

Supporting Information

'One-Dimensional Capillary Liquid Chromatographic Separation Coupled with Tandem Mass Spectrometry Unveils the Proteome of Escherichia coli on a Microarray Scale'

by

Mio Iwasaki, Shohei Miwa, Tohru Ikegami, Masaru Tomita,
Nobuo Tanaka, Yasushi Ishihama

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1. Supplementary Methods

Materials.

Sodium hydroxide, sodium hydrogen carbonate and 4-(2-aminoethyl) benzenesulfonyl fluoride hydrochloride (AEBSF) were from Nacalai (Kyoto, Japan). Tris(2-carboxyethyl)phosphine hydrochloride (TCEP) was from PIERCE (Rockford, IL). C18 Empore disc cartridges and membranes were from 3M (St. Paul, MN). Water was purified by a Millipore Milli-Q system (Bedford, MA, USA). Sodium deoxycholate (SDC), sodium lauroylsarcosinate (SLS), mass spectrometry-grade lysyl endoprotease (Lys-C), ethyl acetate, acetonitrile, acetic acid, methanol, trifluoroacetic acid (TFA), urea, iodoacetamide (IAA), sodium carbonate and all other chemicals were purchased from Wako (Osaka, Japan).

Sample preparation.

Escherichia coli (*E. coli*) strain BW25113 cells grown in Luria-Bertani (LB) cultures at 37 °C were used in this study. The cell pellet was prepared by centrifugation at 4,500 g for 10 min and was resuspended in 10 mL of ice-cold 1 M KCl, 15 mM Tris (pH 7.4). A protease inhibitor AEBSF was added to the final concentration of 1 mM. The cells were lysed by ultrasonication, and the unbroken cells and debris were precipitated at 2,500 g for 5 min. The resultant pellet was used for whole cell lysate analyses.

The whole cell lysate was digested by Lys-C and trypsin according to PTS protocol as described¹. Briefly, the lysates was dissolved in 50 mM sodium carbonate buffer at pH 11 containing 12 mM SDC and 12 mM SLS. Proteins were reduced with a 10-fold molar excess of TCEP at 37°C for 30 min and

alkylated with a 100-fold molar excess of IAA at 37°C for 30 min. The sample solution was diluted 5-fold with 50 mM sodium hydrogen carbonate buffer and digested with Lys-C at 37°C for 3 hours and trypsin at 37°C overnight (protease-to-protein ratio of 1:50 (w/w)). An equal volume of ethyl acetate was added to the solution and the mixture was acidified with the final concentration of 0.5% TFA². The mixture was shaken for 1 min and centrifuged at 15,700 g for 2 min, then the aqueous phase was collected and desalted with C18- StageTips³.

LC-MS/MS system

All nanoLC-MS/MS experiments were performed on an LTQ-Orbitrap XL (Thermo Fisher Scientific, Bremen, Germany) connected to Dionex Ultimate3000 nanoflow pump (Germering, Germany) and HTC-PAL autosampler (CTC Analytics, Zwingen, Switzerland). A self-pulled capillary (15 cm length, 100 µm i.d., 6 µm opening) packed with ReproSil-Pur C18-AQ (3 µm, Dr. Maisch, Ammerbuch, Germany) was used as a C₁₈ silica particle-packed column as described⁴. The spray voltage of 2400 V was applied through a PEEK tee connector with a platinum wire. A 350 cm long monolithic silica-C₁₈ capillary column was prepared from a mixture of tetramethoxysilane and methyltrimethoxysilane in a ratio of 9/2 to form a hybrid structure, as described⁵. The coiled capillary column was connected to a 50 µm i.d. tapered monolithic capillary with the conductive distal coating end, in which the spray voltage was applied. The sample solutions were injected via a 5 µL loop in the autosampler and were directly loaded onto the columns. The flow rate was 500 nL/min. The mobile phases consisted of (A) 0.5% acetic acid and (B) 0.5% acetic

acid and 80% acetonitrile. A two-step linear gradient of 5 % to 40 % B in variable time (70 – 2470 min), 40 % to 100 % B in 5 min, and 100 % B for 10 min was employed throughout this study. The MS scan range was m/z 300-1500, and the top ten precursor ions were selected in MS scan by orbitrap for subsequent MS/MS scans by ion trap in the automated gain control (AGC) mode where AGC values of 5.00e+05 and 1.00e+04 were set for full MS and MS/MS, respectively. The normalized CID was set to be 35.0. A lock mass function was used to obtain stable and accurate m/z values within 3 ppm.

Data analysis and bioinformatics.

The raw data files were analyzed by Mass Navigator v1.2 (Mitsui Knowledge Industry, Tokyo, Japan) to create peak lists on the basis of the recorded fragmentation spectra. In order to improve the quality of MS/MS spectra, Mass Navigator discarded all peaks with an absolute intensity of less than 10, and with an intensity of less than 0.1% of the most intense peak in MS/MS spectra, and an in-house Perl script called “mgf creator” converted the m/z values of the isotope peaks to the corresponding monoisotopic peaks when the isotope peaks were selected as the precursor ions⁶. Peptides and proteins were identified by Mascot v2.2 (Matrix Science, London, U.K.) against the total ORF amino acids sequences of *E. coli* K-12 (BW25113) from GenoBase (<http://ecoli.naist.jp/GB6/search.jsp>) with a precursor mass tolerance of 3 ppm, and strict specificity allowing for up to 2 missed cleavages. For trypsin digestion, carbamidomethylation of cysteine was set as a fixed modification, and methionine oxidation was allowed as a variable modification. Peptides

were rejected if the Mascot score was below the 95% confidence limit based on the “identity” score of each peptide and their length was less than 7 amino acid residues. For protein identification, at least two confident peptides per protein were required. Additionally, higher confident peptides were selected based on significance threshold ($p < 0.01$) for protein identification. False-positive rates (FPR) were estimated by searching against a randomized decoy database created by the Mascot Perl program supplied by Matrix Science.

Mass Navigator was also used for peak integration to measure peak width, peak capacity and peak area using the peak quantitation function. For calculating peak capacity, the elution range was determined by the firstly-eluted peptide (JW1487, GHFFLHPR, 505.769 m/z) and the lastly-eluted peptide (JW3301, ILELAGFLDSYIPEPER, 981.514 m/z).

The grand average hydropathy (GRAVY) values for identified proteins and peptides were calculated according to a previous report⁷. Proteins and peptides exhibiting positive GRAVY values were recognized as hydrophobic. Mapping of transmembrane (TM) domains for the identified proteins was conducted using the TM hidden Markov model (TMHMM) algorithm available at <http://www.cbs.dtu.dk/services/TMHMM-2.0/>, to which FASTA files were submitted in batch mode⁸. Information on the subcellular location of identified proteins was obtained from gene ontology (GO) component terms using GOSlim (<http://www.geneontology.org>).

***E. coli* microarrays.**

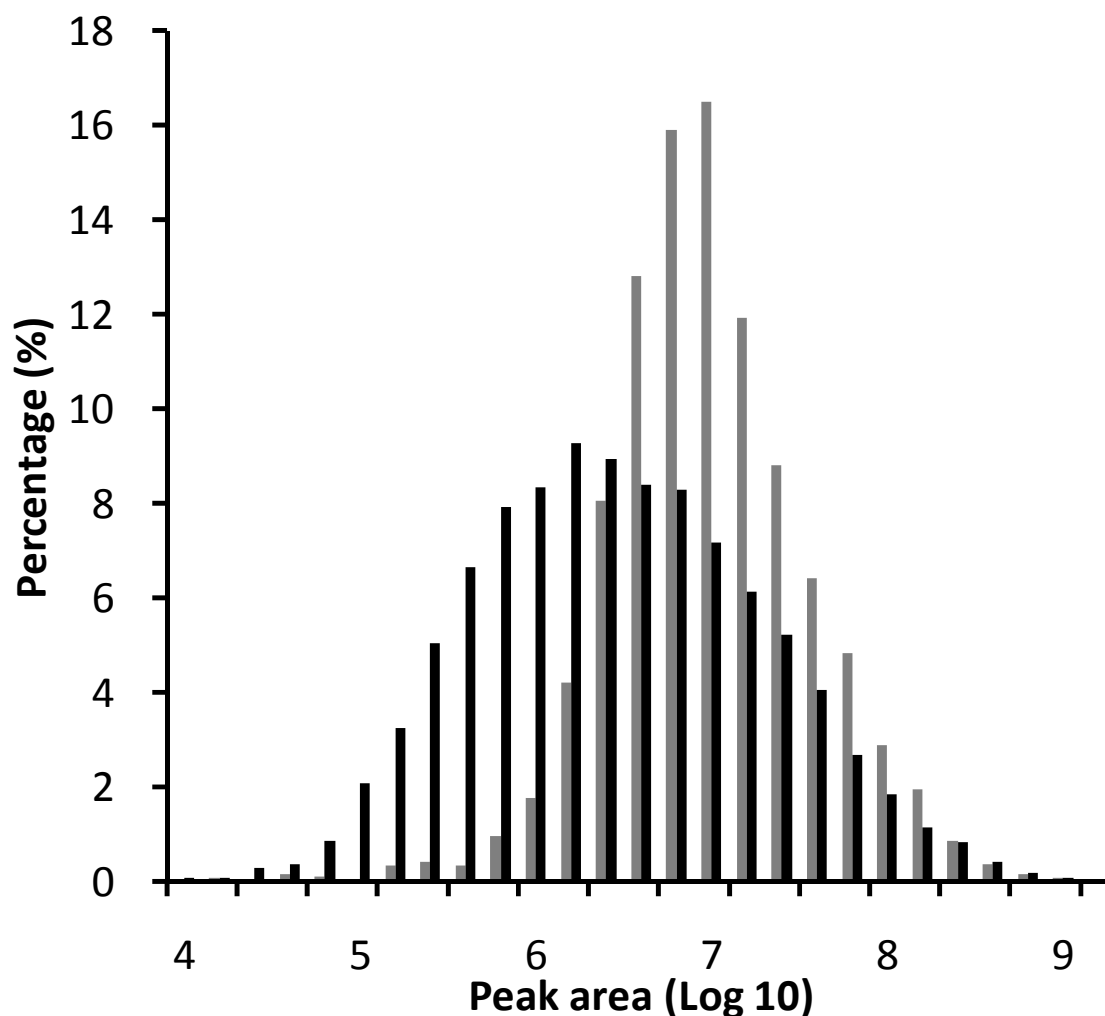
E. coli BW25113 was grown as described previously^{2,9}. For the microarray

experiment, we followed the labeling and hybridization methods of Oshima *et al.*¹⁰. DNA from *E. coli* BW25113 was used for the control channel. Duplicate two-color experiments were performed using an *E. coli* gene array named nara_operonEcoK12, registered on the ArrayExpress database, with an Affymetrix array scanner 428 (Santa Clara, CA). Raw data files were analyzed by the statistical algorithm in the ImaGene version 4.0 (BioDiscovery, Los Angeles, CA), using the default parameters. In the absolute present analysis of mRNA, we set the threshold of 0.1 for signal intensity, and the mRNA signal intensity for each gene was calculated as the mean of values obtained.

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Supplemental Figure S1 Distribution of peak responses obtained by LC-MSMS using the 15 cm long particle-packed column and the 350 cm long monolithic silica column.



The distribution of the peak area of identified peptides was calculated for the results from the monolithic column (black bar) and the particle-packed column (gray bar) shown in Figure 2. The bin of the X-axis is 0.2 and the obtained frequency was normalized to calculate the percentage. The dynamic range for each distribution was calculated, assuming the Gaussian distribution.

Supplementary Table S1 *E. coli* Proteome Analyzed by LC-MS/MS using the Monolithic Silica Column and the 41 Hour Gradient

| Identified number | Transcriptome | Proteome ^a | | | |
|--------------------------------|---------------|-------------------------|-------------------------|-------------------------|-------------------------|
| | | Single LCMS | Single LCMS | Triplicate LCMS | Triplicate LCMS |
| | | Criteria A ^b | Criteria B ^b | Criteria A ^b | Criteria B ^b |
| Non-redundant proteins | 2543 | 1925 ± 59 | 2202 ± 52 | 2404 | 2602 |
| Non-redundant peptides | - | 15993 ± 560 | 16269 ± 557 | 21998 | 22196 |
| Membrane proteins ^c | 919 | 544 ± 16 | 663 ± 22 | 739 | 830 |

^aThe tryptic peptides from the *E. coli* cell lysate were analyzed by LC-MS/MS in triplicate using the 350 cm long monolithic silica column with 2,470 min gradient. Other conditions are described in Figure 2. The transcriptome data was obtained using the same sample.

^bProtein identification was done based on two criteria as follows: (A) at least two non-redundant peptides (not less than 7 AA) per protein. For each peptide, Mascot score should be more than identity score ($p < 0.05$), (B) one non-redundant peptide (not less than 7 AA) per protein, where the Mascot score should be more than identity score ($p < 0.01$) or criteria A.

^cMembrane proteins were defined by using TMHMM, GO terms and GRAVY scores as described in Supplementary method.

Supplementary Table S2 List of identified proteins by LC-MS/MS using the monolithic silica column and the 41 hour gradient

| Accession number | Gene name | Product | GO annotation | GRAVY score | Membrane proteins | Number of predicted transmembrane domains (TMHMM) | Number of identified peptides | Protein score |
|------------------|-----------|---|---|-------------|-------------------|---|-------------------------------|---------------|
| JW3951 | rpoC | RNA polymerase, beta prime subunit | GO:0005737 cytoplasm | -0.240 | 0 | 0 | 76 | 5523 |
| JW3950 | rpoB | RNA polymerase, beta subunit | GO:0005737 cytoplasm | -0.394 | 0 | 0 | 68 | 5260 |
| JW1215 | narG | nitrate reductase 1, alpha subunit | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | -0.512 | 1 | 0 | 67 | 4507 |
| JW2573 | clpB | protein disaggregation chaperone | GO:0005737 cytoplasm | -0.358 | 0 | 0 | 54 | 4068 |
| JW0999 | putA | fused DNA-binding transcriptional regulator - - proline dehydrogenase - - pyrroline-5-carboxylate dehydrogenase | GO:0005737 cytoplasm | -0.131 | 0 | 0 | 60 | 4047 |
| JW0110 | aceE | pyruvate dehydrogenase, decarboxylase component E1, thiamin- | 0 | -0.437 | 0 | 0 | 55 | 3988 |
| JW2541 | purL | phosphoribosylformyl-glycineamide synthetase | GO:0005737 cytoplasm | -0.235 | 0 | 0 | 58 | 3744 |
| JW2871 | gcvP | glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex | 0 | -0.066 | 0 | 0 | 46 | 3739 |
| JW0013 | dnaK | chaperone Hsp70, co-chaperone with DnaJ | GO:0005737 cytoplasm | -0.409 | 0 | 0 | 46 | 3734 |
| JW2667 | alaS | alanyl-tRNA synthetase | GO:0005737 cytoplasm | -0.303 | 0 | 0 | 50 | 3647 |
| JW0031 | carB | carbamoyl-phosphate synthase large subunit | 0 | -0.162 | 0 | 0 | 55 | 3623 |
| JW0114 | acnB | bifunctional aconitate hydratase 2 - - 2-methylisocitrate dehydratase | 0 | -0.117 | 0 | 0 | 46 | 3579 |
| JW1268 | acnA | aconitate hydratase 1 | 0 | -0.234 | 0 | 0 | 48 | 3371 |
| JW1228 | adhE | fused acetaldehyde-CoA dehydrogenase - - iron-dependent alcohol dehydrogenase - - pyruvate- | 0 | -0.066 | 0 | 0 | 46 | 3336 |
| JW3302 | fusA | protein chain elongation factor EF-G | GO:0005737 cytoplasm | -0.286 | 0 | 0 | 38 | 3283 |
| JW0886 | pflB | pyruvate formate lyase I | GO:0005737 cytoplasm | -0.380 | 0 | 0 | 41 | 3272 |
| JW3914 | katG | catalase/hydroperoxidase HPI(I) | 0 | -0.372 | 0 | 0 | 42 | 3092 |
| JW0894 | rpsA | 30S ribosomal subunit protein S1 | GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm | -0.300 | 0 | 0 | 39 | 3008 |
| JW0715 | sucA | 2-oxoglutarate decarboxylase, thiamin-requiring | 0 | -0.441 | 0 | 0 | 44 | 3006 |
| JW1703 | pheT | phenylalanine tRNA synthetase, beta subunit | GO:0005737 cytoplasm | -0.097 | 0 | 0 | 44 | 2971 |
| JW5689 | malP | maltodextrin phosphorylase | 0 | -0.348 | 0 | 0 | 44 | 2957 |
| JW0096 | secA | preprotein translocase subunit, ATPase that targets protein precursors to the SecYE core translocon | GO:0005737 cytoplasm | -0.467 | 0 | 0 | 44 | 2926 |
| JW3530 | glyS | glycine tRNA synthetase, beta subunit | GO:0005737 cytoplasm | -0.219 | 0 | 0 | 38 | 2910 |
| JW0915 | pepN | aminopeptidase N | 0 | -0.325 | 0 | 0 | 41 | 2844 |

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|--------|------|--|---|--------|---|---|----|------|
| JW4103 | groL | Cpn60 chaperonin GroEL, large subunit of GroESL | GO:0005737 cytoplasm | -0.009 | 0 | 0 | 35 | 2832 |
| JW0024 | ileS | isoleucyl-tRNA synthetase | GO:0005737 cytoplasm | -0.263 | 0 | 0 | 43 | 2798 |
| JW4215 | valS | valyl-tRNA synthetase | GO:0005737 cytoplasm | -0.380 | 0 | 0 | 48 | 2731 |
| JW3974 | aceB | malate synthase A | GO:0005737 cytoplasm | -0.316 | 0 | 0 | 36 | 2709 |
| JW0429 | lon | DNA-binding ATP-dependent protease | GO:0005737 cytoplasm | -0.312 | 0 | 0 | 44 | 2703 |
| JW3928 | ppc | phosphoenolpyruvate carboxylase | GO:0005737 cytoplasm | -0.277 | 0 | 0 | 49 | 2676 |
| JW4354 | yjiK | fused predicted transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.478 | 0 | 0 | 37 | 2675 |
| JW1855 | aspS | aspartyl-tRNA synthetase | GO:0005737 cytoplasm | -0.265 | 0 | 0 | 39 | 2647 |
| JW2225 | gyrA | DNA gyrase (type II topoisomerase), subunit A | GO:0005737 cytoplasm | -0.240 | 0 | 0 | 43 | 2642 |
| JW0637 | leuS | leucyl-tRNA synthetase | GO:0005737 cytoplasm | -0.368 | 0 | 0 | 45 | 2627 |
| JW3137 | infB | fused protein chain initiation factor 2, | GO:0005737 cytoplasm | -0.533 | 0 | 0 | 36 | 2600 |
| JW0462 | htpG | molecular chaperone HSP90 family | 0 | -0.524 | 0 | 0 | 35 | 2594 |
| JW3970 | purH | fused IMP cyclohydrolase -!- phosphoribosylaminoimidazolecarboxamide formyltransferase | GO:0005737 cytoplasm | -0.126 | 0 | 0 | 35 | 2571 |
| JW1488 | gadB | glutamate decarboxylase B, PLP-dependent | GO:0005737 cytoplasm | -0.297 | 0 | 0 | 32 | 2557 |
| JW1772 | yeaG | conserved protein with nucleoside triphosphate hydrolase domain | 0 | -0.529 | 0 | 0 | 37 | 2549 |
| JW1071 | rne | fused ribonucleaseE endoribonuclease -!- scaffold for formation of degradosome | GO:0005737 cytoplasm | -0.645 | 0 | 0 | 35 | 2493 |
| JW2278 | nuoG | NADH:ubiquinone oxidoreductase, | GO:0005737 cytoplasm | -0.318 | 0 | 0 | 36 | 2489 |
| JW3710 | atpD | F1 sector of membrane-bound ATP synthase, beta subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.118 | 1 | 0 | 27 | 2477 |
| JW0713 | sdhA | succinate dehydrogenase, flavoprotein subunit | GO:0005737 cytoplasm | -0.324 | 0 | 0 | 30 | 2450 |
| JW3712 | atpA | F1 sector of membrane-bound ATP synthase, alpha subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.045 | 1 | 0 | 29 | 2425 |
| JW3686 | tnaA | tryptophanase/L-cysteine desulfhydrase, PLP-dependent | 0 | -0.216 | 0 | 0 | 30 | 2424 |
| JW2491 | guaA | GMP synthetase (glutamine aminotransferase) | GO:0005737 cytoplasm | -0.096 | 0 | 0 | 33 | 2407 |
| JW0172 | yaeT | conserved protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.483 | 1 | 0 | 36 | 2390 |
| JW5375 | nuoC | NADH:ubiquinone oxidoreductase, chain C,D | GO:0005737 cytoplasm | -0.307 | 0 | 0 | 33 | 2368 |
| JW0907 | mukB | fused chromosome partitioning proteins | 0 | -0.599 | 0 | 0 | 45 | 2361 |
| JW0111 | aceF | pyruvate dehydrogenase, dihydrolipoyltransacetylase component | 0 | 0.004 | 1 | 0 | 30 | 2348 |

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|--------|------|---|---|--------|---|---|----|------|
| JW2447 | maeB | fused malic enzyme predicted oxidoreductase - - predicted phosphotransacetylase | 0 | 0.054 | 1 | 0 | 33 | 2339 |
| JW3835 | polA | fused DNA polymerase I 5'->3' exonuclease - - 3'->5' polymerase - - 3'- >5' exonuclease | GO:0005737 cytoplasm | -0.264 | 0 | 0 | 38 | 2333 |
| JW5625 | gyrB | DNA gyrase, subunit B | GO:0005737 cytoplasm | -0.454 | 0 | 0 | 39 | 2326 |
| JW2449 | tktB | transketolase 2, thiamin-binding | 0 | -0.309 | 0 | 0 | 32 | 2316 |
| JW2101 | metG | methionyl-tRNA synthetase | GO:0005737 cytoplasm | -0.303 | 0 | 0 | 33 | 2311 |
| JW3138 | nusA | transcription termination/antitermination L factor | GO:0005737 cytoplasm | -0.278 | 0 | 0 | 27 | 2283 |
| JW0190 | proS | prolyl-tRNA synthetase | GO:0005737 cytoplasm | -0.243 | 0 | 0 | 32 | 2269 |
| JW2409 | ptsI | PEP-protein phosphotransferase of PTS system (enzyme I) | 0 | -0.120 | 0 | 0 | 30 | 2264 |
| JW4090 | lysU | lysine tRNA synthetase, inducible | GO:0005737 cytoplasm | -0.399 | 0 | 0 | 33 | 2257 |
| JW1266 | topA | DNA topoisomerase I, omega subunit | GO:0005737 cytoplasm | -0.609 | 0 | 0 | 38 | 2246 |
| JW1666 | pykF | pyruvate kinase I | 0 | -0.082 | 0 | 0 | 28 | 2240 |
| JW1604 | fumA | aerobic Class I fumarate hydratase (fumarase A) | 0 | -0.368 | 0 | 0 | 27 | 2211 |
| JW3366 | pck | phosphoenolpyruvate carboxykinase | 0 | -0.315 | 0 | 0 | 26 | 2207 |
| JW4115 | frdA | fumarate reductase (anaerobic) catalytic and NAD/flavoprotein subunit | GO:0005737 cytoplasm | -0.365 | 0 | 0 | 35 | 2196 |
| JW3975 | aceA | isocitrate lyase | GO:0005737 cytoplasm | -0.224 | 0 | 0 | 25 | 2191 |
| JW0675 | pgm | phosphoglucosmutase | GO:0005737 cytoplasm | -0.168 | 0 | 0 | 30 | 2167 |
| JW2228 | nrdA | ribonucleoside diphosphate reductase 1, alpha subunit | 0 | -0.337 | 0 | 0 | 37 | 2159 |
| JW2011 | gnd | gluconate-6-phosphate dehydrogenase, decarboxylating | 0 | -0.200 | 0 | 0 | 26 | 2157 |
| JW0955 | hyaB | hydrogenase 1, large subunit | GO:0019866 inner membrane | -0.210 | 1 | 0 | 31 | 2148 |
| JW5741 | rnR | exoribonuclease R, RNase R | 0 | -0.551 | 0 | 0 | 38 | 2137 |
| JW1709 | thrS | threonyl-tRNA synthetase | GO:0005737 cytoplasm | -0.494 | 0 | 0 | 37 | 2129 |
| JW3145 | ftsH | protease, ATP-dependent zinc-metallo | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | -0.263 | 1 | 2 | 35 | 2125 |
| JW2943 | glcB | malate synthase G | 0 | -0.327 | 0 | 0 | 31 | 2119 |
| JW3465 | prlC | oligopeptidase A | 0 | -0.416 | 0 | 0 | 32 | 2099 |
| JW0426 | tig | peptidyl-prolyl cis/trans isomerase (trigger factor) | GO:0005737 cytoplasm | -0.428 | 0 | 0 | 29 | 2097 |
| JW4135 | purA | adenylosuccinate synthetase | GO:0005737 cytoplasm | -0.200 | 0 | 0 | 26 | 2093 |
| JW1692 | pps | phosphoenolpyruvate synthase | 0 | -0.243 | 0 | 0 | 34 | 2091 |
| JW1412 | aldA | aldehyde dehydrogenase A, NAD-linked | 0 | -0.056 | 0 | 0 | 27 | 2084 |
| JW2294 | pta | phosphate acetyltransferase | 0 | -0.080 | 0 | 0 | 28 | 2073 |
| JW5851 | pnp | polynucleotide phosphorylase/polyadenylase | GO:0005737 cytoplasm | -0.169 | 0 | 0 | 31 | 2060 |
| JW1843 | pykA | pyruvate kinase II | 0 | -0.025 | 0 | 0 | 29 | 2031 |
| JW3897 | glpK | glycerol kinase | 0 | -0.292 | 0 | 0 | 28 | 2014 |
| JW3841 | glnA | glutamine synthetase | GO:0005737 cytoplasm | -0.292 | 0 | 0 | 27 | 2011 |

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|--------|------|---|--|--------|---|---|----|------|
| JW1372 | ydbK | fused predicted Fe-S subunit of pyruvate-flavodoxin oxidoreductase | 0 | -0.191 | 0 | 0 | 40 | 1991 |
| JW0866 | clpA | ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine protease, chaperone activity | GO:0005737 cytoplasm | -0.298 | 0 | 0 | 31 | 1986 |
| JW1235 | oppA | oligopeptide transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597 periplasmic space | -0.436 | 1 | 1 | 26 | 1977 |
| JW4019 | uvrA | ATPase and DNA damage recognition protein of nucleotide excision repair excinuclease UvrABC | GO:0005737 cytoplasm | -0.289 | 0 | 0 | 37 | 1971 |
| JW1865 | argS | arginyl-tRNA synthetase | GO:0005737 cytoplasm | -0.258 | 0 | 0 | 30 | 1969 |
| JW3707 | glmS | L-glutamine:D-fructose-6-phosphate aminotransferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 | -0.101 | 0 | 0 | 28 | 1962 |
| JW2395 | gltX | glutamyl-tRNA synthetase | GO:0005737 cytoplasm | -0.528 | 0 | 0 | 28 | 1932 |
| JW0717 | sucC | succinyl-CoA synthetase, beta subunit | 0 | 0.024 | 1 | 0 | 24 | 1918 |
| JW0431 | ppiD | peptidyl-prolyl cis-trans isomerase (rotamase D) | 0 | -0.405 | 1 | 1 | 32 | 1893 |
| JW2893 | pgk | phosphoglycerate kinase | GO:0005737 cytoplasm | 0.072 | 1 | 0 | 21 | 1880 |
| JW3994 | malE | maltose transporter subunit -!- periplasmic-binding component of ABC | GO:0042597 periplasmic space | -0.251 | 0 | 0 | 23 | 1869 |
| JW2535 | glyA | serine hydroxymethyltransferase | GO:0005737 cytoplasm | -0.233 | 0 | 0 | 23 | 1860 |
| JW3301 | tufA | protein chain elongation factor EF-Tu (duplicate of tufB) | GO:0005737 cytoplasm | -0.196 | 0 | 0 | 24 | 1859 |
| JW1606 | ydgA | conserved protein | 0 | -0.299 | 1 | 1 | 22 | 1848 |
| JW2637 | gabT | 4-aminobutyrate aminotransferase, PLP-dependent | 0 | 0.002 | 1 | 0 | 26 | 1848 |
| JW0666 | glnS | glutamyl-tRNA synthetase | GO:0005737 cytoplasm | -0.518 | 0 | 0 | 30 | 1846 |
| JW0053 | imp | exported protein required for envelope biosynthesis and integrity | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.657 | 1 | 0 | 31 | 1837 |
| JW0165 | tsf | protein chain elongation factor EF-Ts | GO:0005737 cytoplasm | -0.118 | 0 | 0 | 23 | 1821 |
| JW2858 | lysS | lysine tRNA synthetase, constitutive | GO:0005737 cytoplasm | -0.396 | 0 | 0 | 27 | 1819 |
| JW3865 | fdoG | formate dehydrogenase-O, large | GO:0005737 cytoplasm | -0.346 | 0 | 0 | 30 | 1819 |
| JW0599 | ahpF | alkyl hydroperoxide reductase, F52a subunit, FAD/NAD(P)-binding | 0 | -0.123 | 0 | 0 | 26 | 1816 |
| JW1100 | mfd | transcription-repair coupling factor | GO:0005737 cytoplasm | -0.292 | 0 | 0 | 41 | 1783 |
| JW2750 | eno | enolase | GO:0005737 cytoplasm | -0.158 | 0 | 0 | 20 | 1783 |
| JW2194 | napA | nitrate reductase, periplasmic, large subunit | GO:0042597 periplasmic space | -0.438 | 0 | 0 | 32 | 1771 |
| JW2751 | pyrG | CTP synthetase | 0 | -0.139 | 1 | 1 | 29 | 1770 |
| JW4030 | acs | bifunctional acetyl-CoA synthetase -!- propionyl-CoA synthetase | 0 | -0.291 | 0 | 0 | 28 | 1764 |
| JW3756 | rho | transcription termination factor | GO:0005737 cytoplasm | -0.298 | 0 | 0 | 26 | 1742 |
| JW5238 | sfcA | malate dehydrogenase, NAD-requiring (malic enzyme) | 0 | -0.180 | 0 | 0 | 25 | 1738 |

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|--------|------|--|--|--------|---|---|----|------|
| JW2137 | mglB | methyl-galactoside transporter subunit -! periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.273 | 1 | 1 | 22 | 1735 |
| JW0911 | aspC | aspartate aminotransferase, PLP-dependent | GO:0005737 cytoplasm | -0.202 | 0 | 0 | 27 | 1723 |
| JW3205 | mdh | malate dehydrogenase, NAD(P)-binding | 0 | 0.194 | 1 | 0 | 19 | 1715 |
| JW1122 | icd | e14 prophage; isocitrate dehydrogenase, specific for NADP+ | 0 | -0.154 | 0 | 0 | 27 | 1711 |
| JW5551 | sthA | pyridine nucleotide transhydrogenase, soluble | GO:0005737 cytoplasm | -0.227 | 0 | 0 | 23 | 1703 |
| JW4346 | deoB | phosphopentomutase | 0 | -0.271 | 0 | 0 | 24 | 1699 |
| JW0112 | lpd | lipoamide dehydrogenase, E3 component is part of three enzyme | GO:0005737 cytoplasm | -0.011 | 0 | 0 | 22 | 1684 |
| JW0058 | hepA | RNA polymerase-associated helicase protein (ATPase and RNA polymerase recycling factor) | 0 | -0.355 | 0 | 0 | 34 | 1680 |
| JW2499 | ispG | 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase | 0 | -0.157 | 0 | 0 | 25 | 1679 |
| JW0157 | degP | serine endoprotease (protease Do), membrane-associated | GO:0042597 periplasmic space | -0.067 | 0 | 0 | 21 | 1673 |
| JW5118 | dmsA | dimethyl sulfoxide reductase, anaerobic, subunit A | GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner | -0.436 | 1 | 0 | 31 | 1667 |
| JW4345 | deoA | thymidine phosphorylase | 0 | 0.011 | 1 | 0 | 24 | 1660 |
| JW5401 | quaB | IMP dehydrogenase | GO:0005737 cytoplasm | -0.098 | 0 | 0 | 21 | 1654 |
| JW3902 | hslU | molecular chaperone and ATPase component of HslUV protease | GO:0005737 cytoplasm | -0.363 | 0 | 0 | 26 | 1652 |
| JW0913 | asnS | asparaginyl tRNA synthetase | GO:0005737 cytoplasm | -0.257 | 0 | 0 | 25 | 1641 |
| JW5344 | fbaB | fructose-bisphosphate aldolase class I | 0 | -0.148 | 0 | 0 | 23 | 1627 |
| JW3513 | dppA | dipeptide transporter -! periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.463 | 0 | 0 | 22 | 1621 |
| JW1905 | fliY | cystine transporter subunit -! periplasmic-binding component of ABC | GO:0042597 periplasmic space | -0.302 | 0 | 0 | 22 | 1616 |
| JW4001 | plsB | glycerol-3-phosphate O-acyltransferase | GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner | -0.179 | 1 | 0 | 32 | 1614 |
| JW1216 | narH | nitrate reductase 1, beta (Fe-S) subunit | GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner | -0.477 | 1 | 0 | 26 | 1610 |
| JW0855 | poxB | pyruvate dehydrogenase (pyruvate oxidase), thiamin-dependent, FAD- | GO:0005737 cytoplasm | 0.008 | 1 | 0 | 23 | 1599 |
| JW4194 | pmbA | predicted peptidase required for the maturation and secretion of the antibiotic peptide MccB17 | GO:0005737 cytoplasm | -0.160 | 0 | 0 | 22 | 1597 |
| JW0710 | glfA | citrate synthase | 0 | -0.231 | 0 | 0 | 21 | 1596 |
| JW0317 | yahK | predicted oxidoreductase, Zn-dependent and NAD(P)-binding | 0 | -0.183 | 0 | 0 | 23 | 1595 |
| JW0007 | talB | transaldolase B | GO:0005737 cytoplasm | -0.210 | 0 | 0 | 21 | 1593 |
| JW1531 | dcp | dipeptidyl carboxypeptidase II | 0 | -0.331 | 0 | 0 | 25 | 1591 |

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|--------|------|---|--|--------|---|---|----|------|
| JW2636 | gabD | succinate-semialdehyde dehydrogenase I, NADP-dependent | 0 | -0.071 | 0 | 0 | 22 | 1584 |
| JW1841 | zwf | glucose-6-phosphate dehydrogenase | GO:0005737 cytoplasm | -0.374 | 0 | 0 | 25 | 1578 |
| JW3179 | gltB | glutamate synthase, large subunit | 0 | -0.224 | 0 | 0 | 33 | 1566 |
| JW2403 | ligA | DNA ligase, NAD(+)-dependent | GO:0005737 cytoplasm | -0.137 | 0 | 0 | 28 | 1545 |
| JW4220 | yjgR | predicted ATPase | 0 | -0.150 | 0 | 0 | 25 | 1540 |
| JW5478 | tktA | transketolase 1, thiamin-binding | 0 | -0.228 | 0 | 0 | 25 | 1535 |
| JW0876 | serS | seryl-tRNA synthetase, also charges selenocysteinyl-tRNA with serine | GO:0005737 cytoplasm | -0.447 | 0 | 0 | 25 | 1531 |
| JW2082 | gatZ | D-tagatose 1,6-bisphosphate aldolase 2, subunit | 0 | -0.121 | 0 | 0 | 18 | 1529 |
| JW1721 | katE | hydroperoxidase HPil(III) (catalase) | GO:0005737 cytoplasm | -0.498 | 0 | 0 | 25 | 1528 |
| JW2766 | ygdH | conserved protein | 0 | -0.107 | 0 | 0 | 22 | 1525 |
| JW2486 | ppk | polyphosphate kinase, component of RNA degradosome | 0 | -0.341 | 0 | 0 | 31 | 1517 |
| JW3140 | argG | argininosuccinate synthetase | GO:0005737 cytoplasm | -0.371 | 0 | 0 | 25 | 1513 |
| JW3481 | mdtE | multidrug resistance efflux transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.207 | 1 | 0 | 19 | 1507 |
| JW0658 | miaB | isopentenyl-adenosine A37 tRNA methylthiolase | GO:0005737 cytoplasm | -0.378 | 0 | 0 | 24 | 1501 |
| JW0797 | dps | Fe-binding and storage protein | GO:0005737 cytoplasm | -0.214 | 0 | 0 | 19 | 1498 |
| JW2320 | fabB | 3-oxoacyl-[acyl-carrier-protein] synthase | GO:0005737 cytoplasm | 0.008 | 1 | 0 | 17 | 1497 |
| JW1677 | ydiJ | predicted FAD-linked oxidoreductase | 0 | -0.160 | 0 | 0 | 38 | 1496 |
| JW1186 | treA | periplasmic trehalase | GO:0042597 periplasmic space | -0.580 | 0 | 0 | 25 | 1493 |
| JW5905 | hrpA | ATP-dependent helicase | GO:0005737 cytoplasm | -0.439 | 0 | 0 | 32 | 1487 |
| JW4099 | aspA | aspartate ammonia-lyase | GO:0005737 cytoplasm | -0.066 | 0 | 0 | 21 | 1479 |
| JW1035 | mdoG | glucan biosynthesis protein, periplasmic | GO:0042597 periplasmic space | -0.541 | 0 | 0 | 23 | 1470 |
| JW3592 | kbl | glycine C-acetyltransferase | 0 | -0.049 | 0 | 0 | 19 | 1469 |
| JW3594 | rfaD | ADP-L-glycero-D-mannoheptose-6-epimerase, NAD(P)-binding | 0 | -0.284 | 0 | 0 | 18 | 1469 |
| JW2498 | hisS | histidyl tRNA synthetase | GO:0005737 cytoplasm | -0.272 | 0 | 0 | 22 | 1465 |
| JW4347 | deoD | purine-nucleoside phosphorylase | 0 | 0.070 | 1 | 0 | 19 | 1465 |
| JW0428 | clpX | ATPase and specificity subunit of ClpX-ClpP ATP-dependent serine protease | GO:0005737 cytoplasm | -0.238 | 0 | 0 | 21 | 1464 |
| JW0093 | ftsZ | GTP-binding tubulin-like cell division | GO:0005737 cytoplasm | -0.005 | 0 | 0 | 17 | 1463 |
| JW5571 | bipA | GTP-binding protein | 0 | -0.298 | 0 | 0 | 23 | 1462 |
| JW3580 | lldD | L-lactate dehydrogenase, FMN-linked | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.037 | 1 | 0 | 22 | 1454 |
| JW4171 | cpdB | 2':3'-cyclic-nucleotide 2'-phosphodiesterase | GO:0005737 cytoplasm | -0.285 | 0 | 0 | 24 | 1446 |
| JW2504 | yfhM | conserved protein | 0 | -0.321 | 0 | 0 | 30 | 1438 |
| JW2293 | ackA | acetate kinase A and propionate kinase | GO:0005737 cytoplasm | -0.047 | 0 | 0 | 17 | 1430 |
| JW2448 | talA | transaldolase A | 0 | -0.315 | 0 | 0 | 20 | 1425 |
| JW0227 | pepD | aminoacyl-histidine dipeptidase (peptidase D) | GO:0005737 cytoplasm | -0.146 | 0 | 0 | 19 | 1421 |
| JW2970 | yghZ | aldo-keto reductase | 0 | -0.389 | 0 | 0 | 21 | 1420 |

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|--------|------|--|---|--------|---|----|----|------|
| JW3039 | rpoD | RNA polymerase, sigma 70 (sigma D) factor | GO:0005737 cytoplasm | -0.589 | 0 | 0 | 22 | 1413 |
| JW3969 | purD | phosphoribosylglycinamide synthetase phosphoribosylamine-glycine ligase | GO:0005737 cytoplasm | -0.071 | 0 | 0 | 19 | 1409 |
| JW2962 | hybC | hydrogenase 2, large subunit | GO:0019866 inner membrane | -0.140 | 1 | 0 | 23 | 1408 |
| JW3143 | glmM | phosphoglucosamine mutase | GO:0009274 cell wall (sensu Bacteria) - - GO:0009274 cell wall (sensu Bacteria) - - GO:0005737 | 0.013 | 1 | 0 | 22 | 1404 |
| JW2869 | bglA | 6-phospho-beta-glucosidase A | 0 | -0.452 | 0 | 0 | 22 | 1398 |
| JW5867 | aidB | isovaleryl CoA dehydrogenase | 0 | -0.136 | 0 | 0 | 23 | 1398 |
| JW2909 | metK | methionine adenosyltransferase 1 | GO:0005737 cytoplasm | -0.189 | 0 | 0 | 19 | 1391 |
| JW3482 | mdtF | multidrug transporter, RpoS-dependent | GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | 0.318 | 1 | 11 | 23 | 1388 |
| JW1279 | rnb | ribonuclease II | 0 | -0.277 | 0 | 0 | 24 | 1387 |
| JW2569 | pssA | phosphatidylserine synthase (CDP-diacylglycerol-serine O-phosphatidyltransferase) | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane | -0.429 | 1 | 0 | 26 | 1380 |
| JW5907 | yncB | predicted oxidoreductase, Zn-dependent and NAD(P)-binding | 0 | -0.268 | 0 | 0 | 16 | 1379 |
| JW1178 | dadA | D-amino acid dehydrogenase | 0 | -0.216 | 0 | 0 | 19 | 1377 |
| JW2136 | mglA | fused methyl-galactoside transporter subunitsI - - ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.155 | 0 | 0 | 24 | 1377 |
| JW0001 | thrA | fused aspartokinase I - - homoserine dehydrogenase I | GO:0005737 cytoplasm | 0.035 | 1 | 0 | 22 | 1374 |
| JW0473 | copA | copper transporter | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 0.205 | 1 | 8 | 24 | 1367 |
| JW2279 | nuoF | NADH:ubiquinone oxidoreductase, | GO:0005737 cytoplasm | -0.318 | 0 | 0 | 20 | 1364 |
| JW0052 | surA | peptidyl-prolyl cis-trans isomerase (PPIase) | GO:0009279 external outer membrane (sensu Gram-negative | -0.382 | 1 | 0 | 19 | 1360 |
| JW2553 | lepA | GTP binding membrane protein | 0 | -0.200 | 0 | 0 | 22 | 1359 |
| JW2905 | speA | biosynthetic arginine decarboxylase, PLP-binding | GO:0042597 periplasmic space | -0.296 | 0 | 0 | 22 | 1359 |
| JW1117 | purB | adenylosuccinate lyase | GO:0005737 cytoplasm | -0.243 | 0 | 0 | 24 | 1356 |
| JW2133 | yeiT | predicted oxidoreductase | 0 | -0.089 | 0 | 0 | 18 | 1349 |
| JW0762 | uvrB | excinulease of nucleotide excision repair, DNA damage recognition | GO:0005737 cytoplasm | -0.358 | 0 | 0 | 29 | 1342 |
| JW3730 | rbsB | D-ribose transporter subunit - - periplasmic-binding compoent of ABC superfamily | GO:0042597 periplasmic space | -0.031 | 0 | 0 | 16 | 1341 |
| JW5100 | tolB | periplasmic protein | GO:0042597 periplasmic space | -0.215 | 0 | 0 | 15 | 1326 |
| JW4204 | pyrB | aspartate carbamoyltransferase, catalytic subunit | GO:0005737 cytoplasm | -0.105 | 0 | 0 | 19 | 1322 |

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|--------|------|--|--|--------|---|----|----|------|
| JW0890 | serC | 3-phosphoserine/phosphohydroxythreonine aminotransferase | GO:0005737 cytoplasm | -0.113 | 0 | 0 | 18 | 1313 |
| JW5312 | otsA | trehalose-6-phosphate synthase | 0 | -0.281 | 0 | 0 | 21 | 1311 |
| JW5873 | prfC | peptide chain release factor RF-3 | GO:0005737 cytoplasm | -0.326 | 0 | 0 | 22 | 1308 |
| JW4344 | deoC | 2-deoxyribose-5-phosphate aldolase, NAD(P)-linked | GO:0005737 cytoplasm | -0.014 | 0 | 0 | 17 | 1307 |
| JW2317 | pdxB | erythronate-4-phosphate | 0 | -0.037 | 0 | 0 | 26 | 1305 |
| JW1198 | prsA | phosphoribosylpyrophosphate synthase | 0 | 0.096 | 1 | 0 | 14 | 1304 |
| JW3224 | accC | acetyl-CoA carboxylase, biotin carboxylase subunit | GO:0005737 cytoplasm | -0.173 | 0 | 0 | 21 | 1299 |
| JW1420 | mdoD | glucan biosynthesis protein, periplasmic | GO:0042597 periplasmic space | -0.414 | 0 | 0 | 23 | 1296 |
| JW1596 | ydgH | predicted protein | 0 | -0.324 | 0 | 0 | 18 | 1291 |
| JW1737 | astC | succinylornithine transaminase, PLP-dependent | 0 | -0.064 | 0 | 0 | 20 | 1287 |
| JW5427 | ygaT | predicted protein | 0 | -0.375 | 0 | 0 | 22 | 1286 |
| JW3063 | uxaC | uronate isomerase | 0 | -0.429 | 0 | 0 | 30 | 1285 |
| JW4198 | treC | trehalose-6-P hydrolase | GO:0005737 cytoplasm | -0.560 | 0 | 0 | 22 | 1281 |
| JW0451 | acrB | multidrug efflux system protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.266 | 1 | 11 | 25 | 1280 |
| JW3073 | yqjG | predicted S-transferase | 0 | -0.368 | 0 | 0 | 18 | 1280 |
| JW0987 | agp | glucose-1-phosphatase/inositol phosphatase | GO:0042597 periplasmic space | -0.325 | 0 | 0 | 17 | 1279 |
| JW2309 | purF | amidophosphoribosyltransferase | GO:0005737 cytoplasm | -0.243 | 0 | 0 | 19 | 1277 |
| JW3574 | mtlD | mannitol-1-phosphate dehydrogenase, NAD(P)-binding | 0 | -0.040 | 0 | 0 | 20 | 1272 |
| JW1113 | pepT | peptidase T | 0 | -0.215 | 0 | 0 | 21 | 1267 |
| JW3890 | tpiA | triosephosphate isomerase | 0 | 0.010 | 1 | 0 | 18 | 1267 |
| JW5499 | dkgA | 2,5-diketo-D-gluconate reductase A | GO:0005737 cytoplasm | -0.375 | 0 | 0 | 21 | 1267 |
| JW1819 | prc | carboxy-terminal protease for penicillin-binding protein 3 | GO:0009274 cell wall (sensu Bacteria) | -0.482 | 0 | 0 | 24 | 1259 |
| JW3573 | mtlA | fused mannitol-specific PTS enzyme IIABC components | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.329 | 1 | 8 | 17 | 1249 |
| JW5536 | arcB | hybrid sensory histidine kinase in two-component regulatory system with ArcA | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.251 | 1 | 2 | 21 | 1249 |
| JW2866 | ygfZ | predicted folate-dependent regulatory protein | 0 | -0.247 | 0 | 0 | 17 | 1246 |
| JW3429 | ftsY | fused Signal Recognition Particle (SRP) receptor | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.335 | 1 | 0 | 20 | 1245 |
| JW3391 | glgP | glycogen phosphorylase | GO:0005737 cytoplasm | -0.339 | 0 | 0 | 28 | 1243 |
| JW3222 | yhdH | predicted oxidoreductase, Zn-dependent and NAD(P)-binding | 0 | -0.004 | 0 | 0 | 15 | 1242 |
| JW2306 | hisJ | histidine/lysine/arginine/ornithine transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.299 | 1 | 1 | 16 | 1237 |
| JW2663 | gshA | gamma-glutamate-cysteine ligase | 0 | -0.310 | 0 | 0 | 22 | 1234 |

