Supplementary information: Proteome-wide 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, 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. 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. 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
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 proteome-wide 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 and plays an important role during pathogenesis.

Chemotaxis: The L. interrogans genome 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 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 but sub-stoichiometrical in vivo. 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 $V_{\text{max}}$ within the cell, as suggested earlier. In summary, the components of the $L.\text{interrogans}$ 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 $L.\text{interrogans}$ maintains its spiraled cell shape. The contribution of the peptidoglycan layer, the periplasmic flagella and the cytoplasmic filaments has been discussed 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 $B.\text{burgdorferi}$ it is unlikely that the cell shape is determined by the flagellum in $L.\text{interrogans}$. The same arguments can be made for apparent cytoplasmic filaments. These filaments have been visualized using tomography and ascribed to MreB. This protein has a longitudinal subunit spacing of 5.1 nm and occurs in 2500 copies per cell in $Leptospira$, allowing for a maximum of $\sim 13 \, \mu m$ 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 - 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. 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 (Table S2), including several peptidoglycan associated membrane
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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. Thereby, classification due to the Eigenvalue that corresponds to the major codon usage trend (so called axis1) 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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## Table S1 Absolute quantification based on SRM

| Accession Number | Protein description                                                                 | Reference peptide sequence | Control (fmol/ul) | Ciprofloxacin (fmol/ul) | Control (copies/cell SRM*) | Ciprofloxacin (copies/cell SRM*) |
|------------------|--------------------------------------------------------------------------------------|-----------------------------|------------------|------------------------|---------------------------|----------------------------------|
| sp|Q725Y1|ATPA_L EPIC | ATP synthase subunit alpha (EC 3.6.3.14) (ATPase subunit alpha) | ILEVPVGPELLGR | 20.95 | 31.72 | 7424 | 11649 |
| sp|Q725X0|ATPB_L EPIC | ATP synthase subunit beta (EC 3.6.3.14) (ATPase subunit beta) | FSGAQGSEVSALLGR | 15.40 | 21.49 | 4749 | 7189 |
| sp|Q72QJ2|CLPB_L EPIC | Chaperone clpB | AVDLIIDEASSK | 1.02 | 1.13 | 414 | 632 |
| sp|Q72R01|CLPP2_L EPIC | ATP-dependent Clp protease proteolytic subunit 2 (EC 3.4.21.92) | IADIQLEGLR | 1.66 | 2.54 |
| ref|YP_000584.1|Y P_000584.1 | fatty acid synthase subunit beta | TEVITHANLVR | 4.37 | 2.41 | 1348 | 766 |
| ref|YP_001158.1|Y P_001158.1 | flagellar hook protein | VATAVFNAPAGLDK | 0.34 | 0.28 | 105 | 82 |
| ref|YP_001355.1|Y P_001355.1 | flagellar M-ring protein | GPTDPGAPGTEPNIAPOGYK | 0.16 | 0.15 | 43 | 35 |
| ref|YP_001839.1|Y P_001839.1 | flagellin protein | ANLGAYFNR | 47.25 | 72.95 | 18043 |
| sp|P61438|CH60_L EPIC | 60 kDa chaperonin (Protein Cpn60) (GroEL protein) (Heat shock 58 kDa protein) | AVTAAVESIQK | 48.48 | 50.17 | 17711 |
| sp|P61436|CH10_L EPIC | 10 kDa chaperonin (Protein Cpn10) (GroES protein) (Heat shock 10 kDa protein) | VEDALSATR | 47.96 | 60.18 |
| ref|YP_002145.1|Y P_002145.1 | Hsp15-like protein | ILEEVSFGDPDLPESQR | 0.95 | 1.01 |
| sp|Q72QJ2|HSP15_L EPIC | 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 |
| sp|P62217|RECA_L EPIC | Protein recA (Recombinase A) | IVEIYGPRESSK | 2.58 | 33.70 | 795 | 12823 |
| sp|Q72QK0|RS6_L EPIC | 30S ribosomal protein S6 | EFLNQINLR | 19.13 | 11.49 | 5899 | 4077 |
| ref|YP_002772.1|Y P_002772.1 | 30S ribosomal protein S5 | ITNLVLPNNUQIQK | 10.05 | 10.59 | 3100 | 3264 |
| sp|Q72NBI|RPOA_L EPIC | DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) | FTDLGEVGR | 9.70 | 10.35 | 2991 | 3204 |
| sp|Q72UA7|RPOC_L EPIC | DNA-directed RNA polymerase beta chain (EC 2.7.7.6) | FATSOLNDLYR | 9.48 | 8.29 | 2923 | 2535 |

* Selected reaction monitoring
| Accession number | Protein description                                | GO annotation                          | Control (copies/cell MS1) | Ciprofloxacin 24h (copies/cell MS1) | Control (copies/cell Spectral counts) |
|------------------|---------------------------------------------------|----------------------------------------|---------------------------|------------------------------------|--------------------------------------|
| refYP_003221.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 1185                      | 1796                               | 923                                  |
| refYP_001565.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 504                       | 443                                | 85                                   |
| refYP_000417.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 240                       | 394                                | 228                                  |
| refYP_000517.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 386                       | 281                                | 281                                  |
| refYP_000502.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 275                       | 271                                | 75                                   |
| refYP_001503.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 227                       | 209                                | 169                                  |
| refYP_000922.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 217                       | 184                                | 30                                   |
| refYP_000224.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 143                       | 179                                | 75                                   |
| refYP_002457.1    | sulfate ABC transporter periplasmic sulphate-binding protein precursor | ABC-transporter | 275 | 164 | 403 |
| refYP_002606.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 326                       | 207                                | 207                                  |
| refYP_003334.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 143                       | 82                                 | 82                                   |
| refYP_003287.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 47                        | 61                                 | 61                                   |
| refYP_000517.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 27                        | 34                                 | 34                                   |
| refYP_000615.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 21                        | 21                                 | 21                                   |
| refYP_001755.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 17                        | 17                                 | 17                                   |
| refYP_000119.1    | ABC transporter permease protein                  | ABC-transporter                        | 14                        | 14                                 | 14                                   |
| refYP_000119.1    | ABC transporter permease protein                  | ABC-transporter                        | 14                        | 14                                 | 14                                   |
| refYP_000517.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 14                        | 14                                 | 14                                   |
| refYP_003285.1    | dipeptide ABC transport system permease protein  | ABC-transporter                        | 11                        | 11                                 | 11                                   |
| refYP_000615.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 5                         | 5                                  | 5                                    |
| refYP_000655.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 5                         | 5                                  | 5                                    |
| refYP_000564.1    | ABC transporter, ATP-binding protein              | ABC-transporter                        | 5                         | 5                                  | 5                                    |
| refYP_002605.1    | ABC transporter, membrane spanning protein       | ABC-transporter                        | 14                        | 14                                 | 14                                   |
| refYP_000105.1    | ABC transporter integral membrane protein         | ABC-transporter                        | 11                        | 11                                 | 11                                   |
| refYP_001456.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 17                        | 17                                 | 17                                   |
| refYP_000180.1    | ABC transporter permease protein                  | ABC-transporter                        | 27                        | 27                                 | 27                                   |
| refYP_000328.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 82                        | 82                                 | 82                                   |
| refYP_000659.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 30                        | 30                                 | 30                                   |
| refYP_002866.1    | dipeptide/oligopeptide ABC transport system permease protein | ABC-transporter | 85 | 85 | 85 |
| refYP_000132.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 923                       | 923                                | 923                                  |
| refYP_001396.1    | ABC transporter ATP-binding protein               | ABC-transporter                        | 27                        | 27                                 | 27                                   |
| refYP_000517.1    | ABC transporter periplasmic dipeptide-binding protein | ABC-transporter | 217 | 217 | 217 |
| refYP_001756.1    | ABC transporter permease protein                  | ABC-transporter                        | 143                       | 143                                | 143                                  |
| refYP_001806.1    | ABC transporter permease protein                  | ABC-transporter                        | 27                        | 27                                 | 27                                   |
| refYP_002230.1    | ABC transporter permease protein                  | ABC-transporter                        | 27                        | 27                                 | 27                                   |
| refYP_003220.1    | ABC transporter permease protein                  | ABC-transporter                        | 27                        | 27                                 | 27                                   |
| refYP_002455.1    | sulfate ABC transport system permease protein    | ABC-transporter                        | 11                        | 11                                 | 11                                   |
| refYP_000417.1    | cell division protein                             | cell cycle                             | 1713                      | 1200                               | 246                                  |
| refYP_001537.1    | FtsA                                              | cell cycle                             | 433                       | 533                                | 75                                   |
| refYP_001565.1    | cell division ATPase                              | cell cycle                             | 71                        | 71                                 | 71                                   |
| refYP_002882.1    | cell division protein FtsZ                        | cell cycle                             | 50                        | 50                                 | 50                                   |
| refYP_002883.1    | FtsA                                              | cell cycle                             | 238                       | 238                                | 238                                  |
| Ref | YP_002381.1 | YP_002381.1 | Hypothetical protein LIC12452 | Cell cycle | 54 |
|-----|-------------|-------------|-------------------------------|------------|----|
| Ref | YP_000814.1 | YP_000814.1 | Cell division inhibitor       | Cell cycle |      |
| 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 |
| Ref | YP_003091.1 | YP_003091.1 | Methyl-accepting chemotaxis-like | Chemotaxis | 3700 |
| Ref | YP_001482.1 | YP_001482.1 | Chemotaxis protein               | Chemotaxis | 628  |
| Ref | YP_001185.1 | YP_001185.1 | Methyl-accepting chemotaxis transmembrane protein | Chemotaxis | 263  |
| Ref | YP_001681.1 | YP_001681.1 | Histidine kinase response regulator hybrid protein | Chemotaxis | 137  |
| Ref | YP_003195.1 | YP_003195.1 | Histidine kinase sensor protein  | Chemotaxis | 37   |
| Ref | YP_001170.1 | YP_001170.1 | Histidine kinase sensor protein  | Chemotaxis | 17   |
| Ref | P62641| CHEB1_LEPIC | Chemotaxis response regulator protein-gluanate methyl transferase of group 1 operon (EC 3.1.1.61) - Lep | Chemotaxis | 234  |
| Ref | YP_001994.1 | YP_001994.1 | Histidine kinase response regulator hybrid protein | Chemotaxis | 21   |
| 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 | 37   |
| Ref | P62641| CHEB3_LEPIC | Chemotaxis response regulator protein-gluanate methyl transferase of group 3 operon (EC 3.1.1.61) - Lep | Chemotaxis | 27   |
| Ref | YP_001994.1 | YP_001994.1 | Histidine kinase response regulator hybrid protein | Chemotaxis | 21   |
| Ref | YP_002021.1 | YP_002021.1 | Histidine kinase sensor protein  | Chemotaxis | 17   |
| Ref | YP_003019.1 | YP_003019.1 | Histidine kinase response regulator hybrid protein | Chemotaxis | 34   |
| Ref | YP_002994.1 | YP_002994.1 | Histidine kinase response regulator hybrid protein | Chemotaxis | 30   |
| Ref | YP_002031.1 | YP_002031.1 | Histidine kinase sensor protein  | Chemotaxis | 30   |
| Ref | YP_002170.1 | YP_002170.1 | Histidine kinase response regulator hybrid protein | Chemotaxis | 17   |
| 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   |
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| Ref         | Accession         | Protein Description                                      | Chemotaxis |
|-------------|-------------------|----------------------------------------------------------|------------|
| 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|hystidine kinase response regulator hybrid protein|chemotaxis| |
| ref|YP_001401.1|YP_001401.1|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 transmembrane protein|chemotaxis| |
| 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_003130.1|YP_003130.1|methyl-accepting chemotaxis protein|chemotaxis| |
| ref|YP_001996.1|YP_001996.1|histidine kinase protein|chemotaxis| |
| ref|YP_000536.1|YP_000536.1|histidine kinase protein|chemotaxis| |
| ref|YP_000323.1|YP_000323.1|histidine kinase protein|chemotaxis| |
| ref|YP_001258.1|YP_001258.1|histidine kinase sensor protein|chemotaxis| |
| ref|YP_000120.1|YP_000120.1|histidine kinase sensor protein|chemotaxis| |
| ref|YP_003613.1|YP_003613.1|histidine kinase sensor protein|chemotaxis| |
| ref|YP_000096.1|YP_000096.1|histidine kinase sensor protein|chemotaxis| |
| ref|YP_003196.1|YP_003196.1|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_000069.1|YP_000069.1|methyl-accepting chemotaxis transducer transmembrane protein|chemotaxis| |
| ref|YP_000167.1|YP_000167.1|hypoetical protein LIC10175|Cipro induced hypothetical protein|422|39916|657|
| ref|YP_002538.1|YP_002538.1|hypoetical protein LIC12615|Cipro induced hypothetical protein|364|31064|682|
| ref|YP_000168.1|YP_000168.1|hypoetical protein LIC10176|Cipro induced hypothetical protein|224|24432|219|
| ref|YP_000169.1|YP_000169.1|hypoetical protein LIC10177|Cipro induced hypothetical protein|240|13249|230|
| ref|YP_002537.1|YP_002537.1|hypoetical protein LIC12614|Cipro induced hypothetical protein|73|9336|472|
| ref|YP_002539.1|YP_002539.1|hypoetical protein LIC12616|Cipro induced hypothetical protein|8186|207|
| ref|YP_000166.1|YP_000166.1|hypoetical protein LIC10174|Cipro induced hypothetical protein|131|5860|200|
| ref|YP_002523.1|YP_002523.1|hypoetical protein LIC12600|Cipro induced hypothetical protein|145|2242|68|
| ref|YP_002526.1|YP_002526.1|hypoetical protein LIC12603|Cipro induced hypothetical protein|2050|125|
| ref|YP_002536.1|YP_002536.1|hypoetical protein LIC12613|Cipro induced hypothetical protein|1784|151|
| ref|YP_002525.1|YP_002525.1|hypoetical protein LIC12602|Cipro induced hypothetical protein|1720|5|
| Ref | Accession | Protein Name | Membrane Location | Cipro Induced Protein | Copies | Fold Change |
|-----|-----------|--------------|------------------|----------------------|--------|-------------|
| 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_002815.1|YP_002815.1   | Cytoplasmic membrane protein cytoplasmic membrane |           |            |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| 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 membrane |
| ref|YP_003595.1|YP_003595.1 | cytoplasmic membrane protein | cytoplasmic membrane |
| ref|YP_003621.1|YP_003621.1 | cytoplasmic membrane protein | cytoplasmic 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 membrane |
| ref|YP_002307.1|YP_002307.1 | cytoplasmic membrane protein | cytoplasmic membrane |
| ref|YP_000181.1|YP_000181.1 | cytoplasmic membrane protein | cytoplasmic membrane |
| ref|YP_000802.1|YP_000802.1 | cytoplasmic membrane protein | cytoplasmic membrane |
| ref|YP_003621.1|YP_003621.1 | cytoplasmic membrane protein | cytoplasmic membrane |
| ref|YP_000150.1|YP_000150.1 | hypothetical protein LIC10158 | DNA/RNA binding |
| ref|YP_003659.1|YP_003659.1 | ParB | DNA/RNA binding |
| sp|Q72Q67|HFQ_LEPIC | Protein hfq | DNA/RNA binding |
| ref|YP_001152.1|YP_001152.1 | hypothetical protein LIC11182 | DNA/RNA binding |
| ref|YP_003659.1|YP_003659.1 | ParB | DNA/RNA binding |
| sp|Q72Q67|HFQ_LEPIC | Protein hfq | DNA/RNA binding |
| ref|YP_000150.1|YP_000150.1 | hypothetical protein LIC10158 | DNA/RNA binding |
| ref|YP_003659.1|YP_003659.1 | ParB | DNA/RNA binding |
| sp|Q72Q67|HFQ_LEPIC | Protein hfq | DNA/RNA binding |
| ref|YP_0001954.1|YP_0001954.1 | ParB | DNA/RNA binding |
| ref|YP_0001954.1|YP_0001954.1 | ParB | DNA/RNA binding |
| ref|YP_003413.1|YP_003413.1 | ParB | DNA/RNA binding |
| ref|YP_000160.1|YP_000160.1 | ParB family protein | DNA/RNA binding |
| ref|YP_0000905.1|YP_0000905.1 | ParB family protein | DNA/RNA binding |
| ref|YP_0000905.1|YP_0000905.1 | ParB family protein | DNA/RNA binding |
| ref|YP_002583.1|YP_002583.1 | DNA binding protein | DNA/RNA binding |
| ref|YP_003497.1|YP_003497.1 | DNA binding protein | DNA/RNA 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 binding |
| ref|YP_0000157.1|YP_0000157.1 | DNA mismatch repair protein | DNA/RNA binding |
| sp|P62217|RECA_LEPIC | Protein recA (Recombinase A) | DNA/RNA metabolic |
| Reference | Gene ID | Description | Process | Copies | Synthesis | Degradation | Net Difference |
|-----------|---------|-------------|---------|--------|-----------|-------------|----------------|
| ref|YP_002622.1|YP_002622.1|polynucleotide phosphorylase|DNA/RNA metabolic process|1821|1796|2354|
| ref|YP_001743.1|YP_001743.1|ATP-dependent DNA helicase|DNA/RNA metabolic process|1382|1174|611|
| ref|YP_002046.1|YP_002046.1|single-stranded DNA binding protein|DNA/RNA metabolic process|1339|1030|447|
| sp|Q72500|NRDJ_LEPIC|Vitamin B12-dependent ribonucleotide reductase (EC 1.17.4.1) (Ribonucleoside-diphosphate reductase)|DNA/RNA metabolic process|438|598|269|
| ref|YP_003252.1|YP_003252.1|DNA gyrase subunit A|DNA/RNA metabolic process|590|594|395|
| ref|YP_000006.1|YP_000006.1|DNA gyrase subunit A|DNA/RNA metabolic process|536|537|230|
| ref|YP_001639.1|YP_001639.1|endonuclease|DNA/RNA metabolic process|256|443|558|
| ref|YP_000005.1|YP_000005.1|DNA gyrase subunit B|DNA/RNA metabolic process|571|420|242|
| ref|YP_001111.1|YP_001111.1|ribonuclease D|DNA/RNA metabolic process|316|361|223|
| ref|YP_000243.1|YP_000243.1|exonuclease|DNA/RNA metabolic process|196|357|114|
| sp|Q72RM8|UVRA_LEPIC|UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)|DNA/RNA metabolic process|377|342|200|
| ref|YP_003170.1|YP_003170.1|ribonuclease D|DNA/RNA metabolic process|200|172|75|
| sp|P62038|Y2886_LEPIC|UPF0082 protein LIC_12886|DNA/RNA metabolic process|149|62|103|
| ref|YP_001911.1|YP_001911.1|hypotheical protein LIC11971|DNA/RNA metabolic process|281|
| sp|Q72N95|UVRB_LEPIC|UvrABC system protein B (Protein uvrB) (Excinuclease ABC subunit B)|DNA/RNA metabolic process|132|
| sp|Q72S95|XERD_LEPIC|Tyrosine recombinase xerD|DNA/RNA metabolic process|71|
| ref|YP_003490.1|YP_003490.1|phage-related integrase/recombinase|DNA/RNA metabolic process|68|
| ref|YP_002343.1|YP_002343.1|chromosome segregation protein|DNA/RNA metabolic process|54|
| ref|YP_002442.1|YP_002442.1|DNA mismatch repair protein|DNA/RNA metabolic process|40|
| ref|YP_003189.1|YP_003189.1|NAD dependent DNA ligase|DNA/RNA metabolic process|226|
| ref|YP_002043.1|YP_002043.1|replicative DNA helicase|DNA/RNA metabolic process|82|
| Accession | Description                                                                 | Process                          | Count |
|-----------|-----------------------------------------------------------------------------|---------------------------------|-------|
| ref|YP_001112.1|YP_001112.1| RadA          | DNA/RNA metabolic process | 78    |
| ref|YP_001118.1|YP_001118.1| DNA helicase subunit A | DNA/RNA metabolic process | 61    |
| sp|P61669|MUTS_LEPIC| DNA mismatch repair protein mutS | DNA/RNA metabolic process | 61    |
| sp|Q72PL7|SCPA_LEPIC| Segregation and condensation protein A | DNA/RNA metabolic process | 54    |
| sp|P61534|RUVB_LEPIC| Holliday junction ATP | DNA/RNA metabolic process | 50    |
| sp|Q72LS5|RECR_LEPIC| Recombination protein recR | DNA/RNA metabolic process | 50    |
| sp|Q72RZ8|EX7S_LEPIC| Probable exodeoxyribonuclease VII small subunit (EC 3.1.11.6) (Exonuclease VII small subunit) | DNA/RNA metabolic process | 40    |
| ref|YP_001036.1|YP_001036.1| single-stranded DNA exonuclease | DNA/RNA metabolic process | 30    |
| ref|YP_001582.1|YP_001582.1| ATP-dependent DNA helicase | DNA/RNA metabolic process | 24    |
| ref|YP_001413.1|YP_001413.1| exodeoxyribonuclease | DNA/RNA metabolic process | 24    |
| sp|Q72RZ7|EX7L_LEPIC| Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6) (Exonuclease VII large subunit) | DNA/RNA metabolic process | 21    |
| ref|YP_001684.1|YP_001684.1| ATP-dependent DNA helicase | DNA/RNA metabolic process | 17    |
| ref|YP_000903.1|YP_000903.1| Type I restriction enzyme | DNA/RNA metabolic process | 17    |
| ref|YP_002610.1|YP_002610.1| ATP-dependent DNA helicase | DNA/RNA metabolic process | 11    |
| ref|YP_002512.1|YP_002512.1| ATP-dependent DNA helicase | DNA/RNA metabolic process | 8     |
| ref|YP_001711.1|YP_001711.1| Endonuclease III | DNA/RNA metabolic process | 8     |
| ref|YP_000652.1|YP_000652.1| Mrr | DNA/RNA metabolic process | 8     |
| ref|YP_001295.1|YP_001295.1| Ribonuclease BN transmembrane protein | DNA/RNA metabolic process | 8     |
| ref|YP_001226.1|YP_001226.1| Exopolyphosphatase | DNA/RNA metabolic process | 8     |
| sp|Q75FW5|RNC_LEPIC| Ribonuclease III (EC 3.1.26.3) (RNase III) | DNA/RNA metabolic process | 8     |
| ref|YP_002607.1|YP_002607.1| Exodeoxyribonuclease v alpha chain | DNA/RNA metabolic process | 8     |
| Ref | Description                                                                 | Function           |
|-----|------------------------------------------------------------------------------|--------------------|
| YP_002585.1 | IS1500 transposase                                                           | DNA/RNA metabolic process |
| YP_003279.1 | IS1500 transposase                                                           | DNA/RNA metabolic process |
| YP_000229.1 | 3-methyladenine DNA glycosylase                                             | DNA/RNA metabolic process |
| YP_002294.1 | 3-methyladenine DNA glycosylase                                             | DNA/RNA metabolic process |
| YP_002976.1 | 3-methyl-adenine DNA glycosylase I                                         | DNA/RNA metabolic process |
| Q72WD6 | Chromosomal replication initiator protein DNAA                               | DNA/RNA metabolic process |
| YP_000406.1 | DNA helicase II                                                              | DNA/RNA metabolic process |
| YP_002608.1 | Exodeoxyribonuclease V beta chain                                            | DNA/RNA metabolic process |
| YP_002609.1 | Exodeoxyribonuclease V gamma chain                                           | DNA/RNA metabolic process |
| YP_003085.1 | Exonuclease                                                                  | DNA/RNA metabolic process |
| YP_001991.1 | IS1500 transposase                                                           | DNA/RNA metabolic process |
| YP_002642.1 | IS1533 transposase                                                           | DNA/RNA metabolic process |
| YP_000557.1 | IS1533 transposase                                                           | DNA/RNA metabolic process |
| YP_000975.1 | IS1533 transposase                                                           | DNA/RNA metabolic process |
| YP_002641.1 | IS1533 transposase                                                           | DNA/RNA metabolic process |
| YP_001525.1 | Mg chelatase subunit chII                                                   | DNA/RNA metabolic process |
| YP_001510.1 | Primosomal protein N'                                                        | DNA/RNA metabolic process |
| YP_002801.1 | Putative Holliday junction endodeoxyribonuclease protein                     | DNA/RNA metabolic process |
| YP_000954.1 | Transposase, IS1501                                                         | DNA/RNA metabolic process |
| YP_000763.1 | Transposase, IS1501                                                         | DNA/RNA metabolic process |
| YP_000764.1 | Transposase, IS1501                                                         | DNA/RNA metabolic process |
| YP_001311.1 | Transposase, IS1501                                                         | DNA/RNA metabolic process |
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| Ref      | Protein 1 | Protein 2 | Process                         |
|----------|-----------|-----------|---------------------------------|
| ref|YP_001310.1|YP_001310.1|transposase, IS1501 | DNA/RNA metabolic process |
| ref|YP_003281.1|YP_003281.1|transposase, IS1501 | DNA/RNA metabolic process |
| ref|YP_000497.1|YP_000497.1|transposase, IS3      | DNA/RNA metabolic process |
| ref|YP_000487.1|YP_000487.1|transposase, IS3      | DNA/RNA metabolic process |
| ref|YP_003069.1|YP_003069.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000254.1|YP_000254.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000255.1|YP_000255.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000724.1|YP_000724.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000725.1|YP_000725.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000861.1|YP_000861.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000862.1|YP_000862.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000863.1|YP_000863.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000864.1|YP_000864.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_000865.1|YP_000865.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_001001.1|YP_001001.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_001410.1|YP_001410.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_001411.1|YP_001411.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_001412.1|YP_001412.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_001432.1|YP_001432.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_001433.1|YP_001433.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_001434.1|YP_001434.1|transposase, ISlin1    | DNA/RNA metabolic process |
| ref|YP_003067.1|YP_003067.1|transposase, ISlin1    | DNA/RNA |
| Ref | ID | Description | Activity | Activity | Activity |
|-----|-----|-------------|----------|----------|----------|
| ref|YP_002974.1|YP_002974.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_002980.1|YP_002980.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_002981.1|YP_002981.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003023.1|YP_003023.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003024.1|YP_003024.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003025.1|YP_003025.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003068.1|YP_003068.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_000640.1|YP_000640.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_001002.1|YP_001002.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003372.1|YP_003372.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_000035.1|YP_000035.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_002666.1|YP_002666.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_002666.1|YP_002666.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003164.1|YP_003164.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_000137.1|YP_000137.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003326.1|YP_003326.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003165.1|YP_003165.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_001784.1|YP_001784.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_002665.1|YP_002665.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_001587.1|YP_001587.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003326.1|YP_003326.1|metabolic process|DNA/RNA metabolic process|
| ref|YP_003165.1|YP_003165.1|metabolic process|DNA/RNA metabolic process|

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| Accession | Description | Electron Carrier Activity | Copies per Cell |
|-----------|-------------|--------------------------|-----------------|
| sp|Q72VZ9|NUOI_LEPIC | NADH-quinone oxidoreductase subunit I (EC 1.6.99.5) (NADH dehydrogenase I subunit I) [NDH-1 subunit] | 14 |
| ref|YP_002794.1|YP_002794.1 | Hypothetical protein LIC1278 | 316 |
| sp|Q72RB6|QUEF_LEPIC | NADPH-dependent 7-cyano-7-deazaguanine reductase (EC 1.7.1.-) (NADPH-dependent nitrile oxidoreductase) | 114 |
| ref|YP_003524.1|YP_003524.1 | Ferredoxin-like protein | 50 |
| ref|YP_002662.1|YP_002662.1 | NADH dehydrogenase I B subunit | 27 |
| ref|YP_003327.1|YP_003327.1 | Hydrogenase subunit | 8 |
| ref|YP_002669.1|YP_002669.1 | NADH dehydrogenase I K subunit | 8 |
| ref|YP_002672.1|YP_002672.1 | NADH dehydrogenase I N subunit |  |
| ref          | gene ID     | protein Name                  | Structure          | count 1 | count 2 | count 3 |
|--------------|-------------|-------------------------------|--------------------|---------|---------|---------|
| ref[YP_001417.1] | YP_001417.1 | LipL31                        | external encapsulating structure | 1422    | 1412    | 292     |
| ref[YP_000119.1] | YP_000119.1 | LipL45-like protein           | external encapsulating structure | 455     | 604     | 339     |
| ref[YP_003634.1] | YP_003634.1 | peptidoglycan-associated membrane protein | external encapsulating structure | 231     | 339     | 37      |
| ref[YP_000772.1] | YP_000772.1 | surface antigen               | external encapsulating structure | 147     | 105     | 85      |
| ref[YP_003506.1] | YP_003506.1 | LipL45 homologue              | external encapsulating structure |          |         | 177     |
| ref[YP_000050.1] | YP_000050.1 | peptidoglycan-associated membrane protein | external encapsulating structure |          |         | 162     |
| ref[YP_00576.1]  | YP_00576.1  | peptidoglycan-associated membrane protein | external encapsulating structure |          |         | 118     |
| ref[YP_002865.1] | YP_002865.1 | S-layer-like protein          | external encapsulating structure |          |         |         |
| 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 structure |          |         |         |
| ref[YP_000521.1] | YP_000521.1 | peptidoglycan-associated periplasmic protein | external encapsulating structure |          |         |         |
| ref[YP_003380.1] | YP_003380.1 | peptidoglycan-associated cytoplasmic membrane protein | external 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    |
| 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             | flagellum           | 458      | 326     | 89      |
| ref[YP_000607.1] | YP_000607.1 | flagellar motor protein       | flagellum           | 274      | 276     | 44      |
| ref[YP_001355.1] | YP_001355.1 | flagellar M-ring protein      | flagellum           | 237      | 226     | 71      |
| ref[YP_000606.1] | YP_000606.1 | motility protein A            | flagellum           | 193      | 190     | 57      |
| ref[YP_003552.1] | YP_003552.1 | 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           | 117      | 44      |
| ref[YP_001613.1] | YP_001613.1 | FliS                          | flagellum           | 249      | 37      |
| sp[Q725P8]     | FLGI_LEPIC  | Flagellar P-ring protein precursor (Basal body P-ring protein) | flagellum | 122      | 155     |         |
| 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      |
| Accession | Description | Function |
|-----------|-------------|----------|
| ref|YP_001785.1|flagellar motor switch protein | flagellum |
| ref|YP_001357.1|flagellar assembly protein | flagellum |
| ref|YP_001356.1|FlgG | flagellum |
| ref|YP_003353.1|flagellar hook-associated protein | flagellum |
| ref|YP_001356.1|FliG | flagellum |
| ref|YP_001354.1|Flil | flagellum |
| ref|YP_001795.1|flagellar motor switch protein | flagellum |
| ref|YP_000289.1|flagellar basal-body rod protein | flagellum |
| ref|YP_001338.1|flagellar biosynthetic protein | flagellum |
| ref|YP_001337.1|flagellar biosynthetic protein | flagellum |
| ref|YP_001157.1|flagellar hook assembly scaffolding protein | flagellum |
| sp|Q7ZVKO|FLIE_LEPIC Flagellar hook-basal body complex protein fliE | flagellum |
| ref|YP_001339.1|flagellar protein | flagellum |
| ref|YP_001336.1|flagellar protein export system | flagellum |
| ref|YP_002961.1|flagellin protein | flagellum |
| ref|YP_001294.1|flagellin-specific muramidase | flagellum |
| ref|YP_003561.1|MotA/TolQ/ExbB proton channel family | flagellum |
| sp|Q72VM5|EFG_LEPIC Elongation factor G (EF-G) | flagellum |
| ref|YP_001153.1|hypothetical protein | flagellum |
| ref|YP_001208.1|ATP synthase B chain | flagellum |
| sp|Q75FT0|CHED2_LEPIC Probable chemoreceptor glutamine deamidase chED 2 (EC 3.5.1.44) - Leptospira interrogans serogroup I | flagellum |
| ref|YP_002289.1|elongation factor EF-G | flagellum |

