC13140	hypothetical	
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ref YP_000472.1 YP_000472.1	hypothetical protein LIC10488	hypothetical	
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ref YP_002413.1 YP_002413.1	hypothetical protein LIC12485	hypothetical protein	
ref YP 003248.1 YP 003248.1	hypothetical protein LIC13343	hypothetical	
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ref YP 000638.1 YP 000638.1	hypothetical protein LIC10654	hypothetical	
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ref YP_001767.1 YP_001767.1	hypothetical protein LIC11816	hypothetical	
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ref YP_002637.1 YP_002637.1	hypothetical protein LIC12716	hypothetical	
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ref YP_000434.1 YP_000434.1	hypothetical protein LIC10450	hypothetical protein	
ref YP 000717.1 YP 000717.1	hypothetical protein LIC10735	hypothetical	
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ref YP_002242.1 YP_002242.1	hypothetical protein LIC12308	hypothetical	
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ref YP_000801.1 YP_000801.1	hypothetical protein LIC10824	hypothetical	
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ref YP_000086.1 YP_000086.1	hypothetical protein LIC10089	hypothetical protein	
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ref YP_002823.1 YP_002823.1	hypothetical protein LIC12907	hypothetical		
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161 17_000237.1 17_000237.1	hypothetical protein LiC10246	protein	
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ref YP_000252.1 YP_000252.1	hypothetical protein LIC10261	hypothetical	
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ref YP_000393.1 YP_000393.1	hypothetical protein LIC10407	hypothetical		
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ref YP_000394.1 YP_000394.1	hypothetical protein LIC10408	hypothetical		
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ref YP_000420.1 YP_000420.1	hypothetical protein LIC10435	hypothetical		
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ref YP_000438.1 YP_000438.1	hypothetical protein LIC10454	hypothetical		
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ref YP_000446.1 YP_000446.1	hypothetical protein LIC10462	hypothetical		
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ref YP_000451.1 YP_000451.1	hypothetical protein LIC10467	hypothetical protein		
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ref YP_000455.1 YP_000455.1	hypothetical protein LIC10471	hypothetical		
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ref YP_000458.1 YP_000458.1	hypothetical protein LIC10474	hypothetical		
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Clyp code at a lyp code := :	1	protein		
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101711 _001714.1711 _001714.1	hypothetical protein Electivoz	protein	
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	humathatian langtain UC11702	protein	
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SIVE COMOMA ALVE COMOMA	Level attack and the HOMAGO	protein	
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flyp 002022 4 lyp 002022 4	h th - til t-i- UC1 2000	protein	
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ref YP_003209.1 YP_003209.1	hypothetical protein LIC13304	hypothetical	
		protein	
ref YP_003211.1 YP_003211.1	hypothetical protein LIC13306	hypothetical protein	
ref YP_003212.1 YP_003212.1	hypothetical protein LIC13307	hypothetical	
	In potential protein 2.025507	protein	
ref YP_003222.1 YP_003222.1	hypothetical protein LIC13317	hypothetical	
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ref YP_003228.1 YP_003228.1	hypothetical protein LIC13323	hypothetical protein	
ref YP_003232.1 YP_003232.1	hypothetical protein LIC13327	hypothetical	
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ref YP_003234.1 YP_003234.1	hypothetical protein LIC13329	hypothetical	
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ref YP_003240.1 YP_003240.1	hypothetical protein LIC13335	hypothetical protein	
ref YP_003245.1 YP_003245.1	hypothetical protein LIC13340	hypothetical	
		protein	
ref YP_003247.1 YP_003247.1	hypothetical protein LIC13342	hypothetical	
**************************************	humothatical protein LIC12244	protein	
ref YP_003249.1 YP_003249.1	hypothetical protein LIC13344	hypothetical protein	
ref YP 003254.1 YP 003254.1	hypothetical protein LIC13349	hypothetical	
		protein	
ref YP_003257.1 YP_003257.1	hypothetical protein LIC13352	hypothetical	
. (Lyp. 002270 4 Lyp. 002270 4	Level attack and to Head 2205	protein	
ref YP_003270.1 YP_003270.1	hypothetical protein LIC13365	hypothetical protein	
ref YP_003278.1 YP_003278.1	hypothetical protein LIC13373	hypothetical	
		protein	
ref YP_003283.1 YP_003283.1	hypothetical protein LIC13380	hypothetical	
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ref YP_003289.1 YP_003289.1	hypothetical protein LIC13386	hypothetical protein	
ref YP_003291.1 YP_003291.1	hypothetical protein LIC13388	hypothetical	
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ref YP_003293.1 YP_003293.1	hypothetical protein LIC13390	hypothetical	

	T	protein	
ref YP_003294.1 YP_003294.1	hypothetical protein LIC13391	hypothetical	
161 17_003294.1 17_003294.1	hypothetical protein Lic13391	protein	
ref YP_003301.1 YP_003301.1	hypothetical protein LIC13398	hypothetical	
161[11 _003301:1[11 _003301:1	Hypothetical protein Electory	protein	
ref YP_003303.1 YP_003303.1	hypothetical protein LIC13400	hypothetical	
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ref YP_003321.1 YP_003321.1	hypothetical protein LIC13418	hypothetical	
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ref YP_003324.1 YP_003324.1	hypothetical protein LIC13421	hypothetical	
		protein	
ref YP_003328.1 YP_003328.1	hypothetical protein LIC13425	hypothetical	
Clyp access the access t		protein	
ref YP_003329.1 YP_003329.1	hypothetical protein LIC13426	hypothetical	
ref YP_003332.1 YP_003332.1	hypothetical protein LIC13429	protein hypothetical	
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161111 _0033 10:1111 _0033 10:1	Hypothetical protein Elect 137	protein	
ref YP_003343.1 YP_003343.1	hypothetical protein LIC13440	hypothetical	
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ref YP_003348.1 YP_003348.1	hypothetical protein LIC13445	hypothetical	
		protein	
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161 17_003336.1 17_003336.1	hypothetical protein Lic13433	protein	
ref YP_003361.1 YP_003361.1	hypothetical protein LIC13458	hypothetical	
	,,p	protein	
ref YP_003365.1 YP_003365.1	hypothetical protein LIC13462	hypothetical	
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ref YP_003368.1 YP_003368.1	hypothetical protein LIC13466	hypothetical	
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ref YP_003369.1 YP_003369.1	hypothetical protein LIC13467	hypothetical	
ref YP_003370.1 YP_003370.1	hypothetical protein LIC13468	protein hypothetical	
rei[1P_003370.1[1P_003370.1	hypothetical protein LiC13468	protein	
ref YP_003378.1 YP_003378.1	hypothetical protein LIC13477	hypothetical	
161/11 _003370.1/11 _003370.1	Hypothetical protein Elects 177	protein	
ref YP_003385.1 YP_003385.1	hypothetical protein LIC13484	hypothetical	
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		protein	
ref YP_003399.1 YP_003399.1	hypothetical protein LIC20007	hypothetical	
#oflyD 002444 4 lyD 002444 4	humothatical protein LIC20040	protein	
ref YP_003411.1 YP_003411.1	hypothetical protein LIC20019	hypothetical protein	
ref YP 003431.1 YP 003431.1	hypothetical protein LIC20039	hypothetical	
	,potrictical protein Liczooss	protein	
ref YP_003438.1 YP_003438.1	hypothetical protein LIC20046	hypothetical	
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ref YP_003445.1 YP_003445.1	hypothetical protein LIC20053	hypothetical	
		protein	
ref YP_003447.1 YP_003447.1	hypothetical protein LIC20055	hypothetical	
		protein	
ref YP_003448.1 YP_003448.1	hypothetical protein LIC20056	hypothetical	
rofIVD 0034E4 4 IVD 0034E4 4	hypothetical protein LIC2COTO	protein	
ref YP_003451.1 YP_003451.1	hypothetical protein LIC20059	hypothetical protein	
ref YP 003455.1 YP 003455.1	hypothetical protein LIC20063	hypothetical	
	, pour cucur protein Liczooo3	пуроппецеа	

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ref YP_003462.1 YP_003462.1	hypothetical protein LIC20070	hypothetical	
		protein	
ref YP_003465.1 YP_003465.1	hypothetical protein LIC20073	hypothetical protein	
ref YP_003487.1 YP_003487.1	hypothetical protein LIC20095	hypothetical	
Clyp cooler alve cooler		protein	
ref YP_003495.1 YP_003495.1	hypothetical protein LIC20103	hypothetical protein	
ref YP_003499.1 YP_003499.1	hypothetical protein LIC20107	hypothetical	
ref YP_003502.1 YP_003502.1	hypothetical protein LIC20110	protein hypothetical	
101711 _003302.1711 _003302.1	hypothetical protein Elezotto	protein	
ref YP_003508.1 YP_003508.1	hypothetical protein LIC20117	hypothetical	
	h	protein	
ref YP_003509.1 YP_003509.1	hypothetical protein LIC20118	hypothetical protein	
ref YP_003514.1 YP_003514.1	hypothetical protein LIC20123	hypothetical	
		protein	
ref YP_003525.1 YP_003525.1	hypothetical protein LIC20134	hypothetical	
ref YP_003530.1 YP_003530.1	hypothetical protein LIC20139	protein hypothetical	
161 17_005550.1 17_005550.1	hypothetical protein Liczo139	protein	
ref YP_003541.1 YP_003541.1	hypothetical protein LIC20150	hypothetical	
		protein	
ref YP_003543.1 YP_003543.1	hypothetical protein LIC20152	hypothetical	
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ref YP_003548.1 YP_003548.1	hypothetical protein LIC20157	hypothetical	
		protein	
ref YP_003564.1 YP_003564.1	hypothetical protein LIC20173	hypothetical protein	
ref YP_003565.1 YP_003565.1	hypothetical protein LIC20174	hypothetical	
16.11000000.11000000.1	Inflormation protein 2.02017	protein	
ref YP_003580.1 YP_003580.1	hypothetical protein LIC20189	hypothetical	
	h	protein	
ref YP_003590.1 YP_003590.1	hypothetical protein LIC20201	hypothetical protein	
ref YP_003591.1 YP_003591.1	hypothetical protein LIC20202	hypothetical	
		protein	
ref YP_003601.1 YP_003601.1	hypothetical protein LIC20212	hypothetical	
ref YP_003602.1 YP_003602.1	hypothetical protein LIC20213	protein hypothetical	
101111 _003002.1111 _003002.11	hypothetical protein Elezazia	protein	
ref YP_003604.1 YP_003604.1	hypothetical protein LIC20215	hypothetical	
		protein	
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ref YP 003610.1 YP 003610.1	hypothetical protein LIC20221	hypothetical	
	M	protein	
ref YP_003630.1 YP_003630.1	hypothetical protein LIC20245	hypothetical	
	h	protein	
ref YP_003636.1 YP_003636.1	hypothetical protein LIC20252	hypothetical protein	
ref YP_003639.1 YP_003639.1	hypothetical protein LIC20255	hypothetical	
		protein	
ref YP_003641.1 YP_003641.1	hypothetical protein LIC20257	hypothetical	
ref YP_003642.1 YP_003642.1	hypothetical protein LIC20258	protein hypothetical	
161 11_003042.1 11_003042.1	hypothetical protein Liczozoo	protein	
ref YP_003644.1 YP_003644.1	hypothetical protein LIC20260	hypothetical	
the one		protein	
ref YP_003645.1 YP_003645.1	hypothetical protein LIC20261	hypothetical	

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ref YP_003646.1 YP_003646.1	hypothetical protein LIC20262	hypothetical protein			
ref YP_003647.1 YP_003647.1	bun athetical protein LIC202C2	•	+		
rei[17_003647.1[17_003647.1	hypothetical protein LIC20263	hypothetical protein			
ref YP_003651.1 YP_003651.1	hypothetical protein LIC20267	hypothetical			
161[17_003031.1[17_003031.1	hypothetical protein Liczozo/	protein			
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161[11_003032.1[11_003032.1	hypothetical protein Liczozob	protein			
ref YP_003655.1 YP_003655.1	hypothetical protein LIC20271	hypothetical			
161[11_003033.1[11_003033.1	hypothetical protein Elezozy I	protein			
ref YP 001383.1 YP 001383.1	phosphate sodium symporter	ion transport	476	490	40
ref YP 001885.1 YP 001885.1	heavy metal efflux pump	ion transport	362	373	14
sp Q72PE5 CYSA_LEPIC	Sulfate/thiosulfate import ATP-binding	ion transport	376	339	308
34/4/3/3/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2	protein cysA (EC 3.6.3.25) (Sulfate-transporting ATPase)				
ref YP_001236.1 YP_001236.1	periplasmic sulfate-binding protein	ion transport			281
ref YP_001664.1 YP_001664.1	magnesium transporter	ion transport			30
ref YP_001883.1 YP_001883.1	heavy metal efflux pump	ion transport			14
ref YP_001332.1 YP_001332.1	sodium:alanine symporter	ion transport			
	family/phosphatidylserine decarboxylase		<u> </u>		
ref YP_001886.1 YP_001886.1	heavy metal efflux pump	ion transport			
ref YP_002159.1 YP_002159.1	heavy metal efflux pump	ion transport			44
ref YP_001470.1 YP_001470.1	heavy metal efflux pump	ion transport			44
ref YP_002240.1 YP_002240.1	heavy metal efflux pump	ion transport			37
ref YP_003083.1 YP_003083.1	potassium uptake system protein	ion transport			34
ref YP_002336.1 YP_002336.1	disulfide interchange transmembrane protein	ion transport			17
ref YP_003306.1 YP_003306.1	YvrC	ion transport			17
ref YP 000476.1 YP 000476.1	heavy metal efflux pump	ion transport			5
sp Q72TM6 ATKB_LEPIC	Potassium-transporting ATPase B chain	ion transport			
	(EC 3.6.3.12) (Potassium-translocating				
	ATPase B chain) (ATP ph				
ref YP_003342.1 YP_003342.1	putative potassium efflux transporter	ion transport			
ref YP_001956.1 YP_001956.1	sodium-dependent transporter	ion transport			
ref YP_002824.1 YP_002824.1	sodium/glucose cotransport protein	ion transport			
ref YP_002902.1 YP_002902.1	heavy metal efflux pump	ion transport			
ref YP_001882.1 YP_001882.1	heavy metal efflux pump	ion transport			
ref YP_001494.1 YP_001494.1	di-tripeptide proton symporter	ion transport			
ref YP_003267.1 YP_003267.1	chloride channel	ion transport			
ref YP_002052.1 YP_002052.1	divalent anion Na+ symporter	ion transport			
ref YP_001198.1 YP_001198.1	divalent cation transport-related protein	ion transport			
ref YP_003347.1 YP_003347.1	glutathione-regulated potassium-efflux	ion transport			
	system protein		1		
ref YP_001666.1 YP_001666.1	heavy metal efflux pump	ion transport	1		
ref YP_003113.1 YP_003113.1	heavy metal efflux pump	ion transport			
ref YP_002895.1 YP_002895.1	heavy-metal transporting p-type ATPase	ion transport	1		
ref YP_000660.1 YP_000660.1	heme exporter protein B	ion transport	1		
ref YP_000661.1 YP_000661.1	heme exporter protein C	ion transport			
ref YP_002896.1 YP_002896.1	hypothetical protein LIC12983	ion transport	1		
ref YP_003082.1 YP_003082.1	KtrB	ion transport	1		
ref YP_001662.1 YP_001662.1	magnesium transport P-type atpase	ion transport			
ref YP_000264.1 YP_000264.1	potassium uptake protein	ion transport			
sp Q72TM7 ATKA_LEPIC	Potassium-transporting ATPase A chain	ion transport			
	(EC 3.6.3.12) (Potassium-translocating				
	ATPase A chain) (ATP ph		1		
sp Q72TM5 ATKC_LEPIC	Potassium-transporting ATPase C chain	ion transport			
	(EC 3.6.3.12) (Potassium-translocating				
	ATPase C chain) (ATP ph		1	+	
sp Q72V73 KPRS_LEPIC	Ribose-phosphate pyrophosphokinase (EC	kinase activity	227	616	674
	2.7.6.1) (RPPK) (Phosphoribosyl				
cm 0720465 NDV 15046	pyrophosphate synthetase) (P-	kings+' ''	702	FOC	225
sp Q72M65 NDK_LEPIC	Nucleoside diphosphate kinase (EC	kinase activity	702	596	335
	2.7.4.6) (NDK) (NDP kinase) (Nucleoside-2-				

	P kinase)				
ref YP 002825.1 YP 002825.1	aspartokinase	kinase activity	657	520	375
sp Q72NI2 KAD_LEPIC	Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)	kinase activity	872	431	1009
sp Q72U12 PYRH_LEPIC	Uridylate kinase (EC 2.7.4) (UK) (Uridine	kinase activity	569	425	114
	monophosphate kinase) (UMP kinase)				
ref YP_002258.1 YP_002258.1	serine/threonine kinase with GAF domain	kinase activity	392	383	574
ref YP_002135.1 YP_002135.1	ADP-heptose synthetase	kinase activity	407	375	114
ref YP_002278.1 YP_002278.1	ribokinase	kinase activity	444	281	177
ref YP_000703.1 YP_000703.1	polyphosphate kinase	kinase activity	312	226	185
ref YP_001512.1 YP_001512.1	serine/threonine kinase	kinase activity	272	221	27
ref YP_001102.1 YP_001102.1	pyruvate kinase	kinase activity	141	168	166
ref YP_003648.1 YP_003648.1	pyruvate kinase	kinase activity			281
ref YP_001497.1 YP_001497.1	ADP-heptose synthase	kinase activity			162
sp Q72NQ8 PROB_LEPIC	Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK)	kinase activity			151
sp Q72NL9 KTHY_LEPIC	Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	kinase activity			68
ref YP_003480.1 YP_003480.1	diphosphatefructose-6-phosphate 1- phosphotransferase	kinase activity			61
ref YP 002246.1 YP 002246.1	glucokinase	kinase activity		1	50
ref YP 000739.1 YP 000739.1	thiamine-monophosphate kinase protein	kinase activity		1	40
ref YP_001738.1 YP_001738.1	homoserine kinase	kinase activity		+	37
ref YP_001/38.1 YP_001/38.1				+	37
	phoshomethylpyrimidine kinase protein	kinase activity		+	+
ref YP_001498.1 YP_001498.1	glycerol-3-phosphate cytidyltransferase	kinase activity			30
ref YP_003449.1 YP_003449.1	LAO/AO transport system kinase	kinase activity			24
ref YP_003619.1 YP_003619.1	hypothetical protein LIC20231	kinase activity			17
ref YP_002322.1 YP_002322.1	hypothetical protein LIC12390	kinase activity			5
ref YP_002749.1 YP_002749.1	arabinose kinase	kinase activity			
ref YP_001384.1 YP_001384.1	homoserine kinase type II	kinase activity			
ref YP_001274.1 YP_001274.1	acetylglutamate kinase N-acetyl-gamma- glutamyl-phosphate reductase	kinase activity			
ref YP 003513.1 YP 003513.1	cobinamide kinase	kinase activity			
ref YP_003013.1 YP_003013.1	galactokinase	kinase activity			
ref YP_001188.1 YP_001188.1	peroxiredoxin	metabolic process	3608	5736	2052
ref YP_002168.1 YP_002168.1	fructose-bisphosphate aldolase	metabolic process	7001	5529	2138
ref YP_002339.1 YP_002339.1	putative glutamine synthetase protein	metabolic	6674	5461	2543
ref YP_000199.1 YP_000199.1	cytochrome c oxidase polypeptide II	process metabolic	2644	4894	281
. flyp ogoda thyp cooper		process	5422	40.42	2224
ref YP_000944.1 YP_000944.1	acyl-CoA dehydrogenase	metabolic	5423	4843	2234
Shap operation and		process	0.0		100-
ref YP_002024.1 YP_002024.1	glyceraldehyde-3-phosphate dehydrogenase	metabolic process	3645	4777	1305
sp Q72PA2 SUCC_LEPIC	Succinyl-CoA synthetase beta chain (EC 6.2.1.5) (SCS-beta)	metabolic process	4320	4393	2317
ref YP_002016.1 YP_002016.1	cysteine synthase	metabolic process	5375	3745	5019
ref YP_001164.1 YP_001164.1	putative citrate lyase	metabolic process	4158	3519	1371
ref YP_001733.1 YP_001733.1	malate dehydrogenase	metabolic process	3383	3460	2948
ref YP_003456.1 YP_003456.1	3-oxoacyl-(acyl-carrier protein) reductase	metabolic process	5311	3002	537
ref YP_001323.1 YP_001323.1	MaoC	metabolic process	3304	2936	966
ref YP_000200.1 YP_000200.1	cytochrome c oxidase polypeptide I	metabolic process	2532	2902	64
sp Q72VT0 PPCK_LEPIC	Phosphoenolpyruvate carboxykinase	metabolic process	3242	2634	1597
ref YP_002498.1 YP_002498.1	succinyl-CoA synthetase alpha subunit	metabolic process	3096	2621	1543
	1	15.00000	1	1	1

ref YP_001970.1 YP_001970.1	catalase	metabolic	2176	2357	2761
		process			
sp Q72M00 ILVC_LEPIC	Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydr	metabolic process	3176	2322	1610
ref YP_003205.1 YP_003205.1	3-hydroxyacyl-CoA dehydrogenase	metabolic process	2551	2217	2221
ref YP_001941.1 YP_001941.1	succinate dehydrogenase	metabolic process	1473	2088	1195
ref YP_001734.1 YP_001734.1	hypothetical protein LIC11782	metabolic process	1879	2058	375
ref YP_000091.1 YP_000091.1	long-chain-fatty-acid CoA ligase	metabolic process	1229	1903	320
sp Q72NR4 TPX_LEPIC	Probable thiol peroxidase (EC 1.11.1)	metabolic process	1722	1721	1039
ref YP_001065.1 YP_001065.1	adenylate/guanylate cyclase	metabolic process	1760	1601	110
ref YP_000852.1 YP_000852.1	molybdopterin oxidoredutase membrane subunit	metabolic process		1526	40
ref YP_000839.1 YP_000839.1	adenylate/guanylate cyclase	metabolic process	932	1481	188
ref YP_000397.1 YP_000397.1	hypothetical protein LIC10411	metabolic process	2683	1475	1305
ref YP_000046.1 YP_000046.1	proton-translocating transhydrogenase, subunit alpha part 1	metabolic process	1455	1311	1668
ref YP_000280.1 YP_000280.1	H+-translocating transhydrogenase subunit beta	metabolic process	1192	1298	121
ref YP_000854.1 YP_000854.1	hypothetical protein LIC10877	metabolic process	1897	1286	37
ref YP_001400.1 YP_001400.1	peptidyl-prolyl cis-trans isomerase	metabolic process	1361	1234	456
ref YP_001328.1 YP_001328.1	short-chain dehydrogenase	metabolic process	969	1189	1073
ref YP_003070.1 YP_003070.1	phospho-2-dehydro-3-deoxyheptonate aldolase Chorismate mutase	metabolic process	1337	1187	795
sp Q72QZ8 ENO_LEPIC	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	metabolic process	785	1176	808
ref YP_001788.1 YP_001788.1	peptidyl-prolyl cis-trans isomerase	metabolic process	965	1171	177
ref YP_000111.1 YP_000111.1	hypothetical protein LIC10115	metabolic process	1063	1158	96
ref YP_001588.1 YP_001588.1	long-chain-fatty-acid CoA ligase	metabolic process	858	1127	447
ref YP_000567.1 YP_000567.1	acyl-CoA dehydrogenase	metabolic process	1124	1082	766
ref YP_001683.1 YP_001683.1	FKBP-type peptidyl-prolyl cis-trans isomerase	metabolic process	577	1078	411
ref YP_002100.1 YP_002100.1	putative molybdenum cofactor biosynthesis protein	metabolic process	1053	1073	657
ref YP_001916.1 YP_001916.1	cyclic nucleotide binding protein	metabolic process	976	1010	996
sp Q72VY3 FUMC_LEPIC	Fumarate hydratase class II (EC 4.2.1.2) (Fumarase C)	metabolic process	1038	1004	699
sp Q72RC4 LEU2_LEPIC	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) (Isopropylmalate isomerase) (Alpha-IPM iso	metabolic process	942	996	620
ref YP_002745.1 YP_002745.1	citrate synthase	metabolic process	1309	986	488
sp Q72SG7 TIG_LEPIC	Trigger factor (TF)	metabolic process	958	955	1056
ref YP_002659.1 YP_002659.1	MaoC family protein	metabolic process	867	943	919
sp Q72PJ7 ODO1_LEPIC	2-oxoglutarate dehydrogenase E1	metabolic	1461	930	1217

	component (EC 1.2.4.2) (Alpha-	process			
	component (EC 1.2.4.2) (Alpha- ketoglutarate dehydrogenase)	process			
ref YP_002404.1 YP_002404.1	dihydrolipoamide succinyltransferase	metabolic	867	912	1401
ref YP_003151.1 YP_003151.1	isocitrate dehydrogenase	process metabolic	1459	906	1993
		process			
ref YP_002423.1 YP_002423.1	3-hydroxybutyryl-CoA dehydratase	metabolic process	983	883	367
ref YP_001476.1 YP_001476.1	acetyl-CoA carboxylase alpha subunit	metabolic process	895	840	1061
ref YP_001847.1 YP_001847.1	dihydrolipoamide acetyltransferase	metabolic process	675	838	427
ref YP_002101.1 YP_002101.1	alcohol dehydrogenase	metabolic process	1004	820	859
ref YP_001386.1 YP_001386.1	peptidyl-prolyl cis-trans isomerase	metabolic process	716	818	447
ref YP_002922.1 YP_002922.1	acyl-CoA dehydrogenase	metabolic	714	817	703
ref YP_003450.1 YP_003450.1	methylmalonyl-CoA mutase	process metabolic	689	812	435
ref YP_003489.1 YP_003489.1	short-chain dehydrogenase	process metabolic	980	799	129
	and the state of t	process			
ref YP_001276.1 YP_001276.1	bacterioferritin	metabolic	971	762	64
I a a superior superi		process			
sp Q72U22 DAPA_LEPIC	Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDPS)	metabolic process	681	725	779
ref YP_003616.1 YP_003616.1	acireductone dioxygenase enzyme ARD	metabolic	825	688	284
	and ARD'	process			
ref YP_002228.1 YP_002228.1	udp-glucose dehydrogenase	metabolic process	730	683	411
ref YP 001473.1 YP 001473.1	hypothetical protein LIC11514	metabolic	1172	681	47
		process			
ref YP_002615.1 YP_002615.1	glutamate synthase (NADPH) alpha chain precursor	metabolic process	962	672	690
ref YP_003492.1 YP_003492.1	hypothetical protein LIC20100	metabolic	611	672	427
sp Q72RH7 LEU3_LEPIC	2 isopropulmoleto debudrogoposo (FC	process	960	670	537
SPIQ/ZKH/ LEUS_LEPIC	3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH)	metabolic process	960	670	357
sp Q72W72 DCD_LEPIC	Deoxycytidine triphosphate deaminase (EC 3.5.4.13) (dCTP deaminase)	metabolic process	696	641	125
ref YP_000315.1 YP_000315.1	hemolysin	metabolic	640	639	230
sp Q72RJ9 ARGC_LEPIC	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl- glutamate semialdehyde de	metabolic process	501	622	669
ref YP_000045.1 YP_000045.1	dTDP-glucose 4-6-dehydratase	metabolic	598	616	517
ref YP_001168.1 YP_001168.1	adenylate/guanylate cyclase	metabolic process	507	599	850
ref YP_000244.1 YP_000244.1	alcohol dehydrogenase	metabolic	434	597	1069
ref YP_000506.1 YP_000506.1	oxidoreductase family	process metabolic	659	597	480
ref YP 001915.1 YP 001915.1	acyl-CoA dehydrogenase	process metabolic	829	591	288
	, , ,	process			
ref YP_002137.1 YP_002137.1	UDP-glucose 4-epimerase	metabolic process	662	588	578
ref YP_002129.1 YP_002129.1	transketolase beta subunit	metabolic	471	587	707
ref YP_002403.1 YP_002403.1	dihydrolipoamide dehydrogenase	process metabolic	605	566	906
		process	1		
ref YP_003044.1 YP_003044.1	acyl-CoA dehydrogenase	metabolic process	739	549	944