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|--------|------|---|--|--------|---|---|----|------|
| JW3024 | rfaE | fused heptose 7-phosphate kinase -!- heptose 1-phosphate adenylyltransferase | 0 | -0.004 | 0 | 0 | 21 | 1233 |
| JW4355 | slt | lytic murein transglycosylase, soluble | GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597 | -0.503 | 0 | 0 | 26 | 1229 |
| JW2978 | yqhD | alcohol dehydrogenase, NAD(P)-dependent | 0 | -0.129 | 0 | 0 | 20 | 1226 |
| JW5277 | pheS | phenylalanine tRNA synthetase, alpha subunit | GO:0005737 cytoplasm | -0.324 | 0 | 0 | 18 | 1223 |
| JW3418 | ugpB | glycerol-3-phosphate transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.503 | 0 | 0 | 21 | 1222 |
| JW0469 | ushA | bifunctional UDP-sugar hydrolase -!- 5'-nucleotidase | GO:0005737 cytoplasm | -0.411 | 0 | 0 | 19 | 1216 |
| JW0718 | sucD | succinyl-CoA synthetase, NAD(P)-binding, alpha subunit | 0 | 0.162 | 1 | 0 | 16 | 1215 |
| JW2120 | bglX | beta-D-glucoside glucosylhydrolase, periplasmic | GO:0042597 periplasmic space | -0.260 | 0 | 0 | 25 | 1215 |
| JW3587 | gpml | phosphoglycerate mutase III, cofactor-independent | GO:0005737 cytoplasm | -0.195 | 0 | 0 | 18 | 1215 |
| JW0515 | cysS | cysteine tRNA synthetase | GO:0005737 cytoplasm | -0.415 | 0 | 0 | 18 | 1214 |
| JW3203 | degQ | serine endoprotease, periplasmic | 0 | 0.055 | 1 | 1 | 14 | 1211 |
| JW2514 | iscS | cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent | 0 | -0.273 | 0 | 0 | 20 | 1209 |
| JW0233 | proA | gamma-glutamylphosphate reductase | GO:0005737 cytoplasm | -0.005 | 0 | 0 | 18 | 1208 |
| JW0398 | secD | SecYEG protein translocase auxiliary subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.116 | 1 | 6 | 20 | 1208 |
| JW1206 | kdsA | 3-deoxy-D-manno-octulosonate 8-phosphate synthase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.028 | 0 | 0 | 18 | 1208 |
| JW1653 | cfa | cyclopropane fatty acyl phospholipid synthase (unsaturated-phospholipid methyltransferase) | 0 | -0.313 | 0 | 0 | 21 | 1205 |
| JW0657 | ybeZ | predicted protein with nucleoside triphosphate hydrolase domain | 0 | -0.370 | 0 | 0 | 19 | 1203 |
| JW3684 | trmE | GTPase | 0 | -0.095 | 0 | 0 | 19 | 1202 |
| JW1239 | oppF | oligopeptide transporter subunit -!- ATP-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.041 | 0 | 0 | 20 | 1201 |
| JW1095 | ndh | respiratory NADH dehydrogenase 2/cupric reductase | GO:0005737 cytoplasm | -0.129 | 0 | 0 | 20 | 1200 |
| JW1603 | fumC | fumarate hydratase (fumarase C), aerobic Class II | 0 | -0.133 | 0 | 0 | 17 | 1199 |
| JW1327 | uspE | stress-induced protein | 0 | -0.207 | 0 | 0 | 18 | 1189 |
| JW3257 | rpoA | RNA polymerase, alpha subunit | GO:0005737 cytoplasm | -0.228 | 0 | 0 | 18 | 1184 |
| JW4312 | hsdM | DNA methylase M | GO:0005737 cytoplasm | -0.528 | 0 | 0 | 22 | 1181 |
| JW3370 | yhgF | predicted transcriptional accessory | 0 | -0.334 | 0 | 0 | 25 | 1179 |

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|--------|------|--|---|--------|---|---|----|------|
| JW3467 | gor | glutathione oxidoreductase | GO:0005737 cytoplasm | -0.112 | 0 | 0 | 18 | 1179 |
| JW0738 | gpmA | phosphoglyceromutase 1 | 0 | -0.568 | 0 | 0 | 18 | 1173 |
| JW4285 | uxuA | mannonate hydrolase | 0 | -0.402 | 0 | 0 | 20 | 1169 |
| JW3393 | glgC | glucose-1-phosphate | GO:0005737 cytoplasm | -0.267 | 0 | 0 | 17 | 1166 |
| JW2424 | yfeX | conserved protein | 0 | -0.322 | 0 | 0 | 18 | 1161 |
| JW0739 | galM | galactose-1-epimerase (mutarotase) | GO:0042597 periplasmic space | -0.466 | 0 | 0 | 14 | 1158 |
| JW2972 | yghA | predicted glutathionylspermidine synthase, with NAD(P)-binding Rossmann-fold domain | 0 | -0.178 | 0 | 0 | 16 | 1158 |
| JW3947 | rplA | 50S ribosomal subunit protein L1 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.109 | 0 | 0 | 15 | 1155 |
| JW1322 | mppA | murein tripeptide (L-ala-gamma-D-glutamyl-meso-DAP) transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597 periplasmic space | -0.339 | 0 | 0 | 20 | 1154 |
| JW1510 | lsrF | predicted aldolase | 0 | -0.097 | 0 | 0 | 15 | 1154 |
| JW0232 | proB | gamma-glutamate kinase | GO:0005737 cytoplasm | 0.007 | 1 | 0 | 20 | 1153 |
| JW1194 | ychF | predicted GTP-binding protein | 0 | -0.163 | 0 | 0 | 16 | 1149 |
| JW3116 | yraM | conserved protein | 0 | -0.272 | 0 | 0 | 23 | 1149 |
| JW0150 | hemL | glutamate-1-semialdehyde aminotransferase (aminomutase) | 0 | 0.202 | 1 | 0 | 16 | 1146 |
| JW1768 | gapA | glyceraldehyde-3-phosphate dehydrogenase A | GO:0005737 cytoplasm | -0.133 | 0 | 0 | 20 | 1145 |
| JW3706 | pstS | phosphate transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.217 | 1 | 1 | 19 | 1138 |
| JW1605 | manA | mannose-6-phosphate isomerase | GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.126 | 0 | 0 | 15 | 1137 |
| JW2797 | ptsP | fused PEP-protein phosphotransferase (enzyme I) of PTS system | 0 | -0.094 | 0 | 0 | 23 | 1137 |
| JW0823 | dacC | D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6a) | GO:0042597 periplasmic space | -0.078 | 0 | 0 | 15 | 1136 |
| JW0714 | sdhB | succinate dehydrogenase, FeS subunit | GO:0005737 cytoplasm | -0.299 | 0 | 0 | 15 | 1134 |
| JW3775 | hemX | uroporphyrinogen III methylase | 0 | -0.435 | 1 | 1 | 17 | 1134 |
| JW2560 | srmB | ATP-dependent RNA helicase | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.557 | 0 | 0 | 20 | 1133 |
| JW5092 | gltl | glutamate and aspartate transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.473 | 0 | 0 | 15 | 1133 |
| JW3563 | selB | selenocysteinyl-tRNA-specific translation factor | GO:0005737 cytoplasm | -0.354 | 0 | 0 | 23 | 1132 |
| JW5414 | ffh | Signal Recognition Particle (SRP) component with 4.5S RNA (ffs) | 0 | -0.243 | 0 | 0 | 20 | 1132 |
| JW3561 | aldB | aldehyde dehydrogenase B | 0 | -0.116 | 0 | 0 | 15 | 1130 |

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|--------|------|--|--|--------|---|---|----|------|
| JW4011 | qor | quinone oxidoreductase, NADPH-dependent | 0 | -0.059 | 0 | 0 | 17 | 1130 |
| JW0229 | frsA | hydrolase, binds to enzyme IIA(Glc) | 0 | -0.330 | 0 | 0 | 22 | 1128 |
| JW2026 | rfbB | dTDP-glucose 4,6 dehydratase, NAD(P)-binding | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.449 | 0 | 0 | 19 | 1128 |
| JW0409 | yajO | predicted oxidoreductase, NAD(P)- | 0 | -0.404 | 0 | 0 | 19 | 1127 |
| JW4092 | cadA | lysine decarboxylase 1 | GO:0005737 cytoplasm | -0.260 | 0 | 0 | 24 | 1120 |
| JW3711 | atpG | F1 sector of membrane-bound ATP synthase, gamma subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.227 | 1 | 0 | 21 | 1116 |
| JW2461 | purC | phosphoribosylaminoimidazole-succinocarboxamide synthetase | GO:0005737 cytoplasm | -0.370 | 0 | 0 | 16 | 1114 |
| JW0120 | gcd | glucose dehydrogenase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.071 | 1 | 5 | 19 | 1109 |
| JW4197 | nrdD | anaerobic ribonucleoside-triphosphate reductase | 0 | -0.454 | 0 | 0 | 22 | 1104 |
| JW4132 | hflK | modulator for HflB protease specific for phage lambda cII repressor | 0 | -0.632 | 1 | 1 | 16 | 1102 |
| JW5403 | der | predicted GTP-binding protein | 0 | -0.334 | 0 | 0 | 19 | 1102 |
| JW0663 | nagA | N-acetylglucosamine-6-phosphate deacetylase | 0 | 0.080 | 1 | 0 | 17 | 1097 |
| JW2568 | yfiQ | fused predicted acyl-CoA synthetase NAD(P)-binding subunit -!- ATP-binding subunit | 0 | -0.119 | 0 | 0 | 22 | 1097 |
| JW5020 | fadE | acyl coenzyme A dehydrogenase | 0 | 0.006 | 1 | 2 | 22 | 1097 |
| JW0083 | murE | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso-diaminopimelate ligase | GO:0009274 cell wall (sensu Bacteria) | -0.051 | 0 | 0 | 18 | 1096 |
| JW0452 | acrA | multidrug efflux system | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.256 | 1 | 0 | 15 | 1092 |
| JW2233 | glpQ | periplasmic glycerophosphodiester phosphodiesterase | GO:0042597 periplasmic space | -0.553 | 0 | 0 | 19 | 1089 |
| JW2876 | pepP | proline aminopeptidase P II | 0 | -0.308 | 0 | 0 | 16 | 1089 |
| JW1729 | nadE | NAD synthetase, NH3/glutamine- | 0 | -0.370 | 0 | 0 | 15 | 1084 |
| JW2229 | nrdB | ribonucleoside diphosphate reductase 1, beta subunit, ferritin-like | 0 | -0.275 | 0 | 0 | 18 | 1084 |
| JW3396 | asd | aspartate-semialdehyde dehydrogenase, NAD(P)-binding | 0 | -0.029 | 0 | 0 | 14 | 1082 |
| JW1838 | purT | phosphoribosylglycinamide formyltransferase 2 | GO:0005737 cytoplasm | 0.056 | 1 | 0 | 15 | 1077 |
| JW2307 | argT | lysine/arginine/ornithine transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.231 | 0 | 0 | 14 | 1068 |
| JW3985 | pgi | glucosephosphate isomerase | GO:0005737 cytoplasm | -0.268 | 0 | 0 | 21 | 1067 |
| JW1750 | gdhA | glutamate dehydrogenase, NADP- | GO:0005737 cytoplasm | -0.158 | 0 | 0 | 18 | 1066 |
| JW3347 | trpS | tryptophanyl-tRNA synthetase | GO:0005737 cytoplasm | -0.320 | 0 | 0 | 16 | 1065 |
| JW0627 | dacA | D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5) | GO:0019866 inner membrane | -0.137 | 1 | 0 | 17 | 1058 |

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|--------|------|---|--|--------|---|---|----|------|
| JW2021 | glf | UDP-galactopyranose mutase, FAD/NAD(P)-binding | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) | -0.545 | 0 | 0 | 18 | 1058 |
| JW2479 | yfgC | predicted peptidase | 0 | -0.383 | 0 | 0 | 15 | 1055 |
| JW1079 | fabG | 3-oxoacyl-[acyl-carrier-protein] | GO:0005737 cytoplasm | 0.100 | 1 | 0 | 11 | 1054 |
| JW1650 | purR | DNA-binding transcriptional repressor, hypoxanthine-binding | GO:0005737 cytoplasm | -0.240 | 0 | 0 | 19 | 1054 |
| JW2121 | dld | D-lactate dehydrogenase, FAD-binding, NADH independent | GO:0005737 cytoplasm | -0.445 | 0 | 0 | 24 | 1052 |
| JW0161 | dapD | 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase | GO:0005737 cytoplasm | -0.054 | 0 | 0 | 15 | 1049 |
| JW5287 | ynjE | predicted thiosulfate sulfur transferase | 0 | -0.455 | 0 | 0 | 14 | 1048 |
| JW1078 | fabD | malonyl-CoA-[acyl-carrier-protein] transacylase | GO:0005737 cytoplasm | 0.154 | 1 | 0 | 12 | 1039 |
| JW2580 | pheA | fused chorismate mutase P -!- prephenate dehydratase | GO:0005737 cytoplasm | -0.168 | 0 | 0 | 18 | 1039 |
| JW2669 | recA | DNA strand exchange and recombination protein with protease and | GO:0005737 cytoplasm | -0.175 | 0 | 0 | 14 | 1038 |
| JW3823 | pepQ | proline dipeptidase | 0 | -0.241 | 0 | 0 | 16 | 1038 |
| JW0003 | thrC | threonine synthase | GO:0005737 cytoplasm | -0.097 | 0 | 0 | 14 | 1037 |
| JW2496 | yfgL | protein assembly complex, lipoprotein component | 0 | 0.009 | 1 | 0 | 13 | 1036 |
| JW4131 | hflX | predicted GTPase | 0 | -0.332 | 0 | 0 | 20 | 1036 |
| JW0598 | ahpC | alkyl hydroperoxide reductase, C22 subunit | 0 | -0.278 | 0 | 0 | 12 | 1033 |
| JW3979 | metH | homocysteine-N5-methyltetrahydrofolate transmethylase, | 0 | -0.249 | 0 | 0 | 23 | 1031 |
| JW1238 | oppD | oligopeptide transporter subunit -!- ATP-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.009 | 0 | 0 | 17 | 1030 |
| JW2873 | gcvT | aminomethyltransferase, tetrahydrofolate-dependent, subunit (T protein) of glycine cleavage complex | 0 | -0.159 | 0 | 0 | 15 | 1030 |
| JW3249 | fmt | 10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase | GO:0005737 cytoplasm | -0.060 | 0 | 0 | 12 | 1030 |
| JW1281 | fabI | enoyl-[acyl-carrier-protein] reductase, NADH-dependent | GO:0005737 cytoplasm | 0.163 | 1 | 0 | 15 | 1029 |
| JW3708 | glmU | fused N-acetyl glucosamine-1-phosphate uridylyltransferase -!- glucosamine-1-phosphate acetyl | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 | -0.176 | 0 | 0 | 16 | 1026 |
| JW0030 | carA | carbamoyl phosphate synthetase small subunit, glutamine amidotransferase | 0 | -0.199 | 0 | 0 | 14 | 1025 |
| JW1403 | ydbC | predicted oxidoreductase, NAD(P)- | 0 | 0.047 | 1 | 0 | 13 | 1025 |
| JW1439 | ydcW | medium chain aldehyde dehydrogenase | 0 | -0.029 | 0 | 0 | 14 | 1024 |
| JW5187 | dhaK | dihydroxyacetone kinase, N-terminal domain | 0 | -0.113 | 0 | 0 | 14 | 1022 |
| JW0463 | adk | adenylate kinase | GO:0005737 cytoplasm | -0.383 | 0 | 0 | 16 | 1021 |

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|--------|------|---|---|--------|---|---|----|------|
| JW3220 | mreB | cell wall structural complex MreBCD, actin-like component MreB | 0 | 0.057 | 1 | 0 | 15 | 1019 |
| JW1164 | minD | membrane ATPase of the MinC-MinD-MinE system | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.118 | 1 | 0 | 16 | 1018 |
| JW2892 | fbaA | fructose-bisphosphate aldolase, class II | 0 | -0.224 | 0 | 0 | 13 | 1014 |
| JW0716 | sucB | dihydrolipoyltranssuccinase | 0 | -0.217 | 0 | 0 | 15 | 1013 |
| JW1629 | tyrS | tyrosyl-tRNA synthetase | GO:0005737 cytoplasm | -0.334 | 0 | 0 | 15 | 1012 |
| JW5273 | sufB | component of SufBCD complex | 0 | -0.298 | 0 | 0 | 16 | 1008 |
| JW1081 | fabF | 3-oxoacyl-[acyl-carrier-protein] synthase | GO:0005737 cytoplasm | 0.002 | 1 | 0 | 14 | 1007 |
| JW0785 | ybiB | predicted transferase/phosphorylase | 0 | -0.165 | 0 | 0 | 14 | 1003 |
| JW0847 | artI | arginine transporter subunit -!- periplasmic-binding component of ABC | GO:0042597 periplasmic space | -0.329 | 0 | 0 | 13 | 999 |
| JW4014 | tyrB | tyrosine aminotransferase, tyrosine-repressible, PLP-dependent | GO:0005737 cytoplasm | 0.009 | 1 | 0 | 16 | 997 |
| JW1177 | ycgB | conserved protein | 0 | -0.613 | 0 | 0 | 18 | 994 |
| JW3395 | glgB | 1,4-alpha-glucan branching enzyme | GO:0005737 cytoplasm | -0.509 | 0 | 0 | 23 | 993 |
| JW0722 | cydA | cytochrome d terminal oxidase, subunit I | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.397 | 1 | 9 | 16 | 990 |
| JW0931 | ycbY | predicted methyltransferase | 0 | -0.359 | 0 | 0 | 23 | 990 |
| JW1037 | mdoH | glucan biosynthesis: glycosyl transferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.046 | 1 | 6 | 18 | 989 |
| JW3434 | zntA | zinc, cobalt and lead efflux system | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.282 | 1 | 5 | 17 | 986 |
| JW0404 | ribD | fused diaminohydroxyphosphoribosylaminopyr imidine deaminase -!- 5-amino-6-(5-phosphoribosylamino) uracil reductase | 0 | -0.229 | 0 | 0 | 18 | 985 |
| JW0737 | aroG | 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, phenylalanine repressible | 0 | -0.182 | 0 | 0 | 14 | 985 |
| JW0928 | pyrD | dihydro-ototate oxidase, FMN-linked | GO:0005737 cytoplasm | -0.110 | 0 | 0 | 17 | 984 |
| JW1803 | sdaA | L-serine deaminase I | 0 | -0.051 | 0 | 0 | 18 | 983 |
| JW5343 | gatY | D-tagatose 1,6-bisphosphate aldolase 2, catalytic subunit | 0 | -0.091 | 0 | 0 | 16 | 983 |
| JW0180 | accA | acetylCoA carboxylase, carboxytransferase, alpha subunit | GO:0005737 cytoplasm | -0.233 | 0 | 0 | 16 | 978 |
| JW5067 | ybbN | predicted thioredoxin domain-containing protein | 0 | -0.242 | 0 | 0 | 14 | 976 |
| JW0940 | ompA | outer membrane protein A (3a;II*;G;d) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.339 | 1 | 0 | 14 | 975 |
| JW1375 | ldhA | fermentative D-lactate dehydrogenase, NAD-dependent | 0 | -0.101 | 0 | 0 | 15 | 974 |
| JW2119 | yehZ | predicted transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.066 | 0 | 0 | 14 | 972 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW3887 | pfkA | 6-phosphofructokinase I | GO:0005737 cytoplasm | 0.000 | 1 | 0 | 16 | 972 |
| JW0361 | hemB | porphobilinogen synthase | 0 | -0.125 | 0 | 0 | 19 | 971 |
| JW3298 | bfr | bacterioferritin, iron storage and detoxification protein | GO:0005737 cytoplasm | -0.472 | 0 | 0 | 12 | 971 |
| JW5146 | ycdW | 2-ketoacid reductase | 0 | -0.258 | 0 | 0 | 14 | 970 |
| JW0811 | moeA | molybdopterin biosynthesis protein | 0 | 0.027 | 1 | 0 | 13 | 969 |
| JW0963 | appA | phosphoanhydride phosphorylase | GO:0042597 periplasmic space | -0.157 | 0 | 0 | 14 | 969 |
| JW0212 | lpcA | D-sedoheptulose 7-phosphate | GO:0005737 cytoplasm | -0.062 | 0 | 0 | 13 | 965 |
| JW2517 | suhB | inositol monophosphatase | GO:0005737 cytoplasm | -0.171 | 0 | 0 | 16 | 965 |
| JW2462 | nlpB | lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.265 | 1 | 0 | 16 | 962 |
| JW0662 | nagC | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.006 | 0 | 0 | 19 | 958 |
| JW0029 | dapB | dihydrodipicolinate reductase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.019 | 1 | 0 | 18 | 955 |
| JW2640 | ygaU | predicted protein | 0 | -0.458 | 0 | 0 | 14 | 954 |
| JW2312 | folC | bifunctional folylpolyglutamate synthase -!- dihydrofolate synthase | 0 | 0.004 | 1 | 0 | 16 | 953 |
| JW1077 | fabH | 3-oxoacyl-[acyl-carrier-protein] synthase | GO:0005737 cytoplasm | 0.143 | 1 | 0 | 11 | 952 |
| JW0796 | glnH | glutamine transporter subunit -!- periplasmic binding component of ABC superfamily | GO:0042597 periplasmic space | -0.233 | 0 | 0 | 12 | 950 |
| JW1806 | manX | fused mannose-specific PTS enzyme IIAB components | GO:0005737 cytoplasm | -0.058 | 0 | 0 | 15 | 950 |
| JW2703 | mutS | methyl-directed mismatch repair protein | GO:0005737 cytoplasm | -0.238 | 0 | 0 | 19 | 950 |
| JW1714 | yniA | predicted phosphotransferase/kinase | 0 | -0.314 | 0 | 0 | 13 | 947 |
| JW0750 | ybhE | 6-phosphogluconolactonase | 0 | -0.224 | 0 | 0 | 13 | 946 |
| JW0871 | trxB | thioredoxin reductase, FAD/NAD(P)-binding | GO:0005737 cytoplasm | -0.193 | 0 | 0 | 12 | 946 |
| JW5280 | pfkB | 6-phosphofructokinase II | GO:0005737 cytoplasm | 0.012 | 1 | 0 | 14 | 946 |
| JW0746 | modA | molybdate transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.020 | 0 | 0 | 15 | 945 |
| JW5058 | yajQ | predicted nucleotide binding protein | 0 | -0.454 | 0 | 0 | 12 | 944 |
| JW3352 | aroB | 3-dehydroquinate synthase | 0 | 0.168 | 1 | 0 | 14 | 941 |
| JW1447 | yncE | conserved protein | 0 | -0.269 | 0 | 0 | 16 | 940 |
| JW3619 | yicC | conserved protein | 0 | -0.442 | 0 | 0 | 14 | 940 |
| JW0413 | thiI | sulfurtransferase required for thiamine and 4-thiouridine biosynthesis | 0 | -0.222 | 0 | 0 | 19 | 932 |
| JW0897 | msbA | fused lipid transporter subunits -!- membrane component and ATP-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.113 | 1 | 5 | 17 | 932 |
| JW0164 | rpsB | 30S ribosomal subunit protein S2 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.268 | 0 | 0 | 13 | 931 |
| JW3454 | yhlI | predicted HlyD family secretion protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.161 | 1 | 1 | 16 | 931 |
| JW5243 | ydeN | conserved protein | 0 | -0.575 | 0 | 0 | 16 | 931 |

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|--------|------|---|---|--------|---|----|----|-----|
| JW0985 | cbpA | curved DNA-binding protein, DnaJ homologue that functions as a co-chaperone of DnaK | GO:0005737 cytoplasm | -0.592 | 0 | 0 | 15 | 927 |
| JW3753 | rhIB | ATP-dependent RNA helicase | 0 | -0.346 | 0 | 0 | 18 | 927 |
| JW5526 | garR | tartronate semialdehyde reductase | 0 | 0.264 | 1 | 0 | 14 | 927 |
| JW0655 | ybeX | predicted ion transport | GO:0009274 cell wall (sensu | -0.372 | 0 | 0 | 16 | 923 |
| JW2914 | gshB | glutathione synthetase | 0 | -0.261 | 0 | 0 | 12 | 923 |
| JW3583 | gpsA | glycerol-3-phosphate dehydrogenase (NAD+) | GO:0005737 cytoplasm | -0.025 | 0 | 0 | 13 | 923 |
| JW0080 | mraW | S-adenosyl-dependent methyltransferase activity on | 0 | -0.397 | 0 | 0 | 15 | 917 |
| JW3250 | rsmB | 16S rRNA m5C967 methyltransferase, S-adenosyl-L-methionine-dependent | GO:0005737 cytoplasm | -0.394 | 0 | 0 | 16 | 915 |
| JW4191 | fbp | fructose-1,6-bisphosphatase I | GO:0005737 cytoplasm | -0.222 | 0 | 0 | 13 | 915 |
| JW1753 | selD | selenophosphate synthase | GO:0005737 cytoplasm | 0.068 | 1 | 0 | 14 | 914 |
| JW5522 | tdcE | pyruvate formate-lyase 4/2-ketobutyrate formate-lyase | GO:0005737 cytoplasm | -0.294 | 0 | 0 | 21 | 911 |
| JW0162 | glnD | uridylyltransferase | GO:0005737 cytoplasm | -0.294 | 0 | 0 | 19 | 910 |
| JW4192 | mpl | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso- | GO:0009274 cell wall (sensu Bacteria) | -0.051 | 0 | 0 | 18 | 910 |
| JW1297 | pspA | regulatory protein for phage-shock-protein operon | GO:0005737 cytoplasm | -0.722 | 0 | 0 | 15 | 907 |
| JW2987 | parC | DNA topoisomerase IV, subunit A | GO:0005737 cytoplasm | -0.369 | 0 | 0 | 20 | 905 |
| JW0932 | uup | fused predicted transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.467 | 0 | 0 | 20 | 899 |
| JW3258 | rpsD | 30S ribosomal subunit protein S4 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.664 | 0 | 0 | 17 | 898 |
| JW2024 | rfaA | glucose-1-phosphate thymidyltransferase | GO:0005737 cytoplasm | -0.193 | 0 | 0 | 16 | 896 |
| JW2483 | upp | uracil phosphoribosyltransferase | 0 | 0.073 | 1 | 0 | 11 | 896 |
| JW3819 | ubiD | 3-octaprenyl-4-hydroxybenzoate decarboxylase | 0 | -0.248 | 0 | 0 | 17 | 896 |
| JW2134 | yeiA | predicted oxidoreductase | 0 | -0.111 | 0 | 0 | 16 | 893 |
| JW4012 | dnaB | replicative DNA helicase | GO:0005737 cytoplasm | -0.415 | 0 | 0 | 19 | 893 |
| JW0660 | asnB | asparagine synthetase B | GO:0005737 cytoplasm | -0.356 | 0 | 0 | 19 | 891 |
| JW1963 | amn | AMP nucleosidase | GO:0042597 periplasmic space | -0.295 | 0 | 0 | 16 | 890 |
| JW1051 | grxB | glutaredoxin 2 (Grx2) | 0 | -0.264 | 0 | 0 | 12 | 885 |
| JW0665 | nagE | fused N-acetyl glucosamine specific PTS enzyme IICBA components | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.584 | 1 | 10 | 15 | 883 |
| JW3625 | spoT | bifunctional (p)ppGpp synthetase II -!- guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase | GO:0005737 cytoplasm | -0.332 | 0 | 0 | 21 | 881 |
| JW1253 | trpB | tryptophan synthase, beta subunit | GO:0005737 cytoplasm | -0.191 | 0 | 0 | 16 | 880 |

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|--------|------|---|---|--------|---|---|----|-----|
| JW3265 | rpsE | 30S ribosomal subunit protein S5 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.101 | 0 | 0 | 14 | 880 |
| JW2385 | glk | glucokinase | GO:0005737 cytoplasm | 0.154 | 1 | 0 | 13 | 879 |
| JW0804 | ybiT | fused predicted transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.381 | 0 | 0 | 17 | 878 |
| JW2174 | yejK | nucleotide associated protein | GO:0005737 cytoplasm | -0.364 | 0 | 0 | 12 | 878 |
| JW0410 | dxs | 1-deoxyxylulose-5-phosphate synthase, thiamine-requiring, FAD-requiring | 0 | -0.081 | 0 | 0 | 15 | 872 |
| JW2027 | galF | predicted subunit with GalU | GO:0005737 cytoplasm | -0.092 | 0 | 0 | 14 | 872 |
| JW5185 | dhaH | fused predicted dihydroxyacetone-specific PTS enzyme HPr component -!- EI component | 0 | -0.017 | 0 | 0 | 14 | 872 |
| JW4286 | uxuB | D-mannonate oxidoreductase, NAD- | 0 | -0.141 | 0 | 0 | 15 | 871 |
| JW3379 | malQ | 4-alpha-glucanotransferase (amylomaltase) | GO:0005737 cytoplasm | -0.393 | 0 | 0 | 19 | 869 |
| JW3786 | uvrD | DNA-dependent ATPase I and helicase | GO:0005737 cytoplasm | -0.458 | 0 | 0 | 18 | 869 |
| JW5394 | ucpA | predicted oxidoreductase, sulfate metabolism protein | 0 | 0.046 | 1 | 0 | 14 | 867 |
| JW1950 | hchA | Hsp31 molecular chaperone | 0 | -0.224 | 0 | 0 | 12 | 866 |
| JW4180 | ytfN | conserved protein | 0 | -0.183 | 1 | 1 | 17 | 866 |
| JW0347 | frmA | alcohol dehydrogenase class III/glutathione-dependent formaldehyde dehydrogenase | GO:0005737 cytoplasm | -0.012 | 0 | 0 | 14 | 864 |
| JW2755 | relA | (p)ppGpp synthetase I/GTP pyrophosphokinase | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.337 | 0 | 0 | 20 | 864 |
| JW5260 | ynfF | oxidoreductase subunit | 0 | -0.447 | 0 | 0 | 17 | 864 |
| JW3392 | glgA | glycogen synthase | GO:0005737 cytoplasm | 0.003 | 1 | 0 | 14 | 863 |
| JW3495 | yhjJ | predicted zinc-dependent peptidase | 0 | -0.340 | 0 | 0 | 16 | 862 |
| JW0742 | galE | UDP-galactose-4-epimerase | GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.311 | 0 | 0 | 12 | 861 |
| JW2257 | menB | dihydroxynaphthoic acid synthetase | 0 | -0.340 | 0 | 0 | 14 | 861 |
| JW2773 | fucl | L-fucose isomerase | 0 | -0.260 | 0 | 0 | 14 | 861 |
| JW2956 | gss | fused glutathionylspermidine amidase -!- glutathionylspermidine synthetase | 0 | -0.342 | 1 | 1 | 15 | 858 |
| JW3389 | glpD | sn-glycerol-3-phosphate dehydrogenase, aerobic, FAD/NAD(P)- | GO:0005737 cytoplasm | -0.384 | 0 | 0 | 25 | 858 |
| JW2363 | dsdA | D-serine ammonia-lyase | GO:0005737 cytoplasm | -0.087 | 0 | 0 | 14 | 857 |
| JW1672 | sufC | component of SufBCD complex, ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.205 | 0 | 0 | 14 | 856 |
| JW2075 | gatD | galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding | 0 | 0.139 | 1 | 0 | 12 | 855 |
| JW2577 | yfiO | predicted lipoprotein | 0 | -0.484 | 0 | 0 | 14 | 852 |
| JW0396 | tgt | tRNA-guanine transglycosylase | GO:0005737 cytoplasm | -0.412 | 0 | 0 | 15 | 851 |

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|--------|------|---|---|--------|---|---|----|-----|
| JW1509 | lsrB | AI2 transporter -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.151 | 0 | 0 | 9 | 849 |
| JW2313 | accD | acetylCoA carboxylase, beta (carboxyltransferase) subunit | GO:0005737 cytoplasm | -0.129 | 0 | 0 | 15 | 847 |
| JW3911 | metL | fused aspartokinase II -!- homoserine dehydrogenase II | 0 | -0.101 | 0 | 0 | 16 | 846 |
| JW1116 | phoP | DNA-binding response regulator in two-component regulatory system with | GO:0005737 cytoplasm | -0.257 | 0 | 0 | 12 | 844 |
| JW1889 | araF | L-arabinose transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.186 | 0 | 0 | 17 | 843 |
| JW2635 | ygaF | predicted enzyme | 0 | -0.085 | 0 | 0 | 16 | 842 |
| JW5932 | hemC | hydroxymethylbilane synthase | 0 | -0.066 | 0 | 0 | 14 | 838 |
| JW1648 | sodB | superoxide dismutase, Fe | GO:0005737 cytoplasm | -0.169 | 0 | 0 | 11 | 834 |
| JW3279 | rplB | 50S ribosomal subunit protein L2 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.699 | 0 | 0 | 14 | 834 |
| JW5437 | rpoS | RNA polymerase, sigma S (sigma 38) factor | GO:0005737 cytoplasm | -0.460 | 0 | 0 | 14 | 834 |
| JW4161 | rplI | 50S ribosomal subunit protein L9 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.091 | 1 | 0 | 13 | 833 |
| JW0600 | uspG | universal stress protein UP12 | 0 | -0.053 | 0 | 0 | 10 | 832 |
| JW1224 | galU | glucose-1-phosphate uridylyltransferase | GO:0030113 capsule (sensu | 0.031 | 1 | 0 | 11 | 832 |
| JW3403 | yhhX | predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain | 0 | -0.346 | 0 | 0 | 13 | 831 |
| JW1252 | trpA | tryptophan synthase, alpha subunit | GO:0005737 cytoplasm | 0.123 | 1 | 0 | 12 | 829 |
| JW3492 | yhjG | predicted outer membrane biogenesis protein | 0 | -0.227 | 1 | 1 | 18 | 829 |
| JW3564 | selA | selenocysteine synthase | GO:0005737 cytoplasm | -0.055 | 0 | 0 | 20 | 829 |
| JW0167 | frr | ribosome recycling factor | GO:0005737 cytoplasm | -0.534 | 0 | 0 | 12 | 828 |
| JW2594 | grpE | heat shock protein | GO:0005737 cytoplasm | -0.372 | 0 | 0 | 14 | 828 |
| JW2049 | asmA | predicted assembly protein | 0 | -0.422 | 1 | 1 | 18 | 827 |
| JW2487 | ppx | exopolyphosphatase | 0 | -0.239 | 0 | 0 | 19 | 827 |
| JW1627 | gst | glutathione S-transferase | 0 | -0.220 | 0 | 0 | 12 | 826 |
| JW2484 | purM | phosphoribosylaminoimidazole | GO:0005737 cytoplasm | 0.034 | 1 | 0 | 10 | 823 |
| JW3025 | glnE | fused deadenylyltransferase -!- adenyltransferase for glutamine synthetase | 0 | -0.317 | 0 | 0 | 19 | 823 |
| JW0384 | rdgC | DNA-binding protein, non-specific | GO:0005737 cytoplasm | -0.222 | 0 | 0 | 12 | 822 |
| JW0740 | galK | galactokinase | GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.105 | 0 | 0 | 13 | 822 |
| JW5581 | ubiE | bifunctional 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase -!- S-adenosylmethionine:2-DMK methyltransferase | 0 | -0.168 | 0 | 0 | 12 | 822 |
| JW0129 | panC | pantothenate synthetase | GO:0005737 cytoplasm | -0.108 | 0 | 0 | 15 | 820 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW1317 | tpx | lipid hydroperoxide peroxidase | GO:0042597 periplasmic space | 0.256 | 1 | 0 | 9 | 820 |
| JW3270 | rplE | 50S ribosomal subunit protein L5 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.282 | 0 | 0 | 10 | 820 |
| JW1474 | adhP | alcohol dehydrogenase, 1-propanol preferring | 0 | 0.103 | 1 | 0 | 14 | 818 |
| JW5702 | crp | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.225 | 0 | 0 | 13 | 818 |
| JW1054 | yceH | conserved protein | 0 | -0.424 | 0 | 0 | 12 | 810 |
| JW1611 | hdhA | 7alpha-hydroxysteroid dehydrogenase, NAD-dependent | GO:0005737 cytoplasm | 0.139 | 1 | 0 | 14 | 810 |
| JW2510 | hscA | DnaK-like molecular chaperone specific for IscU | GO:0005737 cytoplasm | -0.028 | 0 | 0 | 19 | 804 |
| JW3725 | yieN | fused predicted transcriptional | 0 | -0.219 | 0 | 0 | 16 | 803 |
| JW2505 | sseA | 3-mercaptopyruvate sulfurtransferase | 0 | -0.083 | 0 | 0 | 12 | 802 |
| JW3267 | rplF | 50S ribosomal subunit protein L6 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.227 | 0 | 0 | 10 | 799 |
| JW3822 | fadB | fused 3-hydroxybutyryl-CoA epimerase/delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase/enoyl-CoA hydratase -!- 3-hydroxyacyl-CoA dehydrogenase | 0 | -0.094 | 0 | 0 | 21 | 798 |
| JW3862 | fdhE | formate dehydrogenase formation | 0 | -0.289 | 0 | 0 | 12 | 798 |
| JW3485 | gadA | glutamate decarboxylase A, PLP-dependent | GO:0005737 cytoplasm | -0.278 | 0 | 0 | 14 | 795 |
| JW1938 | yedP | conserved protein | 0 | -0.256 | 0 | 0 | 12 | 794 |
| JW3879 | sodA | superoxide dismutase, Mn | GO:0005737 cytoplasm | -0.429 | 0 | 0 | 11 | 794 |
| JW5492 | yghU | predicted S-transferase | 0 | -0.403 | 1 | 1 | 12 | 794 |
| JW0659 | ubiF | 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol oxygenase | 0 | 0.027 | 1 | 0 | 13 | 791 |
| JW2536 | hmp | fused nitric oxide dioxygenase -!- dihydropteridine reductase 2 | 0 | -0.290 | 0 | 0 | 13 | 791 |
| JW3180 | gltD | glutamate synthase, 4Fe-4S protein, small subunit | 0 | -0.313 | 0 | 0 | 16 | 791 |
| JW2497 | yfgM | conserved protein | 0 | -0.222 | 1 | 1 | 13 | 790 |
| JW0385 | mak | manno(fructo)kinase | 0 | -0.202 | 0 | 0 | 12 | 788 |
| JW4172 | cysQ | PAPS (adenosine 3'-phosphate 5'-phosphosulfate) 3'(2'),5'-bisphosphate nucleotidase | 0 | -0.251 | 0 | 0 | 11 | 787 |
| JW0989 | wrbA | predicted flavoprotein in Trp regulation | GO:0005737 cytoplasm | -0.082 | 0 | 0 | 9 | 786 |
| JW1886 | otsB | trehalose-6-phosphate phosphatase, biosynthetic | GO:0005737 cytoplasm | -0.145 | 0 | 0 | 12 | 786 |
| JW3938 | btuB | vitamin B12/cobalamin outer membrane transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.534 | 1 | 0 | 17 | 785 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW5786 | yjiM | predicted 2-hydroxyglutaryl-CoA dehydratase | 0 | -0.187 | 0 | 0 | 12 | 785 |
| JW4338 | osmY | periplasmic protein | GO:0042597 periplasmic space | -0.292 | 0 | 0 | 9 | 782 |
| JW0101 | guaC | GMP reductase | GO:0005737 cytoplasm | -0.068 | 0 | 0 | 12 | 781 |
| JW1532 | ydfG | L-allo-threonine dehydrogenase, NAD(P)-binding | 0 | -0.175 | 0 | 0 | 12 | 779 |
| JW3315 | yheS | fused predicted transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.463 | 0 | 0 | 18 | 779 |
| JW3213 | tldD | predicted peptidase | 0 | -0.123 | 0 | 0 | 14 | 778 |
| JW1816 | kdgR | predicted DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.278 | 0 | 0 | 13 | 775 |
| JW4068 | phnB | conserved protein | 0 | -0.243 | 0 | 0 | 12 | 774 |
| JW0623 | lipA | lipoate synthase | GO:0005737 cytoplasm | -0.330 | 0 | 0 | 15 | 772 |
| JW1427 | ydcL | predicted lipoprotein | 0 | -0.268 | 0 | 0 | 11 | 771 |
| JW2291 | yfbU | conserved protein | 0 | -0.579 | 0 | 0 | 14 | 771 |
| JW0105 | nadC | quinolinate phosphoribosyltransferase | 0 | -0.234 | 0 | 0 | 14 | 770 |
| JW1595 | pntA | pyridine nucleotide transhydrogenase, alpha subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.273 | 1 | 5 | 13 | 769 |
| JW4169 | ytfG | NAD(P)H:quinone oxidoreductase | 0 | 0.052 | 1 | 0 | 12 | 769 |
| JW2140 | folE | GTP cyclohydrolase I | 0 | -0.121 | 0 | 0 | 13 | 768 |
| JW3896 | glpX | fructose 1,6-bisphosphatase II | GO:0005737 cytoplasm | -0.016 | 0 | 0 | 14 | 768 |
| JW0893 | cmk | cytidylate kinase | GO:0005737 cytoplasm | 0.000 | 0 | 0 | 11 | 766 |
| JW2662 | luxS | S-ribosylhomocysteinease | 0 | -0.323 | 0 | 0 | 10 | 765 |
| JW1419 | ydcJ | conserved protein | 0 | -0.461 | 0 | 0 | 15 | 763 |
| JW3148 | greA | transcription elongation factor | GO:0005737 cytoplasm | -0.366 | 0 | 0 | 13 | 762 |
| JW3948 | rplJ | 50S ribosomal subunit protein L10 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.045 | 1 | 0 | 10 | 762 |
| JW5556 | gldA | glycerol dehydrogenase, NAD | 0 | 0.171 | 1 | 0 | 10 | 762 |
| JW0145 | mrcB | fused glycosyl transferase -!- transpeptidase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.419 | 1 | 1 | 16 | 761 |
| JW0664 | nagB | glucosamine-6-phosphate deaminase | 0 | -0.185 | 0 | 0 | 12 | 761 |
| JW2770 | fucO | L-1,2-propanediol oxidoreductase | 0 | 0.086 | 1 | 0 | 14 | 761 |
| JW3309 | fkpA | FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) | GO:0042597 periplasmic space | -0.458 | 0 | 0 | 12 | 761 |
| JW4358 | ytjC | phosphoglyceromutase 2, co-factor independent | GO:0005737 cytoplasm | -0.371 | 1 | 1 | 12 | 761 |
| JW5656 | tiaE | 2-keto-D-gluconate reductase (glyoxalate reductase) (2-ketoaldonate | GO:0005737 cytoplasm | 0.005 | 1 | 0 | 12 | 759 |
| JW0567 | nfnB | dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive | 0 | -0.211 | 0 | 0 | 14 | 757 |
| JW0835 | nfsA | nitroreductase A, NADPH-dependent, FMN-dependent | 0 | -0.155 | 0 | 0 | 12 | 755 |
| JW3303 | rpsG | 30S ribosomal subunit protein S7 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.460 | 0 | 0 | 13 | 755 |