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| Ref       | Accession       | Gene Description                     | Hydrolyase activity (copies per cell) |
|-----------|-----------------|--------------------------------------|--------------------------------------|
| ref|YP_001110.1|YP_001110.1| alpha-galactosidase | hydrolyase activity | 298 | 234 | 89 |
| ref|YP_000283.1|YP_000283.1| glycerophosphoryl diester phosphodiesterase | hydrolyase activity | 256 | 216 | 71 |
| sp|Q7ZU8|LEPA_LEPIC| GTP-binding protein lepA - Leptospira interrogans serogroup Icterohaemorrhagiae copenhagenii | hydrolyase activity | 234 | 212 | 185 |
| ref|YP_002462.1|YP_002462.1| GTP cyclohydrolase 2 | hydrolyase activity | 220 | 210 | 500 |
| sp|Q7ZU8|HSLU_LEPIC| ATP-dependent hsl protease ATP-binding subunit hslU - Leptospira interrogans serogroup Icterohaemorrhagiae | hydrolyase activity | 217 | 198 | 64 |
| ref|YP_002213.1|YP_002213.1| halocid dehalogenase-like hydrolase | hydrolyase activity | 177 | 30 |
| ref|YP_003275.1|YP_003275.1| sulfate adenylyltransferase subunit 1 | hydrolyase activity | 293 | 167 | 219 |
| ref|YP_001342.1|YP_001342.1| septum site-determining protein | hydrolyase activity | 226 | 159 | 75 |
| ref|YP_001965.1|YP_001965.1| hypothetical protein LIC12027 | hydrolyase activity | 139 | 138 | 242 |
| ref|YP_000940.1|YP_000940.1| hypothetical protein LIC10966 | hydrolyase activity | 133 | 57 |
| ref|YP_001819.1|YP_001819.1| hydrolase | hydrolyase activity | 129 | 37 |
| ref|YP_003469.1|YP_003469.1| polysaccharide deacetylase | hydrolyase activity | 283 | 118 | 211 |
| sp|P62347|HIS2_LEPIC| Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH) - Leptospira interrogans serogroup Icterohaemorrhagiae | hydrolyase activity | 327 | 100 |
| ref|YP_003429.1|YP_003429.1| methanol dehydrogenase regulator | hydrolyase activity | 351 |
| sp|Q7ZU8|SURE_LEPIC| 5'-nucleotidase surE (EC 3.1.3.5) (Nucleoside 5'-monophosphate phosphohydrolase) - Leptospira inter | hydrolyase activity | 269 |
| ref|YP_001659.1|YP_001659.1| fructose-1,6-bisphosphatase | hydrolyase activity | 265 |
| sp|Q7ZU8|GCH1_LEPIC| GTP cyclohydrolase I (EC 3.5.4.16) (GTP-CH-I) - Leptospira interrogans serogroup Icterohaemorrhagiae | hydrolyase activity | 230 |
| ref|YP_001964.1|YP_001964.1| methylenetetrahydrofolate dehydrogenase | hydrolyase activity | 196 |
| sp|Q7ZU8|ATPE_LEPIC| ATP synthase epsilon chain (EC 3.6.3.14) (ATP synthase F1 sector epsilon subunit) - Leptospira inter | hydrolyase activity | 118 |
| ref|YP_002328.1|YP_002328.1| hypothetical protein LIC12396 | hydrolyase activity | 118 |
| sp|Q7ZU8|PHL1_LEPIC| Sphingomyelinase C 1 precursor (EC 3.1.4.12) (Sphingomyelin phosphodiesterase 1) (SMase 1) - Leptospira inter | hydrolyase activity | 110 |
| ref|YP_000211.1|YP_000211.1| ParA | hydrolyase activity | 96 |
| ref|YP_001408.1|YP_001408.1| hydrolase | hydrolyase activity | 75 |
| Ref | Protein Name | Activity |
|-----|--------------|----------|
| ref|YP_002090.1|inositol monophosphatase| hydrolase activity|
| 40 |
| ref|YP_000339.1|hypothetical protein LIC10350| hydrolase activity|
| 34 |
| ref|YP_001672.1|hypothetical protein LIC11720| hydrolase activity|
| 24 |
| ref|YP_002324.1|G-amino-oxoante-cyclic-dimer hydrolase| hydrolase activity|
| 281 |
| ref|YP_000134.1|HD-GYP hydrolase domain protein| hydrolase activity|
| 269 |
| ref|YP_001752.1|hypothetical protein LIC11800| hydrolase activity|
| 215 |
| ref|YP_000260.1|chlorohydrolase family protein| hydrolase activity|
| 181 |
| ref|YP_001076.1|acyltransferase| hydrolase activity|
| 158 |
| ref|YP_000558.1|dihydoorotase| hydrolase activity|
| 158 |
| ref|YP_003088.1|(D)inucleoside polyphosphate hydrolase| hydrolase activity|
| 151 |
| ref|YP_000189.1|inositol monophosphatase| hydrolase activity|
| 147 |
| ref|YP_000123.1|hypothetical protein LIC10127| hydrolase activity|
| 110 |
| ref|YP_001689.1|hypothetical protein LIC11737| hydrolase activity|
| 96 |
| ref|YP_002406.1|hypothetical protein LIC12478| hydrolase activity|
| 96 |
| sp|Q72MG4|Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase) - Leptospira interr| hydrolase activity|
| 96 |
| ref|YP_002253.1|protein phosphatase| hydrolase activity|
| 96 |
| ref|YP_001284.1|N-acetyl-L-amino acid amidohydrolase| hydrolase activity|
| 82 |
| ref|YP_002080.1|polysaccharide deacetylase family protein| hydrolase activity|
| 78 |
| ref|YP_002513.1|hypothetical protein LIC12589| hydrolase activity|
| 75 |
| sp|P61909|Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23) (dUTPase) (dUTP pyrophosphatase) - Leptospira interr| hydrolase activity|
| 61 |
| ref|YP_003086.1|acylphosphatase| hydrolase activity|
| 57 |
| ref|YP_001928.1|hypothetical protein LIC11989| hydrolase activity|
| 57 |
| ref|YP_003419.1|phosphotyrosine protein phosphatase| hydrolase activity|
| 57 |
| ref|YP_002989.1|hypothetical protein LIC13077| hydrolase activity|
| 54 |
| ref|YP_003582.1|hypothetical protein LIC20191| hydrolase activity|
| 54 |
| ref|YP_001680.1|N-acetylmuramoyl-L-alanine amidase| hydrolase activity|
| 54 |
| ref|YP_002842.1|beta-lactamase related protein| hydrolase activity|
| 47 |
| ref|YP_000117.1|hypothetical protein LIC10121| hydrolase activity|
| 47 |
| ref|YP_003412.1|ParA| hydrolase activity|
| 47 |
| ref|YP_000651.1|thioesterase| hydrolase activity|
| 47 |
| ref|YP_002126.1|mutator protein| hydrolase activity|
| 44 |
| Ref | Accession | Description | Activity |
|-----|------------|-------------|----------|
| ref|YP_003471.1| Haloacid dehalogenase-like protein | Hydrolase activity |
| ref|YP_002247.1| HIT family hydrolase | Hydrolase activity |
| sp|Q72MK0|ENGC_LEPIC Probable GTPase engC (EC 3.6.1.) - Leptospira interrogans serogroup Icterohaemorrhagiae serovar cop | Hydrolase activity |
| ref|YP_002800.1| Arylsulfatase | Hydrolase activity |
| ref|YP_000184.1| Hypothetical protein LIC10193 | Hydrolase activity |
| ref|YP_001937.1| Hydrolase | Hydrolase activity |
| ref|YP_002936.1| Hypothetical protein LIC13023 | Hydrolase activity |
| sp|P62392|HIS3_LEPIC Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (PRA-CH) - Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni | Hydrolase activity |
| ref|YP_001727.1| Phosphoserine phosphatase | Hydrolase activity |
| ref|YP_001435.1| Hypothetical protein LIC11474 | Hydrolase activity |
| ref|YP_002096.1| 6-phosphogluconolactonase/glucosamine-6-phosphate isomerase/deaminase | Hydrolase activity |
| ref|YP_000753.1| Hypothetical protein LIC10773 | Hydrolase activity |
| ref|YP_000900.1| Metallo-beta-lactamase | Hydrolase activity |
| sp|Q72M35|COBT_LEPIC Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21) (NN:DBI PRT) | Hydrolase activity |
| ref|YP_001120.1| Nonspecific acid phosphatase precursor | Hydrolase activity |
| sp|Q72VK9|QUEC_LEPIC Queuosine biosynthesis protein queC (EC 3.5.-.-) - Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni | Hydrolase activity |
| ref|YP_001426.1| Hypothetical protein LIC11465 | Hydrolase activity |
| ref|YP_002818.1| Hypothetical protein LIC12902 | Hydrolase activity |
| sp|Q72PP0|LOLD_LEPIC Lipoprotein-releasing system ATP-binding protein loid - Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni | Hydrolase activity |
| ref|YP_003026.1| Metallo-beta-lactamase superfamily hydrolase | Hydrolase activity |
| ref|YP_003022.1| Acyltransferase | Hydrolase activity |
| ref|YP_001997.1| Acyltransferase | Hydrolase activity |
| sp|Q75FQ8|COBB_LEPIC Cobyricin acid A,C-diamide synthase - Leptospira interrogans serogroup Icterohaemorrhagiae serovar cop | Hydrolase activity |
| sp|Q72UV8|HAM1_LEPIC HAM1 protein homolog - Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni | Hydrolase activity |
| ref|YP_002364.1| Phosphoglycerol transferase | Hydrolase activity |
| ref|YP_001957.1| ATP-dependent helicase | Hydrolase activity |
| ref|YP_002077.1| Integral membrane protein | Hydrolase activity |
| Ref     | Accession  | Protein Function                                                                 | Activity     | Value |
|---------|------------|----------------------------------------------------------------------------------|--------------|-------|
| refYP_000721.1| YP_000721.1 | N-acetylmuramoyl-L-alanine amidase hydrolase activity                             |              | 8     |
| refYP_000337.1| YP_000337.1 | Paraoxonase hydrolase activity                                                    |              | 8     |
| refYP_000587.1| YP_000587.1 | Sulfatase family protein hydrolase activity                                       |              | 8     |
| refYP_001151.1| YP_001151.1 | Hypothetical protein LIC11181 hydrolase activity                                 |              | 8     |
| refYP_003459.1| YP_003459.1 | MutT-like protein hydrolase activity                                              |              | 8     |
| refYP_000072.1| YP_000072.1 | Hypothetical protein LIC10072 hydrolase activity                                 |              | 5     |
| refYP_001564.1| YP_001564.1 | Hypothetical protein LIC11606 hydrolase activity                                 |              | 5     |
| refYP_002416.1| YP_002416.1 | Hypothetical protein LIC12488 hydrolase activity                                 |              | 5     |
| refYP_0003090.1| YP_0003090.1 | Glycophosphoryl phosphodiesterase diester hydrolase activity                     |              |       |
| refYP_001474.1| YP_001474.1 | Hypothetical protein LIC11515 hydrolase activity                                 |              |       |
| refYP_003171.1| YP_003171.1 | MutT nudix family protein hydrolase activity                                      |              |       |
| refYP_001856.1| YP_001856.1 | Polysaccharide deacetylase hydrolase activity                                    |              |       |
| refYP_000713.1| YP_000713.1 | Putative lipoprotein hydrolase activity                                           |              |       |
| refYP_001303.1| YP_001303.1 | Deoxyribodipyrimidine photolyase hydrolase activity                             |              |       |
| refYP_003398.1| YP_003398.1 | Haloacid dehalogenase-like protein hydrolase activity                             |              |       |
| refYP_001584.1| YP_001584.1 | Inositol monophosphatase family hydrolase activity                              |              |       |
| refYP_000489.1| YP_000489.1 | Nuclease-like protein hydrolase activity                                          |              |       |
| refYP_003058.1| YP_003058.1 | ATP-dependent DNA helicase protein hydrolase activity                             |              |       |
| refYP_002449.1| YP_002449.1 | Serine/threonine kinase hydrolase activity                                        |              |       |
| refYP_001113.1| YP_001113.1 | Metal dependent phosphohydrolase hydrolase activity                              |              |       |
| refYP_003512.1| YP_003512.1 | Histidinol-phosphate aminotransferase and cobyric acid synthase hydrolase activity |              |       |
| refYP_002522.1| YP_002522.1 | Alpha/beta hydrolase superfamily hydrolase activity                              |              |       |
| refYP_001392.1| YP_001392.1 | Alpha/beta hydrolase superfamily hydrolase activity                              |              |       |
| refYP_001073.1| YP_001073.1 | Alpha/beta hydrolase superfamily hydrolase activity                              |              |       |
| refYP_001207.1| YP_001207.1 | ATP synthase C chain hydrolase activity                                          |              |       |
| refYP_002155.1| YP_002155.1 | Beta-lactamase regulatory protein 1 hydrolase activity                            |              |       |
| sp|Q72RS7|DGTL1_LEPIC | Deoxguanosinetriphosphate triphosphohydrolase-like protein - Leptospira interrogans serogroup Icter hydrolase activity |              |       |
| refYP_000377.1| YP_000377.1 | Hypothetical protein LIC10391 hydrolase activity                                 |              |       |
| refYP_000577.1| YP_000577.1 | Hypothetical protein LIC10593 hydrolase activity                                 |              |       |
| refYP_000582.1| YP_000582.1 | Hypothetical protein LIC10598 hydrolase activity                                 |              |       |
| refYP_001283.1| YP_001283.1 | Hypothetical protein LIC11317 hydrolase activity                                 |              |       |
| Ref          | Accession               | Description                                                                 | Hydrolase Activity |
|--------------|-------------------------|------------------------------------------------------------------------------|--------------------|
| ref|YP_002414.1|YP_002414.1| integral membrane protein                                                                 |
| ref|YP_002078.1|YP_002078.1| integral membrane protein                                                                 |
| ref|YP_000089.1|YP_000089.1| metallo-beta-lactamase                                                                 |
| sp|Q72565|CHED1_LEPIC| Probable chemoreceptor glutamine deamidase cheD 1 (EC 3.5.1.44) - Leptospira interrogans serogroup I |
| ref|YP_000963.1|YP_000963.1| serine/threonine kinase with GAF domain                                                                 |
| ref|YP_001649.1|YP_001649.1| xylanase/chitin deacetylase family protein                                                                 |
| ref|YP_003074.1|YP_003074.1| hypothetical protein LIC13166                                                                 |
| ref|YP_002544.1|YP_002544.1| hypothetical protein LIC12621                                                                 |
| ref|YP_001797.1|YP_001797.1| hypothetical protein LIC11848                                                                 |
| ref|YP_001908.1|YP_001908.1| hypothetical protein LIC11966                                                                 |
| ref|YP_003427.1|YP_003427.1| hypothetical protein LIC20035                                                                 |
| ref|YP_002123.1|YP_002123.1| hypothetical protein LIC12188                                                                 |
| ref|YP_000982.1|YP_000982.1| hypothetical protein LIC11009                                                                 |
| ref|YP_003219.1|YP_003219.1| hypothetical protein LIC13314                                                                 |
| ref|YP_000535.1|YP_000535.1| hypothetical protein LIC10551                                                                 |
| ref|YP_000206.1|YP_000206.1| hypothetical protein LIC10215                                                                 |
| ref|YP_002737.1|YP_002737.1| hypothetical protein LIC12821                                                                 |
| ref|YP_002009.1|YP_002009.1| hypothetical protein LIC12075                                                                 |
| ref|YP_002388.1|YP_002388.1| hypothetical protein LIC12460                                                                 |
| ref|YP_001242.1|YP_001242.1| hypothetical protein LIC11274                                                                 |
| ref|YP_003470.1|YP_003470.1| hypothetical protein LIC20078                                                                 |
| ref|YP_000304.1|YP_000304.1| hypothetical protein LIC10314                                                                 |
| ref|YP_000178.1|YP_000178.1| hypothetical protein LIC10187                                                                 |
| ref|YP_000656.1|YP_000656.1| hypothetical protein LIC10672                                                                 |
| ref|YP_003576.1|YP_003576.1| hypothetical protein LIC20185                                                                 |
| ref|YP_000064.1|YP_000064.1| hypothetical protein LIC10064                                                                 |
| ref|YP_001178.1|YP_001178.1| hypothetical protein LIC11209                                                                 |
| ref|YP_003585.1|YP_003585.1| hypothetical protein LIC20196                                                                 |
| ref|YP_001044.1|YP_001044.1| hypothetical protein LIC11074                                                                 |
| ref|YP_001193.1|YP_001193.1| hypothetical protein LIC11224                                                                 |
| ref|YP_001459.1|YP_001459.1| hypothetical protein LIC11498                                                                 |
| ref|YP_001450.1|YP_001450.1| hypothetical protein LIC11489                                                                 |
| ref          | hypothetical protein | ref          | hypothetical protein | ref          | hypothetical protein | ref          | hypothetical protein |
|--------------|----------------------|--------------|----------------------|--------------|----------------------|--------------|----------------------|
| YP_001794.1 | LIC11845             | YP_001794.1  | hypothetical protein | 778          | 1073                 | 169          |
| YP_000853.1 | LIC10876             | YP_000853.1  | hypothetical protein | 813          | 1031                 | 75           |
| YP_002612.1 | LIC12691             | YP_002612.1  | hypothetical protein | 708          | 1025                 | 44           |
| YP_000180.1 | LIC10189             | YP_000180.1  | hypothetical protein | 1001         |                      |              |
| YP_000155.1 | LIC10163             | YP_000155.1  | hypothetical protein | 991          | 47                   |              |
| YP_003544.1 | LIC20153             | YP_003544.1  | hypothetical protein | 1462         | 979                  | 200          |
| YP_003256.1 | LIC13351             | YP_003256.1  | hypothetical protein | 945          | 937                  | 177          |
| YP_001059.1 | LIC11089             | YP_001059.1  | hypothetical protein | 1344         | 934                  | 107          |
| YP_000646.1 | LIC10662             | YP_000646.1  | hypothetical protein | 828          | 927                  | 114          |
| YP_001166.1 | LIC11196             | YP_001166.1  | hypothetical protein | 954          | 864                  | 504          |
| YP_003488.1 | LIC20096             | YP_003488.1  | hypothetical protein | 815          | 863                  | 288          |
| YP_001368.1 | LIC11405             | YP_001368.1  | hypothetical protein | 977          | 831                  | 281          |
| YP_002166.1 | LIC12231             | YP_002166.1  | hypothetical protein | 801          | 815                  | 47           |
| YP_000113.1 | LIC10117             | YP_000113.1  | hypothetical protein | 618          | 796                  | 82           |
| YP_002198.1 | LIC12263             | YP_002198.1  | hypothetical protein | 924          | 791                  | 889          |
| YP_003625.1 | LIC20240             | YP_003625.1  | hypothetical protein | 893          | 765                  | 328          |
| YP_002329.1 | LIC12397             | YP_002329.1  | hypothetical protein | 745          | 740                  | 147          |
| YP_000467.1 | LIC10483             | YP_000467.1  | hypothetical protein | 717          | 736                  | 665          |
| YP_001793.1 | LIC11844             | YP_001793.1  | hypothetical protein | 333          | 735                  | 82           |
| YP_003337.1 | LIC13434             | YP_003337.1  | hypothetical protein | 621          | 698                  | 162          |
| YP_002871.1 | LIC12958             | YP_002871.1  | hypothetical protein | 1098         | 683                  | 192          |
| YP_000202.1 | LIC10211             | YP_000202.1  | hypothetical protein | 681          | 30                   |              |
| YP_000674.1 | LIC10690             | YP_000674.1  | hypothetical protein | 650          | 678                  | 96           |
| YP_000585.1 | LIC10601             | YP_000585.1  | hypothetical protein | 815          | 658                  | 699          |
| YP_000366.1 | LIC10380             | YP_000366.1  | hypothetical protein | 406          | 637                  | 107          |
| YP_001645.1 | LIC11693             | YP_001645.1  | hypothetical protein | 486          | 627                  | 54           |
| YP_002532.1 | LIC12609             | YP_002532.1  | hypothetical protein | 621          |                      |              |
| YP_000470.1 | LIC10486             | YP_000470.1  | hypothetical protein | 565          | 621                  | 125          |
| YP_002530.1 | LIC12607             | YP_002530.1  | hypothetical protein | 610          | 11                   |              |
| YP_002531.1 | LIC12608             | YP_002531.1  | hypothetical protein | 605          |                      |              |
| YP_000740.1 | LIC10760             | YP_000740.1  | hypothetical protein | 652          | 603                  | 419          |
| YP_000175.1 | LIC10184             | YP_000175.1  | hypothetical protein | 596          |                      |              |
| Ref | Protein ID            | Protein Name                        | Protein Description                     | Protein | Copies | Error |
|-----|-----------------------|-------------------------------------|-----------------------------------------|---------|--------|-------|
| ref| YP_000158.1          | hypothetical protein LIC10166       | hypothetical protein                   |         | 583    | 27    |
| ref| YP_002211.1          | hypothetical protein LIC12277       | hypothetical protein                   |         | 611    | 580   | 14    |
| ref| YP_002142.1          | hypothetical protein LIC12207       | hypothetical protein                   |         | 740    | 577   | 118   |
| ref| YP_000223.1          | hypothetical protein LIC12276       | hypothetical protein                   |         | 286    | 558   | 37    |
| ref| YP_000893.1          | hypothetical protein LIC10918       | hypothetical protein                   |         | 462    | 525   | 351   |
| ref| YP_000226.1          | hypothetical protein LIC10235       | hypothetical protein                   |         | 737    | 516   | 129   |
| ref| YP_001241.1          | hypothetical protein LIC12207       | hypothetical protein                   |         | 479    | 512   | 61    |
| ref| YP_003218.1          | hypothetical protein LIC13313       | hypothetical protein                   |         | 438    | 490   | 89    |
| ref| YP_002331.1          | hypothetical protein LIC12399       | hypothetical protein                   |         | 404    | 484   | 40    |
| ref| YP_001655.1          | hypothetical protein LIC11703       | hypothetical protein                   |         | 743    | 479   | 136   |
| ref| YP_000648.1          | hypothetical protein LIC10664       | hypothetical protein                   |         | 726    | 476   | 226   |
| ref| YP_000120.1          | hypothetical protein LIC10124       | hypothetical protein                   |         | 246    | 474   | 399   |
| ref| YP_002259.1          | hypothetical protein LIC12325       | hypothetical protein                   |         | 441    | 473   | 312   |
| ref| YP_002124.1          | hypothetical protein LIC12189       | hypothetical protein                   |         | 535    | 452   | 96    |
| ref| YP_000172.1          | hypothetical protein LIC10181       | hypothetical protein                   |         | 450    |       |       |
| ref| YP_000825.1          | hypothetical protein LIC10848       | hypothetical protein                   |         | 345    | 450   | 211   |
| ref| YP_001595.1          | hypothetical protein LIC11637       | hypothetical protein                   |         | 657    | 448   | 443   |
| ref| YP_001583.1          | hypothetical protein LIC11625       | hypothetical protein                   |         | 1221   | 435   | 188   |
| ref| YP_001429.1          | hypothetical protein LIC13468       | hypothetical protein                   |         | 312    | 395   | 40    |
| ref| YP_003422.1          | hypothetical protein LIC20030       | hypothetical protein                   |         | 258    | 392   | 8     |
| ref| YP_001609.1          | hypothetical protein LIC11653       | hypothetical protein                   |         | 381    | 103   |       |
| ref| YP_001702.1          | hypothetical protein LIC11750       | hypothetical protein                   |         | 433    | 371   | 395   |
| ref| YP_000210.1          | hypothetical protein LIC10219       | hypothetical protein                   |         | 224    | 363   |       |
| ref| YP_002128.1          | hypothetical protein LIC12193       | hypothetical protein                   |         | 323    | 362   | 403   |
| ref| YP_000769.1          | hypothetical protein LIC10790       | hypothetical protein                   |         | 359    | 44    |       |
| ref| YP_003428.1          | hypothetical protein LIC20036       | hypothetical protein                   |         | 384    | 355   | 17    |
| ref| YP_002533.1          | hypothetical protein LIC12610       | hypothetical protein                   |         | 91     | 350   | 37    |
| ref| YP_000855.1          | hypothetical protein LIC10878       | hypothetical protein                   |         | 337    | 347   | 30    |
| ref| YP_003313.1          | hypothetical protein LIC13410       | hypothetical protein                   |         | 465    | 341   | 8     |
| ref| YP_000542.1          | hypothetical protein LIC10558       | hypothetical protein                   |         | 341    | 325   | 75    |
| ref| YP_000401.1          | hypothetical protein LIC10415       | hypothetical protein                   |         | 516    | 325   | 196   |
| ref         | protein                          | cell copies |   |   |
|------------|----------------------------------|-------------|---|---|
| ref|YP_002113.1|hypothetical protein LIC12178| 317 | 34 |
| ref|YP_000217.1|hypothetical protein LIC10226| 462 | 316 | 541 |
| ref|YP_002983.1|hypothetical protein LIC13071| 1602 | 302 | 1283 |
| ref|YP_002345.1|hypothetical protein LIC12414| 1144 | 299 | 246 |
| ref|YP_000959.1|hypothetical protein LIC10985| 518 | 298 | 103 |
| ref|YP_003001.1|hypothetical protein LIC13089| 287 | 298 | 68 |
| ref|YP_002300.1|hypothetical protein LIC12368| 191 | 294 | 17 |
| ref|YP_001577.1|hypothetical protein LIC11619| 291 | 166 |
| ref|YP_002718.1|hypothetical protein LIC12801| 216 | 290 | 21 |
| ref|YP_000538.1|hypothetical protein LIC10554| 309 | 288 | 85 |
| ref|YP_001029.1|hypothetical protein LIC11059| 78 | 283 | 21 |
| ref|YP_002850.1|hypothetical protein LIC12936| 319 | 281 | 447 |
| ref|YP_002493.1|hypothetical protein LIC12568| 320 | 279 | 246 |
| ref|YP_001132.1|hypothetical protein LIC11162| 314 | 278 | 265 |
| ref|YP_000689.1|hypothetical protein LIC10705| 394 | 275 | 24 |
| ref|YP_000165.1|hypothetical protein LIC10173| 272 | 27 | 11 |
| ref|YP_000424.1|hypothetical protein LIC10439| 187 | 256 | 11 |
| ref|YP_001921.1|hypothetical protein LIC11982| 189 | 251 | 30 |
| ref|YP_001900.1|hypothetical protein LIC11955| 793 | 212 | 200 |