Process	ref YP_001875.1 YP_001875.1	short-chain dehydrogenase	metabolic	506	520	211
Process Proc			process			
	ref YP_002681.1 YP_002681.1	aldehyde dehydrogenase		488	517	211
CTIMD Triose-phosphate isomerase process	Lama et alimpia i socia		•			
	sp Q72QL9 TPIS_LEPIC			562	509	411
Subunit CE 4.2.1.33 (stopropylmalate process Spi 1072UH6 PURO_LEPIC Phosphoribosylformylghcinamidine metabolic process Spi 110	calO73BCELLEUD LEDIC		<u> </u>	621	400	402
	spjQ/2RC5jleUD_lePiC			621	499	492
spig072HJ6 PURQ_LEPIC Phosphorbosylformylgykojnamidine synthase Cs. 5.3.3 (FAM synthase) process synthase Cs. 5.3.3 (FAM synthase) process synthase Cs. 5.3.3 (FAM synthase) process synthase Cs. 5.3.3 (FAM synthase) process synthase Cs. 5.3.3 (FAM synthase) process synthase			process			
synthase EC. 6.3.5.3 CASA Synthase	splO7211H6 DHRO LEDIC		metabolic	507	497	110
ref YP_000468.1 YP_000468.1 threonine synthase process process ref YP_002478.1 YP_002478.1 YP_002478.1 YP_003258.1 YP_003258.1 YP_003258.1 YP_003258.1 YP_003258.1 YP_003258.1 YP_003258.1 YP_003258.1 YP_002645.1 YP_003485.1 3PTQ/20110TT ONQ_EET 10	, , , , , ,		307	437	110	
process	reflyp 000468 1 LVD 000468 1		<u> </u>	564	191	023
ref VP_002478.1 VP_003258.1 VP_00333.1	161[11_000408.1[11_000408.1	threonine synthase		304	434	323
Process	reflyP 002478 1 LYP 002478 1	acyl-CoA dehydrogenase		418	490	246
ref YP_003258.1 YP_002645.1 L-amino acid oxidase	.6.1662 ./6.11662 ./6.1			.20	.50	2.0
Process Proc	reflyP 003258.1 YP 003258.1	L-amino acid oxidase	•	403	478	215
ref YP_002645.1 YP_002541.1 3-hydroxybutyryl-CoA dehydratase process metabolic process metabolic process metabolic process. 510 475 316 ref YP_002541.1 YP_002541.1 diaminopimelate decarboxylase metabolic process metabolic process. 394 454 517 ref YP_003485.1 YP_003485.1 bacterioferritin comigratory protein metabolic process. 672 446 757 ref YP_000333.1 YP_000933.1 monooxygenase metabolic process. 403 444 169 sp P61703 SYA_LEPIC Alany-IRNA synthetase (EC 6.1.1.7) (Alanine-IRNA ligase) (AlaRS) metabolic process 411 436 339 ref YP_001576.1 YP_001576.1 3-ketoacyl-(acyl-carrier-protein) reductase metabolic process 554 413 403 ref YP_003623.1 YP_003623.1 5-adenosylmethionine decarboxylase like protein metabolic protein 275 410 40 ref YP_003102.1 YP_003102.1 Cholesterol oxidase metabolic protein metabolic process 444 407 89 ref YP_002490.1 YP_002490.1 glycerol-3-phosphate dehydrogenase metabolic process 495 401 517 ref YP_000308.1,1YP_001865.1 IMP dehydrogenase (EC 1.2.1.41) (GPR) (Glutamate-5-semiladehyde dehydrogenase (EC 1.2.1.41) (GPR) (Glu						
Process Proc	ref YP 002645.1 YP 002645.1	3-hvdroxybutyryl-CoA dehvdratase		510	475	316
ref YP_002541.1 YP_003485.1 YP_003485.1 YP_003485.1 YP_003485.1 YP_003485.1 YP_003485.1 YP_003485.1 YP_003485.1 YP_003485.1 YP_00333.1 YP_003485.1 YP_00333.1 YP_003303.1 YP_00356.1 YP_0		- , , , ,				
Process Proc	ref YP 002541.1 YP 002541.1	diaminopimelate decarboxylase	•	394	454	517
Process		,	process			
ref YP_000933.1 YP_000933.1 monooxygenase	ref YP 003485.1 YP 003485.1	bacterioferritin comigratory protein	metabolic	672	446	757
Sp P61703 SYA_LEPIC Alanyl-tRNA synthetase (EC 6.1.1.7) metabolic process sp P61703 SYA_LEPIC Alanyl-tRNA synthetase (EC 6.1.1.7) metabolic process sp P61703 SYA_LEPIC Alanyl-tRNA ligase) (AlaRS) metabolic process sp P61703 SYA_LEPIC Alanyl-tRNA ligase) (AlaRS) metabolic process sp P61703 SYA_LEPIC Alanyl-tRNA ligase) (AlaRS) sketoacyl-(acyl-carrier-protein) reductase process metabolic process sp P61703 SYA_LEPIC sketoacyl-(acyl-carrier-protein) reductase metabolic process sp P61703 SYA_LEPIC sketoacyl-(acyl-carrier-protein) reductase metabolic process sp P61703 SYA_LEPIC sketoacyl-(acyl-carrier-protein) reductase metabolic process sp P61703102.1 YP_003623.1 sketoacyl-dehydrogenase metabolic process sp P7203102.1 YP_003102.1 sketoacyl-dehydrogenase metabolic process sp P72003102.1 YP_003490.1 sketoacyl-dehydrogenase metabolic process sp P72003102.1 YP_000555.1 sketoacyl-dehydrogenase metabolic process sp P72003102.1 YP_000555.1 sketoacyl-dehydrogenase metabolic process sketoacyl-dehydrogenase sketoacyl-dehydrog			process			
Sp P61703 SYA_LEPIC Alanyl-tRNA synthetase (EC 6.1.1.7) metabolic process sp P61703 SYA_LEPIC Alanyl-tRNA synthetase (EC 6.1.1.7) metabolic process sp P61703 SYA_LEPIC Alanyl-tRNA ligase) (AlaRS) metabolic process sp P61703 SYA_LEPIC Alanyl-tRNA ligase) (AlaRS) metabolic process sp P61703 SYA_LEPIC Alanyl-tRNA ligase) (AlaRS) sketoacyl-(acyl-carrier-protein) reductase process metabolic process sp P61703 SYA_LEPIC sketoacyl-(acyl-carrier-protein) reductase metabolic process sp P61703 SYA_LEPIC sketoacyl-(acyl-carrier-protein) reductase metabolic process sp P61703 SYA_LEPIC sketoacyl-(acyl-carrier-protein) reductase metabolic process sp P61703102.1 YP_003623.1 sketoacyl-dehydrogenase metabolic process sp P7203102.1 YP_003102.1 sketoacyl-dehydrogenase metabolic process sp P72003102.1 YP_003490.1 sketoacyl-dehydrogenase metabolic process sp P72003102.1 YP_000555.1 sketoacyl-dehydrogenase metabolic process sp P72003102.1 YP_000555.1 sketoacyl-dehydrogenase metabolic process sketoacyl-dehydrogenase sketoacyl-dehydrog	ref YP 000933.1 YP 000933.1	monooxygenase	metabolic	403	444	169
Calanine-HRNA ligase (AlaRS) process	. – . –		process			
ref YP_001576.1 YP_001576.1 3-ketoacyl-(acyl-carrier-protein) reductase process process 554 413 403 ref YP_003418.1 YP_003418.1 short-chain dehydrogenase metabolic process 275 410 40 ref YP_003623.1 YP_003623.1 S-adenosylmethionine decarboxylase like protein metabolic process 444 407 89 ref YP_003102.1 YP_003102.1 cholesterol oxidase metabolic process 495 401 517 ref YP_002490.1 YP_002490.1 glycerol-3-phosphate dehydrogenase metabolic process 331 401 517 ref YP_000555.1 YP_000555.1 homoserine dehydrogenase metabolic process 331 401 324 sp Q72NQ9 PROA_LEPIC Gamma-glutamyl phosphate reductase (EC 1.2.1.41) (GPR) (Glutamate-5-semialdehyde dehydrogenase) (Glu metabolic process 384 242 ref YP_001865.1 YP_001865.1 IMP dehydrogenase metabolic process 293 369 129 ref YP_003084.1 YP_003084.1 Tas metabolic process 399 366 143 ref YP_000714.1 YP_000714.1 bacterioferritin comigratory protein metabolic process 342 <td>sp P61703 SYA_LEPIC</td> <td>Alanyl-tRNA synthetase (EC 6.1.1.7)</td> <td>metabolic</td> <td>411</td> <td>436</td> <td>339</td>	sp P61703 SYA_LEPIC	Alanyl-tRNA synthetase (EC 6.1.1.7)	metabolic	411	436	339
Process Proc		(AlaninetRNA ligase) (AlaRS)	process			
ref YP_003418.1 YP_003428.1 short-chain dehydrogenase metabolic process metabo	ref YP_001576.1 YP_001576.1	3-ketoacyl-(acyl-carrier-protein) reductase	metabolic	554	413	403
Process			process			
Fef YP_003623.1 YP_003623.1 S-adenosylmethionine decarboxylase like protein stability protein prot	ref YP_003418.1 YP_003418.1	short-chain dehydrogenase	metabolic	275	410	40
ref YP_003102.1 YP_003102.1 cholesterol oxidase metabolic process metabolic pr			process			
ref YP_003102.1 YP_003102.1 cholesterol oxidase metabolic process 304 402 140 ref YP_002490.1 YP_002490.1 glycerol-3-phosphate dehydrogenase metabolic process 495 401 517 ref YP_000555.1 YP_000555.1 homoserine dehydrogenase metabolic process 331 401 324 sp Q72NQ9 PROA_LEPIC Gamma-glutamyl phosphate reductase (EC 1.2.1.41) (GPR) (Glutamate-5-semialdehyde dehydrogenase) (Glu metabolic process 210 384 242 ref YP_001865.1 YP_001865.1 IMP dehydrogenase metabolic process 293 369 129 ref YP_003084.1 YP_003084.1 Tas metabolic process 293 369 129 ref YP_000714.1 YP_000714.1 bacterioferritin comigratory protein metabolic process metabolic process 399 366 143 ref YP_000307.1 YP_000307.1 ribose 5-phosphate isomerase B metabolic process 342 365 288 sp Q72U05 TRPB_LEPIC Tryptophan synthase beta chain (EC 4.2.1.20) A2290 metabolic process 379 348 132 ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein process	ref YP_003623.1 YP_003623.1	S-adenosylmethionine decarboxylase like	metabolic	444	407	89
Process Proc		protein	process			
ref YP_002490.1 YP_002490.1 glycerol-3-phosphate dehydrogenase	ref YP_003102.1 YP_003102.1	cholesterol oxidase	metabolic	304	402	140
Process Proc			process			
ref YP_000555.1 YP_000555.1 homoserine dehydrogenase metabolic process metabol	ref YP_002490.1 YP_002490.1	glycerol-3-phosphate dehydrogenase		495	401	517
Sp Q72NQ9 PROA_LEPIC Gamma-glutamyl phosphate reductase (EC 1.2.1.41) (GPR) (Glutamate-5-5emialdehyde dehydrogenase) (Glu GPR) (Glutamate-5-5emialdehyde dehydrogenase) (Glu MP dehydrogenase Metabolic process GPR MP dehydrogenase MP dehydrogen						
Sp Q72NQ9 PROA_LEPIC Gamma-glutamyl phosphate reductase (EC 1.2.1.41) (GPR) (Glutamate-5-semialdehyde dehydrogenase) (Glu metabolic process	ref YP_000555.1 YP_000555.1	homoserine dehydrogenase		331	401	324
CEC 1.2.1.41 GPR Glutamate-5-semialdehyde dehydrogenase Glu	Lamania de la companya	· ·	210	201	2.12	
semialdehyde dehydrogenase Glu	sp Q72NQ9 PROA_LEPIC			210	384	242
ref YP_001865.1 YP_001865.1 IMP dehydrogenase metabolic process 447 382 636 ref YP_003084.1 YP_003084.1 Tas metabolic process 293 369 129 ref YP_000714.1 YP_000714.1 bacterioferritin comigratory protein metabolic process 399 366 143 ref YP_000307.1 YP_000307.1 ribose 5-phosphate isomerase B metabolic process 342 365 288 ref YP_001771.1 YP_001771.1 cysteine synthase metabolic process 210 356 332 sp Q72U05 TRPB_LEPIC Tryptophan synthase beta chain (EC 4.2.1.20) A2290 metabolic process 379 348 132 ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 </td <td></td> <td></td> <td>process</td> <td></td> <td></td> <td></td>			process			
ref YP_003084.1 YP_003084.1 Tas metabolic process 293 369 129 ref YP_000714.1 YP_000714.1 bacterioferritin comigratory protein metabolic process 399 366 143 ref YP_000307.1 YP_000307.1 ribose 5-phosphate isomerase B metabolic process 342 365 288 ref YP_001771.1 YP_001771.1 cysteine synthase metabolic process 210 356 332 sp Q72U05 TRPB_LEPIC Tryptophan synthase beta chain (EC process metabolic process 379 348 132 ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458	*** 1 ND 0019CF 1 ND 0019CF 1		metabalia	447	202	C2C
Tas	ref YP_001865.1 YP_001865.1	livir denydrogenase		447	382	636
Process Proc	roflyn 002094 1 lyn 002094 1	Tac	•	202	360	120
ref YP_000714.1 YP_000714.1 bacterioferritin comigratory protein metabolic process 399 366 143 ref YP_000307.1 YP_000307.1 ribose 5-phosphate isomerase B metabolic process 342 365 288 ref YP_001771.1 YP_001771.1 cysteine synthase metabolic process 210 356 332 sp Q72U05 TRPB_LEPIC Tryptophan synthase beta chain (EC 4.2.1.20) A2290 metabolic process 379 348 132 ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	Ter[17_003084.1[17_003084.1	lds		293	309	129
ref YP_000307.1 YP_000307.1 ribose 5-phosphate isomerase B metabolic process 342 365 288 ref YP_001771.1 YP_001771.1 cysteine synthase metabolic process 210 356 332 sp Q72U05 TRPB_LEPIC Tryptophan synthase beta chain (EC 4.2.1.20) A2290 metabolic process 379 348 132 ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	reflyp 000714 1lvp 000714 1	hacterioferritin comigratory protein		390	366	1/13
ref YP_000307.1 YP_000307.1 ribose 5-phosphate isomerase B metabolic process 342 365 288 ref YP_001771.1 YP_001771.1 cysteine synthase metabolic process 210 356 332 sp Q72U05 TRPB_LEPIC Tryptophan synthase beta chain (EC 4.2.1.20) A2290 metabolic process 379 348 132 ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	161[11_000/14.1[17_000/14.1	Sactemore man comignatory protein		333	300	143
Process Proc	reflyp 000307 1lvp 000307 1	rihose 5-nhosnhate isomerase R	•	342	365	288
ref YP_001771.1 YP_001771.1 cysteine synthase metabolic process 210 356 332 sp Q72U05 TRPB_LEPIC Tryptophan synthase beta chain (EC 4.2.1.20) A2290 metabolic process 379 348 132 ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	161111 _000307.11115_000307.1	110036 3-pilospilate isolilerase b		342	303	200
Sp Q72U05 TRPB_LEPIC	reflyP 001771 1lyP 001771 1	cysteine synthase	•	210	356	332
sp Q72U05 TRPB_LEPIC Tryptophan synthase beta chain (EC 4.2.1.20) A2290 metabolic process 379 348 132 ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	,001//1.1 11 _001//1.1	cysteme synthase		210	330	332
4.2.1.20) A2290 process ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	sn O72U05 TRPR FPIC	Tryptophan synthase heta chain (FC		379	348	132
ref YP_001393.1 YP_001393.1 cyclic nucleotide binding protein metabolic process 333 347 203 ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324					3.3	132
ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	ref YP 001393,1 YP 001393.1			333	347	203
ref YP_001846.1 YP_001846.1 pyruvate dehydrogenase alpha2 subunit protein metabolic process 326 345 332 sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	,	,			-	
protein process sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	ref YP 001846.1 YP 001846.1	pyruvate dehydrogenase alpha2 subunit		326	345	332
sp Q72S57 ISPH_LEPIC 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2) metabolic process 413 338 292 ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324					1 - 1 -	
diphosphate reductase (EC 1.17.1.2) process ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	sp Q72S57 ISPH_LEPIC	1		413	338	292
ref YP_000549.1 YP_000549.1 enoyl-CoA hydratase metabolic process 526 333 513 ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	-1-1-2-1-2-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	· · · · · · · · · · · · · · · · · · ·				 -
ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	ref YP 000549.1 YP 000549.1			526	333	513
ref YP_002058.1 YP_002058.1 dTDP-glucose 4,6-dehydratase metabolic 458 332 324	,	, ,				
	ref YP_002058.1 YP_002058.1	dTDP-glucose 4,6-dehydratase		458	332	324
	,	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,				

ref YP_000019.1 YP_000019.1	3-oxoacyl-acyl carrier protein reductase	metabolic	398	326	529
ref YP_003539.1 YP_003539.1	heme oxygenase	process metabolic process	514	322	257
ref YP_000066.1 YP_000066.1	enoyl-Coa hydratase/isomerase family	metabolic process	299	318	71
ref YP_000932.1 YP_000932.1	alcohol dehydrogenase	metabolic process	407	314	316
ref YP_003598.1 YP_003598.1	methylmalonyl-CoA mutase	metabolic process	276	309	359
ref YP_000152.1 YP_000152.1	malic enzyme	metabolic process		306	431
ref YP_003597.1 YP_003597.1	methylmalonyl-COA mutase small subunit	metabolic process	455	305	553
ref YP_000329.1 YP_000329.1	hemolysin B	metabolic process	504	292	992
ref YP_001651.1 YP_001651.1	glycerol-3-phosphate dehydrogenase	metabolic process	351	290	351
ref YP_001560.1 YP_001560.1	hypothetical protein LIC11602	metabolic process	236	283	82
ref YP_001399.1 YP_001399.1	adenylate/guanylate cyclase	metabolic process	475	282	50
ref YP_003345.1 YP_003345.1	glutathione peroxidase	metabolic process	287	278	192
sp Q72TC0 ILVD_LEPIC	Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD)	metabolic process	247	263	582
ref YP_001860.1 YP_001860.1	udp-n-acetyl-d-mannosamine transferase	metabolic process		260	14
ref YP_002262.1 YP_002262.1	putative lactoylglutathione lyase	metabolic process	298	256	339
ref YP_003477.1 YP_003477.1	B12-dependent homocysteine-N5- methyltetrahydrofolate transmethylase	metabolic process	412	253	753
ref YP_002088.1 YP_002088.1	D-3-phosphoglycerate dehydrogenase	metabolic process	321	252	234
ref YP_000228.1 YP_000228.1	cyclic nucleotide binding protein	metabolic process	284	243	347
ref YP_000566.1 YP_000566.1	anthranilate synthase component I	metabolic process	276	241	192
ref YP_001931.1 YP_001931.1	D-3-phosphoglycerate dehydrogenase	metabolic process	237	239	363
sp Q72W63 DAPF_LEPIC	Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase)	metabolic process	206	235	324
sp Q72VI8 GCSP_LEPIC	Glycine dehydrogenase	metabolic process	480	228	324
ref YP_002075.1 YP_002075.1	UDP-glucose 4-epimerase	metabolic process	204	227	591
ref YP_001891.1 YP_001891.1	hypothetical protein LIC11946	metabolic process	166	224	
ref YP_000368.1 YP_000368.1	acyl-CoA dehydrogenase	metabolic process	250	221	403
sp Q72LS1 SYS_LEPIC	Seryl-tRNA synthetase (EC 6.1.1.11) (SerinetRNA ligase) (SerRS)	metabolic process	184	221	355
ref YP_003076.1 YP_003076.1	GDP-mannose 4,6-dehydratase	metabolic process	268	202	452
ref YP_002601.1 YP_002601.1	thiamine biosynthesis protein ThiC	metabolic process	310	200	82
ref YP_000877.1 YP_000877.1	adenylate/guanylate cyclase	metabolic process	221	200	17
ref YP_002104.1 YP_002104.1	sialic acid synthase	metabolic process	229	190	177
ref YP_003109.1 YP_003109.1	adenylate/guanylate cyclase	metabolic process	269	187	82
sp Q72TR2 ISPG_LEPIC	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (EC 1.17.4.3) (1-	metabolic process	284	186	203

	hydroxy-2-methyl-2-(E)-butenyl				
ref YP_001319.1 YP_001319.1	transketolase	metabolic process	203	177	246
ref YP_000425.1 YP_000425.1	nitrogen regulatory protein pll	metabolic process	266	173	525
ref YP_002571.1 YP_002571.1	glutathione peroxidase	metabolic process	246	173	118
ref YP_002060.1 YP_002060.1	dTDP-4-dehydrorhamnose 3,5-epimerase	metabolic process	255	172	324
ref YP_000988.1 YP_000988.1	adenylosuccinate lyase	metabolic process	226	170	230
ref YP_000431.1 YP_000431.1	phosphomannomutase	metabolic process	215	169	517
ref YP_000530.1 YP_000530.1	lipase	metabolic process	144	168	78
ref YP_002085.1 YP_002085.1	cdp-glucose 4,6-dehydratase	metabolic process	222	163	82
ref YP_003529.1 YP_003529.1	capsular polysaccharide biosynthesis protein	metabolic process	167	155	57
ref YP_003233.1 YP_003233.1	isocitrate dehydrogenase	metabolic process	190	151	375
ref YP_000815.1 YP_000815.1	glyoxalase	metabolic process	401	148	249
ref YP_001600.1 YP_001600.1	hypothetical protein LIC11642	metabolic process		143	118
sp Q75FC8 DHAS_LEPIC	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase) (ASADH)	metabolic process	197	135	439
ref YP_002111.1 YP_002111.1	UDP-glucose 4-epimerase	metabolic process	201	122	96
ref YP_002261.1 YP_002261.1	adenylate/guanylate cyclase	metabolic process	128	103	427
ref YP_002107.1 YP_002107.1	putative UDP-N-acetylglucosamine-2- epimerase	metabolic process	137	87	57
sp P61742 GPDA_LEPIC	Glycerol-3-phosphate dehydrogenase	metabolic process		87	140
ref YP_003182.1 YP_003182.1	hypothetical protein LIC13275	metabolic process	121	76	96
ref YP_002012.1 YP_002012.1	hypothetical protein LIC12078	metabolic process		46	147
ref YP_001691.1 YP_001691.1	hypothetical protein LIC11739	metabolic process	344		253
sp Q72SC4 GATC_LEPIC	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (EC 6.3.5) (Asp/Glu-ADT subunit C) - Le	metabolic process	250		27
ref YP_002040.1 YP_002040.1	hypothetical protein LIC12106	metabolic process	105		14
ref YP_002552.1 YP_002552.1	enoyl-CoA hydratase	metabolic process			521
ref YP_000069.1 YP_000069.1	glyoxylase I	metabolic process			480
ref YP_002130.1 YP_002130.1	transketolase	metabolic process			468
ref YP_002839.1 YP_002839.1	citrate synthase	metabolic process			427
ref YP_003446.1 YP_003446.1	hypothetical protein LIC20054	metabolic process			371
ref YP_002138.1 YP_002138.1	phosphoheptose isomerase	metabolic process			359
sp P62354 HIS4_LEPIC	1-(5-phosphoribosyl)-5-(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase (metabolic process			335
ref YP_001917.1 YP_001917.1	thioredoxin	metabolic process			324

