# Explanatory Notes, pseudo M/A plots, and Data Table ST1, Additional Material for Hendrickson *et al.*

The data table lists our entire set of results calculated from the raw mass spectral data first described in Xia *et al.*, *Proteomics* 2007, **7**: 4323-4337. The data were recalculated based on a search of annotated ORFs from the ATCC 33277 annotation of Naito *et al.*, *DNA Res* 2008, **15**:215-225, as described in the main text. The entire dataset is shown in the form of two pseudo M/A plots that precede Table ST1 below. These additional figures look very similar to those originally published using the W83 annotation, but we include them here as additional material for the sake of completeness. The color codes for the plots follow the data table, with the exception that proteins lacking any significant abundance change are coded black. Following our normal practice, a LOWESS (locally weighted scatter plot smoothing) curve fit to the scatter about zero abundance change, based on replicate control analyses, is superimposed over the plot, following the method of Cleveland, *Amer Statistician* 1981, **35**:54-54. For Table ST1, a key to the individual data fields is given below. The variable naming conventions follow those of Xia *et al.* in the original paper. The equations for the *t*-test, *G*-test and further details regarding their application can be found in Xia *et al.*, *Proteomics* 2007, **7:**2904-2919 and in the electronic supplement to Bosch *et al.*, *Proteomics* 2008, **8**:3494-3505. The forms given in Bosch *et al.* were the ones applied here, which differ from the equations originally described for the *P. gingivalis* internalization studies in Xia *et al.*, *Int Jour Mass spectrum* 2007, **259**:105-116.

## Spectra Count Fields

**ORF number.** The ORF numbers from the three most common naming conventions are given. The field as a whole seems to be gravitating to the use of PGN numbers as assigned by Naito *et al.* for ATCC 33277 and related strains, thus we have ordered the entries by PGN number.

***q*-value.** A measure of false discovery rate, similar to a *p*-value, see Storey and Tibshirani, *Proc Natl Acad Sci USA* 2003, **100**:9440-9445. This q-value reflects the results of a global *G*-test over all replicates following the method popularized by Sokal and Rohlf referenced in the main text. It is worth noting that the global *G*-test as applied here requires that the data be pre-screened for instances where relative abundance trends for the same annotated ORF go in opposite directions from zero ($\log_2$ scale) within the same set of replicates. Such data are rare, but in the absence of such a pre-screen the *G*-test will not be sensitive to the direction of change from zero, thus leading to a call of significant change for data that should be properly coded as qualitative detection only, no abundance change. As noted in the main text, the *q* cut-off for all work reported in Table ST1 is 0.01.

**PP(Norm).** Internalized *P. gingivalis* normalized average total spectral counts over all replicates.

**PPC(Norm).** External control *P. gingivalis* normalized average total spectral counts over all replicates.

**$\log_2$Ratio.** $\log_2$ ratio of PP(Norm)/PPC(norm).

**$\log_2$sum**. $\text{Log}_2$ of the sum of PP(Norm) and PPC(norm).

**Regulation.** A simple color code is given, indicating the direction of abundance change. Red, increased abundance in the internalized *P. gingivalis* cells; green, decreased relative abundance; yellow, qualitative detection in the absence of statistically significant abundance change.

**Protein Intensity Fields**

***q*-value.** A measure of false discovery rate, similar to a *p*-value, see Storey and Tibshirani as noted above. This *q*-value reflects the results of a paired *t*-test over all replicates, according to the method described in Sokal and Rohlf, as given in the main text.

**PP(Norm).** Internalized *P. gingivalis* normalized average total signal intensity for all $\text{MS}^1$ ions over all replicates.

**PPC(Norm).** External control *P. gingivalis* normalized average total signal intensity for all $\text{MS}^1$ ions over all replicates.

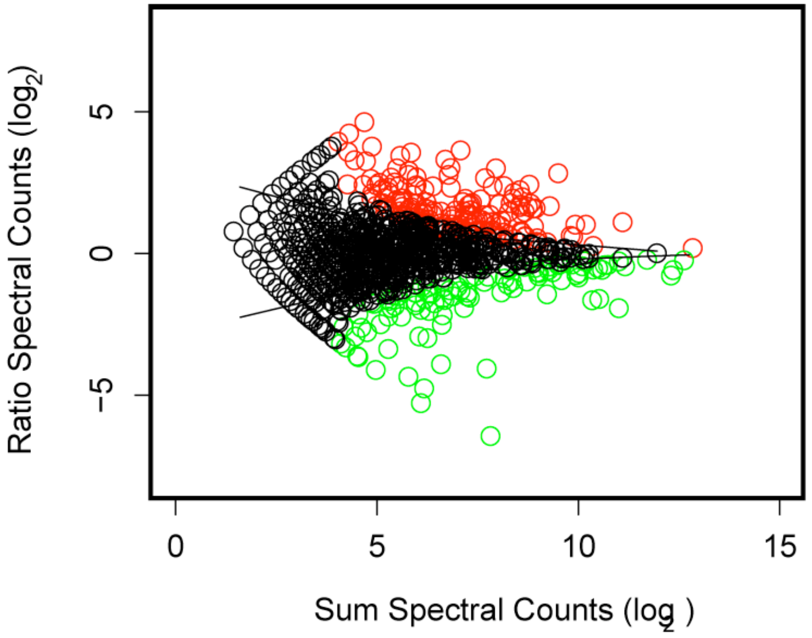
**$\log_2$Ratio.** $\text{Log}_2$ ratio of PP(Norm)/PPC(norm).

**$\log_2$sum**. $\text{Log}_2$ of the sum of normalized average total intensities for PP(Norm) and PPC(norm).

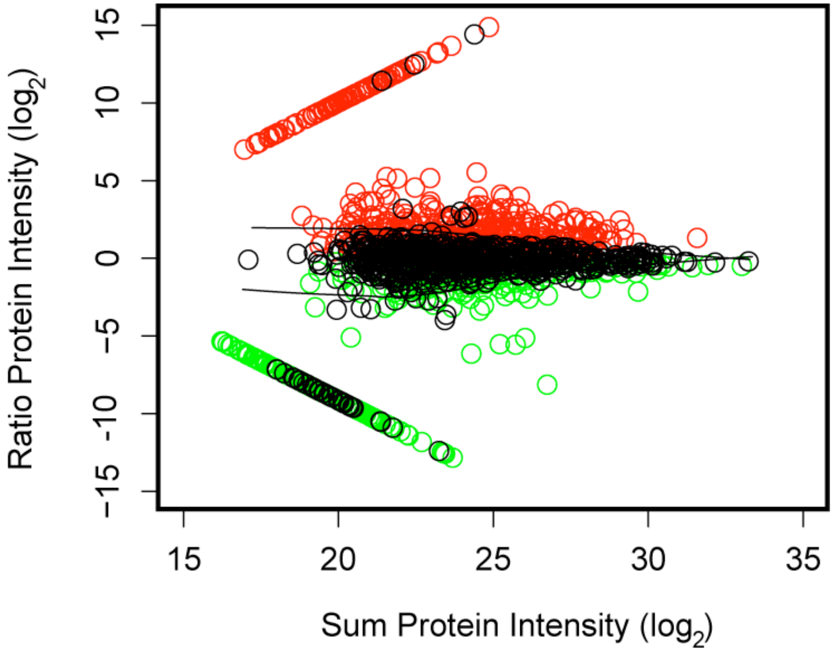
**Regulation.** A simple color code indicating the direction of abundance change. Red, increased abundance in the internalized *P. gingivalis* cells; green, decreased relative abundance; yellow, qualitative detection in the absence of statistically significant abundance change.

**Consensus.**

Readers are urged to consider the spectral count and intensity data separately, but an overall assessment is provided. If all observed trends for a given protein were in the same direction and either spectral counts or intensity were significantly so, then the protein was labeled red or green, if all deviations from zero were greater than 0.1 $\log_2$ units. This rule was *ad hoc* and arbitrary, but yielded results that seemed to fit this dataset reasonably well.



**Pseudo M/A plot for the spectral counting data based on the ATCC 33277 annotation. All protein abundance ratios are internalized/control.**



**Pseudo M/A plot for the summed signal intensity data based on the ATCC 33277 annotation. All protein abundance ratios are internalized/control.**