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Page 32 of 122
| ref | hypothetical protein | protein | copies per cell |
|-----|----------------------|---------|----------------|
| YP_002273.1 | hypothetical protein LIC12341 | 318 | 185 | 82 |
| YP_001927.1 | hypothetical protein LIC11988 | 178 | 11 |
| YP_001622.1 | hypothetical protein LIC11668 | 162 | 176 | 21 |
| YP_000173.1 | hypothetical protein LIC10182 | 174 | 11 |
| YP_003424.1 | hypothetical protein LIC20032 | 255 | 170 | 219 |
| YP_000466.1 | hypothetical protein LIC10482 | 246 | 169 | 68 |
| YP_002500.1 | hypothetical protein LIC12576 | 186 | 155 | 78 |
| YP_002004.1 | hypothetical protein LIC12070 | 249 | 150 | 273 |
| YP_001495.1 | hypothetical protein LIC11536 | 147 | 151 |
| YP_000222.1 | hypothetical protein LIC10231 | 129 | 146 | 17 |
| YP_003547.1 | hypothetical protein LIC20156 | 368 | 142 | 40 |
| YP_001460.1 | hypothetical protein LIC11499 | 1069 | 141 | 439 |
| YP_003537.1 | hypothetical protein LIC20146 | 132 | 21 |
| YP_003527.1 | hypothetical protein LIC20136 | 105 | 132 | 11 |
| YP_000373.1 | hypothetical protein LIC10387 | 129 | 96 |
| YP_002252.1 | hypothetical protein LIC12318 | 126 | 92 |
| YP_002179.1 | hypothetical protein LIC12244 | 120 | 34 |
| YP_000694.1 | hypothetical protein LIC10710 | 111 | 34 |
| YP_001398.1 | hypothetical protein LIC11436 | 166 | 101 | 30 |
| YP_000411.1 | hypothetical protein LIC10425 | 157 | 101 | 54 |
| YP_000448.1 | Ig-like repeat domain protein 3 | 91 | 914 |
| YP_000017.1 | hypothetical protein LIC10017 | 177 | 88 | 92 |
| YP_000583.1 | hypothetical protein LIC10599 | 77 | 44 |
| YP_000639.1 | hypothetical protein LIC10655 | 168 | 32 | 34 |
| YP_001326.1 | hypothetical protein LIC11362 | 445 | 92 |
| YP_002182.1 | hypothetical protein LIC12247 | 421 |
| YP_003204.1 | hypothetical protein LIC13297 | 382 | 21 |
| YP_000068.1 | hypothetical protein LIC10068 | 364 | 75 |
| YP_000745.1 | hypothetical protein LIC10765 | 294 | 118 |
| YP_001006.1 | hypothetical protein LIC11036 | 267 | 40 |
| YP_003346.1 | hypothetical protein LIC13443 | 234 | 92 |
| YP_001005.1 | hypothetical protein LIC11035 | 215 | 8 |
| ref   | hypothetical protein LIC11320 | hypothetical protein |
|-------|------------------------------|---------------------|
| ref   | hypothetical protein LIC10244 | hypothetical protein |
| ref   | hypothetical protein LIC12040 | hypothetical protein |
| ref   | hypothetical protein LIC11046 | hypothetical protein |
| ref   | hypothetical protein LIC12326 | hypothetical protein |
| ref   | hypothetical protein LIC10663 | hypothetical protein |
| ref   | hypothetical protein LIC10318 | hypothetical protein |
| ref   | hypothetical protein LIC13128 | hypothetical protein |
| ref   | hypothetical protein LIC11067 | hypothetical protein |
| ref   | hypothetical protein LIC10640 | hypothetical protein |
| ref   | hypothetical protein LIC12084 | hypothetical protein |
| ref   | hypothetical protein LIC10521 | hypothetical protein |
| ref   | hypothetical protein LIC10947 | hypothetical protein |
| ref   | hypothetical protein LIC10987 | hypothetical protein |
| ref   | hypothetical protein LIC13021 | hypothetical protein |
| ref   | hypothetical protein LIC11406 | hypothetical protein |
| ref   | hypothetical protein LIC12437 | hypothetical protein |
| ref   | hypothetical protein LIC10736 | hypothetical protein |
| ref   | hypothetical protein LIC12337 | hypothetical protein |
| ref   | hypothetical protein LIC12236 | hypothetical protein |
| ref   | hypothetical protein LIC10134 | hypothetical protein |
| ref   | hypothetical protein LIC11635 | hypothetical protein |
| ref   | hypothetical protein LIC13494 | hypothetical protein |
| ref   | hypothetical protein LIC12371 | hypothetical protein |
| ref   | hypothetical protein LIC13360 | hypothetical protein |
| ref   | hypothetical protein LIC10012 | hypothetical protein |
| ref   | hypothetical protein LIC10984 | hypothetical protein |
| ref   | hypothetical protein LIC11595 | hypothetical protein |
| ref   | hypothetical protein LIC12531 | hypothetical protein |
| ref   | hypothetical protein LIC10095 | hypothetical protein |
| ref   | hypothetical protein LIC10104 | hypothetical protein |
| ref | hypothetical protein | hypothetical protein | copies |
|-----|----------------------|----------------------|--------|
| YP_000645.1 | Ref|YP_000645.1 | LIC10661 | 68 |
| YP_001333.1 | Ref|YP_001333.1 | LIC11369 | 68 |
| YP_001573.1 | Ref|YP_001573.1 | LIC11615 | 68 |
| YP_003442.1 | Ref|YP_003442.1 | LIC20050 | 68 |
| YP_001147.1 | Ref|YP_001147.1 | LIC11177 | 61 |
| YP_000145.1 | Ref|YP_000145.1 | LIC10151 | 57 |
| YP_000347.1 | Ref|YP_000347.1 | LIC10358 | 54 |
| YP_001573.1 | Ref|YP_001573.1 | LIC11615 | 68 |
| YP_001573.1 | Ref|YP_001573.1 | LIC11615 | 68 |
| YP_002116.1 | Ref|YP_002116.1 | LIC12181 | 54 |
| YP_002887.1 | Ref|YP_002887.1 | LIC12974 | 47 |
| YP_003310.1 | Ref|YP_003310.1 | LIC13407 | 44 |
| YP_001239.1 | Ref|YP_001239.1 | LIC12181 | 54 |
| YP_001397.1 | Ref|YP_001397.1 | LIC11435 | 40 |
| YP_002996.1 | Ref|YP_002996.1 | LIC13084 | 40 |
| YP_003556.1 | Ref|YP_003556.1 | LIC20165 | 40 |
| YP_001823.1 | Ref|YP_001823.1 | LIC11874 | 37 |
| YP_002314.1 | Ref|YP_002314.1 | LIC12382 | 37 |
| YP_002928.1 | Ref|YP_002928.1 | LIC13015 | 37 |
| YP_003643.1 | Ref|YP_003643.1 | LIC20259 | 37 |
| YP_000503.1 | Ref|YP_000503.1 | LIC10519 | 37 |
| YP_002395.1 | Ref|YP_002395.1 | LIC12467 | 37 |
| YP_001539.1 | Ref|YP_001539.1 | LIC11580 | 34 |
| YP_002733.1 | Ref|YP_002733.1 | LIC12816 | 34 |
| YP_003654.1 | Ref|YP_003654.1 | LIC20270 | 34 |
| YP_002255.1 | Ref|YP_002255.1 | LIC12321 | 30 |
| YP_000822.1 | Ref|YP_000822.1 | LIC10845 | 27 |
| YP_002467.1 | Ref|YP_002467.1 | LIC12539 | 27 |
| YP_002935.1 | Ref|YP_002935.1 | LIC13022 | 27 |
| YP_003362.1 | Ref|YP_003362.1 | LIC13459 | 27 |
| YP_000311.1 | Ref|YP_000311.1 | LIC10321 | 24 |
| YP_001361.1 | Ref|YP_001361.1 | LIC11398 | 24 |
| YP_001922.1 | Ref|YP_001922.1 | LIC11983 | 24 |
| ref                  | protein                        | copies per cell |
|----------------------|-------------------------------|-----------------|
| ref|YP_002476.1|YP_002476.1| hypothetical protein LIC12548 | hypothetical protein | 24 |
| ref|YP_003484.1|YP_003484.1| hypothetical protein LIC20092 | hypothetical protein | 24 |
| ref|YP_000388.1|YP_000388.1| hypothetical protein LIC10402 | hypothetical protein | 21 |
| ref|YP_002105.1|YP_002105.1| hypothetical protein LIC12170 | hypothetical protein | 21 |
| ref|YP_001880.1|YP_001880.1| hypothetical protein LIC11935 | hypothetical protein | 17 |
| ref|YP_002953.1|YP_002953.1| hypothetical protein LIC13041 | hypothetical protein | 17 |
| ref|YP_003558.1|YP_003558.1| hypothetical protein LIC20167 | hypothetical protein | 17 |
| ref|YP_000649.1|YP_000649.1| hypothetical protein LIC10665 | hypothetical protein | 17 |
| ref|YP_002793.1|YP_002793.1| hypothetical protein LIC12877 | hypothetical protein | 14 |
| ref|YP_003175.1|YP_003175.1| hypothetical protein LIC13268 | hypothetical protein | 14 |
| ref|YP_000153.1|YP_000153.1| hypothetical protein LIC10161 | hypothetical protein | 11 |
| ref|YP_002629.1|YP_002629.1| hypothetical protein LIC12708 | hypothetical protein | 8 |
| ref|YP_002750.1|YP_002750.1| hypothetical protein LIC12834 | hypothetical protein | 8 |
| ref|YP_000545.1|YP_000545.1| hypothetical protein LIC10561 | hypothetical protein | 5 |
| ref|YP_001030.1|YP_001030.1| hypothetical protein LIC11060 | hypothetical protein | 5 |
| ref|YP_001126.1|YP_001126.1| hypothetical protein LIC11156 | hypothetical protein | 5 |
| ref|YP_002034.1|YP_002034.1| hypothetical protein LIC12100 | hypothetical protein | 5 |
| ref|YP_000225.1|YP_000225.1| hypothetical protein LIC10234 | hypothetical protein | 5 |
| ref|YP_001631.1|YP_001631.1| hypothetical protein LIC11677 | hypothetical protein | 5 |
| ref|YP_000821.1|YP_000821.1| hypothetical protein LIC10844 | hypothetical protein | 5 |
| ref|YP_001522.1|YP_001522.1| hypothetical protein LIC11563 | hypothetical protein | 383 |
| ref|YP_003656.1|YP_003656.1| hypothetical protein LIC20272 | hypothetical protein | 343 |
| ref|YP_002893.1|YP_002893.1| hypothetical protein LIC12980 | hypothetical protein | 324 |
| ref|YP_001403.1|YP_001403.1| hypothetical protein LIC11441 | hypothetical protein | 316 |
| ref|YP_003331.1|YP_003331.1| hypothetical protein LIC13428 | hypothetical protein | 300 |
| ref|YP_000316.1|YP_000316.1| hypothetical protein LIC10326 | hypothetical protein | 269 |
| ref|YP_002907.1|YP_002907.1| hypothetical protein LIC12994 | hypothetical protein | 249 |
| ref|YP_001833.1|YP_001833.1| hypothetical protein LIC11884 | hypothetical protein | 185 |
| ref|YP_002616.1|YP_002616.1| hypothetical protein LIC12695 | hypothetical protein | 147 |
| ref|YP_003144.1|YP_003144.1| hypothetical protein LIC13237 | hypothetical protein | 140 |
| ref|YP_001599.1|YP_001599.1| hypothetical protein LIC11641 | hypothetical protein | 136 |
| ref|YP_002675.1|YP_002675.1| hypothetical protein LIC12755 | hypothetical protein | 136 |
| Accession | Description | Value |
|-----------|-------------|-------|
| ref|YP_001866.1|hypothetical protein LIC11920|132|
| ref|YP_002713.1|hypothetical protein LIC12796|129|
| ref|YP_003382.1|hypothetical protein LIC13481|129|
| ref|YP_000627.1|hypothetical protein LIC10643|118|
| ref|YP_000683.1|hypothetical protein LIC10699|107|
| ref|YP_001831.1|hypothetical protein LIC11882|107|
| ref|YP_000118.1|hypothetical protein LIC10122|103|
| ref|YP_000405.1|hypothetical protein LIC10419|103|
| ref|YP_001061.1|hypothetical protein LIC11091|103|
| ref|YP_003183.1|hypothetical protein LIC13276|103|
| ref|YP_001918.1|hypothetical protein LIC11979|92|
| ref|YP_002451.1|hypothetical protein LIC12523|92|
| ref|YP_001345.1|hypothetical protein LIC11381|89|
| ref|YP_003339.1|hypothetical protein LIC13436|89|
| ref|YP_000141.1|hypothetical protein LIC10145|85|
| ref|YP_001786.1|hypothetical protein LIC11837|85|
| ref|YP_003114.1|hypothetical protein LIC13206|82|
| ref|YP_001932.1|hypothetical protein LIC11993|78|
| ref|YP_002210.1|hypothetical protein LIC12276|78|
| ref|YP_002340.1|hypothetical protein LIC12408|78|
| ref|YP_002837.1|hypothetical protein LIC12922|78|
| ref|YP_002933.1|hypothetical protein LIC13020|75|
| ref|YP_000077.1|hypothetical protein LIC10077|68|
| ref|YP_001143.1|hypothetical protein LIC11173|68|
| ref|YP_003063.1|hypothetical protein LIC13155|68|
| ref|YP_000989.1|hypothetical protein LIC11017|64|
| ref|YP_001444.1|hypothetical protein LIC11483|64|
| ref|YP_001570.1|hypothetical protein LIC11612|64|
| ref|YP_001787.1|hypothetical protein LIC11838|64|
| ref|YP_001855.1|hypothetical protein LIC11909|61|
| ref|YP_002504.1|hypothetical protein LIC12580|61|
| ref|YP_002856.1|hypothetical protein LIC12942|61|
| Ref          | Accession        | Protein Description                        | Copies Per Cell |
|--------------|------------------|--------------------------------------------|-----------------|
| ref|YP_000384.1|YP_000384.1| hypothetical protein LIC10398 | 57              |
| ref|YP_000779.1|YP_000779.1| hypothetical protein LIC10802 | 57              |
| ref|YP_001502.1|YP_001502.1| hypothetical protein LIC11543 | 57              |
| ref|YP_002065.1|YP_002065.1| hypothetical protein LIC12131 | 57              |
| ref|YP_002097.1|YP_002097.1| hypothetical protein LIC12162 | 57              |
| ref|YP_002285.1|YP_002285.1| hypothetical protein LIC12353 | 57              |
| ref|YP_002995.1|YP_002995.1| hypothetical protein LIC13083 | 57              |
| ref|YP_003397.1|YP_003397.1| hypothetical protein LIC20005 | 57              |
| ref|YP_001509.1|YP_001509.1| hypothetical protein LIC11550 | 54              |
| ref|YP_003039.1|YP_003039.1| hypothetical protein LIC13131 | 54              |
| ref|YP_000079.1|YP_000079.1| hypothetical protein LIC10079 | 50              |
| ref|YP_000966.1|YP_000966.1| hypothetical protein LIC11026 | 50              |
| ref|YP_001083.1|YP_001083.1| hypothetical protein LIC11113 | 50              |
| ref|YP_001107.1|YP_001107.1| hypothetical protein LIC11137 | 50              |
| ref|YP_001424.1|YP_001424.1| hypothetical protein LIC11463 | 50              |
| ref|YP_001566.1|YP_001566.1| hypothetical protein LIC11608 | 50              |
| ref|YP_003437.1|YP_003437.1| hypothetical protein LIC20045 | 50              |
| ref|YP_003628.1|YP_003628.1| hypothetical protein LIC20243 | 50              |
| ref|YP_000232.1|YP_000232.1| hypothetical protein LIC10241 | 47              |
| ref|YP_000435.1|YP_000435.1| hypothetical protein LIC10451 | 47              |
| ref|YP_001912.1|YP_001912.1| hypothetical protein LIC11972 | 47              |
| ref|YP_002542.1|YP_002542.1| hypothetical protein LIC12619 | 47              |
| ref|YP_002597.1|YP_002597.1| hypothetical protein LIC12675 | 47              |
| ref|YP_003441.1|YP_003441.1| hypothetical protein LIC20049 | 47              |
| ref|YP_000193.1|YP_000193.1| hypothetical protein LIC10202 | 44              |
| ref|YP_000271.1|YP_000271.1| hypothetical protein LIC10281 | 44              |
| ref|YP_001240.1|YP_001240.1| hypothetical protein LIC11271 | 44              |
| ref|YP_001351.1|YP_001351.1| hypothetical protein LIC11388 | 44              |
| ref|YP_002505.1|YP_002505.1| hypothetical protein LIC12581 | 44              |
| ref|YP_002654.1|YP_002654.1| hypothetical protein LIC12734 | 44              |
| ref|YP_002982.1|YP_002982.1| hypothetical protein LIC13070 | 44              |
| ref|YP_000250.1|YP_000250.1| hypothetical protein LIC10259 | 40              |
| ref          | protein                   | protein                   | copies |
|--------------|---------------------------|---------------------------|--------|
| ref|YP_000750.1|YP_000750.1| hypothetical protein LIC10770 | hypothetical protein | 40 |
| ref|YP_000794.1|YP_000794.1| hypothetical protein LIC10817 | hypothetical protein | 40 |
| ref|YP_001024.1|YP_001024.1| hypothetical protein LIC11054 | hypothetical protein | 40 |
| ref|YP_001041.1|YP_001041.1| hypothetical protein LIC11071 | hypothetical protein | 40 |
| ref|YP_001562.1|YP_001562.1| hypothetical protein LIC11604 | hypothetical protein | 40 |
| ref|YP_002646.1|YP_002646.1| hypothetical protein LIC12726 | hypothetical protein | 40 |
| ref|YP_003112.1|YP_003112.1| hypothetical protein LIC13204 | hypothetical protein | 40 |
| ref|YP_003439.1|YP_003439.1| hypothetical protein LIC20047 | hypothetical protein | 40 |
| ref|YP_000020.1|YP_000020.1| hypothetical protein LIC10020 | hypothetical protein | 37 |
| ref|YP_000418.1|YP_000418.1| hypothetical protein LIC10433 | hypothetical protein | 37 |
| ref|YP_001446.1|YP_001446.1| hypothetical protein LIC11485 | hypothetical protein | 37 |
| ref|YP_001822.1|YP_001822.1| hypothetical protein LIC11873 | hypothetical protein | 37 |
| ref|YP_001953.1|YP_001953.1| hypothetical protein LIC12014 | hypothetical protein | 37 |
| ref|YP_002007.1|YP_002007.1| hypothetical protein LIC12073 | hypothetical protein | 37 |
| ref|YP_002030.1|YP_002030.1| hypothetical protein LIC12096 | hypothetical protein | 37 |
| ref|YP_002148.1|YP_002148.1| hypothetical protein LIC12213 | hypothetical protein | 37 |
| ref|YP_002232.1|YP_002232.1| hypothetical protein LIC12298 | hypothetical protein | 37 |
| ref|YP_002474.1|YP_002474.1| hypothetical protein LIC12546 | hypothetical protein | 37 |
| ref|YP_002488.1|YP_002488.1| hypothetical protein LIC12561 | hypothetical protein | 37 |
| ref|YP_002496.1|YP_002496.1| hypothetical protein LIC12572 | hypothetical protein | 37 |
| ref|YP_003098.1|YP_003098.1| hypothetical protein LIC13190 | hypothetical protein | 37 |
| ref|YP_0000750.1|YP_0000750.1| hypothetical protein LIC10485 | hypothetical protein | 34 |
| ref|YP_000708.1|YP_000708.1| hypothetical protein LIC10724 | hypothetical protein | 34 |
| ref|YP_0000780.1|YP_0000780.1| hypothetical protein LIC10803 | hypothetical protein | 34 |
| ref|YP_001828.1|YP_001828.1| hypothetical protein LIC11879 | hypothetical protein | 34 |
| ref|YP_002682.1|YP_002682.1| hypothetical protein LIC12762 | hypothetical protein | 34 |
| ref|YP_003207.1|YP_003207.1| hypothetical protein LIC13302 | hypothetical protein | 34 |
| ref|YP_003384.1|YP_003384.1| hypothetical protein LIC13483 | hypothetical protein | 34 |
| ref|YP_003425.1|YP_003425.1| hypothetical protein LIC20033 | hypothetical protein | 34 |
| ref|YP_003612.1|YP_003612.1| hypothetical protein LIC20223 | hypothetical protein | 34 |
| ref|YP_000102.1|YP_000102.1| hypothetical protein LIC10105 | hypothetical protein | 30 |
| Ref          | Protein ID     | Protein Description | Copies |
|--------------|----------------|---------------------|--------|
| ref|YP_000270.1|YP_000270.1|hypothetical protein LIC10280|30|
| ref|YP_000419.1|YP_000419.1|hypothetical protein LIC10434|30|
| ref|YP_001125.1|YP_001125.1|hypothetical protein LIC11155|30|
| ref|YP_001538.1|YP_001538.1|hypothetical protein LIC11579|30|
| ref|YP_002131.1|YP_002131.1|hypothetical protein LIC12196|30|
| ref|YP_000030.1|YP_000030.1|hypothetical protein LIC10030|27|
| ref|YP_000221.1|YP_000221.1|hypothetical protein LIC10230|27|
| ref|YP_000792.1|YP_000792.1|hypothetical protein LIC10815|27|
| ref|YP_000812.1|YP_000812.1|hypothetical protein LIC10835|27|
| ref|YP_000860.1|YP_000860.1|hypothetical protein LIC10883|27|
| ref|YP_002265.1|YP_002265.1|hypothetical protein LIC12333|27|
| ref|YP_002344.1|YP_002344.1|hypothetical protein LIC12413|27|
| ref|YP_002346.1|YP_002346.1|hypothetical protein LIC12415|27|
| ref|YP_002501.1|YP_002501.1|hypothetical protein LIC12577|27|
| ref|YP_002876.1|YP_002876.1|hypothetical protein LIC12963|27|
| ref|YP_002954.1|YP_002954.1|hypothetical protein LIC13042|27|
| ref|YP_003266.1|YP_003266.1|hypothetical protein LIC13361|27|
| ref|YP_003319.1|YP_003319.1|hypothetical protein LIC13416|27|
| ref|YP_003587.1|YP_003587.1|hypothetical protein LIC20198|27|
| ref|YP_001895.1|YP_001895.1|hypothetical protein LIC13950|27|
| ref|YP_000049.1|YP_000049.1|hypothetical protein LIC10049|24|
| ref|YP_000407.1|YP_000407.1|hypothetical protein LIC10421|24|
| ref|YP_001409.1|YP_001409.1|hypothetical protein LIC11447|24|
| ref|YP_001606.1|YP_001606.1|hypothetical protein LIC11650|24|
| ref|YP_001741.1|YP_001741.1|hypothetical protein LIC11789|24|
| ref|YP_002908.1|YP_002908.1|hypothetical protein LIC12995|24|
| ref|YP_002914.1|YP_002914.1|hypothetical protein LIC13001|24|
| ref|YP_003152.1|YP_003152.1|hypothetical protein LIC13245|24|
| ref|YP_000676.1|YP_000676.1|hypothetical protein LIC10692|24|
| ref|YP_003052.1|YP_003052.1|hypothetical protein LIC13144|24|
| ref|YP_000342.1|YP_000342.1|hypothetical protein LIC10353|21|
| ref|YP_000370.1|YP_000370.1|hypothetical protein LIC10384|21|
| Ref | Protein ID | Protein Description | Protein Abundance |
|-----|------------|---------------------|-------------------|
| ref|YP_000894.1| hypothetical protein LIC10919 | 21 |
| ref|YP_001196.1| hypothetical protein LIC11227 | 21 |
| ref|YP_001677.1| hypothetical protein LIC11725 | 21 |
| ref|YP_001893.1| hypothetical protein LIC11948 | 21 |
| ref|YP_001981.1| hypothetical protein LIC12046 | 21 |
| ref|YP_002051.1| hypothetical protein LIC12117 | 21 |
| ref|YP_002387.1| hypothetical protein LIC12459 | 21 |
| ref|YP_002502.1| hypothetical protein LIC12578 | 21 |
| ref|YP_002570.1| hypothetical protein LIC12647 | 21 |
| ref|YP_002738.1| hypothetical protein LIC12822 | 21 |
| ref|YP_003528.1| hypothetical protein LIC20137 | 21 |
| ref|YP_003581.1| hypothetical protein LIC20160 | 21 |
| ref|YP_003611.1| hypothetical protein LIC20190 | 21 |
| ref|YP_003637.1| hypothetical protein LIC20253 | 21 |
| ref|YP_002743.1| hypothetical protein LIC12827 | 21 |
| ref|YP_000620.1| hypothetical protein LIC10636 | 17 |
| ref|YP_000723.1| hypothetical protein LIC10741 | 17 |
| ref|YP_000755.1| hypothetical protein LIC10775 | 17 |
| ref|YP_000879.1| hypothetical protein LIC10902 | 17 |
| ref|YP_000942.1| hypothetical protein LIC10968 | 17 |
| ref|YP_001133.1| hypothetical protein LIC11163 | 17 |
| ref|YP_001232.1| hypothetical protein LIC11263 | 17 |
| ref|YP_001233.1| hypothetical protein LIC11264 | 17 |
| ref|YP_001256.1| hypothetical protein LIC11289 | 17 |
| ref|YP_001347.1| hypothetical protein LIC11383 | 17 |
| ref|YP_001451.1| hypothetical protein LIC11490 | 17 |
| ref|YP_001457.1| hypothetical protein LIC11496 | 17 |
| ref|YP_001722.1| hypothetical protein LIC11770 | 17 |
| ref|YP_001777.1| hypothetical protein LIC11826 | 17 |
| ref|YP_001825.1| hypothetical protein LIC11876 | 17 |
| ref|YP_002165.1| hypothetical protein LIC12230 | 17 |
| Reference                      | Protein Description                  | Value |
|-------------------------------|--------------------------------------|-------|
| ref|YP_003264.1|YP_003264.1 | hypothetical protein LIC13359 | 17 |
| ref|YP_003421.1|YP_003421.1 | hypothetical protein LIC20029 | 17 |
| ref|YP_000103.1|YP_000103.1 | hypothetical protein LIC10106 | 14 |
| ref|YP_000219.1|YP_000219.1 | hypothetical protein LIC10228 | 14 |
| ref|YP_000227.1|YP_000227.1 | hypothetical protein LIC10236 | 14 |
| ref|YP_000993.1|YP_000993.1 | hypothetical protein LIC11023 | 14 |
| ref|YP_001219.1|YP_001219.1 | hypothetical protein LIC11250 | 14 |
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| YP_001056.1 | YP_001056.1              | LIC11086             |
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| YP_001614.1 | YP_001614.1              | LIC11658             |
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| YP_001717.1 | YP_001717.1              | LIC11765             |
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| YP_001863.1 | YP_001863.1              | LIC11917             |
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| ref       | syringomycin channel-forming protein | hypothetical protein |
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| YP_001054.1 | hypothetical protein LIC11084 | hypothetical protein |
| YP_001062.1 | hypothetical protein LIC11092 | hypothetical protein |
| YP_001064.1 | hypothetical protein LIC11094 | hypothetical protein |
| YP_001069.1 | hypothetical protein LIC11099 | hypothetical protein |
| YP_001070.1 | hypothetical protein LIC11100 | hypothetical protein |
| YP_001072.1 | hypothetical protein LIC11102 | hypothetical protein |
| YP_001079.1 | hypothetical protein LIC11109 | hypothetical protein |
| YP_001084.1 | hypothetical protein LIC11114 | hypothetical protein |
| YP_001086.1 | hypothetical protein LIC11116 | hypothetical protein |
| YP_001088.1 | hypothetical protein LIC11118 | hypothetical protein |
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| YP_001108.1 | hypothetical protein LIC11138 | hypothetical protein |
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| YP_001123.1 | hypothetical protein LIC11153 | hypothetical protein |
| YP_001127.1 | hypothetical protein LIC11157 | hypothetical protein |
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| YP_001134.1 | hypothetical protein LIC11164 | hypothetical protein |
| YP_001138.1 | hypothetical protein LIC11168 | hypothetical protein |
| YP_001139.1 | hypothetical protein LIC11169 | hypothetical protein |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

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| YP_001437.1 | hypothetical protein LIC11476 | hypothetical protein |
| YP_001463.1 | hypothetical protein LIC11502 | hypothetical protein |
### Table: Proteome-wide copies per cell measurements