ref YP_001710.1 YP_001710.1	acyl-CoA hydrolase	metabolic	273
		process	
sp Q72S46 PYRG_LEPIC	CTP synthase (EC 6.3.4.2) (UTPammonia	metabolic	261
	ligase) (CTP synthetase)	process	
sp Q72VI2 SERC_LEPIC	Phosphoserine aminotransferase (EC	metabolic	242
	2.6.1.52) (PSAT)	process	
ref YP_002380.1 YP_002380.1	chorismate mutase and prephenate	metabolic	226
	dehydratase	process	
ref YP_003300.1 YP_003300.1	alkaline phosphatase	metabolic	219
		process	
sp Q72N73 NADA_LEPIC	Quinolinate synthetase A	metabolic	203
	,	process	
ref YP_000428.1 YP_000428.1	3-methylcrotonoyl-CoA carboxylase beta	metabolic	188
.6.1666 .26.11666 .26.1	subunit	process	100
sp Q72U21 DAPB_LEPIC	Dihydrodipicolinate reductase (EC	metabolic	185
3P Q/2021 DAI B_EEI IC	1.3.1.26) (DHPR)	process	103
ref YP_001760.1 YP_001760.1			105
rei[1P_001760.1[1P_001760.1	glutaredoxin-related protein	metabolic	185
- Incaccoluuca IEDIO	Later deal control of the delication	process	477
sp P61660 HIS7_LEPIC	Imidazoleglycerol-phosphate dehydratase	metabolic	177
	(EC 4.2.1.19) (IGPD)	process	
ref YP_002710.1 YP_002710.1	hypothetical protein LIC12793	metabolic	169
		process	
ref YP_002471.1 YP_002471.1	hypothetical protein LIC12543	metabolic	155
		process	
ref YP_003402.1 YP_003402.1	delta-aminolevulinic acid dehydratase	metabolic	147
		process	
ref YP_002699.1 YP_002699.1	hydroxymethylglutaryl-CoA lyase	metabolic	132
. = . =		process	
ref YP_002320.1 YP_002320.1	cyclic nucleotide binding protein	metabolic	118
.6.1002020.11002020.1	gyone madicatina amama protein	process	110
ref YP_001268.1 YP_001268.1	phosphoglycolate phosphatase	metabolic	118
161 17_001208.1 17_001208.1	phosphogrycolate phosphatase		110
flyp 004636 4 lyp 004636 4	and Can budgeton	process	107
ref YP_001626.1 YP_001626.1	enoyl-CoA hydratase	metabolic	107
		process	
ref YP_000565.1 YP_000565.1	anthranilate synthase component II	metabolic	92
		process	
ref YP_001252.1 YP_001252.1	hypothetical protein LIC11284	metabolic	89
		process	
ref YP_001718.1 YP_001718.1	phosphomannomutase	metabolic	85
		process	
ref YP_000664.1 YP_000664.1	hypothetical protein LIC10680	metabolic	71
		process	
ref YP_002102.1 YP_002102.1	CMP-N-acetlyneuraminic acid synthetase	metabolic	71
	,	process	
sp Q72RA8 ARLY_LEPIC	Argininosuccinate lyase (EC 4.3.2.1)	metabolic	64
	(Arginosuccinase) (ASAL)	process	
ref YP_003140.1 YP_003140.1	short-chain dehydrogenase	metabolic	64
	Share chain deriyar ogendae	process	
ref YP_002091.1 YP_002091.1	oxidoreductase family protein	metabolic	61
161111-005031.11115-005031.1	Onidoreductase farmiy protein		01
	Assessment distribution (50)	process	
sp Q72QN9 PAND_LEPIC	Aspartate 1-decarboxylase precursor (EC	metabolic	50
	4.1.1.11) (Aspartate alpha-decarboxylase)	process	+
ref YP_002226.1 YP_002226.1	phosphoribosylaminoimidazole	metabolic	50
	carboxylase catalytic subunit protein	process	
sp Q72PM6 PLSX_LEPIC	Fatty acid/phospholipid synthesis protein	metabolic	37
	plsX	process	
ref YP_001699.1 YP_001699.1	long-chain-fatty-acid CoA ligase	metabolic	37
		process	<u> </u>
	1	metabolic	37
ref YP_001452.1 YP_001452.1	hypothetical protein LIC11491	ctabbc	
ref YP_001452.1 YP_001452.1	hypothetical protein LIC11491	process	
	hypothetical protein LIC11491 putative lipoprotein		14
ref YP_001452.1 YP_001452.1 ref YP_001835.1 YP_001835.1		process	14
		process metabolic	14

ref YP_001377.1 YP_001377.1	acyl-CoA thioesterase	metabolic	8
		process	
ref YP_003051.1 YP_003051.1	hemolysin	metabolic	8
		process	
ref YP_001058.1 YP_001058.1	cytochrome c peroxidase	metabolic	
		process	
ref YP_000024.1 YP_000024.1	adenylate/guanylate cyclase	metabolic	
	, , , ,	process	
ref YP_003110.1 YP_003110.1	cholesterol oxidase precursor	metabolic	
	onerester or oxidase presursor	process	
ref YP_000586.1 YP_000586.1	lysophospholipase	metabolic	343
161[17_000380.1[17_000380.1	lysophospholipase		343
china annua china annua c		process	
ref YP_003396.1 YP_003396.1	5,10 methylene tetrahydrofolate	metabolic	304
	reductase	process	
ref YP_003414.1 YP_003414.1	azoreductase	metabolic	269
		process	
sp Q72VB8 GPMI_LEPIC	2,3-bisphosphoglycerate-independent	metabolic	238
_	phosphoglycerate mutase (EC 5.4.2.1)	process	
	(Phosphoglyceromutase) (BPG		
ref YP_002209.1 YP_002209.1	pyrroline-5-carboxylate reductase	metabolic	230
101/11 _002203.1/11 _002203.1	pyrrolline 3 carboxylate reductase		230
#oflyD_000442.41yD_000442.4	adapasina daaminass	process	222
ref YP_000443.1 YP_000443.1	adenosine deaminase	metabolic	223
		process	
sp Q75FF2 ALR_LEPIC	Alanine racemase (EC 5.1.1.1)	metabolic	223
		process	
ref YP_001574.1 YP_001574.1	ADP-L-glycero-D-mannoheptose-6-	metabolic	211
. – . –	epimerase	process	
ref YP_001592.1 YP_001592.1	CsgA	metabolic	203
.6. 661332:1 661332:1	656.1	process	200
on LOZANIJE IMECA JEDIC	Mathylahraval synthesis (FC 4.2.2.2) (MCC)	metabolic	200
sp Q72NU6 MGSA_LEPIC	Methylglyoxal synthase (EC 4.2.3.3) (MGS)		200
cl		process	1
ref YP_002073.1 YP_002073.1	UDP-N-acetylglucosamine 2-epimerase	metabolic	185
		process	
sp Q72T46 MTNA_LEPIC	Probable methylthioribose-1-phosphate	metabolic	173
	isomerase (EC 5.3.1.23) (MTR-1-P	process	
	isomerase) (S-methyl-5-thiori		
ref YP_003061.1 YP_003061.1	UDP-glucose 4-epimerase	metabolic	173
=	, grant sp	process	
ref YP_001314.1 YP_001314.1	acyl-CoA dehydrogenase	metabolic	166
161/11_001314.1/11_001314.1	acyi-con deliyalogellase		100
(IVD 00340C4 IVD 00340C4	1	process	454
ref YP_002186.1 YP_002186.1	L-aspartate oxidase	metabolic	151
		process	
ref YP_001040.1 YP_001040.1	alcohol dehydrogenase	metabolic	140
		process	
ref YP_003277.1 YP_003277.1	phosphoadenosine phosphosulphate	metabolic	140
_	reductase	process	
ref YP_000770.1 YP_000770.1	cyclic nucleotide binding protein	metabolic	136
11222. 12.2[000.70.2	-,	process	
ref YP 000776.1 YP 000776.1	enoyl-CoA hydratase	metabolic	136
10.111_000//0.1117_000//0.1	Choyi-Con hyuratase		130
. flyn oggog the oggos	a fact of the control	process	126
ref YP_002093.1 YP_002093.1	putative hydroxyacid aldolase protein	metabolic	136
		process	
ref YP_002108.1 YP_002108.1	N-acetylneuraminate synthase	metabolic	129
		process	<u> </u>
ref YP_000527.1 YP_000527.1	acyl-CoA dehydrogenase	metabolic	125
· - · -		process	
sp Q72W01 AROC_LEPIC	Chorismate synthase (EC 4.2.3.5) (5-	metabolic	121
SPI Q/2WOITANOC_LLING	enolpyruvylshikimate-3-phosphate		121
		process	
Clyp coocaa : line cooca	phospholyase) - Leptospira inte		1.2.
ref YP_000641.1 YP_000641.1	hemolysin	metabolic	121
		process	1
		process	
sp P62458 HISX_LEPIC	Histidinol dehydrogenase (EC 1.1.1.23)	metabolic	121
sp P62458 HISX_LEPIC	Histidinol dehydrogenase (EC 1.1.1.23) (HDH)		121

		process	
sp Q72U08 DXR_LEPIC	1-deoxy-D-xylulose 5-phosphate	metabolic	107
	reductoisomerase (EC 1.1.1.267) (DXP reductoisomerase) (1-deoxyxylulo	process	
ref YP_001754.1 YP_001754.1	dihydrolipoamide dehydrogenase	metabolic	107
	1 1	process	407
ref YP_003080.1 YP_003080.1	hypothetical protein LIC13172	metabolic process	107
sp Q75FW3 AROB_LEPIC	3-dehydroquinate synthase (EC 4.2.3.4)	metabolic	103
		process	
ref YP_002084.1 YP_002084.1	dTDP-4-dehydrorhamnose epimerase	metabolic	103
ref YP_000444.1 YP_000444.1	hypothetical protein LIC10460	process metabolic	103
161711 _000 11111111 _000 11111	hypothetical protein Electorios	process	
ref YP_000943.1 YP_000943.1	alpha-methylacyl-CoA racemase	metabolic	100
(1) (D. 002.4C2.4 VD. 002.4C2.4	25 0 25 1 25 1 25 1 25 1 25 1 25 1 25 1	process	0.5
ref YP_002463.1 YP_002463.1	riboflavin synthase subunit alpha	metabolic process	96
ref YP_001093.1 YP_001093.1	phosphoribosylaminoimidazole	metabolic	89
	synthetase	process	
ref YP_000185.1 YP_000185.1	short-chain dehydrogenase	metabolic	89
ref YP_003423.1 YP_003423.1	short-chain dehydrogenase	process metabolic	89
161 17_003423.1 17_003423.1	Short-chain denydrogenase	process	65
ref YP_001629.1 YP_001629.1	glycerol-3-phosphate dehydrogenase	metabolic	85
		process	
ref YP_000811.1 YP_000811.1	hypothetical protein LIC10834	metabolic	85
ref YP_001159.1 YP_001159.1	hypothetical protein LIC11189	process metabolic	85
	, , , , , , , , , , , , , , , , , , ,	process	
ref YP_001363.1 YP_001363.1	N-acetylneuraminate synthase	metabolic	85
O721 O4 TDDA LEDIC	Tourstanding numbers alone shall (FC	process	05
sp Q72U04 TRPA_LEPIC	Tryptophan synthase alpha chain (EC 4.2.1.20)	metabolic process	85
ref YP_002554.1 YP_002554.1	hemolysin	metabolic	82
	,	process	
ref YP_002736.1 YP_002736.1	pyridoxal phosphate biosynthesis protein	metabolic	82
ref YP_002309.1 YP_002309.1	capsule biosynthesis protein	process metabolic	82
101/11 _002303.1/11 _002303.1	capsale biosynthesis protein	process	02
ref YP_003336.1 YP_003336.1	dihydroorotate dehydrogenase	metabolic	78
		process	
ref YP_000923.1 YP_000923.1	aldo/keto reductase	metabolic process	75
ref YP 000040.1 YP 000040.1	polysialic acid capsule expression protein	metabolic	75
		process	
ref YP_000778.1 YP_000778.1	acyl-CoA dehydrogenase	metabolic	71
ref YP_001129.1 YP_001129.1	dihydrolipoamide dehydrogenase	process metabolic	71
10.111_001125.1111_001125.1	amyaronpournae aenyarogenase	process	/1
ref YP_000258.1 YP_000258.1	cyclic nucleotide binding protein	metabolic	64
dia ana ana ana ana		process	
ref YP_003407.1 YP_003407.1	coproporphyrinogen III oxidase	metabolic process	64
ref YP 000625.1 YP 000625.1	diguanylate phosphodiesterase	metabolic	64
	G ,	process	
ref YP_001939.1 YP_001939.1	hypothetical protein LIC12000	metabolic	64
sp P62359 HISZ_LEPIC	ATP phosphoribosyltransferase regulatory	process	61
3h1L05333 UI35_FELIC	subunit	metabolic process	01
ref YP_002139.1 YP_002139.1	FAD-dependent oxidoreductase family	metabolic	57
dia and an analysis		process	
ref YP_001253.1 YP_001253.1	hypothetical protein LIC11285	metabolic	57
		process	

ref YP_001701.1 YP_001701.1	hypothetical protein LIC11749	metabolic	57
Clyp cooper the cooper		process	
ref YP_000039.1 YP_000039.1	3-dehydroquinate dehydratase	metabolic	54
China annual china annual chi		process	
ref YP_002059.1 YP_002059.1	dTDP-4-dehydrorhamnose reductase	metabolic	54
		process	
sp Q72MT7 G6PI_LEPIC	Glucose-6-phosphate isomerase (EC	metabolic	50
	5.3.1.9) (GPI) (Phosphoglucose isomerase)	process	
	(PGI) (Phosphohexose iso		
ref YP_000285.1 YP_000285.1	hypothetical protein LIC10295	metabolic	47
		process	
ref YP_002263.1 YP_002263.1	hypothetical protein LIC12331	metabolic	47
	,,	process	
ref YP_003168.1 YP_003168.1	hypothetical protein LIC13261	metabolic	47
	,p	process	
ref YP_002035.1 YP_002035.1	CinA	metabolic	47
101/11_002055.1/11_002055.1	CITIA	process	"'
ref YP_001321.1 YP_001321.1	alaahal dahudraganasa		4.4
Ter TP_001321.1 TP_001321.1	alcohol dehydrogenase	metabolic	44
Clyp codeca dlyp codecad	0.00	process	1
ref YP_001890.1 YP_001890.1	GMP synthase	metabolic	44
		process	
ref YP_000183.1 YP_000183.1	hypothetical protein LIC10192	metabolic	44
		process	
ref YP_001415.1 YP_001415.1	pantoatebeta-alanine ligase	metabolic	44
		process	
ref YP_003050.1 YP_003050.1	pantothenate metabolism flavoprotein	metabolic	44
		process	
ref YP_001264.1 YP_001264.1	hypothetical protein LIC11298	metabolic	44
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	process	
ref YP_001668.1 YP_001668.1	hypothetical protein LIC11716	metabolic	40
101111 _001000.1[11 _001000.1	hypothetical protein Eletty 10	process	10
ref YP_001075.1 YP_001075.1	methylmalonyl-CoA mutase	metabolic	40
161 17_0010/3.1 17_0010/3.1	Inethylmalonyi-Cox mutase		40
	the first of the control of the control of	process	40
ref YP_000710.1 YP_000710.1	riboflavin biosynthesis protein	metabolic	40
Clare and a clare and a clare		process	
ref YP_003640.1 YP_003640.1	pterin-4-alpha-carbinolamine dehydratase	metabolic	37
		process	
ref YP_002079.1 YP_002079.1	putative glycosyltransferase	metabolic	37
		process	
ref YP_003472.1 YP_003472.1	4-hydroxybenzoyl-CoA thioesterase	metabolic	34
		process	
ref YP_000022.1 YP_000022.1	arsenate reductase	metabolic	34
		process	
ref YP_002481.1 YP_002481.1	D-3-phosphoglycerate dehydrogenase	metabolic	34
	, , , ,	process	
ref YP_002901.1 YP_002901.1	lipase	metabolic	34
		process	
ref YP_002495.1 YP_002495.1	hypothetical protein LIC12570	metabolic	34
101111 _002455.1[17_002455.1	hypothetical protein LiC12370	process	34
rofIVD 002122 1 VD 002122 1	putative cytochrome oxidase subunit	metabolic	34
ref YP_003122.1 YP_003122.1	putative cytochronne oxidase subunit		34
	2 Constitut Domathate	process	20
sp Q72UP7 ISPF_LEPIC	2-C-methyl-D-erythritol 2,4-	metabolic	30
	cyclodiphosphate synthase (EC 4.6.1.12)	process	
1	(MECPS) (MECDP-synthase)		
sp Q72PM1 AROA_LEPIC	3-phosphoshikimate 1-	metabolic	30
	carboxyvinyltransferase (EC 2.5.1.19) (5-	process	
	enolpyruvylshikimate-3-phosphate synth		
ref YP_000277.1 YP_000277.1	6-pyruvoyl tetrahydrobiopterin synthase	metabolic	30
		process	
ref YP_001235.1 YP_001235.1	putative 6-pyruvoyl tetrahydrobiopterin	metabolic	30
	synthase	process	
ref YP_002098.1 YP_002098.1	hypothetical protein LIC12163	metabolic	27
	mypothicular protein Elozzas	process	

		process	
ref YP_000194.1 YP_000194.1	oxidoreductase	metabolic process	27
ref YP_003049.1 YP_003049.1	panthotenate metabolism flavoprotein	metabolic process	27
ref YP_001513.1 YP_001513.1	ribulose-5-phosphate 3-epimerase	metabolic process	27
ref YP_002112.1 YP_002112.1	CMP-N-acetlyneuraminic acid synthetase	metabolic process	27
sp Q72V75 ISPE_LEPIC	4-diphosphocytidyl-2-C-methyl-D- erythritol kinase (EC 2.7.1.148) (CMK) (4- (cytidine-5'-diphospho)-2-	metabolic process	24
ref YP_001015.1 YP_001015.1	adenylate or guanylate cyclase	metabolic process	24
ref YP_003239.1 YP_003239.1	GMC oxidoreductase	metabolic process	24
ref YP_001744.1 YP_001744.1	hypothetical protein LIC11792	metabolic process	24
sp Q72NP6 TRPC_LEPIC	Indole-3-glycerol phosphate synthase (EC 4.1.1.48) (IGPS)	metabolic process	24
ref YP_002848.1 YP_002848.1	mannose-6-phosphate isomerase	metabolic process	24
ref YP_002889.1 YP_002889.1	putative lipoprotein	metabolic process	24
ref YP_000313.1 YP_000313.1	2,3-bisphosphoglycerate-independent phosphoglycerate mutase gene	metabolic process	24
ref YP_000790.1 YP_000790.1	cytochrome C biogenesis protein	metabolic process	24
ref YP_000326.1 YP_000326.1	hypothetical protein LIC10336	metabolic	24
sp Q72PF1 PDXH_LEPIC	Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase) (PNPOx)	metabolic process	24
ref YP_002604.1 YP_002604.1	3-oxoacyl-(acyl carrier protein)	metabolic	21
ref YP_003116.1 YP_003116.1	riboflavin-specific deaminase/reductase	process metabolic	21
ref YP_002841.1 YP_002841.1	cytochrome c peroxidase	metabolic	21
ref YP_003583.1 YP_003583.1	hypothetical protein LIC20192	metabolic	21
ref YP_002224.1 YP_002224.1	oligo-1,6- glucosidase	metabolic metabolic	21
sp Q72RD4 GSH1_LEPIC	Glutamatecysteine ligase (EC 6.3.2.2) (Gamma-glutamylcysteine synthetase) (Gamma-ECS) (GCS)	process metabolic process	17
ref YP_003315.1 YP_003315.1	glycerol-3-phosphate acyltransferase	metabolic process	17
ref YP_003041.1 YP_003041.1	NAD(P)H steroid dehydrogenase	metabolic process	17
sp Q75FF4 SPEH_LEPIC	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC) (SamDC)	metabolic process	17
ref YP_003578.1 YP_003578.1	hypothetical protein LIC20187	metabolic process	17
sp Q72TI2 MURI_LEPIC	Glutamate racemase (EC 5.1.1.3)	metabolic process	17
ref YP_002639.1 YP_002639.1	putative enolase-phosphatase E-1	metabolic process	14
ref YP_002071.1 YP_002071.1	UDP-glucose lipid carrier transferase	metabolic process	14
ref YP_000201.1 YP_000201.1	cytochrome/quinol oxidase subunit 3	metabolic process	14
ref YP_002434.1 YP_002434.1	adenylate/guanylate cyclase	metabolic process	11

ref P_003187.1 P_003187.1 Muoc family protein metabolic process				
ref \tau_02379.1 \tau_022379.1 \tau_022379	ref YP_001761.1 YP_001761.1	hypothetical protein LIC11810		11
process			·	
Inter	ref YP_003187.1 YP_003187.1	MaoC family protein		11
process			·	
	ref YP_002379.1 YP_002379.1	prephenate (chorismate) dehydrogenase		11
process			process	
ref YP_003273.1 YP_003273.1 stroheme synthetase	ref YP_001728.1 YP_001728.1	hypothetical protein LIC11776	metabolic	11
process			process	
ref YP_000578.1 YP_003271.1 YP_003271.1 YP_003271.1 YP_003271.1 YP_002916.1 YP_002916.1 YP_002916.1 YP_002916.1 YP_000799.1 YP_00098.1 YP_00099.5 YP_00098.1 YP_00098.1 YP_00098.1 YP_00098.1 YP_00098.1 YP_00098.1 YP_00098.1 YP_00098.1 YP_00098.1 YP_00098.1 YP_000095.1 YP_00098.1 YP_00089.1 YP_0	ref YP_003273.1 YP_003273.1	siroheme synthetase	metabolic	11
process			process	
process	ref YP_000578.1 YP_000578.1	2-dehydropantoate 2-reductase	metabolic	8
Process	. – . –		process	
Process	reflyP 003271.1lyP 003271.1	putative strictosidine synthase		8
ref YP_0002916.1 YP_000789.1 cytochrome c-type biogenesis precursor metabolic process metabolic pro		, , , , , , , , , , , , , , , , , , , ,		
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ref YP_000094.1 YP_000094.1 2'-5' RNA ligase	ref YP_000198.1 YP_000198.1	SCO1/SenC family protein		8
ref YP_001567.1 YP_001567.1 3-octaprenyl-4-hydroxybenzoate metabolic process carboxylase achol dehydrogenase metabolic process 5			process	
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ref YP_001544.1 YP_001544.1 tautomerase metabolic	ref YP_002521.1 YP_002521.1	adenylate/guanylate cyclase permease of the major facilitator	process metabolic process metabolic	
ref YP_001544.1 YP_001544.1 tautomerase metabolic	ref YP_002521.1 YP_002521.1 ref YP_003118.1 YP_003118.1	adenylate/guanylate cyclase permease of the major facilitator superfamily	process metabolic process metabolic process	
	ref YP_002521.1 YP_002521.1 ref YP_003118.1 YP_003118.1	adenylate/guanylate cyclase permease of the major facilitator superfamily	process metabolic process metabolic process metabolic	
process	ref YP_002521.1 YP_002521.1 ref YP_003118.1 YP_003118.1 ref YP_000186.1 YP_000186.1	adenylate/guanylate cyclase permease of the major facilitator superfamily	process metabolic process metabolic process metabolic process metabolic process	
	ref YP_002521.1 YP_002521.1 ref YP_003118.1 YP_003118.1 ref YP_000186.1 YP_000186.1	adenylate/guanylate cyclase permease of the major facilitator superfamily photoproduct lyase	process metabolic process metabolic process metabolic process metabolic process	
ref YP_001568.1 YP_001568.1 4-hydroxybenzoate octaprenyltransferase metabolic	ref YP_002521.1 YP_002521.1 ref YP_003118.1 YP_003118.1 ref YP_000186.1 YP_000186.1	adenylate/guanylate cyclase permease of the major facilitator superfamily photoproduct lyase	process metabolic process metabolic process metabolic process metabolic process metabolic	