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0004 | | 2.98 E-1 | 13.7 | 8 | 0.7751 | 4.4390 | Y | 🟡 | 🔴 | R | 1.15 E-6 | 7.93 E+6 | 2.37 E+6 | 1.7408 | 23.2967 | R | 🔴 |
| *PGN0004* | *PG0004* | *transcriptional regulator Sir2 family* | | | | | | | | | | | | | | | |
| PG0005 | | 6.63 E-2 | 2.6 | 10 | -1.9619 | 3.6516 | Y | 🟡 | 🟢 | G | 4.39 E-5 | 1.28 E+6 | 3.3 E+6 | -1.3635 | 22.1298 | G | 🟢 |
| *PGN0005* | *PG0005* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0010 | | 5.31 E-2 | 9.4 | 2 | 2.2345 | 3.5125 | Y | 🟡 | 🔴 | R | 2.58 E-16 | 4.51 E+6 | 8.59 E+5 | 2.3926 | 22.3556 | R | 🔴 |
| *PGN0008* | *PG0009* | *clpC ATP-dependent Clp protease ATP-binding subunit ClpC* | | | | | | | | | | | | | | | |
| PG0011 | | 5.28 E-2 | 31.7 | 16 | 0.9846 | 5.5747 | Y | 🟡 | 🟡 | Y | 1.08 E-1 | 1.26 E+7 | 1.05 E+7 | 0.2626 | 24.4651 | Y | 🟡 |
| *PGN0009* | *PG0010* | *glycosyl hydrolase family 3* | | | | | | | | | | | | | | | |
| PG0012 | | 9.24 E-9 | 54.8 | 8.5 | 2.6876 | 5.9833 | R | 🔴 | 🔴 | R | 0 | 2.73 E+7 | 4.78 E+6 | 2.5157 | 24.9367 | R | 🔴 |
| *PGN0010* | *PG0011* | *L-threonine-O-3-phosphate decarboxylase putative* | | | | | | | | | | | | | | | |
| PG0016 | | 2.67 E-1 | 9.4 | 4.5 | 1.0646 | 3.7983 | Y | 🟡 | 🔴 | R | 6.34 E-7 | 2.22 E+6 | 6.91 E+5 | 1.6845 | 21.4735 | R | 🔴 |
| *PGN0012* | *PG0013* | *sigma-54 dependent DNA-binding response regulator* | | | | | | | | | | | | | | | |
| PG0017 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 5.11 E+5 | -8.1093 | 18.9682 | Y | 🟡 |
| *PGN0013* | *PG0014* | *sensor histidine kinase* | | | | | | | | | | | | | | | |
| PG0018 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 4.95 E-8 | 1.85 E+3 | 1.54 E+5 | -6.3812 | 17.2521 | G | 🟢 |
| *PGN0014* | *PG0015* | *hypothetical protein PG_0018* | | | | | | | | | | | | | | | |
| PG0020 | | 6.97 E-1 | 3.4 | 3.5 | -0.0323 | 2.7913 | Y | 🟡 | 🟡 | Y | 1.75 E-1 | 1.11 E+6 | 1.29 E+6 | -0.2139 | 21.1945 | Y | 🟡 |
| *PGN0015* | *PG0017* | *transcriptional regulator MarR family* | | | | | | | | | | | | | | | |
| PG0022 | | 4.75 E-1 | 6.8 | 4.5 | 0.6052 | 3.5040 | Y | 🟡 | 🟡 | Y | 4.5 E-2 | 2.49 E+6 | 1.25 E+6 | 1.0013 | 21.8339 | Y | 🟡 |
| *PGN0017* | *PG0019* | *sulfate permease family protein* | | | | | | | | | | | | | | | |
| PG0024 | | 3.76 E-1 | 6.0 | 3 | 0.9975 | 3.1683 | Y | 🟡 | 🟡 | Y | 3.33 E-2 | 4.41 E+6 | 2.66 E+6 | 0.7305 | 22.7544 | Y | 🟡 |
| *PGN0020* | *PG0020* | *DNA-binding protein putative* | | | | | | | | | | | | | | | |
| PG0025 | | 6.97 E-1 | 3.4 | 3.5 | -0.0323 | 2.7913 | Y | 🟡 | 🟡 | Y | 7.32 E-2 | 7.76 E+5 | 9.4 E+5 | -0.2774 | 20.7106 | Y | 🟡 |
| *PGN0021* | *PG0021* | *fumarylacetoacetate hydrolase family protein* | | | | | | | | | | | | | | | |
| PG0026 | | 1.36 E-3 | 17.1 | 45 | -1.3948 | 5.9568 | G | 🟢 | 🟢 | G | 6.45 E-4 | 1.15 E+7 | 3.55 E+7 | -1.6204 | 25.4865 | G | 🟢 |
| *PGN0022* | *PG0022* | *hypothetical protein PG_0026* | | | | | | | | | | | | | | | |
| PG0027 | | 8.17 E-11 | 141.2 | 281.5 | -0.9956 | 8.7234 | G | 🟢 | 🟢 | G | 1.5 E-8 | 8.52 E+7 | 1.65 E+8 | -0.9567 | 27.9014 | G | 🟢 |
| *PGN0023* | *PG0023* | *hypothetical protein PG_0027* | | | | | | | | | | | | | | | |
| PG0028 | | 2.99 E-1 | 6.0 | 11 | -0.8770 | 4.0866 | Y | 🟡 | 🟢 | G | 1.47 E-4 | 1.45 E+6 | 4.78 E+6 | -1.7233 | 22.5698 | G | 🟢 |
| *PGN0024* | *PG0024* | *ispF 2C-methyl-D-erythritol 24-cyclodiphosphate synthase* | | | | | | | | | | | | | | | |
| | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟡 | Y | 2.08 E-2 | 1.85 E+3 | 3.1 E+5 | -7.3867 | 18.2490 | Y | 🟡 |
| *PGN0025* | | | | | | | | | | | | | | | | | |
| PG0030 | | 4.14 E-1 | 6.0 | 9.5 | -0.6655 | 3.9532 | Y | 🟡 | 🟡 | Y | 4.25 E-3 | 3.9 E+6 | 2.15 E+6 | 0.8606 | 22.5266 | Y | 🟡 |
| *PGN0026* | *PG0026* | *cytidine deaminase* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| | | 1.94 E-2 | 47.9 | 25 | 0.9386 | 6.1882 | Y 🟡 | 🟡 Y | 5.07 E-3 | 2.22 E+7 | 1.22 E+7 | 0.8604 | 25.0380 | Y 🟡 |
| *PGN0027* | | | | | | | | | | | | | | |
| PG0031 | | 3.86 E-7 | 1.7 | 29.5 | -4.1075 | 4.9640 | G 🟢 | 🟢 G | 3.46 E-10 | 1.85 E+3 | 1.35 E+7 | -12.8324 | 23.6863 | G 🟢 |
| *PGN0029* | *PG0027* | *hypothetical protein PG_0031* | | | | | | | | | | | | |
| PG0032 | | 3.05 E-1 | 6.8 | 12 | -0.8099 | 4.2361 | Y 🟡 | 🟡 Y | 2.08 E-3 | 9.94 E+5 | 2.11 E+6 | -1.0880 | 21.5672 | Y 🟡 |
| *PGN0030* | *PG0028* | *beta-mannosidase putative* | | | | | | | | | | | | |
| PG0033 | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y 🟡 | 🔴 R | 1.05 E-4 | 1.31 E+6 | 6.85 E+5 | 0.9334 | 20.9273 | R 🔴 |
| *PGN0031* | *PG0029* | *RmuC domain protein* | | | | | | | | | | | | |
| PG0034 | | 6 E-1 | 81.3 | 76.5 | 0.0876 | 7.3018 | Y 🟡 | 🟡 Y | 9.4 E-2 | 1.45 E+8 | 1.17 E+8 | 0.3030 | 27.9661 | Y 🟡 |
| *PGN0033* | *PG0030* | *trx thioredoxin* | | | | | | | | | | | | |
| PG0035 | | 3.56 E-2 | 7.7 | 20.5 | -1.4125 | 4.8177 | Y 🟡 | 🟡 Y | 2.99 E-3 | 1.79 E+6 | 4.3 E+6 | -1.2630 | 22.5391 | Y 🟡 |
| *PGN0034* | *PG0031* | *dnaE DNA polymerase III alpha subunit* | | | | | | | | | | | | |
| PG0037 | | 2.1 E-7 | 52.2 | 10 | 2.3839 | 5.9587 | R 🔴 | 🔴 R | 0 | 4.45 E+7 | 8.57 E+6 | 2.3769 | 25.6615 | R 🔴 |
| *PGN0035* | *PG0032* | *rplS ribosomal protein L19* | | | | | | | | | | | | |
| PG0042 | | 1.38 E-1 | 428.7 | 378 | 0.1815 | 9.6559 | Y 🟡 | 🟡 Y | 1.77 E-2 | 5.22 E+8 | 6.28 E+8 | -0.2653 | 30.0994 | Y 🟡 |
| *PGN0038* | *PG0035* | *glyA serine hydroxymethyltransferase* | | | | | | | | | | | | |
| PG0043 | | 5.43 E-1 | 53.9 | 48.5 | 0.1525 | 6.6782 | Y 🟡 | 🟡 Y | 1.61 E-1 | 1.82 E+7 | 1.9 E+7 | -0.0613 | 25.1489 | Y 🟡 |
| *PGN0039* | *PG0036* | *nahA beta-hexosaminidase* | | | | | | | | | | | | |
| PG0045 | | 7.43 E-2 | 37.6 | 21.5 | 0.8083 | 5.8863 | Y 🟡 | 🟡 Y | 9.26 E-2 | 2.09 E+7 | 1.76 E+7 | 0.2515 | 25.1993 | Y 🟡 |
| *PGN0041* | *PG0038* | *htpG heat shock protein HtpG* | | | | | | | | | | | | |
| PG0046 | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y 🟡 | 🟡 Y | 4.47 E-2 | 6.51 E+5 | 4.6 E+5 | 0.5027 | 20.0837 | Y 🟡 |
| *PGN0042* | *PG0040* | *cdsA phosphatidate cytidylyltransferase* | | | | | | | | | | | | |
| PG0047 | | 9.98 E-4 | 29.1 | 7.5 | 1.9557 | 5.1935 | R 🔴 | 🔴 R | 0 | 1.04 E+7 | 1.8 E+6 | 2.5308 | 23.5437 | R 🔴 |
| *PGN0043* | *PG0041* | *cell division protein FtsH putative* | | | | | | | | | | | | |
| PG0048 | | 2.15 E-1 | 8.6 | 3.5 | 1.2897 | 3.5917 | Y 🟡 | 🟡 Y | 1.43 E-1 | 4.02 E+6 | 2.81 E+6 | 0.5157 | 22.7024 | Y 🟡 |
| *PGN0044* | *PG0042* | *conserved hypothetical protein TIGR00092* | | | | | | | | | | | | |
| | | 4.28 E-2 | 157.4 | 118 | 0.4160 | 8.1056 | Y 🟡 | 🔴 R | 1.45 E-13 | 9.76 E+7 | 4.24 E+7 | 1.2013 | 27.0607 | R 🔴 |
| *PGN0053* | | | | | | | | | | | | | | |
| | | 4.27 E-4 | 106.1 | 56.5 | 0.9091 | 7.3452 | R 🔴 | 🔴 R | 2.58 E-16 | 3.95 E+7 | 1.33 E+7 | 1.5728 | 25.6526 | R 🔴 |
| *PGN0054* | | | | | | | | | | | | | | |
| | | 5.19 E-1 | 11.1 | 8.5 | 0.3881 | 4.2945 | Y 🟡 | 🔴 R | 2.18 E-8 | 3.48 E+6 | 8.49 E+5 | 2.0347 | 22.0457 | R 🔴 |
| *PGN0057* | | | | | | | | | | | | | | |
| | | 9.87 E-3 | 6.8 | 22.5 | -1.7168 | 4.8751 | G 🟢 | 🟢 G | 2.06 E-6 | 2.34 E+6 | 7 E+6 | -1.5769 | 23.1551 | G 🟢 |
| *PGN0058* | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PGN | LANL | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| | | 1.76 E-1 | 50.5 | 35.5 | 0.5080 | 6.4260 | Y 🟡 | 🟡 Y | 8.83 E-2 | 2.63 E+7 | 2.34 E+7 | 0.1677 | 25.5644 | Y 🟡 |
| *PGN0059* | | | | | | | | | | | | | | |
| | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y 🟡 | 🔴 R | 4.17 E-12 | 2.02 E+6 | 1 E+3 | 10.9783 | 20.9448 | R 🔴 |
| *PGN0062* | | | | | | | | | | | | | | |
| | | 1.13 E-1 | 7.7 | 2 | 1.9450 | 3.2781 | Y 🟡 | 🔴 R | 0 | 3.78 E+6 | 1.09 E+5 | 5.1176 | 21.8905 | R 🔴 |
| *PGN0063* | | | | | | | | | | | | | | |
| | | 9.55 E-3 | 10.3 | 1 | 3.3601 | 3.4941 | Y 🟡 | 🔴 R | 0 | 3.98 E+6 | 1 E+3 | 11.9577 | 21.9238 | R 🔴 |
| *PGN0064* | | | | | | | | | | | | | | |
| | | 6.61 E-1 | 13.7 | 15 | -0.1318 | 4.8425 | Y 🟡 | 🟡 Y | 1.97 E-1 | 3.61 E+6 | 3.57 E+6 | 0.0161 | 22.7774 | Y 🟡 |
| *PGN0065* | | | | | | | | | | | | | | |
| | | 1.36 E-1 | 19.7 | 10 | 0.9767 | 4.8914 | Y 🟡 | 🔴 R | 4.42 E-4 | 6.64 E+6 | 2.85 E+6 | 1.2205 | 23.1769 | R 🔴 |
| *PGN0071* | | | | | | | | | | | | | | |
| PG1486 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y 🟡 | 🟢 G | 7.61 E-16 | 1.85 E+3 | 2.41 E+5 | -7.0242 | 17.8890 | G 🟢 |
| *PGN0073* | *PG1301* | *conjugative transposon protein TraA* | | | | | | | | | | | | |
| | | 3.21 E-4 | 43.6 | 14 | 1.6402 | 5.8490 | R 🔴 | 🔴 R | 6.52 E-6 | 2.65 E+7 | 1.09 E+7 | 1.2792 | 25.1546 | R 🔴 |
| *PGN0079* | | | | | | | | | | | | | | |
| PG1447 | | 2.78 E-1 | 40.2 | 29.5 | 0.4470 | 6.1234 | Y 🟡 | 🟡 Y | 1.26 E-1 | 2.01 E+7 | 2.26 E+7 | -0.1693 | 25.3475 | Y 🟡 |
| *PGN0082* | *PG1266* | *transcriptional regulator AraC family* | | | | | | | | | | | | |
| | | 4 E-11 | 122.4 | 36.5 | 1.7451 | 7.3116 | R 🔴 | 🔴 R | 0 | 6.72 E+7 | 1.15 E+7 | 2.5484 | 26.2301 | R 🔴 |
| *PGN0083* | | | | | | | | | | | | | | |
| | | 1.52 E-4 | 59.9 | 22.5 | 1.4125 | 6.3645 | R 🔴 | 🔴 R | 0 | 2.9 E+7 | 5.61 E+6 | 2.3714 | 25.0463 | R 🔴 |
| *PGN0084* | | | | | | | | | | | | | | |
| PG0816 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 2.52 E+5 | -7.0866 | 17.9509 | Y 🟡 |
| *PGN0085* | *PG0734* | *hypothetical protein PG_0816* | | | | | | | | | | | | |
| | | 4.55 E-1 | 5.1 | 3 | 0.7751 | 3.0240 | Y 🟡 | 🔴 R | 6.78 E-4 | 7.91 E+6 | 2.19 E+5 | 5.1765 | 22.9549 | R 🔴 |
| *PGN0086* | | | | | | | | | | | | | | |
| | | 2.1 E-2 | 28.2 | 52 | -0.8809 | 6.3262 | Y 🟡 | 🟢 G | 1.42 E-4 | 8.26 E+6 | 1.35 E+7 | -0.7116 | 24.3769 | G 🟢 |
| *PGN0087* | | | | | | | | | | | | | | |
| | | 9.44 E-2 | 6.0 | 1 | 2.5825 | 2.8052 | Y 🟡 | 🔴 R | 4.46 E-8 | 3.15 E+6 | 1 E+3 | 11.6198 | 21.5861 | R 🔴 |
| *PGN0091* | | | | | | | | | | | | | | |
| PG1113 | | 4.64 E-4 | 15.4 | 1 | 3.9450 | 4.0358 | R 🔴 | 🔴 R | 1.04 E-6 | 3.04 E+7 | 1 E+3 | 14.8900 | 24.8558 | R 🔴 |
| *PGN0094* | *PG0994* | *integrase* | | | | | | | | | | | | |
| PG2189 | | 2.74 E-1 | 8.6 | 4 | 1.0970 | 3.6504 | Y 🟡 | 🔴 R | 3.75 E-6 | 3.31 E+6 | 1.25 E+6 | 1.4028 | 22.1203 | R 🔴 |
| *PGN0096* | *PG1916* | *lysC aspartate kinase* | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Regulation** | | | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Consensus** | |
| PG2190 | | 6.02 E-1 | 5.1 | 4 | 0.3601 | 3.1912 | Y | 🟡 | 🟡 | Y | 1.87 E-1 | 1.4 E+6 | 1.45 E+6 | -0.0460 | 21.4423 | Y | 🟡 |
| *PGN0097* | *PG1917* | *ftsE cell-division ATP-binding protein* | | | | | | | | | | | | | | | |
| | | 2.72 E-1 | 71.0 | 87.5 | -0.3011 | 7.3085 | Y | 🟡 | 🟡 | Y | 1.54 E-2 | 2.69 E+7 | 3.57 E+7 | -0.4075 | 25.8999 | Y | 🟡 |
| *PGN0100* | | | | | | | | | | | | | | | | | |
| | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 1.02 E-6 | 1.85 E+3 | 1.64 E+5 | -6.4683 | 17.3382 | G | 🟢 |
| *PGN0104* | | | | | | | | | | | | | | | | | |
| PG2182 | | 2.67 E-1 | 52.2 | 39.5 | 0.4021 | 6.5188 | Y | 🟡 | 🟡 | Y | 1.99 E-2 | 4.11 E+7 | 3.1 E+7 | 0.4063 | 26.1036 | Y | 🟡 |
| *PGN0114* | *PG1911* | *nqrA NADH:ubiquinone oxidoreductase Na translocating A subunit* | | | | | | | | | | | | | | | |
| PG2181 | | 4.75 E-1 | 17.1 | 21.5 | -0.3292 | 5.2710 | Y | 🟡 | 🟡 | Y | 1.91 E-2 | 3.1 E+6 | 8.65 E+6 | -1.4800 | 23.4858 | Y | 🟡 |
| *PGN0115* | *PG1910* | *nqrB NADH:ubiquinone oxidoreductase Na translocating B subunit* | | | | | | | | | | | | | | | |
| PG2180 | | 4.97 E-1 | 15.4 | 12 | 0.3601 | 4.7762 | Y | 🟡 | 🟡 | Y | 1.47 E-3 | 1.26 E+7 | 8.66 E+6 | 0.5397 | 24.3410 | Y | 🟡 |
| *PGN0116* | *PG1909* | *nqrC NADH:ubiquinone oxidoreductase Na translocating C subunit* | | | | | | | | | | | | | | | |
| PG2178 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.3 E+5 | -6.1398 | 17.0138 | Y | 🟡 |
| *PGN0118* | *PG1907* | *nqrE NADH:ubiquinone oxidoreductase Na translocating E subunit* | | | | | | | | | | | | | | | |
| PG2177 | | 4.98 E-2 | 79.6 | 53 | 0.5863 | 7.0507 | Y | 🟡 | 🟡 | Y | 4.49 E-2 | 3.99 E+7 | 3.27 E+7 | 0.2865 | 26.1130 | Y | 🟡 |
| *PGN0119* | *PG1906* | *nqrF NADH:ubiquinone oxidoreductase Na translocating F subunit* | | | | | | | | | | | | | | | |
| PG2175 | | 1.94 E-2 | 47.9 | 25 | 0.9386 | 6.1882 | Y | 🟡 | 🔴 | R | 2.79 E-8 | 5.54 E+7 | 1.15 E+7 | 2.2698 | 25.9949 | R | 🔴 |
| *PGN0120* | *PG1903* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG2174 | | 3.17 E-2 | 211.3 | 163 | 0.3747 | 8.5482 | Y | 🟡 | 🟡 | Y | 1.91 E-1 | 9.48 E+7 | 9.38 E+7 | 0.0146 | 27.4909 | Y | 🟡 |
| *PGN0121* | *PG1902* | *hypothetical protein PG_2174* | | | | | | | | | | | | | | | |
| PG2173 | | 3.28 E-1 | 71.9 | 86 | -0.2589 | 7.3026 | Y | 🟡 | 🟡 | Y | 9.87 E-3 | 5.13 E+7 | 7.82 E+7 | -0.6096 | 26.9478 | Y | 🟡 |
| *PGN0122* | *PG1901* | *omp28 outer membrane lipoprotein Omp28* | | | | | | | | | | | | | | | |
| PG2172 | | 3.05 E-2 | 48.8 | 27 | 0.8531 | 6.2436 | Y | 🟡 | 🟡 | Y | 1.22 E-1 | 4.27 E+7 | 3.46 E+7 | 0.3026 | 26.2049 | Y | 🟡 |
| *PGN0123* | *PG1899* | *hypothetical protein PG_2172* | | | | | | | | | | | | | | | |
| PG2171 | | 6.64 E-1 | 80.4 | 77.5 | 0.0536 | 7.3032 | Y | 🟡 | 🔴 | R | 2.57 E-6 | 1.51 E+7 | 8.31 E+6 | 0.8632 | 24.4816 | R | 🔴 |
| *PGN0125* | *PG1898* | *D-isomer specific 2-hydroxyacid dehydrogenase family protein* | | | | | | | | | | | | | | | |
| PG2170 | | 4.75 E-1 | 3.4 | 5.5 | -0.6843 | 3.1575 | Y | 🟡 | 🟡 | Y | 6.91 E-3 | 8.21 E+5 | 3.17 E+6 | -1.9506 | 21.9288 | Y | 🟡 |
| *PGN0126* | *PG1897* | *sugar transporter* | | | | | | | | | | | | | | | |
| PG2167 | | 1.13 E-4 | 248.1 | 162 | 0.6152 | 8.6800 | R | 🔴 | 🟡 | Y | 7.12 E-2 | 3.82 E+8 | 3.38 E+8 | 0.1762 | 29.4243 | R | 🔴 |
| *PGN0128* | *PG1893* | *immunoreactive 53 kDa antigen PG123* | | | | | | | | | | | | | | | |
| PG2168 | | 0 | 6.0 | 90 | -3.9094 | 6.5848 | G | 🟢 | 🟢 | G | 2.01 E-5 | 1.15 E+6 | 5.4 E+7 | -5.5588 | 25.7179 | G | 🟢 |
| *PGN0129* | *PG1894* | *hypothetical protein PG_2168* | | | | | | | | | | | | | | | |
| PG2080 | | 4.4 E-1 | 5.1 | 8 | -0.6399 | 3.7152 | Y | 🟡 | 🟡 | Y | 1.99 E-1 | 1.44 E+6 | 1.45 E+6 | -0.0097 | 21.4671 | Y | 🟡 |
| *PGN0133* | *PG1818* | *bioA adenosylmethionine--8-amino-7-oxononanoate aminotransferase* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG2081 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟡 | Y | 2.07 E-2 | 1.85 E+3 | 6.7 E+5 | -8.5007 | 19.3584 | Y | 🟡 |
| *PGN0134* | *PG1819* | *bioB biotin synthetase* | | | | | | | | | | | | | | | |
| PG2082 | | 1.72 E-1 | 30.8 | 45 | -0.5468 | 6.2442 | Y | 🟡 | 🟡 | Y | 2.61 E-3 | 1.85 E+7 | 4.02 E+7 | -1.1149 | 25.8075 | Y | 🟡 |
| *PGN0135* | *PG1820* | *POT family protein* | | | | | | | | | | | | | | | |
| PG2083 | | 5.82 E-3 | 35.1 | 13.5 | 1.3778 | 5.6023 | R | 🔴 | 🟡 | Y | 7.59 E-3 | 1.28 E+7 | 7.84 E+6 | 0.7012 | 24.2956 | R | 🔴 |
| *PGN0136* | *PG1821* | *hypothetical protein PG_2083* | | | | | | | | | | | | | | | |
| PG2085 | | 2.53 E-1 | 33.4 | 45.5 | -0.4473 | 6.3014 | Y | 🟡 | 🟡 | Y | 1.17 E-3 | 1.42 E+7 | 2.37 E+7 | -0.7429 | 25.1762 | Y | 🟡 |
| *PGN0137* | *PG1822* | *trpS tryptophanyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG2086 | | 5.38 E-1 | 71.0 | 64.5 | 0.1389 | 7.0824 | Y | 🟡 | 🟡 | Y | 1.23 E-2 | 2.69 E+7 | 5.82 E+7 | -1.1160 | 26.3425 | Y | 🟡 |
| *PGN0138* | *PG1823* | *hypothetical protein PG_2086* | | | | | | | | | | | | | | | |
| PG2088 | | 6.54 E-1 | 8.6 | 7.5 | 0.1901 | 4.0051 | Y | 🟡 | 🟡 | Y | 5.06 E-2 | 5.46 E+6 | 3.57 E+6 | 0.6132 | 23.1074 | Y | 🟡 |
| *PGN0140* | *PG1826* | *msrA peptide methionine sulfoxide reductase* | | | | | | | | | | | | | | | |
| PG2089 | | 6 E-1 | 6.0 | 7.5 | -0.3244 | 3.7538 | Y | 🟡 | 🟡 | Y | 3.48 E-3 | 1.04 E+6 | 2.69 E+6 | -1.3625 | 21.8309 | Y | 🟡 |
| *PGN0141* | *PG1827* | *hypothetical protein PG_2089* | | | | | | | | | | | | | | | |
| PG2090 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟡 | Y | 6.8 E-3 | 1.85 E+3 | 1.19 E+6 | -9.3244 | 20.1803 | Y | 🟡 |
| *PGN0142* | *PG1828* | *cation efflux family protein* | | | | | | | | | | | | | | | |
| PG2091 | | 5.77 E-2 | 3.4 | 12 | -1.8099 | 3.9470 | Y | 🟡 | 🟢 | G | 7.86 E-6 | 2.93 E+5 | 2.67 E+6 | -3.1868 | 21.4974 | G | 🟢 |
| *PGN0143* | *PG1829* | *folB dihydroneopterin aldolase* | | | | | | | | | | | | | | | |
| PG2092 | | 2.72 E-2 | 12.0 | 28 | -1.2249 | 5.3212 | Y | 🟡 | 🟡 | Y | 1.97 E-2 | 3.81 E+6 | 5.73 E+6 | -0.5893 | 23.1844 | Y | 🟡 |
| *PGN0144* | *PG1830* | *hypothetical protein PG_2092* | | | | | | | | | | | | | | | |
| PG2094 | | 4.8 E-1 | 4.3 | 2.5 | 0.7751 | 2.7609 | Y | 🟡 | 🔴 | R | 0 | 8.39 E+5 | 2.43 E+5 | 1.7854 | 20.0460 | R | 🔴 |
| *PGN0145* | *PG1831* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG2095 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 8.24 E-4 | 1.85 E+3 | 5.76 E+5 | -8.2822 | 19.1406 | G | 🟢 |
| *PGN0147* | *PG1832* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG2096 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 1.5 E-15 | 3.77 E+5 | 1 E+3 | 8.5586 | 18.5282 | R | 🔴 |
| *PGN0148* | *PG1833* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG2097 | | 1.84 E-1 | 113.8 | 91 | 0.3226 | 7.6781 | Y | 🟡 | 🟡 | Y | 9.6 E-2 | 7.05 E+7 | 6.24 E+7 | 0.1756 | 26.9859 | Y | 🟡 |
| *PGN0149* | *PG1834* | *prsA ribose-phosphate pyrophosphokinase* | | | | | | | | | | | | | | | |
| PG2099 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟡 | Y | 1.44 E-1 | 1.03 E+6 | 1.21 E+6 | -0.2274 | 21.0942 | Y | 🟡 |
| *PGN0150* | *PG1835* | *ATP-dependent RNA helicase DEAD/DEAH box family* | | | | | | | | | | | | | | | |
| PG2101 | | 9.37 E-6 | 36.8 | 6.5 | 2.5009 | 5.4361 | R | 🔴 | 🔴 | R | 0 | 3.48 E+7 | 6.63 E+6 | 2.3920 | 25.3042 | R | 🔴 |
| *PGN0151* | *PG1837* | *hypothetical protein PG_2101* | | | | | | | | | | | | | | | |
| PG2102 | | 6.61 E-8 | 690.5 | 923.5 | -0.4194 | 10.6564 | G | 🟢 | 🟡 | Y | 1.46 E-3 | 4.96 E+8 | 6.88 E+8 | -0.4732 | 30.1411 | G | 🟢 |
| *PGN0152* | *PG1838* | *immunoreactive 61 kDa antigen PG91* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG2105 | | 1.51 E-1 | 12.0 | 5 | 1.2605 | 4.0857 | Y 🟡 | 🔴 R | 2.03 E-9 | 8.61 E+6 | 1.9 E+6 | 2.1782 | 23.3250 | R 🔴 |
| *PGN0154* | *PG1839* | *lipoprotein putative* | | | | | | | | | | | | |
| PG2106 | | 4.62 E-1 | 292.6 | 275 | 0.0897 | 9.1488 | Y 🟡 | 🔴 R | 8 E-5 | 9.57 E+7 | 5.91 E+7 | 0.6956 | 27.2064 | R 🔴 |
| *PGN0156* | *PG1840* | *hypothetical protein PG_2106* | | | | | | | | | | | | |