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|--------|------|---|---|--------|---|----|----|-----|
| JW3441 | nikA | nickel transporter subunit -! periplasmic-binding component of ABC | GO:0042597 periplasmic space | -0.261 | 0 | 0 | 18 | 754 |
| JW5836 | cld | regulator of length of O-antigen component of lipopolysaccharide chains | 0 | -0.265 | 1 | 2 | 11 | 754 |
| JW3747 | ilvC | ketol-acid reductoisomerase, NAD(P)- binding | GO:0005737 cytoplasm | -0.205 | 0 | 0 | 17 | 753 |
| JW3722 | asnA | asparagine synthetase A | GO:0005737 cytoplasm | -0.289 | 0 | 0 | 13 | 752 |
| JW5126 | ycbX | predicted 2Fe-2S cluster-containing | 0 | -0.180 | 0 | 0 | 12 | 749 |
| JW2998 | parE | DNA topoisomerase IV, subunit B | GO:0005737 cytoplasm | -0.345 | 0 | 0 | 13 | 748 |
| JW2410 | crr | glucose-specific enzyme IIA component of PTS | GO:0005737 cytoplasm | 0.057 | 1 | 0 | 11 | 747 |
| JW2563 | yfiD | pyruvate formate lyase subunit | 0 | -0.332 | 0 | 0 | 10 | 747 |
| JW0014 | dnaJ | chaperone Hsp40, co-chaperone with DnaK | GO:0005737 cytoplasm | -0.634 | 0 | 0 | 11 | 746 |
| JW0163 | map | methionine aminopeptidase | 0 | -0.162 | 0 | 0 | 11 | 744 |
| JW0372 | ddlA | D-alanine-D-alanine ligase A | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.016 | 1 | 0 | 14 | 744 |
| JW0454 | kefA | fused mechanosensitive channel proteins | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.031 | 1 | 12 | 15 | 744 |
| JW2205 | rscB | DNA-binding response regulator in two- component regulatory system with RcsC and YojN | GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.021 | 1 | 0 | 11 | 739 |
| JW3198 | sspA | stringent starvation protein A | GO:0005737 cytoplasm | -0.265 | 0 | 0 | 9 | 738 |
| JW3714 | atpF | F0 sector of membrane-bound ATP synthase, subunit b | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.213 | 1 | 1 | 9 | 737 |
| JW3933 | oxyR | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.088 | 0 | 0 | 13 | 735 |
| JW2434 | eutB | ethanolamine ammonia-lyase, large subunit, heavy chain | 0 | -0.070 | 0 | 0 | 15 | 732 |
| JW0086 | murD | UDP-N-acetylmuramoyl-L-alanine:D- glutamate ligase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.005 | 1 | 1 | 12 | 731 |
| JW2925 | yggN | predicted protein | 0 | -0.469 | 0 | 0 | 12 | 731 |
| JW3276 | rpsC | 30S ribosomal subunit protein S3 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.422 | 0 | 0 | 14 | 728 |
| JW1225 | hns | global DNA-binding transcriptional dual regulator H-NS | GO:0019861 flagellum -!- GO:0005737 cytoplasm | -0.751 | 0 | 0 | 9 | 726 |
| JW3683 | yidC | cytoplasmic insertase into membrane protein, Sec system | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.122 | 1 | 4 | 11 | 726 |
| JW1654 | ribC | riboflavin synthase, alpha subunit | 0 | -0.100 | 0 | 0 | 12 | 725 |
| JW3774 | hemY | predicted protoheme IX synthesis | 0 | -0.362 | 1 | 2 | 15 | 725 |
| JW0638 | ybeL | conserved protein | 0 | -0.604 | 0 | 0 | 10 | 724 |
| JW3159 | yrbC | predicted ABC-type organic solvent transporter | GO:0005737 cytoplasm | -0.416 | 0 | 0 | 11 | 723 |
| JW3260 | rpsM | 30S ribosomal subunit protein S13 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.424 | 0 | 0 | 10 | 722 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW4133 | hflC | modulator for HflB protease specific for phage lambda cII repressor | 0 | -0.365 | 1 | 1 | 12 | 721 |
| JW1411 | ydcF | conserved protein | 0 | -0.143 | 0 | 0 | 11 | 720 |
| JW3026 | ygiF | predicted adenylate cyclase | 0 | -0.260 | 0 | 0 | 17 | 720 |
| JW4031 | nrfA | nitrite reductase, formate-dependent, cytochrome | GO:0042597 periplasmic space | -0.589 | 0 | 0 | 13 | 720 |
| JW2463 | dapA | dihydrodipicolinate synthase | GO:0005737 cytoplasm | 0.067 | 1 | 0 | 11 | 719 |
| JW2988 | ygiS | predicted transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.374 | 0 | 0 | 16 | 719 |
| JW0885 | pflA | pyruvate formate lyase activating enzyme 1 | GO:0005737 cytoplasm | -0.361 | 0 | 0 | 15 | 718 |
| JW2802 | tas | predicted oxidoreductase, NADP(H)-dependent aldo-keto reductase | 0 | -0.323 | 0 | 0 | 12 | 716 |
| JW1754 | ydjA | predicted oxidoreductase | 0 | -0.168 | 0 | 0 | 9 | 713 |
| JW4333 | rsmC | 16S RNA m2G1207 methylase | GO:0005737 cytoplasm | -0.111 | 0 | 0 | 12 | 713 |
| JW5761 | yjgB | predicted alcohol dehydrogenase, Zn-dependent and NAD(P)-binding | 0 | 0.039 | 1 | 0 | 10 | 713 |
| JW1656 | ydhQ | conserved protein | 0 | 0.025 | 1 | 0 | 11 | 712 |
| JW1912 | amyA | cytoplasmic alpha-amylase | GO:0005737 cytoplasm | -0.381 | 0 | 0 | 13 | 712 |
| JW2316 | usg | predicted semialdehyde dehydrogenase | 0 | 0.061 | 1 | 0 | 10 | 711 |
| JW3052 | fadH | 2,4-dienoyl-CoA reductase, NADH and FMN-linked | 0 | -0.064 | 0 | 0 | 15 | 710 |
| JW4203 | pyrI | aspartate carbamoyltransferase, regulatory subunit | GO:0005737 cytoplasm | -0.273 | 0 | 0 | 12 | 709 |
| JW0460 | ybaB | conserved protein | 0 | -0.473 | 0 | 0 | 8 | 707 |
| JW0474 | ybaS | predicted glutaminase | 0 | 0.057 | 1 | 0 | 11 | 707 |
| JW1700 | btuE | predicted glutathione peroxidase | GO:0042597 periplasmic space | -0.131 | 0 | 0 | 8 | 707 |
| JW0744 | modE | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.021 | 0 | 0 | 11 | 705 |
| JW1615 | add | adenosine deaminase | 0 | -0.024 | 0 | 0 | 14 | 705 |
| JW2204 | rcsD | phosphotransfer intermediate protein in two-component regulatory system with RcsBC | 0 | -0.234 | 1 | 1 | 15 | 705 |
| JW0891 | aroA | 5-enolpyruvylshikimate-3-phosphate synthetase | 0 | -0.005 | 0 | 0 | 17 | 702 |
| JW2465 | bcp | thiol peroxidase, thioredoxin-dependent | GO:0005737 cytoplasm | -0.431 | 0 | 0 | 10 | 700 |
| JW3168 | yhbG | predicted transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.124 | 0 | 0 | 10 | 698 |
| JW3945 | nusG | transcription termination factor | GO:0005737 cytoplasm | -0.391 | 0 | 0 | 10 | 698 |
| JW1112 | potA | polyamine transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.338 | 0 | 0 | 12 | 697 |
| JW1769 | yeaD | conserved protein | 0 | -0.249 | 0 | 0 | 10 | 696 |
| JW1998 | yeeZ | predicted epimerase, with NAD(P)-binding Rossmann-fold domain | 0 | -0.100 | 0 | 0 | 11 | 696 |
| JW3282 | rpIC | 50S ribosomal subunit protein L3 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.235 | 0 | 0 | 12 | 693 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW4121 | psd | phosphatidylserine decarboxylase | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | -0.093 | 1 | 0 | 10 | 693 |
| JW5746 | fkIB | FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) | 0 | -0.081 | 0 | 0 | 10 | 692 |
| JW1200 | lolB | chaperone for lipoproteins | GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.644 | 1 | 0 | 12 | 691 |
| JW3591 | tdh | threonine 3-dehydrogenase, NAD(P)-binding | 0 | 0.051 | 1 | 0 | 11 | 691 |
| JW0732 | ybgF | predicted protein | GO:0042597 periplasmic space | -0.468 | 0 | 0 | 10 | 690 |
| JW2004 | hisB | fused histidinol-phosphatase - - imidazoleglycerol-phosphate | 0 | -0.365 | 0 | 0 | 13 | 689 |
| JW0405 | ribE | riboflavin synthase beta chain | 0 | 0.294 | 1 | 0 | 7 | 688 |
| JW1049 | pyrC | dihydro-orotase | GO:0005737 cytoplasm | -0.123 | 0 | 0 | 15 | 687 |
| JW0168 | dxr | 1-deoxy-D-xylulose 5-phosphate reductoisomerase | 0 | -0.020 | 0 | 0 | 14 | 686 |
| JW3324 | fic | stationary-phase protein, cell division | 0 | -0.361 | 0 | 0 | 10 | 686 |
| JW1106 | cobB | deacetylase of acetyl-CoA synthetase, NAD-dependent | 0 | -0.354 | 0 | 0 | 9 | 685 |
| JW3272 | rplN | 50S ribosomal subunit protein L14 | GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm | -0.128 | 0 | 0 | 8 | 685 |
| JW3509 | dppF | dipeptide transporter - - ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.428 | 0 | 0 | 11 | 685 |
| JW3940 | murB | UDP-N-acetylenolpyruvoylglucosamine reductase, FAD-binding | GO:0009274 cell wall (sensu Bacteria) - - GO:0005737 cytoplasm | -0.204 | 0 | 0 | 12 | 685 |
| JW5111 | yliB | predicted peptide transporter subunit - - periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.253 | 0 | 0 | 14 | 679 |
| JW5947 | aroK | shikimate kinase I | 0 | -0.621 | 0 | 0 | 11 | 679 |
| JW3150 | obgE | GTPase involved in cell partitioning and DNA repair | 0 | -0.452 | 0 | 0 | 9 | 678 |
| JW1738 | xthA | exonuclease III | 0 | -0.555 | 0 | 0 | 14 | 677 |
| JW5808 | pcnB | poly(A) polymerase I | GO:0005737 cytoplasm | -0.531 | 0 | 0 | 17 | 676 |
| JW0166 | pyrH | uridylate kinase | GO:0005737 cytoplasm | 0.133 | 1 | 0 | 8 | 674 |
| JW3368 | ompR | DNA-binding response regulator in two-component regulatory system with EnvZ | GO:0009274 cell wall (sensu Bacteria) - - GO:0005737 cytoplasm | -0.346 | 0 | 0 | 12 | 674 |
| JW0874 | lolA | chaperone for lipoproteins | GO:0042597 periplasmic space | -0.492 | 0 | 0 | 8 | 673 |
| JW0954 | hyaA | hydrogenase 1, small subunit | GO:0019866 inner membrane | -0.205 | 1 | 2 | 10 | 672 |
| JW1212 | narL | DNA-binding response regulator in two-component regulatory system with NarX (or NarQ) | GO:0005737 cytoplasm | -0.153 | 0 | 0 | 12 | 672 |
| JW0937 | fabA | beta-hydroxydecanoyl thioester dehydrase | 0 | -0.012 | 0 | 0 | 10 | 669 |
| JW0155 | pfs | 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase | 0 | 0.306 | 1 | 0 | 8 | 666 |

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|--------|------|--|--|--------|---|---|----|-----|
| JW1202 | prfA | peptide chain release factor RF-1 | GO:0005737 cytoplasm | -0.660 | 0 | 0 | 17 | 666 |
| JW1316 | tyrR | DNA-binding transcriptional dual regulator, tyrosine-binding | GO:0005737 cytoplasm | -0.208 | 0 | 0 | 19 | 666 |
| JW1250 | yciF | conserved protein | 0 | -0.455 | 0 | 0 | 7 | 665 |
| JW2748 | ygcF | conserved protein | 0 | -0.260 | 0 | 0 | 10 | 664 |
| JW4343 | yjil | conserved protein | 0 | -0.280 | 0 | 0 | 13 | 664 |
| JW0731 | pal | peptidoglycan-associated outer membrane lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.454 | 1 | 0 | 7 | 663 |
| JW1670 | sufS | selenocysteine lyase, PLP-dependent | 0 | -0.001 | 0 | 0 | 12 | 663 |
| JW1839 | eda | multifunctional 2-keto-3-deoxygluconate 6-phosphate aldolase -!- 2-keto-4-hydroxyglutarate aldolase -!- oxaloacetate decarboxylase | GO:0005737 cytoplasm | 0.322 | 1 | 0 | 11 | 663 |
| JW0570 | ybdK | gamma-glutamyl:cysteine ligase | 0 | -0.224 | 0 | 0 | 9 | 662 |
| JW2903 | yggG | predicted peptidase | 0 | -0.204 | 0 | 0 | 8 | 661 |
| JW3351 | damX | predicted protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.935 | 1 | 1 | 15 | 661 |
| JW1195 | pth | peptidyl-tRNA hydrolase | GO:0005737 cytoplasm | -0.124 | 0 | 0 | 11 | 660 |
| JW2964 | hybA | hydrogenase 2 4Fe-4S ferredoxin-type component | 0 | -0.451 | 0 | 0 | 11 | 660 |
| JW3194 | nanA | N-acetylneuraminate lyase | 0 | -0.031 | 0 | 0 | 9 | 660 |
| JW5692 | hslO | heat shock protein Hsp33 | 0 | -0.313 | 0 | 0 | 9 | 660 |
| JW5756 | yjgK | conserved protein | 0 | -0.249 | 0 | 0 | 10 | 660 |
| JW0122 | can | carbonic anhydrase | 0 | -0.231 | 0 | 0 | 10 | 658 |
| JW2146 | nfo | endonuclease IV with intrinsic 3'-5' exonuclease activity | 0 | -0.204 | 0 | 0 | 11 | 655 |
| JW3624 | rpoZ | RNA polymerase, omega subunit | GO:0005737 cytoplasm | -0.524 | 0 | 0 | 9 | 654 |
| JW2131 | cdd | cytidine/deoxycytidine deaminase | 0 | 0.001 | 1 | 0 | 10 | 653 |
| JW1263 | yciK | predicted oxoacyl-(acyl carrier protein) reductase, EmrKY-TolC system | 0 | -0.321 | 0 | 0 | 11 | 652 |
| JW4359 | rob | DNA-binding transcriptional activator | GO:0005737 cytoplasm | -0.355 | 0 | 0 | 12 | 651 |
| JW5854 | yigL | predicted hydrolase | 0 | -0.185 | 0 | 0 | 12 | 651 |
| JW0092 | ftsA | ATP-binding cell division protein involved in recruitment of FtsK to Z ring | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.025 | 1 | 0 | 14 | 650 |
| JW5733 | yjdC | predicted transcriptional regulator | 0 | -0.305 | 0 | 0 | 12 | 648 |
| JW2880 | serA | D-3-phosphoglycerate dehydrogenase | GO:0005737 cytoplasm | 0.025 | 1 | 0 | 13 | 647 |
| JW2197 | eco | ecotin, a serine protease inhibitor | GO:0042597 periplasmic space | -0.257 | 0 | 0 | 9 | 645 |
| JW5240 | ddpA | D-Ala-D-Ala transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.474 | 0 | 0 | 17 | 645 |
| JW1264 | sohB | predicted inner membrane peptidase | 0 | -0.354 | 1 | 2 | 12 | 644 |
| JW0422 | cyoA | cytochrome o ubiquinol oxidase subunit II | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.009 | 1 | 3 | 9 | 643 |
| JW3402 | yhhW | predicted protein | 0 | -0.471 | 0 | 0 | 12 | 642 |
| JW0872 | lrp | DNA-binding transcriptional dual regulator, leucine-binding | GO:0005737 cytoplasm | -0.420 | 0 | 0 | 10 | 640 |
| JW1003 | ycdO | conserved protein | 0 | -0.315 | 0 | 0 | 13 | 639 |

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|--------|------|--|---|--------|---|----|----|-----|
| JW1968 | erfK | conserved protein with NAD(P)-binding Rossmann-fold domain | 0 | -0.342 | 0 | 0 | 13 | 639 |
| JW3510 | dppD | dipeptide transporter -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.113 | 0 | 0 | 13 | 638 |
| JW0822 | yliJ | predicted glutathione S-transferase | 0 | -0.198 | 0 | 0 | 9 | 637 |
| JW3263 | rpLO | 50S ribosomal subunit protein L15 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.250 | 0 | 0 | 9 | 637 |
| JW3789 | corA | magnesium/nickel/cobalt transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.156 | 1 | 2 | 11 | 636 |
| JW4110 | blc | outer membrane lipoprotein (lipocalin) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.214 | 1 | 0 | 13 | 636 |
| JW1087 | ptsG | fused glucose-specific PTS enzyme IIBC components | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.618 | 1 | 10 | 11 | 635 |
| JW1594 | pntB | pyridine nucleotide transhydrogenase, beta subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.602 | 1 | 9 | 10 | 634 |
| JW4186 | ytfQ | predicted sugar transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.186 | 1 | 1 | 11 | 634 |
| JW2100 | mrp | antiporter inner membrane protein | 0 | -0.002 | 0 | 0 | 11 | 633 |
| JW3176 | elbB | isoprenoid biosynthesis protein with amidotransferase-like domain | 0 | 0.267 | 1 | 0 | 8 | 633 |
| JW3731 | rbsK | ribokinase | GO:0005737 cytoplasm | 0.046 | 1 | 0 | 10 | 633 |
| JW3832 | dsbA | periplasmic protein disulfide isomerase I | GO:0042597 periplasmic space | -0.131 | 0 | 0 | 9 | 632 |
| JW2418 | cysP | thiosulfate transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.412 | 0 | 0 | 14 | 631 |
| JW2565 | yfiF | predicted methyltransferase | GO:0005737 cytoplasm | -0.682 | 0 | 0 | 12 | 630 |
| JW0880 | ycaC | predicted hydrolase | 0 | -0.127 | 0 | 0 | 8 | 628 |
| JW1808 | manZ | mannose-specific enzyme IID component of PTS | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.407 | 1 | 2 | 11 | 628 |
| JW3713 | atpH | F1 sector of membrane-bound ATP synthase, delta subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.063 | 1 | 0 | 8 | 628 |
| JW3268 | rpsH | 30S ribosomal subunit protein S8 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.100 | 0 | 0 | 10 | 627 |
| JW3531 | glyQ | glycine tRNA synthetase, alpha subunit | GO:0005737 cytoplasm | -0.392 | 0 | 0 | 10 | 627 |
| JW4049 | alsB | D-allose transporter subunit -!- periplasmic-binding component of ABC | GO:0042597 periplasmic space | 0.014 | 1 | 1 | 12 | 627 |
| JW0803 | ybiS | conserved protein | 0 | -0.116 | 1 | 1 | 10 | 626 |
| JW1630 | pdxH | pyridoxine 5'-phosphate oxidase | 0 | -0.621 | 0 | 0 | 12 | 626 |
| JW1683 | aroD | 3-dehydroquinate dehydratase | 0 | 0.065 | 1 | 0 | 12 | 626 |
| JW2996 | mdaB | NADPH quinone reductase | 0 | -0.356 | 0 | 0 | 11 | 626 |
| JW0945 | helD | DNA helicase IV | GO:0005737 cytoplasm | -0.413 | 0 | 0 | 18 | 625 |

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|--------|------|---|---|--------|---|---|----|-----|
| JW1119 | trmU | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase | GO:0005737 cytoplasm | -0.285 | 0 | 0 | 12 | 625 |
| JW2226 | ubiG | bifunctional 3-demethylubiquinone-9 3-methyltransferase -!- 2-octaprenyl-6-hydroxy phenol methylase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | -0.226 | 1 | 0 | 10 | 625 |
| JW4125 | yjeF | predicted carbohydrate kinase | 0 | -0.046 | 0 | 0 | 13 | 625 |
| JW2301 | yfcH | conserved protein with NAD(P)-binding Rossmann-fold domain | 0 | -0.060 | 0 | 0 | 13 | 624 |
| JW2929 | yggX | protein that protects iron-sulfur proteins against oxidative damage | 0 | -0.857 | 0 | 0 | 10 | 624 |
| JW1767 | yeaA | methionine sulfoxide reductase B | 0 | -0.738 | 0 | 0 | 10 | 623 |
| JW2019 | wbbI | conserved protein | 0 | -0.197 | 0 | 0 | 9 | 623 |
| JW0078 | fruR | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.346 | 0 | 0 | 12 | 622 |
| JW4364 | arcA | DNA-binding response regulator in two-component regulatory system with ArcB or CpxA | GO:0005737 cytoplasm | -0.487 | 0 | 0 | 10 | 622 |
| JW3412 | ggt | gamma-glutamyltranspeptidase | 0 | -0.220 | 0 | 0 | 13 | 621 |
| JW5604 | rep | DNA helicase and single-stranded DNA-dependent ATPase | GO:0005737 cytoplasm | -0.408 | 0 | 0 | 16 | 620 |
| JW5829 | infC | protein chain initiation factor IF-3 | GO:0005737 cytoplasm | -0.671 | 0 | 0 | 9 | 620 |
| JW0466 | gsk | inosine/guanosine kinase | 0 | -0.346 | 0 | 0 | 14 | 619 |
| JW3702 | phoU | DNA-binding transcriptional regulator | 0 | -0.272 | 0 | 0 | 11 | 619 |
| JW3864 | fdoH | formate dehydrogenase-O, Fe-S subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.361 | 1 | 0 | 12 | 616 |
| JW2548 | pdxJ | pyridoxine 5'-phosphate synthase | GO:0005737 cytoplasm | -0.091 | 0 | 0 | 10 | 615 |
| JW1267 | cysB | DNA-binding transcriptional dual regulator, O-acetyl-L-serine-binding | GO:0005737 cytoplasm | -0.077 | 0 | 0 | 11 | 614 |
| JW3995 | malK | fused maltose transport subunit, ATP-binding component of ABC superfamily -!- regulatory protein | GO:0005737 cytoplasm | -0.030 | 0 | 0 | 12 | 614 |
| JW3200 | rplM | 50S ribosomal subunit protein L13 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.540 | 0 | 0 | 9 | 613 |
| JW2715 | truD | pseudouridine synthase | 0 | -0.269 | 0 | 0 | 10 | 612 |
| JW3216 | rng | ribonuclease G | GO:0005737 cytoplasm | -0.279 | 0 | 0 | 15 | 612 |
| JW0765 | moaB | molybdopterin biosynthesis protein B | 0 | -0.225 | 0 | 0 | 8 | 611 |
| JW1249 | yciE | conserved protein | 0 | -0.409 | 0 | 0 | 9 | 611 |
| JW5475 | rpiA | ribosephosphate isomerase, constitutive | 0 | 0.230 | 1 | 0 | 10 | 611 |
| JW2002 | hisD | bifunctional histidinal dehydrogenase -!- histidinol dehydrogenase | 0 | -0.013 | 0 | 0 | 11 | 610 |
| JW3119 | yraP | predicted protein | GO:0042597 periplasmic space | 0.045 | 1 | 1 | 8 | 608 |
| JW0483 | tesA | multifunctional acyl-CoA thioesterase I -!- protease I -!- lysophospholipase L1 | GO:0042597 periplasmic space | -0.201 | 1 | 1 | 10 | 607 |
| JW3040 | ygjF | G/U mismatch-specific DNA | GO:0005737 cytoplasm | -0.298 | 0 | 0 | 9 | 606 |
| JW5800 | nadR | bifunctional DNA-binding transcriptional repressor -!- NMN adenyllyltransferase | 0 | -0.361 | 0 | 0 | 12 | 606 |

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|--------|------|---|---|--------|---|---|----|-----|
| JW0401 | tsx | nucleoside channel, receptor of phage T6 and colicin K | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.512 | 1 | 0 | 8 | 605 |
| JW3630 | yicH | conserved protein | 0 | -0.161 | 1 | 1 | 10 | 605 |
| JW3997 | malM | maltose regulon periplasmic protein | GO:0042597 periplasmic space | -0.021 | 0 | 0 | 9 | 605 |
| JW5130 | yccU | predicted CoA-binding protein with NAD(P)-binding Rossmann-fold domain | 0 | 0.096 | 1 | 0 | 8 | 605 |
| JW4158 | rpsF | 30S ribosomal subunit protein S6 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.745 | 0 | 0 | 9 | 604 |
| JW1716 | yniC | predicted hydrolase | 0 | 0.102 | 1 | 0 | 13 | 601 |
| JW1039 | msyB | predicted protein | 0 | -0.833 | 0 | 0 | 6 | 600 |
| JW0673 | ybfF | conserved protein | 0 | -0.213 | 0 | 0 | 13 | 599 |
| JW1477 | osmC | osmotically inducible, stress-inducible membrane protein | 0 | -0.122 | 0 | 0 | 7 | 599 |
| JW0779 | ybhG | predicted membrane fusion protein (MFP) component of efflux pump, membrane anchor | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.364 | 1 | 1 | 10 | 597 |
| JW0794 | glnQ | glutamine transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.138 | 0 | 0 | 8 | 597 |
| JW1046 | solA | N-methyltryptophan oxidase, FAD- | 0 | -0.234 | 0 | 0 | 11 | 597 |
| JW3006 | ygiC | predicted enzyme | 0 | -0.389 | 0 | 0 | 14 | 597 |
| JW5282 | astD | succinylglutamic semialdehyde dehydrogenase | 0 | -0.086 | 0 | 0 | 12 | 596 |
| JW2326 | aroC | chorismate synthase | 0 | -0.267 | 0 | 0 | 12 | 595 |
| JW0669 | fur | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.559 | 0 | 0 | 8 | 594 |
| JW2861 | dsbC | protein disulfide isomerase II | GO:0042597 periplasmic space | -0.103 | 0 | 0 | 10 | 594 |
| JW0741 | galT | galactose-1-phosphate uridylyltransferase | GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.524 | 0 | 0 | 13 | 593 |
| JW3691 | yieF | chromate reductase, Class I, | 0 | 0.060 | 1 | 0 | 8 | 593 |
| JW0849 | ybjP | predicted lipoprotein | 0 | -0.459 | 0 | 0 | 6 | 592 |
| JW2025 | rfbD | dTDP-4-dehydrorhamnose reductase subunit, NAD(P)-binding, of dTDP-L-rhamnose synthase | GO:0005737 cytoplasm | -0.093 | 0 | 0 | 10 | 592 |
| JW0443 | ybaY | predicted outer membrane lipoprotein | 0 | 0.176 | 1 | 0 | 5 | 591 |
| JW5040 | ykgC | predicted oxidoreductase with FAD/NAD(P)-binding domain and dimerization domain | 0 | -0.064 | 0 | 0 | 15 | 590 |
| JW0202 | gloB | predicted hydroxyacylglutathione hydrolase | 0 | -0.227 | 0 | 0 | 8 | 589 |
| JW3115 | yraL | predicted methyltransferase | 0 | -0.168 | 0 | 0 | 12 | 589 |
| JW2513 | iscU | scaffold protein | 0 | -0.355 | 0 | 0 | 8 | 587 |
| JW3162 | yrbF | predicted toluene transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | 0.133 | 1 | 0 | 12 | 587 |

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|--------|------|---|---|--------|---|---|----|-----|
| JW2001 | hisG | ATP phosphoribosyltransferase | GO:0005737 cytoplasm | -0.145 | 0 | 0 | 9 | 586 |
| JW2456 | dapE | N-succinyl-diaminopimelate deacylase | 0 | -0.066 | 0 | 0 | 13 | 586 |
| JW1853 | yebC | conserved protein | 0 | -0.384 | 0 | 0 | 9 | 585 |
| JW3097 | garD | (D)-galactarate dehydrogenase | 0 | -0.014 | 0 | 0 | 14 | 584 |
| JW5158 | ycfP | conserved protein | 0 | -0.591 | 0 | 0 | 10 | 584 |
| JW0304 | betB | betaine aldehyde dehydrogenase, NAD-dependent | 0 | -0.079 | 0 | 0 | 15 | 581 |
| JW3678 | dnaN | DNA polymerase III, beta subunit | GO:0005737 cytoplasm | -0.133 | 0 | 0 | 14 | 581 |
| JW5740 | orn | oligoribonuclease | 0 | -0.372 | 0 | 0 | 11 | 581 |
| JW0424 | yajG | predicted lipoprotein | 0 | -0.090 | 0 | 0 | 6 | 579 |
| JW1114 | ycfD | conserved protein | 0 | -0.436 | 0 | 0 | 9 | 579 |
| JW2407 | cysK | cysteine synthase A, O-acetylserine sulfhydrylase A subunit | GO:0005737 cytoplasm | -0.078 | 0 | 0 | 10 | 579 |
| JW4122 | rsgA | ribosome small subunit-dependent GTPase A | 0 | -0.405 | 0 | 0 | 10 | 579 |
| JW5578 | fadA | 3-ketoacyl-CoA thiolase (thiolase I) | GO:0005737 cytoplasm | 0.131 | 1 | 0 | 12 | 579 |
| JW0458 | apt | adenine phosphoribosyltransferase | GO:0005737 cytoplasm | 0.023 | 1 | 0 | 9 | 577 |
| JW1241 | cls | cardiolipin synthase 1 | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.190 | 1 | 2 | 11 | 577 |
| JW1834 | ptrB | protease II | 0 | -0.507 | 0 | 0 | 12 | 577 |
| JW2287 | yfbQ | predicted aminotransferase | 0 | -0.163 | 0 | 0 | 13 | 576 |
| JW2576 | rluD | 23S rRNA pseudouridine synthase | GO:0005737 cytoplasm | -0.416 | 0 | 0 | 12 | 576 |
| JW4193 | yjgA | conserved protein | 0 | -0.905 | 0 | 0 | 11 | 576 |
| JW0905 | mukF | Involved in chromosome partitioning, Ca2+ binding protein | 0 | -0.375 | 0 | 0 | 12 | 575 |
| JW0554 | ompT | DLP12 prophage; outer membrane protease VII (outer membrane protein 3b) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.645 | 1 | 0 | 15 | 574 |
| JW2017 | wbbK | lipopolysaccharide biosynthesis protein | 0 | -0.158 | 0 | 0 | 11 | 573 |
| JW0159 | yaeH | conserved protein | 0 | -0.811 | 0 | 0 | 10 | 571 |
| JW1512 | tam | trans-aconitate methyltransferase | GO:0005737 cytoplasm | -0.245 | 0 | 0 | 9 | 571 |
| JW3838 | hemN | coproporphyrinogen III oxidase, SAM and NAD(P)H dependent, oxygen- | 0 | -0.346 | 0 | 0 | 12 | 566 |
| JW2564 | ung | uracil-DNA-glycosylase | GO:0005737 cytoplasm | -0.283 | 0 | 0 | 11 | 565 |
| JW0786 | ybiC | predicted dehydrogenase | 0 | -0.084 | 0 | 0 | 8 | 564 |
| JW3038 | dnaG | DNA primase | GO:0005737 cytoplasm | -0.389 | 0 | 0 | 16 | 564 |
| JW5875 | nuoB | NADH:ubiquinone oxidoreductase, | GO:0005737 cytoplasm | -0.320 | 0 | 0 | 11 | 564 |
| JW2555 | rseB | anti-sigma factor | GO:0005737 cytoplasm | -0.257 | 0 | 0 | 11 | 563 |
| JW2889 | yggE | conserved protein | 0 | -0.252 | 0 | 0 | 9 | 561 |
| JW5950 | yjbN | tRNA-dihydrouridine synthase A | 0 | -0.291 | 0 | 0 | 12 | 561 |
| JW0130 | panB | 3-methyl-2-oxobutanoate hydroxymethyltransferase | GO:0005737 cytoplasm | 0.138 | 1 | 0 | 9 | 560 |
| JW1642 | nemA | N-ethylmaleimide reductase, FMN- | 0 | -0.311 | 0 | 0 | 12 | 560 |
| JW3413 | yhhA | conserved protein | 0 | -1.049 | 0 | 0 | 7 | 560 |
| JW5539 | yhcB | conserved protein | 0 | -0.552 | 1 | 1 | 7 | 560 |
| JW0181 | ldcC | lysine decarboxylase 2, constitutive | 0 | -0.189 | 0 | 0 | 14 | 559 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW0661 | nagD | UMP phosphatase | 0 | 0.109 | 1 | 0 | 8 | 559 |
| JW3281 | rplD | 50S ribosomal subunit protein L4 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.235 | 0 | 0 | 7 | 559 |
| JW4114 | frdB | fumarate reductase (anaerobic), Fe-S subunit | GO:0005737 cytoplasm | -0.224 | 0 | 0 | 8 | 559 |
| JW5603 | gpp | guanosine pentaphosphatase/exopolyphosphatase | GO:0005737 cytoplasm | -0.019 | 0 | 0 | 10 | 559 |
| JW0099 | yacF | conserved protein | 0 | -0.155 | 0 | 0 | 9 | 558 |
| JW0854 | ltaE | L-allo-threonine aldolase, PLP- | GO:0005737 cytoplasm | -0.128 | 0 | 0 | 13 | 557 |
| JW1220 | purU | formyltetrahydrofolate hydrolase | GO:0005737 cytoplasm | -0.166 | 0 | 0 | 8 | 557 |
| JW2992 | ygiW | conserved protein | 0 | -0.272 | 0 | 0 | 9 | 557 |
| JW5601 | wzzE | Entobacterial Common Antigen (ECA) polysaccharide chain length modulation protein | GO:0019866 inner membrane | -0.354 | 1 | 2 | 10 | 557 |
| JW3976 | aceK | isocitrate dehydrogenase kinase/phosphatase | 0 | -0.289 | 0 | 0 | 15 | 555 |
| JW5300 | proQ | predicted structural transport element | 0 | -0.776 | 0 | 0 | 8 | 555 |
| JW1287 | sapA | predicted antimicrobial peptide transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.322 | 0 | 0 | 13 | 554 |
| JW1668 | ynhG | conserved protein | 0 | -0.235 | 0 | 0 | 10 | 554 |
| JW5760 | yjgQ | conserved inner membrane protein | GO:0009274 cell wall (sensu | 0.320 | 1 | 6 | 8 | 553 |
| JW5538 | nanK | predicted N-acetylmannosamine kinase | GO:0005737 cytoplasm | 0.272 | 1 | 0 | 8 | 552 |
| JW3820 | fre | flavin reductase | 0 | -0.123 | 0 | 0 | 9 | 551 |
| JW1043 | ycel | predicted protein | 0 | -0.423 | 0 | 0 | 9 | 550 |
| JW2587 | rplS | 50S ribosomal subunit protein L19 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.527 | 0 | 0 | 9 | 550 |
| JW3949 | rplL | 50S ribosomal subunit protein L7/L12 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.295 | 1 | 0 | 8 | 550 |
| JW5668 | kdgK | ketodeoxygluconokinase | 0 | -0.195 | 0 | 0 | 8 | 550 |
| JW5413 | rimM | 16S rRNA processing protein | 0 | -0.290 | 0 | 0 | 9 | 549 |
| JW0377 | proC | pyrroline-5-carboxylate reductase, NAD(P)-binding | GO:0005737 cytoplasm | 0.318 | 1 | 0 | 7 | 548 |
| JW2064 | baeR | DNA-binding response regulator in two-component regulatory system with | GO:0005737 cytoplasm | -0.281 | 0 | 0 | 11 | 548 |
| JW2509 | fdx | [2Fe-2S] ferredoxin | 0 | -0.357 | 0 | 0 | 7 | 548 |
| JW2260 | menF | isochorismate synthase 2 | 0 | -0.340 | 0 | 0 | 11 | 546 |
| JW3474 | slp | outer membrane lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.140 | 1 | 0 | 6 | 546 |
| JW4128 | mutL | methyl-directed mismatch repair protein | GO:0005737 cytoplasm | -0.257 | 0 | 0 | 12 | 546 |
| JW0755 | ybhC | predicted pectinesterase | GO:0009279 external outer membrane (sensu Gram-negative | -0.358 | 1 | 0 | 8 | 545 |

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|--------|------|---|--|--------|---|---|----|-----|
| JW0869 | cydC | fused cysteine transporter subunits -!- membrane component and ATP-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.244 | 1 | 6 | 12 | 544 |
| JW1489 | pqqL | predicted peptidase | GO:0005737 cytoplasm | -0.397 | 1 | 1 | 15 | 542 |
| JW3171 | ptsN | sugar-specific enzyme IIA component of PTS | 0 | -0.167 | 0 | 0 | 8 | 541 |
| JW2261 | elaB | conserved protein | 0 | -0.520 | 1 | 1 | 8 | 540 |
| JW5930 | yihA | GTP-binding protein | 0 | -0.437 | 0 | 0 | 9 | 540 |
| JW2003 | hisC | histidinol-phosphate aminotransferase | 0 | -0.035 | 0 | 0 | 10 | 539 |
| JW0902 | ycbJ | conserved protein | 0 | -0.303 | 0 | 0 | 12 | 537 |
| JW1370 | uspF | stress-induced protein, ATP-binding protein | 0 | 0.022 | 1 | 0 | 8 | 537 |
| JW0050 | ksgA | S-adenosylmethionine-6-N',N'-adenosyl (rRNA) dimethyltransferase | GO:0005737 cytoplasm | -0.101 | 0 | 0 | 10 | 536 |
| JW2733 | cysI | sulfite reductase, beta subunit, NAD(P)-binding | 0 | -0.434 | 0 | 0 | 15 | 535 |
| JW1702 | ihfA | integration host factor (IHF), DNA-binding protein, alpha subunit | GO:0005737 cytoplasm | -0.874 | 0 | 0 | 10 | 534 |
| JW2712 | nlpD | predicted outer membrane lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.403 | 1 | 0 | 9 | 534 |
| JW5642 | dfp | fused 4'-phosphopantothencysteine decarboxylase -!- phosphopantothencysteine synthetase, FMN-binding | GO:0005737 cytoplasm | 0.030 | 1 | 0 | 9 | 534 |
| JW1463 | narZ | nitrate reductase 2 (NRZ), alpha subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.443 | 1 | 0 | 14 | 533 |
| JW3136 | rbfA | 30s ribosome binding factor | GO:0005737 cytoplasm | -0.398 | 0 | 0 | 7 | 533 |
| JW3737 | yifE | conserved protein | 0 | -1.069 | 0 | 0 | 9 | 532 |
| JW1181 | ldcA | L,D-carboxypeptidase A | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.016 | 1 | 0 | 9 | 531 |
| JW1639 | ydhF | predicted oxidoreductase | 0 | -0.120 | 0 | 0 | 10 | 530 |
| JW3623 | gmK | guanylate kinase | GO:0005737 cytoplasm | -0.430 | 0 | 0 | 8 | 530 |
| JW2500 | yfgA | conserved protein | 0 | -0.391 | 1 | 1 | 8 | 529 |
| JW5181 | hlyE | hemolysin E | GO:0005576 extracellular | -0.212 | 1 | 1 | 8 | 529 |
| JW0901 | kdsB | 3-deoxy-manno-octulosonate cytidyltransferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0030113 capsule (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.145 | 0 | 0 | 8 | 527 |
| JW1693 | ydiA | conserved protein | 0 | -0.093 | 0 | 0 | 9 | 527 |
| JW0470 | ybaK | conserved protein | 0 | -0.083 | 0 | 0 | 6 | 526 |
| JW3674 | yidA | predicted hydrolase | 0 | -0.002 | 0 | 0 | 7 | 526 |
| JW0674 | seqA | regulatory protein for replication initiation | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.286 | 1 | 0 | 9 | 525 |
| JW5548 | nudC | NADH pyrophosphatase | 0 | -0.337 | 0 | 0 | 11 | 525 |
| JW0084 | murF | UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine ligase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.165 | 1 | 0 | 10 | 523 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW0090 | ddlB | D-Alanine:D-alanine ligase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.077 | 1 | 0 | 11 | 523 |
| JW1273 | pyrF | orotidine-5'-phosphate decarboxylase | 0 | 0.057 | 1 | 0 | 9 | 523 |
| JW3027 | htrG | predicted signal transduction protein (SH3 domain) | GO:0009274 cell wall (sensu Bacteria) | -0.430 | 1 | 1 | 9 | 522 |
| JW3242 | aroE | dehydroshikimate reductase, NAD(P)-binding | 0 | 0.088 | 1 | 0 | 9 | 522 |
| JW5682 | dcxB | periplasmic protein | 0 | -0.229 | 0 | 0 | 8 | 521 |
| JW0197 | dkgB | 2,5-diketo-D-gluconate reductase B | GO:0005737 cytoplasm | -0.114 | 0 | 0 | 10 | 520 |
| JW0518 | folD | bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase -!- 5,10-methylene-tetrahydrofolate | 0 | 0.048 | 1 | 0 | 8 | 520 |
| JW1072 | rluC | 23S rRNA pseudouridylate synthase | GO:0005737 cytoplasm | -0.461 | 0 | 0 | 15 | 520 |
| JW2765 | yqcD | conserved protein | 0 | -0.530 | 0 | 0 | 10 | 520 |
| JW4217 | pepA | aminopeptidase A, a cyteinyglycine | GO:0005737 cytoplasm | -0.217 | 0 | 0 | 10 | 519 |
| JW3271 | rplX | 50S ribosomal subunit protein L24 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.381 | 0 | 0 | 8 | 518 |
| JW1823 | yebT | conserved protein | GO:0009274 cell wall (sensu Bacteria) | -0.098 | 1 | 1 | 14 | 517 |
| JW5898 | yccW | predicted methyltransferase | 0 | -0.190 | 0 | 0 | 14 | 517 |
| JW4175 | ytfJ | predicted transcriptional regulator | 0 | -0.205 | 0 | 0 | 8 | 513 |
| JW1794 | fadD | acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase) | GO:0009274 cell wall (sensu Bacteria) | -0.098 | 0 | 0 | 11 | 512 |
| JW1982 | flu | CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter | 0 | -0.275 | 1 | 1 | 11 | 512 |
| JW3311 | slyD | FKBP-type peptidyl prolyl cis-trans isomerase (rotamase) | 0 | -0.383 | 0 | 0 | 5 | 512 |
| JW3837 | yihI | conserved protein | 0 | -1.377 | 0 | 0 | 7 | 511 |
| JW1773 | yeaH | conserved protein | 0 | -0.725 | 0 | 0 | 12 | 509 |
| JW3895 | fpr | ferredoxin-NADP reductase | 0 | -0.194 | 0 | 0 | 12 | 509 |
| JW3538 | xylF | D-xylose transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.128 | 0 | 0 | 11 | 508 |
| JW1269 | ribA | GTP cyclohydrolase II | 0 | -0.181 | 0 | 0 | 10 | 507 |
| JW4349 | lplA | lipoate-protein ligase A | GO:0005737 cytoplasm | -0.328 | 0 | 0 | 10 | 506 |
| JW0671 | fldA | flavodoxin 1 | 0 | -0.285 | 0 | 0 | 7 | 505 |
| JW0844 | artJ | arginine transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.281 | 0 | 0 | 10 | 504 |
| JW2007 | hisF | imidazole glycerol phosphate synthase, catalytic subunit with HisF | GO:0005737 cytoplasm | -0.044 | 0 | 0 | 10 | 504 |
| JW3586 | yibN | predicted rhodanese-related sulfurtransferase | 0 | 0.064 | 1 | 1 | 7 | 504 |
| JW1671 | sufD | component of SufBCD complex | 0 | -0.343 | 0 | 0 | 10 | 503 |
| JW1109 | potD | polyamine transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.445 | 0 | 0 | 11 | 502 |