		process			
ref YP_000511.1 YP_000511.1	arsenate reductase	metabolic			
		process			
ref YP_003132.1 YP_003132.1	glycerol-3-phosphate Pi antiporter	metabolic			
		process			
ref YP_003106.1 YP_003106.1	hemolysin/sphingomyelinase-like	metabolic			
		process			
ref YP_002956.1 YP_002956.1	hypothetical protein LIC13044	metabolic			
ref YP_003409.1 YP_003409.1	protoporphyrinogen oxidase	process			
Ter TP_003409.1 TP_003409.1	protoporphyrmogen oxidase	metabolic process			
ref YP_001375.1 YP_001375.1	coproporphyrinogen III oxidase	metabolic			
101711 _001373.1711 _001373.1	coproporphyrmogen in oxiduse	process			
ref YP_003263.1 YP_003263.1	phosphoglycerate mutase	metabolic			
		process			
ref YP_003280.1 YP_003280.1	FAD-dependent oxiredutase	metabolic			
		process			
ref YP_000071.1 YP_000071.1	hypothetical protein LIC10071	metabolic			
-		process			
ref YP_003400.1 YP_003400.1	glutamyl-tRNA reductase	metabolic			
		process			
ref YP_003406.1 YP_003406.1	uroporphyrinogen decarboxylase	metabolic			
ref YP_003046.1 YP_003046.1	UDP-N-acetylenolpyruvoylglucosamine	process metabolic			+
161 17_003046.1 17_003046.1	reductase	process			
ref YP 001809.1 YP 001809.1	3-hydroxyisobutyrate dehydrogenase	metabolic			
101711 _001003.1711 _001003.1	5 Hydroxylsobacyrace dellydrogenase	process			
ref YP_000196.1 YP_000196.1	cytochrome oxidase assembly protein	metabolic			
	, , , , , , , , , , , , , , , , , , , ,	process			
ref YP_001687.1 YP_001687.1	2-dehydropantoate 2-reductase	metabolic			
		process			
ref YP_002254.1 YP_002254.1	3-oxoacyl-acyl-carrier protein] reductase	metabolic			
		process			
ref YP_003614.1 YP_003614.1	3-oxoacyl-acyl-carrier protein] reductase	metabolic			
		process			
ref YP_003486.1 YP_003486.1	adenylate/guanylate cyclase	metabolic			
ref YP_002917.1 YP_002917.1	adenylate/guanylate cyclase	process metabolic			
161 17_002317.1 17_002317.1	adenylate/guanylate cyclase	process			
ref YP_002984.1 YP_002984.1	adenylate/guanylate cyclase	metabolic			
		process			
ref YP_000236.1 YP_000236.1	adenylate/guanylate cyclase	metabolic			
		process			
ref YP_002592.1 YP_002592.1	adenylate/guanylate cyclase	metabolic			
		process			
ref YP_003467.1 YP_003467.1	adenylate/guanylate cyclase	metabolic			
		process			
ref YP_003117.1 YP_003117.1	bacterioferritin-associated ferredoxin	metabolic			
ref YP 001563.1 YP 001563.1	dihydrolipoamide acetyltransferase	process metabolic			
161 17_001303.1 17_001303.1	diffydrolipoarfiide acetyltrafisferase	process			
ref YP_001010.1 YP_001010.1	hemolysin	metabolic			
161711 _001010.1711 _001010.1	Tiernotysiii	process			
ref YP_000274.1 YP_000274.1	hemolysin A	metabolic			
. – –		process			
ref YP_001407.1 YP_001407.1	hydroxypyruvate reductase	metabolic			
		process			
ref YP_000632.1 YP_000632.1	hypothetical protein LIC10648	metabolic			
		process			1
ref YP_002826.1 YP_002826.1	hypothetical protein LIC12910	metabolic			
		process	1		
ref YP_002323.1 YP_002323.1	oxidoreductase	metabolic			
ref YP_003519.1 YP_003519.1	precorrin methylase	process metabolic	 		1
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		process			
ref YP_003463.1 YP_003463.1	putative FAD-dependent dehydrogenase	metabolic			
		process			
ref YP_001115.1 YP_001115.1	short chain dehydrogenase	metabolic			
	, ,	process			
ref YP_000974.1 YP_000974.1	short-chain dehydrogenase	metabolic			
. – –		process			
ref YP_000031.1 YP_000031.1	beta-galactosidase	metabolic			
		process			
ref YP_001390.1 YP_001390.1	capsule biosynthesis protein	metabolic			
		process			
ref YP_001389.1 YP_001389.1	capsule biosynthesis protein	metabolic			
		process			
sp Q75FR2 COBD_LEPIC	Cobalamin biosynthesis protein cobD	metabolic			
		process			
sp Q72M34 COBS_LEPIC	Cobalamin synthase (EC 2)	metabolic			
		process			
ref YP_001169.1 YP_001169.1	cyclic nucleotide binding patatin-like	metabolic			
	phospholipase	process			
ref YP_000195.1 YP_000195.1	cytochrome C oxidase assembly protein	metabolic			
		process			1
ref YP_000946.1 YP_000946.1	cytochrome c peroxidase	metabolic			
		process			1
ref YP_000336.1 YP_000336.1	esterase	metabolic			
		process			
ref YP_002754.1 YP_002754.1	hypothetical protein LIC12838	metabolic			
Clare and a clare and a		process			
ref YP_002149.1 YP_002149.1	putative cytochrome oxidase assembly	metabolic			
Slyp 0040244 lyp 0040244	factor	process			
ref YP_001824.1 YP_001824.1	putative hydrolase	metabolic			
flyp_004024.4 lyp_004024.4	and the line and the	process	F276	4000	4727
ref YP_001834.1 YP_001834.1	putative lipoprotein	no_GO	5276	4808	1727
ref YP_002221.1 YP_002221.1	putative lipoprotein	no_GO	5168	3544	292
ref YP_001318.1 YP_001318.1	S-adenosylmethionine synthetase	no_GO	4492	3211	1494
ref YP_000009.1 YP_000009.1	putative lipoprotein	no_GO	1420	2434	292
ref YP_000856.1 YP_000856.1	putative lipoprotein	no_GO	1415	1606	57
ref YP_001783.1 YP_001783.1	putative lipoprotein	no_GO	1569	1010	249
ref YP_000902.1 YP_000902.1	putative lipoprotein	no_GO	870	967	375
ref YP_002468.1 YP_002468.1 ref YP_002971.1 YP_002971.1	YajC	no_GO	447	723	44
_ ' ' _	putative lipoprotein UPF0234 protein LA 3406	no_GO	556	<u> </u>	110
sp Q8F0T5 Y3406_LEPIN ref YP 000291.1 YP 000291.1	<u> </u>	no_GO	710 425	662	203
	putative lipoprotein	no_GO	585	619	92
ref YP_003157.1 YP_003157.1	apolipoprotein n-acyltransferase	no_GO	_	584	
ref YP_001265.1 YP_001265.1	putative lipoprotein	no_GO	677	571 529	5
ref YP_000491.1 YP_000491.1					34
ref YP_001692.1 YP_001692.1	putative lipoprotein	no_GO	515	<u> </u>	
ref YP_001028.1 YP_001028.1	PmbA	no_GO	515 419	447	363
ref YP_000531.1 YP_000531.1	PmbA putative lipoprotein	no_GO no_GO	419	447 383	363
	PmbA putative lipoprotein putative lipoprotein	no_GO no_GO no_GO	419 582	447 383 369	363 37
ref YP_003246.1 YP_003246.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein	no_GO no_GO no_GO no_GO	419	447 383 369 351	363 37 24
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein	no_GO no_GO no_GO no_GO no_GO	582 175	447 383 369 351 234	363 37 24 8
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD	no_GO no_GO no_GO no_GO no_GO no_GO	582 175	447 383 369 351 234 217	363 37 24 8 166
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein	no_GO no_GO no_GO no_GO no_GO no_GO no_GO	582 175 244 173	447 383 369 351 234	363 37 24 8 166 30
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_000054.1 YP_000054.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein	no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_000054.1 YP_000054.1 ref YP_000697.1 YP_000697.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein	no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO	582 175 244 173	447 383 369 351 234 217	363 37 24 8 166 30 44 129
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_00054.1 YP_00054.1 ref YP_000697.1 YP_000697.1 ref YP_000301.1 YP_000301.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein glycine cleavage T protein	no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44 129 304
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_00054.1 YP_00054.1 ref YP_000697.1 YP_000697.1 ref YP_000301.1 YP_000301.1 ref YP_001018.1 YP_001018.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein glycine cleavage T protein molybdate metabolism regulator	no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44 129 304 230
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_00054.1 YP_00054.1 ref YP_000697.1 YP_000697.1 ref YP_000301.1 YP_000301.1 ref YP_001018.1 YP_001018.1 ref YP_000532.1 YP_000532.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein glycine cleavage T protein molybdate metabolism regulator uracil-DNA glycosylase	no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44 129 304 230 230
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_00054.1 YP_00054.1 ref YP_000697.1 YP_000697.1 ref YP_000301.1 YP_000301.1 ref YP_001018.1 YP_001018.1 ref YP_000532.1 YP_000532.1 ref YP_002223.1 YP_002223.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein glycine cleavage T protein molybdate metabolism regulator uracil-DNA glycosylase putative lipoprotein	no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44 129 304 230 230 57
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_00054.1 YP_00054.1 ref YP_000697.1 YP_000697.1 ref YP_000301.1 YP_000301.1 ref YP_001018.1 YP_001018.1 ref YP_000532.1 YP_000532.1 ref YP_002223.1 YP_002223.1 sp Q72NZ6 Y2681_LEPIC	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein glycine cleavage T protein molybdate metabolism regulator uracil-DNA glycosylase putative lipoprotein UPF0345 protein LIC_12681	no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44 129 304 230 230 57 50
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_00054.1 YP_00054.1 ref YP_000697.1 YP_000697.1 ref YP_000301.1 YP_000301.1 ref YP_001018.1 YP_001018.1 ref YP_001018.1 YP_000532.1 ref YP_002223.1 YP_002223.1 sp Q72NZ6 Y2681_LEPIC ref YP_002421.1 YP_002421.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein glycine cleavage T protein molybdate metabolism regulator uracil-DNA glycosylase putative lipoprotein UPF0345 protein LIC_12681 putative lipoprotein	no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44 129 304 230 230 57 50 47
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_00054.1 YP_00054.1 ref YP_000697.1 YP_000697.1 ref YP_000301.1 YP_000301.1 ref YP_001018.1 YP_001018.1 ref YP_001018.1 YP_000532.1 ref YP_002223.1 YP_002223.1 sp Q72NZ6 Y2681_LEPIC ref YP_003494.1 YP_003494.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein glycine cleavage T protein molybdate metabolism regulator uracil-DNA glycosylase putative lipoprotein UPF0345 protein LIC_12681 putative lipoprotein pheromone shutdown protein	no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44 129 304 230 230 57 50 47 30
ref YP_003246.1 YP_003246.1 ref YP_000242.1 YP_000242.1 ref YP_001693.1 YP_001693.1 ref YP_002811.1 YP_002811.1 ref YP_00054.1 YP_00054.1 ref YP_000697.1 YP_000697.1 ref YP_000301.1 YP_000301.1 ref YP_001018.1 YP_001018.1 ref YP_000532.1 YP_000532.1 ref YP_002223.1 YP_002223.1 sp Q72NZ6 Y2681_LEPIC ref YP_002421.1 YP_002421.1	PmbA putative lipoprotein putative lipoprotein putative lipoprotein Rad50-like protein TldD putative lipoprotein putative lipoprotein putative lipoprotein putative lipoprotein glycine cleavage T protein molybdate metabolism regulator uracil-DNA glycosylase putative lipoprotein UPF0345 protein LIC_12681 putative lipoprotein	no_GO no_GO	419 582 175 244 173 701	447 383 369 351 234 217	363 37 24 8 166 30 44 129 304 230 230 57 50 47

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ref YP_001892.1 YP_001892.1	putative lipoprotein	no_GO	14
ref YP_001663.1 YP_001663.1	putative lipoprotein	no_GO	11
ref YP_000774.1 YP_000774.1	putative lipoprotein	no_GO	11
ref YP_001851.1 YP_001851.1	putative lipoprotein	no_GO	8
ref YP_001940.1 YP_001940.1	succinate dehydrogenase cytochrome B subunit	no_GO	5
ref YP 001705.1 YP 001705.1	exopolysaccharide production protein	no GO	
ref YP_000895.1 YP_000895.1	putative lipoprotein	no_GO	
ref YP_003531.1 YP_003531.1	putative permease	no_GO	
ref YP_000007.1 YP_000007.1	nifR3-like protein	no GO	
ref YP_002863.1 YP_002863.1	shikimate 5-dehydrogenase	no_GO	132
ref YP 002992.1 YP 002992.1	pirin-like protein	no_GO	85
ref YP_002292.1 YP_002292.1	pirin-like protein	no GO	71
ref YP_002939.1 YP_002939.1	ThiJ/PfpI family protein	no GO	61
ref YP 002744.1 YP 002744.1	soluble lytic transglycosylase	no GO	57
ref YP_001092.1 YP_001092.1	putative lipoprotein	no GO	47
ref YP_002978.1 YP_002978.1	putative lipoprotein	no GO	47
ref YP_000131.1 YP_000131.1	SET domain-containing protein	no GO	47
sp Q72SJ7 Y1384 LEPIC	UPF0296 protein LIC_11384	no GO	44
ref YP_001231.1 YP_001231.1	RodA	no_GO	40
ref YP_001104.1 YP_001104.1	histone deacetylase	no GO	37
ref YP_002188.1 YP_002188.1	putative lipoprotein	no GO	37
ref YP 003059.1 YP 003059.1	putative lipoprotein	no_GO	37
ref YP_001246.1 YP_001246.1	putative ipoprotein putative acetyl-coa carboxylase/pyruvate	no_GO	34
	carboxylase	_	34
ref YP_000970.1 YP_000970.1	putative diguanylate phosphodiesterase	no_GO	30
sp Q8CXS1 Y3128_LEPIN	UPF0176 protein LA_3128 - Leptospira interrogans	no_GO	27
ref YP 002048.1 YP 002048.1	putative lipoprotein	no GO	24
sp Q72LS6 Y3475 LEPIC	UPF0133 protein LIC 13475	no_GO	24
ref YP 001759.1 YP 001759.1	BolA-like protein	no GO	24
ref YP 001216.1 YP 001216.1	cGMP-specific phosphodiesterase	no GO	21
ref YP_003243.1 YP_003243.1	putative lipoprotein	no GO	21
ref YP 000910.1 YP 000910.1	fruiting body developmental protein	no GO	17
ref YP 000284.1 YP 000284.1	GlcG	no_GO	14
ref YP_002511.1 YP_002511.1	putative lipoprotein	no GO	14
ref YP 000275.1 YP 000275.1	putativeacetyltransferase	no GO	14
ref YP 003045.1 YP 003045.1	cGMP-specific phosphodiesterase	no GO	8
ref YP_001137.1 YP_001137.1	putative lipoprotein	no_GO	8
ref YP 002143.1 YP 002143.1	putative lipoprotein	no_GO	8
ref YP 002747.1 YP 002747.1	SAM dependent methyltransferase	no GO	8
ref YP_000268.1 YP_000268.1	thioredoxin-like protein	no GO	8
ref YP_003504.1 YP_003504.1	periplasmic protein, LipL45 homologue	no GO	5
ref YP_001526.1 YP_001526.1	putative lipoprotein	no GO	5
ref YP 001725.1 YP 001725.1	N-(5'-phosphoribosyl)anthranilate	no_GO	5
	isomerase	_	
ref YP_000358.1 YP_000358.1	putative lipoprotein	no_GO	5
ref YP_001550.1 YP_001550.1	conserved putative permease protein	no_GO	
ref YP_003186.1 YP_003186.1	putative acetyl CoA acetyltransferase	no_GO	
ref YP_002589.1 YP_002589.1	putative lipoprotein	no_GO	
ref YP_002701.1 YP_002701.1	putative lipoprotein	no_GO	
sp Q72NX1 Y2707_LEPIC	UPF0090 protein LIC_12707	no_GO	
sp Q72M93 Y3295_LEPIC	UPF0189 protein LIC_13295	no_GO	
ref YP_001616.1 YP_001616.1	putative lipoprotein	no_GO	
ref YP_001829.1 YP_001829.1	putative lipoprotein	no_GO	
ref YP_003123.1 YP_003123.1	putative lipoprotein	no_GO	
ref YP_000938.1 YP_000938.1	TonB-dependent outer membrane hemin	no_GO	
this coares the coares	receptor		
ref YP_003166.1 YP_003166.1	putative lipoprotein	no_GO	
ref YP_001162.1 YP_001162.1	Chpl	no_GO	
ref YP_001454.1 YP_001454.1	GldG	no_GO	
ref YP_000492.1 YP_000492.1	putative lipoprotein	no_GO	
ref YP 000909.1 YP 000909.1	fruiting body developmental protein	no_GO	

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ref YP_000493.1 YP_000493.1	putative lipoprotein	no_GO			
ref YP_001122.1 YP_001122.1	pseudouridylate synthase, 23S RNA-	no_GO			
	specific				
ref YP_002582.1 YP_002582.1	putative virulence-associated protein	no_GO			
ref YP_002987.1 YP_002987.1	putative lipoprotein	no_GO			
ref YP_000984.1 YP_000984.1	guanosine polyphosphate	no_GO			
	pyrophosphohydrolase/synthetase				
ref YP_000021.1 YP_000021.1	putative lipoprotein	no_GO			
ref YP_002038.1 YP_002038.1	RecO	no_GO			
ref YP_001948.1 YP_001948.1	1-aminocyclopropane-1-carboxylate	no_GO			
	deaminase				
ref YP_001572.1 YP_001572.1	A/G specific adenine glycosylase	no_GO			
ref YP_001087.1 YP_001087.1	alpha-glucosidase	no_GO			
ref YP_000904.1 YP_000904.1	anticodon nuclease	no_GO			
sp Q72PB6 LNT1_LEPIC	Apolipoprotein N-acyltransferase 1 (EC	no_GO			
	2.3.1) (ALP N-acyltransferase 1)				
ref YP_002874.1 YP_002874.1	ATP-dependent DNA helicase	no_GO			
ref YP_002599.1 YP_002599.1	ATP-dependent DNA ligase	no_GO			
ref YP_001496.1 YP_001496.1	ATP-dependent protease-like La	no_GO			
ref YP_003433.1 YP_003433.1	BatB	no_GO			
ref YP_001757.1 YP_001757.1	BolA-like protein	no_GO			
ref YP_001329.1 YP_001329.1	C-5 sterol desaturase	no_GO			
ref YP_002296.1 YP_002296.1	CagA	no_GO			
sp Q72MJ6 CSRA_LEPIC	Carbon storage regulator homolog	no_GO			
ref YP_000261.1 YP_000261.1	cell wall hydrolase	no_GO			
ref YP_002946.1 YP_002946.1	chitinase	no_GO			
ref YP_001094.1 YP_001094.1	chloride channel	no_GO			
ref YP_001163.1 YP_001163.1	ChpK	no_GO			
ref YP_002963.1 YP_002963.1	ComFC-like protein	no_GO			
ref YP_002319.1 YP_002319.1	conserved putative permease protein	no_GO			
ref YP_003516.1 YP_003516.1	corrinoid ATP adenosyltransferase	no_GO			
ref YP_003417.1 YP_003417.1	cyclic nucleotide binding protein	no_GO			
ref YP_001263.1 YP_001263.1	cyclopropane-fatty-acyl-phospholipid synthase/methyltransferase	no_GO			
ref YP_003374.1 YP_003374.1	cytidine deaminase	no_GO			
ref YP_003444.1 YP_003444.1	fatty acid desaturase	no_GO			
ref YP_002965.1 YP_002965.1	fatty acid desaturase	no_GO			
ref YP_001244.1 YP_001244.1	fatty acyltransferase	no_GO			
ref YP_001309.1 YP_001309.1	ferrichrome-iron receptor	no_GO			
ref YP_003410.1 YP_003410.1	ferrochelatase	no_GO			
sp Q72SI0 FEOB_LEPIC	Ferrous iron transport protein B -	no_GO			
ref YP_003568.1 YP_003568.1	FimH-like protein	no_GO			
ref YP_002602.1 YP_002602.1	FimH-like protein	no_GO			
ref YP_001291.1 YP_001291.1	flagella basal body P-ring formation protein precursor	no_GO			
ref YP_002884.1 YP_002884.1	FtsQ	no_GO			
ref YP_002120.1 YP_002120.1	fucose synthetase	no_GO			
ref YP_001455.1 YP_001455.1	GldF	no_GO			
ref YP_003389.1 YP_003389.1	glucose inhibited division protein B	no_GO			
ref YP_000572.1 YP_000572.1	glutamine amidotransferase	no_GO			
ref YP_000706.1 YP_000706.1	glycerol uptake facilitator protein	no_GO			
ref YP_001382.1 YP_001382.1	GNAT family N-acetyltransferase	no_GO			
sp Q72PQ1 ENGA_LEPIC	GTP-binding protein engA	no_GO			
ref YP_001617.1 YP_001617.1	HNH endonuclease family	no_GO			
ref YP_002847.1 YP_002847.1	HNH endonuclease family	no_GO			
sp Q72U18 ACPS_LEPIC	Holo-acyl-carrier-protein] synthase (EC	no_GO			
, = -	2.7.8.7) (Holo-ACP synthase) (4'-	_			
	phosphopantetheinyl transf				
ref YP_002678.1 YP_002678.1	Hsa	no_GO			
ref YP_000537.1 YP_000537.1	hydrolase	no_GO			
ref YP_000333.1 YP_000333.1	integrase/recombinase	no_GO			
ref YP_003415.1 YP_003415.1	intercellular adhesion protein C	no_GO			
ref YP_001464.1 YP_001464.1	iron-sulfur cluster-binding protein	no_GO			

sp Q72W44 LFTR_LEPIC	Leucyl/phenylalanyl-tRNAprotein	no_GO	
	transferase (EC 2.3.2.6) (L/F-transferase) (Leucyltransferase) (Ph		
ref YP_003545.1 YP_003545.1	lipoprotein	no_GO	
ref YP_003567.1 YP_003567.1	lipoprotein	no_GO	
sp Q72PS8 LSPA_LEPIC	Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal peptidase) (Signal peptidase II)	no_GO	
ref YP_001706.1 YP_001706.1	lipoprotein with phospholipase D domain	no_GO	
sp Q72QP1 LIPB_LEPIC	Lipoyltransferase (EC 2.3.1) (Lipoyl-	no_GO	
ref YP_003466.1 YP_003466.1	long-chain-fatty-acidCoA ligase	no_GO	
ref YP_001038.1 YP_001038.1	lysozyme precursor	no_GO	
sp Q72WC1 Y016_LEPIC	Maf-like protein LIC_10016	no_GO	
ref YP_003142.1 YP_003142.1	malate permease	no_GO	
sp Q75FL1 UBIE_LEPIC	Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1)	no_GO	
ref YP_003159.1 YP_003159.1	methylamine utilization ferredoxin-type protein	no_GO	
ref YP_000666.1 YP_000666.1	methylamine utilization protein/Cytochrome c peroxidase	no_GO	
ref YP_003299.1 YP_003299.1	monooxygenase	no_GO	
ref YP_001229.1 YP_001229.1	MreD	no_GO	
ref YP_000248.1 YP_000248.1	MutT/nudix family protein	no_GO	
ref YP_002201.1 YP_002201.1	Na+/H+ antiporter	no_GO	
ref YP_002632.1 YP_002632.1	N-acetylglutamate synthase/acetyltransferase	no_GO	
ref YP_003077.1 YP_003077.1	NorM	no_GO	
ref YP_001135.1 YP_001135.1	nucleotidyltransferase domain protein	no_GO	
ref YP_002867.1 YP_002867.1	oligopeptide ABC transport system permease protein	no_GO	
ref YP_002293.1 YP_002293.1	permease	no_GO	
ref YP_000956.1 YP_000956.1	permease of the drug/metabolite	no_GO	
ref YP_003596.1 YP_003596.1	transporter superfamily permease of the major facilitator	no_GO	
	superfamily		
ref YP_001131.1 YP_001131.1 ref YP_000673.1 YP_000673.1	phenazine biosynthesis-like protein phosphate transport system protein	no_GO no_GO	
ref YP_001077.1 YP_001077.1	phosphatidylglycerophosphatase B	no_GO	
ref YP_001853.1 YP_001853.1	phosphatidylglycerophosphate synthase related protein	no_GO	
ref YP 002235.1 YP 002235.1	phosphatidylserine synthase	no_GO	
ref YP_003510.1 YP_003510.1	phosphoglycerate mutase	no GO	
ref YP_001364.1 YP_001364.1	phosphoglycerol transferase related protein	no_GO	
ref YP 000143.1 YP 000143.1	polyketide synthase	no GO	
ref YP_002069.1 YP_002069.1	polysaccharide biosynthesis export protein	no_GO	
ref YP_003520.1 YP_003520.1	precorrin-2 C-20 methlytransferase	no_GO	
ref YP_003517.1 YP_003517.1	precorrin-4-methylase	no_GO	
ref YP_003521.1 YP_003521.1	precorrin-6y methylase	no_GO	
ref YP_002354.1 YP_002354.1	prepilin leader peptidase	no_GO	
sp Q72V65 SPEE1_LEPIC	Probable spermidine synthase 1 (EC 2.5.1.16) (Putrescine aminopropyltransferase 1) (SPDSY 1)	no_GO	
sp Q72V37 CRCB_LEPIC	Protein crcB homolog	no_GO	
ref YP_002477.1 YP_002477.1	protein-L-isoaspartate O-methyltransferase	no_GO	
ref YP_000642.1 YP_000642.1	proton antiporter efflux pump	no_GO	
ref YP_000059.1 YP_000059.1	proton antiporter emax pump proton glutamate symport protein	no_GO	
ref YP_000279.1 YP_000279.1	proton-translocating transhydrogenase	no_GO	
-	subunit alpha 2		
ref YP_001605.1 YP_001605.1	pseudouridylate synthase	no_GO	
sp P62642 CHEB2_LEPIC	Putative chemotaxis protein-glutamate methylesterase (EC 3.1.1.61)	no_GO	

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sp P61986 CBID_LEPIC	Putative cobalt-precorrin-6A synthase	no_GO			
ref YP_000668.1 YP_000668.1	putative cytochrome c	no_GO			
ref YP_001867.1 YP_001867.1	putative diguanylate phosphodiesterase	no_GO			
ref YP_003029.1 YP_003029.1	putative diguanylate phosphodiesterase	no_GO			
ref YP_003498.1 YP_003498.1	putative diguanylate phosphodiesterase	no_GO			
ref YP_001156.1 YP_001156.1	putative flagellar protein	no_GO			
ref YP_003087.1 YP_003087.1	putative globin	no_GO			
ref YP_001557.1 YP_001557.1	putative integrase/recombinase protein	no_GO			
ref YP_000018.1 YP_000018.1	putative lipoprotein	no_GO			
ref YP_000251.1 YP_000251.1	putative lipoprotein	no_GO			
ref YP_000363.1 YP_000363.1	putative lipoprotein	no_GO			
ref YP_000445.1 YP_000445.1	putative lipoprotein	no_GO			
ref YP_000447.1 YP_000447.1	putative lipoprotein	no_GO			
ref YP_000478.1 YP_000478.1	putative lipoprotein	no_GO			
ref YP_000546.1 YP_000546.1	putative lipoprotein	no_GO			
ref YP_000688.1 YP_000688.1	putative lipoprotein	no GO			
ref YP 000712.1 YP 000712.1	putative lipoprotein	no GO			
ref YP 000716.1 YP 000716.1	putative lipoprotein	no_GO			
ref YP_000803.1 YP_000803.1	putative lipoprotein	no GO	İ		
ref YP 000991.1 YP 000991.1	putative lipoprotein	no GO	İ		
ref YP 001043.1 YP 001043.1	putative lipoprotein	no_GO	1		
ref YP 001057.1 YP 001057.1	putative lipoprotein	no_GO	1		
ref YP 001060.1 YP 001060.1	putative lipoprotein	no GO	1		
ref YP 001114.1 YP 001114.1	putative lipoprotein	no_GO			
ref YP_001154.1 YP_001154.1	putative lipoprotein	no GO	 	<u> </u>	
ref YP 001324.1 YP 001324.1	putative lipoprotein	no GO			
ref YP 001478.1 YP 001478.1	putative lipoprotein	no GO			
ref YP_001675.1 YP_001675.1	putative lipoprotein	no GO			
ref YP_001836.1 YP_001836.1	putative lipoprotein	no GO			
ref YP 001862.1 YP 001862.1	putative lipoprotein	no GO			
· - · -	1				
ref YP_002222.1 YP_002222.1	putative lipoprotein	no_GO			
ref YP_002656.1 YP_002656.1	putative lipoprotein	no_GO			
ref YP_002796.1 YP_002796.1	putative lipoprotein	no_GO			
ref YP_002808.1 YP_002808.1	putative lipoprotein	no_GO			
ref YP_002822.1 YP_002822.1	putative lipoprotein	no_GO			
ref YP_002878.1 YP_002878.1	putative lipoprotein	no_GO			
ref YP_002924.1 YP_002924.1	putative lipoprotein	no_GO			
ref YP_002948.1 YP_002948.1	putative lipoprotein	no_GO			
ref YP_002988.1 YP_002988.1	putative lipoprotein	no_GO			
ref YP_003162.1 YP_003162.1	putative lipoprotein	no_GO			
ref YP_003163.1 YP_003163.1	putative lipoprotein	no_GO			
ref YP_003210.1 YP_003210.1	putative lipoprotein	no_GO	ļ		
ref YP_003260.1 YP_003260.1	putative lipoprotein	no_GO	ļ		
ref YP_003314.1 YP_003314.1	putative lipoprotein	no_GO	ļ		
ref YP_003350.1 YP_003350.1	putative lipoprotein	no_GO	ļ		
ref YP_003363.1 YP_003363.1	putative lipoprotein	no_GO	ļ		
ref YP_003364.1 YP_003364.1	putative lipoprotein	no_GO			
ref YP_000482.1 YP_000482.1	putative lipoprotein	no_GO			
ref YP_000297.1 YP_000297.1	putative lipoprotein	no_GO	ļ	1	
ref YP_002998.1 YP_002998.1	putative lipoprotein	no_GO			
ref YP_000354.1 YP_000354.1	putative lipoprotein	no_GO			
ref YP_000754.1 YP_000754.1	putative lipoprotein	no_GO			
ref YP_000088.1 YP_000088.1	putative lipoprotein	no_GO			
ref YP_000670.1 YP_000670.1	putative lipoprotein	no_GO			
ref YP_000807.1 YP_000807.1	putative lipoprotein	no_GO			
ref YP_001000.1 YP_001000.1	putative lipoprotein	no_GO			
ref YP_002611.1 YP_002611.1	putative lipoprotein	no_GO			
ref YP_000359.1 YP_000359.1	putative lipoprotein	no_GO			
ref YP_001177.1 YP_001177.1	putative lipoprotein	no_GO			
ref YP_000485.1 YP_000485.1	putative lipoprotein	no_GO			
ref YP_000629.1 YP_000629.1	putative lipoprotein	no_GO			
ref YP_002249.1 YP_002249.1	putative lipoprotein	no GO			
ref YP 001199.1 YP 001199.1	putative lipoprotein	no GO			
	1	,	1	1	l