| PG2107 | | 6.05 E-2 | 79.6 | 54 | 0.5594 | 7.0615 | Y 🟡 | 🟡 Y | 2.19 E-2 | 2.51 E+7 | 2 E+7 | 0.3270 | 25.4290 | Y 🟡 |
| *PGN0157* | *PG1841* | *thiH thiH protein* | | | | | | | | | | | | |
| PG2108 | | 7.02 E-1 | 43.6 | 43.5 | 0.0046 | 6.4452 | Y 🟡 | 🟡 Y | 1.08 E-2 | 2.64 E+7 | 4.66 E+7 | -0.8185 | 26.1216 | Y 🟡 |
| *PGN0158* | *PG1843* | *thiG thiG protein* | | | | | | | | | | | | |
| PG2109 | | 6.69 E-1 | 17.1 | 16 | 0.0970 | 5.0493 | Y 🟡 | 🟡 Y | 5.96 E-2 | 7.05 E+6 | 5.41 E+6 | 0.3839 | 23.5708 | Y 🟡 |
| *PGN0159* | *PG1844* | *hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase* | | | | | | | | | | | | |
| PG2110 | | 1.61 E-1 | 83.0 | 106 | -0.3529 | 7.5622 | Y 🟡 | 🟢 G | 2.88 E-9 | 3.26 E+7 | 7.66 E+7 | -1.2344 | 26.7027 | G 🟢 |
| *PGN0160* | *PG1845* | *thiC thiamine biosynthesis protein ThiC* | | | | | | | | | | | | |
| PG2112 | | 3.5 E-1 | 4.3 | 8 | -0.9030 | 3.6180 | Y 🟡 | 🟢 G | 2.81 E-4 | 3.06 E+5 | 1.46 E+6 | -2.2548 | 20.7512 | G 🟢 |
| *PGN0162* | *PG1848* | *hypothetical protein PG_2112* | | | | | | | | | | | | |
| PG2117 | | 4.89 E-2 | 36.8 | 19.5 | 0.9160 | 5.8149 | Y 🟡 | 🔴 R | 1.82 E-4 | 3.5 E+7 | 1.91 E+7 | 0.8746 | 25.6870 | R 🔴 |
| *PGN0167* | *PG1850* | *rpsP ribosomal protein S16* | | | | | | | | | | | | |
| | | 7.2 E-3 | 36.8 | 15 | 1.2945 | 5.6947 | R 🔴 | 🔴 R | 2.51 E-11 | 2.27 E+7 | 3.61 E+6 | 2.6548 | 24.6492 | R 🔴 |
| *PGN0168* | | | | | | | | | | | | | | |
| PG2120 | | 3.05 E-1 | 2.6 | 6 | -1.2249 | 3.0988 | Y 🟡 | 🟡 Y | 1.28 E-2 | 1.71 E+5 | 1.56 E+6 | -3.1873 | 20.7192 | Y 🟡 |
| *PGN0169* | *PG1853* | *metallo-beta-lactamase superfamily protein* | | | | | | | | | | | | |
| PG2121 | | 1.57 E-2 | 18.0 | 5 | 1.8455 | 4.5216 | Y 🟡 | 🔴 R | 3.67 E-15 | 8.3 E+6 | 2.8 E+6 | 1.5689 | 23.4037 | R 🔴 |
| *PGN0170* | *PG1854* | *ansA L-asparaginase* | | | | | | | | | | | | |
| PG2124 | | 9.97 E-8 | 735.0 | 971.5 | -0.4025 | 10.7368 | G 🟢 | 🟡 Y | 1.01 E-2 | 4.1 E+8 | 5.19 E+8 | -0.3387 | 29.7905 | G 🟢 |
| *PGN0173* | *PG1857* | *gapA glyceraldehyde 3-phosphate dehydrogenase type I* | | | | | | | | | | | | |
| PG2126 | | 2.52 E-1 | 5.1 | 10.5 | -1.0323 | 3.9666 | Y 🟡 | 🟡 Y | 1.9 E-1 | 1.85 E+6 | 1.81 E+6 | 0.0254 | 21.8042 | Y 🟡 |
| *PGN0175* | *PG1859* | *conserved hypothetical protein TIGR00044* | | | | | | | | | | | | |
| PG2127 | | 1.84 E-1 | 28.2 | 41.5 | -0.5555 | 6.1238 | Y 🟡 | 🟡 Y | 1.07 E-1 | 2.13 E+7 | 2.67 E+7 | -0.3246 | 25.5169 | Y 🟡 |
| *PGN0176* | *PG1860* | *hypothetical protein PG_2127* | | | | | | | | | | | | |
| PG2130 | | 0 | 2.6 | 223.5 | -6.4441 | 7.8206 | G 🟢 | 🟢 G | 3.16 E-7 | 3.94 E+5 | 1.11 E+8 | -8.1375 | 26.7318 | G 🟢 |
| *PGN0178* | *PG1863* | *hypothetical protein PG_2130* | | | | | | | | | | | | |
| PG2131 | | 3.11 E-1 | 405.6 | 373 | 0.1208 | 9.6047 | Y 🟡 | 🟡 Y | 5.87 E-2 | 4.57 E+8 | 4.04 E+8 | 0.1790 | 29.6809 | Y 🟡 |
| *PGN0179* | *PG1864* | *60 kDa protein* | | | | | | | | | | | | |
| PG2132 | | 0 | 426.1 | 1623 | -1.9293 | 11.0008 | G 🟢 | 🟢 G | 0 | 1.59 E+8 | 6.94 E+8 | -2.1299 | 29.6669 | G 🟢 |
| *PGN0180* | *PG1865* | *fimA fimbrilin* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| P13793I<br>FMA_PORGI | | 0 | 426.1 | 1623 | -1.9293 | 11.0008 | G | 🟢 | 🟢 | G | 0 | 1.59 E+8 | 6.94 E+8 | -2.1299 | 29.6669 | G | 🟢 |
| *PGN0180* | | *major fimbrillin A, Porphyromonas gingivalis 33277* | | | | | | | | | | | | | | | |
| PG2134 | | 3.03 E-3 | 9.4 | 30 | -1.6724 | 5.3006 | G | 🟢 | 🟢 | G | 4.03 E-10 | 2.83 E+6 | 1.72 E+7 | -2.6066 | 24.2566 | G | 🟢 |
| *PGN0183* | *PG1867* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG2135 | | 4.08 E-10 | 7.7 | 58.5 | -2.9253 | 6.0488 | G | 🟢 | 🟢 | G | 2.96 E-11 | 2.94 E+6 | 2.42 E+7 | -3.0426 | 24.6930 | G | 🟢 |
| *PGN0184* | *PG1868* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG2136 | | 1.74 E-6 | 19.7 | 66.5 | -1.7566 | 6.4293 | G | 🟢 | 🟢 | G | 3.72 E-14 | 8.97 E+6 | 4.11 E+7 | -2.1972 | 25.5778 | G | 🟢 |
| *PGN0185* | *PG1869* | *hypothetical protein PG_2136* | | | | | | | | | | | | | | | |
| PG2140 | | 9.44 E-2 | 6.0 | 1 | 2.5825 | 2.8052 | Y | 🟡 | 🔴 | R | 0 | 1.38 E+6 | 1 E+3 | 10.4275 | 20.3943 | R | 🔴 |
| *PGN0188* | | *rpmF ribosomal protein L32* | | | | | | | | | | | | | | | |
| PG2141 | | 1.97 E-1 | 73.6 | 56 | 0.3940 | 7.0178 | Y | 🟡 | 🟡 | Y | 3.91 E-2 | 4.4 E+7 | 3.4 E+7 | 0.3690 | 26.2168 | Y | 🟡 |
| *PGN0189* | *PG1872* | *fabH 3-oxoacyl-(acyl-carrier-protein) synthase III* | | | | | | | | | | | | | | | |
| PG2142 | | 3.85 E-1 | 5.1 | 2.5 | 1.0381 | 2.9324 | Y | 🟡 | 🟡 | Y | 2.94 E-2 | 3.48 E+6 | 1.76 E+6 | 0.9840 | 22.3192 | Y | 🟡 |
| *PGN0190* | *PG1873* | *era GTP-binding protein Era* | | | | | | | | | | | | | | | |
| PG2143 | | 3.08 E-4 | 26.5 | 5 | 2.4074 | 4.9784 | R | 🔴 | 🟡 | Y | 6.55 E-3 | 4.83 E+6 | 2.41 E+6 | 1.0059 | 22.7871 | R | 🔴 |
| *PGN0191* | *PG1874* | *GTP-binding protein Era/ThdF family* | | | | | | | | | | | | | | | |
| PG2144 | | 6.9 E-1 | 32.5 | 32 | 0.0230 | 6.0116 | Y | 🟡 | 🟡 | Y | 1.61 E-1 | 1.6 E+7 | 1.52 E+7 | 0.0706 | 24.8927 | Y | 🟡 |
| *PGN0192* | *PG1875* | *hypothetical protein PG_2144* | | | | | | | | | | | | | | | |
| PG2145 | | 6.92 E-2 | 4.3 | 13 | -1.6034 | 4.1109 | Y | 🟡 | 🟢 | G | 9.37 E-4 | 9.14 E+5 | 1.93 E+6 | -1.0774 | 21.4384 | G | 🟢 |
| *PGN0193* | *PG1876* | *polysaccharide deacetylase* | | | | | | | | | | | | | | | |
| PG2147 | | 4.75 E-1 | 11.1 | 8 | 0.4755 | 4.2573 | Y | 🟡 | 🟡 | Y | 3.35 E-2 | 2.31 E+6 | 1.65 E+6 | 0.4832 | 21.9164 | Y | 🟡 |
| *PGN0195* | *PG1878* | *xpt xanthine phosphoribosyltransferase* | | | | | | | | | | | | | | | |
| PG2150 | | 5.52 E-3 | 16.3 | 3 | 2.4381 | 4.2673 | R | 🔴 | 🔴 | R | 0 | 5.39 E+6 | 1.26 E+6 | 2.1004 | 22.6634 | R | 🔴 |
| *PGN0198* | *PG1881* | *LysM domain protein* | | | | | | | | | | | | | | | |
| PG2155 | | 2.96 E-2 | 23.1 | 9 | 1.3601 | 5.0046 | Y | 🟡 | 🔴 | R | 1.14 E-6 | 3.14 E+7 | 1.06 E+7 | 1.5628 | 25.3260 | R | 🔴 |
| *PGN0200* | *PG1883* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG2156 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 7.56 E+4 | -5.3524 | 16.2410 | Y | 🟡 |
| *PGN0201* | *PG1884* | *conserved hypothetical protein TIGR00046* | | | | | | | | | | | | | | | |
| PG2157 | | 6.87 E-1 | 29.9 | 30.5 | -0.0264 | 5.9176 | Y | 🟡 | 🟡 | Y | 1.53 E-2 | 1.43 E+7 | 2.01 E+7 | -0.4959 | 25.0344 | Y | 🟡 |
| *PGN0202* | *PG1885* | *glutamine cyclotransferase-related protein* | | | | | | | | | | | | | | | |
| PG2158 | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y | 🟡 | 🔴 | R | 0 | 1.75 E+6 | 1 E+3 | 10.7730 | 20.7396 | R | 🔴 |
| *PGN0203* | *PG1886* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG2159 | | 6.94 E-1 | 7.7 | 7.5 | 0.0381 | 3.9261 | Y | 🟡 | 🟡 | Y | 9.92 E-2 | 1.69 E+6 | 1.38 E+6 | 0.2886 | 21.5495 | Y | 🟡 |
| *PGN0204* | *PG1887* | *protoporphyrinogen oxidase* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG2162 | | 6.54 E-1 | 2.6 | 2 | 0.3601 | 2.1912 | Y | 🟡 | 🔴 | R | 1.52 E-5 | 1.26 E+6 | 3.44 E+5 | 1.8728 | 20.6151 | R | 🔴 |
| *PGN0206* | *PG1889* | *lpxB lipid A disaccharide synthase* | | | | | | | | | | | | | | | |
| PG2163 | | 3.76 E-1 | 15.4 | 21.5 | -0.4812 | 5.2056 | Y | 🟡 | 🟢 | G | 8.02 E-8 | 4.76 E+6 | 1.14 E+7 | -1.2631 | 23.9486 | G | 🟢 |
| *PGN0207* | *PG1890* | *surE stationary-phase survival protein SurE* | | | | | | | | | | | | | | | |
| PG2164 | | 1.02 E-1 | 14.5 | 27 | -0.8923 | 5.3766 | Y | 🟡 | 🟢 | G | 7.53 E-4 | 8.37 E+6 | 1.74 E+7 | -1.0569 | 24.6204 | G | 🟢 |
| *PGN0208* | *PG1891* | *peptidyl-prolyl cis-trans isomerase FKBP-type* | | | | | | | | | | | | | | | |
| PG2165 | | 5.3 E-8 | 47.9 | 7 | 2.7751 | 5.7792 | R | 🔴 | 🔴 | R | 0 | 3.13 E+7 | 4 E+6 | 2.9676 | 25.0739 | R | 🔴 |
| *PGN0209* | *PG1892* | *glyS glycyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG2078 | | 2.74 E-1 | 1.7 | 5 | -1.5468 | 2.7466 | Y | 🟡 | 🟡 | Y | 2.08 E-3 | 2.83 E+5 | 7.07 E+5 | -1.3197 | 19.9167 | Y | 🟡 |
| *PGN0211* | *PG1816* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0104 | | 1.5 E-1 | 1.7 | 6.5 | -1.9253 | 3.0376 | Y | 🟡 | 🟡 | Y | 4.34 E-2 | 7.39 E+5 | 1.87 E+6 | -1.3425 | 21.3172 | Y | 🟡 |
| *PGN0221* | *PG0091* | *topB-1 DNA topoisomerase III* | | | | | | | | | | | | | | | |
| PG0108 | | 5.74 E-1 | 18.8 | 16 | 0.2345 | 5.1220 | Y | 🟡 | 🟡 | Y | 1.69 E-2 | 6.76 E+6 | 4.66 E+6 | 0.5372 | 23.4453 | Y | 🟡 |
| *PGN0224* | *PG0094* | *epsD UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase* | | | | | | | | | | | | | | | |
| PG0111 | | 6.41 E-1 | 6.0 | 5 | 0.2605 | 3.4581 | Y | 🟡 | 🔴 | R | 1.65 E-8 | 1.34 E+6 | 5.62 E+5 | 1.2493 | 20.8552 | R | 🔴 |
| *PGN0228* | *PG0097* | *capsular polysacharride biosynthesis gene putative* | | | | | | | | | | | | | | | |
| | | 6.85 E-1 | 29.1 | 28.5 | 0.0297 | 5.8478 | Y | 🟡 | 🔴 | R | 3.31 E-10 | 1.7 E+7 | 4.65 E+6 | 1.8679 | 24.3666 | R | 🔴 |
| *PGN0229* | | | | | | | | | | | | | | | | | |
| PG0118 | | 6.69 E-1 | 12.0 | 11 | 0.1230 | 4.5223 | Y | 🟡 | 🟢 | G | 5.59 E-4 | 1.53 E+6 | 3.85 E+6 | -1.3282 | 22.3603 | Y | 🟡 |
| *PGN0232* | *PG0103* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | | | | |
| PG0119 | | 2.55 E-1 | 7.7 | 14 | -0.8623 | 4.4397 | Y | 🟡 | 🟡 | Y | 3.45 E-3 | 2.81 E+6 | 5.6 E+6 | -0.9958 | 23.0022 | Y | 🟡 |
| *PGN0233* | *PG0104* | *glycosyl transferase WecB/TagA/CpsF family* | | | | | | | | | | | | | | | |
| PG0120 | | 3.31 E-1 | 20.5 | 14 | 0.5527 | 5.1100 | Y | 🟡 | 🔴 | R | 5.19 E-8 | 9.81 E+6 | 3.73 E+6 | 1.3954 | 23.6910 | R | 🔴 |
| *PGN0234* | *PG0105* | *epsC UDP-N-acetylglucosamine 2-epimerase* | | | | | | | | | | | | | | | |
| PG0121 | | 0 | 371.4 | 69 | 2.4281 | 8.7825 | R | 🔴 | 🔴 | R | 4.01 E-7 | 3.09 E+8 | 1.43 E+8 | 1.1141 | 28.7494 | R | 🔴 |
| *PGN0235* | *PG0106* | *hup-1 DNA-binding protein HU* | | | | | | | | | | | | | | | |
| PG0123 | | 3.21 E-1 | 1.7 | 4.5 | -1.3948 | 2.6349 | Y | 🟡 | 🟡 | Y | 1.72 E-3 | 1.85 E+3 | 1.06 E+6 | -9.1672 | 20.0234 | Y | 🟡 |
| *PGN0236* | *PG0107* | *hypothetical protein PG_0123* | | | | | | | | | | | | | | | |
| PG0125 | | 4.15 E-1 | 2.6 | 5 | -0.9619 | 2.9197 | Y | 🟡 | 🟡 | Y | 3.52 E-3 | 9.2 E+4 | 9.17 E+5 | -3.3170 | 19.9443 | Y | 🟡 |
| *PGN0238* | *PG0109* | *hypothetical protein PG_0125* | | | | | | | | | | | | | | | |
| PG0126 | | 6.55 E-1 | 5.1 | 6 | -0.2249 | 3.4769 | Y | 🟡 | 🟡 | Y | 1.59 E-3 | 1.91 E+6 | 3.46 E+6 | -0.8544 | 22.3560 | Y | 🟡 |
| *PGN0239* | *PG0110* | *type I phosphodiesterase/nucleotide pyrophosphatase family protein* | | | | | | | | | | | | | | | |
| PG0127 | | 6.97 E-1 | 2.6 | 2.5 | 0.0381 | 2.3411 | Y | 🟡 | 🔴 | R | 0 | 2.16 E+6 | 1.7 E+5 | 3.6719 | 21.1547 | R | 🔴 |
| *PGN0240* | *PG0112* | *hemH ferrochelatase* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0128 | | 6.97 E-1 | 2.6 | 2.5 | 0.0381 | 2.3411 | Y | 🟡 | 🔴 | R | 0 | 4.82 E+5 | 1.13 E+5 | 2.0969 | 19.1831 | R | 🔴 |
| *PGN0241* | *PG0113* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG0129 | | 6.69 E-1 | 9.4 | 10 | -0.0874 | 4.2789 | Y | 🟡 | 🟡 | Y | 1.77 E-1 | 2.35 E+6 | 2.2 E+6 | 0.0972 | 22.1155 | Y | 🟡 |
| *PGN0242* | *PG0114* | *mannosyltransferase* | | | | | | | | | | | | | | | |
| PG0130 | | 6.37 E-1 | 157.4 | 152 | 0.0507 | 8.2735 | Y | 🟡 | 🟡 | Y | 1.88 E-1 | 1.43 E+8 | 1.45 E+8 | -0.0238 | 28.0990 | Y | 🟡 |
| *PGN0243* | *PG0115* | *gpm phosphoglycerate mutase* | | | | | | | | | | | | | | | |
| PG0133 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 7.82 E+4 | -5.4011 | 16.2886 | Y | 🟡 |
| *PGN0246* | *PG0118* | *hypothetical protein PG_0133* | | | | | | | | | | | | | | | |
| PG0134 | | 5.17 E-1 | 3.4 | 2 | 0.7751 | 2.4390 | Y | 🟡 | 🟡 | Y | 3.88 E-2 | 9.02 E+5 | 5.33 E+5 | 0.7591 | 20.4530 | Y | 🟡 |
| *PGN0247* | *PG0119* | *mgtE magnesium transporter* | | | | | | | | | | | | | | | |
| PG0136 | | 4.02 E-1 | 4.3 | 2 | 1.0970 | 2.6504 | Y | 🟡 | 🔴 | R | 0 | 1.36 E+6 | 5.22 E+5 | 1.3862 | 20.8468 | R | 🔴 |
| *PGN0249* | *PG0122* | *hypothetical protein PG_0136* | | | | | | | | | | | | | | | |
| PG0137 | | 2.93 E-3 | 124.1 | 183 | -0.5607 | 8.2624 | G | 🟢 | 🟢 | G | 3.51 E-5 | 5.84 E+7 | 1.11 E+8 | -0.9201 | 27.3323 | G | 🟢 |
| *PGN0250* | *PG0123* | *pepD-1 aminoacyl-histidine dipeptidase* | | | | | | | | | | | | | | | |
| PG0138 | | 9.03 E-2 | 82.1 | 110 | -0.4213 | 7.5860 | Y | 🟡 | 🟡 | Y | 2.47 E-3 | 1.12 E+8 | 1.86 E+8 | -0.7243 | 28.1501 | Y | 🟡 |
| *PGN0251* | *PG0124* | *fabD malonyl CoA-acyl carrier protein transacylase* | | | | | | | | | | | | | | | |
| PG0139 | | 6.78 E-1 | 6.8 | 6.5 | 0.0747 | 3.7383 | Y | 🟡 | 🟡 | Y | 4.5 E-2 | 2.16 E+6 | 1.12 E+6 | 0.9507 | 21.6419 | Y | 🟡 |
| *PGN0252* | *PG0125* | *membrane-bound lytic murein transglycosylase D putative* | | | | | | | | | | | | | | | |
| PG0140 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 8.51 E+5 | -8.8458 | 19.7027 | G | 🟢 |
| *PGN0253* | *PG0127* | *hypothetical protein PG_0140* | | | | | | | | | | | | | | | |
| PG0141 | | 6.83 E-1 | 20.5 | 20 | 0.0381 | 5.3411 | Y | 🟡 | 🟡 | Y | 3.72 E-2 | 9.14 E+6 | 1.19 E+7 | -0.3821 | 24.3281 | Y | 🟡 |
| *PGN0254* | *PG0128* | *spo0J spoOJ protein* | | | | | | | | | | | | | | | |
| PG0142 | | 1.86 E-1 | 5.1 | 11.5 | -1.1635 | 4.0561 | Y | 🟡 | 🟡 | Y | 1.32 E-1 | 6.95 E+6 | 5.54 E+6 | 0.3278 | 23.5737 | Y | 🟡 |
| *PGN0255* | *PG0129* | *soj SpoOJ regulator protein* | | | | | | | | | | | | | | | |
| PG0143 | | 2.08 E-2 | 11.1 | 27.5 | -1.3058 | 5.2714 | Y | 🟡 | 🟡 | Y | 9.12 E-3 | 3.17 E+6 | 5.41 E+6 | -0.7727 | 23.0327 | Y | 🟡 |
| *PGN0256* | *PG0130* | *hydrolase carbon-nitrogen family* | | | | | | | | | | | | | | | |
| PG0144 | | 6.92 E-2 | 14.5 | 28.5 | -0.9703 | 5.4278 | Y | 🟡 | 🟡 | Y | 3.17 E-3 | 6.22 E+6 | 1.29 E+7 | -1.0533 | 24.1889 | Y | 🟡 |
| *PGN0257* | *PG0131* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| | | 6.61 E-1 | 11.1 | 10 | 0.1536 | 4.4008 | Y | 🟡 | 🟡 | Y | 1.05 E-1 | 7.21 E+6 | 5.72 E+6 | 0.3340 | 23.6245 | Y | 🟡 |
| *PGN0258* | | | | | | | | | | | | | | | | | |
| PG0146 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 4.41 E+5 | -7.8960 | 18.7558 | Y | 🟡 |
| *PGN0259* | *PG0134* | *hypothetical protein PG_0146* | | | | | | | | | | | | | | | |
| PG0148 | | 1.45 E-1 | 5.1 | 1 | 2.3601 | 2.6168 | Y | 🟡 | 🔴 | R | 0 | 1.23 E+6 | 1 E+3 | 10.2697 | 20.2367 | R | 🔴 |
| *PGN0261* | *PG0136* | *sigma-54-dependent transcriptional regulator* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0149 | | 6.69 E-1 | 2.6 | 3 | -0.2249 | 2.4769 | Y | 🟡 | 🟡 | Y | 9.69 E-2 | 7.01 E+5 | 9.12 E+5 | -0.3794 | 20.6209 | Y | 🟡 |
| *PGN0262* | *PG0137* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG0150 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.14 E+7 | -12.5834 | 23.4373 | G | 🟢 |
| *PGN0263* | *PG0138* | *conserved hypothetical protein TIGR01125* | | | | | | | | | | | | | | | |
| PG0151 | | 1.45 E-1 | 5.1 | 1 | 2.3601 | 2.6168 | Y | 🟡 | 🔴 | R | 6.34 E-7 | 1.45 E+6 | 1 E+3 | 10.5009 | 20.4677 | R | 🔴 |
| *PGN0264* | *PG0139* | *ftsY signal recognition particle-docking protein FtsY* | | | | | | | | | | | | | | | |
| PG0152 | | 5.47 E-3 | 9.4 | 28.5 | -1.5984 | 5.2446 | G | 🟢 | 🟡 | Y | 5.67 E-2 | 2.78 E+6 | 3.55 E+6 | -0.3542 | 22.5936 | G | 🟢 |
| *PGN0265* | *PG0140* | *nspC carboxynorspermidine decarboxylase* | | | | | | | | | | | | | | | |
| PG0153 | | 2.71 E-1 | 101.8 | 121.5 | -0.2549 | 7.8030 | Y | 🟡 | 🟢 | G | 2.14 E-5 | 5.23 E+7 | 8.04 E+7 | -0.6199 | 26.9837 | G | 🟢 |
| *PGN0266* | *PG0141* | *aspS aspartyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG0156 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟡 | Y | 7.27 E-3 | 1.85 E+3 | 6.07 E+5 | -8.3570 | 19.2151 | Y | 🟡 |
| *PGN0268* | *PG0143* | *modification methylase HemK family* | | | | | | | | | | | | | | | |
| PG0159 | | 4.61 E-3 | 516.0 | 625 | -0.2766 | 10.1560 | G | 🟢 | 🟡 | Y | 7.25 E-2 | 4.46 E+8 | 4.94 E+8 | -0.1463 | 29.8075 | G | 🟢 |
| *PGN0271* | *PG0146* | *pepO endopeptidase PepO* | | | | | | | | | | | | | | | |
| PG0160 | | 5.8 E-1 | 78.7 | 73 | 0.1088 | 7.2453 | Y | 🟡 | 🟡 | Y | 1.27 E-1 | 5.52 E+7 | 6.05 E+7 | -0.1319 | 26.7867 | Y | 🟡 |
| *PGN0272* | *PG0147* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG0163 | | 6.61 E-1 | 9.4 | 10.5 | -0.1578 | 4.3156 | Y | 🟡 | 🟡 | Y | 7.32 E-2 | 3.75 E+6 | 2.71 E+6 | 0.4653 | 22.6228 | Y | 🟡 |
| *PGN0275* | *PG0150* | *pfk phosphofructokinase* | | | | | | | | | | | | | | | |
| PG0166 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 4.07 E+5 | -7.7796 | 18.6398 | G | 🟢 |
| *PGN0278* | *PG0153* | *pth peptidyl-tRNA hydrolase* | | | | | | | | | | | | | | | |
| PG0167 | | 6.58 E-12 | 127.5 | 37 | 1.7848 | 7.3619 | R | 🔴 | 🔴 | R | 0 | 1.4 E+8 | 3.03 E+7 | 2.2031 | 27.3407 | R | 🔴 |
| *PGN0279* | *PG0154* | *rplY ribosomal protein L25* | | | | | | | | | | | | | | | |
| PG0170 | | 7.02 E-1 | 131.8 | 131.5 | 0.0030 | 8.0404 | Y | 🟡 | 🟡 | Y | 8.97 E-2 | 7.56 E+7 | 6.81 E+7 | 0.1509 | 27.0986 | Y | 🟡 |
| *PGN0281* | *PG0156* | *metG methionyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG0171 | | 1.77 E-1 | 13.7 | 23.5 | -0.7795 | 5.2169 | Y | 🟡 | 🟡 | Y | 1.4 E-1 | 7.5 E+6 | 8.41 E+6 | -0.1643 | 23.9237 | Y | 🟡 |
| *PGN0282* | *PG0157* | *5'-nucleotidase family protein* | | | | | | | | | | | | | | | |
| PG0172 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.78 E+5 | -6.5842 | 17.4529 | Y | 🟡 |
| *PGN0283* | *PG0158* | *exonuclease* | | | | | | | | | | | | | | | |
| | | 1.56 E-1 | 6.0 | 1.5 | 1.9975 | 2.9049 | Y | 🟡 | 🔴 | R | 0 | 2.02 E+6 | 3.35 E+5 | 2.5881 | 21.1659 | R | 🔴 |
| *PGN0285* | | | | | | | | | | | | | | | | | |
| PG0178 | | 0 | 2104.9 | 3146.5 | -0.5800 | 12.3585 | G | 🟢 | 🟢 | G | 6.61 E-4 | 1.15 E+9 | 1.71 E+9 | -0.5709 | 31.4148 | G | 🟢 |
| *PGN0287* | *PG0163* | | | | | | | | | | | | | | | | |
| PG0179 | | 1.53 E-2 | 162.6 | 217 | -0.4166 | 8.5682 | Y | 🟡 | 🟡 | Y | 1.07 E-2 | 1.06 E+8 | 1.65 E+8 | -0.6375 | 28.0162 | Y | 🟡 |
| *PGN0288* | *PG0164* | *hypothetical protein PG_0179* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0180 | | 5.47 E-12 | 14.5 | 83 | -2.5125 | 6.6080 | G | 🟢 | 🟢 | G | 5.28 E-12 | 7.96 E+6 | 3.12 E+7 | -1.9707 | 25.2234 | G | 🟢 |
| *PGN0289* | *PG0165* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG0181 | | 3.03 E-2 | 76.2 | 110.5 | -0.5371 | 7.5442 | Y | 🟡 | 🟡 | Y | 1.09 E-3 | 5.14 E+7 | 1.21 E+8 | -1.2347 | 27.3603 | Y | 🟡 |