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|--------|------|--|--|--------|---|---|----|-----|
| JW3981 | pepE | (alpha)-aspartyl dipeptidase | 0 | 0.124 | 1 | 0 | 8 | 502 |
| JW5186 | dhaL | dihydroxyacetone kinase, C-terminal domain | 0 | -0.106 | 0 | 0 | 8 | 502 |
| JW0597 | dsbG | periplasmic disulfide isomerase/thiol-disulphide oxidase | GO:0042597 periplasmic space | -0.218 | 0 | 0 | 10 | 501 |
| JW1633 | slyB | outer membrane lipoprotein | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 0.114 | 1 | 0 | 6 | 501 |
| JW3932 | argH | argininosuccinate lyase | GO:0005737 cytoplasm | -0.189 | 0 | 0 | 11 | 501 |
| JW5265 | ydjJ | predicted oxidoreductase | 0 | -0.221 | 0 | 0 | 11 | 500 |
| JW5860 | yidR | conserved protein | 0 | -0.463 | 0 | 0 | 9 | 500 |
| JW1318 | ycjG | L-Ala-D/L-Glu epimerase | 0 | 0.092 | 1 | 0 | 10 | 499 |
| JW2578 | yfiA | cold shock protein associated with 30S ribosomal subunit | GO:0009281 cytosolic ribosome (sensu Bacteria) | -0.535 | 0 | 0 | 6 | 499 |
| JW3961 | hemE | uroporphyrinogen decarboxylase | 0 | -0.156 | 0 | 0 | 11 | 498 |
| JW0198 | yafC | predicted DNA-binding transcriptional regulator | 0 | -0.122 | 0 | 0 | 12 | 497 |
| JW3466 | yhiR | predicted DNA (exogenous) processing protein | 0 | -0.361 | 0 | 0 | 13 | 497 |
| JW3929 | argE | acetylornithine deacetylase | GO:0005737 cytoplasm | -0.181 | 0 | 0 | 8 | 497 |
| JW3156 | murA | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | GO:0009274 cell wall (sensu Bacteria) | 0.070 | 1 | 0 | 11 | 496 |
| JW3904 | ftsN | essential cell division protein | GO:0019866 inner membrane | -1.024 | 1 | 1 | 9 | 496 |
| JW0888 | ycaO | conserved protein | 0 | -0.196 | 0 | 0 | 10 | 495 |
| JW1093 | nagZ | beta N-acetyl-glucosaminidase | 0 | -0.293 | 0 | 0 | 9 | 495 |
| JW2795 | thyA | thymidylate synthetase | GO:0005737 cytoplasm | -0.382 | 0 | 0 | 8 | 495 |
| JW1084 | tmk | thymidylate kinase | 0 | -0.202 | 0 | 0 | 10 | 494 |
| JW1893 | ftn | ferritin iron storage protein (cytoplasmic) | GO:0005737 cytoplasm | -0.568 | 0 | 0 | 8 | 494 |
| JW2789 | ptr | protease III | 0 | -0.369 | 0 | 0 | 16 | 494 |
| JW3326 | ppiA | peptidyl-prolyl cis-trans isomerase A (rotamase A) | 0 | -0.135 | 0 | 0 | 7 | 494 |
| JW5878 | csiE | stationary phase inducible protein | 0 | -0.231 | 0 | 0 | 9 | 494 |
| JW3763 | rffH | glucose-1-phosphate thymidyltransferase | 0 | -0.186 | 0 | 0 | 7 | 493 |
| JW2077 | gatB | galactitol-specific enzyme IIB component of PTS | GO:0005737 cytoplasm | 0.306 | 1 | 0 | 5 | 491 |
| JW0123 | yadG | predicted transporter subunit - - ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.237 | 0 | 0 | 12 | 490 |
| JW1913 | yedD | predicted protein | 0 | -0.195 | 0 | 0 | 8 | 490 |
| JW3779 | cyaY | frataxin, iron-binding and oxidizing | 0 | -0.592 | 0 | 0 | 7 | 490 |
| JW5267 | slyA | DNA-binding transcriptional activator | GO:0005737 cytoplasm | -0.277 | 0 | 0 | 7 | 490 |
| JW2502 | ndk | multifunctional nucleoside diphosphate kinase - - apyrimidinic endonuclease - - 3'-phosphodiesterase | GO:0042597 periplasmic space | -0.082 | 0 | 0 | 6 | 489 |
| JW2551 | rnc | RNase III | 0 | -0.449 | 0 | 0 | 12 | 489 |
| JW3169 | rpoN | RNA polymerase, sigma 54 (sigma N) factor | 0 | -0.435 | 0 | 0 | 8 | 489 |
| JW5559 | yiiM | conserved protein | 0 | -0.417 | 0 | 0 | 10 | 488 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW5841 | prmB | N5-glutamine methyltransferase | 0 | -0.153 | 0 | 0 | 9 | 487 |
| JW0478 | ybbK | predicted protease, membrane | GO:0009274 cell wall (sensu | -0.020 | 1 | 1 | 7 | 486 |
| JW4178 | msrA | methionine sulfoxide reductase A | 0 | -0.333 | 0 | 0 | 6 | 486 |
| JW1226 | tdk | thymidine kinase/deoxyuridine kinase | 0 | -0.320 | 0 | 0 | 8 | 485 |
| JW0210 | ivy | inhibitor of vertebrate C-lysozyme | 0 | -0.103 | 0 | 0 | 6 | 484 |
| JW1860 | yecP | predicted methyltransferase | 0 | -0.241 | 0 | 0 | 10 | 484 |
| JW2173 | rplY | 50S ribosomal subunit protein L25 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.468 | 0 | 0 | 8 | 484 |
| JW3172 | yhbJ | predicted protein with nucleoside triphosphate hydrolase domain | 0 | -0.316 | 0 | 0 | 10 | 484 |
| JW3859 | yiiD | predicted acetyltransferase | 0 | -0.354 | 0 | 0 | 8 | 483 |
| JW2782 | ygdK | predicted Fe-S metabolism protein | 0 | -0.086 | 0 | 0 | 6 | 482 |
| JW1896 | yecA | conserved metal-binding protein | 0 | -0.392 | 0 | 0 | 5 | 481 |
| JW3125 | yhbS | predicted acyltransferase with acyl-CoA N-acyltransferase domain | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.075 | 1 | 0 | 7 | 481 |
| JW0459 | dnaX | DNA polymerase III/DNA elongation factor III, tau and gamma subunits | GO:0005737 cytoplasm | -0.258 | 0 | 0 | 13 | 480 |
| JW1789 | yeaU | predicted dehydrogenase | 0 | -0.221 | 0 | 0 | 13 | 480 |
| JW2501 | yfgB | predicted enzyme | 0 | -0.291 | 0 | 0 | 10 | 478 |
| JW0116 | speD | S-adenosylmethionine decarboxylase | 0 | -0.313 | 0 | 0 | 10 | 477 |
| JW0934 | pqiB | paraquat-inducible protein B | 0 | -0.280 | 1 | 1 | 11 | 477 |
| JW2243 | yfaY | conserved protein | 0 | -0.055 | 0 | 0 | 9 | 477 |
| JW3009 | ribB | 3,4 dihydroxy-2-butanone-4-phosphate synthase | 0 | -0.147 | 0 | 0 | 6 | 477 |
| JW5362 | yeiP | predicted elongation factor | 0 | -0.379 | 0 | 0 | 8 | 476 |
| JW0434 | ybaX | predicted aluminum resistance protein | 0 | -0.095 | 0 | 0 | 10 | 475 |
| JW0089 | murC | UDP-N-acetylmuramate:L-alanine ligase | GO:0009274 cell wall (sensu | -0.161 | 0 | 0 | 12 | 474 |
| JW2758 | gudD | (D)-glucarate dehydratase 1 | 0 | -0.222 | 0 | 0 | 11 | 474 |
| JW3883 | cpxR | DNA-binding response regulator in two-component regulatory system with CpxA | GO:0005737 cytoplasm | -0.344 | 0 | 0 | 8 | 474 |
| JW3058 | ygjR | predicted NAD(P)-binding | 0 | 0.046 | 1 | 0 | 7 | 473 |
| JW3129 | yhbW | predicted enzyme | 0 | -0.166 | 0 | 0 | 11 | 472 |
| JW1167 | ycgK | predicted protein | 0 | -0.634 | 0 | 0 | 7 | 470 |
| JW3252 | mscL | mechanosensitive channel | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.499 | 1 | 2 | 7 | 470 |
| JW1964 | yeeN | conserved protein | 0 | -0.258 | 0 | 0 | 7 | 469 |
| JW1529 | ydeI | conserved protein | 0 | -0.298 | 0 | 0 | 6 | 468 |
| JW2376 | yfdZ | predicted aminotransferase, PLP-dependent | 0 | -0.187 | 0 | 0 | 9 | 467 |
| JW1254 | trpC | fused indole-3-glycerolphosphate synthetase -!- N-(5-phosphoribosyl)anthranilate isomerase | GO:0005737 cytoplasm | -0.025 | 0 | 0 | 11 | 466 |
| JW1781 | yeaO | conserved protein | 0 | -0.641 | 0 | 0 | 9 | 466 |
| JW3251 | trkA | NAD-binding component of Trk potassium transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.015 | 1 | 0 | 11 | 466 |
| JW1261 | rluB | 23S rRNA pseudouridylate synthase | 0 | -0.585 | 0 | 0 | 11 | 465 |

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|--------|------|---|---|--------|---|----|----|-----|
| JW3322 | argD | bifunctional acetylornithine aminotransferase -/- succinyldiaminopimelate | GO:0005737 cytoplasm | 0.045 | 1 | 0 | 10 | 465 |
| JW0514 | ppiB | peptidyl-prolyl cis-trans isomerase B (rotamase B) | GO:0005737 cytoplasm | -0.312 | 0 | 0 | 8 | 464 |
| JW3377 | gntY | predicted gluconate transport associated protein | 0 | -0.256 | 0 | 0 | 7 | 463 |
| JW0601 | ybdR | predicted oxidoreductase, Zn-dependent and NAD(P)-binding | 0 | -0.011 | 0 | 0 | 11 | 462 |
| JW2050 | dcd | 2'-deoxycytidine 5'-triphosphate deaminase | 0 | -0.162 | 0 | 0 | 9 | 462 |
| JW0067 | tbpA | thiamin transporter subunit -/- periplasmic-binding component of ABC | GO:0042597 periplasmic space | -0.176 | 0 | 0 | 7 | 461 |
| JW1248 | ompW | outer membrane protein W | GO:0009274 cell wall (sensu Bacteria) -/- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.027 | 1 | 0 | 7 | 461 |
| JW3277 | rplV | 50S ribosomal subunit protein L22 | GO:0009281 cytosolic ribosome (sensu Bacteria) -/- GO:0005737 cytoplasm | -0.349 | 0 | 0 | 6 | 460 |
| JW3480 | gadE | DNA-binding transcriptional activator | 0 | -0.198 | 0 | 0 | 8 | 460 |
| JW3805 | metE | 5-methyltetrahydropteroyltrimethylhomocysteine S-methyltransferase | GO:0005737 cytoplasm | -0.258 | 0 | 0 | 9 | 460 |
| JW0511 | purK | N5-carboxyaminoimidazole ribonucleotide synthase | GO:0005737 cytoplasm | -0.139 | 0 | 0 | 11 | 459 |
| JW1032 | ymdB | conserved protein | 0 | 0.007 | 1 | 0 | 8 | 457 |
| JW0819 | yliG | predicted SAM-dependent methyltransferase | 0 | -0.280 | 0 | 0 | 10 | 456 |
| JW3900 | rraA | ribonuclease E (RNase E) inhibitor | 0 | 0.054 | 1 | 0 | 6 | 456 |
| JW3703 | pstB | phosphate transporter subunit -/- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.270 | 0 | 0 | 9 | 455 |
| JW4003 | lexA | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.241 | 0 | 0 | 8 | 455 |
| JW3427 | ftsX | predicted transporter subunit -/- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -/- GO:0019866 inner | 0.192 | 1 | 4 | 10 | 454 |
| JW1163 | minE | cell division topological specificity factor | GO:0005737 cytoplasm | -0.294 | 0 | 0 | 7 | 453 |
| JW2674 | srlD | sorbitol-6-phosphate dehydrogenase | 0 | 0.130 | 1 | 0 | 8 | 452 |
| JW4080 | mela | alpha-galactosidase, NAD(P)-binding | 0 | -0.182 | 0 | 0 | 11 | 452 |
| JW4083 | fumB | anaerobic class I fumarate hydratase (fumarase B) | 0 | -0.316 | 0 | 0 | 9 | 452 |
| JW1836 | yebF | predicted protein | 0 | -0.411 | 0 | 0 | 7 | 451 |
| JW3839 | glnG | fused DNA-binding response regulator in two-component regulatory system with GlnL, nitrogen regulator I (NRI) | GO:0005737 cytoplasm | -0.246 | 0 | 0 | 12 | 451 |
| JW3328 | nirB | nitrite reductase, large subunit, NAD(P)H-binding | GO:0005737 cytoplasm | -0.211 | 0 | 0 | 15 | 450 |
| JW0590 | cstA | carbon starvation protein | GO:0009274 cell wall (sensu Bacteria) -/- GO:0019866 inner | 0.782 | 1 | 18 | 8 | 449 |

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|--------|------|---|---|--------|---|---|----|-----|
| JW1658 | ydhS | conserved protein with FAD/NAD(P)-binding domain | 0 | -0.318 | 0 | 0 | 12 | 449 |
| JW1576 | speG | spermidine N1-acetyltransferase | 0 | -0.439 | 0 | 0 | 9 | 447 |
| JW1579 | ynfE | oxidoreductase subunit | 0 | -0.443 | 0 | 0 | 11 | 447 |
| JW2171 | rsuA | 16S rRNA pseudouridylate 516 synthase | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.363 | 0 | 0 | 7 | 447 |
| JW3164 | kdsD | D-arabinose 5-phosphate isomerase | GO:0030113 capsule (sensu | 0.223 | 1 | 0 | 8 | 447 |
| JW4340 | yjiU | predicted esterase | 0 | -0.152 | 0 | 0 | 6 | 447 |
| JW5165 | hflD | predicted lysogenization regulator | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.127 | 1 | 0 | 7 | 447 |
| JW5376 | yfbT | predicted hydrolase or phosphatase | 0 | 0.142 | 1 | 0 | 9 | 447 |
| JW0756 | ybhB | predicted kinase inhibitor | 0 | -0.180 | 0 | 0 | 7 | 446 |
| JW0768 | moaE | molybdopterin synthase, large subunit | 0 | -0.497 | 0 | 0 | 5 | 446 |
| JW2125 | yohF | predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain | 0 | 0.079 | 1 | 0 | 6 | 446 |
| JW3946 | rplK | 50S ribosomal subunit protein L11 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.061 | 0 | 0 | 7 | 446 |
| JW1314 | ycjX | conserved protein with nucleoside triphosphate hydrolase domain | 0 | -0.243 | 0 | 0 | 11 | 445 |
| JW3199 | rpsI | 30S ribosomal subunit protein S9 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.687 | 0 | 0 | 8 | 445 |
| JW3830 | yihD | conserved protein | 0 | -0.424 | 0 | 0 | 6 | 445 |
| JW5606 | ilvE | branched-chain amino-acid aminotransferase | 0 | -0.165 | 0 | 0 | 7 | 445 |
| JW5600 | rffE | UDP-N-acetyl glucosamine-2-epimerase | GO:0005737 cytoplasm | -0.151 | 0 | 0 | 10 | 444 |
| JW5019 | yafV | predicted C-N hydrolase family amidase, NAD(P)-binding | 0 | -0.213 | 0 | 0 | 7 | 443 |
| JW1732 | spy | envelope stress induced periplasmic protein | GO:0042597 periplasmic space | -0.758 | 0 | 0 | 8 | 442 |
| JW2280 | nuoE | NADH:ubiquinone oxidoreductase, | GO:0005737 cytoplasm | -0.392 | 0 | 0 | 6 | 442 |
| JW3496 | dctA | C4-dicarboxylic acid, orotate and citrate transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.872 | 1 | 8 | 9 | 442 |
| JW4311 | hsdS | specificity determinant for hsdM and | GO:0005737 cytoplasm | -0.261 | 0 | 0 | 11 | 442 |
| JW5831 | znuA | zinc transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.211 | 0 | 0 | 8 | 442 |
| JW0636 | rlpB | minor lipoprotein | GO:0019866 inner membrane | -0.252 | 1 | 0 | 9 | 441 |
| JW5529 | yhbO | predicted intracellular protease | 0 | -0.242 | 0 | 0 | 7 | 441 |
| JW3144 | folP | 7,8-dihydropteroate synthase | 0 | -0.022 | 0 | 0 | 11 | 440 |
| JW3256 | rplQ | 50S ribosomal subunit protein L17 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.565 | 0 | 0 | 8 | 440 |
| JW1276 | yciT | predicted DNA-binding transcriptional regulator | 0 | -0.092 | 0 | 0 | 10 | 439 |

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|--------|------|---|---|--------|---|---|----|-----|
| JW1771 | mipA | scaffolding protein for murein synthesizing machinery | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.402 | 1 | 0 | 6 | 438 |
| JW2276 | nuoI | NADH:ubiquinone oxidoreductase, | GO:0005737 cytoplasm | -0.327 | 0 | 0 | 9 | 438 |
| JW5009 | hpt | hypoxanthine phosphoribosyltransferase | GO:0005737 cytoplasm | -0.069 | 0 | 0 | 7 | 438 |
| JW5155 | yceF | predicted protein | 0 | -0.302 | 0 | 0 | 7 | 437 |
| JW0494 | allR | DNA-binding transcriptional regulator | GO:0005737 cytoplasm | 0.073 | 1 | 0 | 8 | 436 |
| JW1530 | ydeJ | conserved protein | 0 | 0.116 | 1 | 0 | 6 | 436 |
| JW3536 | xylB | xylulokinase | 0 | -0.092 | 0 | 0 | 10 | 435 |
| JW3903 | hslV | peptidase component of the HslUV protease | GO:0005737 cytoplasm | -0.034 | 0 | 0 | 8 | 435 |
| JW5655 | yiaF | conserved protein | 0 | -0.151 | 1 | 1 | 7 | 435 |
| JW0427 | clpP | proteolytic subunit of ClpA-ClpP and ClpX-ClpP ATP-dependent serine | GO:0005737 cytoplasm | -0.154 | 0 | 0 | 7 | 434 |
| JW2460 | ypfJ | conserved protein | 0 | -0.512 | 1 | 1 | 6 | 434 |
| JW2575 | yfiH | conserved protein | 0 | -0.141 | 0 | 0 | 7 | 434 |
| JW3831 | yihE | predicted kinase | 0 | -0.317 | 0 | 0 | 12 | 434 |
| JW1179 | dadX | alanine racemase 2, PLP-binding | 0 | -0.026 | 0 | 0 | 10 | 433 |
| JW5946 | gntR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.104 | 0 | 0 | 10 | 433 |
| JW2913 | yggJ | predicted protein | 0 | -0.216 | 0 | 0 | 8 | 432 |
| JW3394 | glgX | glycogen debranching enzyme | GO:0005737 cytoplasm | -0.341 | 0 | 0 | 14 | 432 |
| JW0048 | apaH | diadenosine tetraphosphatase | GO:0005737 cytoplasm | -0.246 | 0 | 0 | 9 | 431 |
| JW0395 | queA | S-adenosylmethionine:tRNA ribosyltransferase-isomerase | GO:0005737 cytoplasm | -0.129 | 0 | 0 | 8 | 431 |
| JW2144 | yeiE | predicted DNA-binding transcriptional regulator | 0 | 0.017 | 1 | 0 | 10 | 431 |
| JW5157 | ycfM | predicted outer membrane lipoprotein | 0 | -0.215 | 0 | 0 | 5 | 431 |
| JW1272 | yciM | conserved protein | 0 | -0.365 | 0 | 0 | 10 | 430 |
| JW1776 | yeaK | conserved protein | 0 | 0.165 | 1 | 0 | 8 | 430 |
| JW2927 | yggH | tRNA (m7G46) methyltransferase, SAM-dependent | 0 | -0.397 | 0 | 0 | 8 | 430 |
| JW5531 | deaD | ATP-dependent RNA helicase | GO:0005737 cytoplasm | -0.586 | 0 | 0 | 7 | 430 |
| JW2700 | hypE | carbamoyl phosphate phosphatase, hydrogenase 3 maturation protein | 0 | 0.329 | 1 | 0 | 10 | 429 |
| JW5790 | yjiA | predicted GTPase | 0 | -0.085 | 0 | 0 | 8 | 428 |
| JW1338 | ydaO | predicted C32 tRNA thiolase | 0 | -0.455 | 0 | 0 | 7 | 427 |
| JW2697 | hypB | GTP hydrolase involved in nickel liganding into hydrogenases | 0 | -0.238 | 0 | 0 | 7 | 427 |
| JW2985 | sufl | repressor protein for FtsI | 0 | -0.175 | 0 | 0 | 10 | 427 |
| JW3646 | ilvB | acetolactate synthase I, large subunit | 0 | 0.041 | 1 | 0 | 10 | 427 |
| JW1755 | sppA | protease IV (signal peptide peptidase) | 0 | -0.111 | 1 | 1 | 12 | 426 |
| JW0051 | pdxA | 4-hydroxy-L-threonine phosphate dehydrogenase, NAD-dependent | GO:0005737 cytoplasm | 0.192 | 1 | 0 | 8 | 425 |
| JW5057 | yajL | conserved protein | 0 | 0.323 | 1 | 0 | 7 | 425 |
| JW1756 | ansA | cytoplasmic L-asparaginase I | GO:0005737 cytoplasm | -0.187 | 0 | 0 | 7 | 424 |

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|--------|------|---|---|--------|---|----|----|-----|
| JW2716 | ispF | 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase | GO:0005737 cytoplasm | 0.089 | 1 | 0 | 6 | 424 |
| JW5566 | yihX | predicted hydrolase | 0 | -0.158 | 0 | 0 | 7 | 424 |
| JW2874 | visC | predicted oxidoreductase, FAD/NAD(P)-binding domain | 0 | -0.132 | 0 | 0 | 9 | 423 |
| JW2644 | stpA | DNA binding protein, nucleoid- | GO:0005737 cytoplasm | -0.794 | 0 | 0 | 7 | 422 |
| JW4020 | ssb | Single-stranded DNA-binding protein | GO:0005737 cytoplasm | -0.708 | 0 | 0 | 7 | 422 |
| JW5676 | rbbA | fused ribosome-associated ATPases | GO:0005737 cytoplasm | 0.077 | 1 | 5 | 11 | 422 |
| JW0387 | sbcC | exonuclease, dsDNA, ATP-dependent | GO:0005737 cytoplasm | -0.635 | 0 | 0 | 9 | 421 |
| JW1694 | aroH | 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tryptophan repressible | 0 | -0.315 | 0 | 0 | 9 | 420 |
| JW5769 | yjhc | KpLE2 phage-like element; predicted oxidoreductase | 0 | -0.266 | 0 | 0 | 8 | 420 |
| JW2339 | yfcY | beta-ketoacyl-CoA thiolase, anaerobic, subunit | 0 | 0.039 | 1 | 0 | 9 | 419 |
| JW2924 | ansB | periplasmic L-asparaginase II | GO:0042597 periplasmic space | -0.114 | 1 | 1 | 7 | 418 |
| JW1821 | yebR | conserved protein | 0 | 0.168 | 1 | 0 | 8 | 417 |
| JW2566 | trxC | thioredoxin 2 | 0 | -0.200 | 0 | 0 | 7 | 417 |
| JW3135 | truB | tRNA pseudouridine synthase | GO:0005737 cytoplasm | -0.368 | 0 | 0 | 9 | 415 |
| JW3331 | cysG | fused siroheme synthase 1,3-dimethyluroporphyriongen III dehydrogenase/siroheme ferrochelatase -!- uroporphyrinogen methyltransferase | 0 | -0.042 | 0 | 0 | 11 | 414 |
| JW5339 | yegP | predicted protein | 0 | -0.711 | 0 | 0 | 6 | 414 |
| JW0467 | ybaL | predicted transporter with NAD(P)-binding Rossmann-fold domain | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.805 | 1 | 12 | 9 | 413 |
| JW1426 | tehB | predicted S-adenosyl-L-methionine-dependent methyltransferase | 0 | -0.376 | 0 | 0 | 9 | 413 |
| JW2156 | fruB | fused fructose-specific PTS enzyme IIA component -!- HPr component | GO:0005737 cytoplasm | -0.029 | 0 | 0 | 7 | 413 |
| JW0603 | rna | ribonuclease I | GO:0005737 cytoplasm | -0.412 | 0 | 0 | 9 | 412 |
| JW2076 | gatC | galactitol-specific enzyme IIC component of PTS | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.824 | 1 | 11 | 5 | 411 |
| JW2552 | lepB | leader peptidase (signal peptidase I) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.156 | 1 | 2 | 9 | 411 |
| JW0421 | cyoB | cytochrome o ubiquinol oxidase subunit I | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.658 | 1 | 14 | 7 | 409 |
| JW2234 | glpT | sn-glycerol-3-phosphate transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.493 | 1 | 12 | 9 | 409 |
| JW5196 | yciO | conserved protein | 0 | -0.311 | 0 | 0 | 7 | 409 |
| JW5804 | ycjY | predicted hydrolase | 0 | -0.387 | 0 | 0 | 9 | 409 |
| JW2066 | yegQ | predicted peptidase | 0 | -0.410 | 0 | 0 | 10 | 408 |
| JW3195 | nanR | DNA-binding transcriptional dual | 0 | -0.408 | 0 | 0 | 8 | 408 |
| JW3259 | rpsK | 30S ribosomal subunit protein S11 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.446 | 0 | 0 | 6 | 408 |

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|--------|------|--|---|--------|---|----|----|-----|
| JW5060 | bolA | regulator of penicillin binding proteins and beta lactamase transcription | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.190 | 0 | 0 | 5 | 407 |
| JW3154 | ispB | octaprenyl diphosphate synthase | 0 | -0.095 | 0 | 0 | 8 | 406 |
| JW3909 | metJ | DNA-binding transcriptional repressor, S-adenosylmethionine-binding | GO:0005737 cytoplasm | -0.748 | 0 | 0 | 7 | 406 |
| JW4072 | proP | proline/glycine betaine transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.558 | 1 | 12 | 7 | 406 |
| JW5302 | yebV | predicted protein | 0 | -0.451 | 0 | 0 | 5 | 406 |
| JW5264 | ynfK | predicted dethiobiotin synthetase | 0 | 0.135 | 1 | 0 | 8 | 405 |
| JW5558 | cpxP | periplasmic protein combats stress | GO:0005737 cytoplasm -!- GO:0042597 periplasmic space | -0.787 | 0 | 0 | 6 | 405 |
| JW3160 | yrbD | predicted ABC-type organic solvent transporter | 0 | -0.068 | 1 | 1 | 7 | 404 |
| JW3428 | ftsE | predicted transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.077 | 0 | 0 | 8 | 404 |
| JW5162 | lolD | outer membrane-specific lipoprotein transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.182 | 0 | 0 | 6 | 404 |
| JW1646 | ydhD | conserved protein | 0 | -0.272 | 0 | 0 | 4 | 403 |
| JW2051 | udk | uridine/cytidine kinase | 0 | -0.258 | 0 | 0 | 9 | 403 |
| JW3283 | rpsJ | 30S ribosomal subunit protein S10 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.352 | 0 | 0 | 6 | 403 |
| JW0908 | ycbB | predicted carboxypeptidase | 0 | -0.276 | 0 | 0 | 13 | 401 |
| JW5672 | yhiQ | predicted SAM-dependent methyltransferase | 0 | -0.009 | 0 | 0 | 7 | 401 |
| JW1213 | narX | sensory histidine kinase in two-component regulatory system with NarL | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.213 | 1 | 2 | 9 | 400 |
| JW1993 | sbcB | exonuclease I | 0 | -0.401 | 0 | 0 | 13 | 400 |
| JW2155 | fruK | fructose-1-phosphate kinase | 0 | 0.060 | 1 | 0 | 9 | 400 |
| JW2768 | sdaB | L-serine deaminase II | 0 | 0.052 | 1 | 0 | 11 | 400 |
| JW3964 | hupA | HU, DNA-binding transcriptional regulator, alpha subunit | GO:0005737 cytoplasm | -0.228 | 0 | 0 | 4 | 400 |
| JW1644 | rnt | ribonuclease T (RNase T) | 0 | -0.051 | 0 | 0 | 6 | 399 |
| JW3028 | cca | fused tRNA nucleotidyl transferase -!- 2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase | GO:0005737 cytoplasm | -0.313 | 0 | 0 | 12 | 399 |
| JW3266 | rplR | 50S ribosomal subunit protein L18 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.395 | 0 | 0 | 6 | 397 |
| JW0117 | speE | spermidine synthase (putrescine aminopropyltransferase) | 0 | -0.170 | 0 | 0 | 7 | 396 |
| JW0939 | ycbG | conserved protein | 0 | -0.779 | 0 | 0 | 8 | 396 |
| JW0958 | hyaE | protein involved in processing of HyaA and HyaB proteins | 0 | -0.282 | 0 | 0 | 7 | 396 |
| JW5853 | ysgA | predicted hydrolase | 0 | -0.210 | 0 | 0 | 6 | 396 |

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|--------|------|---|---|--------|---|----|----|-----|
| JW0870 | cydD | fused cysteine transporter subunits -!- membrane component and ATP-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.162 | 1 | 5 | 12 | 395 |
| JW2493 | xseA | exonuclease VII, large subunit | 0 | -0.528 | 0 | 0 | 9 | 395 |
| JW1017 | ycdX | predicted zinc-binding hydrolase | 0 | -0.118 | 0 | 0 | 7 | 394 |
| JW0188 | nlpE | lipoprotein involved with copper homeostasis and adhesion | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.311 | 1 | 0 | 7 | 393 |
| JW0878 | dmsB | dimethyl sulfoxide reductase, anaerobic, subunit B | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.484 | 1 | 0 | 7 | 393 |
| JW1409 | azoR | NADH-azoreductase, FMN-dependent | 0 | 0.067 | 1 | 0 | 7 | 392 |
| JW5374 | menD | bifunctional 2-oxoglutarate decarboxylase -!- SHCHC synthase | 0 | -0.127 | 0 | 0 | 10 | 392 |
| JW0264 | yagH | CP4-6 prophage; predicted xylosidase/arabinosidase | 0 | -0.465 | 0 | 0 | 6 | 391 |
| JW0407 | thiL | thiamin-monophosphate kinase | 0 | 0.075 | 1 | 0 | 10 | 391 |
| JW3462 | uspA | universal stress global response | GO:0005737 cytoplasm | -0.056 | 0 | 0 | 5 | 391 |
| JW0119 | cueO | multicopper oxidase (laccase) | 0 | -0.165 | 0 | 0 | 10 | 390 |
| JW1089 | hinT | purine nucleoside phosphoramidase | 0 | -0.062 | 0 | 0 | 7 | 390 |
| JW1487 | gadC | predicted glutamate:gamma-aminobutyric acid antiporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.846 | 1 | 12 | 8 | 390 |
| JW2965 | hybO | hydrogenase 2, small subunit | GO:0019866 inner membrane | -0.194 | 1 | 1 | 7 | 390 |
| JW3894 | yjiT | stress-induced protein | 0 | -0.221 | 0 | 0 | 5 | 390 |
| JW4199 | treB | fused trehalose(maltose)-specific enzyme IIBC component of PTS | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.648 | 1 | 10 | 7 | 390 |
| JW3585 | grxC | glutaredoxin 3 | 0 | -0.314 | 0 | 0 | 6 | 389 |
| JW4314 | mrr | methylated adenine and cytosine restriction protein | GO:0005737 cytoplasm | -0.359 | 0 | 0 | 9 | 389 |
| JW5599 | rffD | UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase | GO:0009274 cell wall (sensu Bacteria) | 0.065 | 1 | 0 | 9 | 389 |
| JW2081 | gatA | galactitol-specific enzyme IIA component of PTS | 0 | -0.025 | 0 | 0 | 5 | 388 |
| JW0027 | ispH | 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase, 4Fe-4S protein | GO:0005737 cytoplasm | -0.173 | 0 | 0 | 9 | 387 |
| JW0193 | metQ | DL-methionine transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597 periplasmic space | -0.138 | 0 | 0 | 7 | 387 |
| JW0766 | moaC | molybdopterin biosynthesis, protein C | 0 | -0.037 | 0 | 0 | 9 | 387 |
| JW5431 | gutQ | predicted phosphosugar-binding protein | GO:0030113 capsule (sensu | 0.144 | 1 | 0 | 10 | 387 |
| JW1505 | ydeW | predicted DNA-binding transcriptional regulator | 0 | 0.129 | 1 | 0 | 9 | 385 |
| JW3262 | secY | preprotein translocase membrane subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.602 | 1 | 10 | 8 | 385 |
| JW3615 | dut | deoxyuridinetriphosphatase | 0 | 0.005 | 1 | 0 | 4 | 385 |
| JW5309 | yecM | predicted metal-binding enzyme | 0 | -0.380 | 0 | 0 | 6 | 385 |
| JW5547 | nfi | endonuclease V | 0 | -0.064 | 0 | 0 | 7 | 385 |

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|--------|------|---|---|--------|---|----|----|-----|
| JW3808 | udp | uridine phosphorylase | 0 | 0.022 | 1 | 0 | 8 | 384 |
| JW0430 | hupB | HU, DNA-binding transcriptional regulator, beta subunit | GO:0005737 cytoplasm | -0.042 | 0 | 0 | 5 | 383 |
| JW1265 | yciN | predicted protein | 0 | -0.380 | 0 | 0 | 5 | 383 |
| JW1674 | sufA | Fe-S cluster assembly protein | 0 | -0.103 | 0 | 0 | 6 | 383 |
| JW2516 | yfhQ | predicted methyltransferase | 0 | -0.133 | 0 | 0 | 7 | 383 |
| JW2660 | emrA | multidrug efflux system | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.129 | 1 | 1 | 8 | 383 |
| JW3963 | yjaG | conserved protein | 0 | -0.241 | 0 | 0 | 7 | 383 |
| JW5927 | ygiB | conserved outer membrane protein | 0 | -0.601 | 0 | 0 | 7 | 383 |
| JW1176 | fadR | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.283 | 0 | 0 | 7 | 381 |
| JW3679 | dnaA | chromosomal replication initiator protein DnaA, DNA-binding transcriptional dual regulator | GO:0005737 cytoplasm | -0.364 | 0 | 0 | 10 | 381 |
| JW3719 | gidA | glucose-inhibited cell-division protein | 0 | -0.308 | 0 | 0 | 9 | 381 |
| JW0176 | lpxA | UDP-N-acetylglucosamine acetyltransferase | GO:0005737 cytoplasm | 0.002 | 1 | 0 | 7 | 380 |
| JW2427 | ypeA | predicted acyltransferase with acyl-CoA N-acyltransferase domain | 0 | -0.405 | 0 | 0 | 7 | 380 |
| JW0005 | yaaA | conserved protein | 0 | -0.403 | 0 | 0 | 9 | 378 |
| JW1849 | ruvB | ATP-dependent DNA helicase, component of RuvABC resolvosome | GO:0005737 cytoplasm | -0.089 | 0 | 0 | 10 | 378 |
| JW2006 | hisA | N-(5'-phospho-L-ribosyl-formimino)-5-amino-1-(5'-phosphoribosyl)-4-imidazolecarboxamide isomerase | GO:0005737 cytoplasm | 0.063 | 1 | 0 | 8 | 378 |
| JW3348 | gph | phosphoglycolate phosphatase | 0 | -0.133 | 0 | 0 | 6 | 378 |
| JW5567 | yihW | predicted DNA-binding transcriptional regulator | 0 | -0.054 | 0 | 0 | 7 | 378 |
| JW0702 | ybgK | predicted enzyme subunit | 0 | -0.347 | 0 | 0 | 9 | 377 |
| JW1706 | rplT | 50S ribosomal subunit protein L20 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.336 | 0 | 0 | 8 | 377 |
| JW5090 | ybeB | predicted protein | 0 | 0.034 | 1 | 0 | 5 | 377 |
| JW3192 | nanE | predicted N-acetylmannosamine-6-P epimerase | GO:0005737 cytoplasm | 0.162 | 1 | 0 | 7 | 376 |
| JW3899 | yiiU | conserved protein | 0 | -0.980 | 0 | 0 | 5 | 376 |
| JW0023 | ribF | bifunctional riboflavin kinase -!- FAD synthetase | GO:0005737 cytoplasm | -0.067 | 0 | 0 | 9 | 375 |
| JW0173 | hlpA | periplasmic chaperone | GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597 | -0.473 | 0 | 0 | 6 | 375 |
| JW4120 | yjeP | predicted mechanosensitive channel | GO:0042597 periplasmic space | 0.018 | 1 | 11 | 14 | 375 |
| JW0028 | rihC | ribonucleoside hydrolase 3 | 0 | 0.289 | 1 | 0 | 6 | 374 |
| JW0399 | secF | SecYEG protein translocase auxillary subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.401 | 1 | 6 | 6 | 374 |
| JW2485 | purN | phosphoribosylglycinamide formyltransferase 1 | GO:0005737 cytoplasm | -0.124 | 0 | 0 | 6 | 374 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW4102 | groS | Cpn10 chaperonin GroES, small subunit of GroESL | GO:0005737 cytoplasm | -0.004 | 0 | 0 | 6 | 374 |
| JW0988 | yccJ | predicted protein | 0 | -0.649 | 0 | 0 | 4 | 373 |
| JW2975 | metC | cystathionine beta-lyase, PLP- | GO:0005737 cytoplasm | 0.024 | 1 | 0 | 7 | 373 |
| JW4138 | rlmB | 23S rRNA (Gm2251)-methyltransferase | 0 | -0.033 | 0 | 0 | 8 | 373 |
| JW5755 | yjgF | ketoacid-binding protein | 0 | 0.086 | 1 | 0 | 6 | 373 |
| JW3304 | rpsL | 30S ribosomal subunit protein S12 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.623 | 0 | 0 | 6 | 372 |
| JW3907 | rpmE | 50S ribosomal subunit protein L31 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.649 | 0 | 0 | 5 | 372 |
| JW4366 | yjtD | predicted rRNA methyltransferase | 0 | 0.005 | 1 | 0 | 9 | 372 |
| JW5856 | trxA | thioredoxin 1 | 0 | 0.025 | 1 | 0 | 4 | 372 |
| JW2868 | yqfB | conserved protein | 0 | -0.373 | 0 | 0 | 6 | 371 |
| JW3248 | def | peptide deformylase | 0 | -0.290 | 0 | 0 | 6 | 371 |
| JW1050 | yceB | predicted lipoprotein | 0 | -0.142 | 0 | 0 | 7 | 369 |
| JW2404 | zipA | cell division protein involved in Z ring assembly | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.606 | 1 | 1 | 6 | 369 |
| JW3167 | yhbN | predicted transporter subunit -!- periplasmic-binding component of ABC superfamily | 0 | -0.444 | 0 | 0 | 5 | 369 |
| JW5505 | yqiC | conserved protein | 0 | -0.818 | 0 | 0 | 8 | 369 |
| JW3718 | gidB | methyltransferase, glucose-inhibited cell-division protein | 0 | -0.154 | 0 | 0 | 9 | 368 |
| JW2974 | exbB | membrane spanning protein in TonB-ExbB-ExbD complex | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.265 | 1 | 3 | 7 | 367 |
| JW3153 | rplU | 50S ribosomal subunit protein L21 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.369 | 0 | 0 | 7 | 367 |
| JW3582 | cysE | serine acetyltransferase | GO:0005737 cytoplasm | 0.002 | 1 | 0 | 8 | 367 |
| JW3748 | ppiC | peptidyl-prolyl cis-trans isomerase C (rotamase C) | 0 | -0.105 | 0 | 0 | 7 | 366 |
| JW0088 | murG | N-acetylglucosaminyl transferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.040 | 1 | 0 | 9 | 365 |
| JW3645 | ilvN | acetolactate synthase I, small subunit | 0 | -0.201 | 0 | 0 | 6 | 365 |
| JW1328 | fnr | DNA-binding transcriptional dual regulator, global regulator of anaerobic | GO:0005737 cytoplasm | -0.274 | 0 | 0 | 6 | 364 |
| JW1638 | sodC | superoxide dismutase, Cu, Zn | GO:0042597 periplasmic space | -0.277 | 0 | 0 | 6 | 364 |
| JW2915 | yqgE | predicted protein | 0 | -0.072 | 0 | 0 | 4 | 364 |
| JW3460 | pitA | phosphate transporter, low-affinity | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.523 | 1 | 10 | 7 | 364 |
| JW1795 | yeaY | predicted lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.120 | 1 | 0 | 6 | 363 |

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|--------|------|---|---|--------|---|---|----|-----|
| JW1236 | oppB | oligopeptide transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.767 | 1 | 6 | 6 | 362 |
| JW5605 | ilvD | dihydroxyacid dehydratase | 0 | -0.136 | 0 | 0 | 12 | 362 |
| JW5008 | yacG | conserved protein | 0 | -0.615 | 0 | 0 | 5 | 361 |
| JW4106 | yjeK | predicted lysine aminomutase | 0 | -0.189 | 0 | 0 | 6 | 360 |
| JW0141 | dksA | transcriptional regulator of rRNA transcription, DnaK suppressor protein | GO:0005737 cytoplasm | -0.866 | 0 | 0 | 6 | 359 |
| JW3765 | rffA | TDP-4-oxo-6-deoxy-D-glucose transaminase | 0 | -0.067 | 0 | 0 | 8 | 358 |
| JW3882 | cpxA | sensory histidine kinase in two-component regulatory system with | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.264 | 1 | 2 | 9 | 357 |
| JW0806 | ybiV | predicted hydrolase | 0 | -0.168 | 0 | 0 | 5 | 356 |
| JW2181 | narP | DNA-binding response regulator in two-component regulatory system with NarX or NarX | GO:0005737 cytoplasm | -0.014 | 0 | 0 | 5 | 356 |
| JW5129 | mgsA | methylglyoxal synthase | GO:0005737 cytoplasm | 0.038 | 1 | 0 | 5 | 356 |
| JW0440 | glnK | nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB | 0 | 0.067 | 1 | 0 | 5 | 355 |
| JW1812 | cspC | stress protein, member of the CspA- | 0 | -0.190 | 0 | 0 | 4 | 355 |
| JW0230 | crl | DNA-binding transcriptional regulator | GO:0009289 fimbria -!- GO:0005737 cytoplasm | -0.511 | 0 | 0 | 7 | 354 |
| JW2480 | yfgD | predicted oxidoreductase | 0 | -0.361 | 0 | 0 | 4 | 354 |
| JW4356 | trpR | DNA-binding transcriptional repressor, tryptophan-binding | GO:0005737 cytoplasm | -0.424 | 0 | 0 | 7 | 354 |
| JW5592 | dapF | diaminopimelate epimerase | GO:0005737 cytoplasm | -0.090 | 0 | 0 | 8 | 354 |
| JW5503 | tolC | transport channel | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.427 | 1 | 0 | 7 | 353 |
| JW0900 | ycaR | conserved protein | 0 | -0.127 | 0 | 0 | 6 | 352 |
| JW3959 | rsd | stationary phase protein, binds sigma 70 RNA polymerase subunit | GO:0005737 cytoplasm | -0.277 | 0 | 0 | 5 | 352 |
| JW2008 | hisI | fused phosphoribosyl-AMP cyclohydrolase -!- phosphoribosyl-ATP | GO:0005737 cytoplasm | -0.331 | 0 | 0 | 6 | 351 |
| JW2659 | mprA | DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.638 | 0 | 0 | 7 | 351 |
| JW3076 | yhaJ | predicted DNA-binding transcriptional regulator | 0 | -0.161 | 0 | 0 | 7 | 351 |
| JW5669 | hdeB | acid-resistance protein | 0 | -0.242 | 0 | 0 | 3 | 351 |
| JW5042 | ykgG | predicted transporter | 0 | -0.135 | 0 | 0 | 5 | 350 |
| JW0185 | yaeP | conserved protein | 0 | 0.026 | 1 | 0 | 3 | 349 |
| JW0071 | leuC | 3-isopropylmalate isomerase subunit, dehydratase component | GO:0005737 cytoplasm | -0.174 | 0 | 0 | 8 | 348 |
| JW3132 | nlpl | conserved protein | 0 | -0.321 | 0 | 0 | 7 | 348 |
| JW5608 | yieP | predicted transcriptional regulator | 0 | -0.079 | 0 | 0 | 6 | 348 |

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|--------|------|---|---|--------|---|----|----|-----|
| JW2235 | glpA | sn-glycerol-3-phosphate dehydrogenase (anaerobic), large subunit, FAD/NAD(P)-binding | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | -0.134 | 1 | 0 | 11 | 347 |
| JW2647 | ygaM | predicted protein | 0 | -0.501 | 1 | 1 | 5 | 347 |
| JW4360 | creA | conserved protein | 0 | -0.032 | 0 | 0 | 8 | 347 |
| JW1120 | ymfB | bifunctional thiamin pyrimidine pyrophosphate hydrolase -!- thiamin pyrophosphate hydrolase | 0 | -0.148 | 0 | 0 | 7 | 346 |
| JW2433 | eutC | ethanolamine ammonia-lyase, small subunit (light chain) | 0 | -0.101 | 0 | 0 | 7 | 346 |
| JW3278 | rpsS | 30S ribosomal subunit protein S19 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.620 | 0 | 0 | 7 | 346 |
| JW0895 | ihfB | integration host factor (IHF), DNA-binding protein, beta subunit | GO:0005737 cytoplasm | -0.784 | 0 | 0 | 6 | 345 |
| JW5284 | ynjB | conserved protein | 0 | -0.302 | 0 | 0 | 8 | 345 |
| JW3069 | ycjD | conserved protein | 0 | -0.545 | 1 | 1 | 6 | 344 |
| JW3893 | yiiS | conserved protein | 0 | -0.007 | 0 | 0 | 3 | 344 |
| JW3728 | rbsA | fused D-ribose transporter subunits -!- ATP-binding components ABC | GO:0005737 cytoplasm | -0.088 | 0 | 0 | 7 | 343 |
| JW3486 | yhjA | predicted cytochrome C peroxidase | 0 | -0.395 | 1 | 1 | 10 | 342 |
| JW2343 | vacJ | predicted lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.291 | 1 | 0 | 6 | 341 |
| JW5795 | yjiA | conserved protein | 0 | -0.210 | 0 | 0 | 5 | 341 |
| JW2273 | nuoL | NADH:ubiquinone oxidoreductase, membrane subunit L | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.868 | 1 | 16 | 6 | 339 |
| JW3827 | hemG | protoporphyrin oxidase, flavoprotein | 0 | -0.587 | 0 | 0 | 7 | 339 |
| JW3993 | malF | maltose transporter subunit -!- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.290 | 1 | 8 | 6 | 339 |
| JW0626 | ybeD | conserved protein | 0 | -0.166 | 0 | 0 | 4 | 337 |
| JW2878 | zapA | protein that localizes to the cytokinetic | 0 | -0.733 | 0 | 0 | 5 | 337 |
| JW3584 | secB | protein export chaperone | GO:0005737 cytoplasm | -0.188 | 0 | 0 | 5 | 337 |
| JW1214 | narK | nitrate/nitrite transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.678 | 1 | 12 | 6 | 336 |
| JW4185 | ppa | inorganic pyrophosphatase | GO:0005737 cytoplasm | -0.272 | 0 | 0 | 9 | 336 |
| JW0179 | dnaE | DNA polymerase III alpha subunit | GO:0005737 cytoplasm | -0.241 | 0 | 0 | 12 | 335 |
| JW2721 | cysN | sulfate adenylyltransferase, subunit 1 | 0 | -0.184 | 0 | 0 | 8 | 335 |
| JW3065 | exuR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.524 | 0 | 0 | 9 | 335 |
| JW5473 | ygfB | predicted protein | 0 | -0.362 | 0 | 0 | 5 | 335 |
| JW1534 | ydfZ | conserved protein | 0 | -0.281 | 0 | 0 | 4 | 334 |
| JW2761 | yqcA | predicted flavoprotein | 0 | -0.117 | 0 | 0 | 4 | 334 |
| JW5513 | ygiO | predicted methyltransferase small | 0 | -0.181 | 0 | 0 | 7 | 332 |
| JW2425 | yfeY | predicted protein | 0 | -0.351 | 0 | 0 | 5 | 331 |
| JW5180 | ycgN | conserved protein | 0 | -0.530 | 0 | 0 | 5 | 331 |
| JW1462 | narY | nitrate reductase 2 (NRZ), beta subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.434 | 1 | 0 | 9 | 330 |