ref YP_001223.1 YP_001223.1	putative lipoprotein	no GO	T		
ref YP 003155.1 YP 003155.1	putative lipoprotein	no GO	+		
ref YP_002144.1 YP_002144.1	putative lipoprotein	no GO	+		
ref YP_002919.1 YP_002919.1	putative lipoprotein	no GO	+		
ref YP 000798.1 YP 000798.1	putative lipoprotein	no GO	+		
ref YP 003203.1 YP 003203.1	putative lipoprotein	no GO			
ref YP_002453.1 YP_002453.1	putative lipoprotein	no GO			
ref YP_003092.1 YP_003092.1	putative membrane-bound lytic murein	no_GO	1		
161[11_003032.1[11_003032.1	transglycosylase A transmembrane	110_00			
	protein				
ref YP 002888.1 YP 002888.1	putative phospholipid synthase	no GO			
ref YP_002489.1 YP_002489.1	putative ring hydroxylating dioxygenase	no_GO			
	alpha-subunit				
ref YP_002286.1 YP_002286.1	putative transcriptional regulator	no GO			
ref YP 001428.1 YP 001428.1	regulator of chromosome condensation	no GO			
ref YP_001149.1 YP_001149.1	rhodanese-related thiosulfate	no_GO			
	sulfurtransferase				
ref YP_002748.1 YP_002748.1	rRNA methylase	no_GO			
ref YP_001136.1 YP_001136.1	SAM-dependent methyltransferase	no_GO			
ref YP_000547.1 YP_000547.1	SenC	no_GO			
ref YP_003089.1 YP_003089.1	SET domain-containing protein	no_GO			
ref YP_003491.1 YP_003491.1	shikimate kinase	no_GO			
sp Q72UU3 SSB_LEPIC	Single-stranded DNA-binding protein (SSB)	no_GO			
	(Helix-destabilizing protein)	_			
ref YP_000951.1 YP_000951.1	sodium bile acid symporter family	no_GO			
ref YP_002316.1 YP_002316.1	sodium bile acid symporter family protein	no_GO			
ref YP_001739.1 YP_001739.1	sodium:solute symporter	no_GO			
ref YP_003579.1 YP_003579.1	sodium:solute symporter family	no_GO			
ref YP_003632.1 YP_003632.1	soluble lytic murein transglycosylase	no_GO			
sp Q72PQ0 SSRP_LEPIC	SsrA-binding protein	no_GO			
ref YP_000990.1 YP_000990.1	sterol desaturase	no_GO			
ref YP_002268.1 YP_002268.1	sterol desaturase-related protein	no_GO			
ref YP_001913.1 YP_001913.1	tetracycline resistance protein	no_GO			
ref YP_000699.1 YP_000699.1	thermolysin	no_GO			
ref YP_003226.1 YP_003226.1	thermolysin homolog precursor	no_GO			
ref YP_003227.1 YP_003227.1	thermolysin precursor	no_GO			
ref YP_003225.1 YP_003225.1	thermolysin precursor	no_GO			
ref YP_000866.1 YP_000866.1	TonB	no_GO			
ref YP_000760.1 YP_000760.1	transposase	no_GO			
ref YP_000761.1 YP_000761.1	transposase	no_GO			
ref YP_000935.1 YP_000935.1	transposase	no_GO			
ref YP_000636.1 YP_000636.1	ubiquinone/menaquinone	no_GO			
	methyltransferase	_			
ref YP_002083.1 YP_002083.1	UDP-glucose 4-epimerase	no_GO			
sp P62465 UPPP_LEPIC	Undecaprenyl-diphosphatase (EC 3.6.1.27)	no_GO			
	(Undecaprenyl pyrophosphate				
	phosphatase) (Bacitracin resist				
ref YP_000818.1 YP_000818.1	undecaprenyl-phosphate alpha-N-	no_GO			
	acetylglucosaminyltransferase				
sp Q72QK8 Y2105_LEPIC	UPF0054 protein LIC_12105	no_GO			
sp Q72PQ2 Y2416_LEPIC	UPF0078 membrane protein LIC_12416	no_GO			
sp Q72S23 Y1564_LEPIC	UPF0102 protein LIC_11564	no_GO	1		
sp Q72VY9 Y156_LEPIC	UPF0161 protein LIC_10156	no_GO	1		
sp Q8F5E6 Y1736_LEPIN	UPF0235 protein LA_1736	no_GO			
ref YP_003011.1 YP_003011.1	uracil DNA glycosylase	no_GO			
ref YP_003194.1 YP_003194.1	vancomycin resistance protein	no_GO			
sp P61438 CH60_LEPIC	60 kDa chaperonin (Protein Cpn60) (groEL	nucleotide	17556	15968	14029
	protein) (Heat shock 58 kDa protein)	binding			
ref YP_000349.1 YP_000349.1	electron transfer flavoprotein alpha-	nucleotide	12387	10575	3961
	subunit	binding	1		
sp Q72PK5 CARA_LEPIC	Carbamoyl-phosphate synthase small	nucleotide	3838	7762	351
	chain (EC 6.3.5.5) (Carbamoyl-phosphate	binding	1		
	synthetase glutamine chai	i	1	i i	1

ref YP_001924.1 YP_001924.1	RNA-binding protein	nucleotide binding	8246	4799	1499
ref YP_001227.1 YP_001227.1	MreB	nucleotide binding	2420	3024	1521
sp Q72LY9 ACSA_LEPIC	Acetyl-coenzyme A synthetase (EC 6.2.1.1) (AcetateCoA ligase) (Acyl-activating enzyme)	nucleotide binding	537	2064	284
sp P61436 CH10_LEPIC	10 kDa chaperonin (Protein Cpn10) (groES protein) (Heat shock 10 kDa protein)	nucleotide binding	6358	1943	644
sp P61444 GRPE_LEPIC	Protein grpE (HSP-70 cofactor)	nucleotide binding	1263	1355	383
ref YP_003436.1 YP_003436.1	heat shock protein 90	nucleotide binding	1957	1216	1686
sp P62414 PGK_LEPIC	Phosphoglycerate kinase (EC 2.7.2.3)	nucleotide binding	1148	1101	715
ref YP_000352.1 YP_000352.1	isovaleryl-CoA dehydrogenase	nucleotide binding	596	590	456
sp Q72NF1 CARB_LEPIC	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)	nucleotide binding	716	587	615
ref YP_001889.1 YP_001889.1	translocase	nucleotide binding	787	583	808
sp Q72PA7 PURA_LEPIC	Adenylosuccinate synthetase (EC 6.3.4.4) (IMPaspartate ligase) (AdSS) (AMPSase)	nucleotide binding	546	553	517
ref YP_001372.1 YP_001372.1	acetolactate synthase large subunit	nucleotide binding	395	526	842
ref YP_001431.1 YP_001431.1	thioredoxin reductase	nucleotide binding	607	522	347
ref YP_001751.1 YP_001751.1	glycerol kinase	nucleotide binding	327	467	371
ref YP_001477.1 YP_001477.1	biotin carboxylase subunit of acetyl CoA carboxylase	nucleotide binding	416	457	300
ref YP_003316.1 YP_003316.1	5'-phosphoribosylglycinamide transformylase	nucleotide binding	312	290	308
ref YP_000592.1 YP_000592.1	ATP-dependent protease La	nucleotide binding	190	269	207
sp Q72PR5 PURL_LEPIC	Phosphoribosylformylglycinamidine synthase II (EC 6.3.5.3) (FGAM synthase II)	nucleotide binding	271	264	707
ref YP_001681.1 YP_001681.1	2,4-dienoyl-coa reductase	nucleotide binding	187	253	595
ref YP_001874.1 YP_001874.1	FAD-binding oxidoreductase	nucleotide binding	171	251	64
ref YP_000720.1 YP_000720.1	ATP-dependent RNA helicase	nucleotide binding	162	249	110
ref YP_001628.1 YP_001628.1	alkylglycerone-phosphate synthase	nucleotide binding	169	248	110
ref YP_003658.1 YP_003658.1	ParA	nucleotide binding	208	244	242
ref YP_001571.1 YP_001571.1	GTP-binding protein	nucleotide binding	247	242	423
ref YP_003138.1 YP_003138.1	ATP-dependent RNA helicase	nucleotide binding	241	230	100
ref YP_000037.1 YP_000037.1	GMC oxidoreductase	nucleotide binding	176	189	439
ref YP_001385.1 YP_001385.1	glycine rich RNA-binding protein	nucleotide binding	368	60	185
ref YP_001762.1 YP_001762.1	hypothetical protein LIC11811	nucleotide binding	181		114
ref YP_001530.1 YP_001530.1	general secretory pathway protein E	nucleotide binding			273
sp P61524 ASSY_LEPIC	Argininosuccinate synthase (EC 6.3.4.5) (Citrullineaspartate ligase)	nucleotide binding			249
ref YP_000702.1 YP_000702.1	hypothetical protein LIC10718	nucleotide binding			226

ref YP_001796.1 YP_001796.1	AAA family ATPase	nucleotide	158
		binding	
sp Q75FU1 ARGB_LEPIC	Acetylglutamate kinase (EC 2.7.2.8) (NAG	nucleotide	143
	kinase) (AGK) (N-acetyl-L-glutamate 5- phosphotransferase) -	binding	
ref YP_002203.1 YP_002203.1	putative glycolate oxidase	nucleotide binding	92
ref YP_002041.1 YP_002041.1	phosphate starvation-inducible protein	nucleotide binding	89
ref YP_002692.1 YP_002692.1	GTP-binding protein	nucleotide binding	37
ref YP_002684.1 YP_002684.1	acetolactate synthase I large subunit	nucleotide binding	24
sp Q72RB7 GUAA_LEPIC	Probable GMP synthase	nucleotide binding	277
ref YP_002709.1 YP_002709.1	hypothetical protein LIC12792	nucleotide binding	188
sp Q72U64 THIM_LEPIC	Hydroxyethylthiazole kinase (EC 2.7.1.50)	nucleotide	166
	(4-methyl-5-beta-hydroxyethylthiazole kinase) (Thz kinase)	binding	
ref YP_001245.1 YP_001245.1	acetyl-CoA carboxylase alpha chain	nucleotide binding	147
sp Q72NP4 MURD_LEPIC	UDP-N-acetylmuramoylalanineD-	nucleotide	100
1 2 2	glutamate ligase (EC 6.3.2.9) (UDP-N-acetylmuramoyl-L-alanyl-D-glutam	binding	
ref YP_002225.1 YP_002225.1	UDP-N-acetylmuramyl pentapeptide synthase	nucleotide binding	96
sp Q72UH8 PUR7_LEPIC	Phosphoribosylaminoimidazole-	nucleotide	89
_	succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	binding	
sp Q72R81 MURE_LEPIC	UDP-N-acetylmuramoylalanyl-D-	nucleotide	71
	glutamate2,6-diaminopimelate ligase (EC 6.3.2.13) (UDP-N-acetylmuramy	binding	
sp Q72V31 PUR2_LEPIC	Phosphoribosylamineglycine ligase (EC	nucleotide	68
	6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Ph	binding	
ref YP_003216.1 YP_003216.1	UDP-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- diaminopimelate ligase	nucleotide binding	57
sp Q72MV4 COAE_LEPIC	Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)	nucleotide binding	54
sp Q72R93 DDL_LEPIC	D-alanineD-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)	nucleotide binding	50
ref YP_001493.1 YP_001493.1	hypothetical protein LIC11534	nucleotide binding	50
ref YP_002386.1 YP_002386.1	5-formyltetrahydrofolate cyclo-ligase	nucleotide binding	37
ref YP_003599.1 YP_003599.1	arginine/ornithine transport system ATPase	nucleotide binding	37
sp Q72W11 ENGB_LEPIC	Probable GTP-binding protein engB	nucleotide binding	37
ref YP_001367.1 YP_001367.1	ubiquinone biosynthesis protein	nucleotide binding	37
ref YP_001045.1 YP_001045.1	NH(3)-dependent NAD(+) synthetase	nucleotide binding	34
ref YP_001812.1 YP_001812.1	UDP-N-acetylmuramate-alanine ligase	nucleotide binding	34
ref YP_000459.1 YP_000459.1	RNA-binding protein	nucleotide binding	27
ref YP_001296.1 YP_001296.1	hypothetical protein LIC11332	nucleotide binding	24
ref YP_001270.1 YP_001270.1	d-alanined-alanine ligase	nucleotide binding	17
sp Q72RG6 BIOD_LEPIC	Dethiobiotin synthetase (EC 6.3.3.3)	nucleotide	14

	(Dethiobiotin synthase) (DTB synthetase) (DTBS)	binding			
ref YP_000613.1 YP_000613.1	glycerol kinase	nucleotide binding			14
ref YP_002647.1 YP_002647.1	acetoin- histone deacetylase family	nucleotide binding			11
ref YP_002864.1 YP_002864.1	dihydrofolate synthase	nucleotide binding			11
ref YP_002227.1 YP_002227.1	phosphoribosylaminoimidazole carboxylase atpase subunit protein	nucleotide binding			2
ref YP_000560.1 YP_000560.1	GTP-binding protein	nucleotide binding			
ref YP_000515.1 YP_000515.1	tetraacyldisaccharide 4'-kinase	nucleotide binding			
ref YP_000912.1 YP_000912.1	ATP-dependent RNA helicase	nucleotide binding			
ref YP_003188.1 YP_003188.1	acyl-CoA dehydrogenase	nucleotide binding			
ref YP_002438.1 YP_002438.1	ATPase	nucleotide binding			
ref YP_003128.1 YP_003128.1	ATP-dependent RNA helicase	nucleotide binding			
ref YP_000630.1 YP_000630.1	hypothetical protein LIC10646	nucleotide binding			
ref YP_001021.1 YP_001021.1	hypothetical protein LIC11051	other cellular process	309	193	132
ref YP_003031.1 YP_003031.1	hypothetical protein LIC13122	other cellular process	253	185	132
ref YP_002598.1 YP_002598.1	hypothetical protein LIC12676	other cellular process			30
ref YP_001528.1 YP_001528.1	hypothetical protein LIC11569	other cellular process			24
ref YP_001068.1 YP_001068.1	hypothetical protein LIC11098	other cellular process			75
ref YP_000891.1 YP_000891.1	octaprenyl diphosphate synthase	other cellular			71
ref YP_002817.1 YP_002817.1	molybdate metabolism regulator	other cellular process			64
sp Q72RC1 GMHA_LEPIC	Phosphoheptose isomerase (EC 5.3.1) (Sedoheptulose 7-phosphate isomerase)	other cellular process			44
ref YP_000616.1 YP_000616.1	hypothetical protein LIC10632	other cellular process			30
ref YP_000805.1 YP_000805.1	hypothetical protein LIC10828	other cellular process			27
ref YP_001615.1 YP_001615.1	hypothetical protein LIC11659	other cellular process			14
ref YP_000246.1 YP_000246.1	hypothetical protein LIC10255	other cellular process			
ref YP_001466.1 YP_001466.1	hypothetical protein LIC11505	other cellular process			
ref YP_002807.1 YP_002807.1	putative lipoprotein	other cellular process			
ref YP_001468.1 YP_001468.1	hypothetical protein LIC11507	other cellular process			
ref YP_002195.1 YP_002195.1	hypothetical protein LIC12260	other cellular process			
ref YP_002440.1 YP_002440.1	hypothetical protein LIC12512	other cellular process			
ref YP_003160.1 YP_003160.1	hypothetical protein LIC13253	other cellular process			
ref YP_000851.1 YP_000851.1	molybdopterin oxidoreductase	other celular process	5611	6382	707
ref YP_001260.1 YP_001260.1	hypothetical protein LIC11294	other celular process	1567	1733	203

ref YP_000850.1 YP_000850.1 hypothetical protein LIC10873 ref YP_003272.1 YP_003272.1 sulfite reductase ref YP_000272.1 YP_000272.1 zinc-binding dehydrogenase family ref YP_003594.1 YP_003594.1 hypothetical protein LIC20205 ref YP_00332.1 YP_00332.1 hypothetical protein LIC13123 ref YP_001942.1 YP_001942.1 succinate dehydrogenase ref YP_001167.1 YP_001167.1 hypothetical protein LIC11197 ref YP_002134.1 YP_002134.1 UDP-glucose 4-epimerase ref YP_000562.1 YP_000562.1 hypothetical protein LIC10578 ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_0002405.1 YP_0002405.1 Pbp1A ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000612.1 YP_000612.1 putative lipoprotein	othe process of the p	ess r ess r ess r ess r ess r ess r ess r ess r ess r ess r ess r ess r ess r ess r ess r ess r ess	celular celular celular celular celular celular celular celular celular celular celular celular celular celular	679 777 530 1026 628 306 393 535 630 302 455 763 241 387 341	844 656 616 584 580 539 508 507 501 478 386 373 371 346 312 305	17 1009 166 203 1318 387 242 762 192 75 484 129 121 545
ref YP_000272.1 YP_000272.1 zinc-binding dehydrogenase family ref YP_003594.1 YP_003594.1 hypothetical protein LIC20205 ref YP_003032.1 YP_003032.1 hypothetical protein LIC13123 ref YP_001942.1 YP_001942.1 succinate dehydrogenase ref YP_001167.1 YP_001167.1 hypothetical protein LIC11197 ref YP_002134.1 YP_002134.1 UDP-glucose 4-epimerase ref YP_000562.1 YP_000562.1 hypothetical protein LIC10578 ref YP_002152.1 YP_002152.1 putative lipoprotein ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_0002405.1 YP_002405.1 Pbp1A ref YP_0002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process of the p	r ess r ess	celular celular celular celular celular celular celular celular celular celular	530 1026 628 306 393 535 630 302 455 763 241 387 341	584 580 539 508 507 501 478 386 373 371 346 312	166 203 1318 387 242 762 192 75 484 129 121
ref YP_003594.1 YP_003594.1 hypothetical protein LIC20205 ref YP_003032.1 YP_003032.1 hypothetical protein LIC13123 ref YP_001942.1 YP_001942.1 succinate dehydrogenase ref YP_001167.1 YP_001167.1 hypothetical protein LIC11197 ref YP_002134.1 YP_002134.1 UDP-glucose 4-epimerase ref YP_000562.1 YP_000562.1 hypothetical protein LIC10578 ref YP_002152.1 YP_002152.1 putative lipoprotein ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_0002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process of the p	r ess r ess	celular celular celular celular celular celular celular celular celular	1026 628 306 393 535 630 302 455 763 241 387	584 580 539 508 507 501 478 386 373 371 346 312	203 1318 387 242 762 192 75 484 129 121
ref YP_003032.1 YP_003032.1 hypothetical protein LIC13123 ref YP_001942.1 YP_001942.1 succinate dehydrogenase ref YP_001167.1 YP_001167.1 hypothetical protein LIC11197 ref YP_002134.1 YP_002134.1 UDP-glucose 4-epimerase ref YP_000562.1 YP_000562.1 hypothetical protein LIC10578 ref YP_002152.1 YP_002152.1 putative lipoprotein ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_00028.1 putative lipoprotein ref YP_000327.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process of the p	r ess r ess	celular celular celular celular celular celular celular celular	628 306 393 535 630 302 455 763 241 387 341	580 539 508 507 501 478 386 373 371 346	1318 387 242 762 192 75 484 129 121
ref YP_001942.1 YP_001942.1 succinate dehydrogenase ref YP_001167.1 YP_001167.1 hypothetical protein LIC11197 ref YP_002134.1 YP_002134.1 UDP-glucose 4-epimerase ref YP_000562.1 YP_000562.1 hypothetical protein LIC10578 ref YP_002152.1 YP_002152.1 putative lipoprotein ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_000327.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process of the p	r ess r ess	celular celular celular celular celular celular celular celular	306 393 535 630 302 455 763 241 387 341	539 508 507 501 478 386 373 371 346 312	387 242 762 192 75 484 129 121
ref YP_001167.1 YP_001167.1 hypothetical protein LIC11197 ref YP_002134.1 YP_002134.1 UDP-glucose 4-epimerase ref YP_000562.1 YP_000562.1 hypothetical protein LIC10578 ref YP_002152.1 YP_002152.1 putative lipoprotein ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_000327.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process of the p	r ess r ess	celular celular celular celular celular celular celular	393 535 630 302 455 763 241 387 341	508 507 501 478 386 373 371 346 312	242 762 192 75 484 129 121
ref YP_002134.1 YP_002134.1 UDP-glucose 4-epimerase ref YP_000562.1 YP_000562.1 hypothetical protein LIC10578 ref YP_002152.1 YP_002152.1 putative lipoprotein ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process other process oth	r ess r ess	celular celular celular celular celular celular	535 630 302 455 763 241 387 341	507 501 478 386 373 371 346 312	762 192 75 484 129 121
ref YP_000562.1 YP_000562.1 hypothetical protein LIC10578 ref YP_002152.1 YP_002152.1 putative lipoprotein ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process of the p	r ess r ess	celular celular celular celular celular celular	630 302 455 763 241 387 341	501 478 386 373 371 346 312	192 75 484 129 121
ref YP_002152.1 YP_002152.1 putative lipoprotein ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process other process oth	r ess r ess	celular celular celular celular celular	302 455 763 241 387 341	478 386 373 371 346 312	75 484 129 121
ref YP_001371.1 YP_001371.1 hypothetical protein LIC11408 ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process other process oth	r ess r ess r ess r ess r ess r ess r ess	celular celular celular celular	455 763 241 387 341	386 373 371 346 312	129 121 545
ref YP_000696.1 YP_000696.1 hypothetical protein LIC10712 ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process other process oth	r ess r ess r ess r ess r ess r ess r ess	celular celular celular	763 241 387 341	373 371 346 312	129 121 545
ref YP_002405.1 YP_002405.1 Pbp1A ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process other process oth	r ess r ess r ess r ess r	celular celular celular	241 387 341	371 346 312	121 545
ref YP_000028.1 YP_000028.1 putative lipoprotein ref YP_002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe process other process of the process o	r ess r ess r ess r	celular celular	387	346 312	545
ref YP_002650.1 YP_002650.1 hypothetical protein LIC12730 ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe prod othe prod othe prod	r ess r ess r ess	celular	341	312	
ref YP_000327.1 YP_000327.1 hypothetical protein LIC10337 ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe prod othe prod othe	r ess r ess				
ref YP_000121.1 YP_000121.1 hypothetical protein LIC10125	othe prod othe	r ess	celular	324	305	211
	othe			1		
ref YP_000612.1 YP_000612.1 putative lipoprotein			celular	535	268	699
	othe	r	celular		243	8
ref YP_002122.1 YP_002122.1 perosamine synthetase	othe	r	celular	354	239	242
ref YP_000391.1 YP_000391.1 hypothetical protein LIC10405	othe	r	celular	158	189	37
ref YP_000259.1 YP_000259.1 cyclic nucleotide binding protein	othe	r	celular	150	153	308
ref YP_001903.1 YP_001903.1 ARM repeat superfamily protein	othe	r	celular		128	242
ref YP_000824.1 YP_000824.1 hypothetical protein LIC10847	othe	r	celular	1047		181
ref YP_001404.1 YP_001404.1 hypothetical protein LIC11442	othe	r	celular	344		30
ref YP_002140.1 YP_002140.1 gdp-l-fucose synthetase	othe	r	celular	227		118
ref YP_000998.1 YP_000998.1 hypothetical protein LIC11028	othe	r	celular	111		92
ref YP_003615.1 YP_003615.1 aldolase class II	othe	r	celular	92		34
sp Q72VI7 GCSH_LEPIC Glycine cleavage system H protein	othe	r	celular			177
ref YP_000098.1 YP_000098.1 cystathionine gamma-synthase	othe	r	celular			125
ref YP_000292.1 YP_000292.1 hypothetical protein LIC10302	othe	r	celular			92
ref YP_002870.1 YP_002870.1 hypothetical protein LIC12957	othe	r	celular			71
ref YP_002429.1 YP_002429.1 hypothetical protein LIC12501	othe	r	celular			64

ref YP_000032.1 YP_000032.1	hypothetical protein LIC10032	other	celular	11
ref YP_002651.1 YP_002651.1	hypothetical protein LIC12731	other process	celular	207
ref YP_001117.1 YP_001117.1	nitrilotriacetate monooxygenase component B	other process	celular	158
ref YP_001308.1 YP_001308.1	hypothetical protein LIC11344	other	celular	103
ref YP_000038.1 YP_000038.1	hypothetical protein LIC10038	other process	celular	92
ref YP_000786.1 YP_000786.1	zinc binding dehydrogenase	other process	celular	92
ref YP_001962.1 YP_001962.1	hypothetical protein LIC12024	other process	celular	78
ref YP_002640.1 YP_002640.1	hypothetical protein LIC12719	other process	celular	78
ref YP_000392.1 YP_000392.1	hypothetical protein LIC10406	other process	celular	71
sp Q72RU2 LIPA_LEPIC	Lipoyl synthase (EC 2.8.1) (Lipoic acid synthase) (Lipoate synthase) (Lipoyl-acyl-carrier-protein	other process	celular	57
ref YP_002464.1 YP_002464.1	RibD	other process	celular	57
ref YP_001366.1 YP_001366.1	hypothetical protein LIC11403	other process	celular	50
ref YP_002561.1 YP_002561.1	hypothetical protein LIC12638	other process	celular	50
ref YP_002074.1 YP_002074.1	nucleoside-diphosphate-sugar epimerase	other process	celular	50
ref YP_002838.1 YP_002838.1	hypothetical protein LIC12923	other process	celular	47
ref YP_001447.1 YP_001447.1	hypothetical protein LIC11486	other process	celular	37
ref YP_001269.1 YP_001269.1	L-lysine 2,3-aminomutase	other process	celular	34
sp Q72TL3 TGT_LEPIC	Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (tRNA-guanine transglycosylase) (Guanine insertion enz	other process	celular	34
ref YP_000602.1 YP_000602.1	hypothetical protein LIC10618	other process	celular	30
ref YP_000053.1 YP_000053.1	hypothetical protein LIC10053	other process	celular	27
ref YP_002702.1 YP_002702.1	hypothetical protein LIC12785	other process	celular	27
ref YP_000599.1 YP_000599.1	putative lipoprotein	other process	celular	27
ref YP_003453.1 YP_003453.1	thiol-disulfide interchange like protein	other process	celular	27
ref YP_001624.1 YP_001624.1	hypothetical protein LIC11670	other process	celular	24
ref YP_002243.1 YP_002243.1	hypothetical protein LIC12309	other process	celular	21
ref YP_000580.1 YP_000580.1	putative lipoprotein	other process	celular	21
ref YP_003009.1 YP_003009.1	sugar nucleotide epimerase	other process	celular	17
sp Q72RR0 NPD_LEPIC	NAD-dependent deacetylase (EC 3.5.1) (Regulatory protein SIR2 homolog)	other process	celular	14
sp Q72S29 RIMM_LEPIC	Probable 16S rRNA-processing protein rimM	other process	celular	14
sp Q72TD6 Y1085_LEPIC	Hypothetical RNA methyltransferase LIC 11085 (EC 2.1.1)	other process	celular	11
ref YP_002396.1 YP_002396.1	hypothetical protein LIC12468	other process	celular	8