| *PGN0290* | *PG0166* | *immunoreactive 32 kDa antigen PG49* | | | | | | | | | | | | | | | |
| PG0182 | | 2.44 E-8 | 109.5 | 216.5 | -0.9831 | 8.3488 | G | 🟢 | 🟢 | G | 1.65 E-9 | 7.77 E+7 | 1.44 E+8 | -0.8873 | 27.7226 | G | 🟢 |
| *PGN0291* | *PG0167* | *von Willebrand factor type A domain protein* | | | | | | | | | | | | | | | |
| | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 2.27 E+6 | 1 E+3 | 11.1476 | 21.1141 | R | 🔴 |
| *PGN0292* | | | | | | | | | | | | | | | | | |
| PG0185 | | 1.07 E-7 | 3902.6 | 3413.5 | 0.1932 | 12.8369 | R | 🔴 | 🟢 | G | 4.08 E-6 | 3.63 E+9 | 5.1 E+9 | -0.4891 | 33.0235 | Y | 🟡 |
| *PGN0293* | *PG0170* | *ragA ragA protein* | | | | | | | | | | | | | | | |
| PG0186 | | 3.06 E-2 | 1035.3 | 1153 | -0.1553 | 11.0956 | Y | 🟡 | 🟢 | G | 3.25 E-4 | 1.74 E+9 | 2.35 E+9 | -0.4334 | 31.9293 | G | 🟢 |
| *PGN0294* | *PG0171* | *ragB lipoprotein RagB* | | | | | | | | | | | | | | | |
| | | 4.75 E-1 | 72.7 | 81.5 | -0.1642 | 7.2689 | Y | 🟡 | 🟡 | Y | 3.11 E-2 | 2.68 E+8 | 4.13 E+8 | -0.6211 | 29.3435 | Y | 🟡 |
| *PGN0295* | | | | | | | | | | | | | | | | | |
| PG0188 | | 6.9 E-1 | 26.5 | 27 | -0.0256 | 5.7421 | Y | 🟡 | 🟡 | Y | 4.87 E-2 | 1.34 E+7 | 1.02 E+7 | 0.3890 | 24.4898 | Y | 🟡 |
| *PGN0296* | *PG0172* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG0189 | | 4.82 E-2 | 1.7 | 9 | -2.3948 | 3.4211 | Y | 🟡 | 🟢 | G | 1.56 E-7 | 1.85 E+3 | 2.38 E+6 | -10.3303 | 21.1851 | G | 🟢 |
| *PGN0297* | *PG0173* | *hypothetical protein PG_0189* | | | | | | | | | | | | | | | |
| PG0190 | | 2.52 E-1 | 3.4 | 8 | -1.2249 | 3.5138 | Y | 🟡 | 🟡 | Y | 1.63 E-2 | 9.27 E+5 | 2.78 E+6 | -1.5864 | 21.8238 | Y | 🟡 |
| *PGN0298* | *PG0174* | *uppS undecaprenyl diphosphate synthase* | | | | | | | | | | | | | | | |
| PG0191 | | 3.05 E-1 | 47.1 | 59.5 | -0.3384 | 6.7355 | Y | 🟡 | 🟡 | Y | 8.65 E-2 | 2.92 E+7 | 2.61 E+7 | 0.1625 | 25.7208 | Y | 🟡 |
| *PGN0299* | *PG0175* | *outer membrane protein putative* | | | | | | | | | | | | | | | |
| PG0192 | | 2.83 E-3 | 161.7 | 106.5 | 0.6026 | 8.0673 | R | 🔴 | 🟡 | Y | 1.42 E-2 | 9.62 E+7 | 5.88 E+7 | 0.7106 | 27.2082 | R | 🔴 |
| *PGN0300* | *PG0176* | *ompH-1 cationic outer membrane protein OmpH* | | | | | | | | | | | | | | | |
| PG0193 | | 8.96 E-2 | 103.5 | 76.5 | 0.4366 | 7.4921 | Y | 🟡 | 🟡 | Y | 1.96 E-1 | 1.09 E+8 | 1.1 E+8 | -0.0138 | 27.7060 | Y | 🟡 |
| *PGN0301* | *PG0177* | *ompH-2 cationic outer membrane protein OmpH* | | | | | | | | | | | | | | | |
| PG0195 | | 3.22 E-6 | 101.0 | 186 | -0.8814 | 8.1647 | G | 🟢 | 🟡 | Y | 4.8 E-3 | 4.49 E+7 | 9.18 E+7 | -1.0300 | 27.0264 | G | 🟢 |
| *PGN0302* | *PG0179* | *rubrerythrin* | | | | | | | | | | | | | | | |
| PG0196 | | 1.57 E-1 | 366.2 | 413.5 | -0.1752 | 9.6068 | Y | 🟡 | 🟡 | Y | 1.04 E-1 | 2.98 E+8 | 3.21 E+8 | -0.1058 | 29.2068 | Y | 🟡 |
| *PGN0303* | *PG0180* | *peptidase M16 family* | | | | | | | | | | | | | | | |
| PG0198 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.04 E+6 | -9.1314 | 19.9877 | G | 🟢 |
| *PGN0306* | *PG0182* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0199 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 7.23 E+5 | -8.6107 | 19.4681 | G | 🟢 |
| *PGN0307* | *PG0183* | *TatD family protein* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG0201 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 4.31 E-7 | 1.85 E+3 | 1.84 E+5 | -6.6391 | 17.5073 | G | 🟢 |
| *PGN0309* | *PG0184* | *rnpA ribonuclease P protein component* | | | | | | | | | | | | | | | |
| PG0202 | | 4.23 E-1 | 6.8 | 4 | 0.7751 | 3.4390 | Y | 🟡 | 🔴 | R | 2.81 E-5 | 4.21 E+6 | 8.42 E+5 | 2.3210 | 22.2675 | R | 🔴 |
| *PGN0310* | *PG0185* | *uroporphyrinogen-III synthase HemD putative* | | | | | | | | | | | | | | | |
| PG0205 | | 1.4 E-1 | 14.5 | 6.5 | 1.1621 | 4.3955 | Y | 🟡 | 🟡 | Y | 2.31 E-2 | 5.01 E+6 | 3.35 E+6 | 0.5805 | 22.9964 | Y | 🟡 |
| *PGN0313* | *PG0188* | *prfC peptide chain release factor 3* | | | | | | | | | | | | | | | |
| PG0209 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 6.68 E-8 | 1.85 E+3 | 2.05 E+5 | -6.7916 | 17.6583 | G | 🟢 |
| *PGN0314* | *PG0189* | *formate/nitrite transporter* | | | | | | | | | | | | | | | |
| PG0210 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 1.74 E+5 | 1 E+3 | 7.4469 | 17.4210 | R | 🔴 |
| *PGN0315* | *PG0190* | *precorrin-6x reductase/cobalamin biosynthetic protein CbiD* | | | | | | | | | | | | | | | |
| PG0211 | | 6 E-1 | 5.1 | 6.5 | -0.3404 | 3.5403 | Y | 🟡 | 🟡 | Y | 3.93 E-2 | 2.72 E+6 | 1.94 E+6 | 0.4867 | 22.1539 | Y | 🟡 |
| *PGN0316* | *PG0191* | *cbiGF cobalamin biosynthesis protein CbiG/precorrin-4 C11-methyltransferase* | | | | | | | | | | | | | | | |
| PG0213 | | 2.25 E-1 | 6.8 | 2.5 | 1.4532 | 3.2242 | Y | 🟡 | 🟡 | Y | 2.41 E-2 | 1.29 E+6 | 5.9 E+5 | 1.1326 | 20.8440 | Y | 🟡 |
| *PGN0318* | *PG0193* | *precorrin-3 methylase/precorrin-8X methylmutase* | | | | | | | | | | | | | | | |
| PG0217 | | 1.12 E-2 | 10.3 | 28 | -1.4473 | 5.2581 | Y | 🟡 | 🟢 | G | 1.9 E-4 | 4.36 E+6 | 1.24 E+7 | -1.5057 | 23.9962 | G | 🟢 |
| *PGN0322* | *PG0197* | *hypothetical protein PG_0217* | | | | | | | | | | | | | | | |
| PG0218 | | 4.89 E-1 | 5.1 | 7.5 | -0.5468 | 3.6592 | Y | 🟡 | 🟡 | Y | 1.53 E-2 | 1.13 E+6 | 2.64 E+6 | -1.2264 | 21.8435 | Y | 🟡 |
| *PGN0323* | *PG0198* | *hypothetical protein PG_0218* | | | | | | | | | | | | | | | |
| | | 5.74 E-1 | 4.3 | 3 | 0.5121 | 2.8636 | Y | 🟡 | 🟡 | Y | 6.07 E-3 | 1.12 E+7 | 1.67 E+6 | 2.7523 | 23.6223 | Y | 🟡 |
| *PGN0326* | | | | | | | | | | | | | | | | | |
| PG0226 | | 6.69 E-1 | 142.0 | 144.5 | -0.0248 | 8.1626 | Y | 🟡 | 🟡 | Y | 5.98 E-2 | 7.61 E+7 | 8.39 E+7 | -0.1408 | 27.2531 | Y | 🟡 |
| *PGN0329* | *PG0206* | *transglutaminase-related protein* | | | | | | | | | | | | | | | |
| PG0227 | | 3.21 E-1 | 1.7 | 4.5 | -1.3948 | 2.6349 | Y | 🟡 | 🟡 | Y | 1.99 E-3 | 1.85 E+3 | 6.91 E+5 | -8.5448 | 19.4023 | Y | 🟡 |
| *PGN0330* | *PG0207* | *radA DNA repair protein RadA* | | | | | | | | | | | | | | | |
| PG0228 | | 6.15 E-1 | 14.5 | 16.5 | -0.1818 | 4.9563 | Y | 🟡 | 🟡 | Y | 1.75 E-1 | 8.69 E+6 | 8.38 E+6 | 0.0528 | 24.0247 | Y | 🟡 |
| *PGN0331* | *PG0208* | *DdaH family protein* | | | | | | | | | | | | | | | |
| PG0230 | | 1.17 E-1 | 96.7 | 124.5 | -0.3647 | 7.7891 | Y | 🟡 | 🟡 | Y | 6.61 E-3 | 9.04 E+7 | 1.45 E+8 | -0.6782 | 27.8085 | Y | 🟡 |
| *PGN0333* | *PG0209* | *transaldolase TalC putative* | | | | | | | | | | | | | | | |
| PG0231 | | 6.69 E-1 | 3.4 | 4 | -0.2249 | 2.8919 | Y | 🟡 | 🔴 | R | 1.15 E-7 | 4.35 E+5 | 2.5 E+5 | 0.7977 | 19.3876 | Y | 🟡 |
| *PGN0334* | *PG0211* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0232 | | 5.87 E-2 | 201.1 | 248.5 | -0.3055 | 8.8124 | Y | 🟡 | 🟡 | Y | 3.28 E-2 | 1.95 E+8 | 2.38 E+8 | -0.2843 | 28.6904 | Y | 🟡 |
| *PGN0335* | *PG0212* | *zinc carboxypeptidase putative* | | | | | | | | | | | | | | | |
| | | 1.32 E-2 | 2.6 | 13.5 | -2.3948 | 4.0060 | Y | 🟡 | 🟢 | G | 2.76 E-5 | 5.68 E+5 | 2.2 E+6 | -1.9553 | 21.4030 | G | 🟢 |
| *PGN0336* | | | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG0236 | | 1.12 E-1 | 7.7 | 17 | -1.1424 | 4.6265 | Y | 🟡 | 🟢 | G | 4.24 E-4 | 6.32 E+6 | 1.12 E+7 | -0.8310 | 24.0667 | G | 🟢 |
| *PGN0341* | *PG0215* | *hypothetical protein PG_0236* | | | | | | | | | | | | | | | |
| PG0237 | | 3.33 E-1 | 11.1 | 17 | -0.6119 | 4.8137 | Y | 🟡 | 🟡 | Y | 8.91 E-3 | 2.55 E+6 | 1.82 E+6 | 0.4850 | 22.0614 | Y | 🟡 |
| *PGN0342* | *PG0216* | *ung uracil-DNA glycosylase* | | | | | | | | | | | | | | | |
| PG0240 | | 2.25 E-1 | 1.7 | 5.5 | -1.6843 | 2.8503 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 6.14 E+5 | -8.3753 | 19.2333 | G | 🟢 |
| *PGN0344* | *PG0218* | *hydrolase haloacid dehalogenase-like family* | | | | | | | | | | | | | | | |
| PG0241 | | 3.49 E-2 | 90.7 | 60.5 | 0.5842 | 7.2403 | Y | 🟡 | 🔴 | R | 6.52 E-11 | 1.1 E+8 | 3.93 E+7 | 1.4841 | 27.1535 | R | 🔴 |
| *PGN0345* | *PG0219* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG0242 | | 6.68 E-1 | 20.5 | 22 | -0.0994 | 5.4106 | Y | 🟡 | 🟡 | Y | 6.45 E-2 | 4.97 E+6 | 3.84 E+6 | 0.3718 | 23.0708 | Y | 🟡 |
| *PGN0346* | *PG0220* | *conserved hypothetical protein TIGR00096* | | | | | | | | | | | | | | | |
| PG0243 | | 5.89 E-1 | 7.7 | 9.5 | -0.3029 | 4.1044 | Y | 🟡 | 🟡 | Y | 8.23 E-2 | 3.61 E+6 | 4.7 E+6 | -0.3820 | 22.9855 | Y | 🟡 |
| *PGN0347* | *PG0221* | *hypothetical protein PG_0243* | | | | | | | | | | | | | | | |
| PG0245 | | 0 | 94.1 | 9.5 | 3.3085 | 6.6952 | R | 🔴 | 🔴 | R | 0 | 5.73 E+7 | 3.68 E+6 | 3.9599 | 25.8619 | R | 🔴 |
| *PGN0348* | *PG0222* | *universal stress protein family* | | | | | | | | | | | | | | | |
| PG0246 | | 0 | 220.8 | 27.5 | 3.0050 | 7.9557 | R | 🔴 | 🟡 | Y | 2.85 E-2 | 7.62 E+7 | 5.4 E+7 | 0.4976 | 26.9555 | R | 🔴 |
| *PGN0349* | *PG0223* | *hypothetical protein PG_0246* | | | | | | | | | | | | | | | |
| PG0249 | | 3.12 E-4 | 186.5 | 117 | 0.6729 | 8.2457 | R | 🔴 | 🔴 | R | 8.92 E-4 | 1.38 E+8 | 1.04 E+8 | 0.4168 | 27.8516 | R | 🔴 |
| *PGN0351* | *PG0226* | *oxaloacetate decarboxylase putative* | | | | | | | | | | | | | | | |
| PG0253 | | 6.05 E-2 | 6.8 | 1 | 2.7751 | 2.9718 | Y | 🟡 | 🔴 | R | 0 | 9.37 E+5 | 1 E+3 | 9.8718 | 19.8391 | R | 🔴 |
| *PGN0353* | *PG0228* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0254 | | 3.2 E-6 | 120.6 | 54.5 | 1.1465 | 7.4524 | R | 🔴 | 🔴 | R | 2.97 E-12 | 5.67 E+7 | 2.71 E+7 | 1.0678 | 26.3198 | R | 🔴 |
| *PGN0354* | *PG0229* | *N utilization substance protein A putative* | | | | | | | | | | | | | | | |
| PG0255 | | 1.57 E-5 | 71.0 | 25.5 | 1.4777 | 6.5927 | R | 🔴 | 🔴 | R | 1.14 E-12 | 3.93 E+7 | 1.39 E+7 | 1.4944 | 25.6648 | R | 🔴 |
| *PGN0355* | *PG0230* | *infB translation initiation factor IF-2* | | | | | | | | | | | | | | | |
| PG0257 | | 6.61 E-1 | 9.4 | 10.5 | -0.1578 | 4.3156 | Y | 🟡 | 🟡 | Y | 1.77 E-1 | 4.95 E+6 | 5.29 E+6 | -0.0967 | 23.2882 | Y | 🟡 |
| *PGN0357* | *PG0232* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0258 | | 1.22 E-1 | 41.1 | 26 | 0.6596 | 6.0676 | Y | 🟡 | 🔴 | R | 6.21 E-6 | 2.1 E+7 | 9.51 E+6 | 1.1442 | 24.8642 | R | 🔴 |
| *PGN0358* | *PG0233* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG0259 | | 7.06 E-1 | 12.0 | 12 | -0.0025 | 4.5837 | Y | 🟡 | 🟡 | Y | 8.29 E-3 | 7.54 E+6 | 4.76 E+6 | 0.6634 | 23.5526 | Y | 🟡 |
| *PGN0359* | *PG0235* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0263 | | 0 | 101.0 | 12.5 | 3.0139 | 6.8261 | R | 🔴 | 🔴 | R | 2.11 E-13 | 4.53 E+7 | 1.19 E+7 | 1.9328 | 25.7689 | R | 🔴 |
| *PGN0360* | *PG0237* | *tyrS tyrosyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG0264 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 0 | 6.82 E+5 | 1 E+3 | 9.4130 | 19.3809 | R | 🔴 |
| *PGN0361* | *PG0238* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0267 | | 1.62 E-5 | 83.0 | 33 | 1.3306 | 6.8580 | R | 🔴 | 🔴 | R | 0 | 3.98 E+7 | 1.33 E+7 | 1.5797 | 25.6624 | R | 🔴 |
| *PGN0365* | *PG0239* | *argS arginyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG0268 | | 1.62 E-1 | 8.6 | 3 | 1.5121 | 3.5306 | Y | 🟡 | 🟡 | Y | 1.19 E-1 | 8.17 E+5 | 1.16 E+6 | -0.5118 | 20.9184 | Y | 🟡 |
| *PGN0366* | *PG0240* | *trmU tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase* | | | | | | | | | | | | | | | |
| PG0269 | | 4.53 E-1 | 12.0 | 16 | -0.4175 | 4.8063 | Y | 🟡 | 🟡 | Y | 6.45 E-2 | 5.26 E+6 | 7.11 E+6 | -0.4344 | 23.5614 | Y | 🟡 |
| *PGN0367* | *PG0241* | *xth exodeoxyribonuclease III* | | | | | | | | | | | | | | | |
| PG0270 | | 1.9 E-1 | 12.0 | 5.5 | 1.1230 | 4.1276 | Y | 🟡 | 🟡 | Y | 1.6 E-1 | 3.18 E+6 | 2.92 E+6 | 0.1239 | 22.5416 | Y | 🟡 |
| *PGN0368* | *PG0242* | *oxyR redox-sensitive transcriptional activator OxyR* | | | | | | | | | | | | | | | |
| PG0271 | | 2.32 E-1 | 12.0 | 20 | -0.7395 | 4.9991 | Y | 🟡 | 🟡 | Y | 9.94 E-2 | 5.13 E+6 | 6.58 E+6 | -0.3595 | 23.4813 | Y | 🟡 |
| *PGN0369* | *PG0243* | *ssb single-stranded binding protein* | | | | | | | | | | | | | | | |
| PG0272 | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y | 🟡 | 🔴 | R | 0 | 3.17 E+5 | 1 E+3 | 8.3077 | 18.2780 | R | 🔴 |
| *PGN0370* | *PG0244* | *CBS domain protein* | | | | | | | | | | | | | | | |
| PG0275 | | 2.74 E-1 | 29.1 | 20 | 0.5406 | 5.6174 | Y | 🟡 | 🟡 | Y | 1.85 E-1 | 2.08 E+7 | 2.21 E+7 | -0.0864 | 25.3541 | Y | 🟡 |
| *PGN0373* | *PG0246* | *thioredoxin family protein* | | | | | | | | | | | | | | | |
| PG0276 | | 7.85 E-2 | 39.4 | 23 | 0.7751 | 5.9625 | Y | 🟡 | 🟡 | Y | 6.61 E-2 | 1.52 E+7 | 1.12 E+7 | 0.4413 | 24.6518 | Y | 🟡 |
| *PGN0374* | *PG0248* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1745 | | 8.8 E-3 | 27.4 | 9.5 | 1.5272 | 5.2048 | R | 🔴 | 🟡 | Y | 1.75 E-1 | 8.83 E+6 | 1.02 E+7 | -0.2038 | 24.1794 | Y | 🟡 |
| *PGN0375* | *PG1521* | *phosphoribulokinase family protein* | | | | | | | | | | | | | | | |
| PG1743 | | 1.6 E-1 | 5.1 | 12 | -1.2249 | 4.0988 | Y | 🟡 | 🟢 | G | 6.05 E-4 | 2.39 E+6 | 7.07 E+6 | -1.5654 | 23.1723 | G | 🟢 |
| *PGN0376* | *PG1520* | *kdsA 2-dehydro-3-deoxyphosphooctonate aldolase* | | | | | | | | | | | | | | | |
| PG1741 | | 3.18 E-3 | 339.7 | 258 | 0.3969 | 9.2233 | R | 🔴 | 🔴 | R | 2.14 E-13 | 2.4 E+8 | 9.33 E+7 | 1.3662 | 28.3140 | R | 🔴 |
| *PGN0377* | *PG1518* | *aspA aspartate ammonia-lyase* | | | | | | | | | | | | | | | |
| PG1739 | | 4.75 E-1 | 3.4 | 5.5 | -0.6843 | 3.1575 | Y | 🟡 | 🟡 | Y | 2.94 E-2 | 1.16 E+6 | 6.09 E+5 | 0.9303 | 20.7547 | Y | 🟡 |
| *PGN0378* | *PG1517* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG1735 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.72 E+5 | -6.5356 | 17.4048 | Y | 🟡 |
| *PGN0382* | *PG1513* | *MutT/nudix family protein* | | | | | | | | | | | | | | | |
| PG1731 | | 6 E-1 | 4.3 | 5.5 | -0.3624 | 3.2896 | Y | 🟡 | 🟡 | Y | 4.57 E-2 | 1.51 E+6 | 3.28 E+6 | -1.1224 | 22.1908 | Y | 🟡 |
| *PGN0386* | *PG1509* | *aroQ 3-dehydroquinate dehydratase type II* | | | | | | | | | | | | | | | |
| PG1729 | | 4.52 E-7 | 134.3 | 59.5 | 1.1749 | 7.5987 | R | 🔴 | 🔴 | R | 4.63 E-9 | 1.55 E+8 | 6.93 E+7 | 1.1632 | 27.7427 | R | 🔴 |
| *PGN0388* | *PG1507* | *thiol peroxidase* | | | | | | | | | | | | | | | |
| PG1727 | | 6.97 E-1 | 2.6 | 2.5 | 0.0381 | 2.3411 | Y | 🟡 | 🟢 | G | 0 | 3.97 E+5 | 8.82 E+5 | -1.1509 | 20.2870 | Y | 🟡 |
| *PGN0390* | *PG1505* | *yitL yitL protein* | | | | | | | | | | | | | | | |
| PG1726 | | 8.61 E-4 | 37.6 | 12 | 1.6496 | 5.6337 | R | 🔴 | 🔴 | R | 0 | 1.98 E+7 | 5.58 E+6 | 1.8301 | 24.5985 | R | 🔴 |
| *PGN0391* | *PG1504* | *PDZ domain protein* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG1724 | | 2.6 E-2 | 5.1 | 17 | -1.7274 | 4.4682 | Y 🟡 | 🟢 G | 4.52 E-5 | 1.21 E+6 | 5.03 E+6 | -2.0604 | 22.5733 | G 🟢 |
| *PGN0393* | *PG1502* | *gcp O-sialoglycoprotein endopeptidase* | | | | | | | | | | | | |
| PG1723 | | 2.67 E-7 | 3.4 | 35.5 | -3.3747 | 5.2825 | G 🟢 | 🟢 G | 2.25 E-9 | 2.78 E+6 | 1.41 E+7 | -2.3388 | 24.0072 | G 🟢 |
| *PGN0394* | *PG1501* | *rpsT ribosomal protein S20* | | | | | | | | | | | | |
| PG1721 | | 6.69 E-1 | 24.8 | 23.5 | 0.0785 | 5.5944 | Y 🟡 | 🟡 Y | 2.97 E-3 | 1.05 E+7 | 6.29 E+6 | 0.7359 | 23.9987 | Y 🟡 |
| *PGN0396* | *PG1499* | *vacB ribonuclease R* | | | | | | | | | | | | |
| PG1720 | | 5.43 E-1 | 3.4 | 5 | -0.5468 | 3.0743 | Y 🟡 | 🟡 Y | 2.72 E-2 | 1.07 E+6 | 1.76 E+6 | -0.7251 | 21.4334 | Y 🟡 |
| *PGN0397* | *PG1498* | *conserved domain protein* | | | | | | | | | | | | |
| PG1719 | | 3.05 E-1 | 5.1 | 2 | 1.3601 | 2.8347 | Y 🟡 | 🔴 R | 1.16 E-9 | 2.25 E+6 | 5.7 E+5 | 1.9770 | 21.4251 | R 🔴 |
| *PGN0398* | *PG1497* | *ABC transporter ATP-binding protein MsbA family* | | | | | | | | | | | | |
| PG1715 | | 3.67 E-5 | 13.7 | 48.5 | -1.8248 | 5.9586 | G 🟢 | 🟢 G | 1.77 E-5 | 1.01 E+7 | 2.47 E+7 | -1.2883 | 25.0545 | G 🟢 |
| *PGN0400* | *PG1496* | *hypothetical protein PG_1715* | | | | | | | | | | | | |
| PG1714 | | 6.23 E-2 | 6.8 | 17.5 | -1.3542 | 4.6056 | Y 🟡 | 🟡 Y | 3.5 E-2 | 1.41 E+7 | 6.81 E+6 | 1.0468 | 24.3148 | Y 🟡 |
| *PGN0403* | *PG1495* | *pdxH pyridoxamine-phosphate oxidase* | | | | | | | | | | | | |
| PG1712 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🔴 R | 0 | 6.44 E+5 | 3.36 E+5 | 0.9361 | 19.9022 | Y 🟡 |
| *PGN0405* | *PG1493* | *alpha-12-mannosidase family protein* | | | | | | | | | | | | |
| PG1711 | | 3.5 E-1 | 19.7 | 27 | -0.4562 | 5.5447 | Y 🟡 | 🟡 Y | 1.6 E-1 | 6.38 E+6 | 6.7 E+6 | -0.0705 | 23.6403 | Y 🟡 |
| *PGN0406* | *PG1492* | *alpha-12-mannosidase family protein* | | | | | | | | | | | | |
| PG1705 | | 3.82 E-1 | 8.6 | 5 | 0.7751 | 3.7609 | Y 🟡 | 🔴 R | 3.86 E-8 | 3.32 E+6 | 8.3 E+5 | 2.0006 | 21.9852 | R 🔴 |
| *PGN0410* | *PG1486* | | | | | | | | | | | | | |
| PG1704 | | 1.18 E-1 | 78.7 | 57 | 0.4658 | 7.0845 | Y 🟡 | 🔴 R | 9.77 E-8 | 5.96 E+7 | 3.35 E+7 | 0.8296 | 26.4723 | R 🔴 |
| *PGN0411* | *PG1485* | *thiol:disulfide interchange protein dsbD putative* | | | | | | | | | | | | |
| PG1703 | | 3.09 E-1 | 9.4 | 5 | 0.9126 | 3.8492 | Y 🟡 | 🟡 Y | 6.59 E-2 | 3.58 E+6 | 6.52 E+6 | -0.8647 | 23.2687 | Y 🟡 |
| *PGN0412* | *PG1484* | *MazG family protein* | | | | | | | | | | | | |
| PG1702 | | 5.15 E-9 | 118.1 | 41 | 1.5261 | 7.3136 | R 🔴 | 🔴 R | 0 | 5.42 E+7 | 1.04 E+7 | 2.3859 | 25.9446 | R 🔴 |
| *PGN0413* | *PG1483* | *gyrB DNA gyrase B subunit* | | | | | | | | | | | | |
| PG1701 | | 2.17 E-2 | 12.8 | 30 | -1.2249 | 5.4207 | Y 🟡 | 🟡 Y | 2 E-2 | 5.36 E+6 | 7.18 E+6 | -0.4210 | 23.5804 | Y 🟡 |
| *PGN0414* | *PG1482* | *glutamine amidotransferase class II/dipeptidase* | | | | | | | | | | | | |
| PG1697 | | 2.82 E-1 | 7.7 | 3.5 | 1.1377 | 3.4855 | Y 🟡 | 🔴 R | 1.03 E-6 | 2.92 E+6 | 7.84 E+5 | 1.8957 | 21.8197 | R 🔴 |
| *PGN0415* | *PG1481* | *type II restriction endonuclease putative* | | | | | | | | | | | | |
| PG1694 | | 2.93 E-1 | 6.8 | 3 | 1.1901 | 3.2994 | Y 🟡 | 🔴 R | 1.24 E-4 | 1.18 E+6 | 2.35 E+5 | 2.3241 | 20.4303 | R 🔴 |
| *PGN0418* | *PG1479* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG1693 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 9 E+5 | -8.9261 | 19.7828 | G 🟢 |
| *PGN0419* | *PG1478* | *HesA/MoeB/ThiF family protein* | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Regulation** | | | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Consensus** | |
| PG1692 | | 4.84 E-1 | 4.3 | 6.5 | -0.6034 | 3.4301 | Y | 🟡 | 🟡 | Y | 2.01 E-1 | 1.27 E+6 | 1.27 E+6 | -0.0059 | 21.2751 | Y | 🟡 |
| *PGN0420* | *PG1477* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG1688 | | 4.74 E-5 | 24.0 | 2.5 | 3.2605 | 4.7256 | R | 🔴 | 🔴 | R | 0 | 2.24 E+7 | 1.44 E+6 | 3.9654 | 24.5076 | R | 🔴 |