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|--------|------|---|---|--------|---|----|----|-----|
| JW4250 | fecB | KpLE2 phage-like element; iron-dicitrate transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | 0.026 | 1 | 0 | 8 | 330 |
| JW3459 | yhiN | predicted oxidoreductase, FAD/NAD(P)-binding domain | 0 | -0.036 | 1 | 1 | 6 | 328 |
| JW1018 | ycdY | conserved protein | 0 | -0.166 | 0 | 0 | 5 | 327 |
| JW1105 | ycfX | predicted DNA-binding transcriptional regulator | 0 | -0.071 | 0 | 0 | 7 | 327 |
| JW1863 | cutC | copper homeostasis protein | GO:0005737 cytoplasm | 0.016 | 1 | 0 | 8 | 327 |
| JW2322 | yfcL | predicted protein | 0 | -0.148 | 0 | 0 | 5 | 327 |
| JW0485 | ybbP | predicted inner membrane protein | 0 | 0.255 | 1 | 10 | 8 | 326 |
| JW0618 | cspE | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.213 | 0 | 0 | 5 | 326 |
| JW0867 | infA | translation initiation factor IF-1 | GO:0005737 cytoplasm | -0.354 | 0 | 0 | 4 | 326 |
| JW1511 | lsrG | conserved protein | 0 | -0.529 | 0 | 0 | 5 | 325 |
| JW2296 | yfcD | predicted NUDIX hydrolase | 0 | -0.427 | 0 | 0 | 5 | 325 |
| JW3149 | dacB | D-alanyl-D-alanine carboxypeptidase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597 | -0.051 | 0 | 0 | 8 | 325 |
| JW3776 | hemD | uroporphyrinogen III synthase | 0 | -0.124 | 0 | 0 | 7 | 325 |
| JW5291 | yeaJ | predicted diguanylate cyclase | 0 | -0.207 | 1 | 2 | 9 | 325 |
| JW0860 | ybjD | conserved protein with nucleoside triphosphate hydrolase domain | 0 | -0.326 | 0 | 0 | 8 | 324 |
| JW2639 | csiR | DNA-binding transcriptional dual | 0 | -0.127 | 0 | 0 | 10 | 324 |
| JW3095 | garL | alpha-dehydro-beta-deoxy-D-glucarate aldolase | 0 | 0.071 | 1 | 0 | 7 | 324 |
| JW1288 | ymjA | predicted protein | 0 | -0.469 | 0 | 0 | 5 | 323 |
| JW2300 | folX | D-erythro-7,8-dihydroneopterin triphosphate 2'-epimerase and dihydroneopterin aldolase | 0 | -0.426 | 0 | 0 | 6 | 323 |
| JW3152 | rpmA | 50S ribosomal subunit protein L27 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.638 | 0 | 0 | 5 | 322 |
| JW3770 | rffM | UDP-N-acetyl-D-mannosaminuronic acid transferase | 0 | -0.322 | 0 | 0 | 7 | 321 |
| JW3809 | rnuC | predicted recombination limiting protein | 0 | -0.651 | 1 | 1 | 9 | 321 |
| JW0960 | appC | cytochrome bd-II oxidase, subunit I | GO:0019866 inner membrane | 0.358 | 1 | 9 | 6 | 320 |
| JW2141 | yeiG | predicted esterase | 0 | -0.320 | 0 | 0 | 8 | 320 |
| JW2176 | yejM | predicted hydrolase, inner membrane | 0 | -0.122 | 1 | 5 | 6 | 320 |
| JW2714 | surE | broad specificity 5'(3')-nucleotidase and polyphosphatase | 0 | -0.075 | 0 | 0 | 6 | 320 |
| JW3264 | rpmD | 50S ribosomal subunit protein L30 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.137 | 0 | 0 | 6 | 320 |
| JW5703 | yheO | predicted DNA-binding transcriptional regulator | 0 | -0.163 | 0 | 0 | 4 | 320 |
| JW1844 | lpxM | myristoyl-acyl carrier protein (ACP)-dependent acyltransferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.450 | 1 | 1 | 9 | 319 |

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|--------|------|---|--|--------|---|---|----|-----|
| JW0196 | gmhB | D,D-heptose 1,7-bisphosphate phosphatase | 0 | -0.251 | 0 | 0 | 5 | 318 |
| JW2421 | yfeU | predicted PTS component | 0 | 0.134 | 1 | 0 | 7 | 318 |
| JW3217 | yhdE | conserved protein | 0 | -0.187 | 0 | 0 | 5 | 318 |
| JW5940 | bisC | biotin sulfoxide reductase | 0 | -0.301 | 0 | 0 | 9 | 318 |
| JW0938 | ycbZ | predicted peptidase | 0 | -0.162 | 0 | 0 | 8 | 317 |
| JW4126 | yjeE | ATPase with strong ADP affinity | 0 | -0.086 | 0 | 0 | 4 | 317 |
| JW0406 | nusB | transcription antitermination protein | GO:0005737 cytoplasm | -0.219 | 0 | 0 | 6 | 316 |
| JW0736 | ybgS | conserved protein | 0 | -0.711 | 0 | 0 | 3 | 316 |
| JW0345 | yaiL | nucleoprotein/polynucleotide-associated enzyme | GO:0005737 cytoplasm | -0.473 | 0 | 0 | 7 | 315 |
| JW3201 | yhcM | conserved protein with nucleoside triphosphate hydrolase domain | 0 | -0.289 | 0 | 0 | 7 | 315 |
| JW5295 | yoaB | conserved protein | 0 | 0.024 | 1 | 0 | 5 | 315 |
| JW0445 | ybaA | conserved protein | 0 | -0.393 | 0 | 0 | 4 | 314 |
| JW2154 | fruA | fused fructose-specific PTS enzyme IIB'BC components | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.585 | 1 | 9 | 7 | 314 |
| JW5533 | yhbC | conserved protein | 0 | 0.047 | 1 | 0 | 5 | 314 |
| JW2550 | era | membrane-associated, 16S rRNA-binding GTPase | 0 | -0.192 | 0 | 0 | 10 | 313 |
| JW1074 | yceD | conserved protein | 0 | -0.192 | 0 | 0 | 5 | 311 |
| JW3785 | yigB | predicted hydrolase | 0 | -0.329 | 0 | 0 | 5 | 311 |
| JW0174 | lpxD | UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase | 0 | 0.125 | 1 | 0 | 6 | 310 |
| JW0701 | ybgJ | predicted enzyme subunit | 0 | 0.018 | 1 | 0 | 6 | 310 |
| JW1315 | ycjF | conserved inner membrane protein | 0 | -0.247 | 1 | 3 | 6 | 310 |
| JW1556 | relB | Qin prophage; bifunctional antitoxin of the RelE-RelB toxin-antitoxin system -!- transcriptional repressor | GO:0005737 cytoplasm | -0.359 | 0 | 0 | 5 | 310 |
| JW3478 | hdeA | stress response protein acid-resistance protein | 0 | -0.208 | 1 | 1 | 4 | 310 |
| JW0213 | yafJ | predicted amidotransfease | 0 | -0.313 | 0 | 0 | 7 | 309 |
| JW1086 | ycfH | predicted metallodependent hydrolase | 0 | -0.212 | 0 | 0 | 7 | 309 |
| JW1256 | trpE | component I of anthranilate synthase | 0 | -0.190 | 0 | 0 | 8 | 309 |
| JW1728 | osmE | DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.265 | 1 | 1 | 3 | 308 |
| JW2537 | glnB | regulatory protein P-II for glutamine synthetase | GO:0005737 cytoplasm | 0.009 | 1 | 0 | 6 | 308 |
| JW5283 | ydjY | predicted protein | 0 | -0.242 | 0 | 0 | 6 | 308 |
| JW5832 | yedQ | predicted diguanylate cyclase | 0 | -0.287 | 1 | 2 | 8 | 308 |
| JW1394 | paaX | DNA-binding transcriptional regulator, aryl-CoA responsive | 0 | 0.004 | 1 | 0 | 7 | 307 |
| JW1757 | pncA | nicotinamidase/pyrazinamidase | GO:0005737 cytoplasm | -0.249 | 0 | 0 | 4 | 307 |
| JW2894 | epd | D-erythrose 4-phosphate | GO:0005737 cytoplasm | -0.041 | 0 | 0 | 7 | 307 |
| JW2338 | yfcX | fused enoyl-CoA hydratase-!- epimerase-!-isomerase -!- 3-hydroxyacyl-CoA dehydrogenase, subunit of anaerobic fatty acid oxidation | 0 | -0.050 | 0 | 0 | 9 | 306 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW0054 | djIA | DnaJ-like protein, membrane anchored | 0 | -0.341 | 1 | 1 | 8 | 305 |
| JW0442 | tesB | acyl-CoA thioesterase II | 0 | -0.253 | 0 | 0 | 7 | 305 |
| JW1859 | yecO | predicted methyltransferase | 0 | -0.145 | 0 | 0 | 7 | 305 |
| JW1902 | yecC | predicted transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.147 | 0 | 0 | 5 | 305 |
| JW0171 | yaeL | zinc metalloproteinase | 0 | 0.265 | 1 | 4 | 8 | 303 |
| JW0192 | rcsF | predicted outer membrane protein, | GO:0030113 capsule (sensu | -0.190 | 0 | 0 | 4 | 302 |
| JW1600 | rstA | DNA-binding response regulator in two-component regulatory system with RstB | GO:0005737 cytoplasm | -0.064 | 0 | 0 | 7 | 302 |
| JW5317 | yodD | predicted protein | 0 | -0.731 | 0 | 0 | 4 | 302 |
| JW1991 | sbmC | DNA gyrase inhibitor | GO:0005737 cytoplasm | -0.363 | 0 | 0 | 4 | 301 |
| JW1199 | ispE | 4-diphosphocytidyl-2-C-methylerythritol kinase | GO:0005737 cytoplasm | -0.060 | 0 | 0 | 6 | 300 |
| JW0265 | yagl | CP4-6 prophage; predicted DNA-binding transcriptional regulator | 0 | -0.132 | 0 | 0 | 6 | 299 |
| JW2870 | ygfF | predicted NAD(P)-binding oxidoreductase with NAD(P)-binding Rossmann-fold domain | 0 | 0.118 | 1 | 0 | 6 | 299 |
| JW3424 | yhhK | conserved protein | 0 | -0.360 | 0 | 0 | 5 | 299 |
| JW0321 | yahO | predicted protein | 0 | -0.286 | 0 | 0 | 4 | 297 |
| JW1734 | astB | succinylarginine dihydrolase | 0 | -0.273 | 0 | 0 | 7 | 297 |
| JW2713 | pcm | L-isoaspartate protein carboxylmethyltransferase type II | 0 | -0.158 | 0 | 0 | 7 | 297 |
| JW5550 | murl | glutamate racemase | GO:0009274 cell wall (sensu | 0.187 | 1 | 0 | 7 | 296 |
| JW0848 | artP | arginine transporter subunit -!- ATP-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.134 | 0 | 0 | 6 | 295 |
| JW2511 | hscB | DnaJ-like molecular chaperone specific for IscU | 0 | -0.598 | 0 | 0 | 6 | 295 |
| JW3318 | prkB | predicted phosphoribulokinase | 0 | -0.165 | 0 | 0 | 7 | 295 |
| JW5652 | avtA | valine-pyruvate aminotransferase | 0 | -0.065 | 0 | 0 | 7 | 295 |
| JW3375 | bioH | carboxylesterase of pimeloyl-CoA synthesis | 0 | 0.039 | 1 | 0 | 6 | 294 |
| JW5127 | ymbA | conserved protein | 0 | -0.158 | 0 | 0 | 4 | 294 |
| JW5791 | yjiY | predicted inner membrane protein | 0 | 0.725 | 1 | 16 | 6 | 294 |
| JW0906 | mukE | protein involved in chromosome | 0 | -0.495 | 0 | 0 | 7 | 293 |
| JW3275 | rplP | 50S ribosomal subunit protein L16 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.384 | 0 | 0 | 3 | 293 |
| JW5089 | lipB | lipoyl-protein ligase | 0 | -0.178 | 0 | 0 | 7 | 293 |
| JW1614 | malY | bifunctional beta-cystathionase, PLP-dependent -!- regulator of maltose | GO:0005737 cytoplasm | -0.101 | 0 | 0 | 7 | 292 |
| JW3891 | yjiQ | conserved protein | 0 | -0.294 | 0 | 0 | 6 | 291 |
| JW0094 | lpxC | UDP-3-O-acyl N-acetylglucosamine deacetylase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.050 | 0 | 0 | 8 | 290 |
| JW1899 | uvrY | DNA-binding response regulator in two-component regulatory system with BarA | 0 | -0.056 | 0 | 0 | 7 | 290 |

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|--------|------|---|---|--------|---|---|---|-----|
| JW0216 | dinJ | predicted antitoxin of YafQ-DinJ toxin-antitoxin system | 0 | -0.142 | 0 | 0 | 6 | 289 |
| JW1053 | rimJ | ribosomal-protein-S5-alanine N-acetyltransferase | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.524 | 0 | 0 | 7 | 289 |
| JW2734 | cysJ | sulfite reductase, alpha subunit, flavoprotein | 0 | -0.256 | 0 | 0 | 6 | 288 |
| JW0152 | yadR | conserved protein | 0 | -0.089 | 0 | 0 | 4 | 287 |
| JW1075 | rpmF | 50S ribosomal subunit protein L32 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.974 | 0 | 0 | 4 | 287 |
| JW5449 | amiC | N-acetylmuramoyl-L-alanine amidase | GO:0009274 cell wall (sensu | -0.210 | 0 | 0 | 7 | 287 |
| JW0156 | dgt | deoxyguanosine triphosphate triphosphohydrolase | GO:0005737 cytoplasm | -0.451 | 0 | 0 | 6 | 286 |
| JW0780 | ybiH | predicted DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.113 | 0 | 0 | 6 | 286 |
| JW1242 | kch | voltage-gated potassium channel | GO:0019866 inner membrane | 0.422 | 1 | 7 | 4 | 286 |
| JW2512 | iscA | FeS cluster assembly protein | 0 | -0.103 | 0 | 0 | 6 | 286 |
| JW4351 | serB | 3-phosphoserine phosphatase | GO:0005737 cytoplasm | 0.091 | 1 | 0 | 7 | 286 |
| JW4352 | radA | predicted repair protein | 0 | 0.038 | 1 | 0 | 6 | 286 |
| JW1958 | yeel | conserved protein | 0 | -0.142 | 0 | 0 | 5 | 285 |
| JW2070 | yegS | conserved protein | 0 | 0.030 | 1 | 0 | 5 | 285 |
| JW2857 | idi | isopentenyl diphosphate isomerase | GO:0005737 cytoplasm | -0.292 | 0 | 0 | 5 | 285 |
| JW1718 | ydjN | predicted transporter | 0 | 0.816 | 1 | 9 | 4 | 284 |
| JW2161 | yeiR | predicted enzyme | 0 | -0.229 | 0 | 0 | 8 | 284 |
| JW2764 | syd | predicted protein | GO:0005737 cytoplasm | -0.276 | 0 | 0 | 6 | 284 |
| JW3269 | rpsN | 30S ribosomal subunit protein S14 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.795 | 0 | 0 | 5 | 284 |
| JW3720 | mioC | FMN-binding protein MioC | 0 | -0.159 | 0 | 0 | 5 | 283 |
| JW0628 | rlpA | minor lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.245 | 1 | 0 | 6 | 281 |
| JW1506 | ego | fused A12 transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.051 | 0 | 0 | 7 | 281 |
| JW2408 | ptsH | phosphohistidinoprotein-hexose phosphotransferase component of PTS system (Hpr) | 0 | -0.166 | 0 | 0 | 3 | 281 |
| JW2732 | cysH | 3'-phosphoadenosine 5'-phosphosulfate reductase | 0 | -0.439 | 0 | 0 | 7 | 280 |
| JW4299 | yjiN | conserved inner membrane protein | GO:0009274 cell wall (sensu | -0.048 | 1 | 3 | 7 | 280 |
| JW2875 | ubiH | 2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding | 0 | 0.023 | 1 | 0 | 8 | 279 |
| JW0403 | ybaD | conserved protein | 0 | -0.395 | 0 | 0 | 8 | 278 |
| JW1217 | narJ | molybdenum-cofactor-assembly chaperone subunit (delta subunit) of nitrate reductase 1 | 0 | -0.259 | 0 | 0 | 6 | 278 |
| JW1643 | gloA | glyoxalase I, Ni-dependent | 0 | -0.346 | 0 | 0 | 5 | 278 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW2428 | amiA | N-acetylmuramoyl-L-alanine amidase I | GO:0009274 cell wall (sensu | -0.318 | 0 | 0 | 8 | 278 |
| JW3042 | yqjI | predicted transcriptional regulator | 0 | -0.760 | 0 | 0 | 9 | 278 |
| JW5253 | gnsB | Qin prophage; predicted protein | 0 | -0.481 | 0 | 0 | 4 | 278 |
| JW5714 | zur | DNA-binding transcriptional activator, Zn(II)-binding | GO:0005737 cytoplasm | -0.250 | 0 | 0 | 5 | 278 |
| JW0115 | yacL | conserved protein | 0 | -0.471 | 0 | 0 | 5 | 277 |
| JW2808 | ygeA | predicted racemase | 0 | 0.077 | 1 | 0 | 7 | 277 |
| JW1380 | feaB | phenylacetaldehyde dehydrogenase | 0 | -0.037 | 0 | 0 | 6 | 276 |
| JW4087 | yjdl | conserved protein | 0 | -0.339 | 0 | 0 | 4 | 276 |
| JW4129 | miaA | delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase | GO:0005737 cytoplasm | -0.158 | 0 | 0 | 9 | 276 |
| JW1435 | ydcS | predicted spermidine/putrescine transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.324 | 0 | 0 | 10 | 275 |
| JW1835 | yebE | conserved protein | 0 | -0.237 | 1 | 2 | 6 | 275 |
| JW3170 | yhbH | predicted ribosome-associated, sigma 54 modulation protein | 0 | -0.398 | 0 | 0 | 4 | 275 |
| JW0325 | prpD | 2-methylcitrate dehydratase | 0 | -0.136 | 0 | 0 | 6 | 274 |
| JW1796 | yeaZ | predicted peptidase | 0 | -0.071 | 0 | 0 | 5 | 274 |
| JW2796 | lgt | phosphatidylglycerol-prolipoprotein diacylglycerol transferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.444 | 1 | 5 | 6 | 274 |
| JW3942 | coaA | pantothenate kinase | 0 | -0.247 | 0 | 0 | 6 | 274 |
| JW5070 | ybcJ | predicted RNA-binding protein | 0 | 0.101 | 1 | 0 | 5 | 274 |
| JW0100 | coaE | dephospho-CoA kinase | 0 | -0.116 | 0 | 0 | 5 | 273 |
| JW2005 | hisH | imidazole glycerol phosphate synthase, glutamine amidotransferase subunit | 0 | -0.071 | 0 | 0 | 7 | 273 |
| JW2366 | evgA | DNA-binding response regulator in two-component regulatory system with EvgS | GO:0005737 cytoplasm | -0.094 | 0 | 0 | 4 | 273 |
| JW2451 | yffH | predicted NUDIX hydrolase | 0 | -0.335 | 0 | 0 | 4 | 273 |
| JW3071 | yqjK | conserved protein | 0 | -0.544 | 1 | 1 | 7 | 273 |
| JW3204 | degS | serine endoprotease, periplasmic | GO:0042597 periplasmic space | 0.115 | 1 | 1 | 5 | 273 |
| JW4013 | alr | alanine racemase 1, PLP-binding, biosynthetic | 0 | -0.106 | 0 | 0 | 7 | 273 |
| JW1423 | rimL | ribosomal-protein-L7/L12-serine acetyltransferase | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.370 | 0 | 0 | 5 | 272 |
| JW2926 | yggL | predicted protein | 0 | -0.678 | 0 | 0 | 4 | 272 |
| JW3134 | rpsO | 30S ribosomal subunit protein S15 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.673 | 0 | 0 | 4 | 272 |
| JW2883 | argP | DNA-binding transcriptional activator, replication initiation inhibitor | GO:0005737 cytoplasm | -0.173 | 0 | 0 | 5 | 271 |
| JW1441 | ydcY | predicted protein | 0 | -0.636 | 0 | 0 | 6 | 270 |
| JW4005 | yjbJ | predicted stress response protein | 0 | -1.526 | 0 | 0 | 4 | 270 |

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|--------|------|---|---|--------|---|----|---|-----|
| JW2671 | mltB | membrane-bound lytic murein transglycosylase B | GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.331 | 1 | 0 | 6 | 269 |
| JW3372 | feoB | fused ferrous iron transporter, protein B | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 0.422 | 1 | 10 | 5 | 269 |
| JW5247 | ynel | predicted aldehyde dehydrogenase | 0 | -0.032 | 0 | 0 | 8 | 269 |
| JW5307 | yecD | predicted hydrolase | 0 | -0.031 | 0 | 0 | 6 | 269 |
| JW1989 | yeeX | conserved protein | 0 | -0.694 | 0 | 0 | 5 | 268 |
| JW2464 | gcvR | DNA-binding transcriptional repressor, regulatory protein accessory to GcvA | GO:0005737 cytoplasm | -0.017 | 0 | 0 | 4 | 268 |
| JW3227 | prmA | methylase for 50S ribosomal subunit protein L11 | GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm | -0.065 | 0 | 0 | 6 | 268 |
| JW1080 | acpP | acyl carrier protein (ACP) | 0 | -0.346 | 0 | 0 | 4 | 267 |
| JW1898 | uvrC | excinuclease UvrABC, endonuclease subunit | GO:0005737 cytoplasm | -0.344 | 0 | 0 | 7 | 267 |
| JW2997 | ygiN | quinol monooxygenase | 0 | 0.015 | 1 | 0 | 6 | 267 |
| JW3093 | garK | glycerate kinase I | 0 | 0.079 | 1 | 0 | 7 | 267 |
| JW3941 | birA | bifunctional biotin-[acetylCoA carboxylase] holoenzyme synthetase - - DNA-binding transcriptional repressor, bio-5'-AMP-binding | GO:0005737 cytoplasm | -0.031 | 0 | 0 | 5 | 267 |
| JW5952 | yjhU | KpLE2 phage-like element; predicted DNA-binding transcriptional regulator | 0 | -0.025 | 0 | 0 | 7 | 267 |
| JW1153 | ymgB | predicted protein | 0 | 0.031 | 1 | 0 | 3 | 266 |
| JW2347 | yfdH | CPS-53 (KpLE1) prophage; bactoprenol glucosyl transferase | 0 | 0.079 | 1 | 2 | 6 | 266 |
| JW4179 | ytfM | predicted outer membrane protein and surface antigen | GO:0009274 cell wall (sensu Bacteria) - - GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.415 | 1 | 0 | 8 | 266 |
| JW5920 | rcsC | hybrid sensory kinase in two-component regulatory system with RcsB and YojN | 0 | -0.114 | 1 | 2 | 8 | 266 |
| JW0324 | prpC | 2-methylcitrate synthase | GO:0005737 cytoplasm | -0.289 | 0 | 0 | 7 | 265 |
| JW2277 | nuoH | NADH:ubiquinone oxidoreductase, membrane subunit H | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 0.810 | 1 | 8 | 5 | 265 |
| JW3937 | trmA | tRNA (uracil-5-)-methyltransferase | GO:0005737 cytoplasm | -0.322 | 0 | 0 | 7 | 265 |
| JW2777 | ygdE | predicted methyltransferase | 0 | -0.292 | 0 | 0 | 7 | 264 |
| JW5161 | lolC | outer membrane-specific lipoprotein transporter subunit - - membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane | 0.319 | 1 | 4 | 7 | 264 |
| JW1842 | yebK | predicted DNA-binding transcriptional regulator | 0 | -0.129 | 0 | 0 | 6 | 263 |
| JW2833 | ygeR | Tetratricopeptide repeat transcriptional regulator | GO:0009279 external outer membrane (sensu Gram-negative | -0.254 | 1 | 0 | 6 | 263 |
| JW3577 | yibL | conserved protein | 0 | -0.628 | 0 | 0 | 5 | 263 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW3905 | cytR | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.143 | 0 | 0 | 6 | 263 |
| JW2665 | yqaB | predicted hydrolase | 0 | -0.027 | 0 | 0 | 5 | 262 |
| JW3280 | rplW | 50S ribosomal subunit protein L23 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.373 | 0 | 0 | 4 | 262 |
| JW0729 | tolA | membrane anchored protein in TolA-TolQ-TolR complex | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.610 | 1 | 1 | 7 | 261 |
| JW4026 | yjcE | predicted cation/proton antiporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.633 | 1 | 11 | 5 | 261 |
| JW5857 | rbsD | predicted cytoplasmic sugar-binding protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.101 | 1 | 0 | 4 | 261 |
| JW0142 | sfsA | predicted DNA-binding transcriptional regulator | 0 | -0.340 | 0 | 0 | 6 | 260 |
| JW3675 | yidB | conserved protein | 0 | -0.006 | 0 | 0 | 3 | 260 |
| JW0348 | frmR | regulator protein that represses frmRAB operon | 0 | -0.502 | 0 | 0 | 6 | 259 |
| JW5377 | yfcE | predicted phosphatase | 0 | 0.024 | 1 | 0 | 4 | 259 |
| JW0584 | fepB | iron-enterobactin transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.068 | 0 | 0 | 5 | 258 |
| JW1301 | pspE | thiosulfate:cyanide sulfurtransferase (rhodanese) | 0 | -0.188 | 0 | 0 | 3 | 258 |
| JW1944 | dcm | DNA cytosine methylase | GO:0005737 cytoplasm | -0.450 | 0 | 0 | 8 | 258 |
| JW2263 | elaC | binuclear zinc phosphodiesterase | 0 | -0.061 | 0 | 0 | 8 | 258 |
| JW4069 | phnA | predicted phosphonate metabolizing protein | 0 | -0.532 | 0 | 0 | 5 | 258 |
| JW5156 | plsX | fatty acid/phospholipid synthesis protein | 0 | 0.113 | 1 | 0 | 4 | 258 |
| JW5580 | tatB | TatABCE protein translocation system subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.380 | 1 | 1 | 6 | 258 |
| JW0984 | cbpM | modulator of CbpA co-chaperone | 0 | 0.086 | 1 | 0 | 3 | 257 |
| JW3576 | yibT | predicted protein | GO:0005737 cytoplasm | -0.535 | 0 | 0 | 3 | 257 |
| JW0412 | xseB | exonuclease VII small subunit | GO:0005737 cytoplasm | -0.735 | 0 | 0 | 4 | 256 |
| JW0464 | hemH | ferrochelatase | 0 | -0.187 | 0 | 0 | 5 | 256 |
| JW1713 | ydiZ | predicted protein | 0 | -0.470 | 0 | 0 | 5 | 256 |
| JW3612 | rpmB | 50S ribosomal subunit protein L28 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.650 | 0 | 0 | 6 | 256 |
| JW0047 | folA | dihydrofolate reductase | 0 | -0.294 | 0 | 0 | 4 | 255 |
| JW2596 | uppS | NAD kinase | 0 | -0.072 | 0 | 0 | 4 | 255 |
| JW1210 | ychN | conserved protein | 0 | 0.190 | 1 | 0 | 4 | 254 |
| JW3000 | cpdA | cyclic 3',5'-adenosine monophosphate phosphodiesterase | GO:0005737 cytoplasm | -0.203 | 0 | 0 | 4 | 254 |
| JW3524 | viaG | predicted transcriptional regulator | 0 | -0.397 | 0 | 0 | 5 | 254 |
| JW5415 | yfjD | predicted inner membrane protein | 0 | 0.025 | 1 | 3 | 7 | 254 |
| JW0904 | smtA | S-adenosylmethionine-dependent methyltransferase | 0 | -0.402 | 0 | 0 | 8 | 253 |

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|--------|------|--|---|--------|---|---|----|-----|
| JW1082 | pabC | 4-amino-4-deoxychorismate lyase component of para-aminobenzoate synthase multienzyme complex | 0 | -0.054 | 0 | 0 | 6 | 253 |
| JW1169 | ycgM | predicted isomerase/hydrolase | 0 | -0.106 | 0 | 0 | 5 | 253 |
| JW3565 | yibF | predicted glutathione S-transferase | 0 | -0.027 | 0 | 0 | 9 | 253 |
| JW5063 | ylaC | predicted inner membrane protein | 0 | 0.103 | 1 | 2 | 4 | 253 |
| JW2203 | ompC | outer membrane porin protein C | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.533 | 1 | 0 | 5 | 252 |
| JW2256 | menC | o-succinylbenzoyl-CoA synthase | 0 | -0.117 | 0 | 0 | 7 | 252 |
| JW2214 | atoC | fused response regulator of ato operon, in two-component system with AtoS | GO:0005737 cytoplasm | -0.168 | 0 | 0 | 10 | 251 |
| JW2840 | ygeY | predicted peptidase | 0 | -0.251 | 0 | 0 | 7 | 251 |
| JW2590 | rpsP | 30S ribosomal subunit protein S16 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.329 | 0 | 0 | 4 | 250 |
| JW3598 | rfaK | lipopolysaccharide core biosynthesis | GO:0019866 inner membrane | -0.176 | 1 | 0 | 9 | 249 |
| JW5641 | ttk | division inhibitor | 0 | -0.306 | 0 | 0 | 5 | 249 |
| JW3146 | rrmJ | 23S rRNA methyltransferase | 0 | -0.244 | 0 | 0 | 7 | 248 |
| JW0461 | recR | gap repair protein | GO:0005737 cytoplasm | -0.184 | 0 | 0 | 6 | 247 |
| JW0602 | rnk | regulator of nucleoside diphosphate | 0 | -0.029 | 0 | 0 | 5 | 247 |
| JW2112 | yehS | conserved protein | 0 | -0.327 | 0 | 0 | 6 | 247 |
| JW3319 | yhfA | conserved protein | 0 | 0.069 | 1 | 0 | 6 | 247 |
| JW0749 | ybhA | predicted hydrolase | 0 | -0.126 | 0 | 0 | 4 | 246 |
| JW3568 | yibA | lyase containing HEAT-repeat | 0 | -0.386 | 0 | 0 | 8 | 246 |
| JW4196 | nrdG | anaerobic ribonucleotide reductase activating protein | 0 | -0.376 | 0 | 0 | 6 | 246 |
| JW4335 | rimI | acetylase for 30S ribosomal subunit protein S18 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.184 | 0 | 0 | 5 | 246 |
| JW0182 | yaeR | predicted lyase | 0 | -0.198 | 0 | 0 | 3 | 244 |
| JW0380 | yaiA | predicted protein | 0 | -1.275 | 0 | 0 | 5 | 244 |
| JW5346 | yohN | predicted protein | 0 | -0.238 | 1 | 1 | 4 | 244 |
| JW2411 | pdxK | pyridoxal-pyridoxamine kinase/hydroxymethylpyrimidine kinase | 0 | 0.090 | 1 | 0 | 5 | 243 |
| JW2556 | rseA | anti-sigma factor | GO:0005737 cytoplasm | -0.600 | 0 | 0 | 5 | 243 |
| JW0186 | yaeQ | conserved protein | 0 | -0.357 | 0 | 0 | 4 | 242 |
| JW1759 | ydjF | predicted DNA-binding transcriptional regulator | 0 | -0.189 | 0 | 0 | 7 | 242 |
| JW2115 | mlrA | DNA-binding transcriptional regulator | 0 | -0.349 | 0 | 0 | 6 | 242 |
| JW2756 | rumA | 23S rRNA (uracil-5)-methyltransferase | 0 | -0.230 | 0 | 0 | 8 | 242 |
| JW3070 | ygjE | conserved inner membrane protein | 0 | 0.346 | 1 | 2 | 6 | 242 |
| JW3525 | cspA | major cold shock protein | GO:0005737 cytoplasm | -0.251 | 0 | 0 | 5 | 242 |
| JW4201 | mgtA | magnesium transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.159 | 1 | 7 | 9 | 242 |
| JW5041 | ykgE | predicted oxidoreductase | 0 | 0.037 | 1 | 0 | 6 | 242 |

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|--------|------|--|---|--------|---|---|---|-----|
| JW5107 | ybiN | predicted SAM-dependent methyltransferase | 0 | -0.382 | 0 | 0 | 5 | 242 |
| JW1632 | ydhH | conserved protein | 0 | 0.057 | 1 | 0 | 6 | 241 |
| JW2328 | yfcN | conserved protein | 0 | -0.482 | 0 | 0 | 6 | 241 |
| JW4216 | holC | DNA polymerase III, chi subunit | GO:0005737 cytoplasm | -0.372 | 0 | 0 | 6 | 241 |
| JW0026 | fkpB | FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase) | GO:0005737 cytoplasm | -0.095 | 0 | 0 | 3 | 240 |
| JW0743 | modF | fused subunits of molybdate transporter -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.216 | 0 | 0 | 8 | 240 |
| JW4018 | yjbR | conserved protein | 0 | -0.392 | 0 | 0 | 4 | 240 |
| JW4148 | yjfP | predicted hydrolase | 0 | -0.036 | 0 | 0 | 4 | 240 |
| JW5113 | ybjI | conserved protein | 0 | -0.137 | 0 | 0 | 4 | 240 |
| JW0411 | ispA | geranyltranstransferase | GO:0005737 cytoplasm | -0.121 | 0 | 0 | 6 | 239 |
| JW0864 | cspD | cold shock protein homolog | GO:0005737 cytoplasm | -0.197 | 0 | 0 | 3 | 239 |
| JW0008 | mog | predicted molybdochelatase | GO:0005737 cytoplasm | -0.013 | 0 | 0 | 5 | 238 |
| JW2581 | tyrA | fused chorismate mutase T -!- prephenate dehydrogenase | GO:0005737 cytoplasm | -0.090 | 0 | 0 | 8 | 238 |
| JW2788 | recB | exonuclease V (RecBCD complex), beta subunit | 0 | -0.319 | 0 | 0 | 7 | 238 |
| JW2288 | yfbR | deoxyribonucleoside 5'- | 0 | -0.216 | 0 | 0 | 6 | 237 |
| JW2507 | pepB | aminopeptidase B | 0 | -0.214 | 0 | 0 | 5 | 237 |
| JW3595 | rfaF | ADP-heptose:LPS heptosyltransferase | 0 | -0.185 | 0 | 0 | 6 | 237 |
| JW5535 | yrbB | predicted protein | 0 | 0.032 | 1 | 0 | 4 | 237 |
| JW5735 | dcuA | C4-dicarboxylate antiporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.800 | 1 | 9 | 3 | 237 |
| JW5777 | yjhT | conserved protein | 0 | -0.348 | 0 | 0 | 5 | 237 |
| JW2717 | ispD | 4-diphosphocytidyl-2C-methyl-D-erythritol synthase | GO:0005737 cytoplasm | -0.174 | 0 | 0 | 7 | 236 |
| JW3386 | glpR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.213 | 0 | 0 | 6 | 236 |
| JW4177 | ytfL | predicted inner membrane protein | 0 | 0.238 | 1 | 4 | 5 | 236 |
| JW2340 | yfcZ | conserved protein | 0 | -0.094 | 0 | 0 | 3 | 235 |
| JW2989 | ygiT | predicted DNA-binding transcriptional regulator | 0 | -0.322 | 0 | 0 | 6 | 235 |
| JW1208 | chaB | predicted cation regulator | GO:0005737 cytoplasm | -1.478 | 0 | 0 | 5 | 234 |
| JW1283 | sapF | predicted antimicrobial peptide transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.242 | 0 | 0 | 6 | 234 |
| JW1811 | rrmA | 23S rRNA m1G745 methyltransferase | GO:0005737 cytoplasm | -0.284 | 0 | 0 | 4 | 234 |
| JW0389 | phoB | DNA-binding response regulator in two-component regulatory system with PhoR (or CreC) | GO:0005737 cytoplasm | -0.372 | 0 | 0 | 4 | 233 |
| JW0557 | nfrA | bacteriophage N4 receptor, outer membrane subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.454 | 1 | 0 | 6 | 233 |
| JW0700 | ybgI | conserved metal-binding protein | 0 | -0.125 | 0 | 0 | 4 | 233 |

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|--------|------|---|---|--------|---|---|---|-----|
| JW4212 | yjgD | conserved protein | 0 | -0.605 | 0 | 0 | 4 | 233 |
| JW0415 | panE | 2-dehydropantoate reductase, NADPH-specific | 0 | -0.119 | 0 | 0 | 6 | 232 |
| JW1575 | ynfB | predicted protein | 0 | -0.746 | 0 | 0 | 4 | 232 |
| JW2588 | trmD | tRNA (guanine-1-)-methyltransferase | GO:0005737 cytoplasm | -0.309 | 0 | 0 | 5 | 232 |
| JW3274 | rpmC | 50S ribosomal subunit protein L29 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.657 | 0 | 0 | 3 | 232 |
| JW1504 | ydeV | predicted sugar kinase | 0 | 0.047 | 1 | 0 | 7 | 231 |
| JW3273 | rpsQ | 30S ribosomal subunit protein S17 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.293 | 0 | 0 | 4 | 231 |
| JW3360 | nudE | ADP-ribose diphosphatase | 0 | -0.254 | 0 | 0 | 3 | 231 |
| JW1733 | astE | succinylglutamate desuccinylase | 0 | -0.069 | 0 | 0 | 4 | 230 |
| JW2918 | yggS | predicted enzyme | 0 | -0.200 | 0 | 0 | 6 | 230 |
| JW3423 | livK | leucine transporter subunit -!- periplasmic-binding component of ABC | GO:0042597 periplasmic space | -0.227 | 0 | 0 | 6 | 230 |
| JW0801 | mntR | transcriptional regulator of mntH | 0 | -0.377 | 0 | 0 | 6 | 229 |
| JW2262 | elaA | predicted acyltransferase with acyl-CoA N-acyltransferase domain | 0 | -0.218 | 0 | 0 | 4 | 229 |
| JW5785 | yjiL | predicted ATPase, activator of (R)-hydroxyglutaryl-CoA dehydratase | 0 | 0.133 | 1 | 0 | 5 | 229 |
| JW0944 | yccF | conserved inner membrane protein | 0 | 0.777 | 1 | 3 | 4 | 228 |
| JW2142 | cirA | ferric iron-catecholate outer membrane transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.600 | 1 | 0 | 4 | 228 |
| JW1915 | yedF | conserved protein | 0 | -0.271 | 0 | 0 | 4 | 227 |
| JW3310 | slyX | conserved protein | 0 | -0.478 | 0 | 0 | 3 | 227 |
| JW5847 | prfB | peptide chain release factor RF-2 | GO:0005737 cytoplasm | -1.008 | 0 | 0 | 7 | 227 |
| JW0183 | tilS | tRNA(Ile)-lysidine synthetase | 0 | -0.134 | 0 | 0 | 6 | 226 |
| JW0654 | Int | apolipoprotein N-acyltransferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.273 | 1 | 6 | 6 | 226 |
| JW3537 | xylA | D-xylose isomerase | GO:0005737 cytoplasm | -0.442 | 0 | 0 | 6 | 226 |
| JW4127 | amiB | N-acetylmuramoyl-l-alanine amidase II | GO:0009274 cell wall (sensu | -0.297 | 0 | 0 | 7 | 226 |
| JW2078 | gatA | galactitol-specific enzyme IIA component of PTS | 0 | -0.056 | 0 | 0 | 3 | 225 |
| JW2757 | barA | hybrid sensory histidine kinase, in two-component regulatory system with UvrY | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.109 | 1 | 2 | 8 | 225 |
| JW3490 | yhjD | conserved inner membrane protein | 0 | 0.210 | 1 | 6 | 3 | 225 |
| JW0378 | yail | conserved protein | 0 | -0.211 | 0 | 0 | 6 | 224 |
| JW1243 | ycil | predicted enzyme | 0 | -0.031 | 0 | 0 | 4 | 224 |
| JW1431 | ydcP | predicted peptidase | 0 | -0.311 | 0 | 0 | 9 | 224 |
| JW3709 | atpC | F1 sector of membrane-bound ATP synthase, epsilon subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.095 | 1 | 0 | 4 | 224 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW1255 | trpD | fused glutamine amidotransferase (component II) of anthranilate synthase -!- anthranilate phosphoribosyl | GO:0005737 cytoplasm | -0.007 | 0 | 0 | 5 | 223 |
| JW5131 | yccX | predicted acylphosphatase | 0 | -0.393 | 0 | 0 | 6 | 223 |
| JW5296 | yoaC | predicted protein | 0 | -0.253 | 0 | 0 | 3 | 223 |
| JW0184 | rof | modulator of Rho-dependent transcription termination | GO:0005737 cytoplasm | -0.410 | 0 | 0 | 3 | 222 |
| JW0397 | yajC | SecYEG protein translocase auxillary subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.395 | 1 | 1 | 4 | 222 |
| JW0697 | ybgA | conserved protein | 0 | -0.489 | 0 | 0 | 5 | 222 |
| JW3243 | yrdC | dsRNA-binding protein | 0 | -0.057 | 0 | 0 | 3 | 222 |
| JW5598 | rffG | dTDP-glucose 4,6-dehydratase | 0 | -0.270 | 0 | 0 | 6 | 222 |
| JW0316 | yahJ | predicted deaminase with metallo-dependent hydrolase domain | 0 | -0.245 | 0 | 0 | 7 | 221 |
| JW0369 | yaiW | predicted DNA-binding transcriptional regulator | 0 | -0.377 | 0 | 0 | 7 | 221 |
| JW0647 | gltL | glutamate and aspartate transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.063 | 0 | 0 | 6 | 221 |
| JW1284 | sapD | predicted antimicrobial peptide transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.357 | 0 | 0 | 5 | 221 |
| JW1669 | sufE | sulfur acceptor protein | 0 | -0.171 | 0 | 0 | 5 | 221 |
| JW1914 | yedE | predicted inner membrane protein | 0 | 0.586 | 1 | 10 | 5 | 221 |
| JW3147 | yhbY | predicted RNA-binding protein | 0 | -0.182 | 0 | 0 | 4 | 221 |
| JW5794 | mdbB | phosphoglycerol transferase I | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.236 | 1 | 4 | 9 | 221 |
| JW5943 | yhjK | predicted diguanylate cyclase | 0 | 0.187 | 1 | 2 | 6 | 221 |
| JW0022 | rpsT | 30S ribosomal subunit protein S20 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.705 | 0 | 0 | 3 | 219 |
| JW0106 | ampD | N-acetyl-anhydromuranmyl-L-alanine amidase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.309 | 0 | 0 | 6 | 219 |
| JW0479 | ybbL | predicted transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.212 | 0 | 0 | 6 | 219 |
| JW1165 | minC | cell division inhibitor | GO:0005737 cytoplasm | -0.051 | 0 | 0 | 5 | 219 |
| JW3889 | cdh | CDP-diacylglycerol | 0 | -0.304 | 1 | 1 | 6 | 219 |
| JW0910 | ycbL | predicted metal-binding enzyme | 0 | -0.145 | 0 | 0 | 5 | 218 |
| JW1121 | ymfC | 23S rRNA pseudouridine synthase | 0 | -0.669 | 0 | 0 | 5 | 218 |
| JW3002 | nudF | ADP-ribose pyrophosphatase | 0 | -0.216 | 0 | 0 | 6 | 217 |
| JW3606 | rfaG | glucosyltransferase I | GO:0019866 inner membrane | -0.341 | 1 | 0 | 6 | 217 |
| JW4017 | yjbQ | conserved protein | 0 | -0.396 | 0 | 0 | 4 | 217 |
| JW0704 | nei | endonuclease VIII -!- 5-formyluracil/5-hydroxymethyluracil DNA glycosylase | GO:0005737 cytoplasm | -0.349 | 0 | 0 | 5 | 216 |
| JW3037 | rpsU | 30S ribosomal subunit protein S21 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -1.090 | 0 | 0 | 4 | 216 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW3778 | cyaA | adenylate cyclase | GO:0005737 cytoplasm | -0.292 | 0 | 0 | 8 | 216 |
| JW1884 | yecG | universal stress protein | 0 | 0.127 | 1 | 0 | 4 | 215 |
| JW1041 | lpxL | lauryl-acyl carrier protein (ACP)-dependent acyltransferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.205 | 1 | 1 | 6 | 214 |
| JW2863 | fldB | flavodoxin 2 | 0 | -0.231 | 0 | 0 | 4 | 214 |
| JW4111 | ampC | beta-lactamase/D-alanine carboxypeptidase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0042597 | -0.184 | 0 | 0 | 4 | 214 |
| JW5372 | yfbE | uridine 5'-(beta-1-threo-pentapyranosyl-4-ulose diphosphate) aminotransferase, PLP-dependent | 0 | -0.044 | 0 | 0 | 5 | 214 |
| JW1818 | htpX | predicted endopeptidase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.344 | 1 | 4 | 4 | 213 |
| JW5596 | rffT | TDP-Fuc4NAc:lipidII transferase | 0 | -0.138 | 0 | 0 | 7 | 213 |
| JW0177 | lpxB | tetraacyl-disaccharide-1-P synthase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.007 | 0 | 0 | 6 | 212 |
| JW1334 | ydaL | conserved protein | 0 | -0.600 | 0 | 0 | 8 | 212 |
| JW2138 | galS | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | 0.029 | 1 | 0 | 6 | 212 |
| JW2601 | smpB | trans-translation protein | 0 | -0.581 | 0 | 0 | 4 | 212 |
| JW2860 | recJ | ssDNA exonuclease, 5' --> 3'-specific | 0 | -0.069 | 0 | 0 | 8 | 212 |
| JW4136 | yjeB | predicted DNA-binding transcriptional regulator | 0 | 0.055 | 1 | 0 | 5 | 212 |
| JW4160 | rpsR | 30S ribosomal subunit protein S18 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.775 | 0 | 0 | 3 | 212 |
| JW3487 | treF | cytoplasmic trehalase | GO:0005737 cytoplasm | -0.563 | 0 | 0 | 6 | 211 |
| JW3813 | tatA | TatABCE protein translocation system subunit | 0 | -0.470 | 1 | 1 | 3 | 211 |
| JW0070 | leuD | 3-isopropylmalate isomerase subunit | GO:0005737 cytoplasm | -0.175 | 0 | 0 | 5 | 210 |
| JW0795 | glnP | glutamine transporter subunit -!- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.877 | 1 | 3 | 5 | 210 |
| JW1941 | yedI | conserved inner membrane protein | GO:0009274 cell wall (sensu | 0.804 | 1 | 5 | 4 | 210 |
| JW3036 | ygjD | predicted peptidase | 0 | 0.015 | 1 | 0 | 4 | 209 |
| JW5396 | ypfH | predicted hydrolase | 0 | -0.009 | 0 | 0 | 4 | 209 |
| JW1655 | mdtK | multidrug efflux system transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.760 | 1 | 12 | 3 | 208 |
| JW3219 | mreC | cell wall structural complex MreBCD transmembrane component MreC | GO:0009274 cell wall (sensu Bacteria) | -0.152 | 1 | 1 | 5 | 208 |
| JW0279 | yagS | predicted oxidoreductase with FAD-binding domain | 0 | -0.010 | 0 | 0 | 5 | 207 |
| JW0336 | lacI | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | 0.032 | 1 | 0 | 6 | 207 |
| JW0566 | ybdG | predicted mechanosensitive channel | GO:0042597 periplasmic space | 0.301 | 1 | 5 | 7 | 206 |
| JW3414 | ugpQ | glycerophosphodiester phosphodiesterase, cytosolic | GO:0005737 cytoplasm | -0.213 | 0 | 0 | 4 | 206 |
| JW3844 | yihM | predicted sugar phosphate isomerase | 0 | -0.350 | 0 | 0 | 7 | 206 |
| JW5588 | yigI | conserved protein | 0 | -0.008 | 0 | 0 | 5 | 206 |
| JW5646 | envC | protease with a role in cell division | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.688 | 1 | 1 | 6 | 206 |