ref YP_002150.1 YP_002150.1	hypothetical protein LIC12215	other celular			5
ref YP_003434.1 YP_003434.1	BatC	other celular process			
ref YP_003435.1 YP_003435.1	BatD	other celular process			
ref YP_000657.1 YP_000657.1	hypothetical protein LIC10673	other celular process			
ref YP_000667.1 YP_000667.1	methylamine utilization protein	other celular process			
ref YP_000619.1 YP_000619.1	NifU	other celular process			
ref YP_003432.1 YP_003432.1	BatA	other celular process			
ref YP_003312.1 YP_003312.1	DTDP-4-dehydrorhamnose 3,5-epimerase	other celular process			
ref YP_000052.1 YP_000052.1	hypothetical protein LIC10052	other celular process			
ref YP_000087.1 YP_000087.1	hypothetical protein LIC10090	other celular process			
ref YP_001439.1 YP_001439.1	hypothetical protein LIC11478	other celular process			
ref YP_002220.1 YP_002220.1	hypothetical protein LIC12286	other celular process			
ref YP_002480.1 YP_002480.1	hypothetical protein LIC12553	other celular process			
ref YP_003007.1 YP_003007.1	hypothetical protein LIC13095	other celular process			
sp Q72W54 Y086_LEPIC	Hypothetical RNA methyltransferase LIC_10086 (EC 2.1.1.)	other celular process			
sp Q72VP7 Y249_LEPIC	Hypothetical RNA methyltransferase LIC_10249 (EC 2.1.1.)	other celular process			
ref YP_003618.1 YP_003618.1	L-lysine 2, 3-aminomutase	other celular process			
ref YP_000512.1 YP_000512.1	Pbp3	other celular process			
ref YP_003483.1 YP_003483.1	short-chain dehydrogenase	other celular process			
ref YP_000321.1 YP_000321.1	sugar transferase	other celular process			
ref YP_000947.1 YP_000947.1	outer membrane protein	outermembrane protein	5441	4194	636
ref YP_002473.1 YP_002473.1	outer membrane lipoprotein carrier protein	outermembrane protein	657	685	177
ref YP_000698.1 YP_000698.1	outer membrane receptor protein	outermembrane protein	529	397	265
ref YP_001419.1 YP_001419.1	outer membrane protein, porin superfamily	outermembrane protein	145	103	40
ref YP_001581.1 YP_001581.1	outer membrane protein	outermembrane protein			37
ref YP_002189.1 YP_002189.1	outer membrane protein	outermembrane protein			136
ref YP_000249.1 YP_000249.1	hypothetical protein LIC10258	outermembrane protein			75
ref YP_002241.1 YP_002241.1	outer membrane ToIC superfamily	outermembrane protein			21
ref YP_003479.1 YP_003479.1	outer membrane protein	outermembrane protein			17
ref YP_002306.1 YP_002306.1	outer membrane protein, TonB dependent	outermembrane protein			
ref YP_000483.1 YP_000483.1	outer membrane protein	outermembrane protein			
ref YP_001405.1 YP_001405.1	outer membrane protein	outermembrane protein			

ref YP_001930.1 YP_001930.1	outer membrane protein	outermembrane			
	outer memorane protein	protein			
ref YP_003043.1 YP_003043.1	outer membrane protein	outermembrane			
ref YP_000528.1 YP_000528.1	autar mambrana protain	protein			
[FEI FP_000528.1 FP_000528.1	outer membrane protein	outermembrane protein			
ref YP_001467.1 YP_001467.1	outer membrane protein	outermembrane			
	·	protein			
ref YP_001914.1 YP_001914.1	outer membrane protein	outermembrane			
ref YP 003010.1 YP 003010.1	outer membrane protein with alpha	protein outermembrane			
161/11_003010.1/11_003010.1	integrin like repeat domains	protein			
ref YP_000858.1 YP_000858.1	outer membrane protein, TonB	outermembrane			
	dependent	protein			
ref YP_002729.1 YP_002729.1	serine protease MucD precursor	peptidase activity	2296	1958	1401
ref YP_001745.1 YP_001745.1	endopeptidase IV	peptidase	1315	1203	162
		activity			
ref YP_002185.1 YP_002185.1	carboxy-terminal processing protease	peptidase	1060	979	1108
ref YP_003390.1 YP_003390.1	metallopeptidase	activity peptidase	491	845	37
161 17_005590.1 17_005590.1	metanopeptidase	activity	491	643	37
ref YP_000834.1 YP_000834.1	integral membrane zinc metalloprotease	peptidase	524	645	129
· - · · -		activity			
sp Q72UC6 AMPA_LEPIC	Probable cytosol aminopeptidase (EC	peptidase	520	609	47
	3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase)	activity			
ref YP_000749.1 YP_000749.1	processing metalloprotease	peptidase	474	465	480
	Freezesing measure processes	activity			
ref YP_001202.1 YP_001202.1	signal peptidase I	peptidase	247	396	75
(IVD 000740 4 IVD 000740 4		activity	200	270	453
ref YP_000748.1 YP_000748.1	metalloprotease	peptidase activity	386	370	452
ref YP_003004.1 YP_003004.1	PfaP	peptidase	322	344	103
		activity			
ref YP_003586.1 YP_003586.1	cysteine protease	peptidase	603	335	1152
ref YP_000215.1 YP_000215.1	hypothetical protein LIC10224	activity peptidase	270	331	192
161/11_000213.1/11_000213.1	hypothetical protein Lic10224	activity	270	331	132
ref YP_003535.1 YP_003535.1	HtrA1-like protein	peptidase	356	310	203
		activity			
ref YP_002515.1 YP_002515.1	aminopeptidase N	peptidase activity	362	299	151
ref YP 003295.1 YP 003295.1	polysaccharide deacetylase	peptidase	489	265	745
161711 _003233.1711 _003233.1	porysacenariae acacetylase	activity	103	203	7 13
ref YP_003534.1 YP_003534.1	HtrA1	peptidase	224	196	496
flyn agger thyn aggres t		activity		170	
ref YP_003200.1 YP_003200.1	hypothetical protein LIC13293	peptidase activity	227	170	435
ref YP 001279.1 YP 001279.1	aminopeptidase P	peptidase	128	142	100
		activity			
ref YP_002415.1 YP_002415.1	hypothetical protein LIC12487	peptidase	171	140	61
wellVD_0014C1_4_VD_004.4C4_4	mothics in a position of the control	activity		0.0	122
ref YP_001461.1 YP_001461.1	methionine aminopeptidase	peptidase activity		98	132
ref YP_003383.1 YP_003383.1	hypothetical protein LIC13482	peptidase	308		40
	·	activity			
ref YP_001082.1 YP_001082.1	serine protease	peptidase			162
ref YP 002543.1 YP 002543.1	membrane carboxypeptidase	activity peptidase			37
161117_002545.1 17_002543.1	membrane carboxypeptidase	activity			31
sp Q75FP1 HTPX_LEPIC	Probable protease htpX homolog (EC	peptidase			34
_	3.4.24)	activity			
ref YP_002020.1 YP_002020.1	signal peptidase I	peptidase			17

		activity	
sp Q72RY8 HSLV_LEPIC	ATP-dependent protease hslV (EC 3.4.25)	peptidase activity	8
ref YP_002237.1 YP_002237.1	carboxy-terminal processing protease	peptidase activity	223
ref YP_003367.1 YP_003367.1	carboxypeptidase I	peptidase activity	121
ref YP_003549.1 YP_003549.1	ATP-dependent protease	peptidase activity	78
ref YP_001081.1 YP_001081.1	HtrA2	peptidase activity	61
ref YP_000981.1 YP_000981.1	hypothetical protein LIC11008	peptidase activity	50
ref YP_003060.1 YP_003060.1	D-alanyl-D-alanine carboxypeptidase	peptidase	40
ref YP_002621.1 YP_002621.1	metalloprotease	peptidase	30
ref YP_001670.1 YP_001670.1	protease IV	peptidase	27
ref YP_001007.1 YP_001007.1	periplasmic trypsin-like serine protease	peptidase	24
ref YP_002397.1 YP_002397.1	HtpG	peptidase	21
ref YP_001325.1 YP_001325.1	oligopeptidase A	activity peptidase activity	21
ref YP_001119.1 YP_001119.1	membrane metalloendopeptidase	peptidase activity	14
ref YP_001362.1 YP_001362.1	membrane metalloendopeptidase	peptidase activity	14
ref YP_002236.1 YP_002236.1	O-sialoglycoprotein endopeptidase	peptidase activity	14
ref YP_002569.1 YP_002569.1	membrane carboxypeptidase	peptidase activity	8
ref YP_003242.1 YP_003242.1	zinc carboxypeptidase-related protein	peptidase activity	8
ref YP_000957.1 YP_000957.1	carboxypeptidase T	peptidase activity	5
ref YP_000705.1 YP_000705.1	hypothetical protein LIC10721	peptidase activity	
ref YP_001034.1 YP_001034.1	membrane associated metalloendopeptidase	peptidase activity	
ref YP_001074.1 YP_001074.1	aminopeptidase	peptidase activity	
sp Q72RD1 CLPS_LEPIC	ATP-dependent Clp protease adaptor protein clpS	peptidase activity	
ref YP_003282.1 YP_003282.1	CAAX protease	peptidase activity	
ref YP_001830.1 YP_001830.1	hypothetical protein LIC11881	peptidase activity	
ref YP_002578.1 YP_002578.1	hypothetical protein LIC12655	peptidase activity	
ref YP_002812.1 YP_002812.1	hypothetical protein LIC12896	peptidase activity	
ref YP_003115.1 YP_003115.1	membrane carboxypeptidase	peptidase activity	
ref YP_002545.1 YP_002545.1	membrane metalloendopeptidase	peptidase activity	
ref YP_002191.1 YP_002191.1	membrane metalloendopeptidase	peptidase activity	
ref YP_001527.1 YP_001527.1	membrane peptidase	peptidase activity	
ref YP_002680.1 YP_002680.1	microbial collagenase precursor	peptidase activity	
ref YP_002730.1 YP_002730.1	serine protease	peptidase	

		activity				
ref YP_000462.1 YP_000462.1	signal peptidase I	peptidase activity				
sp P61442 DNAK_LEPIC	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)	response stress	to	3037	8187	3622
ref YP_002145.1 YP_002145.1	Hsp15-like protein	response stress	to	107	3685	177
ref YP_003633.1 YP_003633.1	aconitate hydratase	response stress	to	1514	1974	2170
sp Q72QA1 HSP15_LEPIC	Probable 15 kDa heat shock protein	response stress	to	1600	1681	332
sp Q72R01 CLPP2_LEPIC	ATP-dependent Clp protease proteolytic subunit 2 (EC 3.4.21.92) (Endopeptidase Clp 2)	response stress	to	1587	1585	1043
sp Q72SG6 CLPP1_LEPIC	ATP-dependent Clp protease proteolytic subunit 1 (EC 3.4.21.92) (Endopeptidase Clp 1)	response stress	to	647	651	749
sp P61440 DNAJ_LEPIC	Chaperone protein dnaJ	response stress	to	531	543	399
ref YP_002930.1 YP_002930.1	acriflavine resistance	response stress	to	343	513	92
ref YP_002412.1 YP_002412.1	DNA binding protein	response stress	to	495	466	284
sp Q72QU2 CLPB_LEPIC	Chaperone clpB	response stress	to	476	346	2061
sp Q72SG5 CLPX_LEPIC	ATP-dependent Clp protease ATP-binding subunit clpX	response stress	to	600	325	460
ref YP_002986.1 YP_002986.1	acriflavin resistance	response stress	to	364	296	64
ref YP_003002.1 YP_003002.1	acriflavin resistance	response stress	to	161	230	30
ref YP_000276.1 YP_000276.1	penicillin G acylase precursor	response stress	to	228	149	30
ref YP_003298.1 YP_003298.1	hypothetical protein LIC13395	response stress	to			71
ref YP_000518.1 YP_000518.1	penicillin-binding protein 1	response stress	to			21
ref YP_001765.1 YP_001765.1	ATP-dependent Clp protease, ATP-binding subunit	response stress	to			68
ref YP_001230.1 YP_001230.1	penicillin-binding protein	response stress	to			61
ref YP_000575.1 YP_000575.1	periplasmic divalent cation tolerance	response stress	to			8
ref YP_000247.1 YP_000247.1	carbon starvation protein A	response stress	to			
ref YP_000475.1 YP_000475.1	acriflavin resistance	response stress	to			
ref YP_003042.1 YP_003042.1	acriflavin resistance	response stress	to			
ref YP_000474.1 YP_000474.1	acriflavine resistance	response stress	to			
ref YP_001690.1 YP_001690.1	penicillin binding protein	response stress	to			
ref YP_000941.1 YP_000941.1	small multidrug resistance protein	response stress	to			
ref YP_002383.1 YP_002383.1	response regulator	signal transducer activity		5154	4419	1086
sp Q72RH6 Y1769_LEPIC	Hypothetical protein LIC_11769	signal transducer activity		1490	794	328
ref YP_002892.1 YP_002892.1	hypothetical protein LIC12979	signal transducer		264	389	281

		activity			
ref YP_003405.1 YP_003405.1	response regulator	signal	116	308	71
161111_003403.1111_003403.1	response regulator	transducer	110	308	/1
		activity			
ref YP_001173.1 YP_001173.1	response regulator	signal	141	271	181
161/11_001173.1/11_001173.1	response regulator	transducer	141	2/1	101
		activity			
**************************************	rosponse regulator	,	275	250	328
ref YP_000541.1 YP_000541.1	response regulator	signal	2/5	250	328
		transducer			
flyp 001002 1 lyp 001002 1		activity	272	242	78
ref YP_001902.1 YP_001902.1	response regulator	signal transducer	272	243	/8
	later to the second sec	activity	474	245	460
ref YP_001406.1 YP_001406.1	response regulator	signal	171	215	169
		transducer			
	_	activity			
ref YP_003638.1 YP_003638.1	response regulator	signal		202	504
		transducer			
		activity			
ref YP_002208.1 YP_002208.1	GGDEF family protein	signal	237	149	273
		transducer	1		
		activity			
ref YP_000043.1 YP_000043.1	Aer	signal	104	81	17
		transducer			
		activity			
ref YP_003000.1 YP_003000.1	response regulator	signal			292
		transducer			
		activity			
ref YP_000662.1 YP_000662.1	response regulator	signal			61
		transducer			
		activity			
ref YP_001106.1 YP_001106.1	response regulator	signal			57
	Took and a second	transducer			
		activity			
ref YP_001171.1 YP_001171.1	response regulator	signal			284
161/11_0011/111/11_0011/111	response regulator	transducer			201
		activity			
ref YP_002312.1 YP_002312.1	response regulator	signal			211
161 17_002312.1 17_002312.1	response regulator	transducer			211
**************************************	rosponse regulator	activity			110
ref YP_002022.1 YP_002022.1	response regulator	signal			110
		transducer	1		
		activity	+	_	74
ref YP_002724.1 YP_002724.1	response regulator	signal	1		71
		transducer	1		
		activity	_		
ref YP_001098.1 YP_001098.1	GGDEF family protein	signal			61
		transducer			
		activity			
ref YP_002433.1 YP_002433.1	response regulator	signal			50
		transducer			
		activity			
ref YP_001508.1 YP_001508.1	response regulator	signal			34
		transducer			
		activity			
ref YP_001845.1 YP_001845.1	response regulator	signal			24
_		transducer			
		activity	1		
ref YP_002432.1 YP_002432.1	response regulator	signal			21
, _ , _ , _ , _ , _ , _ , _ , _ , _ , _	. 5	transducer			
		activity			
ref YP_003149.1 YP_003149.1	response regulator	signal	1		21
	- Ispanse regulator	transducer			
		activity			
roflyn 003176 11yn 003176 1	rosponso rogulatas	·	+	+	21
ref YP_003176.1 YP_003176.1	response regulator	signal			21

		transducer			
		activity			
ref YP_002032.1 YP_002032.1	response regulator	signal			17
		transducer			
**************************************	CCDEF family protein	activity	+		11
ref YP_001099.1 YP_001099.1	GGDEF family protein	signal transducer			11
		activity			
ref YP_001266.1 YP_001266.1	GGDEF family protein	signal	+		8
101/11_001200.1/11_001200.1	GODET Turning proteins	transducer			
		activity			
ref YP_000898.1 YP_000898.1	response regulator	signal			5
		transducer			
		activity			
ref YP_000968.1 YP_000968.1	response regulator	signal			
		transducer			
		activity			
ref YP_002250.1 YP_002250.1	response regulator	signal			
		transducer			
*** flyp 003F71 1 lyp 003F71 1	response regulator	activity			
ref YP_003571.1 YP_003571.1	response regulator	signal transducer			
		activity			
ref YP_000322.1 YP_000322.1	response regulator	signal		+	
	response regulator	transducer			
		activity			
ref YP_000563.1 YP_000563.1	response regulator	signal			
		transducer			
		activity			
ref YP_001097.1 YP_001097.1	GGDEF family protein	signal			
		transducer			
		activity			
ref YP_001096.1 YP_001096.1	GGDEF family protein	signal			
		transducer			
		activity	ļ		
ref YP_001101.1 YP_001101.1	GGDEF family protein	signal			
		transducer			
**************************************	GGDEF family protein	activity			
ref YP_003573.1 YP_003573.1	GGDEF family protein	signal transducer			
		activity			
ref YP_001100.1 YP_001100.1	GGDEF family protein	signal			
		transducer			
		activity			
ref YP_001095.1 YP_001095.1	GGDEF family protein	signal			
_		transducer			
		activity			
ref YP_003572.1 YP_003572.1	GGDEF family protein	signal			
		transducer			
Character and the control of the con		activity			
ref YP_001993.1 YP_001993.1	response regulator	signal			
		transducer			
roflyn 002225 41yn 002225 4	rosponso rogulator	activity		+	
ref YP_003235.1 YP_003235.1	response regulator	signal			
		transducer activity			
ref YP_003330.1 YP_003330.1	response regulator	signal		+	
	response regulator	transducer			
		activity			
ref YP_000002.1 YP_000002.1	DNA polymerase III beta subunit	transcription	2486	2486	1459
sp Q72NI8 RPOA_LEPIC	DNA-directed RNA polymerase alpha	transcription	3279	2438	1740
· · ·				1	1
	chain (EC 2.7.7.6) (RNAP alpha subunit)				
sp Q72UA8 RPOB_LEPIC	chain (EC 2.7.7.6) (RNAP alpha subunit)	transcription	2884	2412	3518

	(Transcriptase beta chain) (
sp Q72UA7 RPOC_LEPIC	DNA-directed RNA polymerase beta' chain	transcription	2981	2307	2418
	(EC 2.7.7.6) (RNAP beta' subunit)				
	(Transcriptase beta' chain				
ref YP_000728.1 YP_000728.1	transcription antitermination protein	transcription	1705	1683	566
ref YP_002627.1 YP_002627.1	transcription elongation factor NusA	transcription	2198	1617	1331
ref YP_002559.1 YP_002559.1	transcription termination factor Rho	transcription	1548	1531	1362
ref YP_000768.1 YP_000768.1	transcript cleavage factor/unknown	transcription	1373	1017	1481
. flyp occess a lyp occess a	domain fusion protein		142	44.5	F42
ref YP_000590.1 YP_000590.1	DNA-binding stress protein	transcription	442	415	513
ref YP_003375.1 YP_003375.1 ref YP_001578.1 YP_001578.1	DNA polymerase III gamma subunit DNA repair protein	transcription	347	324	162 300
ref YP 000570.1 YP 000570.1	DNA polymerase I	transcription transcription			50
ref YP 000213.1 YP 000213.1	DNA polymerase III alpha subunit	transcription			158
ref YP 003373.1 YP 003373.1	transcriptional coactivator	transcription			143
ref YP 003073.1 YP 003073.1	DNA replication protein DnaC	transcription			85
ref YP_001654.1 YP_001654.1	DNA primase	transcription			37
sp Q72TG0 FTSK LEPIC	DNA translocase ftsK	transcription			17
ref YP 000041.1 YP 000041.1	transcription activator or transcription	transcription			14
101111 _000041.1111 _000041.1	antitermination factor	transcription			13
ref YP_003394.1 YP_003394.1	DNA polymerase III subunit-related	transcription			8
	protein				
ref YP_002014.1 YP_002014.1	DNA topoisomerase I protein	transcription			
sp Q72WD4 RECF_LEPIC	DNA replication and repair protein recF	transcription			1
sp Q72MY7 DPO4_LEPIC	DNA polymerase IV (EC 2.7.7.7) (Pol IV)	transcription			
ref YP_000600.1 YP_000600.1	DNA processing chain A	transcription			
ref YP_002231.1 YP_002231.1	DNA repair protein	transcription			
ref YP_002849.1 YP_002849.1	DnaJ-like protein	transcription			
ref YP_000390.1 YP_000390.1	transcription antitermination protein	transcription			
ref YP 001575.1 YP 001575.1	NusB transcriptional regulator (ArsR family)	transcription	11947	2023	484
161117_001373.1117_001373.1	transcriptional regulator (Arsk ranniy)	factor &	11947	2025	404
		regulators			
ref YP_000977.1 YP_000977.1	anti-sigma factor antagonist	transcription	1309	1367	484
	anti signia ractor antagonist	factor &	1505	1307	10.
		regulators			
sp P61540 RPOD_LEPIC	RNA polymerase sigma factor rpoD	transcription	1393	1195	359
		factor &			
		regulators			
ref YP_000534.1 YP_000534.1	anti-sigma factor antagonist	transcription	847	733	100
		factor &			
		regulators			1
ref YP_000205.1 YP_000205.1	transcriptional regulator (CarD family)	transcription	804	549	316
		factor &			
meflyp 000004.4 lyp 000000	and sings for the contract of	regulators	722	F42	160
ref YP_000334.1 YP_000334.1	anti-sigma factor antagonist	transcription	722	542	169
		factor &			
ref YP_001344.1 YP_001344.1	sigma factor WhiG	regulators transcription	665	457	200
161 17_001544.1 17_001344.1	Signid idetor willing	factor &	003	437	200
		regulators			
ref YP_002369.1 YP_002369.1	transcriptional regulator	transcription	911	355	288
	a.a.a.a.peroriar regulator	factor &	"	333	
		regulators			
ref YP_002851.1 YP_002851.1	anti-sigma factor antagonist	transcription	327	316	476
· - · -		factor &			
		regulators			
ref YP_002985.1 YP_002985.1	transcriptional regulator (TetR family)	transcription	160	301	188
i	II	factor &	1		
		regulators			
ref YP_002686.1 YP_002686.1	anti-sigma factor antagonist	regulators transcription	222	266	173
ref YP_002686.1 YP_002686.1	anti-sigma factor antagonist	regulators transcription factor &	222	266	173
ref YP_002686.1 YP_002686.1 ref YP_000979.1 YP_000979.1	anti-sigma factor antagonist transcriptional regulator (FUR family)	regulators transcription	222	266	173