| *PGN0423* | *PG1474* | *greA transcription elongation factor GreA* | | | | | | | | | | | | | | | |
| PG1687 | | 3.82 E-1 | 21.4 | 15.5 | 0.4648 | 5.2052 | Y | 🟡 | 🟡 | Y | 5.01 E-2 | 2 E+7 | 1.17 E+7 | 0.7759 | 24.9167 | Y | 🟡 |
| *PGN0424* | *PG1473* | *HIT family protein* | | | | | | | | | | | | | | | |
| PG1684 | | 0 | 1.7 | 66.5 | -5.2802 | 6.0919 | G | 🟢 | 🟢 | G | 1.14 E-7 | 1.85 E+3 | 1.1 E+7 | -12.5345 | 23.3884 | G | 🟢 |
| *PGN0426* | *PG1471* | *hypothetical protein PG_1684* | | | | | | | | | | | | | | | |
| PG1683 | | 1.13 E-1 | 23.1 | 12 | 0.9450 | 5.1335 | Y | 🟡 | 🔴 | R | 1.05 E-10 | 1.04 E+7 | 3.03 E+6 | 1.7769 | 23.6781 | R | 🔴 |
| *PGN0427* | *PG1470* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1682 | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y | 🟡 | 🔴 | R | 0 | 5.82 E+5 | 1 E+3 | 9.1839 | 19.1521 | R | 🔴 |
| *PGN0428* | *PG1469* | *glycosyl transferase group 1 family protein* | | | | | | | | | | | | | | | |
| PG1681 | | 6.42 E-1 | 14.5 | 13 | 0.1621 | 4.7838 | Y | 🟡 | 🟡 | Y | 8.22 E-2 | 4.66 E+6 | 3.59 E+6 | 0.3737 | 22.9756 | Y | 🟡 |
| *PGN0429* | *PG1468* | *glycogen debranching enzyme archaeal type putative* | | | | | | | | | | | | | | | |
| | | 3.05 E-1 | 2.6 | 6 | -1.2249 | 3.0988 | Y | 🟡 | 🟡 | Y | 9.52 E-2 | 8.98 E+5 | 1.1 E+6 | -0.2988 | 20.9336 | Y | 🟡 |
| *PGN0430* | | | | | | | | | | | | | | | | | |
| PG1677 | | 8.08 E-7 | 176.3 | 90 | 0.9697 | 8.0567 | R | 🔴 | 🟡 | Y | 4.49 E-2 | 1.01 E+8 | 8.41 E+7 | 0.2660 | 27.4651 | R | 🔴 |
| *PGN0433* | *PG1465* | *pgk phosphoglycerate kinase* | | | | | | | | | | | | | | | |
| PG1676 | | 1.57 E-12 | 965.2 | 1321.5 | -0.4533 | 11.1590 | G | 🟢 | 🟢 | G | 2.99 E-4 | 6.21 E+8 | 8.35 E+8 | -0.4280 | 30.4391 | G | 🟢 |
| *PGN0434* | *PG1464* | *pckA phosphoenolpyruvate carboxykinase (ATP)* | | | | | | | | | | | | | | | |
| PG1667 | | 6.57 E-3 | 13.7 | 35 | -1.3542 | 5.6056 | G | 🟢 | 🟢 | G | 3.41 E-6 | 6.59 E+6 | 1.66 E+7 | -1.3349 | 24.4689 | G | 🟢 |
| *PGN0444* | *PG1455* | *outer membrane efflux protein* | | | | | | | | | | | | | | | |
| PG1666 | | 5.74 E-1 | 4.3 | 3 | 0.5121 | 2.8636 | Y | 🟡 | 🔴 | R | 0 | 3.09 E+6 | 2.25 E+5 | 3.7845 | 21.6623 | R | 🔴 |
| *PGN0445* | *PG1454* | *efflux transporter MFP component RND family* | | | | | | | | | | | | | | | |
| PG1665 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 1.64 E-6 | 1.85 E+3 | 2.4 E+5 | -7.0216 | 17.8863 | G | 🟢 |
| *PGN0446* | *PG1453* | *ABC transporter permease protein putative* | | | | | | | | | | | | | | | |
| PG1663 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 2.18 E+5 | 1 E+3 | 7.7658 | 17.7382 | R | 🔴 |
| *PGN0448* | *PG1451* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG1662 | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y | 🟡 | 🟢 | G | 1.34 E-4 | 1.74 E+6 | 3.92 E+6 | -1.1697 | 22.4342 | Y | 🟡 |
| *PGN0449* | *PG1450* | *hypothetical protein PG_1662* | | | | | | | | | | | | | | | |
| PG1657 | | 2.57 E-1 | 38.5 | 27.5 | 0.4856 | 6.0445 | Y | 🟡 | 🔴 | R | 2.69 E-5 | 2.37 E+7 | 1.54 E+7 | 0.6200 | 25.2192 | R | 🔴 |
| *PGN0456* | *PG1446* | *mutB methylmalonyl-CoA mutase large subunit* | | | | | | | | | | | | | | | |
| PG1656 | | 3 E-1 | 40.2 | 30 | 0.4228 | 6.1337 | Y | 🟡 | 🟡 | Y | 2.63 E-2 | 1.81 E+7 | 1.21 E+7 | 0.5792 | 24.8475 | Y | 🟡 |
| *PGN0457* | *PG1445* | *mutA methylmalonyl-CoA mutase small subunit* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| | | 2.7 E-1 | 53.9 | 68.5 | -0.3457 | 6.9355 | Y | 🟡 | 🟡 | Y | 3.41 E-3 | 3.74 E+7 | 6.38 E+7 | -0.7719 | 26.5918 | Y | 🟡 |
| *PGN0458* | | | | | | | | | | | | | | | | | |
| PG1653 | | 7.82 E-4 | 48.8 | 18.5 | 1.3985 | 6.0719 | R | 🔴 | 🔴 | R | 4.18 E-5 | 2.52 E+7 | 8.59 E+6 | 1.5532 | 25.0112 | R | 🔴 |
| *PGN0462* | *PG1443* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1652 | | 2.4 E-7 | 15.4 | 63 | -2.0323 | 6.2928 | G | 🟢 | 🟢 | G | 1.23 E-14 | 6.84 E+6 | 3.69 E+7 | -2.4309 | 25.3829 | G | 🟢 |
| *PGN0463* | *PG1442* | *hypothetical protein PG_1652* | | | | | | | | | | | | | | | |
| PG1651 | | 5.08 E-2 | 39.4 | 21.5 | 0.8724 | 5.9274 | Y | 🟡 | 🔴 | R | 7.12 E-14 | 2.5 E+7 | 8.85 E+6 | 1.4964 | 25.0109 | R | 🔴 |
| *PGN0464* | *PG1441* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG1648 | | 2.82 E-1 | 7.7 | 3.5 | 1.1377 | 3.4855 | Y | 🟡 | 🔴 | R | 6.8 E-4 | 5.56 E+6 | 2.35 E+5 | 4.5653 | 22.4655 | R | 🔴 |
| *PGN0465* | *PG1440* | *RelA/SpoT family protein* | | | | | | | | | | | | | | | |
| PG1620 | | 2.32 E-1 | 4.3 | 9.5 | -1.1509 | 3.7843 | Y | 🟡 | 🟡 | Y | 1.06 E-2 | 1.05 E+6 | 6.92 E+6 | -2.7185 | 22.9263 | Y | 🟡 |
| *PGN0470* | *PG1417* | *carboxyl-terminal protease-related protein* | | | | | | | | | | | | | | | |
| PG1621 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 7.48 E+4 | -5.3377 | 16.2267 | Y | 🟡 |
| *PGN0471* | *PG1418* | *hypothetical protein PG_1621* | | | | | | | | | | | | | | | |
| PG1622 | | 3.73 E-1 | 24.0 | 31.5 | -0.3948 | 5.7933 | Y | 🟡 | 🟡 | Y | 3.56 E-2 | 5.93 E+6 | 7.74 E+6 | -0.3841 | 23.7046 | Y | 🟡 |
| *PGN0472* | *PG1419* | *DNA topoisomerase IV A subunit putative* | | | | | | | | | | | | | | | |
| PG1623 | | 5.43 E-1 | 6.8 | 9 | -0.3948 | 3.9860 | Y | 🟡 | 🟡 | Y | 2.41 E-3 | 8.78 E+6 | 4.3 E+6 | 1.0275 | 23.6409 | Y | 🟡 |
| *PGN0473* | *PG1420* | *membrane bound regulatory protein putative* | | | | | | | | | | | | | | | |
| PG1625 | | 1.79 E-1 | 3.4 | 9 | -1.3948 | 3.6349 | Y | 🟡 | 🟡 | Y | 3.84 E-2 | 1.29 E+6 | 1.03 E+6 | 0.3207 | 21.1470 | Y | 🟡 |
| *PGN0476* | *PG1423* | *hypothetical protein PG_1625* | | | | | | | | | | | | | | | |
| PG1626 | | 0 | 2.6 | 69.5 | -4.7589 | 6.1713 | G | 🟢 | 🟢 | G | 8.15 E-7 | 2.87 E+5 | 2.03 E+7 | -6.1440 | 24.2959 | G | 🟢 |
| *PGN0477* | *PG1424* | *hypothetical protein PG_1626* | | | | | | | | | | | | | | | |
| PG1632 | | 1.03 E-2 | 14.5 | 35 | -1.2667 | 5.6307 | Y | 🟡 | 🟢 | G | 2.09 E-5 | 4.16 E+6 | 1.52 E+7 | -1.8714 | 24.2085 | G | 🟢 |
| *PGN0483* | *PG1426* | *galM aldose 1-epimerase* | | | | | | | | | | | | | | | |
| PG1633 | | 3.71 E-2 | 41.9 | 22.5 | 0.8980 | 6.0096 | Y | 🟡 | 🟡 | Y | 1.46 E-1 | 2.43 E+7 | 2.99 E+7 | -0.3012 | 25.6909 | Y | 🟡 |
| *PGN0484* | *PG1427* | *galK galactokinase* | | | | | | | | | | | | | | | |
| PG1635 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 0 | 6.04 E+6 | 1 E+3 | 12.5614 | 22.5274 | R | 🔴 |
| *PGN0486* | *PG1429* | *hypothetical protein PG_1635* | | | | | | | | | | | | | | | |
| PG1636 | | 3.49 E-1 | 15.4 | 10 | 0.6231 | 4.6669 | Y | 🟡 | 🟡 | Y | 1.53 E-3 | 7.12 E+6 | 4.14 E+6 | 0.7808 | 23.4247 | Y | 🟡 |
| *PGN0487* | *PG1430* | *FtsK/SpoIIIE family protein* | | | | | | | | | | | | | | | |
| PG1638 | | 6.69 E-1 | 9.4 | 8.5 | 0.1471 | 4.1629 | Y | 🟡 | 🟡 | Y | 1.7 E-1 | 5.26 E+6 | 4.95 E+6 | 0.0856 | 23.2833 | Y | 🟡 |
| *PGN0488* | *PG1431* | *thioredoxin family protein* | | | | | | | | | | | | | | | |
| PG1641 | | 2.25 E-1 | 1.7 | 5.5 | -1.6843 | 2.8503 | Y | 🟡 | 🟢 | G | 8.22 E-4 | 1.39 E+5 | 4.19 E+5 | -1.5974 | 19.0897 | G | 🟢 |
| *PGN0491* | *PG1433* | *phosphotyrosine protein phosphatase* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| | | 4.76 E-2 | 8.6 | 1.5 | 2.5121 | 3.3301 | Y | 🟡 | 🔴 | R | 4 E-4 | 1.71 E+6 | 1.39 E+5 | 3.6226 | 20.8158 | R | 🔴 |
| *PGN0493* | | | | | | | | | | | | | | | | | |
| PG1616 | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y | 🟡 | 🔴 | R | 0 | 5.02 E+5 | 1 E+3 | 8.9711 | 18.9397 | R | 🔴 |
| *PGN0496* | *PG1414* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1615 | | 1.57 E-1 | 121.5 | 96.5 | 0.3324 | 7.7682 | Y | 🟡 | 🟡 | Y | 1.78 E-1 | 7.65 E+7 | 7.82 E+7 | -0.0313 | 27.2056 | Y | 🟡 |
| *PGN0497* | *PG1413* | *frdA fumarate reductase flavoprotein subunit* | | | | | | | | | | | | | | | |
| PG1614 | | 6.69 E-1 | 41.1 | 39.5 | 0.0563 | 6.3322 | Y | 🟡 | 🟡 | Y | 4.54 E-2 | 3.73 E+7 | 5.12 E+7 | -0.4578 | 26.3989 | Y | 🟡 |
| *PGN0498* | *PG1412* | *frdB fumarate reductase iron-sulfur protein* | | | | | | | | | | | | | | | |
| PG1613 | | 3.93 E-1 | 129.2 | 114.5 | 0.1743 | 7.9290 | Y | 🟡 | 🔴 | R | 4.83 E-4 | 6.69 E+7 | 3.96 E+7 | 0.7560 | 26.6669 | R | 🔴 |
| *PGN0499* | *PG1411* | *glyoxalase family protein* | | | | | | | | | | | | | | | |
| PG1612 | | 1.47 E-6 | 241.3 | 140 | 0.7854 | 8.5748 | R | 🔴 | 🔴 | R | 0 | 2.94 E+8 | 9.57 E+7 | 1.6211 | 28.5397 | R | 🔴 |
| *PGN0500* | *PG1409* | *mmdA methylmalonyl-CoA decarboxylase alpha subunit* | | | | | | | | | | | | | | | |
| PG1611 | | 3.84 E-4 | 35.1 | 9.5 | 1.8847 | 5.4784 | R | 🔴 | 🔴 | R | 0 | 2.17 E+7 | 4.35 E+6 | 2.3184 | 24.6351 | R | 🔴 |
| *PGN0501* | *PG1408* | *hypothetical protein PG_1611* | | | | | | | | | | | | | | | |
| PG1610 | | 9.44 E-2 | 6.0 | 1 | 2.5825 | 2.8052 | Y | 🟡 | 🔴 | R | 4.3 E-7 | 3.63 E+6 | 1 E+3 | 11.8252 | 21.7914 | R | 🔴 |
| *PGN0502* | | *hypothetical protein PG_1610* | | | | | | | | | | | | | | | |
| PG1609 | | 8.35 E-3 | 68.5 | 37.5 | 0.8682 | 6.7273 | R | 🔴 | 🔴 | R | 1.16 E-7 | 1.3 E+8 | 1.57 E+7 | 3.0440 | 27.1167 | R | 🔴 |
| *PGN0503* | *PG1407* | *mmdC methylmalonyl-CoA decarboxylase gamma subunit* | | | | | | | | | | | | | | | |
| PG1608 | | 6.85 E-1 | 4.3 | 4.5 | -0.0729 | 3.1339 | Y | 🟡 | 🟡 | Y | 2.02 E-2 | 9.43 E+5 | 2.32 E+6 | -1.2998 | 21.6379 | Y | 🟡 |
| *PGN0504* | *PG1406* | *mmdB methylmalonyl-CoA decarboxylase beta subunit* | | | | | | | | | | | | | | | |
| PG1605 | | 1.91 E-1 | 104.4 | 83 | 0.3308 | 7.5499 | Y | 🟡 | 🟡 | Y | 9.88 E-2 | 9.36 E+7 | 1.07 E+8 | -0.1890 | 27.5782 | Y | 🟡 |
| *PGN0508* | *PG1404* | *pepC aminopeptidase C* | | | | | | | | | | | | | | | |
| PG1604 | | 3.53 E-3 | 12.0 | 34 | -1.5050 | 5.5229 | G | 🟢 | 🟡 | Y | 1.11 E-1 | 1.79 E+7 | 1.32 E+7 | 0.4329 | 24.8903 | Y | 🟡 |
| *PGN0509* | *PG1403* | *immunoreactive 84 kDa antigen PG93* | | | | | | | | | | | | | | | |
| PG1603 | | 6.03 E-1 | 17.1 | 15 | 0.1901 | 5.0051 | Y | 🟡 | 🟡 | Y | 7.26 E-2 | 6.73 E+6 | 5.46 E+6 | 0.3021 | 23.5382 | Y | 🟡 |
| *PGN0510* | *PG1402* | *HAM1 protein* | | | | | | | | | | | | | | | |
| PG1602 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟡 | Y | 3.83 E-3 | 1.85 E+3 | 1.47 E+6 | -9.6336 | 20.4891 | Y | 🟡 |
| *PGN0511* | *PG1401* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1601 | | 3.6 E-1 | 2.6 | 5.5 | -1.0994 | 3.0120 | Y | 🟡 | 🟡 | Y | 8.33 E-3 | 2.02 E+5 | 1.96 E+6 | -3.2761 | 21.0421 | Y | 🟡 |
| *PGN0512* | *PG1400* | *biotin--acetyl-CoA-carboxylase ligase* | | | | | | | | | | | | | | | |
| PG1597 | | 6 E-1 | 16.3 | 18.5 | -0.1864 | 5.1192 | Y | 🟡 | 🟡 | Y | 2.03 E-2 | 1.99 E+7 | 1.13 E+7 | 0.8103 | 24.8942 | Y | 🟡 |
| *PGN0516* | *PG1396* | *DnaK suppressor protein putative* | | | | | | | | | | | | | | | |
| PG1596 | | 2.31 E-15 | 150.6 | 40 | 1.9126 | 7.5744 | R | 🔴 | 🔴 | R | 0 | 7.62 E+7 | 1.73 E+7 | 2.1416 | 26.4787 | R | 🔴 |
| *PGN0517* | *PG1395* | *isoleucyl-tRNA synthetase putative* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Regulation** | | | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Consensus** | |
| PG1595 | | 9.45 E-12 | 29.9 | 113.5 | -1.9222 | 7.1644 | G | 🟢 | 🟢 | G | 1.29 E-11 | 2.8 E+6 | 7.15 E+6 | -1.3549 | 23.2464 | G | 🟢 |
| *PGN0518* | *PG1394* | *rpe ribulose-phosphate 3-epimerase* | | | | | | | | | | | | | | | |
| PG1592 | | 4.53 E-1 | 9.4 | 13 | -0.4659 | 4.4862 | Y | 🟡 | 🟡 | Y | 3.4 E-2 | 4.31 E+6 | 3.32 E+6 | 0.3779 | 22.8627 | Y | 🟡 |
| *PGN0521* | *PG1391* | *HDIG domain protein* | | | | | | | | | | | | | | | |
| PG1589 | | 6 E-1 | 4.3 | 5.5 | -0.3624 | 3.2896 | Y | 🟡 | 🟡 | Y | 3.81 E-2 | 2.18 E+6 | 3.72 E+6 | -0.7715 | 22.4936 | Y | 🟡 |
| *PGN0522* | *PG1389* | *folP dihydropteroate synthase* | | | | | | | | | | | | | | | |
| PG1587 | | 6.69 E-1 | 6.0 | 5.5 | 0.1230 | 3.5223 | Y | 🟡 | 🟡 | Y | 1.26 E-2 | 3.11 E+5 | 4.18 E+5 | -0.4276 | 19.4761 | Y | 🟡 |
| *PGN0524* | *PG1387* | *PAP2 superfamily protein* | | | | | | | | | | | | | | | |
| PG1586 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 7.26 E+5 | -8.6159 | 19.4733 | Y | 🟡 |
| *PGN0525* | *PG1386* | *batE batE protein* | | | | | | | | | | | | | | | |
| PG1585 | | 6.7 E-1 | 5.1 | 5.5 | -0.0994 | 3.4106 | Y | 🟡 | 🟡 | Y | 8.05 E-3 | 9.87 E+5 | 2.77 E+6 | -1.4919 | 21.8428 | Y | 🟡 |
| *PGN0526* | *PG1385* | *batD batD protein* | | | | | | | | | | | | | | | |
| PG1584 | | 1.06 E-1 | 6.8 | 1.5 | 2.1901 | 3.0610 | Y | 🟡 | 🔴 | R | 5.87 E-11 | 3.32 E+6 | 4.43 E+5 | 2.9045 | 21.8419 | R | 🔴 |
| *PGN0527* | *PG1384* | *batC batC protein* | | | | | | | | | | | | | | | |
| PG1582 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 1.17 E+6 | 1 E+3 | 10.1967 | 20.1637 | R | 🔴 |
| *PGN0529* | *PG1382* | *batA batA protein* | | | | | | | | | | | | | | | |
| PG1581 | | 2.93 E-1 | 6.8 | 3 | 1.1901 | 3.2994 | Y | 🟡 | 🟡 | Y | 1.43 E-1 | 3.2 E+6 | 2.44 E+6 | 0.3905 | 22.4267 | Y | 🟡 |
| *PGN0530* | *PG1381* | *hypothetical protein PG_1581* | | | | | | | | | | | | | | | |
| PG1580 | | 2.99 E-1 | 16.3 | 10 | 0.7011 | 4.7147 | Y | 🟡 | 🔴 | R | 1.55 E-5 | 2.11 E+6 | 7.91 E+5 | 1.4184 | 21.4694 | R | 🔴 |
| *PGN0531* | *PG1380* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1579 | | 4.08 E-3 | 38.5 | 15 | 1.3601 | 5.7416 | R | 🔴 | 🔴 | R | 9.22 E-8 | 2.25 E+7 | 1.12 E+7 | 1.0072 | 25.0038 | R | 🔴 |
| *PGN0532* | *PG1379* | *ATPase MoxR family* | | | | | | | | | | | | | | | |
| PG1578 | | 2.01 E-2 | 8.6 | 23.5 | -1.4576 | 5.0025 | Y | 🟡 | 🟢 | G | 1.15 E-5 | 1.84 E+6 | 5.62 E+6 | -1.6112 | 22.8301 | G | 🟢 |
| *PGN0533* | *PG1378* | *nadA quinolinate synthetase complex subunit A* | | | | | | | | | | | | | | | |
| PG1577 | | 5.8 E-4 | 2.6 | 19.5 | -2.9253 | 4.4638 | G | 🟢 | 🟢 | G | 4.51 E-6 | 1.35 E+6 | 1.21 E+7 | -3.1670 | 23.6795 | G | 🟢 |
| *PGN0534* | *PG1377* | *nadC nicotinate-nucleotide pyrophosphorylase* | | | | | | | | | | | | | | | |
| PG1576 | | 7.06 E-1 | 6.0 | 6 | -0.0025 | 3.5837 | Y | 🟡 | 🟡 | Y | 1.58 E-1 | 7.12 E+5 | 9.2 E+5 | -0.3685 | 20.6381 | Y | 🟡 |
| *PGN0535* | *PG1376* | *nadB L-aspartate oxidase* | | | | | | | | | | | | | | | |
| PG1573 | | 7.56 E-2 | 1.7 | 8 | -2.2249 | 3.2797 | Y | 🟡 | 🟢 | G | 9.68 E-8 | 1.85 E+3 | 8.36 E+5 | -8.8202 | 19.6771 | G | 🟢 |
| *PGN0537* | *PG1375* | *transcriptional regulator Crp family* | | | | | | | | | | | | | | | |
| PG1566 | | 3.83 E-2 | 50.5 | 29 | 0.7998 | 6.3126 | Y | 🟡 | 🔴 | R | 2.71 E-12 | 2.23 E+7 | 8.44 E+6 | 1.4018 | 24.8737 | R | 🔴 |
| *PGN0543* | *PG1371* | *gltX glutamyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG1565 | | 6.69 E-1 | 12.0 | 13 | -0.1180 | 4.6427 | Y | 🟡 | 🔴 | R | 5.17 E-8 | 5.91 E+6 | 7.88 E+5 | 2.9069 | 22.6753 | Y | 🟡 |
| *PGN0544* | *PG1370* | *3-deoxy-D-manno-octulosonic-acid transferase putative* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG1564 | | 6.97 E-1 | 2.6 | 2.5 | 0.0381 | 2.3411 | Y 🟡 | 🟡 Y | 1.62 E-1 | 3.13 E+5 | 3.51 E+5 | -0.1682 | 19.3410 | Y 🟡 |
| *PGN0545* | *PG1369* | *membrane protein putative* | | | | | | | | | | | | |
| PG1563 | | 3.82 E-1 | 21.4 | 15.5 | 0.4648 | 5.2052 | Y 🟡 | 🟡 Y | 6.32 E-2 | 8.32 E+6 | 1.04 E+7 | -0.3228 | 24.1585 | Y 🟡 |
| *PGN0546* | *PG1368* | *rfbA glucose-1-phosphate thymidylyltransferase* | | | | | | | | | | | | |
| PG1562 | | 3.05 E-1 | 15.4 | 9.5 | 0.6971 | 4.6382 | Y 🟡 | 🟡 Y | 1.99 E-1 | 4.25 E+6 | 4.22 E+6 | 0.0085 | 23.0145 | Y 🟡 |
| *PGN0547* | *PG1367* | *rfbC dTDP-4-dehydrorhamnose 35-epimerase* | | | | | | | | | | | | |
| PG1561 | | 6.69 E-1 | 8.6 | 8 | 0.0970 | 4.0493 | Y 🟡 | 🟡 Y | 5.24 E-2 | 2.78 E+6 | 4.19 E+6 | -0.5921 | 22.7327 | Y 🟡 |
| *PGN0548* | *PG1366* | *rfbD dTDP-4-dehydrorhamnose reductase* | | | | | | | | | | | | |
| PG1560 | | 1.98 E-1 | 11.1 | 5 | 1.1536 | 4.0111 | Y 🟡 | 🔴 R | 4.83 E-11 | 5.51 E+6 | 1.3 E+6 | 2.0823 | 22.7002 | R 🔴 |
| *PGN0549* | *PG1365* | *rfbB dTDP-glucose 46-dehydratase* | | | | | | | | | | | | |
| PG1559 | | 6.64 E-1 | 181.4 | 177 | 0.0354 | 8.4854 | Y 🟡 | 🟡 Y | 4.14 E-2 | 1.58 E+8 | 1.35 E+8 | 0.2189 | 28.1258 | Y 🟡 |
| *PGN0550* | *PG1364* | *gcvT glycine cleavage system T protein* | | | | | | | | | | | | |
| PG1555 | | 9.55 E-3 | 10.3 | 1 | 3.3601 | 3.4941 | Y 🟡 | 🔴 R | 0 | 9.92 E+5 | 1 E+3 | 9.9547 | 19.9219 | R 🔴 |
| *PGN0554* | *PG1361* | *conserved domain protein* | | | | | | | | | | | | |
| PG1553 | | 2.28 E-9 | 96.7 | 206.5 | -1.0947 | 8.2441 | G 🟢 | 🟡 Y | 1.15 E-3 | 5.69 E+7 | 1.54 E+8 | -1.4331 | 27.6497 | G 🟢 |
| *PGN0556* | *PG1359* | *CobN/magnesium chelatase family protein* | | | | | | | | | | | | |
| PG1552 | | 2.12 E-12 | 76.2 | 196.5 | -1.3676 | 8.0909 | G 🟢 | 🟢 G | 7.85 E-5 | 2.35 E+7 | 3.88 E+7 | -0.7223 | 25.8936 | G 🟢 |
| *PGN0557* | *PG1358* | *hmuR TonB-dependent receptor HmuR* | | | | | | | | | | | | |
| PG1551 | | 1.4 E-1 | 158.3 | 191.5 | -0.2747 | 8.4504 | Y 🟡 | 🟡 Y | 2.98 E-3 | 1.26 E+8 | 2 E+8 | -0.6689 | 28.2825 | Y 🟡 |
| *PGN0558* | *PG1357* | *hmuY hmuY protein* | | | | | | | | | | | | |
| | | 5.44 E-2 | 14.5 | 29.5 | -1.0201 | 5.4609 | Y 🟡 | 🟢 G | 1.65 E-6 | 3.71 E+6 | 1.17 E+7 | -1.6561 | 23.8771 | G 🟢 |
| *PGN0561* | | | | | | | | | | | | | | |
| PG1545 | | 3.06 E-6 | 195.9 | 309.5 | -0.6595 | 8.9814 | G 🟢 | 🟡 Y | 1.24 E-1 | 2.36 E+8 | 2.61 E+8 | -0.1482 | 28.8874 | G 🟢 |
| *PGN0564* | *PG1354* | *sodB superoxide dismutase Fe-Mn* | | | | | | | | | | | | |
| PG1543 | | 1.21 E-2 | 25.7 | 9 | 1.5121 | 5.1156 | Y 🟡 | 🔴 R | 4.83 E-7 | 9.99 E+6 | 4.43 E+6 | 1.1729 | 23.7812 | R 🔴 |
| *PGN0566* | *PG1350* | *thioesterase family protein* | | | | | | | | | | | | |
| PG1542 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y 🟡 | 🟢 G | 1.27 E-4 | 1.85 E+3 | 8.85 E+5 | -8.9009 | 19.7576 | G 🟢 |
| *PGN0567* | *PG1349* | *prtC collagenase* | | | | | | | | | | | | |
| PG1541 | | 2.93 E-1 | 8.6 | 14.5 | -0.7610 | 4.5271 | Y 🟡 | 🟡 Y | 1.42 E-1 | 3.03 E+6 | 2.7 E+6 | 0.1617 | 22.4501 | Y 🟡 |
| *PGN0568* | *PG1348* | *folK 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase* | | | | | | | | | | | | |
| PG1540 | | 1.63 E-1 | 35.1 | 22.5 | 0.6408 | 5.8475 | Y 🟡 | 🟡 Y | 8.49 E-2 | 1.69 E+7 | 1.45 E+7 | 0.2145 | 24.9039 | Y 🟡 |
| *PGN0569* | *PG1347* | *queA S-adenosylmethionine:tRNA ribosyltransferase-isomerase* | | | | | | | | | | | | |
| PG1539 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y 🟡 | 🔴 R | 4.74 E-9 | 8.59 E+5 | 1 E+3 | 9.7459 | 19.7133 | R 🔴 |
| *PGN0570* | *PG1346* | | | | | | | | | | | | | |