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|--------|------|--|---|--------|---|---|---|-----|
| JW5949 | yrdD | predicted DNA topoisomerase | 0 | -0.315 | 0 | 0 | 5 | 206 |
| JW0781 | rhIE | RNA helicase | 0 | -0.506 | 0 | 0 | 7 | 205 |
| JW4089 | yjdK | predicted protein | 0 | -0.150 | 0 | 0 | 2 | 205 |
| JW5482 | speC | ornithine decarboxylase, constitutive | 0 | -0.162 | 0 | 0 | 5 | 205 |
| JW5823 | ycdH | predicted protein | 0 | -1.024 | 0 | 0 | 4 | 205 |
| JW1319 | mpaA | murein peptide amidase A | 0 | -0.146 | 0 | 0 | 6 | 204 |
| JW2455 | yffB | conserved protein | 0 | -0.338 | 0 | 0 | 5 | 204 |
| JW2801 | ygdR | predicted protein | 0 | -0.200 | 1 | 1 | 2 | 204 |
| JW3626 | trmH | tRNA (Guanosine-2'-O-)- | 0 | -0.223 | 0 | 0 | 6 | 204 |
| JW3866 | fdhD | formate dehydrogenase formation | GO:0005737 cytoplasm | -0.173 | 0 | 0 | 4 | 204 |
| JW5096 | kdpE | DNA-binding response regulator in two-component regulatory system with | GO:0005737 cytoplasm | -0.147 | 0 | 0 | 7 | 204 |
| JW0109 | pdhR | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.551 | 0 | 0 | 4 | 203 |
| JW3664 | ibpA | heat shock chaperone | 0 | -0.525 | 0 | 0 | 4 | 203 |
| JW1586 | dgsA | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | 0.096 | 1 | 0 | 6 | 202 |
| JW2701 | fhlA | DNA-binding transcriptional activator | GO:0005737 cytoplasm | -0.244 | 0 | 0 | 7 | 202 |
| JW4149 | ulaR | DNA-binding transcriptional dual | 0 | -0.179 | 0 | 0 | 5 | 201 |
| JW2599 | yfiF | predicted protein | 0 | -0.584 | 0 | 0 | 5 | 200 |
| JW2921 | yggV | dITP/XTP pyrophosphatase | 0 | -0.122 | 0 | 0 | 3 | 200 |
| JW3359 | mrcA | fused penicillin-binding protein 1a murein transglycosylase -!- murein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.255 | 1 | 1 | 5 | 200 |
| JW5448 | ygdI | predicted protein | 0 | -0.523 | 1 | 1 | 3 | 200 |
| JW0805 | ybiU | predicted protein | 0 | -0.395 | 0 | 0 | 5 | 199 |
| JW2804 | aas | fused 2-acylglycerophospho-ethanolamine acyl transferase -!- acyl-carrier protein synthetase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | -0.042 | 1 | 0 | 9 | 199 |
| JW3609 | coaD | pantetheine-phosphate adenylyltransferase | 0 | 0.006 | 1 | 0 | 4 | 198 |
| JW0810 | moeB | molybdopterin synthase sulfurylase | 0 | 0.164 | 1 | 0 | 4 | 197 |
| JW0862 | macA | macrolide transporter subunit, membrane fusion protein (MFP) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.184 | 1 | 1 | 8 | 197 |
| JW5262 | dmsD | twin-arginine leader-binding protein for DmsA and TorA | 0 | -0.089 | 0 | 0 | 5 | 197 |
| JW0195 | metN | DL-methionine transporter subunit -!- ATP-binding component of ABC | GO:0005737 cytoplasm | -0.072 | 0 | 0 | 4 | 196 |
| JW0821 | ylil | predicted dehydrogenase | 0 | -0.374 | 0 | 0 | 6 | 195 |
| JW2508 | yfhJ | conserved protein | 0 | -0.520 | 0 | 0 | 2 | 195 |
| JW3312 | yheV | predicted protein | GO:0005737 cytoplasm | -0.611 | 0 | 0 | 3 | 195 |
| JW4107 | efp | Elongation factor EF-P | GO:0005737 cytoplasm | -0.221 | 0 | 0 | 3 | 194 |
| JW1218 | narI | nitrate reductase 1, gamma (cytochrome b(NR)) subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.575 | 1 | 5 | 3 | 193 |
| JW2790 | recC | exonuclease V (RecBCD complex), gamma chain | 0 | -0.288 | 0 | 0 | 7 | 193 |
| JW5054 | psiF | conserved protein | 0 | -0.570 | 1 | 1 | 3 | 193 |
| JW2088 | yegW | predicted DNA-binding transcriptional regulator | 0 | -0.306 | 0 | 0 | 5 | 192 |

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|--------|------|--|---|--------|---|---|---|-----|
| JW3197 | sspB | ClpXP protease specificity-enhancing factor | 0 | -0.432 | 0 | 0 | 3 | 192 |
| JW5736 | yjel | conserved protein | 0 | -0.076 | 0 | 0 | 2 | 192 |
| JW0373 | yaiB | predicted protein | 0 | -0.458 | 0 | 0 | 3 | 191 |
| JW2023 | rfbC | dTDP-4-deoxyrhamnose-3,5-epimerase | GO:0005737 cytoplasm -! GO:0005737 cytoplasm | -0.204 | 0 | 0 | 5 | 191 |
| JW3811 | yigP | conserved protein | 0 | 0.021 | 1 | 0 | 3 | 191 |
| JW0107 | ampE | predicted inner membrane protein | GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner | 0.474 | 1 | 4 | 4 | 190 |
| JW1667 | lpp | murein lipoprotein | GO:0009274 cell wall (sensu Bacteria) -! GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner membrane | -0.314 | 1 | 0 | 2 | 190 |
| JW3980 | yjbB | predicted transporter | 0 | 0.432 | 1 | 8 | 6 | 190 |
| JW0482 | ybbO | predicted oxidoreductase with NAD(P)- binding Rossmann-fold domain | 0 | -0.043 | 0 | 0 | 5 | 189 |
| JW2872 | gcvH | glycine cleavage complex lipoylprotein | 0 | -0.139 | 0 | 0 | 3 | 189 |
| JW3307 | yheN | predicted intracellular sulfur oxidation protein | 0 | 0.166 | 1 | 0 | 3 | 189 |
| JW5521 | tdcF | predicted L-PSP (mRNA) | 0 | 0.120 | 1 | 0 | 3 | 189 |
| JW1336 | ydaN | predicted Zn(II) transporter | 0 | -0.050 | 1 | 2 | 5 | 188 |
| JW3098 | sohA | predicted regulator | 0 | -0.578 | 0 | 0 | 3 | 188 |
| JW3512 | dppB | dipeptide transporter-! membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner | 0.692 | 1 | 6 | 3 | 188 |
| JW5819 | ybjS | predicted NAD(P)H oxidoreductase with NAD(P)-binding Rossmann-fold domain | 0 | -0.290 | 0 | 0 | 3 | 187 |
| JW0079 | mraZ | conserved protein | 0 | -0.247 | 0 | 0 | 4 | 186 |
| JW0400 | yajD | conserved protein | 0 | -0.830 | 0 | 0 | 3 | 186 |
| JW0788 | ybil | conserved protein | 0 | -0.882 | 0 | 0 | 5 | 186 |
| JW1083 | yceG | predicted aminodeoxychorismate lyase | 0 | -0.236 | 1 | 1 | 5 | 186 |
| JW1274 | yciH | conserved protein | 0 | -0.419 | 0 | 0 | 3 | 186 |
| JW4085 | dcuR | DNA-binding response regulator in two- component regulatory system with | GO:0005737 cytoplasm | -0.250 | 0 | 0 | 4 | 185 |
| JW4054 | phnO | predicted acyltransferase with acyl-CoA N-acyltransferase domain | 0 | -0.316 | 0 | 0 | 4 | 184 |
| JW2916 | yqgF | predicted Holliday junction resolvase | 0 | -0.257 | 0 | 0 | 3 | 183 |
| JW3446 | nikR | DNA-binding transcriptional regulator, Ni-binding | GO:0005737 cytoplasm | -0.532 | 0 | 0 | 4 | 183 |
| JW0382 | yaiE | conserved protein | 0 | -0.039 | 0 | 0 | 3 | 182 |
| JW1617 | ydgT | predicted regulator | 0 | -0.470 | 0 | 0 | 5 | 182 |
| JW5745 | ytfB | predicted cell envelope opacity- associated protein | 0 | -0.574 | 0 | 0 | 4 | 182 |
| JW0727 | tolQ | membrane spanning protein in TolA- TolQ-TolR complex | GO:0009274 cell wall (sensu Bacteria) -! GO:0019866 inner | 0.226 | 1 | 3 | 4 | 181 |
| JW2299 | yfcG | predicted glutathione S-transferase | 0 | -0.382 | 0 | 0 | 4 | 181 |
| JW3223 | accB | acetyl CoA carboxylase, BCCP subunit | 0 | 0.010 | 1 | 0 | 3 | 181 |
| JW0533 | ybcL | DLP12 prophage; predicted kinase | 0 | -0.121 | 0 | 0 | 3 | 180 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW1782 | yoaF | conserved outer membrane protein | 0 | -0.167 | 0 | 0 | 2 | 180 |
| JW4116 | poxA | predicted lysyl-tRNA synthetase | 0 | -0.291 | 0 | 0 | 5 | 180 |
| JW5116 | ybjT | conserved protein with NAD(P)-binding Rossmann-fold domain | 0 | -0.064 | 1 | 1 | 4 | 180 |
| JW0936 | rmf | ribosome modulation factor | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -1.136 | 0 | 0 | 4 | 179 |
| JW2805 | galR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.069 | 0 | 0 | 5 | 179 |
| JW3784 | xerC | site-specific tyrosine recombinase | 0 | -0.379 | 0 | 0 | 4 | 179 |
| JW1676 | ydil | conserved protein | 0 | -0.064 | 0 | 0 | 3 | 178 |
| JW0046 | kefC | potassium:proton antiporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.457 | 1 | 13 | 5 | 177 |
| JW2515 | iscR | DNA-binding transcriptional activator | 0 | -0.256 | 0 | 0 | 3 | 177 |
| JW2767 | sdaC | predicted serine transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.807 | 1 | 11 | 3 | 177 |
| JW3470 | arsC | arsenate reductase | 0 | -0.280 | 0 | 0 | 4 | 177 |
| JW5657 | yiaD | predicted outer membrane lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.073 | 1 | 3 | 2 | 177 |
| JW0560 | cusR | DNA-binding response regulator in two-component regulatory system with | 0 | 0.075 | 1 | 0 | 5 | 176 |
| JW2557 | rpoE | RNA polymerase, sigma 24 (sigma E) factor | GO:0005737 cytoplasm | -0.254 | 0 | 0 | 4 | 176 |
| JW5758 | yjgM | predicted acetyltransferase | 0 | -0.122 | 0 | 0 | 4 | 176 |
| JW0712 | sdhD | succinate dehydrogenase, membrane subunit, binds cytochrome b556 | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.369 | 1 | 3 | 3 | 175 |
| JW5528 | yraR | predicted nucleoside-diphosphate-sugar epimerase | 0 | -0.095 | 0 | 0 | 2 | 175 |
| JW1237 | oppC | oligopeptide transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.675 | 1 | 6 | 4 | 174 |
| JW2687 | hycl | protease involved in processing C-terminal end of HycE | 0 | 0.023 | 1 | 0 | 3 | 174 |
| JW2999 | yqiA | predicted esterase | 0 | -0.034 | 0 | 0 | 3 | 174 |
| JW4166 | cycA | D-alanine/D-serine/glycine transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.831 | 1 | 12 | 3 | 173 |
| JW0456 | priC | primosomal replication protein N" | GO:0005737 cytoplasm | -0.551 | 0 | 0 | 6 | 172 |
| JW1168 | ycgL | conserved protein | 0 | -0.669 | 0 | 0 | 5 | 172 |
| JW1807 | manY | mannose-specific enzyme IIC component of PTS | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.007 | 1 | 7 | 2 | 172 |
| JW2284 | IrhA | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.011 | 0 | 0 | 5 | 172 |
| JW3608 | kdtA | 3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0030113 capsule (sensu Bacteria) | 0.022 | 1 | 0 | 5 | 172 |
| JW0703 | ybgL | predicted lactam utilization protein | 0 | 0.022 | 1 | 0 | 4 | 171 |
| JW1581 | ynfG | oxidoreductase, Fe-S subunit | 0 | -0.418 | 0 | 0 | 3 | 171 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW3863 | fdol | formate dehydrogenase-O, cytochrome b556 subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.499 | 1 | 4 | 2 | 171 |
| JW2961 | hybD | predicted maturation element for hydrogenase 2 | 0 | 0.298 | 1 | 0 | 4 | 170 |
| JW3602 | rfal | UDP-D-galactose:(glucosyl)lipopolysaccharide-alpha-1,3-D-galactosyltransferase | 0 | -0.221 | 0 | 0 | 6 | 170 |
| JW1436 | ycdT | predicted spermidine/putrescine transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.121 | 0 | 0 | 5 | 169 |
| JW0976 | gnsA | predicted regulator of phosphatidylethanolamine synthesis | GO:0005737 cytoplasm | -0.546 | 0 | 0 | 2 | 168 |
| JW1610 | uidR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.037 | 0 | 0 | 4 | 168 |
| JW1699 | btuD | vitamin B12 transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.132 | 0 | 0 | 4 | 168 |
| JW2960 | hybE | hydrogenase 2-specific chaperone | 0 | -0.054 | 0 | 0 | 3 | 168 |
| JW3644 | uhpA | DNA-binding response regulator in two-component regulatory system with | GO:0005737 cytoplasm | 0.182 | 1 | 0 | 4 | 168 |
| JW3840 | glnL | sensory kinase in two-component regulatory system with GlnG | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.174 | 1 | 0 | 6 | 168 |
| JW0077 | ilvH | acetolactate synthase III, thiamin-dependent, small subunit | 0 | -0.055 | 0 | 0 | 3 | 167 |
| JW0767 | moaD | molybdopterin synthase, small subunit | 0 | 0.202 | 1 | 0 | 2 | 167 |
| JW1828 | yebY | predicted protein | 0 | 0.010 | 1 | 1 | 2 | 167 |
| JW3426 | rpoH | RNA polymerase, sigma 32 (sigma H) factor | GO:0005737 cytoplasm | -0.502 | 0 | 0 | 3 | 167 |
| JW1891 | yecJ | predicted protein | GO:0005737 cytoplasm | 0.082 | 1 | 0 | 4 | 166 |
| JW4325 | dnaC | DNA biosynthesis protein | 0 | -0.481 | 0 | 0 | 3 | 166 |
| JW5553 | argB | acetylglutamate kinase | GO:0005737 cytoplasm | 0.207 | 1 | 0 | 3 | 166 |
| JW5962 | sra | 30S ribosomal subunit protein S22 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -1.269 | 0 | 0 | 4 | 166 |
| JW1222 | rssA | conserved protein | GO:0009274 cell wall (sensu | 0.084 | 1 | 0 | 3 | 165 |
| JW3118 | yraO | DnaA initiator-associating factor for replication initiation | 0 | 0.023 | 1 | 0 | 4 | 165 |
| JW3130 | mtr | tryptophan transporter of high affinity | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.863 | 1 | 11 | 2 | 165 |
| JW4113 | frdC | fumarate reductase (anaerobic), membrane anchor subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.554 | 1 | 3 | 3 | 165 |
| JW4181 | ytfP | conserved protein | 0 | -0.514 | 0 | 0 | 3 | 165 |
| JW1152 | ymgA | predicted protein | 0 | -0.600 | 0 | 0 | 5 | 164 |
| JW1251 | yciG | predicted protein | 0 | -1.673 | 0 | 0 | 3 | 164 |
| JW2837 | ygeV | predicted DNA-binding transcriptional regulator | 0 | -0.130 | 0 | 0 | 5 | 164 |
| JW3102 | agaV | N-acetylgalactosamine-specific enzyme IIB component of PTS | GO:0005737 cytoplasm | 0.226 | 1 | 0 | 4 | 164 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW3611 | rpmG | 50S ribosomal subunit protein L33 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.804 | 0 | 0 | 2 | 164 |
| JW0388 | sbcd | exonuclease, dsDNA, ATP-dependent | GO:0005737 cytoplasm | -0.244 | 0 | 0 | 5 | 163 |
| JW2117 | yehX | predicted transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.119 | 0 | 0 | 7 | 163 |
| JW2283 | nuoA | NADH:ubiquinone oxidoreductase, membrane subunit A | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.565 | 1 | 3 | 2 | 163 |
| JW1727 | chbB | N,N'-diacetylchitobiose-specific enzyme IIB component of PTS | 0 | 0.251 | 1 | 0 | 3 | 162 |
| JW5241 | yddV | predicted diguanylate cyclase | 0 | -0.277 | 0 | 0 | 4 | 162 |
| JW5816 | ybfE | LexA regulated protein | 0 | -0.907 | 0 | 0 | 3 | 162 |
| JW1001 | putP | proline:sodium symporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.785 | 1 | 12 | 5 | 161 |
| JW2389 | nupC | nucleoside (except guanosine) transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.903 | 1 | 8 | 3 | 161 |
| JW3367 | envZ | sensory histidine kinase in two-component regulatory system with | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.060 | 1 | 2 | 6 | 159 |
| JW3484 | gadX | DNA-binding transcriptional dual | 0 | -0.077 | 0 | 0 | 4 | 159 |
| JW4002 | dgkA | diacylglycerol kinase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.881 | 1 | 2 | 3 | 159 |
| JW5338 | mdtA | multidrug efflux system, subunit A | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.223 | 1 | 1 | 3 | 159 |
| JW0002 | thrB | homoserine kinase | GO:0005737 cytoplasm | 0.024 | 1 | 0 | 5 | 158 |
| JW4167 | ytfE | predicted regulator of cell morphogenesis and cell wall | 0 | -0.352 | 0 | 0 | 4 | 158 |
| JW0773 | ybhP | predicted DNase | 0 | -0.295 | 0 | 0 | 3 | 157 |
| JW1517 | yneH | predicted glutaminase | 0 | 0.133 | 1 | 0 | 3 | 157 |
| JW1602 | tus | inhibitor of replication at Ter, DNA-binding protein | GO:0005737 cytoplasm | -0.471 | 0 | 0 | 7 | 157 |
| JW1657 | ydhR | predicted protein | 0 | -0.215 | 0 | 0 | 2 | 157 |
| JW1954 | yedY | predicted reductase | 0 | -0.289 | 0 | 0 | 5 | 157 |
| JW3208 | yhcO | predicted barnase inhibitor | 0 | -0.376 | 0 | 0 | 3 | 157 |
| JW0952 | yccK | predicted sulfite reductase subunit | 0 | -0.304 | 0 | 0 | 3 | 156 |
| JW2545 | yfhH | predicted DNA-binding transcriptional regulator | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.007 | 1 | 0 | 4 | 156 |
| JW2600 | yfjG | conserved protein | 0 | 0.129 | 1 | 0 | 4 | 156 |
| JW5336 | yegH | fused predicted membrane proteins | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.177 | 1 | 7 | 2 | 156 |
| JW5660 | eptB | predicted metal dependent hydrolase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.110 | 1 | 5 | 5 | 156 |
| JW3142 | secG | preprotein translocase membrane subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.375 | 1 | 2 | 2 | 155 |
| JW3906 | priA | Primosome factor n' (replication factor) | GO:0005737 cytoplasm | -0.186 | 0 | 0 | 6 | 155 |
| JW5017 | yafD | conserved protein | 0 | -0.154 | 0 | 0 | 4 | 155 |
| JW5117 | hcr | HCP oxidoreductase, NADH-dependent | 0 | -0.066 | 0 | 0 | 3 | 155 |
| JW0957 | hyaD | protein involved in processing of HyaA and HyaB proteins | 0 | -0.114 | 0 | 0 | 3 | 154 |
| JW1223 | rssB | response regulator of RpoS | GO:0005737 cytoplasm | 0.071 | 1 | 0 | 4 | 154 |

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|--------|------|--|---|--------|---|---|---|-----|
| JW3581 | yibK | predicted rRNA methylase | 0 | -0.243 | 0 | 0 | 4 | 154 |
| JW3716 | atpB | F0 sector of membrane-bound ATP synthase, subunit a | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.807 | 1 | 5 | 3 | 154 |
| JW0057 | rluA | pseudouridine synthase for 23S rRNA (position 746) and tRNA ^{phe} (position 32) | 0 | -0.428 | 0 | 0 | 3 | 153 |
| JW1275 | osmB | lipoprotein | 0 | 0.511 | 1 | 0 | 1 | 153 |
| JW2779 | gcvA | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.143 | 0 | 0 | 4 | 153 |
| JW5182 | dsbB | oxidoreductase that catalyzes reoxidation of DsbA protein disulfide isomerase I | GO:0019861 flagellum -!- GO:0009289 fimbria -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.638 | 1 | 4 | 4 | 153 |
| JW0393 | malZ | maltodextrin glucosidase | GO:0005737 cytoplasm | -0.449 | 0 | 0 | 5 | 152 |
| JW1262 | btuR | cob(I)alamin adenosyltransferase/cobinamide ATP-dependent adenosyltransferase | GO:0005737 cytoplasm | -0.440 | 0 | 0 | 2 | 152 |
| JW3100 | agaR | DNA-binding transcriptional dual | 0 | -0.232 | 0 | 0 | 3 | 152 |
| JW5159 | ycfQ | predicted DNA-binding transcriptional regulator | 0 | -0.254 | 0 | 0 | 3 | 152 |
| JW5479 | yggU | conserved protein | 0 | -0.074 | 0 | 0 | 3 | 152 |
| JW2298 | yfcF | predicted enzyme | 0 | -0.215 | 0 | 0 | 4 | 151 |
| JW4073 | basS | sensory histidine kinase in two-component regulatory system with | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.050 | 1 | 2 | 6 | 151 |
| JW0630 | mrdA | transpeptidase involved in peptidoglycan synthesis (penicillin- | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.353 | 1 | 1 | 6 | 150 |
| JW1696 | ydiU | conserved protein | 0 | -0.425 | 0 | 0 | 5 | 150 |
| JW5486 | glcF | glycolate oxidase iron-sulfur subunit | 0 | -0.275 | 0 | 0 | 4 | 150 |
| JW0772 | ybhO | cardiolipin synthase 2 | 0 | -0.392 | 0 | 0 | 6 | 149 |
| JW2274 | nuoK | NADH:ubiquinone oxidoreductase, membrane subunit K | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.929 | 1 | 3 | 2 | 149 |
| JW2538 | yfhA | predicted DNA-binding response regulator in two-component system | 0 | -0.156 | 0 | 0 | 4 | 149 |
| JW3610 | mutM | formamidopyrimidine/5-formyluracil/ 5-hydroxymethyluracil DNA glycosylase | GO:0005737 cytoplasm | -0.272 | 0 | 0 | 4 | 149 |
| JW5226 | ydcI | predicted DNA-binding transcriptional regulator | 0 | -0.022 | 0 | 0 | 5 | 149 |
| JW1562 | dicA | Qin prophage; predicted regulator for | 0 | -0.789 | 0 | 0 | 4 | 148 |
| JW2922 | yggW | predicted oxidoreductase | 0 | -0.325 | 0 | 0 | 4 | 148 |
| JW3363 | hslR | ribosome-associated heat shock protein Hsp15 | GO:0005737 cytoplasm | -0.941 | 0 | 0 | 5 | 148 |
| JW3381 | malT | DNA-binding transcriptional activator, maltotriose-ATP-binding | GO:0005737 cytoplasm | -0.273 | 0 | 0 | 4 | 148 |
| JW0432 | ybaV | conserved protein | 0 | 0.019 | 1 | 0 | 4 | 147 |
| JW0253 | mmuM | CP4-6 prophage; S-methylmethionine:homocysteine methyltransferase | 0 | -0.030 | 0 | 0 | 3 | 146 |
| JW0726 | ybgC | predicted acyl-CoA thioesterase | 0 | -0.123 | 0 | 0 | 3 | 146 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW1351 | racR | Rac prophage; predicted DNA-binding transcriptional regulator | 0 | -0.469 | 0 | 0 | 3 | 146 |
| JW5062 | ylaB | conserved inner membrane protein | 0 | -0.136 | 1 | 2 | 6 | 146 |
| JW5216 | ydbL | conserved protein | 0 | -0.125 | 1 | 1 | 5 | 146 |
| JW5380 | trmC | fused 5-methylaminomethyl-2-thiouridine forming enzyme methyltransferase -!- FAD-dependent | 0 | -0.280 | 0 | 0 | 4 | 146 |
| JW0138 | folK | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase | 0 | -0.213 | 0 | 0 | 2 | 145 |
| JW0475 | ybaT | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.038 | 1 | 12 | 3 | 145 |
| JW0912 | ompF | outer membrane porin 1a (la;b;F) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.398 | 1 | 0 | 4 | 145 |
| JW0959 | hyaF | protein involved in nickel incorporation into hydrogenase-1 proteins | 0 | -0.159 | 0 | 0 | 2 | 145 |
| JW1278 | gmr | modulator of Rnase II stability | 0 | -0.190 | 0 | 0 | 4 | 145 |
| JW3046 | ebgR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.153 | 0 | 0 | 5 | 145 |
| JW5871 | mcrB | 5-methylcytosine-specific restriction enzyme McrBC, subunit McrB | GO:0005737 cytoplasm | -0.456 | 0 | 0 | 6 | 145 |
| JW0723 | cydB | cytochrome d terminal oxidase, subunit II | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.658 | 1 | 8 | 2 | 144 |
| JW1149 | ycgE | predicted DNA-binding transcriptional regulator | 0 | -0.405 | 0 | 0 | 2 | 144 |
| JW2018 | wbbJ | predicted acyl transferase | 0 | 0.103 | 1 | 0 | 3 | 144 |
| JW2919 | yggT | predicted inner membrane protein | 0 | 1.191 | 1 | 4 | 2 | 144 |
| JW3361 | yrfF | predicted inner membrane protein | 0 | -0.097 | 1 | 5 | 6 | 144 |
| JW4259 | yjhG | KpLE2 phage-like element; predicted dehydratase | 0 | -0.111 | 0 | 0 | 7 | 144 |
| JW5259 | ynfD | predicted protein | 0 | -0.122 | 0 | 0 | 2 | 144 |
| JW0512 | purE | N5-carboxyaminoimidazole ribonucleotide mutase | GO:0005737 cytoplasm | 0.086 | 1 | 0 | 2 | 143 |
| JW1471 | fdnH | formate dehydrogenase-N, Fe-S (beta) subunit, nitrate-inducible | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.271 | 1 | 1 | 3 | 143 |
| JW1623 | rsxG | predicted oxidoreductase | 0 | -0.129 | 0 | 0 | 3 | 143 |
| JW3206 | argR | DNA-binding transcriptional dual regulator, L-arginine-binding | GO:0005737 cytoplasm | -0.007 | 0 | 0 | 4 | 143 |
| JW3596 | rfaC | ADP-heptose:LPS heptosyl transferase | GO:0019866 inner membrane | -0.219 | 1 | 0 | 3 | 143 |
| JW3829 | mobA | molybdopterin-guanine dinucleotide synthase | 0 | -0.191 | 0 | 0 | 4 | 143 |
| JW5701 | yhfK | conserved inner membrane protein | GO:0005737 cytoplasm | 0.047 | 1 | 9 | 4 | 143 |
| JW0204 | rnhA | ribonuclease HI, degrades RNA of DNA-RNA hybrids | GO:0005737 cytoplasm | -0.631 | 0 | 0 | 4 | 142 |
| JW0556 | ybcH | predicted protein | 0 | -0.158 | 1 | 1 | 3 | 142 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW1131 | ymfK | e14 prophage; repressor protein phage e14 | 0 | -0.411 | 0 | 0 | 5 | 142 |
| JW3603 | rfaB | UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase | 0 | -0.143 | 0 | 0 | 4 | 142 |
| JW3982 | yjbC | 23S rRNA pseudouridine synthase | 0 | -0.522 | 0 | 0 | 4 | 142 |
| JW0381 | aroM | conserved protein | 0 | 0.166 | 1 | 0 | 3 | 141 |
| JW4287 | uxuR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.405 | 0 | 0 | 6 | 140 |
| JW1115 | phoQ | sensory histidine kinase in two-component regulatory system with PhoP | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | -0.140 | 1 | 2 | 4 | 139 |
| JW2771 | fucA | L-fucose-1-phosphate aldolase | 0 | -0.046 | 0 | 0 | 3 | 139 |
| JW1329 | ogt | O-6-alkylguanine-DNA:cysteine-protein methyltransferase | GO:0005737 cytoplasm | -0.253 | 0 | 0 | 2 | 138 |
| JW1533 | ydfH | predicted DNA-binding transcriptional regulator | 0 | -0.496 | 0 | 0 | 5 | 138 |
| JW3475 | yhiF | predicted DNA-binding transcriptional regulator | 0 | 0.269 | 1 | 0 | 5 | 138 |
| JW5807 | leuB | 3-isopropylmalate dehydrogenase | GO:0005737 cytoplasm | -0.113 | 0 | 0 | 4 | 138 |
| JW1175 | nhaB | sodium:proton antiporter | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 0.806 | 1 | 12 | 3 | 137 |
| JW3305 | yheL | predicted intracellular sulfur oxidation protein | 0 | 0.091 | 1 | 0 | 2 | 137 |
| JW3640 | ade | cryptic adenine deaminase | 0 | -0.035 | 0 | 0 | 6 | 137 |
| JW1900 | yecF | predicted protein | 0 | -0.258 | 0 | 0 | 3 | 136 |
| JW2175 | yejL | conserved protein | 0 | -0.184 | 0 | 0 | 2 | 136 |
| JW3165 | kdsC | 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase | 0 | 0.239 | 1 | 0 | 2 | 135 |
| JW3818 | rfaH | DNA-binding transcriptional antiterminator | GO:0009289 fimbria - - GO:0005737 cytoplasm | -0.141 | 0 | 0 | 3 | 135 |
| JW5575 | mobB | molybdopterin-guanine dinucleotide biosynthesis protein B | 0 | -0.082 | 0 | 0 | 3 | 135 |
| JW2185 | ccmE | periplasmic heme chaperone | GO:0019866 inner membrane | -0.275 | 1 | 1 | 3 | 134 |
| JW3021 | glgS | predicted glycogen synthesis protein | GO:0005737 cytoplasm | -0.544 | 0 | 0 | 3 | 134 |
| JW5378 | dedD | conserved protein | 0 | -0.306 | 1 | 1 | 3 | 134 |
| JW2182 | ccmH | heme lyase, CcmH subunit | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | -0.169 | 1 | 3 | 4 | 133 |
| JW2891 | mscS | mechanosensitive channel | 0 | 0.494 | 1 | 3 | 2 | 133 |
| JW5368 | yojL | predicted thiamine biosynthesis | 0 | -0.282 | 0 | 0 | 4 | 133 |
| JW5487 | glcE | glycolate oxidase FAD binding subunit | 0 | -0.148 | 0 | 0 | 2 | 133 |
| JW0085 | mraY | phospho-N-acetylmuramoyl-pentapeptide transferase | GO:0009274 cell wall (sensu Bacteria) - - GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane | 0.824 | 1 | 10 | 4 | 132 |
| JW0281 | yagU | conserved inner membrane protein | 0 | 0.337 | 1 | 3 | 3 | 132 |
| JW2798 | nudH | nucleotide hydrolase | 0 | -0.674 | 0 | 0 | 2 | 132 |
| JW5136 | ymdF | conserved protein | GO:0005737 cytoplasm | -1.712 | 0 | 0 | 3 | 132 |
| JW0328 | codA | cytosine deaminase | GO:0005737 cytoplasm | -0.222 | 0 | 0 | 3 | 131 |

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|--------|------|--|--|--------|---|---|---|-----|
| JW1752 | topB | DNA topoisomerase III | GO:0005737 cytoplasm | -0.370 | 0 | 0 | 4 | 131 |
| JW2367 | evgS | hybrid sensory histidine kinase in two-component regulatory system with EvgA | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.199 | 1 | 0 | 4 | 131 |
| JW3369 | greB | transcription elongation factor | GO:0005737 cytoplasm | -0.692 | 0 | 0 | 5 | 131 |
| JW3984 | lysC | aspartokinase III | GO:0005737 cytoplasm | 0.210 | 1 | 0 | 4 | 131 |
| JW4108 | ecnB | entericidin B membrane lipoprotein | 0 | 0.419 | 1 | 1 | 1 | 131 |
| JW5965 | yicS | predicted protein | 0 | -0.319 | 0 | 0 | 4 | 131 |
| JW0711 | sdhC | succinate dehydrogenase, membrane subunit, binds cytochrome b556 | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.837 | 1 | 3 | 2 | 130 |
| JW3546 | yiaJ | predicted DNA-binding transcriptional repressor | 0 | -0.162 | 0 | 0 | 6 | 130 |
| JW0300 | ykgF | predicted amino acid dehydrogenase with NAD(P)-binding domain and ferridoxin-like domain | 0 | -0.313 | 0 | 0 | 4 | 129 |
| JW0824 | deoR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.182 | 0 | 0 | 4 | 129 |
| JW3415 | ugpC | glycerol-3-phosphate transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.224 | 0 | 0 | 2 | 129 |
| JW3812 | ubiB | 2-octaprenylphenol hydroxylase | 0 | -0.140 | 1 | 2 | 4 | 129 |
| JW4218 | yjgP | conserved inner membrane protein | GO:0009274 cell wall (sensu | 0.465 | 1 | 6 | 4 | 129 |
| JW5446 | exo | exonuclease IX (5'-3' exonuclease) | 0 | -0.208 | 0 | 0 | 3 | 129 |
| JW1609 | uidA | beta-D-glucuronidase | 0 | -0.383 | 0 | 0 | 4 | 128 |
| JW2394 | yfeD | predicted DNA-binding transcriptional regulator | 0 | -0.498 | 0 | 0 | 2 | 128 |
| JW2835 | xdhB | xanthine dehydrogenase, FAD-binding subunit | 0 | -0.115 | 0 | 0 | 4 | 128 |
| JW5258 | ynfC | predicted protein | 0 | -0.411 | 0 | 0 | 2 | 128 |
| JW1374 | hslJ | heat-inducible protein | 0 | -0.131 | 0 | 0 | 2 | 127 |
| JW3161 | yrbE | predicted toluene transporter subunit-!- membrane component of ABC | 0 | 0.847 | 1 | 5 | 4 | 127 |
| JW3927 | yijP | conserved inner membrane protein | GO:0009274 cell wall (sensu | -0.323 | 1 | 5 | 5 | 127 |
| JW4348 | yjjJ | predicted DNA-binding transcriptional regulator | 0 | -0.249 | 0 | 0 | 7 | 127 |
| JW5510 | ygjG | putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent | 0 | 0.016 | 1 | 0 | 6 | 127 |
| JW0833 | grxA | glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a) | 0 | -0.571 | 0 | 0 | 3 | 126 |
| JW2582 | aroF | 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase, tyrosine- | 0 | -0.297 | 0 | 0 | 3 | 126 |
| JW1916 | yedK | predicted protein | 0 | -0.388 | 0 | 0 | 3 | 125 |
| JW2643 | ygaP | predicted inner membrane protein with hydrolase activity | 0 | 0.239 | 1 | 2 | 5 | 125 |
| JW3157 | yrbA | predicted DNA-binding transcriptional regulator | 0 | -0.265 | 0 | 0 | 4 | 125 |
| JW4152 | ulaB | L-ascorbate-specific enzyme IIB component of PTS | 0 | 0.091 | 1 | 0 | 3 | 125 |
| JW1940 | yodC | predicted protein | 0 | -0.407 | 0 | 0 | 4 | 124 |

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|--------|------|--|---|--------|---|----|---|-----|
| JW2063 | baeS | sensory histidine kinase in two-component regulatory system with | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.208 | 1 | 2 | 3 | 124 |
| JW2378 | ypdB | predicted response regulator in two-component system with YpdA | 0 | -0.180 | 0 | 0 | 3 | 124 |
| JW5353 | yehU | predicted sensory kinase in two-component system with YehT | 0 | 0.175 | 1 | 6 | 5 | 124 |
| JW2654 | proX | glycine betaine transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.321 | 0 | 0 | 4 | 123 |
| JW3127 | yhbU | predicted peptidase (collagenase-like) | 0 | -0.271 | 0 | 0 | 4 | 123 |
| JW3600 | rfaY | lipopolysaccharide core biosynthesis protein | GO:0019866 inner membrane | -0.517 | 1 | 0 | 4 | 123 |
| JW5402 | yfgJ | predicted protein | 0 | -0.179 | 0 | 0 | 3 | 123 |
| JW5633 | yidQ | conserved outer membrane protein | 0 | -0.035 | 0 | 0 | 3 | 123 |
| JW5645 | yibQ | predicted polysaccharide deacetylase | 0 | -0.229 | 1 | 1 | 3 | 123 |
| JW1298 | pspB | transcriptional regulator of psp operon | GO:0005737 cytoplasm | -0.223 | 1 | 1 | 2 | 122 |
| JW2254 | pmrD | polymyxin resistance protein B | 0 | -0.264 | 0 | 0 | 2 | 122 |
| JW5627 | dgoR | predicted DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.355 | 0 | 0 | 4 | 122 |
| JW0261 | yagE | CP4-6 prophage; predicted | 0 | 0.105 | 1 | 0 | 3 | 121 |
| JW3323 | pabA | aminodeoxychorismate synthase, | 0 | -0.022 | 0 | 0 | 3 | 121 |
| JW3746 | ilvY | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.141 | 0 | 0 | 3 | 121 |
| JW5897 | yliA | fused predicted peptide transport subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.040 | 0 | 0 | 2 | 121 |
| JW0635 | holA | DNA polymerase III, delta subunit | GO:0005737 cytoplasm | -0.099 | 0 | 0 | 4 | 120 |
| JW1805 | yoaE | fused predicted membrane proteins | GO:0009274 cell wall (sensu | 0.452 | 1 | 7 | 3 | 120 |
| JW2592 | ypjD | predicted inner membrane protein | 0 | 0.822 | 1 | 8 | 2 | 120 |
| JW3745 | ilvA | threonine deaminase | 0 | -0.048 | 0 | 0 | 4 | 120 |
| JW5083 | ybdF | conserved protein | 0 | -0.365 | 0 | 0 | 3 | 120 |
| JW5367 | napB | nitrate reductase, small, cytochrome C550 subunit, periplasmic | GO:0042597 periplasmic space | -0.412 | 0 | 0 | 3 | 119 |
| JW5622 | tnaB | tryptophan transporter of low affinity | 0 | 0.719 | 1 | 7 | 2 | 119 |
| JW1104 | lolE | outer membrane-specific lipoprotein transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.411 | 1 | 4 | 3 | 118 |
| JW2993 | qseB | DNA-binding response regulator in two-component regulatory system with | 0 | -0.234 | 0 | 0 | 4 | 118 |
| JW4025 | yjcD | predicted permease | 0 | 1.121 | 1 | 13 | 3 | 118 |
| JW5466 | guaD | guanine deaminase | 0 | -0.368 | 0 | 0 | 6 | 118 |
| JW5542 | yhdP | conserved membrane protein, predicted transporter | 0 | -0.279 | 1 | 1 | 6 | 118 |
| JW0346 | frmB | predicted esterase | 0 | -0.363 | 0 | 0 | 5 | 117 |
| JW0875 | ycaJ | recombination protein | 0 | -0.387 | 0 | 0 | 5 | 117 |
| JW3425 | livJ | leucine/isoleucine/valine transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.189 | 0 | 0 | 3 | 117 |

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|--------|------|---|---|--------|---|----|---|-----|
| JW4028 | actP | acetate transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.793 | 1 | 13 | 3 | 117 |
| JW5066 | ybbM | predicted inner membrane protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.726 | 1 | 7 | 2 | 117 |
| JW2060 | mdtB | multidrug efflux system, subunit B | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | 0.376 | 1 | 11 | 5 | 116 |
| JW2132 | sanA | predicted protein | 0 | 0.014 | 1 | 1 | 5 | 116 |
| JW3166 | yrbK | conserved protein | 0 | -0.372 | 1 | 1 | 4 | 116 |
| JW3435 | yhhP | conserved protein required for cell | 0 | -0.227 | 0 | 0 | 3 | 116 |
| JW4206 | yjgH | predicted mRNA endoribonuclease | 0 | -0.176 | 0 | 0 | 3 | 116 |
| JW0873 | ftsK | DNA-binding membrane protein required for chromosome resolution and | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.407 | 1 | 5 | 5 | 115 |
| JW2315 | truA | pseudouridylate synthase I | GO:0005737 cytoplasm | -0.314 | 0 | 0 | 4 | 115 |
| JW2406 | cysZ | predicted inner membrane protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.549 | 1 | 4 | 3 | 115 |
| JW0453 | acrR | DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.186 | 0 | 0 | 2 | 114 |
| JW0588 | entA | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase | 0 | 0.033 | 1 | 0 | 5 | 114 |
| JW1871 | cheY | chemotaxis regulator transmitting signal to flagellar motor component | GO:0005737 cytoplasm | 0.027 | 1 | 0 | 2 | 114 |
| JW2676 | srlR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.125 | 0 | 0 | 3 | 114 |
| JW2784 | mltA | membrane-bound lytic murein transglycosylase A | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.409 | 1 | 0 | 4 | 114 |
| JW3551 | viaO | predicted transporter | 0 | -0.198 | 0 | 0 | 3 | 114 |
| JW5013 | cdaR | DNA-binding transcriptional regulator | 0 | -0.234 | 0 | 0 | 4 | 114 |
| JW0275 | intF | CP4-6 prophage; predicted phage integrase | 0 | -0.406 | 0 | 0 | 4 | 113 |
| JW5272 | ydhV | predicted oxidoreductase | 0 | -0.333 | 0 | 0 | 4 | 113 |
| JW0049 | apaG | protein associated with Co2+ and Mg2+ efflux | 0 | -0.045 | 0 | 0 | 2 | 112 |
| JW0465 | aes | acetyl esterase | GO:0005737 cytoplasm | -0.191 | 0 | 0 | 3 | 112 |
| JW1459 | yddE | conserved protein | 0 | -0.132 | 0 | 0 | 3 | 112 |
| JW1802 | yeaB | predicted NUDIX hydrolase | 0 | -0.028 | 0 | 0 | 3 | 112 |
| JW4100 | fxsA | inner membrane protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.385 | 1 | 3 | 2 | 111 |
| JW5584 | pldB | lysophospholipase L(2) | 0 | -0.336 | 0 | 0 | 5 | 111 |
| JW3350 | dam | DNA adenine methylase | GO:0005737 cytoplasm | -0.388 | 0 | 0 | 3 | 110 |
| JW2775 | fucU | L-fucose mutarotase | 0 | 0.179 | 1 | 0 | 3 | 109 |
| JW3314 | kefG | component of potassium efflux complex with KefB | 0 | -0.251 | 0 | 0 | 3 | 109 |
| JW5430 | srIE | glucitol/sorbitol-specific enzyme IIB component of PTS | 0 | 0.483 | 1 | 4 | 3 | 108 |
| JW5516 | yqjC | conserved protein | 0 | -0.987 | 0 | 0 | 3 | 108 |

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|--------|------|---|--|--------|---|----|---|-----|
| JW0861 | ybjX | conserved protein | 0 | -0.345 | 0 | 0 | 2 | 107 |
| JW2165 | yejA | predicted oligopeptide transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.433 | 1 | 1 | 3 | 107 |
| JW3430 | yhhF | predicted methyltransferase | 0 | -0.266 | 0 | 0 | 3 | 107 |
| JW4279 | fimC | chaperone, periplasmic | GO:0009289 fimbria -!- GO:0042597 periplasmic space | -0.208 | 1 | 1 | 2 | 107 |
| JW0503 | ylbA | conserved protein | 0 | -0.093 | 0 | 0 | 4 | 106 |
| JW2762 | yqcB | tRNA pseudouridine synthase | 0 | -0.495 | 0 | 0 | 3 | 106 |
| JW2611 | yfjN | CP4-57 prophage; predicted protein | 0 | -0.035 | 0 | 0 | 3 | 105 |
| JW5201 | puuA | gamma-Glu-putrescine synthase | 0 | -0.355 | 0 | 0 | 4 | 105 |
| JW1296 | pspF | DNA-binding transcriptional activator | GO:0005737 cytoplasm | -0.294 | 0 | 0 | 4 | 104 |
| JW1665 | ydhZ | predicted protein | 0 | -0.351 | 0 | 0 | 2 | 104 |
| JW1675 | ydiH | predicted protein | 0 | -0.315 | 0 | 0 | 2 | 104 |
| JW2763 | yqcC | conserved protein | 0 | -0.453 | 0 | 0 | 2 | 104 |
| JW3622 | ligB | DNA ligase, NAD(+)-dependent | 0 | -0.321 | 0 | 0 | 6 | 104 |
| JW3681 | rnvA | protein C5 component of RNase P | GO:0005737 cytoplasm | -0.464 | 0 | 0 | 3 | 104 |
| JW0065 | thiQ | thiamin transporter subunit -!- ATP-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.117 | 1 | 0 | 2 | 103 |
| JW1770 | yeaE | predicted oxidoreductase | 0 | -0.018 | 0 | 0 | 3 | 103 |
| JW1085 | holB | DNA polymerase III, delta prime subunit | GO:0005737 cytoplasm | -0.050 | 0 | 0 | 3 | 102 |
| JW1833 | exoX | DNA exonuclease X | GO:0005737 cytoplasm | -0.219 | 0 | 0 | 2 | 102 |
| JW2052 | yegE | predicted diguanylate cyclase, GGDEF domain signalling protein | 0 | 0.166 | 1 | 11 | 4 | 102 |
| JW5948 | yhfZ | conserved protein | 0 | -0.140 | 0 | 0 | 4 | 102 |
| JW3173 | npr | phosphohistidinoprotein-hexose phosphotransferase component of N-regulated PTS system (Npr) | GO:0005737 cytoplasm | -0.087 | 0 | 0 | 1 | 101 |
| JW3174 | yrbL | predicted protein | 0 | -0.557 | 0 | 0 | 4 | 101 |
| JW3983 | yjbD | conserved protein | 0 | -1.186 | 0 | 0 | 2 | 101 |
| JW2666 | csrA | pleiotropic regulatory protein for carbon source metabolism | GO:0005737 cytoplasm | -0.257 | 0 | 0 | 2 | 100 |
| JW3062 | uxaA | altronate hydrolase | 0 | -0.232 | 0 | 0 | 5 | 100 |
| JW4290 | yjiE | predicted DNA-binding transcriptional regulator | 0 | -0.132 | 0 | 0 | 3 | 100 |
| JW0018 | nhaA | sodium-proton antiporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.005 | 1 | 11 | 2 | 99 |
| JW2709 | ygbM | conserved protein | 0 | -0.205 | 0 | 0 | 2 | 99 |
| JW3635 | nlpA | cytoplasmic membrane lipoprotein-28 | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.165 | 1 | 0 | 2 | 99 |
| JW5352 | yehT | predicted response regulator in two-component system with YehU | 0 | -0.160 | 0 | 0 | 4 | 99 |
| JW0433 | ybaW | conserved protein | 0 | -0.104 | 0 | 0 | 2 | 98 |
| JW1601 | rstB | sensory histidine kinase in two-component regulatory system with RstA | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.026 | 1 | 2 | 3 | 98 |
| JW3783 | yigA | conserved protein | 0 | -0.149 | 0 | 0 | 3 | 98 |
| JW0851 | ybjR | predicted amidase and lipoprotein | 0 | -0.339 | 0 | 0 | 5 | 97 |