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| YP_001492.1 | LIC11533 | hypothetical protein |
| YP_001501.1 | LIC11542 | hypothetical protein |
| YP_001520.1 | LIC11561 | hypothetical protein |
| YP_001533.1 | LIC11574 | hypothetical protein |
| YP_001534.1 | LIC11575 | hypothetical protein |
| YP_001535.1 | LIC11576 | hypothetical protein |
| YP_001540.1 | LIC11581 | hypothetical protein |
| YP_001541.1 | LIC11582 | hypothetical protein |
| YP_001542.1 | LIC11583 | hypothetical protein |
| YP_001547.1 | LIC11589 | hypothetical protein |
| YP_001551.1 | LIC11593 | hypothetical protein |
| YP_001552.1 | LIC11594 | hypothetical protein |
| YP_001561.1 | LIC11603 | hypothetical protein |
| YP_001596.1 | LIC11638 | hypothetical protein |
| YP_001597.1 | LIC11639 | hypothetical protein |
| YP_001598.1 | LIC11640 | hypothetical protein |
| YP_001602.1 | LIC11644 | hypothetical protein |
| YP_001607.1 | LIC11651 | hypothetical protein |
| YP_001620.1 | LIC11664 | hypothetical protein |
| YP_001621.1 | LIC11665 | hypothetical protein |
| YP_001623.1 | LIC11669 | hypothetical protein |
| YP_001633.1 | LIC11679 | hypothetical protein |
| YP_001635.1 | LIC11683 | hypothetical protein |
| YP_001638.1 | LIC11686 | hypothetical protein |
| YP_001640.1 | LIC11688 | hypothetical protein |
| YP_001641.1 | LIC11689 | hypothetical protein |
| YP_001642.1 | LIC11690 | hypothetical protein |
| YP_001644.1 | LIC11692 | hypothetical protein |
| YP_001652.1 | LIC11700 | hypothetical protein |
| YP_001657.1 | LIC11705 | hypothetical protein |
## Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Reference | Description | Protein ID | Protein Description |
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| YP_001674.1 | Hypothetical protein LIC11722 | hypothetical protein |
| YP_001676.1 | Hypothetical protein LIC11724 | hypothetical protein |
| YP_001679.1 | Hypothetical protein LIC11727 | hypothetical protein |
| YP_001682.1 | Hypothetical protein LIC11730 | hypothetical protein |
| YP_001685.1 | Hypothetical protein LIC11733 | hypothetical protein |
| YP_001686.1 | Hypothetical protein LIC11734 | hypothetical protein |
| YP_001689.1 | Hypothetical protein LIC11744 | hypothetical protein |
| YP_001707.1 | Hypothetical protein LIC11755 | hypothetical protein |
| YP_001713.1 | Hypothetical protein LIC11761 | hypothetical protein |
| YP_001714.1 | Hypothetical protein LIC11762 | hypothetical protein |
| YP_001715.1 | Hypothetical protein LIC11763 | hypothetical protein |
| YP_001723.1 | Hypothetical protein LIC11771 | hypothetical protein |
| YP_001724.1 | Hypothetical protein LIC11772 | hypothetical protein |
| YP_001735.1 | Hypothetical protein LIC11783 | hypothetical protein |
| YP_001737.1 | Hypothetical protein LIC11785 | hypothetical protein |
| YP_001747.1 | Hypothetical protein LIC11795 | hypothetical protein |
| YP_001750.1 | Hypothetical protein LIC11798 | hypothetical protein |
| YP_001758.1 | Hypothetical protein LIC11807 | hypothetical protein |
| YP_001769.1 | Hypothetical protein LIC11818 | hypothetical protein |
| YP_001779.1 | Hypothetical protein LIC11830 | hypothetical protein |
| YP_001782.1 | Hypothetical protein LIC11833 | hypothetical protein |
| YP_001791.1 | Hypothetical protein LIC11842 | hypothetical protein |
| YP_001792.1 | Hypothetical protein LIC11843 | hypothetical protein |
| YP_001799.1 | Hypothetical protein LIC11850 | hypothetical protein |
| YP_001805.1 | Hypothetical protein LIC11856 | hypothetical protein |
| YP_001811.1 | Hypothetical protein LIC11862 | hypothetical protein |
| YP_001817.1 | Hypothetical protein LIC11868 | hypothetical protein |
| YP_001826.1 | Hypothetical protein LIC11877 | hypothetical protein |
| YP_001827.1 | Hypothetical protein LIC11878 | hypothetical protein |
| YP_001840.1 | Hypothetical protein LIC11891 | hypothetical protein |
| YP_001841.1 | Hypothetical protein LIC11892 | hypothetical protein |
| ref | hypothetical protein LIC11894 | hypothetical protein |
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| YP_001843.1 | hypothetical protein LIC11901 | hypothetical protein |
| YP_001850.1 | hypothetical protein LIC11902 | hypothetical protein |
| YP_001854.1 | hypothetical protein LIC11908 | hypothetical protein |
| YP_001868.1 | hypothetical protein LIC11922 | hypothetical protein |
| YP_001871.1 | hypothetical protein LIC11925 | hypothetical protein |
| YP_001877.1 | hypothetical protein LIC11931 | hypothetical protein |
| YP_001878.1 | hypothetical protein LIC11933 | hypothetical protein |
| YP_001881.1 | hypothetical protein LIC11936 | hypothetical protein |
| YP_001884.1 | hypothetical protein LIC11939 | hypothetical protein |
| YP_001887.1 | hypothetical protein LIC11942 | hypothetical protein |
| YP_001894.1 | hypothetical protein LIC11949 | hypothetical protein |
| YP_001897.1 | hypothetical protein LIC11952 | hypothetical protein |
| YP_001898.1 | hypothetical protein LIC11953 | hypothetical protein |
| YP_001901.1 | hypothetical protein LIC11956 | hypothetical protein |
| YP_001906.1 | hypothetical protein LIC11964 | hypothetical protein |
| YP_001907.1 | hypothetical protein LIC11965 | hypothetical protein |
| YP_001909.1 | hypothetical protein LIC11969 | hypothetical protein |
| YP_001923.1 | hypothetical protein LIC11984 | hypothetical protein |
| YP_001925.1 | hypothetical protein LIC11986 | hypothetical protein |
| YP_001926.1 | hypothetical protein LIC11987 | hypothetical protein |
| YP_001933.1 | hypothetical protein LIC11994 | hypothetical protein |
| YP_001934.1 | hypothetical protein LIC11995 | hypothetical protein |
| YP_001935.1 | hypothetical protein LIC11996 | hypothetical protein |
| YP_001936.1 | hypothetical protein LIC11997 | hypothetical protein |
| YP_001938.1 | hypothetical protein LIC11999 | hypothetical protein |
| YP_001943.1 | hypothetical protein LIC12004 | hypothetical protein |
| YP_001945.1 | hypothetical protein LIC12006 | hypothetical protein |
| YP_001946.1 | hypothetical protein LIC12007 | hypothetical protein |
| YP_001950.1 | hypothetical protein LIC12011 | hypothetical protein |
| YP_001952.1 | hypothetical protein LIC12013 | hypothetical protein |
| YP_001959.1 | hypothetical protein LIC12021 | hypothetical protein |
| ref          | hypothetical protein LIC12023 | hypothetical protein LIC12036 |
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| ref          | hypothetical protein LIC12044 | hypothetical protein LIC12045 |
| ref          | hypothetical protein LIC12048 | hypothetical protein LIC12049 |
| ref          | hypothetical protein LIC12050 | hypothetical protein LIC12051 |
| ref          | hypothetical protein LIC12052 | hypothetical protein LIC12053 |
| ref          | hypothetical protein LIC12054 | hypothetical protein LIC12055 |
| ref          | hypothetical protein LIC12055 | hypothetical protein LIC12056 |
| ref          | hypothetical protein LIC12057 | hypothetical protein LIC12058 |
| ref          | hypothetical protein LIC12059 | hypothetical protein LIC12060 |
| ref          | hypothetical protein LIC12061 | hypothetical protein LIC12062 |
| ref          | hypothetical protein LIC12063 | hypothetical protein LIC12064 |
| ref          | hypothetical protein LIC12065 | hypothetical protein LIC12066 |
| ref          | hypothetical protein LIC12067 | hypothetical protein LIC12068 |
| ref          | hypothetical protein LIC12069 | hypothetical protein LIC12070 |
| ref          | hypothetical protein LIC12071 | hypothetical protein LIC12072 |
| ref          | hypothetical protein LIC12073 | hypothetical protein LIC12074 |
| ref          | hypothetical protein LIC12075 | hypothetical protein LIC12076 |
| ref          | hypothetical protein LIC12077 | hypothetical protein LIC12078 |
| ref          | hypothetical protein LIC12079 | hypothetical protein LIC12080 |
| ref          | hypothetical protein LIC12081 | hypothetical protein LIC12082 |
| ref          | hypothetical protein LIC12083 | hypothetical protein LIC12084 |
| ref          | hypothetical protein LIC12085 | hypothetical protein LIC12086 |
| ref          | hypothetical protein LIC12087 | hypothetical protein LIC12088 |
| ref          | hypothetical protein LIC12089 | hypothetical protein LIC12090 |
| ref          | hypothetical protein LIC12091 | hypothetical protein LIC12092 |
| ref          | hypothetical protein LIC12093 | hypothetical protein LIC12094 |
| ref          | hypothetical protein LIC12095 | hypothetical protein LIC12096 |
| ref          | hypothetical protein LIC12097 | hypothetical protein LIC12098 |
| ref          | hypothetical protein LIC12099 | hypothetical protein LIC12100 |
| ref          | hypothetical protein LIC12101 | hypothetical protein LIC12102 |
| ref          | hypothetical protein LIC12103 | hypothetical protein LIC12104 |
| ref          | hypothetical protein LIC12105 | hypothetical protein LIC12106 |
| ref          | hypothetical protein LIC12107 | hypothetical protein LIC12108 |
| ref          | hypothetical protein LIC12109 | hypothetical protein LIC12110 |
| ref          | hypothetical protein LIC12111 | hypothetical protein LIC12112 |
| ref          | hypothetical protein LIC12113 | hypothetical protein LIC12114 |
| ref          | hypothetical protein LIC12115 | hypothetical protein LIC12116 |
| ref          | hypothetical protein LIC12117 | hypothetical protein LIC12118 |
| ref          | hypothetical protein LIC12119 | hypothetical protein LIC12120 |
| ref          | hypothetical protein LIC12121 | hypothetical protein LIC12122 |
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| ref          | hypothetical protein LIC12125 | hypothetical protein LIC12126 |
| ref          | hypothetical protein LIC12127 | hypothetical protein LIC12128 |
| ref          | hypothetical protein LIC12129 | hypothetical protein LIC12130 |
| ref          | hypothetical protein LIC12131 | hypothetical protein LIC12132 |
| ref          | hypothetical protein LIC12133 | hypothetical protein LIC12134 |
| ref          | hypothetical protein LIC12135 | hypothetical protein LIC12136 |
| ref          | hypothetical protein LIC12137 | hypothetical protein LIC12138 |
| ref          | hypothetical protein LIC12139 | hypothetical protein LIC12140 |
| ref          | hypothetical protein LIC12141 | hypothetical protein LIC12142 |
| ref          | hypothetical protein LIC12143 | hypothetical protein LIC12144 |
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| ref          | hypothetical protein LIC12153 | hypothetical protein LIC12154 |
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| ref          | hypothetical protein LIC12161 | hypothetical protein LIC12162 |
| ref          | hypothetical protein LIC12163 | hypothetical protein LIC12164 |
| ref          | hypothetical protein LIC12165 | hypothetical protein LIC12166 |
| ref          | hypothetical protein LIC12167 | hypothetical protein LIC12168 |
| ref          | hypothetical protein LIC12169 | hypothetical protein LIC12170 |
| ref          | hypothetical protein LIC12171 | hypothetical protein LIC12172 |
| ref          | hypothetical protein LIC12173 | hypothetical protein LIC12174 |
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| ref          | hypothetical protein LIC12179 | hypothetical protein LIC12180 |
| ref          | hypothetical protein LIC12181 | hypothetical protein LIC12182 |
| ref          | hypothetical protein LIC12183 | hypothetical protein LIC12184 |
| ref          | hypothetical protein LIC12185 | hypothetical protein LIC12186 |
| ref          | hypothetical protein LIC12187 | hypothetical protein LIC12188 |
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| ref          | hypothetical protein LIC12191 | hypothetical protein LIC12192 |
| ref          | hypothetical protein LIC12193 | hypothetical protein LIC12194 |
| ref          | hypothetical protein LIC12195 | hypothetical protein LIC12196 |
| ref          | hypothetical protein LIC12197 | hypothetical protein LIC12198 |
| ref          | hypothetical protein LIC12199 | hypothetical protein LIC12200 |
| ref          | hypothetical protein LIC12201 | hypothetical protein LIC12202 |
| ref          | hypothetical protein LIC12203 | hypothetical protein LIC12204 |
| ref          | hypothetical protein LIC12205 | hypothetical protein LIC12206 |
| ref          | hypothetical protein LIC12207 | hypothetical protein LIC12208 |
| ref          | hypothetical protein LIC12209 | hypothetical protein LIC12210 |
| ref          | hypothetical protein LIC12211 | hypothetical protein LIC12212 |
| ref          | hypothetical protein LIC12213 | hypothetical protein LIC12214 |
| ref          | hypothetical protein LIC12215 | hypothetical protein LIC12216 |
| ref          | hypothetical protein LIC12217 | hypothetical protein LIC12218 |
| ref          | hypothetical protein LIC12219 | hypothetical protein LIC12220 |
| ref         | protein                  | protein                  |
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| YP_002158.1 | hypothetical LIC12223   | hypothetical LIC12223   |
| YP_002161.1 | hypothetical LIC12226   | hypothetical LIC12226   |
| YP_002163.1 | hypothetical LIC12228   | hypothetical LIC12228   |
| YP_002164.1 | hypothetical LIC12229   | hypothetical LIC12229   |
| YP_002169.1 | hypothetical LIC12234   | hypothetical LIC12234   |
| YP_002172.1 | hypothetical LIC12237   | hypothetical LIC12237   |
| YP_002174.1 | hypothetical LIC12239   | hypothetical LIC12239   |
| YP_002176.1 | hypothetical LIC12241   | hypothetical LIC12241   |
| YP_002177.1 | hypothetical LIC12242   | hypothetical LIC12242   |
| YP_002184.1 | hypothetical LIC12249   | hypothetical LIC12249   |
| YP_002190.1 | hypothetical LIC12255   | hypothetical LIC12255   |
| YP_002193.1 | hypothetical LIC12258   | hypothetical LIC12258   |
| YP_002196.1 | hypothetical LIC12261   | hypothetical LIC12261   |
| YP_002199.1 | hypothetical LIC12264   | hypothetical LIC12264   |
| YP_002200.1 | hypothetical LIC12265   | hypothetical LIC12265   |
| YP_002205.1 | hypothetical LIC12270   | hypothetical LIC12270   |
| YP_002206.1 | hypothetical LIC12271   | hypothetical LIC12271   |
| YP_002207.1 | hypothetical LIC12272   | hypothetical LIC12272   |
| YP_002212.1 | hypothetical LIC12278   | hypothetical LIC12278   |
| YP_002215.1 | hypothetical LIC12281   | hypothetical LIC12281   |
| YP_002217.1 | hypothetical LIC12283   | hypothetical LIC12283   |
| YP_002218.1 | hypothetical LIC12284   | hypothetical LIC12284   |
| YP_002233.1 | hypothetical LIC12299   | hypothetical LIC12299   |
| YP_002234.1 | hypothetical LIC12300   | hypothetical LIC12300   |
| YP_002248.1 | hypothetical LIC12314   | hypothetical LIC12314   |
| YP_002270.1 | hypothetical LIC12338   | hypothetical LIC12338   |
| YP_002275.1 | hypothetical LIC12343   | hypothetical LIC12343   |
| YP_002276.1 | hypothetical LIC12344   | hypothetical LIC12344   |
| YP_002277.1 | hypothetical LIC12345   | hypothetical LIC12345   |
| YP_002280.1 | hypothetical LIC12348   | hypothetical LIC12348   |
| YP_002283.1 | hypothetical LIC12351   | hypothetical LIC12351   |
| YP_002284.1 | hypothetical LIC12352   | hypothetical LIC12352   |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| ref | hypothetical protein LIC12356 |
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| YP_002288.1 | hypothetical protein |
| YP_002290.1 | hypothetical protein |
| YP_002291.1 | hypothetical protein |
| YP_002295.1 | hypothetical protein |
| YP_002299.1 | hypothetical protein |
| YP_002301.1 | hypothetical protein |
| YP_002302.1 | hypothetical protein |
| YP_002308.1 | hypothetical protein |
| YP_002313.1 | hypothetical protein |
| YP_002315.1 | hypothetical protein |
| YP_002317.1 | hypothetical protein |
| YP_002326.1 | hypothetical protein |
| YP_002327.1 | hypothetical protein |
| YP_002335.1 | hypothetical protein |
| YP_002337.1 | hypothetical protein |
| YP_002338.1 | hypothetical protein |
| YP_002341.1 | hypothetical protein |
| YP_002342.1 | hypothetical protein |
| YP_002351.1 | hypothetical protein |
| YP_002355.1 | hypothetical protein |
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| YP_002358.1 | hypothetical protein |
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| YP_002365.1 | hypothetical protein |
| YP_002366.1 | hypothetical protein |
| YP_002370.1 | hypothetical protein |
| YP_002371.1 | hypothetical protein |
| YP_002372.1 | hypothetical protein |
| YP_002392.1 | hypothetical protein |
| YP_002401.1 | hypothetical protein |
| YP_002408.1 | hypothetical protein |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| ref|YP_002411.1|YP_002411.1 | hypothetical protein LIC12483 |
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| ref|YP_002419.1|YP_002419.1 | hypothetical protein LIC12491 |
| ref|YP_002425.1|YP_002425.1 | hypothetical protein LIC12497 |
| ref|YP_002431.1|YP_002431.1 | hypothetical protein LIC12503 |
| ref|YP_002435.1|YP_002435.1 | hypothetical protein LIC12507 |
| ref|YP_002439.1|YP_002439.1 | hypothetical protein LIC12511 |
| ref|YP_002445.1|YP_002445.1 | hypothetical protein LIC12517 |
| ref|YP_002446.1|YP_002446.1 | hypothetical protein LIC12518 |
| ref|YP_002447.1|YP_002447.1 | hypothetical protein LIC12519 |
| ref|YP_002450.1|YP_002450.1 | hypothetical protein LIC12522 |
| ref|YP_002458.1|YP_002458.1 | hypothetical protein LIC12530 |
| ref|YP_002460.1|YP_002460.1 | hypothetical protein LIC12532 |
| ref|YP_002461.1|YP_002461.1 | hypothetical protein LIC12533 |
| ref|YP_002479.1|YP_002479.1 | hypothetical protein LIC12552 |
| ref|YP_002482.1|YP_002482.1 | hypothetical protein LIC12555 |
| ref|YP_002484.1|YP_002484.1 | hypothetical protein LIC12557 |
| ref|YP_002485.1|YP_002485.1 | hypothetical protein LIC12558 |
| ref|YP_002486.1|YP_002486.1 | hypothetical protein LIC12559 |
| ref|YP_002507.1|YP_002507.1 | hypothetical protein LIC12583 |
| ref|YP_002508.1|YP_002508.1 | hypothetical protein LIC12584 |
| ref|YP_002509.1|YP_002509.1 | hypothetical protein LIC12585 |
| ref|YP_002516.1|YP_002516.1 | hypothetical protein LIC12592 |
| ref|YP_002517.1|YP_002517.1 | hypothetical protein LIC12594 |
| ref|YP_002520.1|YP_002520.1 | hypothetical protein LIC12597 |
| ref|YP_002527.1|YP_002527.1 | hypothetical protein LIC12604 |
| ref|YP_002529.1|YP_002529.1 | hypothetical protein LIC12606 |
| ref|YP_002534.1|YP_002534.1 | hypothetical protein LIC12611 |
| ref|YP_002535.1|YP_002535.1 | hypothetical protein LIC12612 |
| ref|YP_002546.1|YP_002546.1 | hypothetical protein LIC12623 |
| ref|YP_002547.1|YP_002547.1 | hypothetical protein LIC12624 |
| ref|YP_002548.1|YP_002548.1 | hypothetical protein LIC12625 |
| ref|YP_002549.1|YP_002549.1 | hypothetical protein LIC12626 |
| Ref | Hypothetical Protein | Hypothetical Protein |
|-----|----------------------|----------------------|
| YP_002551.1 | LIC12628 | Hypothetical protein |
| YP_002553.1 | LIC12630 | Hypothetical protein |
| YP_002563.1 | LIC12640 | Hypothetical protein |
| YP_002564.1 | LIC12641 | Hypothetical protein |
| YP_002565.1 | LIC12642 | Hypothetical protein |
| YP_002573.1 | LIC12650 | Hypothetical protein |
| YP_002575.1 | LIC12652 | Hypothetical protein |
| YP_002579.1 | LIC12656 | Hypothetical protein |
| YP_002580.1 | LIC12657 | Hypothetical protein |
| YP_002581.1 | LIC12658 | Hypothetical protein |
| YP_002584.1 | LIC12661 | Hypothetical protein |
| YP_002586.1 | LIC12664 | Hypothetical protein |
| YP_002587.1 | LIC12665 | Hypothetical protein |
| YP_002594.1 | LIC12672 | Hypothetical protein |
| YP_002595.1 | LIC12673 | Hypothetical protein |
| YP_002596.1 | LIC12674 | Hypothetical protein |
| YP_002600.1 | LIC12678 | Hypothetical protein |
| YP_002617.1 | LIC12696 | Hypothetical protein |
| YP_002618.1 | LIC12697 | Hypothetical protein |
| YP_002619.1 | LIC12698 | Hypothetical protein |
| YP_002631.1 | LIC12710 | Hypothetical protein |
| YP_002633.1 | LIC12712 | Hypothetical protein |
| YP_002634.1 | LIC12713 | Hypothetical protein |
| YP_002636.1 | LIC12715 | Hypothetical protein |
| YP_002644.1 | LIC12724 | Hypothetical protein |
| YP_002648.1 | LIC12728 | Hypothetical protein |
| YP_002649.1 | LIC12729 | Hypothetical protein |
| YP_002652.1 | LIC12732 | Hypothetical protein |
| YP_002655.1 | LIC12735 | Hypothetical protein |
| YP_002673.1 | LIC12753 | Hypothetical protein |
| YP_002674.1 | LIC12754 | Hypothetical protein |
| YP_002683.1 | LIC12763 | Hypothetical protein |
| Ref       | Protein                                      | Protein                                      |
|-----------|----------------------------------------------|----------------------------------------------|
| YP_002687.1 | hypothetical protein LIC12767                | hypothetical protein LIC12767                |
| YP_002688.1 | hypothetical protein LIC12769                | hypothetical protein LIC12769                |
| YP_002694.1 | hypothetical protein LIC12775                | hypothetical protein LIC12775                |
| YP_002696.1 | hypothetical protein LIC12779                | hypothetical protein LIC12779                |
| YP_002698.1 | hypothetical protein LIC12781                | hypothetical protein LIC12781                |
| YP_002706.1 | hypothetical protein LIC12789                | hypothetical protein LIC12789                |
| YP_002707.1 | hypothetical protein LIC12790                | hypothetical protein LIC12790                |
| YP_002708.1 | hypothetical protein LIC12791                | hypothetical protein LIC12791                |
| YP_002711.1 | hypothetical protein LIC12794                | hypothetical protein LIC12794                |
| YP_002714.1 | hypothetical protein LIC12797                | hypothetical protein LIC12797                |
| YP_002716.1 | hypothetical protein LIC12799                | hypothetical protein LIC12799                |
| YP_002720.1 | hypothetical protein LIC12803                | hypothetical protein LIC12803                |
| YP_002721.1 | hypothetical protein LIC12804                | hypothetical protein LIC12804                |
| YP_002723.1 | hypothetical protein LIC12806                | hypothetical protein LIC12806                |
| YP_002726.1 | hypothetical protein LIC12809                | hypothetical protein LIC12809                |
| YP_002727.1 | hypothetical protein LIC12810                | hypothetical protein LIC12810                |
| YP_002732.1 | hypothetical protein LIC12815                | hypothetical protein LIC12815                |
| YP_002734.1 | hypothetical protein LIC12818                | hypothetical protein LIC12818                |
| YP_002735.1 | hypothetical protein LIC12819                | hypothetical protein LIC12819                |
| YP_002739.1 | hypothetical protein LIC12823                | hypothetical protein LIC12823                |
| YP_002741.1 | hypothetical protein LIC12825                | hypothetical protein LIC12825                |
| YP_002742.1 | hypothetical protein LIC12826                | hypothetical protein LIC12826                |
| YP_002746.1 | hypothetical protein LIC12830                | hypothetical protein LIC12830                |
| YP_002751.1 | hypothetical protein LIC12835                | hypothetical protein LIC12835                |
| YP_002753.1 | hypothetical protein LIC12837                | hypothetical protein LIC12837                |
| YP_002756.1 | hypothetical protein LIC12840                | hypothetical protein LIC12840                |
| YP_002758.1 | hypothetical protein LIC12842                | hypothetical protein LIC12842                |
| YP_002759.1 | hypothetical protein LIC12843                | hypothetical protein LIC12843                |
| YP_002760.1 | hypothetical protein LIC12844                | hypothetical protein LIC12844                |
| YP_002795.1 | hypothetical protein LIC12879                | hypothetical protein LIC12879                |
| YP_002797.1 | hypothetical protein LIC12881                | hypothetical protein LIC12881                |
| YP_002798.1 | hypothetical protein LIC12882                | hypothetical protein LIC12882                |
| ref          | hypothetical protein LIC12887       | protein |
|--------------|-------------------------------------|---------|
| ref|YP_002803.1|YP_002803.1| hypothetical protein |
| ref|YP_002805.1|YP_002805.1| hypothetical protein |
| ref|YP_002806.1|YP_002806.1| hypothetical protein |
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| ref|YP_002813.1|YP_002813.1| hypothetical protein |
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| ref|YP_002816.1|YP_002816.1| hypothetical protein |
| ref|YP_002819.1|YP_002819.1| hypothetical protein |
| ref|YP_002821.1|YP_002821.1| hypothetical protein |
| ref|YP_002827.1|YP_002827.1| hypothetical protein |
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| ref|YP_002844.1|YP_002844.1| hypothetical protein |
| ref|YP_002846.1|YP_002846.1| hypothetical protein |
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| ref|YP_002881.1|YP_002881.1| hypothetical protein |
| ref|YP_002886.1|YP_002886.1| hypothetical protein |
| ref|YP_002890.1|YP_002890.1| hypothetical protein |
| ref|YP_002898.1|YP_002898.1| hypothetical protein |
| Ref | Hypothetical Protein LIC1296 | Hypothetical Protein LIC12986 |
|-----|-----------------------------|-----------------------------|
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| YP_002900.1 | hypothetical protein LIC1297 | hypothetical protein LIC12987 |
| YP_002903.1 | hypothetical protein LIC12990 | hypothetical protein LIC12991 |
| YP_002904.1 | hypothetical protein LIC12992 | hypothetical protein LIC12993 |
| YP_002906.1 | hypothetical protein LIC12994 | hypothetical protein LIC12995 |
| YP_002908.1 | hypothetical protein LIC12996 | hypothetical protein LIC12997 |
| YP_002912.1 | hypothetical protein LIC12998 | hypothetical protein LIC13000 |
| YP_002913.1 | hypothetical protein LIC13001 | hypothetical protein LIC13002 |
| YP_002918.1 | hypothetical protein LIC13003 | hypothetical protein LIC13004 |
| YP_002920.1 | hypothetical protein LIC13005 | hypothetical protein LIC13006 |
| YP_002921.1 | hypothetical protein LIC13007 | hypothetical protein LIC13008 |
| YP_002926.1 | hypothetical protein LIC13009 | hypothetical protein LIC13010 |
| YP_002927.1 | hypothetical protein LIC13011 | hypothetical protein LIC13012 |
| YP_002931.1 | hypothetical protein LIC13013 | hypothetical protein LIC13014 |
| YP_002932.1 | hypothetical protein LIC13015 | hypothetical protein LIC13016 |
| YP_002937.1 | hypothetical protein LIC13017 | hypothetical protein LIC13018 |
| YP_002938.1 | hypothetical protein LIC13019 | hypothetical protein LIC13020 |
| YP_002939.1 | hypothetical protein LIC13021 | hypothetical protein LIC13022 |
| YP_002940.1 | hypothetical protein LIC13023 | hypothetical protein LIC13024 |
| YP_002943.1 | hypothetical protein LIC13025 | hypothetical protein LIC13026 |
| YP_002947.1 | hypothetical protein LIC13027 | hypothetical protein LIC13028 |
| YP_002952.1 | hypothetical protein LIC13029 | hypothetical protein LIC13030 |
| YP_002957.1 | hypothetical protein LIC13031 | hypothetical protein LIC13032 |
| YP_002959.1 | hypothetical protein LIC13033 | hypothetical protein LIC13034 |
| YP_002960.1 | hypothetical protein LIC13035 | hypothetical protein LIC13036 |
| YP_002966.1 | hypothetical protein LIC13037 | hypothetical protein LIC13038 |
| YP_002969.1 | hypothetical protein LIC13039 | hypothetical protein LIC13040 |
| YP_002991.1 | hypothetical protein LIC13041 | hypothetical protein LIC13042 |
| YP_002993.1 | hypothetical protein LIC13043 | hypothetical protein LIC13044 |
| YP_003003.1 | hypothetical protein LIC13045 | hypothetical protein LIC13046 |
| YP_003008.1 | hypothetical protein LIC13047 | hypothetical protein LIC13048 |
| YP_003015.1 | hypothetical protein LIC13049 | hypothetical protein LIC13050 |
| YP_003016.1 | hypothetical protein LIC13051 | hypothetical protein LIC13052 |
| ref        | hypothetical protein LIC13109 | hypothetical protein LIC13112 |
|------------|--------------------------------|-------------------------------|
| ref        | hypothetical protein LIC13119 | hypothetical protein LIC13121 |
| ref        | hypothetical protein LIC13125 | hypothetical protein LIC13127 |
| ref        | hypothetical protein LIC13132 | hypothetical protein LIC13139 |
| ref        | hypothetical protein LIC13149 | hypothetical protein LIC13156 |
| ref        | hypothetical protein LIC13157 | hypothetical protein LIC13158 |
| ref        | hypothetical protein LIC13167 | hypothetical protein LIC13170 |
| ref        | hypothetical protein LIC13171 | hypothetical protein LIC13173 |
| ref        | hypothetical protein LIC13186 | hypothetical protein LIC13188 |
| ref        | hypothetical protein LIC13191 | hypothetical protein LIC13197 |
| ref        | hypothetical protein LIC13199 | hypothetical protein LIC13200 |
| ref        | hypothetical protein LIC13203 | hypothetical protein LIC13211 |
| ref        | hypothetical protein LIC13213 | hypothetical protein LIC13217 |
| ref        | hypothetical protein LIC13225 | hypothetical protein LIC13226 |
| ref        | hypothetical protein LIC13227 | hypothetical protein LIC13228 |
| ref        | hypothetical protein LIC13229 | hypothetical protein LIC13239 |
| Ref       | Hypothetical Protein | Hypothetical Protein |
|-----------|----------------------|----------------------|
| YP_003148.1 | LIC13241              | LIC13241              |
| YP_003150.1 | LIC13243              | LIC13243              |
| YP_003153.1 | LIC13246              | LIC13246              |
| YP_003161.1 | LIC13254              | LIC13254              |
| YP_003167.1 | LIC13260              | LIC13260              |
| YP_003172.1 | LIC13265              | LIC13265              |
| YP_003174.1 | LIC13267              | LIC13267              |
| YP_003184.1 | LIC13277              | LIC13277              |
| YP_003191.1 | LIC13284              | LIC13284              |
| YP_003197.1 | LIC13290              | LIC13290              |
| YP_003199.1 | LIC13292              | LIC13292              |
| YP_003201.1 | LIC13294              | LIC13294              |
| YP_003208.1 | LIC13303              | LIC13303              |
| YP_003209.1 | LIC13304              | LIC13304              |
| YP_003211.1 | LIC13306              | LIC13306              |
| YP_003212.1 | LIC13307              | LIC13307              |
| YP_003222.1 | LIC13317              | LIC13317              |
| YP_003228.1 | LIC13323              | LIC13323              |
| YP_003232.1 | LIC13327              | LIC13327              |
| YP_003234.1 | LIC13329              | LIC13329              |
| YP_003240.1 | LIC13335              | LIC13335              |
| YP_003245.1 | LIC13340              | LIC13340              |
| YP_003247.1 | LIC13342              | LIC13342              |
| YP_003249.1 | LIC13344              | LIC13344              |
| YP_003254.1 | LIC13349              | LIC13349              |
| YP_003257.1 | LIC13352              | LIC13352              |
| YP_003270.1 | LIC13365              | LIC13365              |
| YP_003278.1 | LIC13373              | LIC13373              |
| YP_003283.1 | LIC13380              | LIC13380              |
| YP_003289.1 | LIC13386              | LIC13386              |
| YP_003291.1 | LIC13388              | LIC13388              |
| YP_003293.1 | LIC13390              | LIC13390              |
| Ref     | Protein Name               |
|---------|----------------------------|
| ref|YP_003294.1| hypothetical protein LIC13391 |
| ref|YP_003301.1| hypothetical protein LIC13398 |
| ref|YP_003303.1| hypothetical protein LIC13400 |
| ref|YP_003321.1| hypothetical protein LIC13418 |
| ref|YP_003324.1| hypothetical protein LIC13421 |
| ref|YP_003328.1| hypothetical protein LIC13425 |
| ref|YP_003329.1| hypothetical protein LIC13426 |
| ref|YP_003332.1| hypothetical protein LIC13429 |
| ref|YP_003340.1| hypothetical protein LIC13437 |
| ref|YP_003343.1| hypothetical protein LIC13440 |
| ref|YP_003348.1| hypothetical protein LIC13445 |
| ref|YP_003349.1| hypothetical protein LIC13446 |
| ref|YP_003355.1| hypothetical protein LIC13452 |
| ref|YP_003357.1| hypothetical protein LIC13454 |
| ref|YP_003358.1| hypothetical protein LIC13455 |
| ref|YP_003361.1| hypothetical protein LIC13458 |
| ref|YP_003365.1| hypothetical protein LIC13462 |
| ref|YP_003368.1| hypothetical protein LIC13466 |
| ref|YP_003369.1| hypothetical protein LIC13467 |
| ref|YP_003370.1| hypothetical protein LIC13468 |
| ref|YP_003378.1| hypothetical protein LIC13477 |
| ref|YP_003385.1| hypothetical protein LIC13484 |
| ref|YP_002087.1| hypothetical protein LIC13510 |
| ref|YP_003399.1| hypothetical protein LIC20007 |
| ref|YP_003411.1| hypothetical protein LIC20019 |
| ref|YP_003431.1| hypothetical protein LIC20039 |
| ref|YP_003438.1| hypothetical protein LIC20046 |
| ref|YP_003445.1| hypothetical protein LIC20053 |
| ref|YP_003447.1| hypothetical protein LIC20055 |
| ref|YP_003448.1| hypothetical protein LIC20056 |
| ref|YP_003451.1| hypothetical protein LIC20059 |
| ref|YP_003455.1| hypothetical protein LIC20063 |
Supplement: Malmstroem, Beck *et al.* Proteome-wide copies per cell measurements

| Ref     | Protein Name             | Copy Number |
|---------|--------------------------|-------------|
| refYP_003462.1| hypothetical protein LIC20070 | 122         |
| refYP_003465.1| hypothetical protein LIC20073 | 122         |
| refYP_003487.1| hypothetical protein LIC20095 | 122         |
| refYP_003495.1| hypothetical protein LIC20103 | 122         |
| refYP_003499.1| hypothetical protein LIC20107 | 122         |
| refYP_003502.1| hypothetical protein LIC20110 | 122         |
| refYP_003508.1| hypothetical protein LIC20117 | 122         |
| refYP_003509.1| hypothetical protein LIC20118 | 122         |
| refYP_003514.1| hypothetical protein LIC20123 | 122         |
| refYP_003525.1| hypothetical protein LIC20134 | 122         |
| refYP_003530.1| hypothetical protein LIC20139 | 122         |
| refYP_003541.1| hypothetical protein LIC20150 | 122         |
| refYP_003543.1| hypothetical protein LIC20152 | 122         |
| refYP_003546.1| hypothetical protein LIC20155 | 122         |
| refYP_003548.1| hypothetical protein LIC20157 | 122         |
| refYP_003564.1| hypothetical protein LIC20173 | 122         |
| refYP_003565.1| hypothetical protein LIC20174 | 122         |
| refYP_003580.1| hypothetical protein LIC20189 | 122         |
| refYP_003590.1| hypothetical protein LIC20201 | 122         |
| refYP_003591.1| hypothetical protein LIC20202 | 122         |
| refYP_003601.1| hypothetical protein LIC20212 | 122         |
| refYP_003602.1| hypothetical protein LIC20213 | 122         |
| refYP_003604.1| hypothetical protein LIC20215 | 122         |
| refYP_003608.1| hypothetical protein LIC20219 | 122         |
| refYP_003610.1| hypothetical protein LIC20221 | 122         |
| refYP_003630.1| hypothetical protein LIC20245 | 122         |
| refYP_003636.1| hypothetical protein LIC20252 | 122         |
| refYP_003639.1| hypothetical protein LIC20255 | 122         |
| refYP_003641.1| hypothetical protein LIC20257 | 122         |
| refYP_003642.1| hypothetical protein LIC20258 | 122         |
| refYP_003644.1| hypothetical protein LIC20260 | 122         |
| refYP_003645.1| hypothetical protein LIC20261 | 122         |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| ref | YP_003646.1 | hypothetical protein LIC2062 | hypothetical protein |
| ref | YP_003647.1 | hypothetical protein LIC2063 | hypothetical protein |
| ref | YP_003651.1 | hypothetical protein LIC2067 | hypothetical protein |
| ref | YP_003652.1 | hypothetical protein LIC2068 | hypothetical protein |
| ref | YP_003655.1 | hypothetical protein LIC2071 | hypothetical protein |
| ref | YP_001383.1 | phosphate sodium symporter | ion transport |
| sp | Q72PE5 | CysA_LEPIC | Sulfate/thiosulfate import ATP-binding protein CysA (EC 3.6.3.25) (Sulfate-transporting ATPase) |
| ref | YP_001885.1 | heavy metal efflux pump | ion transport |
| ref | YP_001236.1 | periplasmic sulfate-binding protein | ion transport |
| ref | YP_001664.1 | magnesium transporter | ion transport |
| ref | YP_001883.1 | heavy metal efflux pump | ion transport |
| ref | YP_001332.1 | sodium:alanine symporter family/phosphatidylserine decarboxylase | ion transport |
| ref | YP_001886.1 | heavy metal efflux pump | ion transport |
| ref | YP_001470.1 | heavy metal efflux pump | ion transport |
| ref | YP_001236.1 | sodium:alanine symporter family/phosphatidylserine decarboxylase | ion transport |
| ref | YP_001332.1 | sodium:alanine symporter family/phosphatidylserine decarboxylase | ion transport |
| ref | YP_001470.1 | heavy metal efflux pump | ion transport |
| ref | YP_001882.1 | heavy metal efflux pump | ion transport |
| ref | YP_001885.1 | heavy metal efflux pump | ion transport |
| ref | YP_002159.1 | heavy metal efflux pump | ion transport |
| ref | YP_003083.1 | potassium uptake system protein | ion transport |
| ref | YP_001332.1 | sodium:alanine symporter family/phosphatidylserine decarboxylase | ion transport |
| ref | YP_001885.1 | heavy metal efflux pump | ion transport |
| ref | YP_003083.1 | potassium uptake system protein | ion transport |
| ref | YP_002336.1 | disulfide interchange transmembrane protein | ion transport |
| ref | YP_003306.1 | YwrC | ion transport |
| ref | YP_000476.1 | heavy metal efflux pump | ion transport |
| sp | Q72TM6 | ATKB_LEPIC | Potassium-transporting ATPase B chain (EC 3.6.3.12) (Potassium-translocating ATPase B chain) (ATP ph |
| ref | YP_001342.1 | putative potassium efflux transporter | ion transport |
| ref | YP_001956.1 | sodium-dependent transporter | ion transport |
| ref | YP_001883.1 | heavy metal efflux pump | ion transport |
| ref | YP_001884.1 | heavy metal efflux pump | ion transport |
| ref | YP_001494.1 | di-tripeptide proton symporter | ion transport |
| ref | YP_003267.1 | chloride channel | ion transport |
| ref | YP_000264.1 | potassium uptake protein | ion transport |
| sp | Q72TM7 | ATKA_LEPIC | Potassium-transporting ATPase A chain (EC 3.6.3.12) (Potassium-translocating ATPase A chain) (ATP ph |
| ref | YP_001666.1 | heavy metal efflux pump | ion transport |
| ref | YP_001667.1 | heavy metal efflux pump | ion transport |
| ref | YP_001082.1 | YP_000660.1 | heme exporter protein B | ion transport |
| ref | YP_000661.1 | heme exporter protein C | ion transport |
| ref | YP_003082.1 | YP_000822.1 | KtrB | ion transport |
| ref | YP_001662.1 | magnesium transport P-type atpase | ion transport |
| ref | YP_000264.1 | potassium uptake protein | ion transport |
| sp | Q72TM5 | ATKC_LEPIC | Potassium-transporting ATPase C chain (EC 3.6.3.12) (Potassium-translocating ATPase C chain) (ATP ph |
| ref | YP_002902.1 | heavy metal efflux pump | ion transport |
| sp | Q72V73 | KPRS_LEPIC | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) (RPPK) (Phosphoribosyl pyrophosphate synthetase) (P- |
| sp | Q72M65 | NDK_LEPIC | Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase) (Nucleoside-2- | kinase activity |