| **TIGR** | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1536 | | 6.97 E-1 | 3.4 | 3.5 | -0.0323 | 2.7913 | Y | 🟡 | 🟡 | Y | 8.62 E-2 | 1.38 E+6 | 9.88 E+5 | 0.4817 | 21.1752 | Y | 🟡 |
| *PGN0573* | *PG1343* | *cell division protein FtsX putative* | | | | | | | | | | | | | | | |
| | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 6 E+5 | 1 E+3 | 9.2289 | 19.1971 | R | 🔴 |
| *PGN0580* | | | | | | | | | | | | | | | | | |
| PG1519 | | 1.45 E-1 | 5.1 | 1 | 2.3601 | 2.6168 | Y | 🟡 | 🔴 | R | 1.11 E-5 | 1.06 E+6 | 1 E+3 | 10.0564 | 20.0235 | R | 🔴 |
| *PGN0583* | *PG1329* | *hypothetical protein PG_1519* | | | | | | | | | | | | | | | |
| | | 3.64 E-1 | 18.8 | 13 | 0.5341 | 4.9921 | Y | 🟡 | 🔴 | R | 3.19 E-5 | 1.01 E+7 | 4.94 E+6 | 1.0349 | 23.8447 | R | 🔴 |
| *PGN0590* | | | | | | | | | | | | | | | | | |
| PG1286 | | 2.72 E-1 | 320.9 | 288.5 | 0.1534 | 9.2512 | Y | 🟡 | 🟡 | Y | 1.73 E-1 | 4.64 E+8 | 4.45 E+8 | 0.0595 | 29.7603 | Y | 🟡 |
| *PGN0604* | *PG1133* | *ftn ferritin* | | | | | | | | | | | | | | | |
| PG1285 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟢 | G | 1.16 E-8 | 1.85 E+3 | 3.18 E+5 | -7.4229 | 18.2850 | G | 🟢 |
| *PGN0606* | *PG1132* | *glucosamine-6-phosphate isomerase putative* | | | | | | | | | | | | | | | |
| PG1283 | | 5.25 E-3 | 125.8 | 181.5 | -0.5291 | 8.2634 | G | 🟢 | 🟡 | Y | 2.29 E-3 | 6.88 E+7 | 9.27 E+7 | -0.4302 | 27.2665 | G | 🟢 |
| *PGN0607* | *PG1131* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1281 | | 3.52 E-1 | 12.8 | 8 | 0.6820 | 4.3809 | Y | 🟡 | 🟡 | Y | 6.91 E-2 | 4.12 E+6 | 3.33 E+6 | 0.3052 | 22.8284 | Y | 🟡 |
| *PGN0609* | *PG1129* | *hypothetical protein PG_1281* | | | | | | | | | | | | | | | |
| PG1280 | | 0 | 227.6 | 82.5 | 1.4641 | 8.2766 | R | 🔴 | 🔴 | R | 0 | 2.32 E+8 | 5.83 E+7 | 1.9932 | 28.1137 | R | 🔴 |
| *PGN0610* | *PG1128* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1279 | | 0 | 311.5 | 78.5 | 1.9883 | 8.6072 | R | 🔴 | 🔴 | R | 0 | 1.74 E+8 | 3.19 E+7 | 2.4474 | 27.6161 | R | 🔴 |
| *PGN0611* | *PG1127* | *D-isomer specific 2-hydroxyacid dehydrogenase family protein* | | | | | | | | | | | | | | | |
| PG1278 | | 2.1 E-10 | 590.4 | 845.5 | -0.5181 | 10.4877 | G | 🟢 | 🟢 | G | 4.9 E-4 | 6.97 E+8 | 9.92 E+8 | -0.5090 | 30.6535 | G | 🟢 |
| *PGN0612* | *PG1126* | *serC phosphoserine aminotransferase* | | | | | | | | | | | | | | | |
| PG1277 | | 3.58 E-1 | 6.8 | 3.5 | 0.9677 | 3.3709 | Y | 🟡 | 🟡 | Y | 6.85 E-3 | 3.9 E+6 | 2.08 E+6 | 0.9058 | 22.5114 | Y | 🟡 |
| *PGN0613* | *PG1125* | *UDP-glucose-6 dehydrogenase putative* | | | | | | | | | | | | | | | |
| | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟡 | Y | 1.26 E-2 | 1.85 E+3 | 3.9 E+5 | -7.7202 | 18.5807 | Y | 🟡 |
| *PGN0614* | | | | | | | | | | | | | | | | | |
| | | 3.78 E-2 | 34.2 | 17 | 1.0096 | 5.6788 | Y | 🟡 | 🔴 | R | 1.35 E-10 | 7.49 E+6 | 1.6 E+6 | 2.2242 | 23.1164 | R | 🔴 |
| *PGN0616* | | | | | | | | | | | | | | | | | |
| PG0571 | | 2.28 E-2 | 51.3 | 28 | 0.8746 | 6.3100 | Y | 🟡 | 🔴 | R | 5.03 E-5 | 1.7 E+7 | 7.84 E+6 | 1.1132 | 24.5633 | R | 🔴 |
| *PGN0618* | *PG0514* | *asd aspartate-semialdehyde dehydrogenase* | | | | | | | | | | | | | | | |
| PG0573 | | 2.22 E-1 | 2.6 | 7 | -1.4473 | 3.2581 | Y | 🟡 | 🟡 | Y | 3.28 E-2 | 1.88 E+6 | 1.52 E+6 | 0.3058 | 21.6972 | Y | 🟡 |
| *PGN0620* | *PG0515* | *mraW S-adenosyl-methyltransferase MraW* | | | | | | | | | | | | | | | |
| PG0575 | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y | 🟡 | 🔴 | R | 1.22 E-11 | 9.61 E+5 | 1 E+3 | 9.9082 | 19.8755 | R | 🔴 |
| *PGN0622* | *PG0517* | *penicillin-binding protein 2 putative* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG0576 | | 1.03 E-1 | 6.8 | 16 | -1.2249 | 4.5138 | Y 🟡 | 🟡 Y | 1.47 E-3 | 2.36 E+6 | 5.79 E+6 | -1.2979 | 22.9581 | Y 🟡 |
| *PGN0623* | *PG0518* | *murE UDP-N-acetylmuramoylalanyl-D-glutamyl-2 6-diaminopimelate ligase* | | | | | | | | | | | | |
| PG0577 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y 🟡 | 🟢 G | 9.22 E-8 | 1.85 E+3 | 8.75 E+5 | -8.8851 | 19.7419 | G 🟢 |
| *PGN0624* | *PG0519* | *mraY phospho-N-acetylmuramoyl-pentapeptide-transferase* | | | | | | | | | | | | |
| PG0578 | | 4.53 E-1 | 10.3 | 14 | -0.4473 | 4.6010 | Y 🟡 | 🟡 Y | 2.2 E-3 | 1.64 E+7 | 2.56 E+6 | 2.6837 | 24.1788 | Y 🟡 |
| *PGN0625* | *PG0520* | *murD UDP-N-acetylmuramoylalanine--D-glutamate ligase* | | | | | | | | | | | | |
| PG0580 | | 8.52 E-2 | 3.4 | 11 | -1.6843 | 3.8503 | Y 🟡 | 🟢 G | 8.6 E-4 | 6.77 E+5 | 2.25 E+6 | -1.7307 | 21.4796 | G 🟢 |
| *PGN0627* | *PG0522* | *murG UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase* | | | | | | | | | | | | |
| PG0581 | | 2.15 E-1 | 13.7 | 7 | 0.9677 | 4.3709 | Y 🟡 | 🔴 R | 3.84 E-4 | 7.11 E+6 | 2.76 E+6 | 1.3653 | 23.2345 | R 🔴 |
| *PGN0628* | *PG0523* | *murC UDP-N-acetylmuramate--alanine ligase* | | | | | | | | | | | | |
| PG0583 | | 8.63 E-2 | 47.9 | 30 | 0.6756 | 6.2839 | Y 🟡 | 🟡 Y | 2.78 E-2 | 1.5 E+7 | 1.13 E+7 | 0.4144 | 24.6490 | Y 🟡 |
| *PGN0630* | *PG0525* | *ftsA cell division protein FtsA* | | | | | | | | | | | | |
| PG0584 | | 4.23 E-1 | 19.7 | 25.5 | -0.3738 | 5.4976 | Y 🟡 | 🟡 Y | 1.53 E-1 | 1.09 E+7 | 1.16 E+7 | -0.0845 | 24.4208 | Y 🟡 |
| *PGN0631* | *PG0526* | *ftsz cell division protein FtsZ* | | | | | | | | | | | | |
| PG0585 | | 6.69 E-1 | 7.7 | 8.5 | -0.1424 | 4.0180 | Y 🟡 | 🟡 Y | 1.11 E-1 | 4.89 E+6 | 4.23 E+6 | 0.2114 | 23.1202 | Y 🟡 |
| *PGN0632* | *PG0527* | *YqeY family protein* | | | | | | | | | | | | |
| PG0588 | | 4.92 E-1 | 9.4 | 12.5 | -0.4093 | 4.4537 | Y 🟡 | 🟡 Y | 5.98 E-2 | 6.53 E+6 | 1.02 E+7 | -0.6379 | 23.9934 | Y 🟡 |
| *PGN0634* | *PG0530* | *panB 3-methyl-2-oxobutanoate hydroxymethyltransferase* | | | | | | | | | | | | |
| PG0589 | | 2.19 E-5 | 82.1 | 33 | 1.3157 | 6.8473 | R 🔴 | 🔴 R | 0 | 3.97 E+7 | 1.2 E+7 | 1.7285 | 25.6232 | R 🔴 |
| *PGN0635* | *PG0531* | *guaA GMP synthase* | | | | | | | | | | | | |
| PG0592 | | 8.11 E-5 | 32.5 | 6.5 | 2.3226 | 5.2859 | R 🔴 | 🔴 R | 3.06 E-13 | 2.44 E+7 | 4.06 E+6 | 2.5866 | 24.7601 | R 🔴 |
| *PGN0636* | *PG0534* | *rpmE ribosomal protein L31* | | | | | | | | | | | | |
| PG0593 | | 3.9 E-1 | 61.6 | 51.5 | 0.2585 | 6.8215 | Y 🟡 | 🟡 Y | 3 E-2 | 3.75 E+7 | 2.38 E+7 | 0.6600 | 25.8696 | Y 🟡 |
| *PGN0637* | *PG0535* | *htrA htrA protein* | | | | | | | | | | | | |
| PG0594 | | 2.32 E-4 | 19.7 | 2 | 3.2987 | 4.4383 | R 🔴 | 🔴 R | 6.99 E-7 | 3.79 E+6 | 7.37 E+5 | 2.3648 | 22.1116 | R 🔴 |
| *PGN0638* | *PG0536* | *rpoD RNA polymerase sigma-70 factor* | | | | | | | | | | | | |
| PG0595 | | 5.73 E-11 | 53.1 | 4.5 | 3.5594 | 5.8468 | R 🔴 | 🔴 R | 0 | 3.74 E+7 | 2.17 E+6 | 4.1047 | 25.2388 | R 🔴 |
| *PGN0639* | *PG0537* | *rpsF ribosomal protein S6* | | | | | | | | | | | | |
| PG0596 | | 1.84 E-1 | 49.6 | 35 | 0.5038 | 6.4031 | Y 🟡 | 🟡 Y | 1.74 E-2 | 3.69 E+7 | 2.69 E+7 | 0.4525 | 25.9277 | Y 🟡 |
| *PGN0640* | *PG0538* | *rpsR ribosomal protein S18* | | | | | | | | | | | | |
| PG0597 | | 6.23 E-9 | 43.6 | 4 | 3.4475 | 5.5740 | R 🔴 | 🔴 R | 2.09 E-8 | 3.93 E+7 | 2.62 E+6 | 3.9081 | 25.3224 | R 🔴 |
| *PGN0641* | *PG0540* | *rplI ribosomal protein L9* | | | | | | | | | | | | |
| PG0598 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🔴 R | 0 | 4.96 E+5 | 2.29 E+5 | 1.1164 | 19.4670 | Y 🟡 |
| *PGN0642* | *PG0541* | *hypothetical protein PG_0598* | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0599 | | 4.65 E-1 | 76.2 | 85.5 | -0.1670 | 7.3368 | Y | 🟡 | 🟡 | Y | 5.19 E-2 | 5.44 E+7 | 7.06 E+7 | -0.3765 | 26.8969 | Y | 🟡 |
| *PGN0643* | *PG0542* | *ribBA 34-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II* | | | | | | | | | | | | | | | |
| PG0602 | | 9.33 E-12 | 8.6 | 67.5 | -2.9798 | 6.2490 | G | 🟢 | 🟢 | G | 3.63 E-13 | 2.19 E+6 | 2.26 E+7 | -3.3685 | 24.5623 | G | 🟢 |
| *PGN0645* | *PG0543* | *hypothetical protein PG_0602* | | | | | | | | | | | | | | | |
| PG0603 | | 9.55 E-3 | 10.3 | 1 | 3.3601 | 3.4941 | Y | 🟡 | 🔴 | R | 0 | 4.66 E+6 | 1 E+3 | 12.1866 | 22.1527 | R | 🔴 |
| *PGN0646* | *PG0544* | *cmk cytidylate kinase* | | | | | | | | | | | | | | | |
| PG0604 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟢 | G | 7.52 E-4 | 1.85 E+3 | 3.25 E+5 | -7.4575 | 18.3194 | G | 🟢 |
| *PGN0647* | *PG0545* | *ispH hydroxymethylbutenyl pyrophosphate reductase* | | | | | | | | | | | | | | | |
| PG0611 | | 3.82 E-1 | 53.9 | 64.5 | -0.2589 | 6.8876 | Y | 🟡 | 🟡 | Y | 8.76 E-3 | 2.54 E+7 | 4.53 E+7 | -0.8364 | 26.0739 | Y | 🟡 |
| *PGN0654* | *PG0550* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG0613 | | 2.25 E-1 | 1.7 | 5.5 | -1.6843 | 2.8503 | Y | 🟡 | 🟡 | Y | 1.99 E-2 | 1.85 E+3 | 1.3 E+6 | -9.4556 | 20.3114 | Y | 🟡 |
| *PGN0656* | *PG0551* | *hypothetical protein PG_0613* | | | | | | | | | | | | | | | |
| PG0614 | | 2.6 E-2 | 6.0 | 18.5 | -1.6270 | 4.6141 | Y | 🟡 | 🟡 | Y | 1.5 E-3 | 4.76 E+6 | 1.51 E+7 | -1.6634 | 24.2411 | Y | 🟡 |
| *PGN0657* | *PG0552* | *hypothetical protein PG_0614* | | | | | | | | | | | | | | | |
| PG0615 | | 5.89 E-1 | 19.7 | 17 | 0.2112 | 5.1969 | Y | 🟡 | 🟡 | Y | 7.7 E-2 | 7.4 E+6 | 5.82 E+6 | 0.3454 | 23.6560 | Y | 🟡 |
| *PGN0658* | *PG0553* | *typA GTP-binding protein TypA* | | | | | | | | | | | | | | | |
| PG0616 | | 0 | 367.1 | 659.5 | -0.8453 | 10.0036 | G | 🟢 | 🟡 | Y | 5.12 E-3 | 5.06 E+8 | 6.8 E+8 | -0.4273 | 30.1434 | G | 🟢 |
| *PGN0659* | *PG0554* | *thioredoxin putative* | | | | | | | | | | | | | | | |
| PG0618 | | 1.38 E-6 | 140.3 | 66 | 1.0883 | 7.6888 | R | 🔴 | 🔴 | R | 7.42 E-6 | 1.84 E+8 | 1 E+8 | 0.8746 | 28.0794 | R | 🔴 |
| *PGN0660* | *PG0556* | *alkyl hydroperoxide reductase C subunit* | | | | | | | | | | | | | | | |
| PG0619 | | 9.3 E-2 | 18.8 | 8.5 | 1.1471 | 4.7721 | Y | 🟡 | 🟡 | Y | 1.06 E-1 | 3.66 E+6 | 4.35 E+6 | -0.2499 | 22.9334 | Y | 🟡 |
| *PGN0661* | *PG0557* | *alkyl hydroperoxide reductase F subunit* | | | | | | | | | | | | | | | |
| PG0620 | | 1.17 E-2 | 73.6 | 42.5 | 0.7920 | 6.8591 | Y | 🟡 | 🔴 | R | 0 | 2.84 E+7 | 7.83 E+6 | 1.8616 | 25.1122 | R | 🔴 |
| *PGN0662* | *PG0558* | *lon ATP-dependent protease La* | | | | | | | | | | | | | | | |
| PG0621 | | 4.75 E-1 | 12.8 | 9.5 | 0.4341 | 4.4812 | Y | 🟡 | 🟡 | Y | 2.39 E-3 | 4.33 E+6 | 2.59 E+6 | 0.7412 | 22.7223 | Y | 🟡 |
| *PGN0663* | *PG0559* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0622 | | 3.76 E-1 | 6.0 | 3 | 0.9975 | 3.1683 | Y | 🟡 | 🟡 | Y | 1.52 E-1 | 2.08 E+6 | 1.81 E+6 | 0.1990 | 21.8943 | Y | 🟡 |
| *PGN0664* | *PG0560* | *hypothetical protein PG_0622* | | | | | | | | | | | | | | | |
| PG0623 | | 4.23 E-1 | 361.9 | 339.5 | 0.0923 | 9.4542 | Y | 🟡 | 🟢 | G | 2.73 E-4 | 2.01 E+8 | 3.94 E+8 | -0.9721 | 29.1476 | Y | 🟡 |
| *PGN0665* | *PG0561* | *tpiA triosephosphate isomerase* | | | | | | | | | | | | | | | |
| PG0624 | | 9.44 E-2 | 6.0 | 1 | 2.5825 | 2.8052 | Y | 🟡 | 🔴 | R | 0 | 1.7 E+6 | 1 E+3 | 10.7313 | 20.6980 | R | 🔴 |
| *PGN0666* | *PG0562* | *hypothetical protein PG_0624* | | | | | | | | | | | | | | | |
| PG0625 | | 4.75 E-1 | 18.0 | 14 | 0.3601 | 4.9986 | Y | 🟡 | 🟡 | Y | 6.08 E-2 | 7.13 E+6 | 2.12 E+7 | -1.5689 | 24.7536 | Y | 🟡 |
| *PGN0667* | *PG0563* | *folE GTP cyclohydrolase I* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0627 | | 2.4 E-1 | 20.5 | 12.5 | 0.7162 | 5.0460 | Y | 🟡 | 🔴 | R | 1.77 E-10 | 1.8 E+7 | 6.25 E+6 | 1.5220 | 24.5291 | R | 🔴 |
| *PGN0668* | *PG0565* | *RNA-binding protein* | | | | | | | | | | | | | | | |
| | | 6.54 E-1 | 2.6 | 2 | 0.3601 | 2.1912 | Y | 🟡 | 🟡 | Y | 1.17 E-2 | 1.04 E+6 | 1.44 E+6 | -0.4646 | 21.2430 | Y | 🟡 |
| *PGN0669* | | | | | | | | | | | | | | | | | |
| PG0629 | | 4.75 E-1 | 3.4 | 5.5 | -0.6843 | 3.1575 | Y | 🟡 | 🟡 | Y | 1.36 E-3 | 8.6 E+5 | 3.29 E+6 | -1.9333 | 21.9834 | Y | 🟡 |
| *PGN0670* | *PG0568* | *ppnK ATP-NAD kinase* | | | | | | | | | | | | | | | |
| PG0630 | | 5.99 E-2 | 32.5 | 53 | -0.7049 | 6.4181 | Y | 🟡 | 🟡 | Y | 7.1 E-2 | 1.73 E+7 | 2 E+7 | -0.2131 | 25.1515 | Y | 🟡 |
| *PGN0671* | *PG0569* | *pdxJ pyridoxal phosphate biosynthetic protein PdxJ* | | | | | | | | | | | | | | | |
| PG0631 | | 9.84 E-2 | 17.1 | 7.5 | 1.1901 | 4.6214 | Y | 🟡 | 🟡 | Y | 1.44 E-1 | 8.39 E+6 | 7.1 E+6 | 0.2407 | 23.8844 | Y | 🟡 |
| *PGN0672* | *PG0570* | *MotA/TolQ/ExbB proton channel family protein* | | | | | | | | | | | | | | | |
| PG0632 | | 1.31 E-3 | 13.7 | 1 | 3.7751 | 3.8768 | Y | 🟡 | 🔴 | R | 0 | 3.82 E+6 | 1 E+3 | 11.8991 | 21.8653 | R | 🔴 |
| *PGN0673* | *PG0571* | *biopolymer transport protein ExbD putative* | | | | | | | | | | | | | | | |
| PG0633 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 2.36 E-4 | 1.85 E+3 | 9.73 E+5 | -9.0384 | 19.8948 | G | 🟢 |
| *PGN0674* | *PG0573* | *hypothetical protein PG_0633* | | | | | | | | | | | | | | | |
| PG0634 | | 4.86 E-2 | 33.4 | 17 | 0.9730 | 5.6545 | Y | 🟡 | 🟡 | Y | 1.23 E-1 | 1.76 E+7 | 2.29 E+7 | -0.3833 | 25.2719 | Y | 🟡 |
| *PGN0675* | *PG0575* | *ThiJ/PfpI family protein* | | | | | | | | | | | | | | | |
| PG0637 | | 3.93 E-1 | 4.3 | 7.5 | -0.8099 | 3.5581 | Y | 🟡 | 🟢 | G | 8.35 E-5 | 2.4 E+5 | 4.31 E+5 | -0.8461 | 19.3544 | G | 🟢 |
| *PGN0678* | *PG0578* | *thiL thiamine monophosphate kinase* | | | | | | | | | | | | | | | |
| PG0638 | | 6 E-1 | 6.8 | 5.5 | 0.3157 | 3.6259 | Y | 🟡 | 🟡 | Y | 2.71 E-3 | 3.97 E+6 | 4.36 E+5 | 3.1872 | 22.0702 | Y | 🟡 |
| *PGN0679* | *PG0579* | *lpxK tetraacyldisaccharide 4'-kinase* | | | | | | | | | | | | | | | |
| PG0639 | | 4.31 E-1 | 46.2 | 54.5 | -0.2382 | 6.6540 | Y | 🟡 | 🟡 | Y | 2.16 E-3 | 3.08 E+7 | 4.56 E+7 | -0.5675 | 26.1865 | Y | 🟡 |
| *PGN0680* | *PG0580* | *sppA signal peptide peptidase SppA 67K type* | | | | | | | | | | | | | | | |
| | | 2.4 E-2 | 203.6 | 260 | -0.3525 | 8.8569 | Y | 🟡 | 🟢 | G | 6.19 E-5 | 1.06 E+8 | 1.69 E+8 | -0.6745 | 28.0328 | G | 🟢 |
| *PGN0683* | | | | | | | | | | | | | | | | | |
| PG0645 | | 3.82 E-1 | 3.4 | 6.5 | -0.9253 | 3.3107 | Y | 🟡 | 🟡 | Y | 1.51 E-2 | 1.21 E+6 | 3.2 E+6 | -1.4038 | 22.0714 | Y | 🟡 |
| *PGN0684* | *PG0583* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG0648 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟢 | G | 2.98 E-9 | 1.85 E+3 | 4.24 E+5 | -7.8408 | 18.7008 | G | 🟢 |
| *PGN0687* | *PG0586* | *iron compound ABC transporter periplasmic iron compound-binding protein putative* | | | | | | | | | | | | | | | |
| PG0651 | | 1.84 E-1 | 1.7 | 6 | -1.8099 | 2.9470 | Y | 🟡 | 🟢 | G | 9.27 E-6 | 1.85 E+3 | 1.16 E+6 | -9.2937 | 20.1497 | G | 🟢 |
| *PGN0690* | *PG0589* | *HDIG domain protein* | | | | | | | | | | | | | | | |
| PG0652 | | 1.06 E-1 | 22.2 | 37 | -0.7339 | 5.8887 | Y | 🟡 | 🟡 | Y | 5.24 E-2 | 4.65 E+6 | 6.28 E+6 | -0.4337 | 23.3822 | Y | 🟡 |
| *PGN0691* | *PG0590* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0653 | | 7.86 E-6 | 39.4 | 7.5 | 2.3918 | 5.5503 | R | 🔴 | 🔴 | R | 5.38 E-8 | 1.05 E+7 | 4.15 E+6 | 1.3363 | 23.8017 | R | 🔴 |
| *PGN0692* | *PG0591* | *serB phosphoserine phosphatase* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG0654 | | 3.58 E-1 | 33.4 | 42.5 | -0.3489 | 6.2455 | Y | 🟡 | 🟡 | Y | 2.53 E-3 | 3.24 E+7 | 6.24 E+7 | -0.9451 | 26.4990 | Y | 🟡 |
| *PGN0693* | *PG0592* | *hypothetical protein PG_0654* | | | | | | | | | | | | | | | |
| PG0658 | | 1.54 E-1 | 10.3 | 19.5 | -0.9253 | 4.8957 | Y | 🟡 | 🟢 | G | 4.01 E-4 | 3.94 E+6 | 1.08 E+7 | -1.4525 | 23.8123 | G | 🟢 |
| *PGN0696* | *PG0594* | *phosphatase YrbI family* | | | | | | | | | | | | | | | |
| PG0659 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟡 | Y | 2.95 E-2 | 1.85 E+3 | 7.7 E+5 | -8.6999 | 19.5570 | Y | 🟡 |
| *PGN0697* | *PG0595* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0660 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 2.06 E-6 | 6.51 E+5 | 2.99 E+6 | -2.2023 | 21.7978 | G | 🟢 |
| *PGN0698* | *PG0596* | *nitroreductase family protein* | | | | | | | | | | | | | | | |
| PG0664 | | 6.27 E-1 | 22.2 | 24.5 | -0.1392 | 5.5468 | Y | 🟡 | 🔴 | R | 2.9 E-4 | 8.14 E+6 | 4.19 E+6 | 0.9604 | 23.5555 | Y | 🟡 |
| *PGN0700* | *PG0597* | *oxidoreductase Gfo/Idh/MocA family* | | | | | | | | | | | | | | | |
| PG0665 | | 9.53 E-2 | 7.7 | 17.5 | -1.1843 | 4.6554 | Y | 🟡 | 🟢 | G | 1.36 E-4 | 8.77 E+5 | 3.74 E+6 | -2.0927 | 22.1390 | G | 🟢 |
| *PGN0701* | *PG0598* | *lacZ-1 beta-galactosidase* | | | | | | | | | | | | | | | |
| | | 5.95 E-1 | 6.8 | 8.5 | -0.3124 | 3.9397 | Y | 🟡 | 🟡 | Y | 1.74 E-1 | 1.84 E+6 | 1.97 E+6 | -0.0991 | 21.8614 | Y | 🟡 |
| *PGN0702* | | | | | | | | | | | | | | | | | |
| | | 4.75 E-1 | 6.8 | 4.5 | 0.6052 | 3.5040 | Y | 🟡 | 🔴 | R | 1.29 E-4 | 2.55 E+6 | 9.46 E+5 | 1.4277 | 21.7355 | R | 🔴 |
| *PGN0703* | | | | | | | | | | | | | | | | | |
| PG0668 | | 0 | 261.8 | 502.5 | -0.9405 | 9.5781 | G | 🟢 | 🟢 | G | 3.56 E-6 | 1.05 E+8 | 1.94 E+8 | -0.8816 | 28.1542 | G | 🟢 |
| *PGN0704* | *PG0601* | *TonB-dependent receptor* | | | | | | | | | | | | | | | |
| PG0669 | | 4.32 E-5 | 32.5 | 79.5 | -1.2899 | 6.8075 | G | 🟢 | 🟢 | G | 7.69 E-11 | 1.76 E+7 | 6.67 E+7 | -1.9187 | 26.3297 | G | 🟢 |
| *PGN0705* | *PG0602* | *fetB heme-binding protein FetB* | | | | | | | | | | | | | | | |
| PG0670 | | 4.53 E-1 | 8.6 | 12 | -0.4879 | 4.3615 | Y | 🟡 | 🟢 | G | 5.33 E-4 | 3.83 E+6 | 7.16 E+6 | -0.9048 | 23.3898 | G | 🟢 |
| *PGN0706* | *PG0603* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG0672 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.75 E+5 | -6.5627 | 17.4316 | G | 🟢 |
| *PGN0708* | *PG0605* | *iron compound ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG0674 | | 6.61 E-8 | 59.9 | 12.5 | 2.2605 | 6.1778 | R | 🔴 | 🔴 | R | 0 | 6.21 E+7 | 8.06 E+6 | 2.9456 | 26.0648 | R | 🔴 |
| *PGN0709* | *PG0606* | *iorB indolepyruvate ferredoxin oxidoreductase beta subunit* | | | | | | | | | | | | | | | |
| PG0675 | | 9.88 E-4 | 118.1 | 68 | 0.7962 | 7.5398 | R | 🔴 | 🔴 | R | 7.88 E-8 | 1.06 E+8 | 4.93 E+7 | 1.1068 | 27.2109 | R | 🔴 |
| *PGN0710* | *PG0607* | *iorA indolepyruvate ferredoxin oxidoreductase alpha subunit* | | | | | | | | | | | | | | | |
| PG0676 | | 3.58 E-1 | 33.4 | 42.5 | -0.3489 | 6.2455 | Y | 🟡 | 🟡 | Y | 5.24 E-3 | 2.13 E+7 | 3.25 E+7 | -0.6108 | 25.6798 | Y | 🟡 |
| *PGN0711* | *PG0608* | *oxidoreductase short chain dehydrogenase/reductase family* | | | | | | | | | | | | | | | |
| PG0677 | | 7.02 E-6 | 47.9 | 11.5 | 2.0589 | 5.8928 | R | 🔴 | 🔴 | R | 0 | 3.53 E+7 | 3.8 E+6 | 3.2134 | 25.2192 | R | 🔴 |
| *PGN0713* | *PG0609* | *LYS1 saccharopine dehydrogenase* | | | | | | | | | | | | | | | |
| PG0678 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 2.74 E-6 | 1.85 E+3 | 8.31 E+5 | -8.8106 | 19.6675 | G | 🟢 |
| *PGN0714* | *PG0610* | *pyrazinamidase/nicotinamidase putative* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | q-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | q-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus |
| | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y 🟡 | 🔴 R | 2.08 E-11 | 3.46 E+6 | 1.42 E+6 | 1.2812 | 22.2181 | R 🔴 |
| *PGN0721* | | | | | | | | | | | | | | |
| PG0686 | | 1.45 E-1 | 60.8 | 43 | 0.4986 | 6.6970 | Y 🟡 | 🔴 R | 1.63 E-8 | 2.37 E+7 | 1.14 E+7 | 1.0583 | 25.0612 | R 🔴 |
| *PGN0722* | *PG0620* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG0687 | | 8.11 E-5 | 926.7 | 1123.5 | -0.2779 | 11.0015 | G 🟢 | 🟡 Y | 3.86 E-2 | 7.79 E+8 | 6.94 E+8 | 0.1684 | 30.4560 | Y 🟡 |
| *PGN0723* | *PG0621* | *sucD succinate-semialdehyde dehydrogenase* | | | | | | | | | | | | |
| PG0689 | | 2.67 E-1 | 475.7 | 435.5 | 0.1275 | 9.8317 | Y 🟡 | 🟡 Y | 2.01 E-1 | 4.04 E+8 | 4.04 E+8 | -0.0012 | 29.5904 | Y 🟡 |
| *PGN0724* | *PG0622* | *4hbD NAD-dependent 4-hydroxybutyrate dehydrogenase* | | | | | | | | | | | | |
| PG0690 | | 1.43 E-1 | 280.7 | 324 | -0.2072 | 9.2400 | Y 🟡 | 🟡 Y | 1.94 E-2 | 2.12 E+8 | 2.72 E+8 | -0.3595 | 28.8498 | Y 🟡 |
| *PGN0725* | *PG0623* | *abfT-1 4-hydroxybutyrate CoA-transferase* | | | | | | | | | | | | |
| PG0691 | | 4.65 E-1 | 2.6 | 4.5 | -0.8099 | 2.8211 | Y 🟡 | 🟡 Y | 1.74 E-2 | 7.31 E+5 | 1.33 E+6 | -0.8602 | 20.9721 | Y 🟡 |
| *PGN0726* | *PG0624* | *NifU-related protein* | | | | | | | | | | | | |
| PG0692 | | 7.34 E-5 | 1542.7 | 1795.5 | -0.2189 | 11.7049 | G 🟢 | 🟡 Y | 2.34 E-2 | 1.18 E+9 | 1.39 E+9 | -0.2342 | 31.2597 | G 🟢 |
| *PGN0727* | *PG0625* | *abfD 4-hydroxybutyryl-CoA dehydratase* | | | | | | | | | | | | |
| PG0694 | | 0 | 363.7 | 1101.5 | -1.5988 | 10.5168 | G 🟢 | 🟢 G | 3.7 E-4 | 5.59 E+8 | 7.66 E+8 | -0.4550 | 30.3032 | G 🟢 |
| *PGN0728* | *PG0626* | *immunoreactive 42 kDa antigen PG33* | | | | | | | | | | | | |
| PG0695 | | 0 | 313.2 | 982 | -1.6488 | 10.3389 | G 🟢 | 🟢 G | 5.77 E-5 | 4.91 E+8 | 8.23 E+8 | -0.7442 | 30.2917 | G 🟢 |
| *PGN0729* | *PG0627* | *immunoreactive 43 kDa antigen PG32* | | | | | | | | | | | | |
| PG0698 | | 6.05 E-2 | 6.8 | 1 | 2.7751 | 2.9718 | Y 🟡 | 🔴 R | 3.06 E-4 | 2.59 E+6 | 1 E+3 | 11.3400 | 21.3063 | R 🔴 |
| *PGN0732* | *PG0628* | *lipoprotein putative* | | | | | | | | | | | | |
| PG0699 | | 2.18 E-7 | 41.9 | 109.5 | -1.3850 | 7.2425 | G 🟢 | 🟢 G | 2.75 E-10 | 1.94 E+7 | 4.72 E+7 | -1.2809 | 25.9892 | G 🟢 |
| *PGN0733* | *PG0629* | *malP maltodextrin phosphorylase* | | | | | | | | | | | | |
| PG0701 | | 5.43 E-1 | 6.0 | 8 | -0.4175 | 3.8063 | Y 🟡 | 🟡 Y | 5.81 E-2 | 1.46 E+6 | 1.21 E+6 | 0.2684 | 21.3497 | Y 🟡 |
| *PGN0735* | *PG0631* | *cobU cobinamide kinase/cobinamide phosphate guanylyltransferase* | | | | | | | | | | | | |
| PG0702 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y 🟡 | 🟢 G | 2.23 E-5 | 1.85 E+3 | 5.31 E+5 | -8.1650 | 19.0237 | G 🟢 |
| *PGN0736* | *PG0632* | *nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase putative* | | | | | | | | | | | | |
| PG0704 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y 🟡 | 🟢 G | 1.98 E-4 | 1.85 E+3 | 7.54 E+5 | -8.6712 | 19.5285 | G 🟢 |
| *PGN0738* | *PG0634* | *phosphoglycerate mutase family protein* | | | | | | | | | | | | |
| PG0705 | | 6.78 E-1 | 25.7 | 25 | 0.0381 | 5.6630 | Y 🟡 | 🔴 R | 2.4 E-11 | 1.73 E+7 | 7.32 E+6 | 1.2406 | 24.5537 | R 🔴 |
| *PGN0739* | *PG0635* | *murI glutamate racemase* | | | | | | | | | | | | |
| PG0706 | | 4.93 E-1 | 7.7 | 10.5 | -0.4473 | 4.1859 | Y 🟡 | 🟡 Y | 1.08 E-1 | 4.71 E+6 | 5.68 E+6 | -0.2716 | 23.3091 | Y 🟡 |
| *PGN0740* | *PG0636* | *hypothetical protein PG_0706* | | | | | | | | | | | | |
| PG0707 | | 0 | 160.9 | 436.5 | -1.4402 | 9.2225 | G 🟢 | 🟢 G | 7.61 E-16 | 6.17 E+7 | 2.34 E+8 | -1.9211 | 28.1370 | G 🟢 |
| *PGN0741* | *PG0637* | *TonB-dependent receptor putative* | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Regulation** | | | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Consensus** | |
| PG0708 | | 6.89 E-8 | 253.3 | 401 | -0.6629 | 9.3537 | G | 🟢 | 🟡 | Y | 1.2 E-2 | 8.98 E+7 | 1.53 E+8 | -0.7657 | 27.8540 | G | 🟢 |
| *PGN0742* | *PG0639* | *peptidyl-prolyl cis-trans isomerase FKBP-type* | | | | | | | | | | | | | | | |
| PG0709 | | 1.31 E-1 | 44.5 | 29 | 0.6176 | 6.1996 | Y | 🟡 | 🟡 | Y | 3.21 E-2 | 6.24 E+7 | 4.35 E+7 | 0.5201 | 26.6591 | Y | 🟡 |
| *PGN0743* | *PG0640* | *fkpA peptidyl-prolyl cis-trans isomerase FkpA FKBP-type* | | | | | | | | | | | | | | | |
| PG0710 | | 2.31 E-4 | 24.8 | 4 | 2.6331 | 4.8487 | R | 🔴 | 🔴 | R | 5.17 E-9 | 1.26 E+7 | 2.46 E+6 | 2.3504 | 23.8409 | R | 🔴 |
| *PGN0744* | *PG0641* | *peptidyl-prolyl cis-trans isomerase FKBP-type* | | | | | | | | | | | | | | | |
| PG0712 | | 4.91 E-1 | 10.3 | 13.5 | -0.3948 | 4.5709 | Y | 🟡 | 🟡 | Y | 7.61 E-2 | 4.4 E+6 | 3.59 E+6 | 0.2942 | 22.9300 | Y | 🟡 |
| *PGN0746* | *PG0642* | *hypothetical protein PG_0712* | | | | | | | | | | | | | | | |
| PG0713 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟢 | G | 5.69 E-6 | 1.85 E+3 | 3.9 E+5 | -7.7184 | 18.5790 | G | 🟢 |
| *PGN0747* | *PG0643* | *trpG anthranilate synthase component II* | | | | | | | | | | | | | | | |
| | | 5.17 E-1 | 73.6 | 66.5 | 0.1461 | 7.1302 | Y | 🟡 | 🟡 | Y | 4.8 E-2 | 3.72 E+7 | 3.31 E+7 | 0.1698 | 26.0665 | Y | 🟡 |
| *PGN0748* | | | | | | | | | | | | | | | | | |
| PG0714 | | 2.84 E-2 | 1.7 | 10 | -2.5468 | 3.5498 | Y | 🟡 | 🟡 | Y | 3.74 E-2 | 7.93 E+5 | 1.03 E+6 | -0.3812 | 20.8009 | Y | 🟡 |
| *PGN0750* | *PG0644* | *cutC copper homeostasis protein CutC* | | | | | | | | | | | | | | | |
| PG0715 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 9.82 E+5 | 1 E+3 | 9.9391 | 19.9064 | R | 🔴 |
| *PGN0751* | *PG0645* | *transporter* | | | | | | | | | | | | | | | |
| PG0724 | | 1.44 E-2 | 167.7 | 223.5 | -0.4143 | 8.6118 | Y | 🟡 | 🟢 | G | 2.34 E-5 | 9.48 E+7 | 1.59 E+8 | -0.7500 | 27.9209 | G | 🟢 |
| *PGN0756* | *PG0652* | *prolyl oligopeptidase family protein* | | | | | | | | | | | | | | | |
| PG0725 | | 1.45 E-1 | 5.1 | 1 | 2.3601 | 2.6168 | Y | 🟡 | 🔴 | R | 2.92 E-10 | 2.6 E+6 | 1 E+3 | 11.3430 | 21.3093 | R | 🔴 |
| *PGN0757* | *PG0653* | *hydrolase haloacid dehalogenase-like family* | | | | | | | | | | | | | | | |
| PG0726 | | 1.52 E-4 | 22.2 | 59.5 | -1.4193 | 6.3531 | G | 🟢 | 🟡 | Y | 1.22 E-3 | 2.61 E+7 | 7.08 E+7 | -1.4379 | 26.5303 | G | 🟢 |
| *PGN0758* | *PG0654* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG0728 | | 6.69 E-1 | 9.4 | 10 | -0.0874 | 4.2789 | Y | 🟡 | 🟡 | Y | 4.54 E-2 | 3.86 E+6 | 2.55 E+6 | 0.5950 | 22.6119 | Y | 🟡 |
| *PGN0759* | *PG0655* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0729 | | 6.92 E-2 | 3.4 | 11.5 | -1.7485 | 3.8994 | Y | 🟡 | 🟢 | G | 1.95 E-4 | 8.58 E+5 | 3.95 E+6 | -2.2028 | 22.1968 | G | 🟢 |
| *PGN0760* | *PG0656* | *ddlA D-alanine--D-alanine ligase* | | | | | | | | | | | | | | | |
| PG0733 | | 1.92 E-1 | 38.5 | 26 | 0.5665 | 6.0113 | Y | 🟡 | 🔴 | R | 8.36 E-4 | 2.24 E+7 | 1.31 E+7 | 0.7717 | 25.0825 | R | 🔴 |
| *PGN0764* | *PG0661* | *ribE riboflavin synthase alpha subunit* | | | | | | | | | | | | | | | |
| PG0734 | | 6.45 E-2 | 18.0 | 33.5 | -0.8987 | 5.6856 | Y | 🟡 | 🟡 | Y | 1.51 E-2 | 7.66 E+6 | 1.24 E+7 | -0.6925 | 24.2557 | Y | 🟡 |
| *PGN0765* | *PG0662* | *nitroreductase family protein* | | | | | | | | | | | | | | | |
| PG0735 | | 4.4 E-1 | 21.4 | 27 | -0.3359 | 5.5967 | Y | 🟡 | 🔴 | R | 2.24 E-6 | 8.25 E+6 | 3.93 E+6 | 1.0690 | 23.5379 | Y | 🟡 |
| *PGN0766* | *PG0663* | *aminotransferase class V* | | | | | | | | | | | | | | | |
| PG0737 | | 1.45 E-1 | 5.1 | 1 | 2.3601 | 2.6168 | Y | 🟡 | 🔴 | R | 2.13 E-13 | 1.23 E+6 | 1 E+3 | 10.2692 | 20.2361 | R | 🔴 |
| *PGN0768* | *PG0665* | *hypothetical protein PG_0737* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus |
| PG0738 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 7.02 E-8 | 1.85 E+3 | 1.98 E+5 | -6.7403 | 17.6075 | G 🟢 |
| *PGN0769* | *PG0666* | *cytidine/deoxycytidylate deaminase family protein* | | | | | | | | | | | | |
| PG0739 | | 3.71 E-1 | 9.4 | 5.5 | 0.7751 | 3.8984 | Y 🟡 | 🟡 Y | 1.08 E-1 | 1.24 E+6 | 1.72 E+6 | -0.4731 | 21.4951 | Y 🟡 |
| *PGN0770* | *PG0667* | *metallo-beta-lactamase family protein* | | | | | | | | | | | | |
| PG0745 | | 3.64 E-1 | 5.1 | 9 | -0.8099 | 3.8211 | Y 🟡 | 🟡 Y | 8.85 E-2 | 3.05 E+6 | 2.2 E+6 | 0.4697 | 22.3231 | Y 🟡 |
| *PGN0773* | *PG0673* | *lactoylglutathione lyase putative* | | | | | | | | | | | | |
| PG0747 | | 6.33 E-1 | 7.7 | 6.5 | 0.2446 | 3.8279 | Y 🟡 | 🔴 R | 1.59 E-6 | 1.73 E+6 | 5.41 E+5 | 1.6811 | 21.1173 | R 🔴 |
| *PGN0775* | *PG0675* | *sigma-54 dependent DNA-binding response regulator* | | | | | | | | | | | | |
| PG0750 | | 5.17 E-1 | 3.4 | 2 | 0.7751 | 2.4390 | Y 🟡 | 🔴 R | 1.5 E-4 | 1.15 E+6 | 6.66 E+5 | 0.7863 | 20.7917 | R 🔴 |
| *PGN0777* | *PG0676* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | |
| PG0751 | | 6.69 E-5 | 1.7 | 21 | -3.6172 | 4.5053 | G 🟢 | 🟢 G | 5.43 E-6 | 1.85 E+3 | 6.74 E+6 | -11.8297 | 22.6838 | G 🟢 |
| *PGN0778* | *PG0677* | *porT porT protein* | | | | | | | | | | | | |
| PG0752 | | 8.33 E-5 | 14.5 | 48 | -1.7224 | 5.9668 | G 🟢 | 🟢 G | 8.31 E-6 | 1.03 E+7 | 2.63 E+7 | -1.3469 | 25.1273 | G 🟢 |
| *PGN0779* | *PG0678* | *uracil phosphoribosyltransferase putative* | | | | | | | | | | | | |
| PG0753 | | 4.21 E-1 | 3.4 | 1.5 | 1.1901 | 2.2994 | Y 🟡 | 🔴 R | 9.64 E-4 | 1.26 E+6 | 1.62 E+5 | 2.9580 | 20.4364 | R 🔴 |
| *PGN0780* | *PG0679* | *prtQ protease* | | | | | | | | | | | | |
| PG0754 | | 1.21 E-2 | 25.7 | 9 | 1.5121 | 5.1156 | Y 🟡 | 🔴 R | 2.26 E-5 | 6.49 E+6 | 2.82 E+6 | 1.2007 | 23.1502 | R 🔴 |
| *PGN0781* | *PG0680* | *topA DNA topoisomerase I* | | | | | | | | | | | | |
| | | 5.43 E-1 | 12.0 | 9.5 | 0.3345 | 4.4249 | Y 🟡 | 🟡 Y | 3.11 E-3 | 4.81 E+6 | 2.71 E+6 | 0.8296 | 22.8422 | Y 🟡 |
| *PGN0783* | | | | | | | | | | | | | | |
| | | 3.43 E-1 | 24.0 | 17 | 0.4950 | 5.3561 | Y 🟡 | 🟡 Y | 4.1 E-3 | 8.27 E+6 | 4.87 E+6 | 0.7641 | 23.6483 | Y 🟡 |
| *PGN0784* | | | | | | | | | | | | | | |
| PG0756 | | 1.61 E-1 | 6.8 | 2 | 1.7751 | 3.1449 | Y 🟡 | 🟡 Y | 6.07 E-2 | 9.57 E+5 | 6.69 E+5 | 0.5163 | 20.6324 | Y 🟡 |
| *PGN0786* | *PG0682* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG0758 | | 6.96 E-1 | 68.5 | 69 | -0.0115 | 7.1028 | Y 🟡 | 🟡 Y | 1.82 E-1 | 4.38 E+7 | 4.47 E+7 | -0.0289 | 26.3996 | Y 🟡 |
| *PGN0788* | *PG0684* | *dcp-1 peptidyl-dipeptidase Dcp* | | | | | | | | | | | | |
| PG0759 | | 6.69 E-1 | 26.5 | 28 | -0.0781 | 5.7689 | Y 🟡 | 🟡 Y | 6.34 E-2 | 6.25 E+6 | 7.75 E+6 | -0.3112 | 23.7392 | Y 🟡 |
| *PGN0789* | *PG0685* | *TPR domain protein* | | | | | | | | | | | | |
| PG0762 | | 5.43 E-1 | 112.9 | 105 | 0.1052 | 7.7678 | Y 🟡 | 🔴 R | 6.82 E-10 | 1.12 E+8 | 5.52 E+7 | 1.0260 | 27.3216 | R 🔴 |
| *PGN0791* | *PG0687* | *trigger factor putative* | | | | | | | | | | | | |
| PG0766 | | 1.45 E-1 | 287.5 | 331 | -0.2033 | 9.2726 | Y 🟡 | 🟡 Y | 1.96 E-1 | 2.58 E+8 | 2.59 E+8 | -0.0068 | 28.9453 | Y 🟡 |
| *PGN0792* | *PG0690* | *pnpA polyribonucleotide nucleotidyltransferase* | | | | | | | | | | | | |
| PG0767 | | 1.26 E-2 | 19.7 | 42 | -1.0937 | 5.9467 | Y 🟡 | 🟡 Y | 4.68 E-3 | 5.49 E+6 | 9.28 E+6 | -0.7587 | 23.8161 | Y 🟡 |
| *PGN0793* | *PG0691* | *malQ 4-alpha-glucanotransferase* | | | | | | | | | | | | |