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|--------|------|--|---|--------|---|---|---|----|
| JW1271 | yciS | conserved inner membrane protein | 0 | 0.680 | 1 | 2 | 2 | 97 |
| JW1514 | uxaB | altronate oxidoreductase, NAD- | 0 | -0.188 | 0 | 0 | 2 | 97 |
| JW2783 | ygdL | conserved protein | 0 | 0.089 | 1 | 1 | 5 | 97 |
| JW3858 | dtd | D-Tyr-tRNA(Tyr) deacylase | GO:0005737 cytoplasm | -0.173 | 0 | 0 | 2 | 97 |
| JW4154 | ulaD | 3-keto-L-gulonate 6-phosphate decarboxylase | 0 | 0.104 | 1 | 0 | 4 | 97 |
| JW4334 | holD | DNA polymerase III, psi subunit | GO:0005737 cytoplasm | -0.157 | 0 | 0 | 2 | 97 |
| JW5391 | yfeA | predicted diguanylate cyclase | 0 | 0.306 | 1 | 8 | 2 | 97 |
| JW5453 | yqeF | predicted acyltransferase | 0 | 0.109 | 1 | 0 | 2 | 97 |
| JW5607 | hdfR | DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.284 | 0 | 0 | 2 | 97 |
| JW0097 | mutT | nucleoside triphosphate pyrophosphohydrolase, marked preference for dGTP | GO:0005737 cytoplasm | -0.475 | 0 | 0 | 4 | 96 |
| JW0322 | prpR | DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.135 | 0 | 0 | 3 | 96 |
| JW0863 | macB | fused macrolide transporter subunits -!- ATP-binding component and membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.129 | 1 | 4 | 5 | 96 |
| JW1801 | pabB | aminodeoxychorismate synthase, | 0 | -0.289 | 0 | 0 | 3 | 96 |
| JW1850 | ruvA | component of RuvABC resolvosome, regulatory subunit | GO:0005737 cytoplasm | 0.057 | 1 | 0 | 2 | 96 |
| JW4039 | yjcO | conserved protein | 0 | -0.289 | 0 | 0 | 2 | 96 |
| JW5530 | yhbV | predicted protease | 0 | -0.114 | 0 | 0 | 2 | 96 |
| JW5713 | ubiC | chorismate pyruvate lyase | GO:0005737 cytoplasm | -0.155 | 0 | 0 | 4 | 96 |
| JW5776 | sgcX | KpLE2 phage-like element; predicted endoglucanase with Zn-dependent exopeptidase domain | 0 | 0.011 | 1 | 0 | 3 | 96 |
| JW0323 | prpB | 2-methylisocitrate lyase | GO:0005737 cytoplasm | -0.015 | 0 | 0 | 3 | 95 |
| JW0337 | mhpR | DNA-binding transcriptional activator, 3HPP-binding | GO:0005737 cytoplasm | -0.181 | 0 | 0 | 3 | 95 |
| JW2245 | yfaO | predicted NUDIX hydrolase | 0 | -0.391 | 0 | 0 | 2 | 95 |
| JW2341 | fadL | long-chain fatty acid outer membrane transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.300 | 1 | 0 | 2 | 95 |
| JW4112 | frdD | fumarate reductase (anaerobic), membrane anchor subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.007 | 1 | 3 | 3 | 95 |
| JW5877 | ypeB | predicted protein | GO:0005737 cytoplasm | -0.194 | 0 | 0 | 2 | 95 |
| JW0178 | rnhB | ribonuclease HII, degrades RNA of DNA-RNA hybrids | GO:0005737 cytoplasm | -0.006 | 0 | 0 | 3 | 94 |
| JW1621 | rsxC | fused predicted 4Fe-4S ferredoxin-type protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.416 | 1 | 0 | 4 | 94 |
| JW2444 | eutQ | conserved protein | 0 | -0.115 | 0 | 0 | 3 | 94 |
| JW0486 | rhsD | rhsD element protein | 0 | -0.717 | 0 | 0 | 6 | 93 |
| JW0728 | tolR | membrane spanning protein in TolA-TolQ-TolR complex | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.204 | 1 | 1 | 2 | 93 |

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|--------|------|---|---|--------|---|----|---|----|
| JW1286 | sapB | predicted antimicrobial peptide transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.737 | 1 | 5 | 2 | 93 |
| JW2092 | yohL | conserved protein | 0 | -0.292 | 0 | 0 | 3 | 93 |
| JW3857 | rbn | tRNA processing exoribonuclease BN | GO:0005737 cytoplasm | 0.615 | 1 | 6 | 2 | 93 |
| JW4208 | yjgJ | predicted transcriptional regulator | 0 | -0.167 | 0 | 0 | 3 | 93 |
| JW0082 | ftsI | transpeptidase involved in septal peptidoglycan synthesis (penicillin-binding protein 3) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | -0.150 | 1 | 1 | 6 | 92 |
| JW1736 | astA | arginine succinyltransferase | 0 | -0.197 | 0 | 0 | 3 | 92 |
| JW3031 | ygiH | conserved inner membrane protein | 0 | 0.579 | 1 | 5 | 1 | 92 |
| JW3325 | yhfG | predicted protein | 0 | -0.924 | 0 | 0 | 2 | 92 |
| JW3543 | malS | alpha-amylase | GO:0042597 periplasmic space | -0.469 | 0 | 0 | 3 | 92 |
| JW3815 | tatC | TatABCE protein translocation system subunit | 0 | 0.749 | 1 | 6 | 2 | 92 |
| JW1800 | yoaH | conserved protein | 0 | -0.468 | 0 | 0 | 2 | 91 |
| JW3193 | nanT | sialic acid transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.689 | 1 | 12 | 2 | 91 |
| JW0476 | cueR | DNA-binding transcriptional activator | 0 | -0.579 | 0 | 0 | 3 | 90 |
| JW1299 | pspC | transcriptional activator | GO:0005737 cytoplasm | 0.281 | 1 | 1 | 2 | 90 |
| JW2168 | yefF | fused predicted oligopeptide transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.063 | 0 | 0 | 2 | 90 |
| JW2598 | smpA | small membrane lipoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.087 | 1 | 0 | 1 | 90 |
| JW3329 | nirD | nitrite reductase, NAD(P)H-binding, small subunit | GO:0005737 cytoplasm | -0.211 | 0 | 0 | 2 | 90 |
| JW5104 | ybhF | fused predicted transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.183 | 0 | 0 | 3 | 90 |
| JW5876 | yfeH | predicted inner membrane protein | 0 | 0.826 | 1 | 8 | 2 | 90 |
| JW0154 | btuF | vitamin B12 transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.120 | 0 | 0 | 4 | 89 |
| JW0307 | yahA | predicted DNA-binding transcriptional regulator | 0 | -0.045 | 0 | 0 | 3 | 89 |
| JW0646 | rihA | ribonucleoside hydrolase 1 | 0 | 0.105 | 1 | 0 | 3 | 89 |
| JW1507 | IsrC | A12 transporter -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.893 | 1 | 9 | 1 | 89 |
| JW1598 | folM | dihydrofolate reductase isozyme | 0 | -0.066 | 0 | 0 | 3 | 89 |
| JW1857 | yecE | conserved protein | 0 | -0.354 | 0 | 0 | 2 | 89 |
| JW3677 | recF | gap repair protein | GO:0005737 cytoplasm | -0.423 | 0 | 0 | 3 | 89 |
| JW5801 | yjyX | thiamin metabolism associated protein | 0 | 0.034 | 1 | 0 | 3 | 89 |
| JW1337 | dbpA | ATP-dependent RNA helicase specific for 23S rRNA | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.014 | 1 | 0 | 3 | 88 |

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|--------|------|--|---|--------|---|----|---|----|
| JW2810 | kduD | 2-deoxy-D-gluconate 3-dehydrogenase | 0 | 0.148 | 1 | 0 | 3 | 88 |
| JW0222 | yafN | predicted antitoxin of the YafO-YafN toxin-antitoxin system | 0 | -0.654 | 0 | 0 | 3 | 87 |
| JW1424 | ydcK | predicted enzyme | 0 | -0.033 | 0 | 0 | 4 | 87 |
| JW1587 | ynfL | predicted DNA-binding transcriptional regulator | 0 | -0.053 | 0 | 0 | 3 | 87 |
| JW1742 | ynjA | conserved protein | 0 | 0.037 | 1 | 0 | 3 | 87 |
| JW1953 | yedX | conserved protein | 0 | -0.328 | 0 | 0 | 1 | 87 |
| JW5408 | yfhB | conserved protein | 0 | -0.040 | 1 | 1 | 2 | 87 |
| JW5821 | emtA | lytic murein endotransglycosylase E | GO:0009274 cell wall (sensu Bacteria) - - GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner membrane | -0.203 | 1 | 0 | 2 | 87 |
| JW0059 | polB | DNA polymerase II | GO:0005737 cytoplasm | -0.451 | 0 | 0 | 5 | 86 |
| JW0205 | dnaQ | DNA polymerase III epsilon subunit | GO:0005737 cytoplasm | -0.162 | 0 | 0 | 3 | 86 |
| JW0491 | ybbB | tRNA 2-selenouridine synthase, selenophosphate-dependent | 0 | -0.371 | 0 | 0 | 2 | 86 |
| JW1056 | mviN | predicted inner membrane protein | 0 | 0.880 | 1 | 13 | 3 | 86 |
| JW1203 | prmC | N5-glutamine methyltransferase, modifies release factors RF-1 and RF-2 | 0 | -0.202 | 0 | 0 | 2 | 86 |
| JW2457 | ypfN | predicted protein | GO:0031225 anchored to | -0.689 | 1 | 1 | 2 | 86 |
| JW2699 | hypD | protein required for maturation of hydrogenases | 0 | -0.092 | 0 | 0 | 3 | 86 |
| JW5670 | yhiD | predicted Mg(2+) transport ATPase inner membrane protein | 0 | 0.535 | 1 | 5 | 2 | 86 |
| JW1854 | nudB | dATP pyrophosphohydrolase | 0 | -0.268 | 0 | 0 | 3 | 85 |
| JW3228 | dusB | tRNA-dihydrouridine synthase B | 0 | -0.246 | 0 | 0 | 3 | 85 |
| JW3254 | zntR | DNA-binding transcriptional activator | GO:0005737 cytoplasm | -0.504 | 0 | 0 | 3 | 85 |
| JW4053 | phnP | carbon-phosphorus lyase complex accessory protein | 0 | -0.115 | 0 | 0 | 2 | 85 |
| JW4200 | treR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.085 | 0 | 0 | 1 | 85 |
| JW5313 | yedO | D-cysteine desulfhydrase, PLP- | 0 | 0.123 | 1 | 0 | 3 | 85 |
| JW0368 | sbmA | predicted transporter | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 0.535 | 1 | 8 | 2 | 84 |
| JW2337 | sixA | phosphohistidine phosphatase | 0 | 0.200 | 1 | 0 | 1 | 84 |
| JW3721 | asnC | DNA-binding transcriptional dual | GO:0005737 cytoplasm | 0.062 | 1 | 0 | 2 | 84 |
| JW5173 | icdC | conserved protein (pseudogene) | GO:0005737 cytoplasm | 0.048 | 1 | 0 | 1 | 84 |
| JW0191 | yaeb | conserved protein | 0 | -0.149 | 0 | 0 | 3 | 83 |
| JW0887 | focA | formate transporter | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 0.772 | 1 | 6 | 3 | 83 |
| JW1590 | ydgD | predicted peptidase | 0 | -0.207 | 0 | 0 | 3 | 83 |
| JW1994 | yeeD | conserved protein | 0 | 0.215 | 1 | 0 | 1 | 83 |
| JW4032 | nrfB | nitrite reductase, formate-dependent, penta-heme cytochrome c | GO:0042597 periplasmic space | -0.540 | 0 | 0 | 2 | 83 |
| JW1625 | nth | DNA glycosylase and apyrimidinic (AP) lyase (endonuclease III) | GO:0005737 cytoplasm | -0.120 | 0 | 0 | 2 | 82 |

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|--------|------|---|---|--------|---|----|---|----|
| JW2061 | mdtC | multidrug efflux system, subunit C | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | 0.283 | 1 | 10 | 4 | 82 |
| JW3781 | yifL | predicted lipoprotein | GO:00016020 membrane | -0.437 | 1 | 1 | 3 | 82 |
| JW4223 | idnO | 5-keto-D-gluconate-5-reductase | GO:0005737 cytoplasm | 0.083 | 1 | 0 | 2 | 82 |
| JW5501 | ygiQ | conserved protein | 0 | -0.519 | 0 | 0 | 4 | 82 |
| JW3384 | rtcB | conserved protein | 0 | -0.221 | 0 | 0 | 3 | 81 |
| JW3852 | yihT | predicted aldolase | 0 | -0.048 | 0 | 0 | 2 | 81 |
| JW5381 | yfcM | conserved protein | 0 | -0.416 | 0 | 0 | 2 | 81 |
| JW2128 | dusC | tRNA-dihydrouridine synthase C | 0 | -0.164 | 0 | 0 | 4 | 80 |
| JW3729 | rbsC | D-ribose transporter subunit -!- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.924 | 1 | 8 | 1 | 80 |
| JW4088 | yjdJ | predicted acyltransferase with acyl-CoA N-acyltransferase domain | 0 | -0.704 | 0 | 0 | 2 | 80 |
| JW5108 | ybiO | predicted mechanosensitive channel | 0 | 0.393 | 1 | 11 | 3 | 80 |
| JW5308 | yecN | predicted inner membrane protein | 0 | 0.654 | 1 | 3 | 1 | 80 |
| JW5389 | ypdH | predicted enzyme IIB component of | 0 | -0.030 | 0 | 0 | 1 | 80 |
| JW1500 | hipA | regulator with hipB | GO:0009274 cell wall (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.152 | 0 | 0 | 3 | 79 |
| JW2862 | xerD | site-specific tyrosine recombinase | 0 | -0.330 | 0 | 0 | 4 | 79 |
| JW0634 | nadD | nicotinic acid mononucleotide adenyltransferase, NAD(P)-dependent | 0 | -0.457 | 0 | 0 | 2 | 78 |
| JW0846 | artQ | arginine transporter subunit -!- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.718 | 1 | 4 | 2 | 78 |
| JW0956 | hyaC | hydrogenase 1, b-type cytochrome subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.297 | 1 | 4 | 2 | 78 |
| JW1908 | fliC | flagellar filament structural protein (flagellin) | GO:0019861 flagellum | -0.366 | 0 | 0 | 3 | 78 |
| JW2705 | ygbI | predicted DNA-binding transcriptional regulator | 0 | 0.071 | 1 | 0 | 4 | 78 |
| JW3511 | dppC | dipeptide transporter -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.807 | 1 | 5 | 3 | 78 |
| JW3627 | recG | ATP-dependent DNA helicase | GO:0005737 cytoplasm | -0.127 | 0 | 0 | 2 | 78 |
| JW4264 | sgcA | KpLE2 phage-like element; predicted phosphotransferase enzyme IIA component | 0 | 0.024 | 1 | 0 | 2 | 78 |
| JW2543 | tadA | tRNA-specific adenosine deaminase | 0 | -0.135 | 0 | 0 | 2 | 77 |
| JW3604 | rfaS | lipopolysaccharide core biosynthesis protein | GO:0019866 inner membrane | -0.339 | 1 | 0 | 4 | 77 |
| JW5301 | yebU | predicted methyltransferase | GO:0005737 cytoplasm | -0.195 | 0 | 0 | 3 | 77 |
| JW5382 | yfdI | CPS-53 (KpLE1) prophage; predicted inner membrane protein | 0 | 0.488 | 1 | 10 | 2 | 77 |
| JW0239 | ykfB | CP4-6 prophage; predicted protein | 0 | -0.280 | 0 | 0 | 2 | 76 |
| JW0587 | entB | isochorismatase | GO:0005737 cytoplasm | -0.288 | 0 | 0 | 2 | 76 |
| JW3506 | bcsG | predicted inner membrane protein | 0 | 0.022 | 1 | 4 | 2 | 76 |

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|--------|------|--|---|--------|---|----|---|----|
| JW2272 | nuoM | NADH:ubiquinone oxidoreductase, membrane subunit M | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.821 | 1 | 14 | 3 | 75 |
| JW2303 | hisP | histidine/lysine/arginine/ornithine transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.243 | 0 | 0 | 2 | 75 |
| JW2318 | flk | predicted flagella assembly protein | 0 | -0.308 | 1 | 1 | 3 | 75 |
| JW4097 | cutA | copper binding protein, copper | 0 | -0.026 | 0 | 0 | 2 | 75 |
| JW0441 | amtB | ammonium transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.937 | 1 | 12 | 1 | 74 |
| JW0879 | dmsC | dimethyl sulfoxide reductase, anaerobic, subunit C | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.064 | 1 | 8 | 2 | 74 |
| JW2135 | mglC | methyl-galactoside transporter subunit -!- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.002 | 1 | 9 | 2 | 74 |
| JW2781 | csdA | cysteine sulfinate desulfinate | 0 | 0.041 | 1 | 0 | 2 | 74 |
| JW4033 | nrfC | formate-dependent nitrite reductase, 4Fe4S subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.162 | 1 | 0 | 2 | 74 |
| JW4050 | rpiR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | 0.066 | 1 | 0 | 2 | 74 |
| JW1460 | narV | nitrate reductase 2 (NRZ), gamma subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.550 | 1 | 5 | 2 | 73 |
| JW1897 | pgsA | phosphatidylglycerophosphate synthetase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.824 | 1 | 4 | 3 | 73 |
| JW2183 | ccmG | periplasmic thioredoxin of cytochrome c-type biogenesis | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.188 | 1 | 1 | 2 | 73 |
| JW2932 | nupG | nucleoside transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.830 | 1 | 12 | 3 | 73 |
| JW3996 | lamB | maltose outer membrane porin (maltoporin) | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.516 | 1 | 0 | 1 | 73 |
| JW5849 | yqhC | predicted DNA-binding transcriptional regulator | 0 | -0.149 | 0 | 0 | 3 | 73 |
| JW0420 | cyoC | cytochrome o ubiquinol oxidase subunit III | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.721 | 1 | 5 | 1 | 72 |
| JW1969 | cobT | nicotinate-nucleotide dimethylbenzimidazole-P phosphoribosyl transferase | 0 | 0.342 | 1 | 0 | 1 | 72 |
| JW2022 | rfbX | predicted polysiprenol-linked O-antigen transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.917 | 1 | 10 | 2 | 72 |
| JW2787 | recD | exonuclease V (RecBCD complex), alpha chain | 0 | -0.201 | 0 | 0 | 3 | 72 |
| JW5056 | yajL | predicted lipoprotein | 0 | -0.129 | 0 | 0 | 2 | 72 |
| JW5189 | ychM | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.831 | 1 | 11 | 3 | 72 |
| JW0763 | ybhK | predicted transferase with NAD(P)-binding Rossmann-fold domain | 0 | 0.039 | 1 | 0 | 3 | 71 |
| JW1240 | yciU | predicted protein | 0 | -0.328 | 0 | 0 | 2 | 71 |
| JW1715 | yniB | predicted inner membrane protein | 0 | 0.504 | 1 | 3 | 2 | 71 |

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|--------|------|---|---|--------|---|----|---|----|
| JW2152 | yeiN | conserved protein | 0 | 0.194 | 1 | 0 | 2 | 71 |
| JW5783 | yjiH | conserved inner membrane protein | 0 | 0.522 | 1 | 4 | 3 | 71 |
| JW0278 | yagR | predicted oxidoreductase with molybdenum-binding domain | 0 | -0.214 | 0 | 0 | 4 | 70 |
| JW2271 | nuoN | NADH:ubiquinone oxidoreductase, membrane subunit N | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 0.916 | 1 | 12 | 1 | 70 |
| JW2865 | ygfY | conserved protein | 0 | -0.559 | 0 | 0 | 2 | 70 |
| JW5555 | ptsA | fused predicted PTS enzymes Hpr component - - enzyme I component - - enzyme IIA component | 0 | -0.090 | 0 | 0 | 3 | 70 |
| JW0578 | entF | enterobactin synthase multienzyme complex component, ATP-dependent | GO:0005737 cytoplasm | -0.079 | 0 | 0 | 2 | 69 |
| JW0903 | ybcC | conserved inner membrane protein | 0 | 0.044 | 1 | 2 | 1 | 69 |
| JW2806 | lysA | diaminopimelate decarboxylase, PLP-binding | 0 | -0.155 | 0 | 0 | 3 | 69 |
| JW4029 | yjch | conserved inner membrane protein involved in acetate transport | 0 | 0.424 | 1 | 2 | 2 | 69 |
| JW4326 | dnaT | DNA biosynthesis protein (primosomal protein I) | GO:0005737 cytoplasm | -0.081 | 0 | 0 | 2 | 69 |
| JW5298 | yobH | predicted protein | 0 | 0.601 | 1 | 1 | 1 | 69 |
| JW2241 | yfaW | predicted enolase | 0 | -0.208 | 0 | 0 | 3 | 68 |
| JW0246 | insl | CP4-6 prophage; IS30 transposase | 0 | -0.763 | 0 | 0 | 4 | 67 |
| JW0586 | entE | 2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex | GO:0009274 cell wall (sensu Bacteria) - - GO:0005737 cytoplasm | -0.147 | 0 | 0 | 3 | 67 |
| JW1707 | rpml | 50S ribosomal subunit protein L35 | GO:0009281 cytosolic ribosome (sensu Bacteria) - - GO:0005737 cytoplasm | -0.617 | 0 | 0 | 1 | 67 |
| JW1971 | cobU | bifunctional cobinamide kinase - - cobinamide phosphate | 0 | -0.135 | 0 | 0 | 1 | 67 |
| JW2162 | yeiU | undecaprenyl pyrophosphate | 0 | 0.685 | 1 | 5 | 1 | 67 |
| JW2289 | yfbS | predicted transporter | 0 | 0.730 | 1 | 10 | 2 | 67 |
| JW2344 | yfdC | predicted inner membrane protein | 0 | 0.170 | 1 | 6 | 2 | 67 |
| JW2546 | yfhL | predicted 4Fe-4S cluster-containing | 0 | -0.310 | 0 | 0 | 2 | 67 |
| JW5105 | ybiX | conserved protein | 0 | -0.361 | 0 | 0 | 1 | 67 |
| JW5404 | sseB | rhodanase-like enzyme, sulfur transfer from thiosulfate | 0 | -0.176 | 0 | 0 | 2 | 67 |
| JW0342 | mhpF | acetaldehyde-CoA dehydrogenase II, NAD-binding | GO:0005737 cytoplasm | 0.099 | 1 | 0 | 2 | 66 |
| JW0998 | ycdC | predicted DNA-binding transcriptional regulator | 0 | 0.069 | 1 | 0 | 2 | 66 |
| JW1221 | ychJ | conserved protein | 0 | -0.280 | 0 | 0 | 2 | 66 |
| JW2946 | glcD | glycolate oxidase subunit, FAD-linked | 0 | 0.051 | 1 | 0 | 3 | 66 |
| JW3479 | hdeD | acid-resistance membrane protein | 0 | 1.271 | 1 | 6 | 2 | 66 |
| JW3715 | atpE | F0 sector of membrane-bound ATP synthase, subunit c | GO:0009274 cell wall (sensu Bacteria) - - GO:0019866 inner | 1.267 | 1 | 2 | 2 | 66 |

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|--------|------|---|---|--------|---|----|---|----|
| JW5086 | fepA | iron-enterobactin outer membrane transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.581 | 1 | 0 | 2 | 66 |
| JW5698 | frlR | predicted DNA-binding transcriptional regulator | 0 | -0.346 | 0 | 0 | 3 | 66 |
| JW5942 | bcsC | cellulose synthase subunit | 0 | -0.592 | 0 | 0 | 4 | 66 |
| JW0063 | araC | DNA-binding transcriptional dual | GO:0005737 cytoplasm | -0.315 | 0 | 0 | 2 | 65 |
| JW1151 | ycgZ | predicted protein | 0 | -0.362 | 0 | 0 | 1 | 65 |
| JW1376 | ydbH | predicted protein | 0 | -0.164 | 1 | 1 | 3 | 65 |
| JW2167 | yejE | predicted oligopeptide transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.378 | 1 | 6 | 2 | 64 |
| JW2539 | yfhG | conserved protein | 0 | -0.745 | 0 | 0 | 1 | 64 |
| JW0390 | phoR | sensory histidine kinase in two-component regulatory system with | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.305 | 1 | 1 | 4 | 63 |
| JW1722 | chbG | conserved protein | 0 | -0.051 | 0 | 0 | 2 | 63 |
| JW1887 | araH | fused L-arabinose transporter subunits -!- membrane components of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 1.035 | 1 | 10 | 1 | 63 |
| JW2029 | wcaL | predicted glycosyl transferase | 0 | -0.108 | 0 | 0 | 3 | 63 |
| JW2090 | thiD | bifunctional hydroxy-methylpyrimidine kinase -!- hydroxy-phosphomethylpyrimidine kinase | 0 | -0.037 | 0 | 0 | 2 | 63 |
| JW2472 | hyfG | hydrogenase 4, subunit | 0 | -0.284 | 0 | 0 | 4 | 63 |
| JW2928 | mutY | adenine DNA glycosylase | GO:0005737 cytoplasm | -0.146 | 0 | 0 | 1 | 63 |
| JW3388 | glpE | thiosulfate:cyanide sulfurtransferase (rhodanese) | 0 | -0.265 | 0 | 0 | 1 | 63 |
| JW3617 | pyrE | orotate phosphoribosyltransferase | GO:0005737 cytoplasm | -0.058 | 0 | 0 | 2 | 63 |
| JW5434 | ascG | DNA-binding transcriptional regulator | GO:0005737 cytoplasm | -0.066 | 0 | 0 | 3 | 63 |
| JW5747 | ytfH | predicted transcriptional regulator | 0 | -0.123 | 0 | 0 | 2 | 63 |
| JW0144 | hrpB | predicted ATP-dependent helicase | GO:0005737 cytoplasm | -0.171 | 0 | 0 | 3 | 62 |
| JW0502 | glxK | glycerate kinase II | 0 | 0.335 | 1 | 0 | 2 | 62 |
| JW0608 | citE | citrate lyase, citryl-ACP lyase (beta) subunit | GO:0005737 cytoplasm | -0.165 | 0 | 0 | 3 | 62 |
| JW1645 | lhr | predicted ATP-dependent helicase | GO:0005737 cytoplasm | -0.174 | 0 | 0 | 4 | 62 |
| JW1720 | cedA | cell division modulator | 0 | -0.518 | 0 | 0 | 2 | 62 |
| JW1760 | ydgJ | predicted oxidoreductase | 0 | -0.093 | 0 | 0 | 4 | 62 |
| JW2236 | glpB | sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.062 | 1 | 0 | 4 | 62 |
| JW5012 | clcA | chloride channel, voltage-gated | 0 | 0.636 | 1 | 11 | 2 | 62 |
| JW5286 | ynjD | predicted transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | 0.024 | 1 | 0 | 2 | 62 |
| JW0769 | ybhL | predicted inner membrane protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.815 | 1 | 7 | 1 | 61 |
| JW1058 | flgM | anti-sigma factor for FlhA (sigma 28) | GO:0019861 flagellum -!- GO:0005737 cytoplasm | -0.504 | 0 | 0 | 1 | 61 |

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|--------|------|--|---|--------|---|---|---|----|
| JW1551 | ydFT | Qin prophage; predicted antitermination protein Q | 0 | -0.313 | 0 | 0 | 4 | 61 |
| JW1573 | rspA | predicted dehydratase | 0 | -0.297 | 0 | 0 | 3 | 61 |
| JW1970 | cobS | cobalamin 5'-phosphate synthase | 0 | 0.868 | 1 | 4 | 4 | 61 |
| JW2884 | yliK | methylmalonyl-CoA mutase | 0 | -0.122 | 0 | 0 | 4 | 61 |
| JW3123 | yhbP | conserved protein | 0 | -0.276 | 0 | 0 | 1 | 61 |
| JW3317 | yheU | conserved protein | 0 | -0.513 | 0 | 0 | 1 | 61 |
| JW3843 | yihL | predicted DNA-binding transcriptional regulator | 0 | -0.459 | 0 | 0 | 2 | 61 |
| JW5366 | ccmA | heme exporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.232 | 0 | 0 | 2 | 61 |
| JW0656 | ybeY | conserved protein | 0 | -0.311 | 0 | 0 | 1 | 60 |
| JW0764 | moaA | molybdopterin biosynthesis protein A | 0 | -0.354 | 0 | 0 | 3 | 60 |
| JW2199 | yojI | fused predicted multidrug transport subunits -!- membrane component and ATP-binding component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.194 | 1 | 6 | 2 | 60 |
| JW4000 | ubiA | p-hydroxybenzoate octaprenyltransferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.690 | 1 | 7 | 1 | 60 |
| JW5644 | htrL | predicted protein | 0 | -0.268 | 0 | 0 | 2 | 60 |
| JW0496 | hyi | hydroxypyruvate isomerase | GO:0005737 cytoplasm | -0.343 | 0 | 0 | 2 | 59 |
| JW0868 | aat | leucyl/phenylalanyl-tRNA-protein transferase | GO:0005737 cytoplasm | -0.247 | 0 | 0 | 1 | 59 |
| JW0974 | cspG | DNA-binding transcriptional regulator | 0 | -0.363 | 0 | 0 | 1 | 59 |
| JW0980 | torR | DNA-binding response regulator in two-component regulatory system with TorS | GO:0005737 cytoplasm | -0.178 | 0 | 0 | 2 | 59 |
| JW1456 | ycdE | 4-oxalocrotonate tautomerase | 0 | -0.262 | 0 | 0 | 1 | 59 |
| JW1990 | yeeA | conserved inner membrane protein | GO:0009274 cell wall (sensu | 0.282 | 1 | 5 | 2 | 59 |
| JW2248 | yfbF | undecaprenyl phosphate-L-Ara4FN transferase | 0 | 0.073 | 1 | 2 | 1 | 59 |
| JW3518 | tag | 3-methyl-adenine DNA glycosylase I, constitutive | GO:0005737 cytoplasm | -0.280 | 0 | 0 | 1 | 59 |
| JW5292 | yeaP | predicted diguanylate cyclase | 0 | -0.235 | 0 | 0 | 1 | 59 |
| JW5395 | yfeW | predicted periplasmic esterase | 0 | -0.284 | 0 | 0 | 2 | 59 |
| JW0203 | yafS | predicted S-adenosyl-L-methionine-dependent methyltransferase | 0 | -0.126 | 0 | 0 | 1 | 58 |
| JW2365 | emrK | EmrKY-TolC multidrug resistance efflux pump, membrane fusion protein | 0 | -0.237 | 1 | 1 | 4 | 58 |
| JW2904 | speB | agmatinase | 0 | -0.105 | 0 | 0 | 2 | 58 |
| JW4074 | basR | DNA-binding response regulator in two-component regulatory system with BasS | GO:0005737 cytoplasm | -0.150 | 0 | 0 | 1 | 58 |
| JW5906 | gapC | glyceraldehyde-3-phosphate dehydrogenase C, C-ter fragment (pseudogene) | 0 | 0.028 | 1 | 0 | 3 | 58 |
| JW0285 | yagX | predicted aromatic compound | 0 | -0.351 | 0 | 0 | 3 | 57 |
| JW0379 | aroL | shikimate kinase II | GO:0005737 cytoplasm | -0.014 | 0 | 0 | 1 | 57 |
| JW0800 | ybiP | predicted hydrolase, inner membrane | GO:0009274 cell wall (sensu | -0.117 | 1 | 4 | 3 | 57 |

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|--------|------|--|---|--------|---|----|---|----|
| JW1788 | yeaT | predicted DNA-binding transcriptional regulator | 0 | -0.007 | 0 | 0 | 2 | 57 |
| JW2190 | napC | nitrate reductase, cytochrome c-type, periplasmic | GO:0019866 inner membrane | -0.623 | 1 | 1 | 3 | 57 |
| JW2571 | kgtP | alpha-ketoglutarate transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.617 | 1 | 12 | 2 | 57 |
| JW2910 | galP | D-galactose transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.599 | 1 | 12 | 2 | 57 |
| JW3241 | yrdB | conserved protein | 0 | -0.748 | 0 | 0 | 2 | 57 |
| JW3605 | rfaP | kinase that phosphorylates core heptose of lipopolysaccharide | GO:0019866 inner membrane | -0.275 | 1 | 0 | 2 | 57 |
| JW3886 | fieF | zinc transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.378 | 1 | 6 | 2 | 57 |
| JW5150 | ymdC | predicted hydrolase | 0 | -0.163 | 0 | 0 | 2 | 57 |
| JW0250 | insH | CP4-6 prophage; IS5 transposase and trans-activator | 0 | -0.534 | 0 | 0 | 2 | 56 |
| JW0449 | hha | modulator of gene expression, with H- | 0 | -0.569 | 0 | 0 | 3 | 56 |
| JW2237 | glpC | sn-glycerol-3-phosphate dehydrogenase (anaerobic), small subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.214 | 1 | 0 | 3 | 56 |
| JW2670 | ygaD | conserved protein | 0 | -0.114 | 0 | 0 | 2 | 56 |
| JW3910 | metB | cystathionine gamma-synthase, PLP-dependent | GO:0005737 cytoplasm | -0.021 | 0 | 0 | 1 | 56 |
| JW0146 | fhuA | ferrichrome outer membrane transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.481 | 1 | 0 | 3 | 55 |
| JW1793 | rnd | ribonuclease D | GO:0005737 cytoplasm | -0.150 | 0 | 0 | 2 | 55 |
| JW5444 | ygcE | predicted kinase | 0 | -0.103 | 0 | 0 | 2 | 55 |
| JW1245 | yciA | predicted hydrolase | 0 | 0.118 | 1 | 0 | 2 | 54 |
| JW1313 | ycjW | predicted DNA-binding transcriptional regulator | GO:0042597 periplasmic space | -0.089 | 0 | 0 | 2 | 54 |
| JW1377 | ynbE | predicted lipoprotein | 0 | 0.297 | 1 | 0 | 2 | 54 |
| JW1749 | ynjH | predicted protein | 0 | -0.104 | 0 | 0 | 1 | 54 |
| JW1903 | yecS | predicted transporter subunit -!- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.435 | 1 | 3 | 2 | 54 |
| JW2966 | yghW | predicted protein | 0 | -0.473 | 0 | 0 | 2 | 54 |
| JW5061 | mdlB | fused predicted multidrug transporter subunits -!- ATP binding components of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.252 | 1 | 4 | 2 | 54 |
| JW5729 | yjcZ | conserved protein | 0 | -0.183 | 0 | 0 | 3 | 54 |
| JW0484 | ybbA | predicted transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.147 | 0 | 0 | 2 | 53 |
| JW1830 | yobA | conserved protein | 0 | -0.262 | 0 | 0 | 2 | 53 |
| JW2160 | yeiQ | predicted dehydrogenase, NAD- | 0 | -0.114 | 0 | 0 | 2 | 53 |
| JW2187 | ccmC | heme exporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.586 | 1 | 6 | 2 | 53 |

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|--------|------|--|---|--------|---|----|---|----|
| JW3601 | rfaJ | UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase | 0 | -0.152 | 1 | 1 | 2 | 53 |
| JW3992 | malG | maltose transporter subunit -!- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.836 | 1 | 6 | 1 | 53 |
| JW4341 | yjiV | predicted DNase | 0 | -0.243 | 0 | 0 | 2 | 53 |
| JW5970 | yccV | DNA-binding protein, hemimethylated | 0 | -0.397 | 0 | 0 | 1 | 53 |
| JW0341 | mhpD | 2-keto-4-pentenoate hydratase | 0 | -0.033 | 0 | 0 | 1 | 52 |
| JW1247 | yciC | predicted inner membrane protein | GO:0009274 cell wall (sensu | 1.068 | 1 | 6 | 2 | 52 |
| JW2030 | wcaK | predicted pyruvyl transferase | 0 | -0.018 | 0 | 0 | 3 | 52 |
| JW5917 | rscC | hybrid sensory kinase in two-component regulatory system with RcsB and YojN | 0 | -0.152 | 0 | 0 | 1 | 52 |
| JW5931 | tatD | DNase, magnesium-dependent | GO:0005737 cytoplasm | -0.156 | 0 | 0 | 2 | 52 |
| JW0733 | nadA | quinolinate synthase, subunit A | GO:0005737 cytoplasm | -0.141 | 0 | 0 | 1 | 51 |
| JW1763 | ydjJ | predicted oxidoreductase, Zn-dependent and NAD(P)-binding | 0 | 0.018 | 1 | 0 | 1 | 51 |
| JW2432 | eutL | predicted carboxysome structural protein with predicted role in ethanolamine utilization | 0 | 0.191 | 1 | 0 | 2 | 51 |
| JW5128 | yccS | predicted inner membrane protein | 0 | 0.098 | 1 | 9 | 3 | 51 |
| JW5233 | yncA | predicted acyltransferase with acyl-CoA N-acyltransferase domain | 0 | -0.217 | 0 | 0 | 2 | 51 |
| JW5325 | yeeL | predicted protein, C-ter fragment (pseudogene) | 0 | 0.097 | 1 | 0 | 3 | 51 |
| JW0076 | ilvI | acetolactate synthase III, large subunit | 0 | -0.051 | 0 | 0 | 2 | 50 |
| JW0438 | mdlA | fused predicted multidrug transporter subunits -!- ATP-binding components of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.085 | 1 | 6 | 3 | 50 |
| JW0817 | yliE | conserved inner membrane protein | 0 | -0.083 | 1 | 2 | 3 | 50 |
| JW0857 | hcp | hybrid-cluster [4Fe-2S-2O] protein in anaerobic terminal reductases | 0 | 0.035 | 1 | 0 | 3 | 50 |
| JW2097 | yehC | predicted periplasmic pilin chaperone | 0 | -0.136 | 1 | 1 | 3 | 50 |
| JW2522 | hcaE | 3-phenylpropionate dioxygenase, large (alpha) subunit | 0 | -0.484 | 0 | 0 | 3 | 50 |
| JW2813 | yqeG | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.940 | 1 | 10 | 2 | 50 |
| JW3599 | rfaZ | lipopolysaccharide core biosynthesis protein | GO:0019866 inner membrane | -0.248 | 1 | 0 | 2 | 50 |
| JW3758 | rfe | UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase | 0 | 0.767 | 1 | 11 | 2 | 50 |
| JW1926 | fliJ | flagellar protein | GO:0019861 flagellum | -0.981 | 0 | 0 | 3 | 49 |
| JW1945 | yedJ | predicted phosphohydrolase | 0 | -0.271 | 0 | 0 | 2 | 49 |
| JW2275 | nuoJ | NADH:ubiquinone oxidoreductase, membrane subunit J | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.913 | 1 | 5 | 1 | 49 |
| JW2754 | chpR | antitoxin of the ChpA-ChpR toxin-antitoxin system | 0 | -0.299 | 0 | 0 | 2 | 49 |

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|--------|------|---|---|--------|---|----|---|----|
| JW4034 | nrfD | formate-dependent nitrite reductase, membrane subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.995 | 1 | 8 | 1 | 49 |
| JW5251 | ynfO | Qin prophage; predicted protein | 0 | -1.009 | 0 | 0 | 1 | 49 |
| JW5887 | yfdT | CPS-53 (KpLE1) prophage; predicted protein | 0 | -0.711 | 0 | 0 | 3 | 49 |
| JW0045 | kefF | flavoprotein subunit for the KefC potassium efflux system | 0 | -0.228 | 0 | 0 | 2 | 48 |
| JW2559 | yfiC | predicted methyltransferase | 0 | -0.095 | 0 | 0 | 1 | 48 |
| JW2753 | chpA | toxin of the ChpA-ChpR toxin-antitoxin system, endoribonuclease | 0 | -0.093 | 0 | 0 | 1 | 48 |
| JW3120 | yraQ | predicted permease | 0 | 0.856 | 1 | 9 | 1 | 48 |
| JW3221 | yhdA | conserved inner membrane protein | 0 | -0.192 | 1 | 2 | 2 | 48 |
| JW3261 | rpmJ | 50S ribosomal subunit protein L36 | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.611 | 0 | 0 | 1 | 48 |
| JW3631 | yicl | predicted alpha-glucosidase | 0 | -0.397 | 0 | 0 | 3 | 48 |
| JW3978 | iclR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.051 | 0 | 0 | 3 | 48 |
| JW5540 | yhcN | conserved protein | 0 | -0.087 | 0 | 0 | 1 | 48 |
| JW5784 | kptA | 2'-phosphotransferase | GO:0005737 cytoplasm | -0.259 | 0 | 0 | 2 | 48 |
| JW0147 | fhuC | iron-hydroxamate transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | 0.015 | 1 | 0 | 3 | 47 |
| JW0228 | gpt | guanine-hypoxanthine phosphoribosyltransferase | GO:0005737 cytoplasm | -0.048 | 0 | 0 | 1 | 47 |
| JW2172 | yejH | predicted ATP-dependet helicase | 0 | -0.278 | 0 | 0 | 2 | 47 |
| JW4159 | priB | primosomal protein N | GO:0005737 cytoplasm | -0.101 | 0 | 0 | 1 | 47 |
| JW4211 | argI | ornithine carbamoyltransferase 1 | GO:0005737 cytoplasm | -0.233 | 0 | 0 | 2 | 47 |
| JW4362 | creC | sensory histidine kinase in two-component regulatory system with CreB or PhoB, regulator of the CreBC regulon | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.006 | 1 | 2 | 3 | 47 |
| JW5010 | yadD | predicted transposase | 0 | -0.269 | 0 | 0 | 3 | 47 |
| JW5520 | tdcG | L-serine dehydratase 3 | 0 | 0.071 | 1 | 0 | 3 | 47 |
| JW0091 | ftsQ | membrane anchored protein involved in growth of wall at septum | GO:0019866 inner membrane | -0.504 | 1 | 1 | 3 | 46 |
| JW1678 | ydiK | predicted inner membrane protein | 0 | 1.029 | 1 | 9 | 1 | 46 |
| JW2255 | menE | o-succinylbenzoate-CoA ligase | 0 | -0.067 | 0 | 0 | 2 | 46 |
| JW2619 | yfjU | CP4-57 prophage; conserved protein | 0 | -0.190 | 0 | 0 | 1 | 46 |
| JW2803 | ygeD | predicted inner membrane protein | 0 | 0.898 | 1 | 10 | 1 | 46 |
| JW5087 | citF | citrate lyase, citrate-ACP transferase (alpha) subunit | GO:0005737 cytoplasm | -0.094 | 0 | 0 | 2 | 46 |
| JW5397 | hda | ATPase regulatory factor involved in DnaA inactivation | 0 | -0.115 | 0 | 0 | 1 | 46 |
| JW5433 | hypF | carbamoyl phosphate phosphatase and maturation protein for [NiFe] | GO:0005737 cytoplasm | -0.091 | 0 | 0 | 2 | 46 |

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|--------|------|---|---|--------|---|----|---|----|
| JW5481 | mltC | membrane-bound lytic murein transglycosylase C | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | -0.351 | 1 | 0 | 1 | 46 |
| JW0280 | yagT | predicted xanthine dehydrogenase, 2Fe-2S subunit | 0 | -0.126 | 0 | 0 | 1 | 45 |
| JW0374 | phoA | alkaline phosphatase | GO:0042597 periplasmic space | -0.313 | 0 | 0 | 3 | 45 |
| JW1196 | ychH | predicted inner membrane protein | 0 | -0.001 | 1 | 2 | 1 | 45 |
| JW1464 | narU | nitrate/nitrite transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.783 | 1 | 12 | 2 | 45 |
| JW2358 | yfdR | CPS-53 (KpLE1) prophage; conserved protein | 0 | -0.044 | 0 | 0 | 3 | 45 |
| JW2400 | yfeR | predicted DNA-binding transcriptional regulator | 0 | -0.054 | 0 | 0 | 3 | 45 |
| JW2459 | ypfI | predicted hydrolase | 0 | -0.223 | 0 | 0 | 2 | 45 |
| JW2488 | yfgF | predicted inner membrane protein | 0 | 0.256 | 1 | 9 | 3 | 45 |
| JW3099 | yhaV | conserved protein | 0 | -0.758 | 0 | 0 | 2 | 45 |
| JW3190 | yhcH | conserved protein | 0 | -0.184 | 0 | 0 | 2 | 45 |
| JW3433 | yhhN | conserved inner membrane protein | 0 | 0.974 | 1 | 6 | 2 | 45 |
| JW4040 | fdhF | formate dehydrogenase-H, selenopolypeptide subunit | 0 | -0.326 | 0 | 0 | 3 | 45 |
| JW4224 | idnD | L-idonate 5-dehydrogenase, NAD- | 0 | -0.017 | 0 | 0 | 2 | 45 |
| JW5059 | yajR | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.691 | 1 | 12 | 2 | 45 |
| JW5793 | yjiN | predicted oxidoreductase, Zn-dependent and NAD(P)-binding | 0 | 0.004 | 1 | 0 | 3 | 45 |
| JW0081 | ftsL | membrane bound cell division protein at septum containing leucine zipper motif | 0 | -0.026 | 1 | 1 | 3 | 44 |
| JW0194 | metI | DL-methionine transporter subunit -!- membrane component protein of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.994 | 1 | 5 | 2 | 44 |
| JW0698 | phr | deoxyribodipyrimidine photolyase, FAD-binding | GO:0005737 cytoplasm | -0.395 | 0 | 0 | 3 | 44 |
| JW0748 | modC | molybdate transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.050 | 0 | 0 | 2 | 44 |
| JW1366 | stfR | Rac prophage; predicted tail fiber | 0 | -0.327 | 0 | 0 | 3 | 44 |
| JW2728 | ygcJ | predicted protein | 0 | -0.241 | 0 | 0 | 2 | 44 |
| JW2911 | sprT | conserved protein | 0 | -0.522 | 0 | 0 | 2 | 44 |
| JW3229 | fis | global DNA-binding transcriptional dual regulator | GO:0005737 cytoplasm | -0.531 | 0 | 0 | 1 | 44 |
| JW3405 | yhhY | predicted acetyltransferase | 0 | -0.428 | 0 | 0 | 2 | 44 |
| JW4288 | yjiC | predicted protein | 0 | -0.290 | 0 | 0 | 3 | 44 |
| JW5200 | yciW | predicted oxidoreductase | 0 | -0.222 | 0 | 0 | 2 | 44 |
| JW5205 | abgA | predicted peptidase, aminobenzoyl-glutamate utilization protein | 0 | -0.096 | 0 | 0 | 3 | 44 |