			&			
ref YP_000216.1 YP_000216.1	RNA polymerase ECF-type sigma factor		&	194	209	114
ref YP_000128.1 YP_000128.1	sigma 54 activator	regulators transcription factor regulators	&	231	181	177
ref YP_003566.1 YP_003566.1	dnaK suppressor	transcription	&	933	130	230
sp P61446 HRCA_LEPIC	Heat-inducible transcription repressor hrcA	transcription	&		99	82
ref YP_000372.1 YP_000372.1	RNA polymerase ECF-type sigma factor	transcription	&	393		151
ref YP_001972.1 YP_001972.1	transcriptional regulator (FUR family)	transcription	&	139		50
ref YP_001124.1 YP_001124.1	transcriptional regulator	transcription	&			219
ref YP_002704.1 YP_002704.1	anti-sigma factor antagonist	transcription	&			147
ref YP_003481.1 YP_003481.1	sigma factor regulatory protein	transcription	&			89
ref YP_002418.1 YP_002418.1	RNA polymerase ECF-type sigma factor	transcription	&			78
ref YP_000554.1 YP_000554.1	anti-sigma factor antagonist	transcription	&			71
ref YP_001753.1 YP_001753.1	anti-sigma factor antagonist	transcription	&			37
ref YP_000995.1 YP_000995.1	anti-sigma factor antagonist	transcription	&			284
ref YP_002330.1 YP_002330.1	anti-sigma factor antagonist	transcription	&			238
ref YP_003440.1 YP_003440.1	anti-sigma factor antagonist	transcription	&			203
ref YP_001630.1 YP_001630.1	transcriptional regulator (TetR family)	transcription	&			118
ref YP_003507.1 YP_003507.1	RNA polymerase ECF-type sigma factor	transcription	&			75
ref YP_002558.1 YP_002558.1	hypothetical protein LIC12635	transcription	&			54
ref YP_001416.1 YP_001416.1	transcription-repair coupling factor	transcription	&			34
ref YP_000610.1 YP_000610.1	anti-sigma factor antagonist	transcription	&			34
ref YP_001475.1 YP_001475.1	anti-sigma factor antagonist	transcription	&			34

ref YP_001128.1 YP_001128.1	transcriptional regulator (FUR family)	transcription factor & regulators	30
ref YP_001441.1 YP_001441.1	anti-sigma factor antagonist	transcription factor & regulators	30
ref YP_000140.1 YP_000140.1	RNA polymerase ECF-type sigma factor	transcription factor & regulators	21
ref YP_001200.1 YP_001200.1	transcriptional regulator (TetR family)	transcription factor & regulators	17
ref YP_002239.1 YP_002239.1	transcriptional repressor (LexA family)	transcription factor & regulators	17
ref YP_003012.1 YP_003012.1	anti-sigma factor antagonist	transcription factor & regulators	17
ref YP_000924.1 YP_000924.1	sigma factor regulatory protein	transcription factor & regulators	14
ref YP_002141.1 YP_002141.1	transcriptional regulator (MarR family)	transcription factor & regulators	14
ref YP_002658.1 YP_002658.1	transcriptional regulator (MarR family)	transcription factor & regulators	14
ref YP_001951.1 YP_001951.1	anti-sigma factor antagonist	transcription factor & regulators	14
ref YP_001504.1 YP_001504.1	RNA polymerase sigma-54 factor	transcription factor & regulators	11
ref YP_003538.1 YP_003538.1	transcriptional regulator (FUR family)	transcription factor & regulators	11
ref YP_003173.1 YP_003173.1	RNA polymerase ECF-type sigma factor	transcription factor & regulators	11
ref YP_002951.1 YP_002951.1	transcriptional regulator (MarR family)	transcription factor & regulators	8
ref YP_000290.1 YP_000290.1	anti-sigma factor antagonist	transcription factor & regulators	8
ref YP_003192.1 YP_003192.1	RNA polymerase ECF-type sigma factor	transcription factor & regulators	5
ref YP_003657.1 YP_003657.1	putative transcriptional regulator	transcription factor & regulators	
ref YP_001748.1 YP_001748.1	sigma factor regulatory protein	transcription factor & regulators	
ref YP_002424.1 YP_002424.1	sigma factor regulatory protein	transcription factor & regulators	
ref YP_003318.1 YP_003318.1	transcriptional regulator (AraC family)	transcription factor & regulators	
ref YP_001543.1 YP_001543.1	transcriptional regulator (TetR family)	transcription factor & regulators	
ref YP_000381.1 YP_000381.1	transcriptional regulator (TetR family)	transcription factor &	

		regulators			
ref YP_003500.1 YP_003500.1	anti-sigma factor antagonist	transcription			
		factor	&		
		regulators			
ref YP_000650.1 YP_000650.1	transcriptional regulator (ArsR family)	transcription			
		factor	&		
Slyp codess alve codess a	505	regulators			
ref YP_001768.1 YP_001768.1	RNA polymerase ECF-type sigma factor	transcription	0		
		factor regulators	&		
ref YP_003474.1 YP_003474.1	transcriptional regulator (ArsR family)	transcription			
101111 _003474.1111 _003474.1	transcriptional regulator (Arsicianily)	factor	&		
		regulators			
ref YP_002715.1 YP_002715.1	transcriptional regulator (TetR family)	transcription			
		factor	&		
		regulators			
ref YP_000628.1 YP_000628.1	RNA polymerase ECF-type sigma factor	transcription			
		factor	&		
	siana fasta na ulatan matain	regulators			
ref YP_001388.1 YP_001388.1	sigma factor regulatory protein	transcription factor	&		
		regulators	Q		
ref YP_003569.1 YP_003569.1	DNA binding protein	transcription			
.5.,11 _003303.1111 _003303.1	2 Small protein	factor	&		
		regulators			
ref YP_001116.1 YP_001116.1	putative transcriptional regulator (DeoR	transcription			
	family)	factor	&		
		regulators			
ref YP_000543.1 YP_000543.1	RNA polymerase ECF-type sigma factor	transcription			
		factor	&		
		regulators			
ref YP_002677.1 YP_002677.1	RNA polymerase ECF-type sigma factor	transcription factor	&		
		regulators	α		
ref YP_000013.1 YP_000013.1	sigma 54 activator	transcription			
		factor	&		
		regulators			
ref YP_003180.1 YP_003180.1	sigma factor regulatory protein	transcription			
		factor	&		
		regulators			
ref YP_003503.1 YP_003503.1	sigma factor regulatory protein	transcription			
		factor	&		
ref YP_003034.1 YP_003034.1	transcriptional regulator (AraC family)	regulators transcription			
10111 _003034.1 11 _003034.1	danscriptional regulator (Arac faililly)	factor	&		
		regulators	~		
ref YP_003093.1 YP_003093.1	transcriptional regulator (AraC family)	transcription			
		factor	&		
		regulators			
ref YP_000949.1 YP_000949.1	transcriptional regulator (AraC family)	transcription			
		factor	&		
	Annualistic and annual to 10 and 5 and 5	regulators			
ref YP_002506.1 YP_002506.1	transcriptional regulator (ArsR family)	transcription factor	&		
		regulators	α		
ref YP_003311.1 YP_003311.1	transcriptional regulator (ArsR family)	transcription			
	2012001 (100000)	factor	&		
		regulators	_		<u> </u>
ref YP_001445.1 YP_001445.1	transcriptional regulator (Crp family)	transcription			
		factor	&		
		regulators			
ref YP_003344.1 YP_003344.1	transcriptional regulator (MarR family)	transcription			
		factor	&		
roflyp_002000 4 lyp_002000 4	transcriptional regulator /MarD family	regulators			
ref YP_002000.1 YP_002000.1	transcriptional regulator (MarR family)	transcription			

	T	factor &			
		factor & regulators			
ref YP_000364.1 YP_000364.1	transcriptional regulator (PadR family)	transcription			
101111 _000304.1111 _000304.1	transcriptional regulator (radik ranniy)	factor &			
		regulators			
ref YP_000361.1 YP_000361.1	transcriptional regulator (TetR family)	transcription			
		factor &			
		regulators			
ref YP_002362.1 YP_002362.1	transcriptional regulator (TetR family)	transcription			
		factor &			
		regulators			
ref YP_003473.1 YP_003473.1	transcriptional regulator (TetR family)	transcription			
		factor &			
Character and the control of		regulators	+		
ref YP_001161.1 YP_001161.1	transcriptional regulator	transcription			
		factor &			
. (LVD 002577.4 LVD 002577.4	1	regulators	+		
ref YP_002577.1 YP_002577.1	transcriptional repressor (LexA family)	transcription			
		factor &			
ref YP_001484.1 YP_001484.1	anti-sigma factor antagonist	regulators			
161117_001484.1117_001484.1	anti-signia factor antagonist	transcription factor &			
		regulators			
ref YP_002712.1 YP_002712.1	acetyl-CoA acetyltransferase	transferase	3927	3387	2663
161 17_002/12.1 17_002/12.1	acetyl-coa acetylti alisiei ase	activity	3927	3307	2003
ref YP_002133.1 YP_002133.1	aminotransferase	transferase	2628	2420	1313
161 17_002133.1 17_002133.1	allillott alistel ase	activity	2028	2420	1515
sp Q72RT8 TAL_LEPIC	Probable transaldolase (EC 2.2.1.2)	transferase	1474	1645	1069
SPIQIZITIO I TAL_LLI IC	Trobable transaldolase (LC 2.2.1.2)	activity	1474	1045	1003
ref YP_003206.1 YP_003206.1	acetyl-CoA acetyltransferase	transferase	1556	1520	774
101111 _003200.1111 _003200.1	dectyl contactylliansiciase	activity	1330	1320	,,,,
ref YP_000382.1 YP_000382.1	acetyl-CoA acetyltransferase	transferase	1593	1345	1160
		activity	2000	13 .3	1100
ref YP_000948.1 YP_000948.1	acetyl-CoA acetyltransferase	transferase	2158	1209	983
	,	activity			
ref YP_003223.1 YP_003223.1	fatty acid synthase subunit beta	transferase	1633	1169	1039
		activity			
ref YP_000430.1 YP_000430.1	glutamine-fructose-6-phosphate	transferase	736	1055	399
	transaminase	activity			
ref YP_000395.1 YP_000395.1	2-isopropylmalate synthase	transferase	77	1055	129
		activity			
ref YP_001085.1 YP_001085.1	thiosulfate sulfurtransferase	transferase	1036	1050	846
		activity			
ref YP_000584.1 YP_000584.1	fatty acid synthase subunit beta	transferase	1171	1032	460
		activity			
ref YP_000436.1 YP_000436.1	glycosyltransferase	transferase	788	1022	121
		activity			
ref YP_001742.1 YP_001742.1	aspartate aminotransferase	transferase	1058	995	1287
		activity	1		
ref YP_001801.1 YP_001801.1	O-acetylhomoserine (thiol) lyase	transferase	507	866	1226
1-2-2-2		activity	1		
sp P61656 KDSA_LEPIC	2-dehydro-3-deoxyphosphooctonate	transferase	454	765	379
	aldolase (EC 2.5.1.55) (Phospho-2-	activity			
- flyp oogsoo styp oogsoo	dehydro-3-deoxyoctonate aldolase)		440=	755	447
ref YP_002103.1 YP_002103.1	aspartate aminotransferase	transferase	1107	755	447
LDC4724 LDICD LEDIC	C.7 dissabled 0. 11.11 House 1	activity	402	700	101
sp P61724 RISB_LEPIC	6,7-dimethyl-8-ribityllumazine synthase	transferase	492	708	181
	(EC 2.5.1.9) (DMRL synthase) (Lumazine	activity			
	synthase) (Riboflavin	+f	770	602	F 4.4
sp Q72RH8 ARGD_LEPIC	Acetylornithine aminotransferase (EC	transferase	779	682	541
roflyD 00375741VD 0037574	2.6.1.11) (ACOAT)	activity	777	665	1221
ref YP_002757.1 YP_002757.1	aspartate aminotransferase	transferase	777	665	1331
ref YP 000591.1 YP 000591.1	aminotransferase	activity	916	642	1020
[161] 15_00023TT] 15_00023TT	anninotransierase	transferase	816	643	1030

		activity			
sp Q72PY2 GLYA_LEPIC	Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase) (SHMT)	transferase activity	663	634	682
ref YP_000413.1 YP_000413.1	UDP-N-acetylglucosamine pyrophosphorylase	transferase activity	559	556	304
ref YP_002132.1 YP_002132.1	aminotransferase	transferase activity	654	550	757
ref YP_003563.1 YP_003563.1	lipoprotein	transferase activity	306	536	50
ref YP_001704.1 YP_001704.1	glycosyl transferase	transferase activity	263	463	177
ref YP_002958.1 YP_002958.1	UDP glucosamine N-acyltransferase	transferase activity	568	439	288
sp Q72PD0 TRPD_LEPIC	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	transferase activity	501	419	71
ref YP_002167.1 YP_002167.1	thymidylate synthase	transferase activity	346	406	300
ref YP_003393.1 YP_003393.1	branched-chain amino acid aminotransferase	transferase activity	398	359	226
ref YP_003062.1 YP_003062.1	UDP-N-acetylglucosamine acyltransferase	transferase activity	353	330	320
ref YP_003403.1 YP_003403.1	glutamate-1-semialdehyde aminotransferase	transferase activity	439	324	300
ref YP_002353.1 YP_002353.1	aspartate aminotransferase a	transferase activity	420	318	431
ref YP_002257.1 YP_002257.1	type III beta-ketoacyl synthase-like protein	transferase activity	298	316	707
ref YP_001678.1 YP_001678.1	2-isopropylmalate synthase	transferase activity	401	298	476
ref YP_002114.1 YP_002114.1	sugar transferase	transferase activity		295	30
ref YP_003104.1 YP_003104.1	putative O-methyl transferase	transferase activity	343	288	82
ref YP_002657.1 YP_002657.1	site-specific modification DNA- methyltransferase	transferase activity	332	281	155
ref YP_002115.1 YP_002115.1	methyltransferase	transferase activity	268	280	78
ref YP_001947.1 YP_001947.1	hypothetical protein LIC12008	transferase activity	326	244	253
ref YP_001813.1 YP_001813.1	UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase	transferase activity		235	27
ref YP_001035.1 YP_001035.1	poly A polymerase	transferase activity	247	231	155
ref YP_003130.1 YP_003130.1	lauroyl/myristoyl acyltransferase	transferase activity	196	224	17
ref YP_000429.1 YP_000429.1	glucose-1-phosphate thymidylyltransferase	transferase activity		211	75
sp Q72RT5 PUR9_LEPIC	Bifunctional purine biosynthesis protein purH	transferase activity	286	202	452
sp Q72TF8 LGT_LEPIC	Prolipoprotein diacylglyceryl transferase (EC 2.4.99)	transferase activity	172	194	
ref YP_002136.1 YP_002136.1	mannose-1-phosphate guanyltransferase	transferase activity	182	190	21
ref YP_001703.1 YP_001703.1	lipopolysaccharide core biosynthesis protein	transferase activity	545	189	
ref YP_001555.1 YP_001555.1	2-isopropylmalate synthase 2	transferase activity	229	169	335
ref YP_002057.1 YP_002057.1	glucose-1-phosphate thymidylyltransferase	transferase activity	244	150	207
ref YP_001373.1 YP_001373.1	acetolactate synthase small subunit	transferase activity		123	125
ref YP_002106.1 YP_002106.1	nucleoside-diphosphate-sugar pyrophosphorylase	transferase activity	136	105	85
ref YP_002072.1 YP_002072.1	colanic acid biosynthesis glycosyl-	transferase		101	8

	transferase	activity			
ref YP_002251.1 YP_002251.1	beta-ketoacyl synthase	transferase activity	71	72	103
ref YP_002162.1 YP_002162.1	hypothetical protein LIC12227	transferase activity	929		21
ref YP_003158.1 YP_003158.1	UDP-N-acetylglucosamine 1- carboxyvinyltransferase	transferase activity	236		121
ref YP_001637.1 YP_001637.1	hypothetical protein LIC11685	transferase activity	210		132
ref YP_000888.1 YP_000888.1	transketolase alpha subunit protein	transferase activity			395
ref YP_002092.1 YP_002092.1	3-deoxy-manno-octulosonate cytidylyltransferase	transferase activity			173
sp Q75FP0 APT_LEPIC	Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT)	transferase activity			169
ref YP_000055.1 YP_000055.1	serine acetyltransferase	transferase activity			169
sp Q72LZ4 MTNP_LEPIC	Probable 5'-methylthioadenosine phosphorylase (EC 2.4.2.28) (MTA phosphorylase)	transferase activity			162
ref YP_000618.1 YP_000618.1	selenocysteine reductase	transferase activity			155
ref YP_002325.1 YP_002325.1	ankyrin-like protein	transferase activity			151
ref YP_003593.1 YP_003593.1	cysteine desulfurase	transferase activity			143
ref YP_000604.1 YP_000604.1	glycosyl transferase	transferase activity			136
ref YP_002099.1 YP_002099.1	hypothetical protein LIC12164	transferase activity			136
ref YP_001764.1 YP_001764.1	gamma-glutamyltranspeptidase	transferase activity			132
ref YP_001327.1 YP_001327.1	glutathione-S-transferase	transferase activity			89
sp Q72NJ5 PYRB_LEPIC	Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase)	transferase activity			75
ref YP_002125.1 YP_002125.1	SAM-dependent methyltransferase	transferase activity			57
ref YP_001746.1 YP_001746.1	alginate O-acetyltransferase protein	transferase activity			47
ref YP_002061.1 YP_002061.1	glycosyl transferase	transferase activity			24
sp Q72U01 DXS_LEPIC	1-deoxy-D-xylulose-5-phosphate synthase (EC 2.2.1.7) (1-deoxyxylulose-5-phosphate synthase) (DXP syn	transferase activity			21
ref YP_001872.1 YP_001872.1	dolichol-P-glucose synthetase	transferase activity			21
ref YP_002700.1 YP_002700.1	dolichyl-phosphate-mannose-protein mannosyltransferase	transferase activity			21
ref YP_002109.1 YP_002109.1	acetyl transferase	transferase activity			17
ref YP_000994.1 YP_000994.1	glycosyltransferase	transferase activity			14
ref YP_002719.1 YP_002719.1	hypothetical protein LIC12802	transferase activity			11
ref YP_002304.1 YP_002304.1	ankyrin repeat protein	transferase activity			8
ref YP_001971.1 YP_001971.1	ankyrin like protein	transferase activity			
ref YP_002470.1 YP_002470.1	phosphatidylglycerophosphate synthase	transferase activity			
ref YP_003169.1 YP_003169.1	glutamine phosphoribosylpyrophosphate amidotransferase	transferase activity			300

ref YP_002894.1 YP_002894.1	glutathione S-transferase	transferase	292
ref YP_002183.1 YP_002183.1	pyridoxal phosphate biosynthetic protein	activity transferase activity	234
ref YP_003276.1 YP_003276.1	sulfate adenylyltransferase subunit 2	transferase activity	181
sp P62062 ARGJ_LEPIC	Arginine biosynthesis bifunctional protein argJ	transferase activity	177
sp Q72PG3 HIS8_LEPIC	Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase)	transferase activity	173
ref YP_001008.1 YP_001008.1	hypothetical protein LIC11038	transferase activity	169
sp Q72R95 METX_LEPIC	Homoserine O-acetyltransferase (EC 2.3.1.31) (Homoserine O-trans-acetylase) (Homoserine transacetyla	transferase activity	158
ref YP_001729.1 YP_001729.1	biotin synthase	transferase activity	155
ref YP_002064.1 YP_002064.1	aminotransferase	transferase activity	147
ref YP_002256.1 YP_002256.1	glutaconate CoA transferase-like protein	transferase activity	136
sp Q72S40 HPRK_LEPIC	HPr kinase/phosphorylase (EC 2.7.11) (EC 2.7.4) (HPrK/P) (HPr(Ser) kinase/phosphorylase)	transferase activity	136
ref YP_002019.1 YP_002019.1	carbonic anhydrase	transferase activity	132
ref YP_000257.1 YP_000257.1	protoporphyrinogen oxidase	transferase activity	129
ref YP_002086.1 YP_002086.1	glucose-1-phosphate cytidylyltransferase	transferase activity	125
ref YP_002110.1 YP_002110.1	aminotransferase	transferase activity	118
sp P59119 HIS61_LEPIN	Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3) (IGP synthase cyclase subunit) (IGP	transferase activity	107
sp Q72T26 OTC_LEPIC	Ornithine carbamoyltransferase (EC 2.1.3.3) (OTCase)	transferase activity	107
ref YP_003401.1 YP_003401.1	porphobilinogen deaminase	transferase activity	103
sp Q72MN0 PANB_LEPIC	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferas	transferase activity	100
ref YP_003072.1 YP_003072.1	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase	transferase activity	71
ref YP_001861.1 YP_001861.1	thiamine phosphate pyrophosphorylase	transferase activity	71
ref YP_001046.1 YP_001046.1	uridine 5-monophosphate synthase	transferase activity	71
ref YP_002944.1 YP_002944.1	aminotransferase	transferase activity	68
sp Q72M66 COAD_LEPIC	Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine-phosphate adenylyltransferase) (PPA	transferase activity	68
ref YP_001803.1 YP_001803.1	putative methyltransferase	transferase activity	61
ref YP_000609.1 YP_000609.1	3-deoxy-manno-octulosonate cytidylyltransferase	transferase activity	54
ref YP_000075.1 YP_000075.1	hypothetical protein LIC10075	transferase activity	54
sp P59118 HIS51_LEPIN	Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2) (IGP synthase glutamine amidotransfe	transferase activity	54

ref YP_000983.1 YP_000983.1	nicotinate-nucleotide pyrophosphorylase	transferase activity	54
ref YP_002089.1 YP_002089.1	3-demethylubiquinone-9 3-	transferase	50
ref YP_001732.1 YP_001732.1	methyltransferase 8-amino-7-oxononanoate synthase	activity transferase	50
161 11_001/32:1 11_001/32:1	d unino 7 oxononanoate synthase	activity	30
ref YP_001277.1 YP_001277.1	acetyl-CoA C-acyltransferase	transferase	50
	h a sana a bhi a a sana a sana bhi a a	activity	50
ref YP_003341.1 YP_003341.1	hypoxanthine-guanine-xanthine phosphoribosyltransferase	transferase activity	50
ref YP_000571.1 YP_000571.1	glycosyl transferase	transferase	47
		activity	
ref YP_002409.1 YP_002409.1	putative amino-acid acetyltransferase	transferase activity	47
sp Q72P59 ISPD_LEPIC	2-C-methyl-D-erythritol 4-phosphate	transferase	44
3713	cytidylyltransferase (EC 2.7.7.60) (4-diphosphocytidyl-2C-methyl	activity	
ref YP_002178.1 YP_002178.1	mannose-1-phosphate	transferase	44
	guanylyltransferase	activity	
ref YP_003552.1 YP_003552.1	mannosyltransferase	transferase activity	44
sp P62382 HIS1_LEPIC	ATP phosphoribosyltransferase (EC	transferase	40
551. 62562161_226	2.4.2.17) (ATP-PRTase) (ATP-PRT)	activity	
ref YP_000701.1 YP_000701.1	carbon-nitrogen hydrolase	transferase	40
Clyp coarse alve coarse		activity	
ref YP_001585.1 YP_001585.1	mannosyltransferase	transferase activity	40
ref YP_003588.1 YP_003588.1	UTP-glucose-1-phosphate uridyltransferase	transferase activity	40
ref YP_000144.1 YP_000144.1	valinepyruvate transaminase	transferase	40
		activity	
ref YP_003557.1 YP_003557.1	alginate O-acetyltransferase	transferase	34
ref YP_000273.1 YP_000273.1	farnesyl-diphosphate synthase	activity transferase	30
161 17_0002/3.1 17_0002/3.1	Tarriesyi-dipriospilate synthase	activity	30
ref YP_001910.1 YP_001910.1	hypothetical protein LIC11970	transferase	30
		activity	
ref YP_000353.1 YP_000353.1	hypothetical protein LIC10364	transferase activity	27
ref YP_000906.1 YP_000906.1	type I restriction enzyme	transferase	27
	,	activity	
ref YP_001262.1 YP_001262.1	dolichyl-phosphate mannose synthase	transferase	24
ref YP_001032.1 YP_001032.1	hypothetical protein LIC11062	activity transferase	24
161/17_001032.1/17_001032.1	hypothetical protein Lici1002	activity	24
ref YP_003468.1 YP_003468.1	putative S-adenosyl methionine	·	24
	dependent methyltransferase like protein	activity	
ref YP_002310.1 YP_002310.1	3-demethylubiquinone-9 3-O- methyltransferase	transferase activity	21
ref YP_000051.1 YP_000051.1	7,8-dihydropteroate synthase protein	transferase	21
		activity	
ref YP_000317.1 YP_000317.1	hypothetical protein LIC10327	transferase	21
ref YP_000442.1 YP_000442.1	hypothetical protein LIC10458	activity transferase	21
101111_000442.1 117_000442.1	hypothetical protein Lic10436	activity	21
ref YP_002503.1 YP_002503.1	lipid-a-disaccharide synthase protein	transferase activity	21
ref YP_001612.1 YP_001612.1	phosphoribosylglycinamide formyltransferase	transferase activity	17
ref YP_002068.1 YP_002068.1	sugar transferase	transferase	17
thus against the same		activity	
ref YP_001879.1 YP_001879.1	polynucleotide adenyltransferase-like protein	transferase activity	17
ref YP_001730.1 YP_001730.1	adenosylmethionine-8-amino-7-	transferase	14
			- t

	oxononanoate aminotransferase	activity	
ref YP_001278.1 YP_001278.1	lipopolysaccharide heptosyltransferase II	transferase	14
101111 _001270.1111 _001270.1	iipoporysaccitariae rieptosytti arisierase ri	activity	1 4
ref YP_003241.1 YP_003241.1	putative aminotransferase	transferase	14
101711 _005241.1711 _005241.1	patative arimotransierase	activity	1 4
sp Q72R21 ATE_LEPIC	Putative arginyl-tRNAprotein transferase	transferase	14
351Q/21(21)/112_22110	(EC 2.3.2.8) (R-transferase)	activity	1.
	(Arginyltransferase)		
ref YP_003126.1 YP_003126.1	carbonic anhydrase/acetyltransferase	transferase	14
		activity	
ref YP_003555.1 YP_003555.1	alginate O-acetyltransferase	transferase	11
	,	activity	
ref YP_003027.1 YP_003027.1	amino-sugar biosynthesis protein	transferase	11
		activity	
ref YP_003143.1 YP_003143.1	ankyrin-like protein	transferase	11
	, .	activity	
ref YP_000552.1 YP_000552.1	hypothetical protein LIC10568	transferase	11
		activity	
sp P62472 MRAW_LEPIC	S-adenosyl-methyltransferase mraW (EC	transferase	11
_	2.1.1)	activity	
ref YP_003305.1 YP_003305.1	methylated-DNAprotein-cysteine	transferase	8
	methyltransferase transcription regulator	activity	
ref YP_003309.1 YP_003309.1	mannosyltransferase	transferase	8
		activity	
ref YP_002192.1 YP_002192.1	hypothetical protein LIC12257	transferase	5
		activity	
ref YP_000191.1 YP_000191.1	glycosyltransferase	transferase	5
		activity	
ref YP_000751.1 YP_000751.1	hypothetical protein LIC10771	transferase	5
		activity	
ref YP_000073.1 YP_000073.1	3-demethylubiquinone-9 3-	transferase	2
	methyltransferase	activity	
ref YP_000014.1 YP_000014.1	hypothetical protein LIC10014	transferase	
		activity	
ref YP_000719.1 YP_000719.1	3-demethylubiquinone-9 3-	transferase	
	methyltransferase	activity	
ref YP_002420.1 YP_002420.1	alginate O-acetyltransferase	transferase	
		activity	
ref YP_002049.1 YP_002049.1	ankyrin-like protein	transferase	
		activity	
ref YP_002157.1 YP_002157.1	DNA methyltransferase	transferase	
		activity	
ref YP_002062.1 YP_002062.1	glycosyl transferase	transferase	
thyp pages thyp pages :	Later the section of	activity	
ref YP_002066.1 YP_002066.1	glycosyltransferase	transferase	
	h	activity	
ref YP_003452.1 YP_003452.1	hypothetical protein LIC20060	transferase	
**************************************	C adapagulmathianina + PP1A	activity	
ref YP_003550.1 YP_003550.1	S-adenosylmethioninetRNA	transferase	
roflyD 004042 4 lyD 004042 1	ribosyltransferase-isomerase	activity	
ref YP_001042.1 YP_001042.1	tetrapyrrole (corrin/porphyrin) methylase	transferase	
	h	activity	
ref YP_001275.1 YP_001275.1	hypothetical protein LIC11309	transferase	
ref YP_001458.1 YP_001458.1	methyltransferase	activity	
	methyltransierase	transferase	
rofIVD 003E10 1 VD 003E40 4	processin 2 C 17 methylese	activity	
ref YP_003518.1 YP_003518.1	precorrin-3 C-17 methylase	transferase	
sp Q72U10 UPPS_LEPIC	Undecaprenyl pyrophosphate synthetase	activity transferase	
3PTC/2010[0FF3_LEFIC	(EC 2.5.1.31) (UPP synthetase) (Di-	activity	
	trans,poly-cis-decaprenylci	activity	
ref YP_003097.1 YP_003097.1	acetyltransferase	transferase	
	accepter unitaries use	activity	
ref YP 002055.1 YP 002055.1	dTDP-rhamnosyl transferase	transferase	
101111 _002033.1111 _002033.1	arer mannosyrtransierase	transiciase	

		activity	
sp Q72NR0 NADD_LEPIC	Probable nicotinate-nucleotide	transferase	
	adenylyltransferase (EC 2.7.7.18)	activity	
	(Deamido-NAD(+) pyrophosphorylase)		
ref YP_003274.1 YP_003274.1	uroporphyrinogen-III C-methyltransferase	transferase	
		activity	
ref YP_001778.1 YP_001778.1	lipopolysaccharide biosynthesis	transferase	
	glycosyltransferase	activity	
ref YP_003017.1 YP_003017.1	sugar-phosphate nucleotidyl transferase	transferase	
ref YP_001289.1 YP_001289.1	methyltransferase DNA modification	activity transferase	
161 17_001289.1 17_001289.1	enzyme	activity	
ref YP_000832.1 YP_000832.1	CDP-diglyceride synthetase	transferase	
101111 _000032.1111 _000032.11	CD1 digiyeeride synthetase	activity	
ref YP_000133.1 YP_000133.1	protein-PII] uridylyltransferase	transferase	
	, , ,	activity	
ref YP_002214.1 YP_002214.1	3-deoxy-d-manno-octulosonic acid	transferase	
	transferase	activity	
ref YP_000684.1 YP_000684.1	3-oxoacyl-	transferase	
		activity	
ref YP_002119.1 YP_002119.1	acetyl transferase	transferase	
the constant the constant	l	activity	
ref YP_000525.1 YP_000525.1	acetyltransferase	transferase	
ref YP_002400.1 YP_002400.1	acetyltransferase	activity transferase	
ref[YP_002400.1]YP_002400.1	acetyitransferase	activity	
ref YP_002588.1 YP_002588.1	acetyltransferase	transferase	
161 17_002388.1 17_002388.1	acetyittansierase	activity	
ref YP_003653.1 YP_003653.1	alginate O-acetyltransferase	transferase	
		activity	
ref YP_001436.1 YP_001436.1	alginate o-acetyltransferase	transferase	
		activity	
ref YP_001217.1 YP_001217.1	alginate o-acetyltransferase	transferase	
		activity	
ref YP_002298.1 YP_002298.1	alginate O-acetyltransferase	transferase	
		activity	
ref YP_003198.1 YP_003198.1	ankyrin domain containing protein	transferase activity	
ref YP_001020.1 YP_001020.1	ankyrin G domain containing protein	transferase	
101111 _001020.1111 _001020.1	dikyiii d domaii containing protein	activity	
ref YP_001627.1 YP_001627.1	ankyrin repeat protein	transferase	
	, , ,	activity	
ref YP_002350.1 YP_002350.1	ankyrin repeats-containing protein	transferase	
		activity	
ref YP_000239.1 YP_000239.1	ankyrin-like protein	transferase	
		activity	
ref YP_002923.1 YP_002923.1	ankyrin-like protein	transferase	
ref YP_001716.1 YP_001716.1		activity	
161117_001/16.11179_001/16.1	aspartate aminotransferase	transferase	
ref YP 000343.1 YP 000343.1	dimethyladenosine transferase	activity transferase	
.5.711_000545.1711_000545.1	aestryiadenositie transferase	activity	
ref YP_000784.1 YP_000784.1	glutathione S-transferase	transferase	
,		activity	
ref YP_002076.1 YP_002076.1	glycosyl transferase	transferase	
		activity	
ref YP_001063.1 YP_001063.1	glycosyl transferase	transferase	
		activity	
ref YP_002053.1 YP_002053.1	glycosyl transferase	transferase	
ref YP_002860.1 YP_002860.1	alveocyl transforace	activity	
161117_002000.1 17_002860.1	glycosyl transferase	transferase activity	
ref YP_000192.1 YP_000192.1	glycosyl transferase	transferase	
	0,,	activity	
j	i	, ,	l .