| **TIGR** | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0768 | | 2.14 E-1 | 3.4 | 8.5 | -1.3124 | 3.5756 | Y | 🟡 | 🟡 | Y | 1.92 E-3 | 9.63 E+5 | 4.37 E+6 | -2.1807 | 22.3461 | Y | 🟡 |
| *PGN0794* | *PG0692* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0769 | | 6.18 E-2 | 12.8 | 26.5 | -1.0459 | 5.2977 | Y | 🟡 | 🟡 | Y | 1.35 E-1 | 1.57 E+7 | 1.23 E+7 | 0.3486 | 24.7410 | Y | 🟡 |
| *PGN0795* | *PG0693* | *fibronectin type III domain protein* | | | | | | | | | | | | | | | |
| PG0774 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 3.27 E+5 | -7.4660 | 18.3279 | Y | 🟡 |
| *PGN0798* | *PG0695* | *hypothetical protein PG_0774* | | | | | | | | | | | | | | | |
| PG0775 | | 6.34 E-3 | 160.0 | 109 | 0.5538 | 8.0715 | R | 🔴 | 🟡 | Y | 1.86 E-3 | 1.12 E+8 | 7.09 E+7 | 0.6559 | 27.4451 | R | 🔴 |
| *PGN0799* | *PG0696* | *acyl-CoA dehydrogenase family protein* | | | | | | | | | | | | | | | |
| PG0776 | | 4.76 E-7 | 126.6 | 54.5 | 1.2164 | 7.5009 | R | 🔴 | 🔴 | R | 0 | 7.17 E+7 | 2.27 E+7 | 1.6614 | 26.4909 | R | 🔴 |
| *PGN0800* | *PG0697* | *etfA-1 electron transfer flavoprotein alpha subunit* | | | | | | | | | | | | | | | |
| PG0777 | | 0 | 124.9 | 10 | 3.6430 | 7.0760 | R | 🔴 | 🔴 | R | 0 | 6.12 E+7 | 1.21 E+7 | 2.3394 | 26.1277 | R | 🔴 |
| *PGN0801* | *PG0698* | *etfB-1 electron transfer flavoprotein beta subunit* | | | | | | | | | | | | | | | |
| PG0778 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 1.46 E-5 | 1.85 E+3 | 8.05 E+5 | -8.7657 | 19.6227 | G | 🟢 |
| *PGN0802* | *PG0699* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0779 | | 1.64 E-2 | 51.3 | 27 | 0.9271 | 6.2917 | Y | 🟡 | 🔴 | R | 1.37 E-4 | 4.49 E+7 | 2.27 E+7 | 0.9833 | 26.0118 | R | 🔴 |
| *PGN0803* | *PG0700* | *hypothetical protein PG_0779* | | | | | | | | | | | | | | | |
| PG0780 | | 3.29 E-4 | 89.0 | 43.5 | 1.0326 | 7.0497 | R | 🔴 | 🔴 | R | 2.45 E-9 | 8.66 E+7 | 3.59 E+7 | 1.2711 | 26.8673 | R | 🔴 |
| *PGN0804* | *PG0701* | *hypothetical protein PG_0780* | | | | | | | | | | | | | | | |
| PG0782 | | 5.89 E-6 | 242.1 | 145.5 | 0.7349 | 8.5986 | R | 🔴 | 🟡 | Y | 2.6 E-2 | 5.61 E+8 | 4.42 E+8 | 0.3449 | 29.9015 | R | 🔴 |
| *PGN0806* | *PG0703* | *MotA/TolQ/ExbB proton channel family protein* | | | | | | | | | | | | | | | |
| PG0784 | | 4.23 E-1 | 14.5 | 19.5 | -0.4228 | 5.0894 | Y | 🟡 | 🟡 | Y | 5.26 E-3 | 6.58 E+6 | 3.97 E+6 | 0.7303 | 23.3306 | Y | 🟡 |
| *PGN0808* | *PG0705* | *polyprenyl synthetase* | | | | | | | | | | | | | | | |
| PG0785 | | 6.81 E-6 | 35.1 | 5.5 | 2.6732 | 5.3428 | R | 🔴 | 🔴 | R | 0 | 5.22 E+7 | 5.7 E+6 | 3.1953 | 25.7880 | R | 🔴 |
| *PGN0809* | *PG0707* | *tonB protein putative* | | | | | | | | | | | | | | | |
| PG0788 | | 1.76 E-2 | 6.0 | 19.5 | -1.7030 | 4.6718 | Y | 🟡 | 🟡 | Y | 3.64 E-3 | 1.87 E+6 | 3.14 E+6 | -0.7443 | 22.2578 | Y | 🟡 |
| *PGN0811* | *PG0709* | *hypothetical protein PG_0788* | | | | | | | | | | | | | | | |
| PG0789 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 4.27 E+6 | 1 E+3 | 12.0608 | 22.0269 | R | 🔴 |
| *PGN0812* | *PG0710* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0790 | | 6.05 E-2 | 6.8 | 1 | 2.7751 | 2.9718 | Y | 🟡 | 🔴 | R | 0 | 3.05 E+6 | 1 E+3 | 11.5760 | 21.5422 | R | 🔴 |
| *PGN0813* | *PG0711* | *obg GTP-binding protein Obg* | | | | | | | | | | | | | | | |
| PG0791 | | 2.92 E-4 | 37.6 | 10.5 | 1.8422 | 5.5894 | R | 🔴 | 🔴 | R | 0 | 1.62 E+7 | 2.34 E+6 | 2.7936 | 24.1481 | R | 🔴 |
| *PGN0814* | *PG0712* | *adk adenylate kinase* | | | | | | | | | | | | | | | |
| PG0792 | | 2.37 E-2 | 3.4 | 14 | -2.0323 | 4.1229 | Y | 🟡 | 🟢 | G | 1.81 E-7 | 1.62 E+6 | 6.28 E+6 | -1.9504 | 22.9142 | G | 🟢 |
| *PGN0815* | *PG0713* | *hpt hypoxanthine phosphoribosyltransferase* | | | | | | | | | | | | | | | |