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|--------|------|---|---|--------|---|----|---|----|
| JW0148 | fhuD | iron-hydroxamate transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | 0.067 | 1 | 0 | 3 | 43 |
| JW0169 | ispU | undecaprenyl pyrophosphate synthase | GO:0005737 cytoplasm | -0.396 | 0 | 0 | 2 | 43 |
| JW0579 | fepE | regulator of length of O-antigen component of lipopolysaccharide chains | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.171 | 1 | 2 | 2 | 43 |
| JW0649 | gltJ | glutamate and aspartate transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.605 | 1 | 5 | 3 | 43 |
| JW1361 | ynaA | Rac prophage; predicted tail protein | 0 | -0.413 | 0 | 0 | 2 | 43 |
| JW1723 | chbF | cryptic phospho-beta-glucosidase, NAD(P)-binding | GO:0005737 cytoplasm | -0.104 | 0 | 0 | 3 | 43 |
| JW2776 | fucR | DNA-binding transcriptional activator | GO:0005737 cytoplasm | -0.321 | 0 | 0 | 1 | 43 |
| JW3313 | kefB | potassium:proton antiporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.454 | 1 | 13 | 3 | 43 |
| JW3385 | rtcR | sigma 54-dependent transcriptional regulator of rtcBA expression | GO:0005737 cytoplasm | -0.363 | 0 | 0 | 3 | 43 |
| JW3541 | xylR | DNA-binding transcriptional activator, xylose-binding | GO:0005737 cytoplasm | -0.331 | 0 | 0 | 3 | 43 |
| JW5011 | ligT | 2'-5' RNA ligase | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | -0.235 | 0 | 0 | 1 | 43 |
| JW5177 | ymgD | predicted protein | 0 | 0.036 | 1 | 0 | 1 | 43 |
| JW5892 | yadB | glutamyl-Q tRNA(Asp) synthetase | 0 | -0.272 | 0 | 0 | 1 | 43 |
| JW0922 | ycbR | predicted periplasmic pilin chaperone | 0 | -0.057 | 0 | 0 | 2 | 42 |
| JW1258 | yciV | conserved protein | 0 | -0.301 | 0 | 0 | 2 | 42 |
| JW1381 | tynA | tyramine oxidase, copper-requiring | GO:0042597 periplasmic space | -0.390 | 0 | 0 | 2 | 42 |
| JW2096 | yehB | predicted outer membrane protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.493 | 1 | 0 | 2 | 42 |
| JW2105 | yehl | conserved protein | 0 | -0.330 | 0 | 0 | 3 | 42 |
| JW2193 | napG | ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB) | 0 | -0.155 | 0 | 0 | 1 | 42 |
| JW2201 | ada | fused DNA-binding transcriptional dual regulator -!- O6-methylguanine-DNA methyltransferase | GO:0005737 cytoplasm | -0.349 | 0 | 0 | 1 | 42 |
| JW2222 | yfaS | predicted protein, N-ter fragment (pseudogene) | 0 | -0.334 | 0 | 0 | 3 | 42 |
| JW0021 | insA | IS1 repressor protein InsA | 0 | -0.316 | 0 | 0 | 3 | 41 |
| JW0358 | tauB | taurine transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.034 | 0 | 0 | 3 | 41 |
| JW1831 | holE | DNA polymerase III, theta subunit | GO:0005737 cytoplasm | -0.454 | 0 | 0 | 1 | 41 |
| JW1868 | flhA | predicted flagellar export pore protein | GO:0019861 flagellum -!- GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.378 | 1 | 7 | 2 | 41 |

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|--------|------|---|---|--------|---|----|---|----|
| JW2053 | alkA | 3-methyl-adenine DNA glycosylase II | GO:0005737 cytoplasm | -0.036 | 0 | 0 | 2 | 41 |
| JW2164 | rtn | conserved protein | 0 | 0.105 | 1 | 2 | 2 | 41 |
| JW2503 | pbpC | fused transglycosylase -!- | GO:0009274 cell wall (sensu | -0.218 | 1 | 1 | 3 | 41 |
| JW1292 | puuR | DNA-binding transcriptional repressor | 0 | -0.325 | 0 | 0 | 2 | 40 |
| JW1321 | ycjZ | predicted DNA-binding transcriptional regulator | 0 | -0.078 | 0 | 0 | 2 | 40 |
| JW1631 | ydhA | predicted lipoprotein | 0 | -0.314 | 0 | 0 | 2 | 40 |
| JW3077 | yhaK | predicted pirin-related protein | 0 | -0.269 | 0 | 0 | 1 | 40 |
| JW3151 | yhbE | conserved inner membrane protein | GO:0009274 cell wall (sensu | 0.852 | 1 | 10 | 1 | 40 |
| JW3234 | acrF | multidrug efflux system protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.322 | 1 | 12 | 2 | 40 |
| JW3235 | yhdV | predicted outer membrane protein | 0 | 0.396 | 1 | 1 | 1 | 40 |
| JW3342 | php | predicted hydrolase | 0 | -0.236 | 0 | 0 | 2 | 40 |
| JW3400 | gntK | gluconate kinase 2 -!- gluconate transport, GNT I system | 0 | -0.318 | 0 | 0 | 1 | 40 |
| JW3845 | yihN | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.731 | 1 | 12 | 3 | 40 |
| JW3957 | thiE | thiamin phosphate synthase (thiamin phosphate pyrophosphorylase) | 0 | 0.032 | 1 | 0 | 2 | 40 |
| JW5016 | yaeF | predicted lipoprotein | 0 | -0.014 | 0 | 0 | 2 | 40 |
| JW0923 | ycbS | predicted outer membrane usher protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.364 | 1 | 1 | 2 | 39 |
| JW1651 | ydhB | predicted DNA-binding transcriptional regulator | 0 | -0.240 | 0 | 0 | 2 | 39 |
| JW2249 | yfbG | fused UDP-L-Ara4N formyltransferase -!- UDP-GlcA C-4'-decarboxylase | 0 | -0.183 | 0 | 0 | 2 | 39 |
| JW2947 | glcC | DNA-binding transcriptional dual regulator, glycolate-binding | GO:0005737 cytoplasm | -0.253 | 0 | 0 | 2 | 39 |
| JW3698 | bglH | carbohydrate-specific outer membrane porin, cryptic | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.588 | 1 | 0 | 2 | 39 |
| JW4130 | hfq | HF-I, host factor for RNA phage Q beta replication | 0 | -0.505 | 0 | 0 | 1 | 39 |
| JW5174 | ycgG | conserved inner membrane protein | 0 | 0.149 | 1 | 2 | 2 | 39 |
| JW5407 | yfhK | predicted sensory kinase in two-component system | 0 | -0.140 | 1 | 2 | 2 | 39 |
| JW0303 | betA | choline dehydrogenase, a flavoprotein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.468 | 1 | 0 | 2 | 38 |
| JW2482 | uraA | uracil transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.045 | 1 | 12 | 1 | 38 |
| JW2525 | hcaB | 2,3-dihydroxy-2,3-dihydrophenylpropionate | 0 | 0.166 | 1 | 0 | 2 | 38 |
| JW2864 | ygfX | predicted protein | 0 | -0.059 | 1 | 1 | 1 | 38 |
| JW3050 | ygiJ | conserved protein | 0 | -0.476 | 0 | 0 | 2 | 38 |

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|--------|------|---|---|--------|---|----|---|----|
| JW3109 | agaD | N-acetylgalactosamine-specific enzyme IID component of PTS | 0 | 0.566 | 1 | 5 | 2 | 38 |
| JW3662 | yidE | predicted transporter | 0 | 0.694 | 1 | 10 | 2 | 38 |
| JW3930 | argC | N-acetyl-gamma-glutamylphosphate reductase, NAD(P)-binding | GO:0005737 cytoplasm | 0.163 | 1 | 0 | 2 | 38 |
| JW5757 | yjgL | predicted protein | 0 | -0.596 | 0 | 0 | 2 | 38 |
| JW0683 | kdpD | fused sensory histidine kinase in two-component regulatory system with | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.090 | 1 | 4 | 2 | 37 |
| JW1055 | mviM | predicted oxidoreductase, NAD(P)-binding Rossmann-fold domain | 0 | -0.098 | 0 | 0 | 1 | 37 |
| JW1295 | puuE | GABA aminotransferase, PLP- | GO:0005737 cytoplasm | 0.042 | 1 | 0 | 2 | 37 |
| JW1472 | fdnI | formate dehydrogenase-N, cytochrome B556 (gamma) subunit, nitrate-inducible | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.359 | 1 | 4 | 1 | 37 |
| JW1571 | intQ | Qin prophage; predicted defective integrase | 0 | -0.428 | 0 | 0 | 2 | 37 |
| JW3023 | yqiK | conserved protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.311 | 1 | 2 | 2 | 37 |
| JW5363 | bcr | bicyclomycin/multidrug efflux system | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.948 | 1 | 12 | 1 | 37 |
| JW5469 | ygfT | fused predicted oxidoreductase Fe-S subunit -!- nucleotide-binding subunit | 0 | -0.142 | 0 | 0 | 2 | 37 |
| JW5775 | yjhH | KpLE2 phage-like element; predicted lyase/synthase | 0 | 0.096 | 1 | 0 | 2 | 37 |
| JW0564 | cusA | copper/silver efflux system, membrane component | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.283 | 1 | 12 | 2 | 36 |
| JW0919 | ssuA | alkanesulfonate transporter subunit -!- periplasmic-binding component of ABC superfamily | GO:0042597 periplasmic space | -0.077 | 0 | 0 | 2 | 36 |
| JW1522 | marC | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.819 | 1 | 5 | 2 | 36 |
| JW1995 | yeeE | predicted inner membrane protein | 0 | 0.716 | 1 | 9 | 2 | 36 |
| JW2382 | ypdF | predicted peptidase | 0 | -0.108 | 0 | 0 | 2 | 36 |
| JW2531 | yphE | fused predicted sugar transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.028 | 0 | 0 | 2 | 36 |
| JW2849 | xdhD | fused predicted xanthine/hypoxanthine oxidase, molybdopterin-binding subunit -!- Fe-S binding subunit | 0 | -0.132 | 0 | 0 | 2 | 36 |
| JW3107 | agaB | N-acetylgalactosamine-specific enzyme IIB component of PTS | GO:0005737 cytoplasm | -0.126 | 0 | 0 | 2 | 36 |
| JW3575 | mtlR | DNA-binding transcriptional repressor | GO:0005737 cytoplasm | -0.195 | 0 | 0 | 2 | 36 |
| JW4124 | yjeS | predicted Fe-S electron transport | 0 | -0.250 | 0 | 0 | 2 | 36 |
| JW5065 | ybbJ | conserved inner membrane protein | 0 | 0.366 | 1 | 3 | 1 | 36 |
| JW5507 | yqiG | predicted outer membrane usher protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.526 | 1 | 0 | 2 | 36 |

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|--------|------|--|--|--------|---|----|---|----|
| JW5519 | yhaO | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.894 | 1 | 11 | 1 | 36 |
| JW1932 | fliP | flagellar biosynthesis protein | GO:0019861 flagellum -!- GO:0009274 cell wall (sensu | 0.801 | 1 | 5 | 2 | 35 |
| JW1951 | yedV | predicted sensory kinase in two-component regulatory system with | 0 | -0.051 | 1 | 2 | 2 | 35 |
| JW2372 | yfdX | predicted protein | 0 | -0.326 | 0 | 0 | 2 | 35 |
| JW2467 | hyfB | hydrogenase 4, membrane subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.888 | 1 | 16 | 2 | 35 |
| JW2752 | mazG | nucleoside triphosphate pyrophosphohydrolase | 0 | -0.515 | 0 | 0 | 2 | 35 |
| JW3944 | secE | preprotein translocase membrane subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.876 | 1 | 3 | 1 | 35 |
| JW4048 | alsA | fused D-allose transporter subunits -!- ATP-binding components of ABC superfamily | GO:0005737 cytoplasm | -0.085 | 0 | 0 | 2 | 35 |
| JW4059 | phnJ | carbon-phosphorus lyase complex | 0 | -0.388 | 0 | 0 | 1 | 35 |
| JW4329 | yjjQ | predicted DNA-binding transcriptional regulator | 0 | -0.160 | 0 | 0 | 2 | 35 |
| JW5018 | mltD | predicted membrane-bound lytic murein transglycosylase D | GO:0005737 cytoplasm | -0.407 | 0 | 0 | 2 | 35 |
| JW5923 | ygfK | predicted oxidoreductase, Fe-S subunit | 0 | -0.291 | 0 | 0 | 2 | 35 |
| JW0175 | fabZ | (3R)-hydroxymyristol acyl carrier protein dehydratase | GO:0005737 cytoplasm | 0.054 | 1 | 0 | 2 | 34 |
| JW1042 | yceA | conserved protein | 0 | -0.427 | 0 | 0 | 2 | 34 |
| JW1134 | ymfM | e14 prophage; predicted protein | 0 | -0.347 | 0 | 0 | 2 | 34 |
| JW1389 | paaG | acyl-CoA hydratase | 0 | -0.094 | 0 | 0 | 2 | 34 |
| JW1434 | ydcR | fused predicted DNA-binding transcriptional regulator -!- predicted amino transferase | 0 | -0.192 | 0 | 0 | 1 | 34 |
| JW1502 | ydeU | conserved protein, predicted | 0 | -0.754 | 0 | 0 | 2 | 34 |
| JW2478 | yfgO | predicted inner membrane protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.041 | 1 | 7 | 1 | 34 |
| JW2952 | yghR | predicted protein with nucleoside triphosphate hydrolase domain | 0 | -0.274 | 0 | 0 | 2 | 34 |
| JW4086 | dcuS | sensory histidine kinase in two-component regulatory system with DcuR, regulator of anaerobic fumarate | GO:0009274 cell wall (sensu Bacteria) | -0.109 | 1 | 2 | 2 | 34 |
| JW5388 | ypdA | predicted sensory kinase in two-component system with YpdB | 0 | 0.283 | 1 | 6 | 2 | 34 |
| JW5610 | yleM | predicted von Willibrand factor containing protein | 0 | -0.306 | 0 | 0 | 1 | 34 |
| JW5697 | yhfU | predicted protein | 0 | 0.153 | 1 | 1 | 2 | 34 |
| JW0260 | yagA | CP4-6 prophage; predicted DNA-binding transcriptional regulator | 0 | -0.656 | 0 | 0 | 2 | 33 |
| JW0262 | yagF | CP4-6 prophage; predicted dehydratase | 0 | -0.024 | 0 | 0 | 2 | 33 |

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|--------|------|--|--|--------|---|----|---|----|
| JW0437 | ybaO | predicted DNA-binding transcriptional regulator | 0 | -0.001 | 0 | 0 | 2 | 33 |
| JW1308 | ycjS | predicted oxidoreductase, NADH- | 0 | -0.102 | 0 | 0 | 2 | 33 |
| JW1470 | fdnG | formate dehydrogenase-N, alpha subunit, nitrate-inducible | GO:0005737 cytoplasm | -0.421 | 0 | 0 | 2 | 33 |
| JW1922 | fliF | flagellar basal-body MS-ring and collar protein | GO:0019861 flagellum -!- GO:0019866 inner membrane | -0.476 | 1 | 2 | 2 | 33 |
| JW4070 | yjdA | conserved protein with nucleoside triphosphate hydrolase domain | 0 | -0.293 | 0 | 0 | 2 | 33 |
| JW4258 | yjhF | KpLE2 phage-like element; predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.114 | 1 | 12 | 2 | 33 |
| JW5103 | ybhJ | predicted hydratase | 0 | -0.142 | 0 | 0 | 2 | 33 |
| JW0964 | yccC | cryptic autophosphorylating protein tyrosine kinase Etk | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.309 | 1 | 2 | 2 | 32 |
| JW1023 | csgD | DNA-binding transcriptional activator in two-component regulatory system | 0 | -0.415 | 0 | 0 | 1 | 32 |
| JW1309 | ycjT | predicted hydrolase | 0 | -0.324 | 0 | 0 | 2 | 32 |
| JW1445 | yncC | predicted DNA-binding transcriptional regulator | 0 | -0.142 | 0 | 0 | 1 | 32 |
| JW1546 | ydfQ | Qin prophage; predicted lysozyme | 0 | -0.401 | 1 | 1 | 2 | 32 |
| JW1607 | uidC | predicted outer membrane porin protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.333 | 1 | 1 | 2 | 32 |
| JW2609 | yfiL | CP4-57 prophage; predicted protein | 0 | -0.407 | 0 | 0 | 2 | 32 |
| JW3344 | yhfX | predicted amino acid racemase | 0 | -0.001 | 0 | 0 | 2 | 32 |
| JW3457 | yhiL | predicted protein | 0 | -0.467 | 0 | 0 | 2 | 32 |
| JW4015 | aphA | acid phosphatase/phosphotransferase, class B, non-specific | GO:0005737 cytoplasm | -0.283 | 0 | 0 | 1 | 32 |
| JW5084 | hokE | toxic polypeptide, small | 0 | 0.782 | 1 | 1 | 1 | 32 |
| JW5925 | yghJ | predicted inner membrane lipoprotein | 0 | -0.540 | 0 | 0 | 2 | 32 |
| JW0504 | allC | allantoate amidohydrolase | 0 | -0.230 | 0 | 0 | 2 | 31 |
| JW0505 | allD | ureidoglycolate dehydrogenase | 0 | -0.136 | 0 | 0 | 2 | 31 |
| JW0695 | ybfL | predicted transposase (pseudogene) | 0 | -0.320 | 0 | 0 | 2 | 31 |
| JW0808 | ybiY | predicted pyruvate formate lyase activating enzyme | 0 | -0.108 | 0 | 0 | 2 | 31 |
| JW0916 | ssuB | alkanesulfonate transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.009 | 0 | 0 | 2 | 31 |
| JW1166 | ycgJ | predicted protein | 0 | -0.208 | 0 | 0 | 2 | 31 |
| JW1943 | vsr | DNA mismatch endonuclease of very short patch repair | 0 | -0.360 | 0 | 0 | 2 | 31 |
| JW2265 | yfbK | conserved protein | 0 | -0.478 | 0 | 0 | 2 | 31 |
| JW2314 | dedA | conserved inner membrane protein | GO:0009274 cell wall (sensu | 0.809 | 1 | 4 | 1 | 31 |
| JW2345 | intS | CPS-53 (KpLE1) prophage; predicted prophage CPS-53 integrase | 0 | -0.387 | 0 | 0 | 2 | 31 |
| JW2759 | gudX | predicted glucarate dehydratase | 0 | -0.195 | 0 | 0 | 2 | 31 |
| JW3089 | tdcA | DNA-binding transcriptional activator | GO:0005737 cytoplasm | 0.092 | 1 | 0 | 2 | 31 |
| JW3182 | yhcA | predicted periplasmic chaperone protein | 0 | -0.366 | 0 | 0 | 2 | 31 |

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|--------|------|---|---|--------|---|----|---|----|
| JW3956 | thiF | thiamin (thiazole moiety) biosynthesis protein | 0 | -0.039 | 1 | 1 | 2 | 31 |
| JW4065 | phnE | phosphonate/organophosphate ester transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.313 | 1 | 3 | 2 | 31 |
| JW4254 | insA | KpLE2 phage-like element; IS1 repressor protein InsA | 0 | -0.376 | 0 | 0 | 2 | 31 |
| JW5451 | ppdB | conserved protein | GO:0009289 fimbria | 0.032 | 1 | 1 | 2 | 31 |
| JW5803 | ybhR | predicted transporter subunit -!- membrane component of ABC | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.391 | 1 | 6 | 2 | 31 |
| JW0073 | leuA | 2-isopropylmalate synthase | GO:0005737 cytoplasm | -0.188 | 0 | 0 | 1 | 30 |
| JW1145 | mcrA | e14 prophage; 5-methylcytosine-specific restriction endonuclease B | 0 | -0.436 | 0 | 0 | 2 | 30 |
| JW1354 | ydaU | Rac prophage; conserved protein | 0 | -0.539 | 0 | 0 | 2 | 30 |
| JW1416 | ydcA | predicted protein | 0 | 0.084 | 1 | 0 | 1 | 30 |
| JW1568 | ydfE | Qin prophage; predicted protein | 0 | -0.452 | 0 | 0 | 2 | 30 |
| JW2086 | yegU | predicted hydrolase | 0 | 0.031 | 1 | 0 | 1 | 30 |
| JW2695 | hycA | regulator of the transcriptional regulator FhIA | GO:0005737 cytoplasm | -0.356 | 0 | 0 | 2 | 30 |
| JW2722 | cysD | sulfate adenylyltransferase, subunit 2 | 0 | -0.537 | 0 | 0 | 2 | 30 |
| JW2811 | kdul | predicted 5-keto 4-deoxyuronate isomerase | 0 | -0.190 | 0 | 0 | 1 | 30 |
| JW3558 | yiaV | membrane fusion protein (MFP) component of efflux pump, signal | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.028 | 1 | 2 | 2 | 30 |
| JW3688 | mdtL | multidrug efflux system protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.991 | 1 | 11 | 2 | 30 |
| JW3989 | yjbH | predicted porin | 0 | -0.502 | 0 | 0 | 2 | 30 |
| JW4313 | hsdR | endonuclease R | GO:0005737 cytoplasm | -0.489 | 0 | 0 | 2 | 30 |
| JW5184 | cvrA | predicted cation/proton antiporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.668 | 1 | 11 | 2 | 30 |
| JW5228 | ydcM | predicted transposase | 0 | -0.653 | 0 | 0 | 2 | 30 |
| JW5406 | yphH | predicted DNA-binding transcriptional regulator | 0 | -0.197 | 0 | 0 | 1 | 30 |
| JW5688 | rtcA | RNA 3'-terminal phosphate cyclase | GO:0005737 cytoplasm | 0.130 | 1 | 0 | 2 | 30 |
| JW5908 | yddM | predicted DNA-binding transcriptional regulator | 0 | -0.161 | 0 | 0 | 1 | 30 |
| JW0126 | yadE | predicted polysaccharide deacetylase lipoprotein | 0 | -0.278 | 1 | 1 | 2 | 29 |
| JW0498 | ybbV | predicted protein | 0 | -0.023 | 1 | 1 | 2 | 29 |
| JW0689 | rhsC | rhsC element core protein RshC | 0 | -0.715 | 0 | 0 | 2 | 29 |
| JW0850 | ybjQ | conserved protein | 0 | 0.034 | 1 | 0 | 1 | 29 |
| JW0967 | ymcA | conserved protein | 0 | -0.456 | 0 | 0 | 2 | 29 |
| JW1007 | ydcQ | predicted glycosyl transferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.296 | 1 | 5 | 2 | 29 |
| JW1637 | ydhK | conserved inner membrane protein | 0 | 0.255 | 1 | 10 | 2 | 29 |
| JW1766 | yeaC | conserved protein | 0 | -0.369 | 0 | 0 | 2 | 29 |

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|--------|------|---|---|--------|---|----|---|----|
| JW1923 | fliG | flagellar motor switching and energizing component | GO:0019861 flagellum | -0.108 | 0 | 0 | 2 | 29 |
| JW1955 | yedZ | conserved inner membrane protein | 0 | 0.543 | 1 | 6 | 1 | 29 |
| JW2054 | yegD | predicted chaperone | 0 | -0.118 | 0 | 0 | 2 | 29 |
| JW2192 | napH | ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB) | 0 | 0.397 | 1 | 4 | 2 | 29 |
| JW2200 | alkB | oxidative demethylase of N1-methyladenine or N3-methylcytosine DNA lesions | GO:0005737 cytoplasm | -0.286 | 0 | 0 | 1 | 29 |
| JW2623 | yfiW | CP4-57 prophage; predicted inner membrane protein | 0 | 0.285 | 1 | 5 | 2 | 29 |
| JW2686 | ascB | cryptic 6-phospho-beta-glucosidase | 0 | -0.355 | 0 | 0 | 2 | 29 |
| JW2912 | endA | DNA-specific endonuclease I | 0 | -0.739 | 0 | 0 | 2 | 29 |
| JW2923 | yggM | conserved protein | 0 | -0.794 | 0 | 0 | 2 | 29 |
| JW3029 | bacA | undecaprenyl pyrophosphate phosphatase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.930 | 1 | 7 | 1 | 29 |
| JW3354 | hofQ | predicted fimbrial transporter | 0 | -0.117 | 0 | 0 | 2 | 29 |
| JW3455 | yhiJ | predicted protein | 0 | -0.341 | 0 | 0 | 2 | 29 |
| JW3643 | uhpB | sensory histidine kinase in two-component regulatory sytem with UhpA | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.268 | 1 | 7 | 2 | 29 |
| JW4261 | yjhl | KpLE2 phage-like element; predicted DNA-binding transcriptional regulator | 0 | -0.233 | 0 | 0 | 2 | 29 |
| JW5031 | ykgK | predicted regulator | 0 | -0.522 | 0 | 0 | 2 | 29 |
| JW5082 | cusS | sensory histidine kinase in two-component regulatory system with CusR, senses copper ions | GO:0019866 inner membrane | 0.012 | 1 | 2 | 2 | 29 |
| JW5218 | paaK | phenylacetyl-CoA ligase | 0 | -0.345 | 0 | 0 | 1 | 29 |
| JW5316 | fliO | flagellar biosynthesis protein | GO:0019861 flagellum | 0.318 | 1 | 1 | 2 | 29 |
| JW5512 | ygiJ | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.787 | 1 | 12 | 2 | 29 |
| JW5690 | gntT | gluconate transporter, high-affinity GNT I system | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.029 | 1 | 11 | 2 | 29 |
| JW0308 | yahB | predicted DNA-binding transcriptional regulator | 0 | -0.102 | 0 | 0 | 2 | 28 |
| JW0340 | mhpC | 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase | 0 | -0.202 | 0 | 0 | 1 | 28 |
| JW0685 | kdpB | potassium translocating ATPase, subunit B | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.358 | 1 | 7 | 2 | 28 |
| JW0836 | rimK | ribosomal protein S6 modification protein | GO:0009281 cytosolic ribosome (sensu Bacteria) -!- GO:0005737 cytoplasm | 0.022 | 1 | 0 | 2 | 28 |
| JW1005 | phoH | conserved protein with nucleoside triphosphate hydrolase domain | GO:0005737 cytoplasm | -0.242 | 0 | 0 | 2 | 28 |
| JW1285 | sapC | predicted antimicrobial peptide transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.749 | 1 | 5 | 1 | 28 |

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|--------|------|--|--|--------|---|----|---|----|
| JW1355 | ydaV | Rac prophage; predicted DNA replication protein | 0 | -0.476 | 0 | 0 | 2 | 28 |
| JW1613 | malX | fused maltose and glucose-specific PTS enzyme IIBC components | 0 | 0.700 | 1 | 8 | 2 | 28 |
| JW1684 | ydiF | fused predicted acetyl-CoA:acetoacetyl-CoA transferase: alpha subunit -/- beta subunit | 0 | 0.008 | 1 | 0 | 2 | 28 |
| JW2368 | yfdE | predicted CoA-transferase, NAD(P)-binding | 0 | -0.116 | 0 | 0 | 2 | 28 |
| JW2415 | cysA | sulfate/thiosulfate transporter subunit -/- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.273 | 0 | 0 | 1 | 28 |
| JW2549 | recO | gap repair protein | GO:0005737 cytoplasm | -0.257 | 0 | 0 | 2 | 28 |
| JW2638 | gabP | gamma-aminobutyrate transporter | GO:0009274 cell wall (sensu Bacteria) -/- GO:0019866 inner | 0.826 | 1 | 12 | 2 | 28 |
| JW3483 | gadW | DNA-binding transcriptional activator | 0 | -0.154 | 0 | 0 | 2 | 28 |
| JW3500 | bcsB | regulator of cellulose synthase, cyclic di-GMP binding | 0 | -0.126 | 1 | 2 | 2 | 28 |
| JW3901 | menA | 1,4-dihydroxy-2-naphthoate octaprenyltransferase | GO:0009274 cell wall (sensu Bacteria) -/- GO:0019866 inner | 0.664 | 1 | 9 | 1 | 28 |
| JW3967 | zraS | sensory histidine kinase in two-component regulatory system with ZraR | GO:0009274 cell wall (sensu Bacteria) -/- GO:0019866 inner | -0.061 | 1 | 2 | 1 | 28 |
| JW5007 | secM | regulator of secA translation | 0 | -0.281 | 1 | 1 | 1 | 28 |
| JW5385 | yfdN | CPS-53 (KpLE1) prophage; predicted protein | 0 | -0.815 | 0 | 0 | 2 | 28 |
| JW5424 | ypjC | predicted protein | 0 | -0.456 | 0 | 0 | 1 | 28 |
| JW5707 | gspD | general secretory pathway component, cryptic | 0 | -0.184 | 0 | 0 | 2 | 28 |
| JW5710 | yrdA | conserved protein | 0 | -0.206 | 0 | 0 | 1 | 28 |
| JW5743 | yjfO | conserved protein | 0 | -0.055 | 1 | 1 | 1 | 28 |
| JW5748 | ytfl | predicted protein | 0 | -0.374 | 0 | 0 | 2 | 28 |
| JW5855 | recQ | ATP-dependent DNA helicase | GO:0005737 cytoplasm | -0.269 | 0 | 0 | 2 | 28 |
| JW5910 | ydiD | short chain acyl-CoA synthetase, anaerobic | 0 | -0.060 | 0 | 0 | 2 | 28 |
| JW5967 | sgcB | predicted enzyme IIB component of | GO:0005737 cytoplasm | 0.152 | 1 | 0 | 2 | 28 |
| JW0444 | ybaZ | predicted methyltransferase | 0 | -0.400 | 0 | 0 | 2 | 27 |
| JW0629 | mrdB | cell wall shape-determining protein | GO:0009274 cell wall (sensu Bacteria) -/- GO:0019866 inner | 0.908 | 1 | 9 | 1 | 27 |
| JW0783 | ybiA | conserved protein | 0 | -0.764 | 0 | 0 | 2 | 27 |
| JW1490 | yddB | predicted porin protein | 0 | -0.584 | 0 | 0 | 2 | 27 |
| JW1840 | edd | 6-phosphogluconate dehydratase | 0 | -0.023 | 0 | 0 | 2 | 27 |
| JW1872 | cheB | fused chemotaxis regulator -/- protein-glutamate methylesterase, in two-component regulatory system with | GO:0005737 cytoplasm | 0.050 | 1 | 0 | 2 | 27 |
| JW2047 | wza | lipoprotein required for capsular polysaccharide translocation through the outer membrane | 0 | -0.216 | 0 | 0 | 2 | 27 |

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|--------|------|--|--|--------|---|----|---|----|
| JW2058 | yegL | conserved protein | 0 | -0.083 | 0 | 0 | 2 | 27 |
| JW2102 | molR | DNA-binding transcriptional regulator, N-ter fragment (pseudogene) | 0 | -0.306 | 0 | 0 | 2 | 27 |
| JW2143 | lysP | lysine transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.616 | 1 | 12 | 1 | 27 |
| JW2453 | narQ | sensory histidine kinase in two-component regulatory system with NarP | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.152 | 1 | 2 | 1 | 27 |
| JW2723 | iap | aminopeptidase in alkaline phosphatase isozyme conversion | 0 | -0.372 | 0 | 0 | 1 | 27 |
| JW2809 | araE | arabinose transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.628 | 1 | 12 | 2 | 27 |
| JW2841 | hyuA | D-stereospecific phenylhydantoinase | 0 | -0.161 | 0 | 0 | 2 | 27 |
| JW2843 | yqeB | conserved protein with NAD(P)-binding Rossmann fold | 0 | 0.125 | 1 | 0 | 2 | 27 |
| JW2944 | glcG | conserved protein | 0 | 0.158 | 1 | 0 | 1 | 27 |
| JW3357 | yrfC | predicted fimbrial assembly protein | 0 | -0.345 | 1 | 1 | 2 | 27 |
| JW3365 | yhgE | predicted inner membrane protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.454 | 1 | 11 | 2 | 27 |
| JW3528 | insK | IS150 conserved protein InsB | 0 | -0.671 | 0 | 0 | 2 | 27 |
| JW3965 | yjaH | conserved protein | 0 | -0.539 | 0 | 0 | 1 | 27 |
| JW4066 | phnD | phosphonate/organophosphate ester transporter subunit -!- periplasmic binding component of ABC superfamily | GO:0042597 periplasmic space | -0.328 | 0 | 0 | 2 | 27 |
| JW4101 | yjeH | predicted transporter | 0 | 0.960 | 1 | 11 | 2 | 27 |
| JW4143 | yjfM | conserved protein | 0 | -0.791 | 0 | 0 | 2 | 27 |
| JW4247 | fecE | KpLE2 phage-like element; iron-dicitrate transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.065 | 0 | 0 | 2 | 27 |
| JW5135 | torS | hybrid sensory histidine kinase in two-component regulatory system with TorR | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.154 | 1 | 2 | 1 | 27 |
| JW5142 | ycdR | predicted enzyme associated with biofilm formation | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -0.379 | 1 | 0 | 1 | 27 |
| JW5188 | dhaR | predicted DNA-binding transcriptional regulator, dihydroxyacetone | 0 | -0.085 | 0 | 0 | 1 | 27 |
| JW5595 | yifK | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.843 | 1 | 12 | 2 | 27 |
| JW5749 | ytfK | conserved protein | 0 | -0.157 | 0 | 0 | 1 | 27 |
| JW0812 | iaaA | L-asparaginase | 0 | 0.101 | 1 | 0 | 2 | 26 |
| JW1060 | flgB | flagellar component of cell-proximal portion of basal-body rod | GO:0019861 flagellum -!- GO:0042597 periplasmic space | -0.469 | 0 | 0 | 2 | 26 |
| JW1067 | flgI | predicted flagellar basal body protein | GO:0019861 flagellum | 0.055 | 1 | 0 | 2 | 26 |
| JW1219 | tpr | predicted protamine-like protein | GO:0005737 cytoplasm | -1.924 | 0 | 0 | 1 | 26 |
| JW1294 | puuB | gamma-Glu-putrescine oxidase, FAD/NAD(P)-binding | 0 | -0.244 | 0 | 0 | 2 | 26 |
| JW1344 | recE | Rac prophage; exonuclease VIII, 5' -> 3' specific dsDNA exonuclease | GO:0005737 cytoplasm | -0.578 | 0 | 0 | 2 | 26 |
| JW1508 | lsrD | A12 transporter -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.103 | 1 | 9 | 2 | 26 |

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|--------|------|---|---|--------|---|----|---|----|
| JW2310 | cvpA | membrane protein required for colicin V production | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.961 | 1 | 4 | 2 | 26 |
| JW2973 | exbD | membrane spanning protein in TonB-ExbB-ExbD complex | 0 | 0.013 | 1 | 1 | 1 | 26 |
| JW3096 | garP | predicted (D)-galactarate transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.704 | 1 | 11 | 2 | 26 |
| JW4008 | yjbM | predicted protein | 0 | -0.419 | 0 | 0 | 2 | 26 |
| JW4041 | yjcP | predicted outer membrane factor of efflux pump | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.122 | 1 | 0 | 2 | 26 |
| JW4304 | yjiS | conserved protein | 0 | -0.976 | 0 | 0 | 2 | 26 |
| JW4361 | creB | DNA-binding response regulator in two-component regulatory system with CreC | GO:0005737 cytoplasm | -0.132 | 0 | 0 | 2 | 26 |
| JW5455 | yqeJ | predicted protein | 0 | -0.272 | 1 | 1 | 2 | 26 |
| JW5858 | yidX | predicted lipoproteinC | 0 | -0.122 | 1 | 1 | 1 | 26 |
| JW0548 | ybcW | DLP12 prophage; predicted protein | 0 | -0.113 | 0 | 0 | 1 | 25 |
| JW0914 | pncB | nicotinate phosphoribosyltransferase | GO:0042597 periplasmic space | -0.298 | 0 | 0 | 1 | 25 |
| JW1731 | ydjR | conserved protein | 0 | -0.134 | 0 | 0 | 1 | 25 |
| JW2651 | nrdF | ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like | GO:0005737 cytoplasm | -0.255 | 0 | 0 | 1 | 25 |
| JW3953 | thiH | thiamin biosynthesis ThiGH complex subunit | 0 | -0.468 | 0 | 0 | 1 | 25 |
| JW5412 | yfiL | predicted protein | 0 | -0.440 | 0 | 0 | 1 | 25 |
| JW5859 | dgoT | D-galactonate transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.680 | 1 | 11 | 1 | 25 |
| JW5881 | ychS | predicted protein | 0 | 0.014 | 1 | 0 | 1 | 25 |
| JW0680 | speF | ornithine decarboxylase isozyme, | 0 | -0.235 | 0 | 0 | 1 | 24 |
| JW1597 | ydgl | predicted arginine/ornithine antiporter transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.971 | 1 | 13 | 1 | 24 |
| JW2454 | acrD | aminoglycoside/multidrug efflux system | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.160 | 1 | 11 | 1 | 24 |
| JW2490 | yfgI | conserved protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | -1.118 | 1 | 0 | 1 | 24 |
| JW2954 | yghT | predicted protein with nucleoside triphosphate hydrolase domain | 0 | -0.151 | 0 | 0 | 1 | 24 |
| JW3189 | yhcG | conserved protein | 0 | -0.375 | 0 | 0 | 1 | 24 |
| JW5046 | mhpT | predicted 3-hydroxyphenylpropionic transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.964 | 1 | 12 | 1 | 24 |
| JW0042 | fixC | predicted oxidoreductase, FAD/NAD(P)-binding domain | 0 | 0.056 | 1 | 0 | 1 | 23 |
| JW0831 | ybjL | predicted transporter | 0 | 0.554 | 1 | 9 | 1 | 23 |
| JW1098 | ycfR | predicted protein | 0 | 0.029 | 1 | 0 | 1 | 23 |
| JW2184 | ccmF | heme lyase, CcmF subunit | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.641 | 1 | 15 | 1 | 23 |

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|--------|------|---|---|--------|---|----|---|----|
| JW2380 | ypdD | fused predicted PTS enzymes Hpr component -!- enzyme I component -!- enzyme IIA component | 0 | -0.148 | 0 | 0 | 1 | 23 |
| JW2842 | yqeA | predicted amino acid kinase | 0 | -0.019 | 0 | 0 | 1 | 23 |
| JW3692 | yieG | predicted inner membrane protein | 0 | 0.997 | 1 | 13 | 1 | 23 |
| JW5036 | insE | IS3 element protein | 0 | -0.962 | 0 | 0 | 1 | 23 |
| JW5422 | ypjA | adhesin-like autotransporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.359 | 1 | 1 | 1 | 23 |
| JW5818 | potG | putrescine transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | -0.130 | 0 | 0 | 1 | 23 |
| JW0068 | sgrR | DNA-binding transcriptional regulator | GO:0042597 periplasmic space | -0.324 | 0 | 0 | 1 | 22 |
| JW0455 | ybaM | predicted protein | 0 | -0.391 | 0 | 0 | 1 | 22 |
| JW0648 | gltK | glutamate and aspartate transporter subunit -!- membrane component of ABC superfamily | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner membrane | 0.868 | 1 | 5 | 1 | 22 |
| JW1384 | paaB | predicted multicomponent oxygenase/reductase subunit for phenylacetic acid degradation | 0 | -0.561 | 0 | 0 | 1 | 22 |
| JW1395 | paaY | predicted hexapeptide repeat acetyltransferase | 0 | -0.064 | 0 | 0 | 1 | 22 |
| JW1402 | ydbA | predicted outer membrane protein, C-ter fragment (pseudogene) | 0 | -0.270 | 0 | 0 | 1 | 22 |
| JW2330 | yfcP | predicted fimbrial-like adhesin protein | GO:0009289 fimbria | 0.064 | 1 | 1 | 1 | 22 |
| JW2917 | yggR | predicted transporter | 0 | -0.135 | 0 | 0 | 1 | 22 |
| JW2986 | plsC | 1-acyl-sn-glycerol-3-phosphate acyltransferase | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.073 | 1 | 1 | 1 | 22 |
| JW3689 | yidZ | predicted DNA-binding transcriptional regulator | 0 | -0.226 | 0 | 0 | 1 | 22 |
| JW0471 | ybaP | conserved protein | 0 | -0.228 | 0 | 0 | 1 | 21 |
| JW0609 | citD | citrate lyase, acyl carrier (gamma) | GO:0005737 cytoplasm | 0.028 | 1 | 0 | 1 | 21 |
| JW0807 | ybiW | predicted pyruvate formate lyase | 0 | -0.245 | 0 | 0 | 1 | 21 |
| JW0884 | ycaK | conserved protein | 0 | -0.381 | 0 | 0 | 1 | 21 |
| JW1293 | puuC | gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, | GO:0005737 cytoplasm | -0.116 | 0 | 0 | 1 | 21 |
| JW1479 | ddpD | D-Ala-D-Ala transporter subunit -!- ATP-binding component of ABC superfamily | GO:0005737 cytoplasm | 0.024 | 1 | 0 | 1 | 21 |
| JW1779 | yeaM | predicted DNA-binding transcriptional regulator | 0 | -0.142 | 0 | 0 | 1 | 21 |
| JW2335 | yfcU | predicted export usher protein | GO:0009274 cell wall (sensu Bacteria) -!- GO:0009279 external outer membrane (sensu Gram-negative Bacteria) | -0.631 | 1 | 0 | 1 | 21 |
| JW2547 | acpS | holo-[acyl-carrier-protein] synthase 1 | GO:0005737 cytoplasm | 0.013 | 1 | 0 | 1 | 21 |
| JW3101 | kbaZ | tagatose 6-phosphate aldolase 1, kbaZ subunit | 0 | -0.175 | 0 | 0 | 1 | 21 |

| | | | | | | | | |
|--------|------|---|--|--------|---|----|---|----|
| JW3349 | rpe | D-ribulose-5-phosphate 3-epimerase | 0 | 0.066 | 1 | 0 | 1 | 21 |
| JW3553 | sgbH | 3-keto-L-gulonate 6-phosphate decarboxylase | 0 | 0.028 | 1 | 0 | 1 | 21 |
| JW3700 | bglF | fused beta-glucoside-specific PTS enzyme IIABC components | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.617 | 1 | 10 | 1 | 21 |
| JW3701 | bglG | transcriptional antiterminator of the bgl operon | GO:0005737 cytoplasm | -0.204 | 0 | 0 | 1 | 21 |
| JW0133 | yadL | predicted fimbrial-like adhesin protein | 0 | 0.152 | 1 | 1 | 1 | 20 |
| JW0332 | cynX | predicted cyanate transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 0.857 | 1 | 12 | 1 | 20 |
| JW0784 | dinG | ATP-dependent DNA helicase | GO:0005737 cytoplasm | -0.243 | 0 | 0 | 1 | 20 |
| JW1201 | hemA | glutamyl tRNA reductase | GO:0005737 cytoplasm | -0.188 | 0 | 0 | 1 | 20 |
| JW1555 | relE | Qin prophage; toxin of the RelE-RelB toxin-antitoxin system | GO:0005737 cytoplasm | -0.348 | 0 | 0 | 1 | 20 |
| JW2098 | yehD | predicted fimbrial-like adhesin protein | GO:0009289 fimbria | 0.048 | 1 | 1 | 1 | 20 |
| JW2362 | dsdX | predicted transporter | GO:0009274 cell wall (sensu Bacteria) -!- GO:0019866 inner | 1.122 | 1 | 12 | 1 | 20 |
| JW2608 | yfjK | CP4-57 prophage; conserved protein | 0 | -0.184 | 0 | 0 | 1 | 20 |
| JW2848 | ygfM | predicted oxidoreductase | 0 | -0.127 | 0 | 0 | 1 | 20 |
| JW2897 | yggF | predicted hexoseP phosphatase | 0 | 0.018 | 1 | 0 | 1 | 20 |
| JW3685 | tnaC | tryptophanase leader peptide | 0 | -0.117 | 0 | 0 | 1 | 20 |
| JW3699 | bglB | cryptic phospho-beta-glucosidase B | 0 | -0.304 | 0 | 0 | 1 | 20 |
| JW3913 | metF | 5,10-methylenetetrahydrofolate | 0 | -0.235 | 0 | 0 | 1 | 20 |
| JW5484 | yghF | predicted secretion pathway protein, C-type protein | 0 | -0.218 | 0 | 0 | 1 | 20 |
| JW5683 | yhhL | conserved inner membrane protein | 0 | 0.734 | 1 | 2 | 1 | 20 |
| JW5737 | ecnA | entericidin A membrane lipoprotein, antidote entericidin B | 0 | 0.473 | 1 | 0 | 1 | 20 |