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| Ref | YP_002825.1 | YP_002825.1 |
|-----|------------|------------|
| Kinase activity | aspartokinase | 657 |

| Ref | YP_002528.1 | YP_002528.1 |
|-----|------------|------------|
| Kinase activity | Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase) | 872 |

| Ref | YP_002528.1 | YP_002528.1 |
|-----|------------|------------|
| Kinase activity | Serine/threonine kinase with GAF domain | 392 |

| Ref | YP_002135.1 | YP_002135.1 |
|-----|------------|------------|
| Kinase activity | ADP-ribose synthetase | 407 |

| Ref | YP_002278.1 | YP_002278.1 |
|-----|------------|------------|
| Kinase activity | Ribokinase | 444 |

| Ref | YP_000703.1 | YP_000703.1 |
|-----|------------|------------|
| Kinase activity | Polyphosphate kinase | 312 |

| Ref | YP_000112.1 | YP_000112.1 |
|-----|------------|------------|
| Kinase activity | Serine/threonine kinase | 272 |

| Ref | YP_001102.1 | YP_001102.1 |
|-----|------------|------------|
| Kinase activity | Pyruvate kinase | 141 |

| Ref | YP_0003480.1 | YP_003480.1 |
|-----|------------|------------|
| Kinase activity | Phosphatase–fructose-6-phosphate 1-phosphotransferase | 68 |

| Ref | YP_000118.1 | YP_001188.1 |
|-----|------------|------------|
| Kinase activity | Peroxiredoxin | 3608 |

| Ref | YP_002166.1 | YP_002166.1 |
|-----|------------|------------|
| Metabolic process | Fructose-bisphosphate aldolase | 7001 |

| Ref | YP_000199.1 | YP_001999.1 |
|-----|------------|------------|
| Metabolic process | Cytochrome c oxidase polypeptide | 281 |

| Ref | YP_000944.1 | YP_000944.1 |
|-----|------------|------------|
| Metabolic process | Acyl-CoA dehydrogenase | 2234 |

| Ref | YP_003456.1 | YP_003456.1 |
|-----|------------|------------|
| Metabolic process | 3-oxoacyl-(acyl-carrier protein) reductase | 537 |

| Ref | YP_001323.1 | YP_001323.1 |
|-----|------------|------------|
| Metabolic process | MacoC | 966 |

| Ref | YP_002001.1 | YP_002001.1 |
|-----|------------|------------|
| Metabolic process | Cytochrome c oxidase polypeptide | 64 |

| Ref | YP_002498.1 | YP_002498.1 |
|-----|------------|------------|
| Metabolic process | Succinyl-CoA synthetase alpha subunit | 1543 |
| Ref       | Protein ID   | Description                                                                 | Metabolic Process | 2176 | 2357 | 2761 |
|-----------|--------------|-----------------------------------------------------------------------------|-------------------|------|------|------|
| ref|YP_001970.1|catalase|metabolic process|1576|2322|1610|
| sp|Q72M00|llvc_lepic|Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acid isomerase) (Alpha-keto-beta-hydration) metabolic process|3176|2217|2221|
| ref|YP_003205.1|3-hydroxyacyl-CoA dehydrogenase metabolic process|2551|1903|320|
| ref|YP_001941.1|succinate dehydrogenase metabolic process|1473|2088|1195|
| ref|YP_001734.1|hypothetical protein LIC11782 metabolic process|1879|2058|375|
| ref|YP_000091.1|long-chain-fatty-acid CoA ligase metabolic process|1229|1903|320|
| sp|Q72NR4|tpx_lepic|Probable thiol peroxidase (EC 1.11.1.22) metabolic process|1722|1721|1039|
| ref|YP_001065.1|adenylate/guanylate cyclase metabolic process|1760|1601|110|
| ref|YP_001798.1|molybdopterin oxidoreductase membrane subunit metabolic process|3176|2217|2221|
| ref|YP_000397.1|hypothetical protein LIC0411 metabolic process|2551|1903|320|
| ref|YP_000046.1|proton-translocating NADH transhydrogenase, subunit alpha part 1|1455|1311|1688|
| ref|YP_000280.1|H+-translocating NADH transhydrogenase subunit beta|1192|1298|121|
| ref|YP_000385.1|hypothetical protein LIC0877 metabolic process|1526|40|
| ref|YP_001400.1|peptidyl-prolyl cis-trans isomerase metabolic process|932|1481|188|
| ref|YP_001328.1|short-chain dehydrogenase metabolic process|969|1189|1073|
| ref|YP_000307.1|phospho-2-dehydro-3-deoxyheptonate aldolase Chorismate mutase metabolic process|2683|1475|1305|
| ref|YP_001788.1|peptidyl-prolyl cis-trans isomerase metabolic process|1897|1286|37|
| ref|YP_000111.1|hypothetical protein LIC0115 metabolic process|1229|1903|320|
| ref|YP_001588.1|long-chain-fatty-acid CoA ligase metabolic process|1897|1286|37|
| ref|YP_000567.1|acyl-CoA dehydrogenase metabolic process|1455|1311|1688|
| ref|YP_001583.1|FKBP-type peptidyl-prolyl cis-trans isomerase metabolic process|1192|1298|121|
| ref|YP_002100.1|putative molybdenum cofactor biosynthesis protein metabolic process|1063|1158|96|
| ref|YP_001916.1|cyclic nucleotide binding protein metabolic process|858|1127|447|
| sp|Q72VY3|fumc_lepic|Fumarate hydratase class II (EC 4.2.1.2) (Fumarase C) metabolic process|1053|1073|456|
| sp|Q72RC4|leu2_lepic|3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) (Isopropylmalate isomerase) (Alpha-IPM iso) metabolic process|1053|1073|456|
| ref|YP_002745.1|citrate synthase metabolic process|1309|986|488|
| sp|Q72SG7|tig_lepic|Trigger factor (TF) metabolic process|958|995|1056|
| ref|YP_002659.1|mamC family protein metabolic process|867|943|919|
| sp|Q72PI7|odo1_lepic|2-oxoglutarate dehydrogenase E1 metabolic process|1461|930|1217|
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Ref | PDB | Component | EC (Alpha-ketoglutarate dehydrogenase) | Process | Copies per Cell |
|-----|-----|-----------|----------------------------------------|---------|----------------|
| YP_002404.1 | YP_002404.1 | Dihydrolipoamide succinyltransferase | | Metabolic process | 867 912 1401 |
| YP_003151.1 | YP_003151.1 | Isocitrate dehydrogenase | | Metabolic process | 1459 906 1993 |
| YP_002423.1 | YP_002423.1 | 3-Hydroxybutyryl-CoA dehydratase | | Metabolic process | 983 883 367 |
| YP_001476.1 | YP_001476.1 | Acetyl-CoA carboxylase alpha subunit | | Metabolic process | 895 840 1061 |
| YP_002101.1 | YP_002101.1 | Alcohol dehydrogenase | | Metabolic process | 1004 820 859 |
| YP_001386.1 | YP_001386.1 | Peptidyl-prolyl cis-trans isomerase | | Metabolic process | 716 818 447 |
| YP_002922.1 | YP_002922.1 | Acyl-CoA dehydrogenase | | Metabolic process | 714 817 703 |
| YP_003450.1 | YP_003450.1 | Methylmalonyl-CoA mutase | | Metabolic process | 689 812 435 |
| YP_003489.1 | YP_003489.1 | Short-chain dehydrogenase | | Metabolic process | 980 799 129 |
| YP_001276.1 | YP_001276.1 | Bacterioferritin | | Metabolic process | 971 762 64 |
| YP_003616.1 | YP_003616.1 | Acireductone dioxygenase enzyme ARD and ARD' | | Metabolic process | 825 688 284 |
| YP_001473.1 | YP_001473.1 | Hypothetical protein LIC11514 | | Metabolic process | 1172 681 47 |
| YP_002615.1 | YP_002615.1 | Glutamate synthase (NADPH) alpha chain precursor | | Metabolic process | 962 672 690 |
| YP_003492.1 | YP_003492.1 | Hypothetical protein LIC20100 | | Metabolic process | 611 672 427 |
| YP_000315.1 | YP_000315.1 | Hemolysin | | Metabolic process | 640 639 230 |
| YP_000045.1 | YP_000045.1 | DTD-P-glucose 4-6-dehydratase | | Metabolic process | 598 616 517 |
| YP_001168.1 | YP_001168.1 | Adenylate/guanilate cyclase | | Metabolic process | 507 599 850 |
| YP_000244.1 | YP_000244.1 | Alcohol dehydrogenase | | Metabolic process | 434 597 1069 |
| YP_000506.1 | YP_000506.1 | Oxidoreductase family | | Metabolic process | 659 597 480 |
| YP_001915.1 | YP_001915.1 | Acyl-CoA dehydrogenase | | Metabolic process | 829 591 288 |
| YP_002137.1 | YP_002137.1 | UDP-glucose 4-epimerase | | Metabolic process | 662 588 578 |
| YP_001219.1 | YP_001219.1 | Transketolase beta subunit | | Metabolic process | 471 587 707 |
| YP_002403.1 | YP_002403.1 | Dihydrolipoamide dehydrogenase | | Metabolic process | 605 566 906 |
| Reference | Description | Process | Start | End | Length |
|-----------|-------------|---------|-------|-----|--------|
| ref|YP_001875.1|YP_001875.1|short-chain dehydrogenase|metabolic process|506|520|211|
| ref|YP_002681.1|YP_002681.1|aldehyde dehydrogenase|metabolic process|488|517|211|
| sp|Q7ZLQ9|TPIS_LEPIC|Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase)|metabolic process|562|509|411|
| sp|Q7ZRC5|LEUD_LEPIC|3-isopropylmalate dehydrogenase small subunit (EC 4.2.1.33) (Isopropylmalate isomerase) (Alpha-IPM iso)|metabolic process|621|499|492|
| sp|Q7ZUH6|PURQ_LEPIC|Phosphoribosylformylglycinamidine synthase I (EC 5.3.1.1) (FGAM synthase I)|metabolic process|507|497|110|
| ref|YP_000468.1|YP_000468.1|threonine synthase|metabolic process|564|494|923|
| ref|YP_002478.1|YP_002478.1|acyl-CoA dehydrogenase|metabolic process|418|490|246|
| ref|YP_003258.1|YP_003258.1|L-amino acid oxidase|metabolic process|403|478|215|
| ref|YP_002645.1|YP_002645.1|3-hydroxybutyryl-CoA dehydratase|metabolic process|510|475|316|
| ref|YP_002541.1|YP_002541.1|diaminopimelate decarboxylase|metabolic process|394|454|517|
| ref|YP_003485.1|YP_003485.1|bacterioferritin comigratory protein|metabolic process|672|446|757|
| ref|YP_000933.1|YP_000933.1|monoxygenase|metabolic process|403|444|169|
| sp|P61703|SYA_LEPIC|Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA 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_003418.1|YP_003418.1|short-chain dehydrogenase|metabolic process|275|410|40|
| ref|YP_000555.1|YP_000555.1|homoerine dehydrogenase|metabolic process|331|401|324|
| sp|Q7ZNQ9|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|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_003071.1|YP_003071.1|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|Q7ZU05|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|metabolic process|326|345|332|
| sp|Q7ZS57|ISP5_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 process|458|332|324|
Supplement: Malmstroem, Beck *et al*. Proteome-wide copies per cell measurements

| Ref | Gene Accession | Protein Name | Process | Copies |
|-----|----------------|--------------|---------|--------|
| ref|YP_000019.1|YP_000019.1|3-oxoacyl-acyl carrier protein reductase|metabolic process|398|326|529|
| ref|YP_003539.1|YP_003539.1|heme oxygenase|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|292|992|
| ref|YP_003597.1|YP_003597.1|methylmalonyl-CoA mutase small subunit|metabolic process|455|305|553|
| 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|292|992|
| ref|YP_003597.1|YP_003597.1|methylmalonyl-CoA mutase small subunit|metabolic process|455|305|553|
| 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|292|992|
| ref|YP_003597.1|YP_003597.1|methylmalonyl-CoA mutase small subunit|metabolic process|455|305|553|
| 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|292|992|
| ref|YP_003597.1|YP_003597.1|methylmalonyl-CoA mutase small subunit|metabolic process|455|305|553|
| 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|292|992|
| ref|YP_003597.1|YP_003597.1|methylmalonyl-CoA mutase small subunit|metabolic process|455|305|553|
| 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|292|992|
| ref|YP_003597.1|YP_003597.1|methylmalonyl-CoA mutase small subunit|metabolic process|455|305|553|
| 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|292|992|
| ref|YP_003597.1|YP_003597.1|methylmalonyl-CoA mutase small subunit|metabolic process|455|305|553|
| 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|292|992|
| ref|YP_003597.1|YP_003597.1|methylmalonyl-CoA mutase small subunit|metabolic process|455|305|553|
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Reference | Gene ID | Protein Description | Process | Copies Per Cell |
|-----------|---------|---------------------|---------|-----------------|
| ref|YP_001319.1|transketolase|metabolic process|203|177|246|
| ref|YP_000425.1|nitrogen regulatory protein pII|metabolic process|266|173|525|
| ref|YP_002571.1|glutathione peroxidase|metabolic process|246|173|118|
| ref|YP_002060.1|dTDP-4-dehydrorhamnose 3,5-epimerase|metabolic process|255|172|324|
| ref|YP_000988.1|adenylsuccinate lyase|metabolic process|226|170|230|
| ref|YP_000431.1|phosphomannomutase|metabolic process|215|169|517|
| ref|YP_000530.1|lipase|metabolic process|144|168|78|
| ref|YP_002085.1|cdp-glucose 4,6-dehydratase|metabolic process|222|163|82|
| ref|YP_003529.1|capsular polysaccharide biosynthesis protein|metabolic process|167|155|57|
| ref|YP_003233.1|isocitrate dehydrogenase|metabolic process|190|151|375|
| ref|YP_000815.1|glyoxalase|metabolic process|401|148|249|
| ref|YP_001600.1|hypothetical protein LIC11642|metabolic process|143|118|
| sp|Q75FCB|Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase) (ASADH)|metabolic process|197|135|439|
| ref|YP_002111.1|UDP-glucose 4-epimerase|metabolic process|201|122|96|
| ref|YP_002261.1|adenylate/guanylate cyclase|metabolic process|128|103|427|
| ref|YP_002107.1|putative UDP-N-acetylglucosamine-2-epimerase|metabolic process|137|87|57|
| sp|P61742|Glycerol-3-phosphate dehydrogenase|metabolic process|87|140|
| ref|YP_003182.1|hypothetical protein LIC13275|metabolic process|
| ref|YP_002012.1|hypothetical protein LIC12078|metabolic process|46|147|
| ref|YP_001691.1|hypothetical protein LIC11739|metabolic process|344|253|
| sp|Q72SC4|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|hypothetical protein LIC12106|metabolic process|105|14|
| ref|YP_002552.1|enoyl-CoA hydratase|metabolic process|521|
| ref|YP_000069.1|glyoxylase |metabolic process|480|
| ref|YP_002130.1|transketolase|metabolic process|468|
| ref|YP_002839.1|citrate synthase|metabolic process|427|
| ref|YP_003446.1|hypothetical protein LIC20054|metabolic process|371|
| ref|YP_002138.1|phosphoheptose isomerase|metabolic process|359|
| sp|P62354|1-(5-phosphoribosyl)-5-(5-phosphoribosylaminomethylideneamino)imidazole-4-carboxamide isomerase |metabolic process|335|
| ref|YP_001917.1|thioredoxin|metabolic process|324|
| Reference | Accession | Description | Process | Proportion |
|-----------|-----------|-------------|---------|------------|
| ref|YP_001710.1|YP_001710.1|acyl-CoA hydrolase|metabolic process|273|
| sp|Q72546|PYRG_LEPIC|CTP synthase (EC 6.3.4.2) (UTP–ammonia ligase) (CTP synthetase)|metabolic process|261|
| sp|Q72V2|SERC_LEPIC|Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT)|metabolic process|242|
| ref|YP_002380.1|YP_002380.1|chorismate mutase and prephenate dehydratase|metabolic process|226|
| ref|YP_003300.1|YP_003300.1|alkaline phosphatase|metabolic process|219|
| sp|Q72N73|NADA_LEPIC|Quinolinate synthetase A|metabolic process|203|
| ref|YP_000428.1|YP_000428.1|3-methylcrotonoyl-CoA carboxylase beta subunit|metabolic process|188|
| sp|Q72U21|DAPB_LEPIC|Dihydroripocollinate reductase (EC 1.3.1.26) (DHPR)|metabolic process|185|
| ref|YP_001760.1|YP_001760.1|glutaredoxin-related protein|metabolic process|185|
| sp|P61660|HIS7_LEPIC|Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) (IGPD)|metabolic process|177|
| ref|YP_002710.1|YP_002710.1|hypothetical protein LIC12793|metabolic process|169|
| ref|YP_002471.1|YP_002471.1|hypothetical protein LIC12543|metabolic process|155|
| ref|YP_003402.1|YP_003402.1|delta-aminolevulinic acid dehydratase|metabolic process|147|
| ref|YP_002699.1|YP_002699.1|hydroxymethylglutaryl-CoA lyase|metabolic process|132|
| ref|YP_002320.1|YP_002320.1|cyclic nucleotide binding protein|metabolic process|118|
| ref|YP_001268.1|YP_001268.1|phosphoglycolate phosphatase|metabolic process|118|
| ref|YP_001626.1|YP_001626.1|enoyl-CoA hydratase|metabolic process|107|
| ref|YP_000565.1|YP_000565.1|anthranilate synthase component II|metabolic process|92|
| ref|YP_001252.1|YP_001252.1|hypothetical protein LIC11284|metabolic process|89|
| ref|YP_001718.1|YP_001718.1|phosphomannomutase|metabolic process|85|
| ref|YP_000664.1|YP_000664.1|hypothetical protein LIC10680|metabolic process|71|
| ref|YP_002102.1|YP_002102.1|CMP-N-acetylneuraminic acid synthetase|metabolic process|71|
| sp|Q72RA8|ARLY_LEPIC|Argininosuccinate lyase (EC 4.3.2.1) (Arginosuccinase) (ASAL)|metabolic process|64|
| ref|YP_003140.1|YP_003140.1|short-chain dehydrogenase|metabolic process|64|
| ref|YP_002091.1|YP_002091.1|oxidoreductase family protein|metabolic process|61|
| sp|Q72QN9|PAND_LEPIC|Aspartate 1-decarboxylase precursor (EC 4.1.1.11) (Aspartate alpha-decarboxylase)|metabolic process|61|
| ref|YP_002226.1|YP_002226.1|phosphoribosylaminomidazole carboxylase catalytic subunit protein|metabolic process|50|
| sp|Q72PM6|PLSX_LEPIC|Fatty acid/phospholipid synthesis protein plx|metabolic process|37|
| ref|YP_001699.1|YP_001699.1|long-chain-fatty-acid CoA ligase|metabolic process|37|
| ref|YP_001452.1|YP_001452.1|hypothetical protein LIC11491|metabolic process|37|
| ref|YP_001835.1|YP_001835.1|putative lipoprotein|metabolic process|14|
| ref|YP_003609.1|YP_003609.1|glutamate synthase|metabolic process|11|
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Ref| YP| Function | Process |
|---|---|---|---|
| ref|YP_001377.1|YP_001377.1|acyl-CoA thioesterase|metabolic process|8|
| ref|YP_003051.1|YP_003051.1|hemolysin|metabolic process|8|
| ref|YP_001058.1|YP_001058.1|cytochrome c peroxidase|metabolic process|
| ref|YP_000024.1|YP_000024.1|adenylate/guanulate cyclase|metabolic process|
| ref|YP_003110.1|YP_003110.1|cholesterol oxidase precursor|metabolic process|
| ref|YP_000586.1|YP_000586.1|lyso phospholipase|metabolic process|343|
| ref|YP_003396.1|YP_003396.1|5,10 methylene tetrahydrofolate reductase|metabolic process|304|
| ref|YP_003414.1|YP_003414.1|azoreductase|metabolic process|269|
| sp|Q72VB8|GPMI_LEPIC|2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC 5.4.2.1] (Phosphoglyceromutase) (BPG)|metabolic process|238|
| ref|YP_002209.1|YP_002209.1|pyrroline-5-carboxylate reductase|metabolic process|230|
| ref|YP_000443.1|YP_000443.1|adenosine deaminase|metabolic process|223|
| sp|Q75FF2|AIRP_LEPIC|Alanine racemase (EC 5.1.1.1)|metabolic process|223|
| ref|YP_001574.1|YP_001574.1|ADP-L-glycero-D-mannoheptose-6-epimerase|metabolic process|211|
| ref|YP_001592.1|YP_001592.1|CsgA|metabolic process|203|
| sp|Q72NU6|MGSA_LEPIC|Methylglyoxal synthase (EC 4.2.3.3) (MGS)|metabolic process|200|
| ref|YP_002073.1|YP_002073.1|UDP-N-acetylglycosamine 2-epimerase|metabolic process|185|
| sp|Q72T46|MTNA_LEPIC|Probable methylthioribose-1-phosphate isomerase (EC 5.3.1.23) (MTR-1-P isomerase) (S-methyl-5-thioribose isomerase) (S-methyl-5-thioribose isomerase)|metabolic process|173|
| ref|YP_003061.1|YP_003061.1|UDP-glucose 4-epimerase|metabolic process|173|
| ref|YP_001314.1|YP_001314.1|acyl-CoA dehydrogenase|metabolic process|166|
| ref|YP_002186.1|YP_002186.1|L-aspartate oxidase|metabolic process|151|
| ref|YP_001040.1|YP_001040.1|alcohol dehydrogenase|metabolic process|140|
| ref|YP_003277.1|YP_003277.1|phosphoadenosine phosphosulphate reductase|metabolic process|140|
| ref|YP_000770.1|YP_000770.1|cyclic nucleotide binding protein|metabolic process|136|
| ref|YP_000776.1|YP_000776.1|enoyl-CoA hydratase|metabolic process|136|
| ref|YP_002093.1|YP_002093.1|putative hydroxyacid aldolase protein|metabolic process|136|
| ref|YP_002108.1|YP_002108.1|N-acetylmuraminate synthase|metabolic process|129|
| ref|YP_000527.1|YP_000527.1|acyl-CoA dehydrogenase|metabolic process|125|
| sp|Q72W01|AROC_LEPIC|Chorismate synthase (EC 4.2.3.5) (5-enolpyruvylyshikimate-3-phosphate phospholylase) - Leptospira inte|metabolic process|121|
| ref|YP_000641.1|YP_000641.1|hemolysin|metabolic process|121|
| sp|PE2458|HISX_LEPIC|Histidinol dehydrogenase (EC 1.1.1.23) (HDH)|metabolic process|121|
| ref|YP_002444.1|YP_002444.1|acetocacetyl-CoA synthetase|metabolic process|114|
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| accession | name | description | process | fold_change |
|-----------|------|-------------|---------|-------------|
| sp|Q72U07|DXR_LEPIC | 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (DXP reductoisomerase) [1-deoxyxylulose] | metabolic | 107 |
| ref|YP_001754.1|YP_001754.1 | dihydrodiploamid dehydrogenase | metabolic | 107 |
| ref|YP_003080.1|YP_003080.1 | hypothetical protein LIC13172 | metabolic | 107 |
| sp|Q75FW3|AROB_LEPIC | 3-dehydroquinate synthase (EC 4.2.3.4) | metabolic | 103 |
| ref|YP_002084.1|YP_002084.1 | dTDP-4-dehydrorhamnose epimerase | metabolic | 103 |
| ref|YP_000444.1|YP_000444.1 | hypothetical protein LIC10460 | metabolic | 103 |
| ref|YP_000943.1|YP_000943.1 | alpha-methylacyl-CoA racemase | metabolic | 100 |
| ref|YP_002463.1|YP_002463.1 | riboflavin synthase subunit alpha | metabolic | 96 |
| ref|YP_001093.1|YP_001093.1 | phosphoribosylaminooimidazole synthetase | metabolic | 89 |
| ref|YP_000185.1|YP_000185.1 | short-chain dehydrogenase | metabolic | 89 |
| ref|YP_003423.1|YP_003423.1 | short-chain dehydrogenase | metabolic | 89 |
| ref|YP_001629.1|YP_001629.1 | glycerol-3-phosphate dehydrogenase | metabolic | 85 |
| ref|YP_000811.1|YP_000811.1 | hypothetical protein LIC10834 | metabolic | 85 |
| ref|YP_001159.1|YP_001159.1 | hypothetical protein LIC11189 | metabolic | 85 |
| ref|YP_001363.1|YP_001363.1 | N-acetylneuraminate synthase | metabolic | 85 |
| sp|Q72U04|TRPA_LEPIC | Tryptophan synthase alpha chain (EC 4.2.1.20) | metabolic | 85 |
| ref|YP_002554.1|YP_002554.1 | hemolysin | metabolic | 82 |
| ref|YP_002736.1|YP_002736.1 | pyridoxal phosphate biosynthesis protein | metabolic | 82 |
| ref|YP_002309.1|YP_002309.1 | capsule biosynthesis protein | metabolic | 82 |
| ref|YP_003336.1|YP_003336.1 | dihydroorotate dehydrogenase | metabolic | 78 |
| ref|YP_000923.1|YP_000923.1 | aldo/keto reductase | metabolic | 75 |
| ref|YP_000040.1|YP_000040.1 | polysialic acid capsule expression protein | metabolic | 75 |
| ref|YP_000778.1|YP_000778.1 | acyl-CoA dehydrogenase | metabolic | 71 |
| ref|YP_001129.1|YP_001129.1 | dihydriopaid dehydrogenase | metabolic | 71 |
| ref|YP_000258.1|YP_000258.1 | cyclic nucleotide binding protein | metabolic | 64 |
| ref|YP_003407.1|YP_003407.1 | coproporphyrinogen III oxidase | metabolic | 64 |
| ref|YP_000625.1|YP_000625.1 | diguanylate phosphodiesterase | metabolic | 64 |
| ref|YP_001939.1|YP_001939.1 | hypothetical protein LIC12000 | metabolic | 64 |
| sp|P62359|HISZ_LEPIC | ATP phosphoribosyltransferase regulatory subunit | metabolic | 61 |
| ref|YP_002139.1|YP_002139.1 | FAD-dependent oxidoreductase family | metabolic | 57 |
| ref|YP_001253.1|YP_001253.1 | hypothetical protein LIC11285 | metabolic | 57 |
| Reference | Protein ID | Protein Name | Process | Value |
|-----------|------------|--------------|---------|-------|
| ref|YP_001701.1| hypothetical protein LIC11749 | metabolic process | 57 |
| ref|YP_000039.1| 3-dehydroquinate dehydratase | metabolic process | 54 |
| ref|YP_002059.1| dTDP-4-dehydrorhamnose reductase | metabolic process | 54 |
| sp|Q72MT7|Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucone isomerase) (PGI) (Phosphohexose isomerase) | metabolic process | 50 |
| ref|YP_000285.1| hypothetical protein LIC10295 | metabolic process | 47 |
| ref|YP_002059.1| dTDP-4-dehydrorhamnose reductase | metabolic process | 47 |
| ref|YP_002035.1| CinA | metabolic process | 47 |
| ref|YP_001321.1| alcohol dehydrogenase | metabolic process | 44 |
| ref|YP_001890.1| GMP synthase | metabolic process | 44 |
| ref|YP_000183.1| hypothetical protein LIC10192 | metabolic process | 44 |
| ref|YP_001415.1| pantoate–beta-alanine ligase | metabolic process | 44 |
| ref|YP_003050.1| pantothenate metabolism flavoprotein | metabolic process | 44 |
| ref|YP_001264.1| hypothetical protein LIC11298 | metabolic process | 44 |
| ref|YP_001668.1| hypothetical protein LIC11716 | metabolic process | 40 |
| ref|YP_001075.1| methylmalonyl-CoA mutase | metabolic process | 40 |
| ref|YP_000710.1| riboflavin biosynthesis protein | metabolic process | 40 |
| ref|YP_003460.1| pterin-4-alpha-carbinolamine dehydratase | metabolic process | 37 |
| ref|YP_002079.1| putative glycosyltransferase | metabolic process | 37 |
| ref|YP_003472.1| 4-hydroxybenzoyl-CoA thioesterase | metabolic process | 34 |
| ref|YP_000022.1| arsenate reductase | metabolic process | 34 |
| ref|YP_002481.1| D-3-phosphoglycerate dehydrogenase | metabolic process | 34 |
| ref|YP_002901.1| lipase | metabolic process | 34 |
| ref|YP_002495.1| hypothetical protein LIC12570 | metabolic process | 34 |
| ref|YP_003122.1| putative cytochrome oxidase subunit | metabolic process | 34 |
| sp|Q72UP7|2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12) (MECP synthase) | metabolic process | 30 |
| sp|Q72PM1|3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) | metabolic process | 30 |
| ref|YP_000277.1| 6-pyruvoyl tetrahydrobiopterin synthase | metabolic process | 30 |
| ref|YP_001235.1| putative 6-pyruvoyl tetrahydrobiopterin synthase | metabolic process | 30 |
| ref|YP_002098.1| hypothetical protein LIC12163 | metabolic process | 27 |
| ref|YP_002266.1| lipoate-protein ligase a | metabolic process | 27 |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Reference | Description |
|-----------|-------------|
| 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-acetyleneuraminic acid synthetase | metabolic process | 27 |
| sp|Q72V75|ISPETYPEPIC | 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 |
| sp|Q72V77|TRPCLETEPIC | 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 LIC1036 | metabolic process | 24 |
| sp|Q72PF1|PDHXLETEPIC | 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 process | 24 |
| ref|YP_003116.1|YP_003116.1 | riboflavin-specific deaminase/reductase | metabolic process | 24 |
| ref|YP_002841.1|YP_002841.1 | cytochrome c peroxidase | metabolic process | 24 |
| ref|YP_003358.1|YP_003358.1 | hypothetical protein LIC20192 | metabolic process | 24 |
| ref|YP_002224.1|YP_002224.1 | oligo-1,6-glucosidase | metabolic process | 24 |
| sp|Q72RD4|GSH1LETEPIC | Glutamate--cysteine ligase (EC 6.3.2.2) (Gamma-glutamylcysteine synthetase) (Gamma-ECS) (GCS) | 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|Q72FF4|SPEHLETEPIC | 5-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|MURILETEPIC | 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_000244.1|YP_000244.1 | adenylylguanylyl cyclase | metabolic process | 11 |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Ref | Accession | Description | Process | Copies |
|-----|-----------|-------------|---------|--------|
| ref|YP_001761.1|hypothetical protein LIC11810|metabolic|11|
| ref|YP_003187.1|Maoc family protein|metabolic|11|
| ref|YP_002379.1|prephenate (chorismate) dehydrogenase|metabolic|11|
| ref|YP_001728.1|hypothetical protein LIC11776|metabolic|11|
| ref|YP_003273.1|siroheme synthetase|metabolic|11|
| ref|YP_000578.1|2-dehydrodopantoate 2-reductase|metabolic|8|
| ref|YP_003271.1|putative strictosidine synthase|metabolic|8|
| ref|YP_002916.1|short-chain dehydrogenase|metabolic|8|
| ref|YP_000198.1|SCO1/SenC family protein|metabolic|8|
| ref|YP_00094.1|2'-5' RNA ligase|metabolic|5|
| ref|YP_001567.1|3-oxaprenyl-4-hydroxybenzoate carboxylase|metabolic|5|
| ref|YP_001545.1|alcohol dehydrogenase|metabolic|5|
| ref|YP_000245.1|hypothetical protein LIC10254|metabolic|5|
| ref|YP_000095.1|para-aminobenzoate synthase component I|metabolic|5|
| ref|YP_000878.1|adenylate/guanylate cyclase|metabolic|2|
| ref|YP_003214.1|4-hydroxybenzoyl-CoA thioesterase|metabolic|2|
| ref|YP_000617.1|benzene 1,2-dioxygenase system ferredoxin component|metabolic|2|
| ref|YP_003103.1|cholesterol oxidase precursor|metabolic|2|
| ref|YP_002518.1|fumarylacetoacetate hydrolase family protein|metabolic|2|
| ref|YP_008601.1|gamma-glutamyl carboxylase-like protein|metabolic|2|
| ref|YP_002613.1|hypothetical protein LIC12692|metabolic|2|
| ref|YP_000186.1|photoproduct lyase|metabolic|2|
| sp|Q7Z8R2|MRAY_LEPIC|Phospho-N-acetylumuramoyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-MurNAc-pentapeptide phosphotransferase)|metabolic|2|
| ref|YP_003522.1|precorrin isomerase|metabolic|2|
| ref|YP_000791.1|cytochrome c-type biogenesis protein|metabolic|2|
| ref|YP_003584.1|4-hydroxybutyrate CoA transferase|metabolic|2|
| ref|YP_001307.1|adenylate/guanylate cyclase|metabolic|2|
| ref|YP_002521.1|adenylate/guanylate cyclase|metabolic|2|
| ref|YP_003118.1|permease of the major facilitator superfamily|metabolic|2|
| ref|YP_000186.1|photoproduct lyase|metabolic|2|
| ref|YP_001544.1|tautomerase|metabolic|2|
| ref|YP_001568.1|4-hydroxybenzoyl octaprenyltransferase|metabolic|2|
### Table of Enzymes and Processes