ref YP_002063.1 YP_002063.1	glycosyltransferase	transferase			
		activity			
ref YP_002056.1 YP_002056.1	glycosyltransferase	transferase			
		activity			
ref YP_002082.1 YP_002082.1	glycosyltransferase	transferase			
		activity			
ref YP_000190.1 YP_000190.1	glycosyltransferase	transferase			
		activity			
ref YP_002873.1 YP_002873.1	glycosyltransferase	transferase			
		activity			
ref YP_001857.1 YP_001857.1	glycosyltransferase	transferase			
		activity			
ref YP_001394.1 YP_001394.1	histidine kinase response regulator hybrid	transferase			
	protein	activity			
ref YP_001121.1 YP_001121.1	hypothetical protein LIC11151	transferase			
		activity			
ref YP_000115.1 YP_000115.1	methylated-DNAprotein-cysteine	transferase			
-, =	methyltransferase	activity			
ref YP_003038.1 YP_003038.1	protein-pll uridylyltransferase	transferase			
	. , , , , , , , , , , , , , , , , , , ,	activity			
ref YP_003627.1 YP_003627.1	putative acyltransferase	transferase			
		activity			
ref YP_003371.1 YP_003371.1	UDP-3-O-	transferase			
		activity			
ref YP_001591.1 YP_001591.1	UDP-3-O-	transferase			
101711 _001331.1711 _001331.1	051 3 0	activity			
ref YP_001420.1 YP_001420.1	UDP-glucosyltransferase	transferase			
161/11_001420.1/11_001420.1	ODF-glucosyltransierase	activity			
sp Q72NG2 RL4_LEPIC	50S ribosomal protein L4	translation	4724	4232	375
sp Q72NG4 RL2_LEPIC	50S ribosomal protein L2	translation	3508	3203	284
sp Q72NI6 RS11 LEPIC	30S ribosomal protein S11	translation	2748	2439	136
ref YP_002772.1 YP_002772.1	·		3630	2368	335
<u> </u>	30S ribosomal protein S5	translation			
sp Q72UB1 RL1_LEPIC	50S ribosomal protein L1	translation	3830	2193	238
sp Q72NG1 RL3_LEPIC	50S ribosomal protein L3	translation	2474	1939	324
ref YP_002695.1 YP_002695.1	50S ribosomal protein L21	translation	3487	1764	166
sp P62436 RL11_LEPIC	50S ribosomal protein L11	translation	2168	1638	383
sp Q72NG7 RS3_LEPIC	30S ribosomal protein S3	translation	2467	1595	207
sp Q72NG6 RL22_LEPIC	50S ribosomal protein L22	translation	1517	1550	332
sp Q72U13 EFTS_LEPIC	Elongation factor Ts (EFTs)	translation	1517	1416	603
sp Q72NH3 RL5_LEPIC	50S ribosomal protein L5	translation	1794	1411	517
sp Q72UA9 RL7_LEPIC	50S ribosomal protein L7/L12	translation	6683	1350	707
sp Q72QK3 RL9_LEPIC	50S ribosomal protein L9	translation	1996	1347	480
ref YP_002377.1 YP_002377.1	30S ribosomal protein S1	translation	1564	1224	1521
sp Q72U14 RS2_LEPIC	30S ribosomal protein S2	translation	1783	1015	407
sp Q72V72 RL25_LEPIC	50S ribosomal protein L25 (General stress	translation	1385	996	591
	protein CTC)				
ref YP_002779.1 YP_002779.1	50S ribosomal protein L14	translation	1349	992	151
sp Q72NH5 RS8_LEPIC	30S ribosomal protein S8	translation	944	944	304
ref YP_000741.1 YP_000741.1	50S ribosomal protein L13	translation	1514	901	234
sp Q72NG3 RL23_LEPIC	50S ribosomal protein L23	translation	1552	869	219
sp Q72UB0 RL10_LEPIC	50S ribosomal protein L10	translation	1794	865	736
sp Q72NI9 RL17_LEPIC	50S ribosomal protein L17	translation	2120	846	185
sp Q72PK6 SYT_LEPIC	Threonyl-tRNA synthetase (EC 6.1.1.3)	translation	876	830	850
	(Threonine-tRNA ligase) (ThrRS)				
sp Q72QK0 RS6_LEPIC	30S ribosomal protein S6	translation	1235	824	443
sp Q72S27 RL19 LEPIC	50S ribosomal protein L19	translation	1034	818	121
sp Q72UA5 RS7 LEPIC	30S ribosomal protein S7	translation	1839	774	492
sp Q72VS5 GATB LEPIC	Aspartyl/glutamyl-tRNA(Asn/Gln)	translation	847	767	624
39147243310A1D_LL110	amidotransferase subunit B (EC 6.3.5.)	ti an siation	047	/ / /	324
	(Asp/Glu-ADT subunit B)				
sp Q72NG8 RL16_LEPIC	50S ribosomal protein L16	translation	729	755	207
sp Q72Ni7 RS4_LEPIC	30S ribosomal protein S4	translation	1330	743	200
sp Q72NH6 RL6_LEPIC	50S ribosomal protein 54		1081	721	395
I SPIC/ZINIIO NLO_LEPIC	אסט וואטטטווומו או אוואטטטווו בטכ	translation	TOOT	141	333

sp Q72PR7 SYI_LEPIC	Isoleucyl-tRNA synthetase (EC 6.1.1.5) (IsoleucinetRNA ligase) (IleRS)	translation	457	505	312
sp Q72NI0 RL15_LEPIC	50S ribosomal protein L15	translation	1853	465	129
sp Q72SC3 GATA_LEPIC	Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5) (Glu-ADT subunit A)	translation	574	464	525
sp Q72PK8 IF3_LEPIC	Translation initiation factor IF-3 -	translation	350	425	54
sp Q72UA6 RS12_LEPIC	30S ribosomal protein S12	translation	592	401	8
sp Q72NQ6 RL27_LEPIC	50S ribosomal protein L27	translation	955	382	89
sp Q72NG0 RS10_LEPIC	30S ribosomal protein S10	translation	1671	379	435
sp Q72PW7 SYG_LEPIC	Glycyl-tRNA synthetase (EC 6.1.1.14) (GlycinetRNA ligase) (GlyRS)	translation	272	353	249
sp Q72QT4 SYN_LEPIC	Asparaginyl-tRNA synthetase (EC 6.1.1.22) (AsparaginetRNA ligase) (AsnRS)	translation	231	331	200
sp Q72S74 DEF_LEPIC	Peptide deformylase (EC 3.5.1.88) (PDF) (Polypeptide deformylase)	translation	494	321	196
sp Q72MR4 SYM_LEPIC	Methionyl-tRNA synthetase (EC 6.1.1.10) (MethioninetRNA ligase) (MetRS)	translation	350	306	636
sp Q72NH2 RL24_LEPIC	50S ribosomal protein L24	translation	496	302	21
sp Q72NI5 RS13_LEPIC	30S ribosomal protein S13	translation	465	277	110
ref YP_000416.1 YP_000416.1	peptidyl-tRNA hydrolase	translation	251	248	196
sp Q72U06 SYP_LEPIC	Prolyl-tRNA synthetase (EC 6.1.1.15)	translation	316	239	427
	(ProlinetRNA ligase) (ProRS)				
ref YP 002858.1 YP 002858.1	30S ribosomal protein S1	translation	334	233	281
sp Q72RI5 RL28_LEPIC	50S ribosomal protein L28	translation	753	226	24
sp Q72QK5 SYD_LEPIC	Aspartyl-tRNA synthetase (EC 6.1.1.12) (AspartatetRNA ligase) (AspRS) -	translation	297	225	253
sp Q72NH4 RS14_LEPIC	30S ribosomal protein S14	translation	770	192	
sp Q72R38 SYK_LEPIC	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine- -tRNA ligase) (LysRS)	translation		179	211
sp Q72M80 SYFA_LEPIC	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (PhenylalaninetRNA ligase alpha chain) (Phe	translation	168	176	181
sp Q72U99 RS9 LEPIC	30S ribosomal protein S9	translation	282	129	47
sp Q72NX6 RS15_LEPIC	30S ribosomal protein S15	translation	405	120	54
sp Q72UY6 SYL_LEPIC	Leucyl-tRNA synthetase (EC 6.1.1.4) (LeucinetRNA ligase) (LeuRS)	translation	147	113	37
ref YP 001514.1 YP 001514.1	30S ribosomal protein S16	translation	2003	95	277
sp Q72PK9 RL35 LEPIC	50S ribosomal protein L35	translation	619	89	14
sp Q72U11 RRF_LEPIC	Ribosome recycling factor (Ribosome- releasing factor) (RRF)	translation	881		533
sp Q72RP1 RS21 LEPIC	30S ribosomal protein S21	translation	649		47
sp Q72NG9 RL29_LEPIC	50S ribosomal protein L29	translation	616		
sp Q72NH0 RS17 LEPIC	30S ribosomal protein S17	translation	596		21
sp Q72QL1 SYR_LEPIC	Arginyl-tRNA synthetase (EC 6.1.1.19) (ArgininetRNA ligase) (ArgRS)	translation	218		100
ref YP_001248.1 YP_001248.1	peptide chain release factor 3	translation	218		129
ref YP_003127.1 YP_003127.1	phenylalanyl-tRNA synthetase beta chain	translation	149		230
sp Q72V30 SYV_LEPIC	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine- -tRNA ligase) (ValRS)	translation			238
sp Q72RP6 SYY_LEPIC	Tyrosyl-tRNA synthetase (EC 6.1.1.1) (TyrosinetRNA ligase) (TyrRS) -	translation			103
ref YP_002767.1 YP_002767.1	translation initiation factor IF-1	translation			92
sp Q72P39 RL31_LEPIC	50S ribosomal protein L31	translation			75
sp Q72NH9 RL30_LEPIC	50S ribosomal protein L30	translation			71
sp Q72QK2 RS18_LEPIC	30S ribosomal protein S18	translation			64
sp Q72W38 RF1_LEPIC	Peptide chain release factor 1 (RF-1)	translation			50
sp Q72PL0 RL20_LEPIC	50S ribosomal protein L20	translation			47
ref YP_002204.1 YP_002204.1	tRNA (5-methylaminomethyl-2- thiouridylate)-methyltransferase	translation			47
sp Q72NH7 RL18_LEPIC	50S ribosomal protein L18	translation			30
sp Q72NG5 RS19_LEPIC	30S ribosomal protein S19	translation			24
sp Q72M46 SYE_LEPIC	Glutamyl-tRNA synthetase (EC 6.1.1.17) (GlutamatetRNA ligase) (GluRS)	translation			496

ref YP_000346.1 YP_000346.1	tryptophanyl-tRNA synthetase	translation			269
sp P62371 SYH LEPIC	Histidyl-tRNA synthetase (EC 6.1.1.21)	translation			257
-F1. 020. 210111_EE110	(HistidinetRNA ligase) (HisRS)	- cransiación			237
ref YP_002717.1 YP_002717.1	methionine sulfoxide reductase B	translation			121
ref YP 000596.1 YP 000596.1	ribosomal protein S18 acetyltransferase	translation			100
sp Q72QT1 SYC_LEPIC	Cysteinyl-tRNA synthetase (EC 6.1.1.16)	translation			96
-1-1-2	(CysteinetRNA ligase) (CysRS)				
sp Q72V33 RF2_LEPIC	Peptide chain release factor 2 (RF-2)	translation			96
ref YP 002792.1 YP 002792.1	elongation factor G	translation			85
sp Q72S34 FMT_LEPIC	Methionyl-tRNA formyltransferase (EC	translation			75
	2.1.2.9)				
sp Q72LR0 GIDA_LEPIC	tRNA uridine 5-	translation			75
	carboxymethylaminomethyl modification				
	enzyme gidA (Glucose-inhibited division				
	protein				
ref YP_002121.1 YP_002121.1	methionyl-tRNA(fmet) n-	translation			61
	formyltransferase				
sp Q72S28 TRMD_LEPIC	tRNA (guanine-N(1)-)-methyltransferase	translation			47
	(EC 2.1.1.31) (M1G-methyltransferase)				
	(trna				
ref YP_000529.1 YP_000529.1	peptide methionine sulfoxide reductase	translation			30
sp Q72PX0 PRMA_LEPIC	Ribosomal protein L11 methyltransferase	translation			30
	(EC 2.1.1) (L11 Mtase)				
sp Q72RZ0 PTH_LEPIC	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	translation			24
	(PTH)				
ref YP_001967.1 YP_001967.1	tRNA/rRNA methyltransferase	translation			24
ref YP_002181.1 YP_002181.1	tRNA delta(2)-isopentenylpyrophosphate	translation			21
	transferase		_		
sp Q72V55 RS20_LEPIC	30S ribosomal protein S20	translation			11
sp Q72VY6 TRME_LEPIC	tRNA modification GTPase trmE	translation			8
ref YP_003635.1 YP_003635.1	lysyl-tRNA synthetase homolog	translation			5
sp Q72NX4 RBFA_LEPIC	Ribosome-binding factor A	translation			
sp Q72W10 TILS_LEPIC	tRNA(IIe)-lysidine synthase (EC 6.3.4)	translation			
	(tRNA(IIe)-lysidine synthetase) (tRNA(IIe)-				
LOZONATINI 22 LEDIO	2-lysyl-cytidine				
sp Q72PM5 RL32_LEPIC	50S ribosomal protein L32	translation			
ref YP_000621.1 YP_000621.1	ribosomal protein serine acetyltransferase	translation			
sp Q72VZ0 RL34_LEPIC	50S ribosomal protein L34	translation	_		
sp Q72NI4 RL36_LEPIC	50S ribosomal protein L36	translation			
ref YP_001709.1 YP_001709.1	peptide chain release factor 2-like protein	translation			
flyp 002202 4 lyp 002202 4					
ref YP_002202.1 YP_002202.1	ribosomal large subunit pseudouridine	translation			
	ribosomal large subunit pseudouridine synthase C	translation			
ref YP_002202.1 YP_002202.1 ref YP_000813.1 YP_000813.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-				
ref YP_000813.1 YP_000813.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine- acetyltransferase	translation translation			
	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine- acetyltransferase tRNA (guanine-N(7)-)-methyltransferase	translation			
ref YP_000813.1 YP_000813.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-	translation translation			
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase)	translation translation translation			
ref YP_000813.1 YP_000813.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC	translation translation			
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55	translation translation translation			
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-	translation translation translation translation			
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-tRNA/rRNA methyltransferase	translation translation translation translation translation	1397	2237	114
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-	translation translation translation translation translation transport	1397	2237 1709	114 242
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_002466.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-tRNA/rRNA methyltransferase general secretory pathway protein G SecD	translation translation translation translation translation	1397 1431 1044	1709	
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_002466.1 sp Q72VY8 OXAA_LEPIC	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-tRNA/rRNA methyltransferase general secretory pathway protein G	translation translation translation translation translation transport transport	1431 1044	1709 1275	242 125
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_002466.1 sp Q72VY8 OXAA_LEPIC ref YP_003605.1 YP_003605.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-tRNA/rRNA methyltransferase general secretory pathway protein G SecD Inner membrane protein oxaA ExbB	translation translation translation translation translation transport transport transport transport transport	1431 1044 784	1709 1275 1256	242 125 47
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_002466.1 sp Q72VY8 0XAA_LEPIC ref YP_003605.1 YP_003605.1 ref YP_001529.1 YP_001529.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-tRNA/rRNA methyltransferase general secretory pathway protein G SecD Inner membrane protein oxaA ExbB general secretory pathway protein D	translation translation translation translation translation transport transport transport transport transport transport transport transport	1431 1044 784 658	1709 1275 1256 691	242 125 47 158
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_002466.1 sp Q72VY8 OXAA_LEPIC ref YP_003605.1 YP_003605.1 ref YP_001529.1 YP_001529.1 ref YP_000985.1 YP_000985.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-tRNA/rRNA methyltransferase general secretory pathway protein G SecD Inner membrane protein oxaA ExbB general secretory pathway protein D OppA	translation translation translation translation translation transport transport transport transport transport transport transport transport transport transport	1431 1044 784 658 555	1709 1275 1256 691 610	242 125 47 158 114
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_002466.1 sp Q72VY8 OXAA_LEPIC ref YP_003605.1 YP_003605.1 ref YP_001529.1 YP_001529.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine-acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA-tRNA/rRNA methyltransferase general secretory pathway protein G SecD Inner membrane protein oxaA ExbB general secretory pathway protein D OppA Pyrophosphate-energized proton pump	translation translation translation translation translation transport transport transport transport transport transport transport transport	1431 1044 784 658	1709 1275 1256 691	242 125 47 158
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_002466.1 sp Q72VY8 OXAA_LEPIC ref YP_003605.1 YP_003605.1 ref YP_001529.1 YP_001529.1 ref YP_000985.1 YP_000985.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine- acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)- methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA- tRNA/rRNA methyltransferase general secretory pathway protein G SecD Inner membrane protein oxaA ExbB general secretory pathway protein D OppA Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-energized	translation translation translation translation translation transport transport transport transport transport transport transport transport transport transport	1431 1044 784 658 555	1709 1275 1256 691 610	242 125 47 158 114
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_001532.1 sp Q72VY8 OXAA_LEPIC ref YP_003605.1 YP_003605.1 ref YP_001529.1 YP_001529.1 sp Q72Q29 HPPA_LEPIC	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine- acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)- methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA- tRNA/rRNA methyltransferase general secretory pathway protein G SecD Inner membrane protein oxaA ExbB general secretory pathway protein D OppA Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-energized inorganic pyrophosphatase)	translation translation translation translation translation transport transport transport transport transport transport transport transport transport transport transport	1431 1044 784 658 555 450	1709 1275 1256 691 610 578	242 125 47 158 114 162
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_001532.1 sp Q72VY8 OXAA_LEPIC ref YP_003605.1 YP_003605.1 ref YP_001529.1 YP_001529.1 sp Q72Q29 HPPA_LEPIC ref YP_003606.1 YP_003606.1	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine- acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)- methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA- tRNA/rRNA methyltransferase general secretory pathway protein G SecD Inner membrane protein oxaA ExbB general secretory pathway protein D OppA Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-energized inorganic pyrophosphatase) ExbD	translation translation translation translation translation transport transport transport transport transport transport transport transport transport transport	1431 1044 784 658 555 450	1709 1275 1256 691 610 578	242 125 47 158 114 162
ref YP_000813.1 YP_000813.1 sp Q72W15 TRMB_LEPIC sp Q72NX5 TRUB_LEPIC ref YP_002857.1 YP_002857.1 ref YP_001532.1 YP_001532.1 ref YP_002466.1 YP_001532.1 sp Q72VY8 OXAA_LEPIC ref YP_003605.1 YP_003605.1 ref YP_001529.1 YP_001529.1 sp Q72Q29 HPPA_LEPIC	ribosomal large subunit pseudouridine synthase C ribosomal-protein-serine- acetyltransferase tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)- methyltransferase) tRNA pseudouridine synthase B (EC 5.4.99) (tRNA pseudouridine 55 synthase) (Psi55 synthase) (tRNA- tRNA/rRNA methyltransferase general secretory pathway protein G SecD Inner membrane protein oxaA ExbB general secretory pathway protein D OppA Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-energized inorganic pyrophosphatase)	translation translation translation translation translation transport transport transport transport transport transport transport transport transport transport transport	1431 1044 784 658 555 450	1709 1275 1256 691 610 578	242 125 47 158 114 162

ref YP_002614.1 YP_002614.1	hypothetical protein LIC12693	transport	377	344	219
ref YP_001580.1 YP_001580.1	biopolymer transport exbd-related	transport	223	241	8
	transmembrane protein				
ref YP_002905.1 YP_002905.1	sulfate Permease	transport		116	
ref YP_000348.1 YP_000348.1	hypothetical protein LIC10359	transport		69	17
sp Q75FW6 ACP_LEPIC	Acyl carrier protein (ACP)	transport			324
ref YP_003379.1 YP_003379.1	cystine-binding periplasmic protein	transport			143
	precursor				
ref YP_002868.1 YP_002868.1	nitrogen regulatory IIA protein	transport			50
ref YP_002465.1 YP_002465.1	SecF	transport			44
ref YP_002029.1 YP_002029.1	SecG	transport			34
ref YP_002274.1 YP_002274.1	export protein	transport			17
ref YP_002443.1 YP_002443.1	cystine-binding periplasmic protein precursor	transport			114
ref YP_002452.1 YP_002452.1	fatty acid transport protein	transport			61
ref YP_002676.1 YP_002676.1	DshA	transport			44
ref YP_001531.1 YP_001531.1	general secretory pathway protein F	transport			17
ref YP_003542.1 YP_003542.1	tonB-dependent outer membrane receptor	transport			14
ref YP_003607.1 YP_003607.1	hypothetical protein LIC20218	transport			14
ref YP_003335.1 YP_003335.1	hypothetical protein LIC13432	transport			11
ref YP_002156.1 YP_002156.1	cation:proton antiporter	transport			
ref YP_001506.1 YP_001506.1	phosphocarrier protein hpr	transport			
ref YP_001536.1 YP_001536.1	type II secretion pathway related protein	transport			
	etpK-like protein				
ref YP_001590.1 YP_001590.1	phosphotransferase system enzyme I	transport			
ref YP_003603.1 YP_003603.1	hypothetical protein LIC20214	transport			
ref YP_002949.1 YP_002949.1	amino acid transporter	transport			
ref YP_000426.1 YP_000426.1	ammonium transporter	transport			
ref YP_000573.1 YP_000573.1	ammonium transporter	transport			
ref YP_002514.1 YP_002514.1	drug proton antiporter	transport			
ref YP_002318.1 YP_002318.1	drug/metabolite exporter	transport			
ref YP_000058.1 YP_000058.1	drug:Na+ antiporter of the multi antimicrobial extrusion family	transport			
ref YP_000972.1 YP_000972.1	hypothetical protein LIC10998	transport			
ref YP_003540.1 YP_003540.1	multidrug-efflux transporter	transport			
ref YP_002638.1 YP_002638.1	putative 4-hydroxybenzoate transporter transmembrane protein	transport			
ref YP_003461.1 YP_003461.1	small conductance mechanosensitive ion channel	transport			
ref YP_002593.1 YP_002593.1	small conductance mechanosensitive ion	transport			
	channel				
ref YP_000873.1 YP_000873.1	TonB-dependent outer membrane	transport			
roflyD 002011 1 JyD 002011 1	receptor TonB-dependent outer membrane	transport			
ref YP_002911.1 YP_002911.1	receptor	transport			
ref YP_001646.1 YP_001646.1	TonB-dependent outer membrane receptor	transport			
ref YP_003592.1 YP_003592.1	bile acid Na+ symporter	transport			
ref YP_000869.1 YP_000869.1	biopolymer transport exbB-like protein	transport			
ref YP_000867.1 YP_000867.1	ExbD	transport			
ref YP_000868.1 YP_000868.1	ExbD	transport			
ref YP_003560.1 YP_003560.1	ExbD/TolR biopolymer transport protein	transport			
ref YP_001078.1 YP_001078.1	polysaccharide exporter	transport			
ref YP_000727.1 YP_000727.1	SecE	transport			
ref YP_001920.1 YP_001920.1	sec-independent protein translocase	transport			
sp Q72QX8 TATA_LEPIC	Sec-independent protein translocase	transport			
	protein tatA/E homolog -				