| Ref             | Protein Description                                      | Process                      |
|-----------------|----------------------------------------------------------|------------------------------|
| YP_000511.1     | arsenate reductase                                        | metabolic process            |
| YP_003132.1     | glycerol-3-phosphate Pi antiporter                       | metabolic process            |
| YP_003106.1     | hemolysin/sphingomyelinase-like                          | metabolic process            |
| YP_002956.1     | hypothetical protein LIC13044                            | metabolic process            |
| YP_003409.1     | protoporphyrinogen oxidase                               | metabolic process            |
| YP_001375.1     | coproporphyrinogen III oxidase                           | metabolic process            |
| YP_003263.1     | phosphoglycerate mutase                                  | metabolic process            |
| YP_003280.1     | FAD-dependent oxireductase                               | metabolic process            |
| YP_000071.1     | hypothetical protein LIC10071                            | metabolic process            |
| YP_003400.1     | glutamyl-tRNA reductase                                   | metabolic process            |
| YP_003406.1     | uroporphyrinogen decarboxylase                           | metabolic process            |
| YP_003046.1     | UDP-N-acetylenolpyruvoylglucosamine reductase            | metabolic process            |
| YP_001809.1     | 3-hydroxyisobutyrate dehydrogenase                       | metabolic process            |
| YP_000196.1     | cytochrome oxidase assembly protein                       | metabolic process            |
| YP_001687.1     | 2-dehydropantoate 2-reductase                            | metabolic process            |
| YP_002254.1     | 3-oxoacyl-acyl-carrier protein reductase                  | metabolic process            |
| YP_003614.1     | 3-oxoacyl-acyl-carrier protein reductase                  | metabolic process            |
| YP_003486.1     | adenylate/guanylate cyclase                               | metabolic process            |
| YP_002917.1     | adenylate/guanylate cyclase                               | metabolic process            |
| YP_002984.1     | adenylate/guanylate cyclase                               | metabolic process            |
| YP_000236.1     | adenylate/guanylate cyclase                               | metabolic process            |
| YP_002592.1     | adenylate/guanylate cyclase                               | metabolic process            |
| YP_003467.1     | adenylate/guanylate cyclase                               | metabolic process            |
| YP_003117.1     | bacterioferritin-associated ferredoxin                   | metabolic process            |
| YP_001563.1     | dihydrolipoamide acetyltransferase                       | metabolic process            |
| YP_001010.1     | hemolysin                                                | metabolic process            |
| YP_000274.1     | hemolysin A                                              | metabolic process            |
| YP_001407.1     | hydroxypyruvate reductase                                 | metabolic process            |
| YP_000632.1     | hypothetical protein LIC10648                            | metabolic process            |
| YP_002826.1     | hypothetical protein LIC12910                            | metabolic process            |
| YP_002323.1     | oxidoreductase                                           | metabolic process            |
| YP_003519.1     | precorrin methylase                                      | metabolic process            |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| 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 |
| 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 phospholipase| metabolic process |
| ref|YP_000195.1|YP_000195.1 |cytochrome C oxidase assembly protein| metabolic process |
| ref|YP_000946.1|YP_000946.1 |cytochrome c peroxidase| metabolic process |
| ref|YP_000336.1|YP_000336.1 |esterase| metabolic process |
| ref|YP_001824.1|YP_001824.1 |putative hydrolase| metabolic process |
| ref|YP_001834.1|YP_001834.1 |putative lipoprotein| no_GO |
| ref|YP_002221.1|YP_002221.1 |putative lipoprotein| no_GO |
| ref|YP_001318.1|YP_001318.1 |S-adenosylmethionine synthetase| no_GO |
| ref|YP_000009.1|YP_000009.1 |putative lipoprotein| no_GO |
| ref|YP_000031.1|YP_000031.1 |putative lipoprotein| no_GO |
| ref|YP_000974.1|YP_000974.1 |putative lipoprotein| no_GO |
| ref|YP_001169.1|YP_001169.1 |putative lipoprotein| no_GO |
| ref|YP_000491.1|YP_000491.1 |putative lipoprotein| no_GO |
| ref|YP_000856.1|YP_000856.1 |putative lipoprotein| no_GO |
| ref|YP_000902.1|YP_000902.1 |putative lipoprotein| no_GO |
| ref|YP_000946.1|YP_000946.1 |putative lipoprotein| no_GO |
| ref|YP_001824.1|YP_001824.1 |putative lipoprotein| no_GO |
| ref|YP_001834.1|YP_001834.1 |putative lipoprotein| no_GO |
| ref|YP_002221.1|YP_002221.1 |putative lipoprotein| no_GO |
| ref|YP_001318.1|YP_001318.1 |putative lipoprotein| no_GO |
| ref|YP_000974.1|YP_000974.1 |putative lipoprotein| no_GO |
| ref|YP_001824.1|YP_001824.1 |putative lipoprotein| no_GO |
| ref|YP_001834.1|YP_001834.1 |putative lipoprotein| no_GO |
| ref|YP_002221.1|YP_002221.1 |putative lipoprotein| no_GO |
| ref|YP_001318.1|YP_001318.1 |putative lipoprotein| no_GO |
| ref|YP_000974.1|YP_000974.1 |putative lipoprotein| no_GO |
| ref|YP_001824.1|YP_001824.1 |putative lipoprotein| no_GO |
| ref|YP_001834.1|YP_001834.1 |putative lipoprotein| no.GO |
| Ref | YP000492.1 | putative lipoprotein | no_GO | 14 |
|----|------------|----------------------|-------|----|
| Ref | YP001663.1 | putative lipoprotein | no_GO | 11 |
| Ref | YP000774.1 | putative lipoprotein | no_GO | 11 |
| Ref | YP001851.1 | putative lipoprotein | no_GO | 8 |
| Ref | YP000190.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP001705.1 | exopolysaccharide production protein | no_GO | 57 |
| Ref | YP000895.1 | putative lipoprotein | no_GO | 57 |
| Ref | YP003531.1 | putative permease | no_GO | 47 |
| Ref | YP000007.1 | nifR3-like protein | no_GO | 47 |
| Ref | YP002863.1 | shikimate 5-dehydrogenase | no_GO | 132 |
| Ref | YP002992.1 | pirin-like protein | no_GO | 85 |
| Ref | YP002292.1 | pirin-like protein | no_GO | 71 |
| Ref | YP002939.1 | Thü/PPI family protein | no_GO | 61 |
| Ref | YP002744.1 | soluble lytic transglycosylase | no_GO | 57 |
| Ref | YP001092.1 | putative lipoprotein | no_GO | 47 |
| Ref | YP002978.1 | putative lipoprotein | no_GO | 47 |
| Ref | YP001311.1 | SET domain-containing protein | no_GO | 47 |
| Sp | Q72S75|Y3384_LEPIC | UFP0176 protein LIC_13184 | no_GO | 44 |
| Ref | YP001231.1 | RodA | no_GO | 40 |
| Ref | YP001104.1 | histone deacetylase | no_GO | 37 |
| Ref | YP002188.1 | putative lipoprotein | no_GO | 37 |
| Ref | YP003059.1 | putative lipoprotein | no_GO | 37 |
| Ref | YP001246.1 | putative acetyl-coa carboxylase/pyruvate carboxylase | no_GO | 34 |
| Ref | YP000970.1 | putative diguanylate phosphodiesterase | no_GO | 30 |
| Sp | Q8CK51|Y328_LEPIN | UFP0176 protein LA_3128 - Leptospira interrogans | no_GO | 27 |
| Ref | YP002048.1 | putative lipoprotein | no_GO | 24 |
| Sp | Q72L65|Y3475_LEPIC | UFP0133 protein LIC_13475 | no_GO | 24 |
| Ref | YP001759.1 | BolA-like protein | no_GO | 24 |
| Ref | YP001216.1 | cGMP-specific phosphodiesterase | no_GO | 21 |
| Ref | YP003243.1 | putative lipoprotein | no_GO | 21 |
| Ref | YP000910.1 | fruiting body developmental protein | no_GO | 17 |
| Ref | YP000284.1 | GlcG | no_GO | 14 |
| Ref | YP002511.1 | putative lipoprotein | no_GO | 14 |
| Ref | YP000275.1 | putative aceyltransferase | no_GO | 14 |
| Ref | YP003405.1 | cGMP-specific phosphodiesterase | no_GO | 8 |
| Ref | YP001137.1 | putative lipoprotein | no_GO | 8 |
| Ref | YP000163.1 | putative lipoprotein | no_GO | 8 |
| Ref | YP002747.1 | SAM dependent methyltransferase | no_GO | 8 |
| Ref | YP000268.1 | thioredoxin-like protein | no_GO | 8 |
| Ref | YP003504.1 | periplasmic protein, LipL45 homologue | no_GO | 5 |
| Ref | YP001526.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP001725.1 | N-(5'-phosphoribosyl)anthranilate isomerase | no_GO | 5 |
| Ref | YP000358.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP001550.1 | conserved putative permease protein | no_GO | 5 |
| Ref | YP003186.1 | putative acetyl CoA acetyltransferase | no_GO | 5 |
| Ref | YP002589.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP002701.1 | putative lipoprotein | no_GO | 5 |
| Sp | Q72NX1|Y5707_LEPIC | UFP0090 protein LIC_12707 | no_GO | 5 |
| Sp | Q72M93|Y3929_LEPIC | UFP0189 protein LIC_13295 | no_GO | 5 |
| Ref | YP001616.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP001829.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP003123.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP000938.1 | TonB-dependent outer membrane hemin receptor | no_GO | 5 |
| Ref | YP003166.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP001162.1 | Chlp | no_GO | 5 |
| Ref | YP001454.1 | GldG | no_GO | 5 |
| Ref | YP000492.1 | putative lipoprotein | no_GO | 5 |
| Ref | YP000909.1 | fruiting body developmental protein | no_GO | 5 |
| Ref| YP | Description | GO Status |
|---|---|---|---|
| ref|YP_000493.1|YP_000493.1|putative lipoprotein|no_GO|
| ref|YP_001122.1|YP_001122.1|pseudouridylate synthase, 23S RNA-specific|no_GO|
| ref|YP_000258.1|YP_000258.1|putative virulence-associated protein|no_GO|
| ref|YP_000298.1|YP_000298.1|putative lipoprotein|no_GO|
| ref|YP_000984.1|YP_000984.1|guanosine polyphosphate pyrophosphohydrolase/synthetase|no_GO|
| ref|YP_000021.1|YP_000021.1|putative lipoprotein|no_GO|
| ref|YP_002038.1|YP_002038.1|RecO|no_GO|
| ref|YP_001122.1|YP_001122.1|pseudouridylate synthase, 23S RNA-specific|no_GO|
| ref|YP_000090.1|YP_000090.1|anticodon nuclease|no_GO|
| ref|YP_000021.1|YP_000021.1|putative lipoprotein|no_GO|
| ref|YP_002038.1|YP_002038.1|RecO|no_GO|
| ref|YP_001122.1|YP_001122.1|pseudouridylate synthase, 23S RNA-specific|no_GO|
| ref|YP_002987.1|YP_002987.1|putative lipoprotein|no_GO|
| ref|YP_002038.1|YP_002038.1|RecO|no_GO|
| ref|YP_001122.1|YP_001122.1|pseudouridylate synthase, 23S RNA-specific|no_GO|
| ref|YP_000090.1|YP_000090.1|anticodon nuclease|no_GO|
| ref|YP_000021.1|YP_000021.1|putative lipoprotein|no_GO|
| ref|YP_002038.1|YP_002038.1|RecO|no_GO|
| ref|YP_001122.1|YP_001122.1|pseudouridylate synthase, 23S RNA-specific|no_GO|
| ref|YP_000090.1|YP_000090.1|anticodon nuclease|no_GO|
| ref|YP_000021.1|YP_000021.1|putative lipoprotein|no_GO|
| ref|YP_002038.1|YP_002038.1|RecO|no_GO|
| sp|Q72PB6|LNT1_LEPIC|Apolipoprotein N-acyltransferase 1 (EC 2.3.1.-) (ALP N-acyltransferase 1)|no_GO|
| 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_003417.1|YP_003417.1|cyclic nucleotide binding 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_000904.1|YP_000904.1|anticodon nuclease|no_GO|
| ref|YP_001464.1|YP_001464.1|iron-sulfur cluster-binding protein|no_GO|
| ref|YP_000537.1|YP_000537.1|hydrolase|no_GO|
| ref|YP_000335.1|YP_000335.1|integrase/recombinase|no_GO|
| ref|YP_000341.1|YP_000341.1|intercellular adhesion protein C|no_GO|

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| sp|Q72W44|LFTP_LEPIC | Leucyl/phenylalanyl-tRNA–protein transferase (EC 2.3.2.6) [L(F-transferase) (Leucyltransferase) (Ph  | no_GO |
| 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 II) (Signal peptidase II) | no_GO |
| ref|YP_001706.1|YP_001706.1 | lipoprotein with phospholipase D domain | no_GO |
| sp|Q72OP1|LIPB_LEPIC | Lipoyltransferase (EC 2.3.1.-) (Lipoyltransferase) (Ph no_GO ref|YP_003466.1|YP_003466.1 | lipoyltransferase ubiE (EC 2.1.1.-) | no_GO |
| ref|YP_003142.1|YP_003142.1 | malate permease | no_GO |
| sp|Q75FL1|UBE_LEPIC | Menaquinone biosynthesis methyltransferase ubE (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 | MrEo | 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 | nucleotidytransferase 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 transporter superfamily | no_GO |
| ref|YP_003596.1|YP_003596.1 | permease of the major facilitator superfamily | no_GO |
| ref|YP_001131.1|YP_001131.1 | phenazine biosynthesis-like protein | no_GO |
| ref|YP_000673.1|YP_000673.1 | phosphate transport system protein | no_GO |
| ref|YP_001077.1|YP_001077.1 | phosphatidylethanolamine synthase | no_GO |
| ref|YP_001853.1|YP_001853.1 | phosphatidylethanolamine 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 methyltransferase | 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_000254.1|YP_000254.1 | prepilin leader peptidase | no_GO |
| sp|Q72V65|SPE1_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-isoadipate-O-methyltransferase | no_GO |
| ref|YP_000642.1|YP_000642.1 | proton antiporter efflux pump | no_GO |
| ref|YP_000599.1|YP_000599.1 | proton glutamate symport protein | no_GO |
| ref|YP_002791.1|YP_002791.1 | proton-translocating transhydrogenase subunit alpha 2 | no_GO |
| ref|YP_001605.1|YP_001605.1 | pseudouridylate synthase | no_GO |
| sp|P62642|CHEB2_LEPIC | Putative chemotaxis protein-glutamate methyltransferase (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_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_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_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_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_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_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_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_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_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_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_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_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 | Protein ID | Description |
|-----|------------|-------------|
| ref|YP_001223.1| putative lipoprotein |
| ref|YP_001223.1| putative lipoprotein |
| ref|YP_003155.1| putative lipoprotein |
| ref|YP_002919.1| putative lipoprotein |
| ref|YP_000798.1| putative lipoprotein |
| ref|YP_003203.1| putative lipoprotein |
| ref|YP_001428.1| regulator of chromosome condensation |
| ref|YP_001149.1| rhodanese-related thiosulfate sulfurtransferase |
| ref|YP_000798.1| putative lipoprotein |
| ref|YP_003203.1| putative lipoprotein |
| ref|YP_002453.1| putative lipoprotein |
| ref|YP_003092.1| putative membrane-bound lytic murein transglycosylase A transmembrane protein |
| ref|YP_002888.1| putative phospholipid synthase |
| ref|YP_002489.1| putative ring hydroxylating dioxygenase alpha-subunit |
| ref|YP_003155.1| putative lipoprotein |
| ref|YP_001149.1| rhodanese-related thiosulfate sulfurtransferase |
| ref|YP_000798.1| putative lipoprotein |
| ref|YP_003203.1| putative lipoprotein |
| ref|YP_002453.1| putative lipoprotein |

**Gene Ontology (GO) Information:**

- **GO:000699.1** | sodium acid symporter |
- **GO:000136.1** | sodium acid symporter family |
- **GO:000636.1** | sodium:solute symporter |
- **GO:003632.1** | sodium:solute symporter family |
- **GO:000809.1** | soluble lytic murein transglycosylase |
- **GO:000995.1** | sodium acid symporter family |
- **GO:000818.1** | sodium acid symporter family |
- **GO:001739.1** | sodium:solute symporter |
- **GO:002526.1** | sodium:solute symporter |
- **GO:000866.1** | sodium:solute symporter |
- **GO:000995.1** | sodium acid symporter family |
- **GO:000636.1** | sodium acid symporter family |
- **GO:001739.1** | sodium:solute symporter |
- **GO:003226.1** | sodium:solute symporter |
- **GO:000866.1** | sodium:solute symporter |
- **GO:000818.1** | sodium acid symporter family |
- **GO:000866.1** | sodium:solute symporter |
- **GO:000995.1** | sodium acid symporter family |
- **GO:000636.1** | sodium acid symporter family |
- **GO:001739.1** | sodium:solute symporter |
- **GO:002526.1** | sodium:solute symporter |
- **GO:000866.1** | sodium:solute symporter |
- **GO:000995.1** | sodium acid symporter family |
- **GO:000636.1** | sodium acid symporter family |
- **GO:001739.1** | sodium:solute symporter |
- **GO:000866.1** | sodium:solute symporter |
- **GO:000995.1** | sodium acid symporter family |
- **GO:000636.1** | sodium acid symporter family |
- **GO:001739.1** | sodium:solute symporter |
- **GO:000866.1** | sodium:solute symporter |
- **GO:000995.1** | sodium acid symporter family |
- **GO:000636.1** | sodium acid symporter family |
- **GO:001739.1** | sodium:solute symporter |
- **GO:000866.1** | sodium:solute symporter |
- **GO:000995.1** | sodium acid symporter family |
- **GO:000636.1** | sodium acid symporter family |
- **GO:001739.1** | sodium:solute symporter |
- **GO:000866.1** | sodium:solute symporter |
- **GO:000995.1** | sodium acid symporter family |
- **GO:000636.1** | sodium acid symporter family |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Ref       | Accession  | Enzyme Name                                         | Function                                      | Nucleotide Binding |
|-----------|------------|-----------------------------------------------------|-----------------------------------------------|--------------------|
| ref|YP_001924.1|YP_001924.1  | RNA-binding protein                              | 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)          | nucleotide binding                              | 537                | 2064               | 284                |
| sp|P61436|CH10_LEPIC  | Acetyl-coenzyme A synthetase (EC 6.2.1.1)          | Acetylating enzyme                              | 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   | 716                | 587                | 615                |
| ref|YP_001889.1|YP_001889.1  | translocase                                        | nucleotide binding                              | 787                | 583                | 808                |
| sp|Q72PA7|PURU_LEPIC  | Adenosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate 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  | S'-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|PURU_LEPIC  | Phosphoribosylformylglycinamide 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  | alkyglycerone-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) (Citribine--aspartate ligase) | nucleotide binding                              |                   | 249                |                   |
| ref|YP_000702.1|YP_000702.1  | Hypothetical protein LIC10718                     | nucleotide binding                              |                   | 226                |                   |
| Ref                  | Accession          | Description                                                                 | Binding       | Value |
|---------------------|--------------------|-----------------------------------------------------------------------------|---------------|-------|
| ref                 | YP_001796.1        | AAA family ATPase                                                          | nucleotide    | 158   |
| sp                  | Q7SFU1             | Acetylglutamate kinase (EC 2.7.2.8) (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-phosphotransferase) | nucleotide    | 143   |
| ref                 | YP_002203.1        | Putative glycolate oxidase                                                 | nucleotide    | 92    |
| ref                 | YP_002041.1        | Phosphate starvation-inducible protein                                     | nucleotide    | 89    |
| ref                 | YP_002692.1        | GTP-binding protein                                                        | nucleotide    | 37    |
| ref                 | YP_002684.1        | Acetolactate synthase I large subunit                                      | nucleotide    | 24    |
| sp                  | Q7R87              | Probable GMP synthase                                                      | nucleotide    | 277   |
| ref                 | YP_002709.1        | Hypothetical protein LIC12792                                             | nucleotide    | 188   |
| sp                  | Q7U64              | Hydroxyethylthiazole kinase (EC 2.7.1.50) (4-methyl-5-beta-hydroxyethylthiazole kinase) (Thz kinase) | nucleotide    | 166   |
| ref                 | YP_001245.1        | Acetyl-CoA carboxylase alpha chain                                         | nucleotide    | 147   |
| sp                  | Q7NP4              | UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (UDP-N-acetylmuramoyl-L-alanyl-D-glutam) | nucleotide    | 100   |
| ref                 | YP_002225.1        | UDP-N-acetylmuramyl pentapeptide synthase                                  | nucleotide    | 96    |
| sp                  | Q7UH8              | Phosphoribosylaminomimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)  | nucleotide    | 89    |
| sp                  | Q7R81              | UDP-N-acetylmuramoylalanine--D-glutamate 2.6-diaminopimelate ligase (EC 6.3.2.13) (UDP-N-acetylmuramy) | nucleotide    | 71    |
| sp                  | Q7V31              | Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GAR) (Glycinamide ribonucleotide synthetase) (Ph) | nucleotide    | 68    |
| ref                 | YP_003216.1        | UDP-N-acetylmuramate-L-alanyl-gamma-d-glutamyl-meso-diaminopimelate ligase | nucleotide    | 57    |
| sp                  | Q7MV4              | Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)            | nucleotide    | 54    |
| sp                  | Q7R93              | D-alanine--D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase) (D-Ala-D-Ala ligase) | nucleotide    | 50    |
| ref                 | YP_001493.1        | Hypothetical protein LIC11534                                             | nucleotide    | 50    |
| ref                 | YP_002386.1        | S-formyltetrahydrofolate cyclo-ligase                                      | nucleotide    | 37    |
| ref                 | YP_003599.1        | Arginine/ornithine transport system ATPase                                | nucleotide    | 37    |
| sp                  | Q7W11              | Probable GTP-binding protein engB                                          | nucleotide    | 37    |
| ref                 | YP_001367.1        | Ubiquinone biosynthesis protein                                            | nucleotide    | 37    |
| ref                 | YP_001045.1        | NH(3)-dependent NAD(+) synthetase                                          | nucleotide    | 34    |
| ref                 | YP_001812.1        | UDP-N-acetylmuramate-alanine ligase                                        | nucleotide    | 34    |
| ref                 | YP_000459.1        | RNA-binding protein                                                        | nucleotide    | 27    |
| ref                 | YP_001296.1        | Hypothetical protein LIC11332                                             | nucleotide    | 24    |
| ref                 | YP_001270.1        | D-alanine--D-alanine ligase                                                | nucleotide    | 17    |
| sp                  | Q7RG6              | Dethiobiotin synthetase (EC 6.3.3.3)                                       | nucleotide    | 14    |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Reference | Protein Description                                      | Binding   | Copies per Cell |
|-----------|----------------------------------------------------------|-----------|-----------------|
| ref|YP_000613.1| (Dethiobiotin synthase) (DTB synthetase) binding | | |
| ref|YP_002647.1| Glycerol kinase nucleotide binding | 14 | |
| ref|YP_002647.1| Acetoin- histone deacetylase family nucleotide binding | 11 | |
| ref|YP_002864.1| Dihydrofolate synthase nucleotide binding | 11 | |
| ref|YP_002227.1| Phosphoribosylaminomimidazole carboxylase atpase subunit protein nucleotide binding | 2 | |
| ref|YP_000560.1| GTP-binding protein nucleotide binding | | |
| ref|YP_000515.1| Acetoin- histone deacetylase family nucleotide binding | | |
| ref|YP_000912.1| ATP-dependent RNA helicase nucleotide binding | | |
| ref|YP_003188.1| Acyl-CoA dehydrogenase nucleotide binding | | |
| ref|YP_002438.1| ATPase nucleotide binding | | |
| ref|YP_003128.1| ATP-dependent RNA helicase nucleotide binding | | |
| ref|YP_000630.1| Hypothetical protein LIC10646 nucleotide binding | | |
| ref|YP_003031.1| Hypothetical protein LIC11051 other cellular process | 309 | 193 | 132 |
| ref|YP_003031.1| Hypothetical protein LIC13122 other cellular process | 253 | 185 | 132 |
| ref|YP_002598.1| Hypothetical protein LIC12676 other cellular process | 30 | | |
| ref|YP_001528.1| Hypothetical protein LIC11569 other cellular process | 24 | | |
| ref|YP_001068.1| Hypothetical protein LIC11098 other cellular process | 75 | | |
| ref|YP_000891.1| Octaprenyl diphosphate synthase other cellular process | 71 | | |
| ref|YP_002817.1| Molybdate metabolism regulator other cellular process | 64 | | |
| sp|Q72RC1| GMHA_LEPIC Phosphoheptose isomerase (EC 5.3.1.-) other cellular process | 44 | | |
| ref|YP_000616.1| Hypothetical protein LIC10632 other cellular process | 30 | | |
| ref|YP_000805.1| Hypothetical protein LIC10828 other cellular process | 27 | | |
| ref|YP_001615.1| Hypothetical protein LIC11659 other cellular process | 14 | | |
| ref|YP_00246.1| Hypothetical protein LIC10255 other cellular process | | | |
| ref|YP_001466.1| Hypothetical protein LIC11505 other cellular process | | | |
| ref|YP_002807.1| Putative lipoprotein other cellular process | | | |
| ref|YP_001468.1| Hypothetical protein LIC11507 other cellular process | | | |
| ref|YP_002195.1| Hypothetical protein LIC12260 other cellular process | | | |
| ref|YP_002440.1| Hypothetical protein LIC12512 other cellular process | | | |
| ref|YP_003160.1| Hypothetical protein LIC13253 other cellular process | | | |
| ref|YP_000851.1| Molybdopterin oxidoreductase other cellular process | 5611 | 6382 | 707 |
| ref|YP_001260.1| Hypothetical protein LIC13294 other cellular process | 1567 | 1733 | 203 |
| Ref     | Accession 1 | Accession 2 | Description                          | Cellular Process | Frequency | Relative Frequency |
|---------|-------------|-------------|--------------------------------------|------------------|-----------|--------------------|
| ref|YP_000850.1|YP_000850.1| hypothetical protein LIC10873       | other process    | 679       | 844                |
| ref|YP_003272.1|YP_003272.1| sulfite reductase                   | other process    | 777       | 656                |
| ref|YP_000272.1|YP_000272.1| zinc-binding dehydrogenase family   | other process    | 530       | 616                |
| ref|YP_003594.1|YP_003594.1| hypothetical protein LIC20205       | other process    | 1026      | 584                |
| ref|YP_003032.1|YP_003032.1| hypothetical protein LIC13123       | other process    | 628       | 580                |
| ref|YP_001942.1|YP_001942.1| succinate dehydrogenase             | other process    | 306       | 539                |
| ref|YP_001167.1|YP_001167.1| hypothetical protein LIC11197       | other process    | 393       | 508                |
| ref|YP_002134.1|YP_002134.1| UDP-glucose 4-epimerase             | other process    | 535       | 507                |
| ref|YP_000562.1|YP_000562.1| hypothetical protein LIC10578       | other process    | 630       | 501                |
| ref|YP_002152.1|YP_002152.1| putative lipoprotein                | other process    | 302       | 478                |
| ref|YP_001371.1|YP_001371.1| hypothetical protein LIC11408       | other process    | 455       | 386                |
| ref|YP_000696.1|YP_000696.1| hypothetical protein LIC10712       | other process    | 763       | 373                |
| ref|YP_002405.1|YP_002405.1| Pbp1A                               | other process    | 241       | 371                |
| ref|YP_000028.1|YP_000028.1| putative lipoprotein                | other process    | 387       | 346                |
| ref|YP_002650.1|YP_002650.1| hypothetical protein LIC12730       | other process    | 341       | 312                |
| ref|YP_000327.1|YP_000327.1| hypothetical protein LIC10337       | other process    | 324       | 305                |
| ref|YP_000121.1|YP_000121.1| hypothetical protein LIC10125       | other process    | 535       | 268                |
| ref|YP_000612.1|YP_000612.1| putative lipoprotein                | other process    | 243       | 8                  |
| ref|YP_002122.1|YP_002122.1| perosamine synthetase               | other process    | 354       | 239                |
| ref|YP_000391.1|YP_000391.1| hypothetical protein LIC10405       | other process    | 158       | 189                |
| ref|YP_000259.1|YP_000259.1| cyclic nucleotide binding protein   | other process    | 150       | 153                |
| ref|YP_001903.1|YP_001903.1| ARM repeat superfamily protein      | other process    | 128       | 242                |
| ref|YP_000824.1|YP_000824.1| hypothetical protein LIC10847       | other process    | 1047      | 181                |
| ref|YP_001404.1|YP_001404.1| hypothetical protein LIC13442       | other process    | 344       | 30                 |
| ref|YP_002140.1|YP_002140.1| gdp-l-fucose synthetase             | other process    | 227       | 118                |
| ref|YP_000998.1|YP_000998.1| hypothetical protein LIC11028       | other process    | 111       | 92                 |
| ref|YP_003615.1|YP_003615.1| aldolase class II                   | other process    | 92        | 34                 |
| sp|Q72V7F|GCSH_LEPIC| Glycine cleavage system H protein   | other process    | 177       |                    |
| ref|YP_000098.1|YP_000098.1| cystathionine gamma-synthase         | other process    | 125       |                    |
| ref|YP_000292.1|YP_000292.1| hypothetical protein LIC10302       | other process    | 92        |                    |
| ref|YP_002870.1|YP_002870.1| hypothetical protein LIC12957       | other process    | 71        |                    |
| ref|YP_002429.1|YP_002429.1| hypothetical protein LIC12501       | other process    | 64        |                    |
| Ref | UniProt ID | Description | Cellular Process | Copies |
|-----|-----------|-------------|-----------------|--------|
| ref|YP_000032.1| hypothetical protein LIC10032 | other cellular process | 11 |
| ref|YP_002651.1| hypothetical protein LIC12731 | other cellular process | 207 |
| ref|YP_001117.1| nitrilotriacetate monoxygenase component B | other cellular process | 158 |
| ref|YP_001308.1| hypothetical protein LIC11344 | other cellular process | 103 |
| ref|YP_000038.1| hypothetical protein LIC10038 | other cellular process | 92 |
| ref|YP_000786.1| zinc binding dehydrogenase | other cellular process | 92 |
| ref|YP_001962.1| hypothetical protein LIC12024 | other cellular process | 78 |
| ref|YP_002640.1| hypothetical protein LIC12719 | other cellular process | 78 |
| ref|YP_000392.1| hypothetical protein LIC10406 | other cellular process | 71 |
| sp|Q72RU2| Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase) (Lipoate synthase) (Lipoyl-acyl-carrier-protein | other cellular process | 57 |
| ref|YP_002464.1| RibD | other cellular process | 57 |
| ref|YP_001366.1| hypothetical protein LIC11403 | other cellular process | 50 |
| ref|YP_002561.1| hypothetical protein LIC12638 | other cellular process | 50 |
| ref|YP_002074.1| nucleoside-diphosphate-sugar epimerase | other cellular process | 50 |
| ref|YP_002838.1| hypothetical protein LIC12923 | other cellular process | 47 |
| ref|YP_001447.1| hypothetical protein LIC11486 | other cellular process | 37 |
| ref|YP_001269.1| L-lysine 2,3-aminomutase | other cellular process | 34 |
| sp|Q72TL3| Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (tRNA-guanine transglycosylase) (Guanine insertion enzyme) | other cellular process | 34 |
| ref|YP_000602.1| hypothetical protein LIC10618 | other cellular process | 30 |
| ref|YP_000053.1| hypothetical protein LIC10053 | other cellular process | 27 |
| ref|YP_002702.1| hypothetical protein LIC12785 | other cellular process | 27 |
| ref|YP_000599.1| putative lipoprotein | other cellular process | 27 |
| ref|YP_003453.1| thiol-disulfide interchange like protein | other cellular process | 27 |
| ref|YP_001624.1| hypothetical protein LIC11670 | other cellular process | 24 |
| ref|YP_002243.1| hypothetical protein LIC12309 | other cellular process | 21 |
| ref|YP_000580.1| putative lipoprotein | other cellular process | 21 |
| ref|YP_003009.1| sugar nucleotide epimerase | other cellular process | 17 |
| sp|Q72RRO| NAD-dependent deacetylase (EC 3.5.1.-) (Regulatory protein SIR2 homolog) | other cellular process | 14 |
| sp|Q72S29| Probable 16S rRNA-processing protein rimM | other cellular process | 14 |
| sp|Q72TD6| Hypothetical RNA methyltransferase LIC_11085 (EC 2.1.1.-) | other cellular process | 11 |
| ref|YP_002396.1| hypothetical protein LIC12468 | other cellular process | 8 |
| Ref | Accession | Description                                      | Process                     | Count |
|-----|-----------|--------------------------------------------------|-----------------------------|-------|
| ref| YP_002150.1 | YP_002150.1 | hypothetical protein LIC12215 | other cellular process | 5     |
| ref| YP_003434.1 | YP_003434.1 | BatC | other cellular process |       |
| ref| YP_003435.1 | YP_003435.1 | BatD | other cellular process |       |
| ref| YP_000657.1 | YP_000657.1 | hypothetical protein LIC10673 | other cellular process |       |
| ref| YP_000667.1 | YP_000667.1 | methylamine utilization protein | other cellular process |       |
| ref| YP_000619.1 | YP_000619.1 | NifU | other cellular process |       |
| ref| YP_003432.1 | YP_003432.1 | BatA | other cellular process |       |
| ref| YP_003312.1 | YP_003312.1 | DTDP-4-dehydrorhamnose 3,5-epimerase | other cellular process |       |
| ref| YP_000052.1 | YP_000052.1 | hypothetical protein LIC10052 | other cellular process |       |
| ref| YP_000087.1 | YP_000087.1 | hypothetical protein LIC10090 | other cellular process |       |
| ref| YP_001439.1 | YP_001439.1 | hypothetical protein LIC11478 | other cellular process |       |
| ref| YP_002220.1 | YP_002220.1 | hypothetical protein LIC12286 | other cellular process |       |
| ref| YP_000300.1 | YP_000300.1 | hypothetical protein LIC13095 | other cellular process |       |
| sp | Q72W54/Y086_LEPIC | Hypothetical RNA methyltransferase LIC_10086 (EC 2.1.1.) | other cellular process |       |
| sp | Q72VP7/Y249_LEPIC | Hypothetical RNA methyltransferase LIC_10249 (EC 2.1.1.) | other cellular process |       |
| ref| YP_003618.1 | YP_003618.1 | L-lysine 2, 3-aminomutase | other cellular process |       |
| ref| YP_000512.1 | YP_000512.1 | Pbp3 | other cellular process |       |
| ref| YP_003483.1 | YP_003483.1 | short-chain dehydrogenase | other cellular process |       |
| ref| YP_000321.1 | YP_000321.1 | sugar transferase | other cellular process |       |
| ref| YP_000947.1 | YP_000947.1 | outer membrane protein | outer membrane protein | 5441  4194  636 |
| ref| YP_002473.1 | YP_002473.1 | outer membrane lipoprotein carrier protein | outer membrane protein | 657   685   177 |
| ref| YP_000698.1 | YP_000698.1 | outer membrane receptor protein | outer membrane protein | 529   397   265 |
| ref| YP_001419.1 | YP_001419.1 | outer membrane protein, porin superfamily | outer membrane protein | 145   103   40  |
| ref| YP_001581.1 | YP_001581.1 | outer membrane protein | outer membrane protein | 37    |       |
| ref| YP_002189.1 | YP_002189.1 | outer membrane protein | outer membrane protein | 136   |       |
| ref| YP_000249.1 | YP_000249.1 | hypothetical protein LIC10258 | outer membrane protein | 75    |       |
| ref| YP_002241.1 | YP_002241.1 | outer membrane TolC superfamily | outer membrane protein | 21    |       |
| ref| YP_003479.1 | YP_003479.1 | outer membrane protein | outer membrane protein | 17    |       |
| ref| YP_002306.1 | YP_002306.1 | outer membrane protein, TonB dependent | outer membrane protein |       |
| ref| YP_000483.1 | YP_000483.1 | outer membrane protein | outer membrane protein |       |
| ref| YP_001405.1 | YP_001405.1 | outer membrane protein | outer membrane protein |       |
| Ref | Accession | Description | Peptidase Activity |
|-----|------------|-------------|--------------------|
| ref|YP_001930.1|outer membrane protein|outer membrane protein|
| ref|YP_003043.1|outer membrane protein|outer membrane protein|
| ref|YP_000528.1|outer membrane protein|outer membrane protein|
| ref|YP_001467.1|outer membrane protein|outer membrane protein|
| ref|YP_001914.1|outer membrane protein|outer membrane protein|
| ref|YP_003043.1|outer membrane protein|outer membrane protein|
| ref|YP_000528.1|outer membrane protein|outer membrane protein|
| ref|YP_001467.1|outer membrane protein|outer membrane protein|
| ref|YP_001914.1|outer membrane protein|outer membrane protein|
| ref|YP_000858.1|outer membrane protein, TonB dependent|outer membrane protein|
| ref|YP_002729.1|serine protease MucD precursor|peptidase activity|
| ref|YP_001745.1|endopeptidase IV|peptidase activity|
| ref|YP_002185.1|carboxy-terminal processing protease|peptidase activity|
| ref|YP_003390.1|metalloprotease|peptidase activity|
| ref|YP_000834.1|integral membrane zinc metalloprotease|peptidase activity|
| sp|Q72UC6|AMPA_LEPIC|Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase)|peptidase activity|
| ref|YP_000749.1|processing metalloprotease|peptidase activity|
| ref|YP_001202.1|signal peptidase I|peptidase activity|
| ref|YP_0000748.1|metalloprotease|peptidase activity|
| ref|YP_003004.1|PfaP|peptidase activity|
| ref|YP_003586.1|cysteine protease|peptidase activity|
| ref|YP_000215.1|hypothetical protein LIC10224|peptidase activity|
| ref|YP_003535.1|HtrA-like protein|peptidase activity|
| ref|YP_002515.1|aminopeptidase N|peptidase activity|
| ref|YP_003295.1|polysaccharide deacetylase|peptidase activity|
| ref|YP_003534.1|HtrA1|peptidase activity|
| ref|YP_003200.1|hypothetical protein LIC13293|peptidase activity|
| ref|YP_001279.1|aminopeptidase P|peptidase activity|
| ref|YP_002415.1|hypothetical protein LIC12487|peptidase activity|
| ref|YP_001461.1|methionine aminopeptidase|peptidase activity|
| ref|YP_003383.1|hypothetical protein LIC13482|peptidase activity|
| ref|YP_001082.1|serine protease|peptidase activity|
| ref|YP_002543.1|membrane carboxypeptidase|peptidase activity|
| sp|Q75FP1|HtpX_LEPIC|Probable protease htpX homolog (EC 3.4.24.-)|peptidase activity|
| ref|YP_002020.1|signal peptidase I|peptidase activity|
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| Gene ID | Description | Peptidase Activity |
|---------|-------------|--------------------|
| sp|Q72RY8|HSLV_LEPIC | ATP-dependent protease hslV (EC 3.4.25.-) | peptidase activity |
| ref|YP_002237.1|YP_002237.1 | carboxy-terminal processing protease | peptidase activity |
| ref|YP_003367.1|YP_003367.1 | carboxypeptidase I | peptidase activity |
| ref|YP_003549.1|YP_003549.1 | ATP-dependent protease | peptidase activity |
| ref|YP_001081.1|YP_001081.1 | HtrA2 | peptidase activity |
| ref|YP_000981.1|YP_000981.1 | hypothetical protein LIC11008 | peptidase activity |
| ref|YP_003060.1|YP_003060.1 | D-alanyl-D-alanine carboxypeptidase | peptidase activity |
| ref|YP_002621.1|YP_002621.1 | metalloprotease | peptidase activity |
| ref|YP_001670.1|YP_001670.1 | protease IV | peptidase activity |
| ref|YP_001007.1|YP_001007.1 | periplasmic trypsin-like serine protease | peptidase activity |
| ref|YP_002397.1|YP_002397.1 | HtpG | peptidase activity |
| ref|YP_001325.1|YP_001325.1 | oligopeptidase A | peptidase activity |
| ref|YP_001119.1|YP_001119.1 | membrane metalloendopeptidase | peptidase activity |
| ref|YP_001362.1|YP_001362.1 | membrane metalloendopeptidase | peptidase activity |
| ref|YP_002236.1|YP_002236.1 | O-sialoglycoprotein endopeptidase | peptidase activity |
| ref|YP_002569.1|YP_002569.1 | membrane carboxypeptidase | peptidase activity |
| ref|YP_003242.1|YP_003242.1 | zinc carboxypeptidase-related protein | peptidase activity |
| ref|YP_000957.1|YP_000957.1 | carboxypeptidase T | peptidase activity |
| ref|YP_000705.1|YP_000705.1 | hypothetical protein LIC10721 | peptidase activity |
| ref|YP_001034.1|YP_001034.1 | membrane metalloendopeptidase | peptidase activity |
| ref|YP_001074.1|YP_001074.1 | aminopeptidase | peptidase activity |
| sp|Q72RD1|CLPS_LEPIC | ATP-dependent Clp protease adaptor | 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 |
Table 1: Proteome-wide copies per cell measurements

| Accession | Description                                                                 | Activity                      |
|-----------|------------------------------------------------------------------------------|-------------------------------|
| ref|YP_000462.1|YP_000462.1| signal peptidase I | peptidase activity | 105 | 122 |
| sp|P61442|DNAK_LEPIC| Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) | response to stress | 3037 | 8187 | 3622 |
| ref|YP_002145.1|YP_002145.1| Hsp15-like protein | response to stress | 107 | 3685 | 177 |
| ref|YP_003633.1|YP_003633.1| aconitate hydratase | response to stress | 1514 | 1974 | 2170 |
| sp|Q72QAI1|HSP35_LEPIC| Probable 15 kDa heat shock protein | response to stress | 1600 | 1681 | 332 |
| sp|Q72R01|CLPP2_LEPIC| ATP-dependent Clp protease proteolytic subunit 2 (EC 3.4.21.92) (Endopeptidase Clp 2) | response to stress | 1587 | 1585 | 1043 |
| sp|Q725G6|CLPP1_LEPIC| ATP-dependent Clp protease proteolytic subunit 1 (EC 3.4.21.92) (Endopeptidase Clp 1) | response to stress | 647 | 651 | 749 |
| sp|P61440|DNAJ_LEPIC| Chaperone protein dnaJ | response to stress | 531 | 543 | 399 |
| ref|YP_002930.1|YP_002930.1| acriflavine resistance | response to stress | 343 | 513 | 92 |
| ref|YP_002412.1|YP_002412.1| DNA binding protein | response to stress | 495 | 466 | 284 |
| sp|Q72Q21|CLPB_LEPIC| Chaperone clpB | response to stress | 476 | 346 | 2061 |
| sp|Q725G5|CLPX_LEPIC| ATP-dependent Clp protease ATP-binding subunit clpX | response to stress | 600 | 325 | 460 |
| ref|YP_002986.1|YP_002986.1| acriflavin resistance | response to stress | 364 | 296 | 64 |
| ref|YP_003002.1|YP_003002.1| acriflavin resistance | response to stress | 161 | 230 | 30 |
| ref|YP_000276.1|YP_000276.1| penicillin G acylase precursor | response to stress | 228 | 149 | 30 |
| ref|YP_003298.1|YP_003298.1| hypothetical protein LIC13395 | response to stress | 71 |
| ref|YP_000518.1|YP_000518.1| penicillin-binding protein | response to stress | 21 |
| ref|YP_001765.1|YP_001765.1| ATP-dependent Clp protease, ATP-binding subunit | response to stress | 68 |
| ref|YP_001230.1|YP_001230.1| penicillin-binding protein | response to stress | 61 |
| ref|YP_000575.1|YP_000575.1| periplasmic divalent cation tolerance | response to stress | 8 |
| ref|YP_000247.1|YP_000247.1| carbon starvation protein A | response to stress | |
| ref|YP_000475.1|YP_000475.1| acriflavin resistance | response to stress | |
| ref|YP_003042.1|YP_003042.1| acriflavin resistance | response to stress | |
| ref|YP_000474.1|YP_000474.1| acriflavine resistance | response to stress | |
| ref|YP_001690.1|YP_001690.1| penicillin binding protein | response to stress | |
| ref|YP_000941.1|YP_000941.1| small multidrug resistance protein | response to stress | |
| 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 |
| Ref| YP_XXXX | YP_YYYY | Activity                     | Value 1 | Value 2 | Value 3 |
|----|---------|---------|------------------------------|---------|---------|---------|
| ref| YP_003405.1 | YP_003405.1 | response regulator          | signal  | transducer activity | 116     | 308     | 71      |
| ref| YP_001173.1 | YP_001173.1 | response regulator          | signal  | transducer activity | 141     | 271     | 181     |
| ref| YP_000541.1 | YP_000541.1 | response regulator          | signal  | transducer activity | 275     | 250     | 328     |
| ref| YP_001902.1 | YP_001902.1 | response regulator          | signal  | transducer activity | 272     | 243     | 78      |
| ref| YP_001406.1 | YP_001406.1 | response regulator          | signal  | transducer activity | 171     | 215     | 169     |
| ref| YP_003638.1 | YP_003638.1 | response regulator          | signal  | transducer activity | 202     | 504     |         |
| ref| YP_002208.1 | YP_002208.1 | GGDEF family protein        | signal  | transducer activity | 237     | 149     | 273     |
| ref| YP_000043.1 | YP_000043.1 | Aer                         | signal  | transducer activity | 104     | 81      | 17      |
| ref| YP_003000.1 | YP_003000.1 | response regulator          | signal  | transducer activity |         | 292     |         |
| ref| YP_000662.1 | YP_000662.1 | response regulator          | signal  | transducer activity |         | 61      |         |
| ref| YP_001106.1 | YP_001106.1 | response regulator          | signal  | transducer activity |         | 57      |         |
| ref| YP_001171.1 | YP_001171.1 | response regulator          | signal  | transducer activity |         | 284     |         |
| ref| YP_002312.1 | YP_002312.1 | response regulator          | signal  | transducer activity |         | 211     |         |
| ref| YP_002022.1 | YP_002022.1 | response regulator          | signal  | transducer activity |         | 110     |         |
| ref| YP_002724.1 | YP_002724.1 | response regulator          | signal  | transducer activity |         | 71      |         |
| ref| YP_001098.1 | YP_001098.1 | GGDEF family protein        | signal  | transducer activity |         | 61      |         |
| ref| YP_002433.1 | YP_002433.1 | response regulator          | signal  | transducer activity |         | 50      |         |
| ref| YP_001508.1 | YP_001508.1 | response regulator          | signal  | transducer activity |         | 34      |         |
| ref| YP_001845.1 | YP_001845.1 | response regulator          | signal  | transducer activity |         | 24      |         |
| ref| YP_002432.1 | YP_002432.1 | response regulator          | signal  | transducer activity |         | 21      |         |
| ref| YP_003149.1 | YP_003149.1 | response regulator          | signal  | transducer activity |         | 21      |         |
| ref| YP_003176.1 | YP_003176.1 | response regulator          | signal  |                 |         | 21      |         |
| Accession | Description                                      | Activity             | Value 1 | Value 2 | Value 3 |
|-----------|--------------------------------------------------|----------------------|---------|---------|---------|
| ref|YP_002032.1|YP_002032.1|response regulator|signal transducer activity|17|
| ref|YP_001099.1|YP_001099.1|GGDEF family protein|signal transducer activity|11|
| ref|YP_001266.1|YP_001266.1|GGDEF family protein|signal transducer activity|8|
| ref|YP_000898.1|YP_000898.1|response regulator|signal transducer activity|5|
| ref|YP_000968.1|YP_000968.1|response regulator|signal transducer activity| |
| ref|YP_002250.1|YP_002250.1|response regulator|signal transducer activity| |
| ref|YP_003571.1|YP_003571.1|response regulator|signal transducer activity| |
| ref|YP_000322.1|YP_000322.1|response regulator|signal 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| |
| ref|YP_001101.1|YP_001101.1|GGDEF family protein|signal transducer 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 activity| |
| ref|YP_001993.1|YP_001993.1|response regulator|signal transducer activity| |
| ref|YP_003235.1|YP_003235.1|response regulator|signal transducer activity| |
| ref|YP_003330.1|YP_003330.1|response regulator|signal transducer activity| |
| ref|YP_000002.1|YP_000002.1|DNA polymerase III beta subunit|transcription|2486|2486|1459|
| sp|Q72NB8|RPOA_LEPIC|DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (RNAP alpha subunit) (Transcriptase alpha chain)|transcription|3279|2438|1740|
| sp|Q72UA8|RPOB_LEPIC|DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (RNAP beta subunit)|transcription|2884|2412|3518|
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| GenBank Accession | Description | Transcription |
|-------------------|-------------|---------------|
| sp|Q72UA7|RPOC_LEPIC | DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (RNAP beta' subunit) | transcription |
| ref|YP_000728.1|YP_000728.1 | transcription antitermination protein | transcription |
| ref|YP_002627.1|YP_002627.1 | transcription elongation factor NusA | transcription |
| ref|YP_002559.1|YP_002559.1 | transcription termination factor Rho | transcription |
| ref|YP_000766.1|YP_000766.1 | transcript cleavage factor/unknown domain fusion protein | transcription |
| ref|YP_000590.1|YP_000590.1 | DNA-binding stress protein | transcription |
| ref|YP_003375.1|YP_003375.1 | DNA polymerase III gamma subunit | transcription |
| ref|YP_000768.1|YP_000768.1 | transcription antitermination protein | transcription |
| ref|YP_000590.1|YP_000590.1 | DNA repair protein | transcription |
| ref|YP_0003373.1|YP_0003373.1 | transcriptional coactivator | transcription |
| ref|YP_002627.1|YP_002627.1 | DNA translocase ftsK | transcription |
| ref|YP_000041.1|YP_000041.1 | transcription activator or transcription antitermination factor | transcription |
| ref|YP_003394.1|YP_003394.1 | DNA polymerase III subunit-related protein | transcription |
| ref|YP_002014.1|YP_002014.1 | DNA topoisomerase I protein | transcription |
| sp|Q72WD4|RECF_LEPIC | DNA replication and repair protein recF | transcription |
| sp|Q72MY7|DPO4_LEPIC | DNA polymerase IV (EC 2.7.7.7) (Pol IV) | transcription |
| ref|YP_000534.1|YP_000534.1 | anti-sigma factor antagonist | transcription |
| ref|YP_00205.1|YP_00205.1 | transcriptional regulator (CarD family) | transcription |
| ref|YP_000334.1|YP_000334.1 | anti-sigma factor antagonist | transcription |
| ref|YP_001344.1|YP_001344.1 | sigma factor WhiG | transcription |
| ref|YP_002369.1|YP_002369.1 | transcriptional regulator | transcription |
| ref|YP_002851.1|YP_002851.1 | anti-sigma factor antagonist | transcription |
| ref|YP_002985.1|YP_002985.1 | transcriptional regulator (TetR family) | transcription |
| ref|YP_002686.1|YP_002686.1 | anti-sigma factor antagonist | transcription |
| ref|YP_000979.1|YP_000979.1 | transcriptional regulator (FUR family) | transcription |
| ref                      | Accession       | Description                                  | Factor & Regulators | Copies per Cell |
|-------------------------|-----------------|----------------------------------------------|---------------------|-----------------|
| ref|YP_000216.1|YP_000216.1 | RNA polymerase ECF-type sigma factor          | transcription factor & regulators | 194          |
| ref|YP_000128.1|YP_000128.1 | sigma 54 activator                           | transcription factor & regulators | 233          |
| ref|YP_003566.1|YP_003566.1 | dnaK suppressor                              | transcription factor & regulators | 933          |
| sp|P61446|HRCA_LEPIC | Heat-inducible transcription repressor hrcA   | transcription factor & regulators | 99           |
| ref|YP_00372.1|YP_00372.1 | RNA polymerase ECF-type sigma factor          | transcription factor & regulators | 393          |
| ref|YP_001972.1|YP_001972.1 | transcriptional regulator (FUR family)        | transcription factor & regulators | 139          |
| ref|YP_001124.1|YP_001124.1 | transcriptional regulator                    | transcription factor & regulators | 219          |
| ref|YP_002704.1|YP_002704.1 | anti-sigma factor antagonist                  | transcription factor & regulators | 147          |
| ref|YP_003481.1|YP_003481.1 | sigma factor regulatory protein               | transcription factor & regulators | 89           |
| ref|YP_002418.1|YP_002418.1 | RNA polymerase ECF-type sigma factor          | transcription factor & regulators | 78           |
| ref|YP_000554.1|YP_000554.1 | anti-sigma factor antagonist                  | transcription factor & regulators | 71           |
| ref|YP_001753.1|YP_001753.1 | anti-sigma factor antagonist                  | transcription factor & regulators | 37           |
| ref|YP_000995.1|YP_000995.1 | anti-sigma factor antagonist                  | transcription factor & regulators | 284          |
| ref|YP_002330.1|YP_002330.1 | anti-sigma factor antagonist                  | transcription factor & regulators | 238          |
| ref|YP_003440.1|YP_003440.1 | anti-sigma factor antagonist                  | transcription factor & regulators | 203          |
| ref|YP_001630.1|YP_001630.1 | transcriptional regulator (TetR family)       | transcription factor & regulators | 118          |
| ref|YP_003507.1|YP_003507.1 | RNA polymerase ECF-type sigma factor          | transcription factor & regulators | 75           |
| ref|YP_002558.1|YP_002558.1 | hypothetical protein LIC12635                | transcription factor & regulators | 54           |
| ref|YP_001416.1|YP_001416.1 | transcription-repair coupling factor          | transcription factor & regulators | 34           |
| ref|YP_000610.1|YP_000610.1 | anti-sigma factor antagonist                  | transcription factor & regulators | 34           |
| ref|YP_001475.1|YP_001475.1 | anti-sigma factor antagonist                  | transcription factor & regulators | 34           |
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| Ref | Description | Transcription Factor & Regulators | Copies |
|-----|-------------|-----------------------------------|--------|
| ref|YP_001128.1|transcriptional regulator (FUR family)|30|
| ref|YP_001128.1|transcription factor & regulators| |
| ref|YP_001441.1|anti-sigma factor antagonist|30|
| ref|YP_001441.1|transcription factor & regulators| |
| ref|YP_000140.1|RNA polymerase ECF-type sigma factor|21|
| ref|YP_000140.1|transcription factor & regulators| |
| ref|YP_001200.1|transcriptional regulator (TetR family)|17|
| ref|YP_001200.1|transcription factor & regulators| |
| ref|YP_002239.1|transcriptional repressor (LexA family)|17|
| ref|YP_002239.1|transcription factor & regulators| |
| ref|YP_003012.1|anti-sigma factor antagonist|17|
| ref|YP_003012.1|transcription factor & regulators| |
| ref|YP_000924.1|sigma factor regulatory protein|14|
| ref|YP_000924.1|transcription factor & regulators| |
| ref|YP_002141.1|transcriptional regulator (MarR family)|14|
| ref|YP_002141.1|transcription factor & regulators| |
| ref|YP_002658.1|transcriptional regulator (MarR family)|14|
| ref|YP_002658.1|transcription factor & regulators| |
| ref|YP_001951.1|anti-sigma factor antagonist|14|
| ref|YP_001951.1|transcription factor & regulators| |
| ref|YP_001504.1|RNA polymerase sigma-54 factor|11|
| ref|YP_001504.1|transcription factor & regulators| |
| ref|YP_003538.1|transcriptional regulator (FUR family)|11|
| ref|YP_003538.1|transcription factor & regulators| |
| ref|YP_003173.1|RNA polymerase ECF-type sigma factor|11|
| ref|YP_003173.1|transcription factor & regulators| |
| ref|YP_002951.1|transcriptional regulator (MarR family)|8|
| ref|YP_002951.1|transcription factor & regulators| |
| ref|YP_000290.1|anti-sigma factor antagonist|8|
| ref|YP_000290.1|transcription factor & regulators| |
| ref|YP_003192.1|RNA polymerase ECF-type sigma factor|5|
| ref|YP_003192.1|transcription factor & regulators| |
| ref|YP_003657.1|putative transcriptional regulator|5|
| ref|YP_003657.1|transcription factor & regulators| |
| ref|YP_001748.1|sigma factor regulatory protein|5|
| ref|YP_001748.1|transcription factor & regulators| |
| ref|YP_002424.1|sigma factor regulatory protein|5|
| ref|YP_002424.1|transcription factor & regulators| |
| ref|YP_003318.1|transcriptional regulator (AraC family)|5|
| ref|YP_003318.1|transcription factor & regulators| |
| ref|YP_001543.1|transcriptional regulator (TetR family)|5|
| ref|YP_001543.1|transcription factor & regulators| |
| ref|YP_000381.1|transcriptional regulator (TetR family)|5|
| ref|YP_000381.1|transcription factor & regulators| |

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| ref | protein name | function | regulator type |
|-----|--------------|----------|---------------|
| YP_003500.1 | anti-sigma factor antagonist | transcription factor & regulators |
| YP_000650.1 | transcriptional regulator (ArsR family) | transcription factor & regulators |
| YP_001768.1 | RNA polymerase ECF-type sigma factor | transcription factor & regulators |
| YP_003474.1 | transcriptional regulator (ArsR family) | transcription factor & regulators |
| YP_002715.1 | transcriptional regulator (TetR family) | transcription factor & regulators |
| YP_000628.1 | RNA polymerase ECF-type sigma factor | transcription factor & regulators |
| YP_001388.1 | sigma factor regulatory protein | transcription factor & regulators |
| YP_003569.1 | DNA binding protein | transcription factor & regulators |
| YP_001116.1 | putative transcriptional regulator (DeoR family) | transcription factor & regulators |
| YP_000543.1 | RNA polymerase ECF-type sigma factor | transcription factor & regulators |
| YP_002677.1 | RNA polymerase ECF-type sigma factor | transcription factor & regulators |
| YP_000013.1 | sigma 54 activator | transcription factor & regulators |
| YP_003180.1 | sigma factor regulatory protein | transcription factor & regulators |
| YP_003503.1 | sigma factor regulatory protein | transcription factor & regulators |
| YP_003034.1 | transcriptional regulator (AraC family) | transcription factor & regulators |
| YP_003093.1 | transcriptional regulator (AraC family) | transcription factor & regulators |
| YP_000949.1 | transcriptional regulator (AraC family) | transcription factor & regulators |
| YP_002506.1 | transcriptional regulator (ArsR family) | transcription factor & regulators |
| YP_003311.1 | transcriptional regulator (ArsR family) | transcription factor & regulators |
| YP_001445.1 | transcriptional regulator (Crp family) | transcription factor & regulators |
| YP_003344.1 | transcriptional regulator (MarR family) | transcription factor & regulators |
| YP_002000.1 | transcriptional regulator (MarR family) | transcription |
| Ref | Protein ID | Description | Activity | CPM 1 | CPM 2 | CPM 3 |
|-----|------------|-------------|----------|-------|-------|-------|
| ref|YP_000364.1|transcriptional regulator (PadR family) | transcription factor & regulators | 3927 | 3387 | 2663 |
| ref|YP_000361.1|transcriptional regulator (TetR family) | transcription factor & regulators | 2628 | 2420 | 1313 |
| sp|Q72RT8|Probable transaldolase (EC 2.2.1.2) | transferase activity | 1474 | 1645 | 1069 |
| ref|YP_003206.1|acetyl-CoA acetyltransferase | transferase activity | 1556 | 1520 | 774 |
| ref|YP_000382.1|acetyl-CoA acetyltransferase | transferase activity | 1593 | 1345 | 1160 |
| ref|YP_000948.1|acetyl-CoA acetyltransferase | transferase activity | 2158 | 1209 | 983 |
| ref|YP_003223.1|fatty acid synthase subunit beta | transferase activity | 1633 | 1169 | 1039 |
| ref|YP_000430.1|glutamine-fructose-6-phosphate transaminase | transferase activity | 736 | 1055 | 399 |
| ref|YP_000395.1|2-isopropylmalate synthase | transferase activity | 77 | 1055 | 129 |
| ref|YP_001085.1|thiosulfate sulfurtransferase | transferase activity | 1036 | 1050 | 846 |
| ref|YP_000584.1|fatty acid synthase subunit beta | transferase activity | 1171 | 1032 | 460 |
| ref|YP_000436.1|glycosyltransferase | transferase activity | 788 | 1022 | 121 |
| ref|YP_001742.1|aspartate aminotransferase | transferase activity | 1058 | 995 | 1287 |
| ref|YP_001801.1|O-acetylhomoserine (thiol) lyase | transferase activity | 507 | 866 | 1226 |
| sp|P61656|2-dehydro-3-deoxyphosphochononate aldolase (EC 2.5.1.55) (Phospho-2-dehydro-3-deoxyoctonate aldolase) | transferase activity | 454 | 765 | 379 |
| ref|YP_002103.1|aspartate aminotransferase | transferase activity | 1107 | 755 | 447 |
| sp|P61724|6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase) (Lumazine synthase) (Riboflavin synthase) | transferase activity | 492 | 708 | 181 |
| sp|Q72RH8|Acetylornithine aminotransferase (EC 2.6.1.11) (ACOAT) | transferase activity | 779 | 682 | 541 |
| ref|YP_002757.1|aspartate aminotransferase | transferase activity | 777 | 665 | 1331 |
| ref|YP_000591.1|aminotransferase | transferase activity | 816 | 643 | 1030 |
| Reference | Activity Description | Activity | Activity | Activity |
|-----------|----------------------|----------|----------|----------|
| sp|Q72PY2|GLYA_LEPIC | Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase) (SHMT) transferase | 663 | 634 | 682 |
| ref|YP_000413.1|YP_000413.1 | UDP-N-acetylglucosamine pyrophosphorylase transferase | 599 | 556 | 304 |
| ref|YP_002132.1|YP_002132.1 | aminotransferase transferase | 654 | 550 | 757 |
| ref|YP_003563.1|YP_003563.1 | lipoprotein transferase | 306 | 536 | 50 |
| ref|YP_001704.1|YP_001704.1 | glycosyl transferase transferase | 263 | 463 | 177 |
| ref|YP_002958.1|YP_002958.1 | UDP glucosamine N-acetyltransferase transferase | 588 | 439 | 288 |
| sp|Q72PD0|TRPD_LEPIC | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) transferase | 501 | 419 | 71 |
| ref|YP_002167.1|YP_002167.1 | thymidylate synthase transferase | 346 | 406 | 300 |
| ref|YP_003393.1|YP_003393.1 | branched-chain amino acid aminotransferase transferase | 398 | 359 | 226 |
| ref|YP_003062.1|YP_003062.1 | UDP-N-acetylglucosamine acetyltransferase transferase | 353 | 330 | 320 |
| ref|YP_003403.1|YP_003403.1 | glutamate-1-semialdehyde aminotransferase transferase | 439 | 324 | 300 |
| ref|YP_002353.1|YP_002353.1 | aspartate aminotransferase transferase | 420 | 318 | 431 |
| ref|YP_001678.1|YP_001678.1 | 2-isopropylmalate synthase transferase | 298 | 316 | 707 |
| ref|YP_002114.1|YP_002114.1 | sugar transferase transferase | 295 | 298 | 476 |
| ref|YP_003104.1|YP_003104.1 | putative O-methyl transferase transferase | 343 | 288 | 82 |
| ref|YP_002657.1|YP_002657.1 | site-specific modification DNA-methyltransferase transferase | 332 | 281 | 155 |
| ref|YP_002115.1|YP_002115.1 | methyltransferase transferase | 268 | 280 | 78 |
| ref|YP_001947.1|YP_001947.1 | hypothetical protein LIC12008 transferase | 326 | 244 | 253 |
| ref|YP_001813.1|YP_001813.1 | UDP-N-acetylglucosamine:lipid A-N-acetylglucosamine transferase transferase | 235 | 27 |
| ref|YP_001035.1|YP_001035.1 | poly A polymerase transferase | 247 | 231 | 155 |
| ref|YP_003130.1|YP_003130.1 | lauroyl/myristoyl acyltransferase transferase | 196 | 224 | 17 |
| ref|YP_000429.1|YP_000429.1 | glucose-1-phosphate thymidyltransferase transferase | 211 | 75 |
| sp|Q72RT5|PUR9_LEPIC | Bifunctional purine biosynthesis protein purH transferase | 286 | 202 | 452 |
| sp|Q72TF8|LGT_LEPIC | Proline protein diacylglycerol transferase (EC 2.4.99.-) transferase | 172 | 194 |
| ref|YP_002316.1|YP_002316.1 | mannose-1-phosphate guanylyltransferase transferase | 182 | 190 | 21 |
| ref|YP_001703.1|YP_001703.1 | lipopolysaccharide core biosynthesis protein transferase | 545 | 189 |
| ref|YP_001555.1|YP_001555.1 | 2-isopropylmalate synthase 2 transferase | 229 | 169 | 335 |
| ref|YP_002057.1|YP_002057.1 | glucose-1-phosphate thymidyltransferase transferase | 244 | 150 | 207 |
| ref|YP_001373.1|YP_001373.1 | acetolactate synthase small subunit transferase | 123 | 125 |
| ref|YP_002106.1|YP_002106.1 | nucleoside-diphosphate-sugar pyrophosphorylase transferase | 136 | 105 | 85 |
| ref|YP_002072.1|YP_002072.1 | colanic acid biosynthesis glycosyltransferase transferase | 101 | 8 |
| 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 carboxyvinyltransferase 1-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 | Gluthionine-S-transferase transferase activity | 89 | | |
| Sp        | Q72NS5     | 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 synthase) 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 | | |
| Reference | Protein ID | Description | Transferase Activity |
|-----------|------------|-------------|----------------------|
| Ref|YP_002894.1|Glutathione S-transferase|292|
| Ref|YP_002183.1|Pyridoxal phosphate biosynthetic protein|234|
| Ref|YP_003276.1|Sulfate adenylyltransferase subunit 2|181|
| Sp|P62062|Arginine biosynthesis bifunctional protein argJ|177|
| Sp|YP_002183.1|Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Histidinol-phosphate transaminase)|173|
| Ref|YP_001008.1|Hypothetical protein LIC11058|169|
| Sp|YP_003276.1|Sulfate adenylyltransferase subunit 2|158|
| Ref|YP_001729.1|Biotin synthase|155|
| Ref|YP_002064.1|Aminotransferase|147|
| Ref|YP_002256.1|Glutaconate CoA transferase-like protein|136|
| Sp|YP_002256.1|Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Histidinol-phosphate transaminase)|136|
| Ref|YP_002019.1|Carboxic anhydrase|132|
| Ref|YP_00257.1|Protoporphyrinogen oxidase|129|
| Ref|YP_002086.1|Glucose-1-phosphate cytidylyltransferase|125|
| Ref|YP_002110.1|Aminotransferase|118|
| Sp|P59119|Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP synthase cyclase subunit) (IGP synthase aminotransferase)|107|
| Sp|YP_002109.1|Ornithine carbamoyltransferase (EC 2.1.3.3) (OTCase)|107|
| Ref|YP_003401.1|Porphobilinogen deaminase|103|
| Sp|YP_003072.1|2-Amino-4-hydroxy-6-hydroxymethylpyrrolophosphokinase|100|
| Ref|YP_002894.1|Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase glutamine amidotransferase)|71|
| Ref|YP_002183.1|Putative methyltransferase|61|
| Ref|YP_000609.1|3-Deoxy-manno-octulosonate cytidylyltransferase|54|
| Ref|YP_000075.1|Hypothetical protein LIC10075|54|
| Sp|P59118|Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase glutamine amidotransferase)|54|
| Ref | Accession | Description |
|-----|-----------|-------------|
| ref| YP_000983.1 | nicotinate-nucleotide pyrophosphorylase transferase activity |
| ref| YP_002089.1 | 3-demethylubiquinone-9 methyltransferase transferase activity |
| ref| YP_001732.1 | 8-amino-7-oxononanoyl transferase activity |
| ref| YP_001277.1 | acetyl-CoA C-acyltransferase transferase activity |
| ref| YP_003341.1 | hypoxanthine-guanine-xanthine phosphoribosyltransferase transferase activity |
| ref| YP_000571.1 | glycosyl transferase transferase activity |
| ref| YP_002409.1 | putative amino-acid acetyltransferase transferase activity |
| sp| Q72PS9 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60) (4-diphosphocytidyl-2C-methyltransferase) activity |
| ref| YP_0022178.1 | mannose-1-phosphate guanylyltransferase transferase activity |
| ref| YP_003552.1 | mannosyltransferase transferase activity |
| sp| P63752 | ATP phosphoribosyltransferase (EC 2.4.2.17) (ATP-PRTase) (ATP-PRT) transferase activity |
| ref| YP_000701.1 | carbon-nitrogen hydrolase transferase activity |
| ref| YP_001585.1 | mannosyltransferase transferase activity |
| ref| YP_003588.1 | UTP-glucose-1-phosphate uridylyltransferase transferase activity |
| ref| YP_000144.1 | valine-pyruvate transaminase transferase activity |
| ref| YP_003557.1 | alginate O-acetyltransferase transferase activity |
| ref| YP_000273.1 | farnesyl-diphosphate synthase transferase activity |
| ref| YP_001910.1 | hypothetical protein LIC11970 transferase activity |
| ref| YP_000355.1 | hypothetical protein LIC10364 transferase activity |
| ref| YP_000906.1 | type I restriction enzyme transferase activity |
| ref| YP_001262.1 | dolichyl-phosphate mannosyltransferase transferase activity |
| ref| YP_001032.1 | hypothetical protein LIC11062 transferase activity |
| ref| YP_003468.1 | putative S-adenosyl methionine dependent methyltransferase like protein transferase activity |
| ref| YP_002310.1 | 3-demethylubiquinone-9 3-O-methyltransferase transferase activity |
| ref| YP_000051.1 | 7,8-dihydropteroyl synthase protein transferase activity |
| ref| YP_000317.1 | hypothetical protein LIC10327 transferase activity |
| ref| YP_000442.1 | hypothetical protein LIC10458 transferase activity |
| ref| YP_002503.1 | lipid-a-disaccharide synthase protein transferase activity |
| ref| YP_001612.1 | phosphoribosylglycinamide formyltransferase transferase activity |
| ref| YP_002068.1 | sugar transferase transferase activity |
| ref| YP_001879.1 | polynucleotide adenyltransferase-like protein transferase activity |
| ref| YP_001730.1 | adenosylmethionine-8-amino-7-ribosyltransferase transferase activity |
| accession | description | activity | count |
|-----------|-------------|----------|-------|
| ref|YP_001278.1|lipopolysaccharide heptosyltransferase II|transferase activity|14|
| ref|YP_0003241.1|putative aminotransferase|transferase activity|14|
| sp|Q72R21|ATE_LEPIC|Putative arginyl-tRNA--protein transferase ((EC 2.3.2.8) (Arginyltransferase)|transferase activity|14|
| ref|YP_003126.1|carbonic anhydrase/acetyltransferase|transferase activity|14|
| ref|YP_003555.1|alginate O-acetyltransferase|transferase activity|11|
| ref|YP_003027.1|putative aminotransferase|transferase activity|11|
| ref|YP_003143.1|ankyrin-like protein|transferase activity|11|
| sp|P62472|MRAW_LEPIC|S-adenosyl-methyltransferase mraW (EC 2.1.1.7)|transferase activity|11|
| ref|YP_003305.1|methylated-DNA--protein-cysteine methyltransferase transcription regulator|transferase activity|8|
| ref|YP_003309.1|mannosyltransferase|transferase activity|8|
| ref|YP_002192.1|hypothetical protein LIC12257|transferase activity|5|
| ref|YP_000191.1|glycosyltransferase|transferase activity|5|
| ref|YP_000751.1|hypothetical protein LIC10771|transferase activity|5|
| ref|YP_000073.1|3-demethylubiquinone-9 methyltransferase|3-methyltransferase activity|2|
| ref|YP_000014.1|hypothetical protein LIC0014|transferase activity|5|
| ref|YP_000719.1|3-demethylubiquinone-9 methyltransferase|3-methyltransferase activity|5|
| ref|YP_002420.1|alginate O-acetyltransferase|transferase activity|5|
| ref|YP_002049.1|ankyrin-like protein|transferase activity|5|
| ref|YP_002157.1|DNA methyltransferase|transferase activity|5|
| ref|YP_002062.1|glycosyl transferase|transferase activity|5|
| ref|YP_002066.1|glycosyltransferase|transferase activity|5|
| ref|YP_003452.1|hypothetical protein LIC20060|transferase activity|5|
| ref|YP_003550.1|5-adenosylmethionine--tRNA ribosyltransferase-isomerase|transferase activity|5|
| ref|YP_001042.1|tetrapyrrole (corrin/porphyrin) methylase|transferase activity|5|
| ref|YP_001275.1|hypothetical protein LIC11309|transferase activity|5|
| ref|YP_001458.1|methyltransferase|transferase activity|5|
| ref|YP_003518.1|precorrin-3 C-17 methylase|transferase activity|5|
| sp|Q72U10|UPPS_LEPIC|Undecaprenyl pyrophosphate synthetase (EC 2.5.1.31) (UPP synthetase) (Di-trans,poly-cis-decaprenylpyrophosphate synthetase)|transferase activity|5|
| ref|YP_003097.1|acetyltransferase|transferase activity|5|
| ref|YP_002055.1|dTDP-rhamnosyl transferase|transferase activity|5|
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| sp|Q72NR0|NADD_LEPIC | Probable nicotinate-nucleotide adenyltransferase (EC 2.7.7.18) (Deamido-NAD(+) pyrophosphorylase) | transferase activity |
|---|---|---|---|---|
| ref|YP_003274.1|YP_003274.1 | uroporphyrinogen-III C-methyltransferase | transferase activity |
| ref|YP_001778.1|YP_001778.1 | lipopolysaccharide biosynthesis glycosyltransferase | transferase activity |
| ref|YP_003017.1|YP_003017.1 | sugar-phosphate nucleotidyl transferase | transferase activity |
| ref|YP_001289.1|YP_001289.1 | methyltransferase DNA modification enzyme | transferase activity |
| ref|YP_000832.1|YP_000832.1 | CDP-diglyceride synthetase | transferase activity |
| ref|YP_000138.1|YP_000138.1 | protein-PII uridylyltransferase | transferase activity |
| ref|YP_002214.1|YP_002214.1 | 3-deoxy-d-manno-octulosonic acid transferase | transferase activity |
| ref|YP_006841.1|YP_006841.1 | 3-oxoacyl- | transferase activity |
| ref|YP_002119.1|YP_002119.1 | acetyltransferase | transferase activity |
| ref|YP_000525.1|YP_000525.1 | acetyltransferase | transferase activity |
| ref|YP_002400.1|YP_002400.1 | acetyltransferase | transferase activity |
| ref|YP_002588.1|YP_002588.1 | acetyltransferase | transferase 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_000120.1|YP_000120.1 | ankyrin G domain containing protein | transferase 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 activity |
| ref|YP_001716.1|YP_001716.1 | aspartate aminotransferase | transferase activity |
| ref|YP_000343.1|YP_000343.1 | dimethyladenosine transferase | transferase activity |
| ref|YP_000784.1|YP_000784.1 | glutathione S-transferase | transferase activity |
| ref|YP_002076.1|YP_002076.1 | glycosyltransferase | transferase activity |
| ref|YP_001063.1|YP_001063.1 | glycosyltransferase | transferase activity |
| ref|YP_002531.1|YP_002531.1 | glycosyltransferase | transferase activity |
| ref|YP_002800.1|YP_002800.1 | glycosyltransferase | transferase activity |
| ref|YP_000192.1|YP_000192.1 | glycosyltransferase | transferase activity |
Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements

| Ref | Accession | Protein Name | Function |
|-----|-----------|--------------|----------|
| 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_001394.1 | YP_001394.1 | histidine kinase response regulator hybrid protein transferase activity |
| ref| YP_001121.1 | YP_001121.1 | hypothetical protein LIC11151 transferase activity |
| ref| YP_000115.1 | YP_000115.1 | methylated-DNA-protein-cysteine methyltransferase transferase activity |
| ref| YP_003038.1 | YP_003038.1 | protein-pII uridylyltransferase transferase activity |
| ref| YP_003627.1 | YP_003627.1 | putative acyltransferase transferase activity |
| ref| YP_001591.1 | YP_001591.1 | UDP-3-O- transferase activity |
| ref| YP_001420.1 | YP_001420.1 | UDP-glucosyltransferase transferase activity |
| sp| Q72NG2| RL4_LEPIC | 30S ribosomal protein L4 translation 4724 4232 375 |
| sp| Q72NG4| RL2_LEPIC | 30S ribosomal protein L2 translation 3508 3203 284 |
| sp| Q72N6| RS11_LEPIC | 30S ribosomal protein S11 translation 2748 2439 250 |
| ref| YP_002722.1 | YP_002722.1 | 30S ribosomal protein S5 translation 3630 2368 335 |
| sp| Q72UB1| RL1_LEPIC | 30S 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 338 |
| sp| Q72NG7| RS3_LEPIC | 50S 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| Q72U9| 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 | 50S ribosomal protein S2 translation 1783 1015 407 |
| sp| Q72V72| EFTS_LEPIC | Elongation factor Ts (EFTs) translation 1517 1416 603 |
| sp| Q72NH5| RL15_LEPIC | 50S ribosomal protein L15 translation 1385 996 591 |
| sp| Q72U19| RL7_LEPIC | 30S ribosomal protein S1 translation 1034 818 121 |
| sp| Q72QK0| RS6_LEPIC | 30S ribosomal protein S6 translation 1235 824 443 |
| sp| Q72S27| RL19_LEPIC | 30S ribosomal protein L19 translation 847 767 624 |
| sp| Q72N9| RS17_LEPIC | 30S ribosomal protein S17 translation 2120 846 185 |
| sp| Q72PK6| SYT_LEPIC | Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine-tRNA ligase) (ThrRS) translation 876 830 850 |
| sp| Q72QKO| RS6_LEPIC | 30S ribosomal protein S6 translation 1235 824 443 |
| sp| Q72S27| RS19_LEPIC | 30S ribosomal protein L19 translation 1034 818 121 |
| sp| Q72UAS| RS7_LEPIC | 30S ribosomal protein S7 translation 1839 774 492 |
| sp| Q72V5S| GATD_LEPIC | Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (EC 6.3.5.) (Asp/Glu-ADT subunit B) translation 847 767 624 |
| sp| Q72NG8| RL16_LEPIC | 30S ribosomal protein L16 translation 729 755 207 |
| sp| Q72N7| RS4_LEPIC | 30S ribosomal protein S4 translation 1330 743 200 |
| sp| Q72NH6| RL6_LEPIC | 30S ribosomal protein L6 translation 1081 721 395 |

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| Accession | Protein ID | Description | Gene | Translation |
|-----------|------------|-------------|------|-------------|
| sp|Q72PR7|SYI_LEPIC|Isoleucyl-tRNA synthetase (EC 6.1.1.5) | (Isoleucine--tRNA ligase) (IleRS) | 457 505 312 |
| sp|Q72NO|RL15_LEPIC|50S ribosomal protein L15 | | 1853 465 129 |
| sp|Q72SC3|GATA_LEPIC|Glutamyl-tRNA (Gln) amidotransferase subunit A (EC 6.3.5.7) | (Glu-ADT subunit A) | 574 464 525 |
| sp|Q72PK8|IF3_LEPIC|Translation initiation factor IF-3 | | 350 425 54 |
| sp|Q72UA6|RS12_LEPIC|30S ribosomal protein S12 | | 592 401 8 |
| sp|Q72NO6|RL27_LEPIC|50S ribosomal protein L27 | | 955 382 89 |
| sp|Q72NG0|RS10_LEPIC|30S ribosomal protein S10 | | 1671 379 435 |
| sp|Q72PW7|SYG_LEPIC|Glycyl-tRNA synthetase (EC 6.1.1.14) | (Glycine--tRNA ligase) (GlyRS) | 272 353 249 |
| sp|Q72QTX|SYN_LEPIC|Asparaginyl-tRNA synthetase | (Asparagine--tRNA ligase) (AsnRS) | 231 331 200 |
| sp|Q72ST4|DEF_LEPIC|Peptide deformylase (EC 3.5.1.88) | (Polypeptide deformylase) | 494 321 196 |
| sp|Q72MR4|SYM_LEPIC|Methionyl-tRNA synthetase (EC 6.1.1.10) | (Methionine--tRNA ligase) (MetRS) | 350 306 636 |
| sp|Q72NO9|RL24_LEPIC|50S ribosomal protein L24 | | 496 302 21 |
| sp|Q72N15|RS13_LEPIC|30S ribosomal protein S13 | | 465 277 110 |
| ref|YP_000416.1|YP_000416.1|peptidyl-tRNA hydrolase | | 251 248 196 |
| sp|Q72U06|SYF_LEPIC|Prolyl-tRNA synthetase (EC 6.1.1.15) | (Proline--tRNA ligase) (ProRS) | 316 239 427 |
| ref|YP_002858.1|YP_002858.1|30S ribosomal protein S1 | | 334 233 281 |
| sp|Q72RS5|RL28_LEPIC|50S ribosomal protein L28 | | 753 226 24 |
| sp|Q72QKS|SYD_LEPIC|Aspartyl-tRNA synthetase (EC 6.1.1.12) | (Aspartate--tRNA ligase) (AspRS) | 297 225 253 |
| sp|Q72NH4|RS14_LEPIC|30S ribosomal protein S14 | | 770 192 |
| sp|Q72R38|SYK_LEPIC|Lysyl-tRNA synthetase (EC 6.1.1.6) | (Lysine--tRNA ligase) (LysRS) | 179 211 |
| sp|Q72MB0|SYF_A_LEPIC|Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) | (Phenylalanine--tRNA ligase alpha chain) (PheRS) | 168 176 181 |
| sp|Q72U99|RS9_LEPIC|30S ribosomal protein S9 | | 282 129 47 |
| sp|Q72NX6|RS15_LEPIC|30S ribosomal protein S15 | | 405 120 54 |
| sp|Q72UY6|SYL_LEPIC|Leucyl-tRNA synthetase (EC 6.1.1.4) | (Leucine--tRNA ligase) (LeuRS) | 147 113 37 |
| ref|YP_001514.1|YP_001514.1|30S ribosomal protein S16 | | 2003 95 277 |
| sp|Q72PK9|RL35_LEPIC|50S ribosomal protein L35 | | 619 89 14 |
| sp|Q72UI1|RRF_LEPIC|Ribosome recycling factor (Ribosome-releasing factor) (RRF) | | 881 533 |
| sp|Q72PR1|RS21_LEPIC|30S ribosomal protein S21 | | 649 47 |
| sp|Q72N29|RL29_LEPIC|50S ribosomal protein L29 | | 616 |
| sp|Q72NH0|RS17_LEPIC|30S ribosomal protein S17 | | 596 21 |
| sp|Q72QL1|SVR_LEPIC|Arginyl-tRNA synthetase (EC 6.1.1.19) | (Arginine--tRNA ligase) (ArgRS) | 218 100 |
| ref|YP_001248.1|YP_001248.1|peptide chain release factor 3 | | 218 |
| ref|YP_003127.1|YP_003127.1|phenylalanyl-tRNA synthetase beta chain | | 149 |
| sp|Q72V30|SYV_LEPIC|Valyl-tRNA synthetase (EC 6.1.1.9) | (Valine--tRNA ligase) (ValRS) | 238 |
| sp|Q72RP6|SYV_LEPIC|Tyr(3)-tRNA synthetase | (Tyrinosine--tRNA ligase) (TyrRS) | 103 |
| ref|YP_000276.1|YP_000276.1|translation initiation factor IF-1 | | 92 |
| sp|Q72P39|RL31_LEPIC|50S ribosomal protein L31 | | 75 |
| sp|Q72NH9|RL30_LEPIC|50S ribosomal protein L30 | | 71 |
| sp|Q72QK2|RS18_LEPIC|30S ribosomal protein S18 | | 64 |
| sp|Q72W38|RF1_LEPIC|Peptide chain release factor 1 (RF-1) | | 50 |
| sp|Q72PL0|RL20_LEPIC|50S ribosomal protein L20 | | 47 |
| ref|YP_002204.1|YP_002204.1|tRNA (5-methylamino-2-thiouridylate)--methyltransferase | | 47 |
| sp|Q72NH7|RL38_LEPIC|50S ribosomal protein L18 | | 30 |
| sp|Q72NGS|RS19_LEPIC|30S ribosomal protein S19 | | 24 |
| sp|Q72M46|SYE_LEPIC|Glutamyl-tRNA synthetase (EC 6.1.1.17) | (Glutamate--tRNA ligase) (GluRS) | 496 |

Supplement: Malmstroem, Beck et al. Proteome-wide copies per cell measurements
| Refrence | Name                  | Function                                                                 |
|----------|-----------------------|--------------------------------------------------------------------------|
| ref|YP_000346.1|YP_000346.1| tryptophanyl-tRNA synthetase translation |
| sp|P62371|YPH_LEPIC| Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase) [HisRS] translation |
| ref|YP_002717.1|YP_002717.1| methionine sulfoxide reductase B translation |
| sp|Q7ZQ17|STC_LEPIC| Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase) [CysRS] translation |
| sp|Q7ZV33|RF2_LEPIC| Peptide chain release factor 2 (RF-2) translation |
| ref|YP_002792.1|YP_002792.1| elongation factor G translation |
| sp|Q7ZS34|FMT_LEPIC| Methionyl-tRNA formyltransferase (EC 2.1.2.9) translation |
| ref|YP_000346.1|YP_000346.1| tryptophanyl-tRNA synthetase translation |
| sp|P62371|YPH_LEPIC| Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase) [HisRS] translation |
| ref|YP_002717.1|YP_002717.1| methionine sulfoxide reductase B translation |
| sp|Q7ZQ17|STC_LEPIC| Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase) [CysRS] translation |
| sp|Q7ZV33|RF2_LEPIC| Peptide chain release factor 2 (RF-2) translation |
| ref|YP_002792.1|YP_002792.1| elongation factor G translation |
| sp|Q7ZS34|FMT_LEPIC| Methionyl-tRNA formyltransferase (EC 2.1.2.9) translation |
| ref|YP_000346.1|YP_000346.1| tryptophanyl-tRNA synthetase translation |
| sp|P62371|YPH_LEPIC| Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase) [HisRS] translation |
| ref|YP_002717.1|YP_002717.1| methionine sulfoxide reductase B translation |
| sp|Q7ZQ17|STC_LEPIC| Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase) [CysRS] translation |
| sp|Q7ZV33|RF2_LEPIC| Peptide chain release factor 2 (RF-2) translation |
| ref|YP_002792.1|YP_002792.1| elongation factor G translation |
| sp|Q7ZS34|FMT_LEPIC| Methionyl-tRNA formyltransferase (EC 2.1.2.9) translation |
| ref|YP_000346.1|YP_000346.1| tryptophanyl-tRNA synthetase translation |
| sp|P62371|YPH_LEPIC| Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase) [HisRS] translation |
| ref|YP_002717.1|YP_002717.1| methionine sulfoxide reductase B translation |
| sp|Q7ZQ17|STC_LEPIC| Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase) [CysRS] translation |
| sp|Q7ZV33|RF2_LEPIC| Peptide chain release factor 2 (RF-2) translation |
| ref|YP_002792.1|YP_002792.1| elongation factor G translation |
| sp|Q7ZS34|FMT_LEPIC| Methionyl-tRNA formyltransferase (EC 2.1.2.9) translation |

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| Ref | YP_002614.1 | Protein Name | Transport Type | Copies Per Cell |
|-----|-------------|--------------|----------------|----------------|
| YP_001580.1 | hypothetical protein LIC12693 | transport | 377 | |
| YP_002905.1 | sulfate Permease | transport | 223 | 8 |
| YP_003379.1 | cystine-binding periplasmic protein precursor | transport | 143 | |
| YP_002614.1 | hypothetical protein LIC10359 | transport | 69 | 17 |
| YP_002868.1 | nitrogen regulatory IIA protein | transport | 50 | |
| YP_001580.1 | biopolymer transport exbd-related transmembrane protein | transport | 324 | |
| YP_001580.1 | Acyl carrier protein (ACP) | transport | 377 | |
| YP_002905.1 | cystine-binding periplasmic protein precursor | transport | 241 | |
| YP_003379.1 | cystine-binding periplasmic protein precursor | transport | 219 | |
| YP_001580.1 | biopolymer transport exbd-related transmembrane protein | transport | 223 | |
| YP_001580.1 | biopolymer transport exbd-related transmembrane protein | transport | 344 | |