| **TIGR** | | PP PPC / Pg Spectral Count | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG0793 | | 3.9 E-3 | 95.0 | 55 | 0.7882 | 7.2286 | R 🔴 | 🔴 R | 1.89 E-14 | 4.82 E+7 | 2.27 E+7 | 1.0861 | 26.0783 | R 🔴 |
| *PGN0816* | *PG0714* | *fbp fructose-16-bisphosphatase* | | | | | | | | | | | | |
| PG0794 | | 6.1 E-5 | 18.8 | 1 | 4.2345 | 4.3092 | R 🔴 | 🔴 R | 1.87 E-8 | 1.31 E+7 | 1 E+3 | 13.6786 | 23.6445 | R 🔴 |
| *PGN0817* | *PG0715* | *penicillin-binding protein 1A putative* | | | | | | | | | | | | |
| PG0796 | | 1.16 E-2 | 51.3 | 26 | 0.9815 | 6.2731 | Y 🟡 | 🔴 R | 5.14 E-16 | 2.15 E+7 | 7.05 E+6 | 1.6071 | 24.7660 | R 🔴 |
| *PGN0819* | *PG0717* | *leuS leucyl-tRNA synthetase* | | | | | | | | | | | | |
| PG0800 | | 3.82 E-1 | 3.4 | 6.5 | -0.9253 | 3.3107 | Y 🟡 | 🟡 Y | 1.12 E-2 | 1.39 E+6 | 8.25 E+5 | 0.7522 | 21.0790 | Y 🟡 |
| *PGN0823* | *PG0719* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG0801 | | 6.55 E-1 | 5.1 | 6 | -0.2249 | 3.4769 | Y 🟡 | 🟡 Y | 5.72 E-2 | 8.71 E+5 | 1.17 E+6 | -0.4264 | 20.9616 | Y 🟡 |
| *PGN0824* | *PG0720* | *polyA polymerase family protein* | | | | | | | | | | | | |
| PG0802 | | 1.19 E-2 | 124.9 | 175 | -0.4863 | 8.2285 | Y 🟡 | 🟢 G | 2.42 E-4 | 4.43 E+7 | 7.91 E+7 | -0.8355 | 26.8792 | G 🟢 |
| *PGN0826* | *PG0721* | *pdhD alpha keto acid dehydrogenase complex E3 component lipoamide dehydrogenase* | | | | | | | | | | | | |
| PG0803 | | 4.21 E-1 | 6.8 | 10.5 | -0.6172 | 4.1165 | Y 🟡 | 🟡 Y | 5.41 E-2 | 5.07 E+6 | 1.19 E+7 | -1.2276 | 24.0147 | Y 🟡 |
| *PGN0827* | *PG0722* | *nagB glucosamine-6-phosphate isomerase* | | | | | | | | | | | | |
| PG0804 | | 2.31 E-1 | 94.1 | 75.5 | 0.3181 | 7.4062 | Y 🟡 | 🟡 Y | 7.86 E-2 | 4.52 E+7 | 5.47 E+7 | -0.2757 | 26.5745 | Y 🟡 |
| *PGN0828* | *PG0723* | *flavodoxin* | | | | | | | | | | | | |
| PG0805 | | 2.74 E-1 | 1.7 | 5 | -1.5468 | 2.7466 | Y 🟡 | 🟢 G | 4.21 E-7 | 3.43 E+5 | 2.81 E+6 | -3.0377 | 21.5896 | G 🟢 |
| *PGN0829* | *PG0724* | *lgt prolipoprotein diacylglyceryl transferase* | | | | | | | | | | | | |
| PG0806 | | 3.05 E-1 | 20.5 | 29 | -0.4979 | 5.6304 | Y 🟡 | 🟡 Y | 4.32 E-3 | 9.83 E+6 | 1.56 E+7 | -0.6688 | 24.6012 | Y 🟡 |
| *PGN0830* | *PG0725* | *oxidoreductase Gfo/Idh/MocA family* | | | | | | | | | | | | |
| PG0807 | | 5.8 E-1 | 16.3 | 19 | -0.2249 | 5.1399 | Y 🟡 | 🟡 Y | 1.73 E-1 | 8.13 E+6 | 8.59 E+6 | -0.0794 | 23.9947 | Y 🟡 |
| *PGN0831* | *PG0726* | *NusB family protein* | | | | | | | | | | | | |
| PG0809 | | 2.27 E-4 | 21.4 | 57 | -1.4139 | 6.2926 | G 🟢 | 🟢 G | 2.26 E-6 | 9.17 E+6 | 1.99 E+7 | -1.1148 | 24.7904 | G 🟢 |
| *PGN0832* | *PG0727* | *hypothetical protein PG_0809* | | | | | | | | | | | | |
| PG0811 | | 3.4 E-1 | 12.8 | 19 | -0.5659 | 4.9925 | Y 🟡 | 🟡 Y | 1.03 E-1 | 6.31 E+6 | 7.13 E+6 | -0.1774 | 23.6798 | Y 🟡 |
| *PGN0833* | *PG0729* | *ruvA Holliday junction DNA helicase RuvA* | | | | | | | | | | | | |
| PG1493 | | 4.81 E-2 | 4.3 | 14 | -1.7103 | 4.1921 | Y 🟡 | 🟢 G | 2.59 E-5 | 1.41 E+6 | 5.51 E+6 | -1.9689 | 22.7221 | G 🟢 |
| *PGN0836* | *PG1308* | *hypothetical protein PG_1493* | | | | | | | | | | | | |
| PG1492 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y 🟡 | 🔴 R | 0 | 2.49 E+6 | 1 E+3 | 11.2818 | 21.2481 | R 🔴 |
| *PGN0837* | *PG1307* | *hypothetical protein PG_1492* | | | | | | | | | | | | |
| PG1433 | | 2.72 E-1 | 4.3 | 9 | -1.0729 | 3.7310 | Y 🟡 | 🟡 Y | 1.03 E-2 | 8.47 E+5 | 5.09 E+6 | -2.5867 | 22.5014 | Y 🟡 |
| *PGN0840* | *PG1256* | *hydrolase* | | | | | | | | | | | | |
| PG1434 | | 2.74 E-1 | 8.6 | 4 | 1.0970 | 3.6504 | Y 🟡 | 🔴 R | 3.57 E-4 | 2.41 E+6 | 1.15 E+6 | 1.0742 | 21.7623 | R 🔴 |
| *PGN0841* | *PG1257* | *ispD 4-diphosphocytidyl-2C-methyl-D-erythritol synthase* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG1374 | | 6.41 E-1 | 63.3 | 60 | 0.0777 | 6.9462 | Y 🟡 | 🟡 Y | 1.27 E-3 | 2.82 E+7 | 5.91 E+7 | -1.0680 | 26.3798 | Y 🟡 |
| *PGN0852* | *PG1208* | *immunoreactive 47 kDa antigen PG97* | | | | | | | | | | | | |
| PG1378 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟡 Y | 9.81 E-3 | 1.85 E+3 | 6.2 E+5 | -8.3882 | 19.2462 | Y 🟡 |
| *PGN0856* | *PG1209* | *mutY A/G-specific adenine glycosylase* | | | | | | | | | | | | |
| PG1379 | | 1.06 E-1 | 12.8 | 24.5 | -0.9327 | 5.2224 | Y 🟡 | 🟢 G | 1.11 E-4 | 6.02 E+6 | 1.67 E+7 | -1.4690 | 24.4348 | G 🟢 |
| *PGN0857* | *PG1210* | *ABC transporter periplasmic substrate-binding protein putative* | | | | | | | | | | | | |
| PG1382 | | 3.15 E-9 | 40.2 | 118 | -1.5530 | 7.3057 | G 🟢 | 🟢 G | 1.29 E-8 | 1.83 E+7 | 9.53 E+7 | -2.3827 | 26.7587 | G 🟢 |
| *PGN0860* | *PG1213* | *hypothetical protein PG_1382* | | | | | | | | | | | | |
| | | 2.25 E-1 | 6.8 | 2.5 | 1.4532 | 3.2242 | Y 🟡 | 🟡 Y | 3.14 E-3 | 1.25 E+6 | 4.39 E+5 | 1.5065 | 20.6860 | Y 🟡 |
| *PGN0862* | | | | | | | | | | | | | | |
| | | 5.74 E-1 | 4.3 | 3 | 0.5121 | 2.8636 | Y 🟡 | 🟡 Y | 1.28 E-2 | 2.28 E+6 | 8.8 E+5 | 1.3727 | 21.5910 | Y 🟡 |
| *PGN0863* | | | | | | | | | | | | | | |
| PG1397 | | 6.94 E-1 | 18.8 | 18.5 | 0.0251 | 5.2220 | Y 🟡 | 🟡 Y | 1.37 E-1 | 1.03 E+7 | 1.15 E+7 | -0.1526 | 24.3782 | Y 🟡 |
| *PGN0865* | *PG1228* | *purH phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase* | | | | | | | | | | | | |
| PG1396 | | 6.36 E-1 | 62.5 | 66 | -0.0795 | 7.0052 | Y 🟡 | 🟡 Y | 1.12 E-1 | 3.17 E+7 | 3.68 E+7 | -0.2171 | 26.0298 | Y 🟡 |
| *PGN0866* | *PG1227* | *mreB cell shape-determining protein MreB* | | | | | | | | | | | | |
| PG1393 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 1.63 E+5 | -6.4615 | 17.3315 | Y 🟡 |
| *PGN0869* | *PG1224* | *penicillin-binding protein 2 putative* | | | | | | | | | | | | |
| PG1389 | | 3.82 E-1 | 7.7 | 12 | -0.6399 | 4.3002 | Y 🟡 | 🟡 Y | 1.11 E-1 | 1.54 E+7 | 1.17 E+7 | 0.3980 | 24.6938 | Y 🟡 |
| *PGN0872* | *PG1221* | *DNA-binding protein histone-like family* | | | | | | | | | | | | |
| PG1388 | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y 🟡 | 🟡 Y | 1.69 E-3 | 2.19 E+7 | 1 E+3 | 14.4218 | 24.3877 | Y 🟡 |
| *PGN0873* | *PG1220* | *hypothetical protein PG_1388* | | | | | | | | | | | | |
| PG1387 | | 9.48 E-2 | 1.7 | 7.5 | -2.1318 | 3.2034 | Y 🟡 | 🟢 G | 1.34 E-4 | 1.85 E+3 | 5.04 E+6 | -11.4116 | 22.2658 | G 🟢 |
| *PGN0874* | *PG1218* | *hypothetical protein PG_1387* | | | | | | | | | | | | |
| PG1386 | | 3.7 E-7 | 111.2 | 44 | 1.3380 | 7.2783 | R 🔴 | 🔴 R | 7.39 E-10 | 7.03 E+7 | 2.79 E+7 | 1.3322 | 26.5491 | R 🔴 |
| *PGN0875* | *PG1217* | *gyrA DNA gyrase A subunit* | | | | | | | | | | | | |
| PG1385 | | 0 | 282.4 | 90.5 | 1.6416 | 8.5425 | R 🔴 | 🔴 R | 0 | 3.44 E+8 | 9.58 E+7 | 1.8437 | 28.7120 | R 🔴 |
| *PGN0876* | *PG1216* | *TPR domain protein* | | | | | | | | | | | | |
| | | 3.05 E-1 | 6.8 | 12 | -0.8099 | 4.2361 | Y 🟡 | 🟡 Y | 1.24 E-1 | 3.08 E+6 | 2.61 E+6 | 0.2428 | 22.4397 | Y 🟡 |
| *PGN0877* | | | | | | | | | | | | | | |
| PG1401 | | 5.92 E-1 | 566.4 | 581 | -0.0366 | 10.1642 | Y 🟡 | 🟡 Y | 1.72 E-1 | 5.95 E+8 | 5.83 E+8 | 0.0309 | 30.1339 | Y 🟡 |
| *PGN0880* | *PG1232* | *beta-eliminating lyase* | | | | | | | | | | | | |
| PG1402 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 3.73 E+5 | -7.6556 | 18.5164 | G 🟢 |
| *PGN0881* | *PG1233* | *AP endonuclease domain protein* | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Regulation** | | | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Consensus** | |
| PG1405 | | 5.47 E-2 | 2.6 | 10.5 | -2.0323 | 3.7079 | Y | 🟡 | 🟢 | G | 2.6 E-6 | 6.84 E+5 | 3.46 E+6 | -2.3395 | 21.9835 | G | 🟢 |
| *PGN0884* | *PG1236* | *hypothetical protein PG_1405* | | | | | | | | | | | | | | | |
| PG1407 | | 1.84 E-1 | 1.7 | 6 | -1.8099 | 2.9470 | Y | 🟡 | 🟡 | Y | 5.66 E-2 | 6.04 E+5 | 7.94 E+5 | -0.3948 | 20.4154 | Y | 🟡 |
| *PGN0885* | *PG1237* | *nitroimidazole resistance protein putative* | | | | | | | | | | | | | | | |
| PG1408 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 6.38 E+5 | -8.4285 | 19.2864 | G | 🟢 |
| *PGN0886* | *PG1238* | *heavy metal efflux pump CzcD family* | | | | | | | | | | | | | | | |
| PG1411 | | 6.49 E-1 | 4.3 | 3.5 | 0.2897 | 2.9594 | Y | 🟡 | 🟡 | Y | 3.45 E-2 | 8.25 E+5 | 3.75 E+5 | 1.1375 | 20.1939 | Y | 🟡 |
| *PGN0889* | *PG1240* | *potassium uptake protein TrkA putative* | | | | | | | | | | | | | | | |
| PG1414 | | 1.03 E-8 | 189.1 | 327.5 | -0.7924 | 9.0129 | G | 🟢 | 🟢 | G | 7.27 E-4 | 1.27 E+8 | 1.85 E+8 | -0.5458 | 28.2151 | G | 🟢 |
| *PGN0890* | *PG1242* | *hypothetical protein PG_1414* | | | | | | | | | | | | | | | |
| PG1416 | | 5.93 E-1 | 59.0 | 54.5 | 0.1154 | 6.8271 | Y | 🟡 | 🟡 | Y | 8.74 E-2 | 3.48 E+7 | 4.33 E+7 | -0.3156 | 26.2174 | Y | 🟡 |
| *PGN0891* | *PG1243* | *fabK enoyl-(acyl-carrier-protein) reductase II* | | | | | | | | | | | | | | | |
| PG1417 | | 7.41 E-3 | 95.8 | 58 | 0.7245 | 7.2652 | R | 🔴 | 🟡 | Y | 1.42 E-2 | 5.69 E+7 | 4.39 E+7 | 0.3734 | 26.5873 | R | 🔴 |
| *PGN0893* | *PG1244* | *fumB fumarate hydratase class I anaerobic* | | | | | | | | | | | | | | | |
| PG1418 | | 6 E-1 | 3.4 | 2.5 | 0.4532 | 2.5662 | Y | 🟡 | 🔴 | R | 0 | 5.89 E+5 | 1.52 E+5 | 1.9536 | 19.4981 | R | 🔴 |
| *PGN0894* | *PG1245* | *dnaX DNA polymerase III gamma and tau subunits* | | | | | | | | | | | | | | | |
| PG1422 | | 6.69 E-1 | 10.3 | 9.5 | 0.1121 | 4.3051 | Y | 🟡 | 🟡 | Y | 1.68 E-1 | 1.92 E+6 | 1.74 E+6 | 0.1435 | 21.8006 | Y | 🟡 |
| *PGN0896* | *PG1248* | *dacB D-alanyl-D-alanine carboxypeptidase* | | | | | | | | | | | | | | | |
| PG1424 | | 6.78 E-15 | 367.1 | 623 | -0.7632 | 9.9514 | G | 🟢 | 🟢 | G | 9.11 E-8 | 2.79 E+8 | 5.34 E+8 | -0.9397 | 29.5983 | G | 🟢 |
| *PGN0898* | *PG1249* | *peptidylarginine deiminase* | | | | | | | | | | | | | | | |
| PG1427 | | 7.99 E-4 | 3.4 | 21 | -2.6172 | 4.6101 | G | 🟢 | 🟢 | G | 1.04 E-6 | 1.24 E+6 | 8.43 E+6 | -2.7619 | 23.2055 | G | 🟢 |
| *PGN0900* | *PG1251* | *thiol protease/hemagglutinin PrtT precursor putative* | | | | | | | | | | | | | | | |
| PG1428 | | 5.17 E-1 | 7.7 | 5.5 | 0.4856 | 3.7226 | Y | 🟡 | 🟡 | Y | 9.57 E-3 | 6.51 E+6 | 3.57 E+6 | 0.8681 | 23.2653 | Y | 🟡 |
| *PGN0901* | *PG1252* | *ribH riboflavin synthase beta subunit* | | | | | | | | | | | | | | | |
| PG1430 | | 6.05 E-2 | 118.1 | 86.5 | 0.4490 | 7.6765 | Y | 🟡 | 🟡 | Y | 1.4 E-2 | 1.01 E+8 | 7.41 E+7 | 0.4522 | 27.3861 | Y | 🟡 |
| *PGN0902* | *PG1253* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG1431 | | 6.64 E-1 | 4.3 | 5 | -0.2249 | 3.2139 | Y | 🟡 | 🟡 | Y | 2 E-2 | 4.89 E+5 | 3.21 E+6 | -2.7146 | 21.8186 | Y | 🟡 |
| *PGN0903* | *PG1254* | *DNA-binding response regulator LuxR family* | | | | | | | | | | | | | | | |
| PG1432 | | 6 E-1 | 4.3 | 5.5 | -0.3624 | 3.2896 | Y | 🟡 | 🔴 | R | 3.11 E-6 | 2.61 E+6 | 4.95 E+5 | 2.4009 | 21.5682 | Y | 🟡 |
| *PGN0904* | *PG1255* | *sensor histidine kinase* | | | | | | | | | | | | | | | |
| PG1065 | | 9.03 E-2 | 14.5 | 27.5 | -0.9188 | 5.3939 | Y | 🟡 | 🟢 | G | 7.8 E-4 | 5.5 E+6 | 1.22 E+7 | -1.1450 | 24.0747 | G | 🟢 |
| *PGN0905* | *PG0947* | *pyrD dihydroorotate dehydrogenase* | | | | | | | | | | | | | | | |
| PG1064 | | 2.72 E-1 | 4.3 | 9 | -1.0729 | 3.7310 | Y | 🟡 | 🟡 | Y | 1.83 E-2 | 7.77 E+5 | 1.46 E+6 | -0.9097 | 21.0930 | Y | 🟡 |
| *PGN0906* | *PG0946* | *dihydroorotate dehydrogenase putative* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | | **33277** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Regulation** | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Consensus** |
| PG1063 | | 6.97 E-1 | 3.4 | 3.5 | -0.0323 | 2.7913 | Y 🟡 | 🔴 R | 3.67 E-4 | 1.57 E+6 | 7.42 E+5 | 1.0790 | 21.1399 | Y 🟡 |
| *PGN0907* | *PG0945* | *transcriptional regulator putative* | | | | | | | | | | | | |
| PG1213 | | 6.54 E-1 | 2.6 | 2 | 0.3601 | 2.1912 | Y 🟡 | 🔴 R | 6.77 E-4 | 1.28 E+6 | 3.75 E+5 | 1.7737 | 20.6618 | R 🔴 |
| *PGN0911* | *PG1074* | *rnhA ribonuclease H* | | | | | | | | | | | | |
| PG1212 | | 5.81 E-2 | 18.8 | 7.5 | 1.3276 | 4.7183 | Y 🟡 | 🟡 Y | 3.21 E-3 | 1.49 E+7 | 2.44 E+6 | 2.6109 | 24.0499 | Y 🟡 |
| *PGN0912* | *PG1073* | *TPR domain protein* | | | | | | | | | | | | |
| PG1211 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y 🟡 | 🟢 G | 6.8 E-4 | 1.85 E+3 | 1.61 E+6 | -9.7690 | 20.6244 | G 🟢 |
| *PGN0913* | *PG1072* | *hexapeptide transferase family protein* | | | | | | | | | | | | |
| PG1210 | | 3.92 E-4 | 259.3 | 357 | -0.4615 | 9.2674 | G 🟢 | 🟢 G | 5.79 E-5 | 2.04 E+8 | 3.1 E+8 | -0.6063 | 28.9384 | G 🟢 |
| *PGN0914* | *PG1071* | *peptidase M24 family* | | | | | | | | | | | | |
| PG1209 | | 4.23 E-1 | 35.9 | 43.5 | -0.2755 | 6.3117 | Y 🟡 | 🟡 Y | 1.34 E-2 | 1.42 E+7 | 1.08 E+7 | 0.4021 | 24.5753 | Y 🟡 |
| *PGN0915* | *PG1070* | *hypothetical protein PG_1209* | | | | | | | | | | | | |
| PG1208 | | 3.05 E-1 | 393.6 | 427.5 | -0.1192 | 9.6814 | Y 🟡 | 🟡 Y | 4.13 E-2 | 2.73 E+8 | 2.38 E+8 | 0.2006 | 28.9277 | Y 🟡 |
| *PGN0916* | *PG1069* | *dnaK dnaK protein* | | | | | | | | | | | | |
| | | 7.31 E-2 | 18.0 | 33 | -0.8770 | 5.6715 | Y 🟡 | 🟡 Y | 6.83 E-2 | 1.24 E+7 | 1.51 E+7 | -0.2872 | 24.7149 | Y 🟡 |
| *PGN0928* | | | | | | | | | | | | | | |
| | | 4.4 E-1 | 26.5 | 21 | 0.3370 | 5.5706 | Y 🟡 | 🔴 R | 4.95 E-5 | 1.52 E+7 | 4.78 E+6 | 1.6651 | 24.2487 | R 🔴 |
| *PGN0929* | | | | | | | | | | | | | | |
| | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y 🟡 | 🟢 G | 2.19 E-10 | 1.85 E+3 | 2.59 E+6 | -10.4507 | 21.3054 | G 🟢 |
| *PGN0930* | | | | | | | | | | | | | | |
| | | 2.72 E-1 | 14.5 | 22.5 | -0.6293 | 5.2112 | Y 🟡 | 🟡 Y | 9.57 E-3 | 4.48 E+6 | 7.28 E+6 | -0.7004 | 23.4873 | Y 🟡 |
| *PGN0933* | | | | | | | | | | | | | | |
| PG1189 | | 2.04 E-3 | 142.9 | 90 | 0.6669 | 7.8635 | R 🔴 | 🔴 R | 5.53 E-6 | 1.12 E+8 | 6.89 E+7 | 0.7059 | 27.4347 | R 🔴 |
| *PGN0935* | *PG1059* | *hypothetical protein PG_1189* | | | | | | | | | | | | |
| PG1190 | | 3.85 E-1 | 5.1 | 2.5 | 1.0381 | 2.9324 | Y 🟡 | 🔴 R | 0 | 2.22 E+6 | 4.86 E+5 | 2.1899 | 21.3675 | R 🔴 |
| *PGN0936* | *PG1060* | *hprA glycerate dehydrogenase* | | | | | | | | | | | | |
| PG1195 | | 6.15 E-1 | 9.4 | 11 | -0.2249 | 4.3514 | Y 🟡 | 🟡 Y | 1.52 E-1 | 2.47 E+6 | 2.3 E+6 | 0.1058 | 22.1867 | Y 🟡 |
| *PGN0938* | *PG1061* | *bioF-2 8-amino-7-oxononanoate synthase* | | | | | | | | | | | | |
| | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 3.02 E+5 | -7.3508 | 18.2133 | G 🟢 |
| *PGN0945* | | | | | | | | | | | | | | |
| | | 4.15 E-1 | 2.6 | 5 | -0.9619 | 2.9197 | Y 🟡 | 🟡 Y | 1.08 E-1 | 1.26 E+6 | 1.18 E+6 | 0.0969 | 21.2172 | Y 🟡 |
| *PGN0946* | | | | | | | | | | | | | | |
| | | 6.52 E-2 | 6.0 | 16 | -1.4175 | 4.4587 | Y 🟡 | 🟢 G | 8.04 E-4 | 1.79 E+6 | 4.39 E+6 | -1.2910 | 22.5600 | G 🟢 |
| *PGN0948* | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $log_2$Ratio | $log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $log_2$Ratio | $log_2$Sum | Consensus | |
| | | 4.5 E-1 | 6.8 | 10 | -0.5468 | 4.0743 | Y | 🟡 | 🟡 | Y | 3.81 E-2 | 3.35 E+6 | 2.56 E+6 | 0.3900 | 22.4939 | Y | 🟡 |
| *PGN0949* | | | | | | | | | | | | | | | | | |
| | | 5.43 E-1 | 3.4 | 5 | -0.5468 | 3.0743 | Y | 🟡 | 🟡 | Y | 2.62 E-3 | 2.25 E+6 | 1.27 E+6 | 0.8280 | 21.7476 | Y | 🟡 |
| *PGN0950* | | | | | | | | | | | | | | | | | |
| | | 6.36 E-5 | 55.6 | 18.5 | 1.5880 | 6.2117 | R | 🔴 | 🔴 | R | 1.93 E-11 | 3.15 E+7 | 1.14 E+7 | 1.4730 | 25.3548 | R | 🔴 |
| *PGN0952* | | | | | | | | | | | | | | | | | |
| PG0992 | | 0 | 201.1 | 60.5 | 1.7328 | 8.0311 | R | 🔴 | 🔴 | R | 0 | 7.67 E+7 | 2.86 E+7 | 1.4236 | 26.6491 | R | 🔴 |
| *PGN0962* | *PG0888* | *thrS threonyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG0991 | | 2.68 E-4 | 18.0 | 1.5 | 3.5825 | 4.2831 | R | 🔴 | 🔴 | R | 0 | 2.4 E+7 | 2.28 E+6 | 3.3970 | 24.6467 | R | 🔴 |
| *PGN0963* | *PG0887* | *infC translation initiation factor IF-3* | | | | | | | | | | | | | | | |
| PG0990 | | 6.49 E-1 | 4.3 | 3.5 | 0.2897 | 2.9594 | Y | 🟡 | 🔴 | R | 2.56 E-4 | 4.08 E+6 | 5.58 E+5 | 2.8698 | 22.1441 | R | 🔴 |
| *PGN0964* | | *rpmI ribosomal protein L35* | | | | | | | | | | | | | | | |
| PG0989 | | 3.61 E-1 | 31.7 | 40.5 | -0.3553 | 6.1731 | Y | 🟡 | 🟡 | Y | 3.5 E-2 | 2.49 E+7 | 1.88 E+7 | 0.4051 | 25.3812 | Y | 🟡 |
| *PGN0965* | *PG0886* | *rplT ribosomal protein L20* | | | | | | | | | | | | | | | |
| PG0982 | | 1.85 E-3 | 54.8 | 24 | 1.1901 | 6.2994 | R | 🔴 | 🔴 | R | 1.63 E-12 | 1.61 E+7 | 6.56 E+6 | 1.2962 | 24.4346 | R | 🔴 |
| *PGN0972* | *PG0878* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG0980 | | 6.69 E-1 | 2.6 | 3 | -0.2249 | 2.4769 | Y | 🟡 | 🟡 | Y | 4.22 E-2 | 3.42 E+5 | 2.63 E+5 | 0.3774 | 19.2080 | Y | 🟡 |
| *PGN0973* | *PG0877* | *hypothetical protein PG_0980* | | | | | | | | | | | | | | | |
| PG0978 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟡 | Y | 2.16 E-3 | 1.85 E+3 | 2.62 E+5 | -7.1444 | 18.0083 | Y | 🟡 |
| *PGN0974* | *PG0875* | *aroE shikimate 5-dehydrogenase* | | | | | | | | | | | | | | | |
| PG0977 | | 2.92 E-1 | 3.4 | 7.5 | -1.1318 | 3.4492 | Y | 🟡 | 🟡 | Y | 5.61 E-3 | 1.07 E+6 | 2.23 E+6 | -1.0603 | 21.6516 | Y | 🟡 |
| *PGN0975* | *PG0874* | *ubiE ubiquinone/menaquinone biosynthesis methyltransferase UbiE* | | | | | | | | | | | | | | | |
| PG0976 | | 1.85 E-3 | 65.0 | 31 | 1.0688 | 6.5854 | R | 🔴 | 🔴 | R | 6.02 E-4 | 3.99 E+7 | 2.41 E+7 | 0.7307 | 25.9314 | R | 🔴 |
| *PGN0976* | *PG0873* | *phosphoribosylaminoimidazole-succinocarboxamide synthase putative* | | | | | | | | | | | | | | | |
| PG0975 | | 4.88 E-1 | 8.6 | 6 | 0.5121 | 3.8636 | Y | 🟡 | 🟡 | Y | 1.83 E-2 | 1.23 E+6 | 5.75 E+5 | 1.0933 | 20.7820 | Y | 🟡 |
| *PGN0977* | *PG0872* | *PhoH family protein* | | | | | | | | | | | | | | | |
| PG0973 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 2.27 E+5 | 1 E+3 | 7.8236 | 17.7957 | R | 🔴 |
| *PGN0980* | *PG0871* | *alpha-12-mannosidase family protein* | | | | | | | | | | | | | | | |
| PG0968 | | 6.85 E-1 | 4.3 | 4.5 | -0.0729 | 3.1339 | Y | 🟡 | 🔴 | R | 5.11 E-11 | 3.75 E+6 | 7.22 E+5 | 2.3753 | 22.0920 | Y | 🟡 |
| *PGN0982* | *PG0866* | *mrr Mrr restriction system protein* | | | | | | | | | | | | | | | |
| PG0965 | | 1.76 E-2 | 11.1 | 28 | -1.3318 | 5.2900 | Y | 🟡 | 🟡 | Y | 1.69 E-3 | 3.13 E+6 | 8.99 E+6 | -1.5225 | 23.5310 | Y | 🟡 |
| *PGN0984* | *PG0865* | *phosphatidylserine decarboxylase-related protein* | | | | | | | | | | | | | | | |
| PG0962 | | 5.47 E-4 | 52.2 | 20 | 1.3839 | 6.1738 | R | 🔴 | 🔴 | R | 5.03 E-5 | 2.38 E+7 | 1.08 E+7 | 1.1342 | 25.0439 | R | 🔴 |
| *PGN0987* | *PG0861* | *proS prolyl-tRNA synthetase* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0961 | | 4.55 E-1 | 5.1 | 3 | 0.7751 | 3.0240 | Y | 🟡 | 🟡 | Y | 1.88 E-3 | 3.12 E+6 | 1.37 E+6 | 1.1821 | 22.0996 | Y | 🟡 |
| *PGN0988* | *PG0860* | *hypothetical protein PG_0961* | | | | | | | | | | | | | | | |
| PG0960 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 0 | 1.18 E+6 | 1 E+3 | 10.2070 | 20.1740 | R | 🔴 |
| *PGN0989* | *PG0859* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0959 | | 1.74 E-1 | 18.0 | 9.5 | 0.9195 | 4.7797 | Y | 🟡 | 🟡 | Y | 5.71 E-2 | 8.94 E+6 | 6.04 E+6 | 0.5651 | 23.8365 | Y | 🟡 |
| *PGN0990* | *PG0858* | *mrp ATP-binding protein Mrp/Nbp35 family* | | | | | | | | | | | | | | | |
| PG0958 | | 2.74 E-1 | 6.8 | 12.5 | -0.8688 | 4.2739 | Y | 🟡 | 🟡 | Y | 2.25 E-2 | 1.21 E+6 | 2.82 E+6 | -1.2263 | 21.9404 | Y | 🟡 |
| *PGN0991* | *PG0857* | *ribonuclease BN putative* | | | | | | | | | | | | | | | |
| PG0957 | | 3.05 E-1 | 2.6 | 6 | -1.2249 | 3.0988 | Y | 🟡 | 🟡 | Y | 7.25 E-2 | 8.35 E+5 | 1.01 E+6 | -0.2691 | 20.8130 | Y | 🟡 |
| *PGN0992* | *PG0856* | *ribF riboflavin biosynthesis protein RibF* | | | | | | | | | | | | | | | |
| PG0956 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 0 | 6.42 E+5 | 1 E+3 | 9.3272 | 19.2953 | R | 🔴 |
| *PGN0993* | *PG0855* | *peptidase M23/M37 family putative* | | | | | | | | | | | | | | | |
| PG0955 | | 2.93 E-1 | 6.8 | 3 | 1.1901 | 3.2994 | Y | 🟡 | 🟡 | Y | 8.01 E-3 | 2.52 E+6 | 1.1 E+6 | 1.1955 | 21.7892 | Y | 🟡 |
| *PGN0994* | *PG0854* | *hypothetical protein PG_0955* | | | | | | | | | | | | | | | |
| PG0954 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 1.7 E+6 | 1 E+3 | 10.7318 | 20.6984 | R | 🔴 |
| *PGN0996* | *PG0853* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG0953 | | 2.96 E-2 | 3.4 | 13.5 | -1.9798 | 4.0809 | Y | 🟡 | 🟡 | Y | 4.96 E-3 | 6.72 E+5 | 1.07 E+7 | -3.9871 | 23.4343 | Y | 🟡 |
| *PGN0997* | *PG0852* | *dut deoxyuridine 5'-triphosphate nucleotidohydrolase* | | | | | | | | | | | | | | | |
| PG0952 | | 2.97 E-2 | 16.3 | 34 | -1.0644 | 5.6513 | Y | 🟡 | 🟡 | Y | 4.15 E-3 | 5.11 E+6 | 1.51 E+7 | -1.5652 | 24.2696 | Y | 🟡 |
| *PGN0998* | *PG0851* | *ispG 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase* | | | | | | | | | | | | | | | |
| PG0951 | | 4.4 E-1 | 18.0 | 13.5 | 0.4125 | 4.9758 | Y | 🟡 | 🟡 | Y | 5.2 E-2 | 1.24 E+7 | 9.09 E+6 | 0.4533 | 24.3596 | Y | 🟡 |
| *PGN0999* | *PG0850* | *purE phosphoribosylaminoimidazole carboxylase PurE protein* | | | | | | | | | | | | | | | |
| PG0950 | | 7.04 E-1 | 35.1 | 35 | 0.0034 | 6.1310 | Y | 🟡 | 🟡 | Y | 6.41 E-2 | 4.69 E+7 | 7.06 E+7 | -0.5898 | 26.8086 | Y | 🟡 |
| *PGN1000* | *PG0848* | *gcvH glycine cleavage system H protein* | | | | | | | | | | | | | | | |
| PG0949 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟢 | G | 4.51 E-6 | 1.85 E+3 | 4.57 E+5 | -7.9485 | 18.8080 | G | 🟢 |
| *PGN1001* | *PG0847* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0948 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 6.44 E+5 | 1 E+3 | 9.3310 | 19.2990 | R | 🔴 |
| *PGN1002* | *PG0846* | *AMP nucleosidase putative* | | | | | | | | | | | | | | | |
| PG0946 | | 3.31 E-1 | 16.3 | 10.5 | 0.6307 | 4.7419 | Y | 🟡 | 🔴 | R | 4.42 E-4 | 1.19 E+7 | 6.43 E+6 | 0.8946 | 24.1314 | R | 🔴 |
| *PGN1004* | *PG0844* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG0945 | | 5.71 E-1 | 18.0 | 21 | -0.2249 | 5.2842 | Y | 🟡 | 🟡 | Y | 1.6 E-2 | 1.19 E+7 | 1.82 E+7 | -0.6120 | 24.8448 | Y | 🟡 |
| *PGN1005* | *PG0843* | *ABC transporter permease protein putative* | | | | | | | | | | | | | | | |
| PG0937 | | 5.76 E-5 | 18.0 | 55 | -1.6139 | 6.1892 | G | 🟢 | 🟡 | Y | 3.54 E-3 | 8.59 E+6 | 2.19 E+7 | -1.3487 | 24.8612 | G | 🟢 |
| *PGN1010* | *PG0836* | *hypothetical protein PG_0937* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG0936 | | 3.06 E-1 | 4.3 | 1.5 | 1.5121 | 2.5306 | Y 🟡 | 🔴 R | 1.34 E-6 | 7.29 E+6 | 6.74 E+5 | 3.4350 | 22.9253 | R 🔴 |
| *PGN1011* | *PG0835* | *xanthine/uracil permease family protein* | | | | | | | | | | | | |
| PG0935 | | 2.25 E-1 | 1.7 | 5.5 | -1.6843 | 2.8503 | Y 🟡 | 🟡 Y | 3.57 E-3 | 1.85 E+3 | 1.07 E+6 | -9.1776 | 20.0338 | Y 🟡 |
| *PGN1012* | *PG0834* | *ispE 4-diphosphocytidyl-2C-methyl-D-erythritol kinase* | | | | | | | | | | | | |
| PG0934 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 2.12 E+5 | -6.8385 | 17.7048 | Y 🟡 |
| *PGN1013* | *PG0833* | *radical SAM domain protein* | | | | | | | | | | | | |
| PG0933 | | 8.74 E-2 | 579.3 | 650.5 | -0.1673 | 10.2642 | Y 🟡 | 🟡 Y | 9.55 E-3 | 6.3 E+8 | 5.42 E+8 | 0.2170 | 30.1257 | Y 🟡 |
| *PGN1014* | *PG0832* | *translation elongation factor G putative* | | | | | | | | | | | | |
| PG0932 | | 6.64 E-1 | 6.8 | 6 | 0.1901 | 3.6832 | Y 🟡 | 🔴 R | 5.08 E-5 | 2.51 E+6 | 1.05 E+6 | 1.2602 | 21.7620 | R 🔴 |
| *PGN1015* | *PG0831* | *DNA polymerase III delta prime subunit putative* | | | | | | | | | | | | |
| | | 4.21 E-1 | 3.4 | 1.5 | 1.1901 | 2.2994 | Y 🟡 | 🔴 R | 0 | 1.25 E+6 | 1.1 E+5 | 3.4982 | 20.3727 | R 🔴 |
| *PGN1018* | | | | | | | | | | | | | | |
| PG0928 | | 6.96 E-1 | 33.4 | 33 | 0.0161 | 6.0525 | Y 🟡 | 🔴 R | 4.23 E-12 | 1.91 E+7 | 8.15 E+6 | 1.2263 | 24.6974 | R 🔴 |
| *PGN1019* | *PG0827* | *response regulator* | | | | | | | | | | | | |
| PG0927 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 3.65 E+5 | -7.6226 | 18.4837 | G 🟢 |
| *PGN1020* | *PG0826* | *conserved hypothetical protein TIGR00150* | | | | | | | | | | | | |
| PG0925 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y 🟡 | 🟢 G | 2.01 E-9 | 6.33 E+4 | 5.62 E+5 | -3.1502 | 19.2535 | G 🟢 |
| *PGN1022* | *PG0825* | *tmk thymidine kinase* | | | | | | | | | | | | |
| PG0924 | | 2.02 E-1 | 6.0 | 12.5 | -1.0614 | 4.2086 | Y 🟡 | 🟡 Y | 4.4 E-3 | 9.59 E+5 | 2.76 E+6 | -1.5247 | 21.8264 | Y 🟡 |
| *PGN1023* | *PG0824* | *5'-nucleotidase lipoprotein e(P4) family* | | | | | | | | | | | | |
| PG0923 | | 1.52 E-2 | 9.4 | 1 | 3.2345 | 3.3802 | Y 🟡 | 🔴 R | 0 | 3.75 E+6 | 1 E+3 | 11.8714 | 21.8375 | R 🔴 |
| *PGN1024* | *PG0823* | *rbfA ribosome-binding factor A* | | | | | | | | | | | | |
| PG0920 | | 1.62 E-1 | 7.7 | 2.5 | 1.6231 | 3.3506 | Y 🟡 | 🔴 R | 9.19 E-10 | 1.01 E+7 | 1.91 E+6 | 2.3952 | 23.5130 | R 🔴 |
| *PGN1026* | *PG0820* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | |
| PG0919 | | 5.67 E-4 | 9.4 | 34 | -1.8529 | 5.4400 | G 🟢 | 🟢 G | 2.62 E-9 | 3.65 E+6 | 1.33 E+7 | -1.8658 | 24.0136 | G 🟢 |
| *PGN1027* | *PG0819* | *pyrC dihydroorotase* | | | | | | | | | | | | |
| PG0918 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y 🟡 | 🟢 G | 2.26 E-6 | 1.85 E+3 | 1.73 E+6 | -9.8649 | 20.7202 | G 🟢 |
| *PGN1028* | *PG0818* | *hypothetical protein PG_0918* | | | | | | | | | | | | |
| PG0914 | | 1.49 E-1 | 12.0 | 22 | -0.8770 | 5.0866 | Y 🟡 | 🟢 G | 8.18 E-4 | 4.47 E+6 | 9.4 E+6 | -1.0730 | 23.7255 | G 🟢 |
| *PGN1032* | *PG0815* | *hypothetical protein PG_0914* | | | | | | | | | | | | |
| PG0909 | | 6.41 E-1 | 6.0 | 5 | 0.2605 | 3.4581 | Y 🟡 | 🟡 Y | 2.91 E-2 | 2.53 E+6 | 1.61 E+6 | 0.6478 | 21.9808 | Y 🟡 |
| *PGN1035* | *PG0811* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG0906 | | 8.7 E-2 | 40.2 | 24 | 0.7447 | 6.0049 | Y 🟡 | 🟡 Y | 1.62 E-1 | 1.01 E+8 | 1.11 E+8 | -0.1363 | 27.6637 | Y 🟡 |
| *PGN1037* | *PG0809* | *lipoprotein putative* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG0903 | | 1.84 E-1 | 1.7 | 6 | -1.8099 | 2.9470 | Y 🟡 | 🟢 G | 3.46 E-8 | 1.85 E+3 | 4.19 E+6 | -11.1447 | 21.9991 | G 🟢 |
| *PGN1038* | *PG0806* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG0900 | | 5.43 E-1 | 8.6 | 6.5 | 0.3966 | 3.9123 | Y 🟡 | 🟡 Y | 2.38 E-2 | 3.23 E+6 | 5.28 E+6 | -0.7096 | 23.0200 | Y 🟡 |
| *PGN1041* | *PG0803* | *cydA cytochrome d ubiquinol oxidase subunit I* | | | | | | | | | | | | |
| PG0898 | | 6.02 E-1 | 5.1 | 4 | 0.3601 | 3.1912 | Y 🟡 | 🔴 R | 0 | 1.86 E+6 | 4.46 E+5 | 2.0585 | 21.1360 | R 🔴 |
| *PGN1043* | *PG0801* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG0897 | | 7.56 E-2 | 1.7 | 8 | -2.2249 | 3.2797 | Y 🟡 | 🟢 G | 1.11 E-5 | 1.85 E+3 | 1.12 E+6 | -9.2457 | 20.1018 | G 🟢 |
| *PGN1044* | *PG0800* | *alpha-amylase family protein* | | | | | | | | | | | | |
| PG0890 | | 1.76 E-2 | 78.7 | 117 | -0.5717 | 7.6126 | Y 🟡 | 🟢 G | 4.89 E-7 | 4.45 E+7 | 9.07 E+7 | -1.0267 | 27.0112 | G 🟢 |
| *PGN1049* | *PG0796* | *alkaline phosphatase putative* | | | | | | | | | | | | |
| PG0889 | | 5.14 E-1 | 16.3 | 20 | -0.2989 | 5.1802 | Y 🟡 | 🟡 Y | 1.5 E-1 | 8.64 E+6 | 8.13 E+6 | 0.0868 | 23.9996 | Y 🟡 |
| *PGN1050* | *PG0795* | *peptidase M24 family* | | | | | | | | | | | | |
| PG0886 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 8.61 E+4 | -5.5399 | 16.4243 | Y 🟡 |
| *PGN1052* | *PG0794* | *hypothetical protein PG_0886* | | | | | | | | | | | | |
| PG0885 | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y 🟡 | 🟡 Y | 1.85 E-1 | 8 E+5 | 7.55 E+5 | 0.0836 | 20.5677 | Y 🟡 |
| *PGN1053* | *PG0793* | *phospho-2-dehydro-3-deoxyheptonate aldolase/chorismate mutase* | | | | | | | | | | | | |
| PG0884 | | 4.23 E-1 | 3.4 | 6 | -0.8099 | 3.2361 | Y 🟡 | 🟡 Y | 1.91 E-1 | 9.95 E+5 | 9.77 E+5 | 0.0264 | 20.9115 | Y 🟡 |
| *PGN1054* | *PG0792* | *hypothetical protein PG_0884* | | | | | | | | | | | | |
| PG0883 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y 🟡 | 🟢 G | 3.18 E-5 | 3.21 E+5 | 8.31 E+5 | -1.3720 | 20.1353 | G 🟢 |
| *PGN1055* | *PG0791* | *hypothetical protein PG_0883* | | | | | | | | | | | | |
| PG0882 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y 🟡 | 🟢 G | 2.39 E-4 | 1.85 E+3 | 6.08 E+5 | -8.3605 | 19.2186 | G 🟢 |
| *PGN1056* | *PG0790* | *hypothetical protein PG_0882* | | | | | | | | | | | | |
| PG0881 | | 2.7 E-2 | 77.9 | 49 | 0.6682 | 6.9871 | Y 🟡 | 🟡 Y | 2.77 E-3 | 6.39 E+7 | 4.19 E+7 | 0.6106 | 26.6562 | Y 🟡 |
| *PGN1057* | *PG0789* | *recA recA protein* | | | | | | | | | | | | |
| PG0880 | | 5.94 E-2 | 11.1 | 3 | 1.8906 | 3.8200 | Y 🟡 | 🔴 R | 7.03 E-9 | 3.81 E+6 | 1.04 E+6 | 1.8686 | 22.2090 | R 🔴 |
| *PGN1058* | *PG0788* | *bcp bacterioferritin comigratory protein* | | | | | | | | | | | | |
| PG0877 | | 4.02 E-1 | 4.3 | 2 | 1.0970 | 2.6504 | Y 🟡 | 🔴 R | 1.22 E-5 | 2 E+6 | 1 E+6 | 0.9958 | 21.5197 | R 🔴 |
| *PGN1061* | *PG0787* | *hypothetical protein PG_0877* | | | | | | | | | | | | |
| PG0876 | | 2.52 E-1 | 3.4 | 8 | -1.2249 | 3.5138 | Y 🟡 | 🟡 Y | 9.23 E-2 | 1.31 E+6 | 1.67 E+6 | -0.3485 | 21.5051 | Y 🟡 |
| *PGN1062* | *PG0786* | *thdF thiophene and furan oxidation protein ThdF* | | | | | | | | | | | | |
| | | 4.75 E-1 | 23.1 | 18.5 | 0.3205 | 5.3786 | Y 🟡 | 🟡 Y | 8.26 E-2 | 2.98 E+6 | 3.51 E+6 | -0.2374 | 22.6300 | Y 🟡 |
| *PGN1071* | | | | | | | | | | | | | | |
| | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y 🟡 | 🔴 R | 0 | 1.29 E+6 | 1 E+3 | 10.3300 | 20.2969 | R 🔴 |
| *PGN1072* | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| | | 5.17 E-1 | 3.4 | 2 | 0.7751 | 2.4390 | Y 🟡 | 🟡 Y | 6.07 E-2 | 1.67 E+6 | 9.2 E+5 | 0.8606 | 21.3053 | Y 🟡 |
| *PGN1074* | | | | | | | | | | | | | | |
| PG1288 | | 2.49 E-2 | 26.5 | 49 | -0.8854 | 6.2389 | Y 🟡 | 🟢 G | 9.78 E-7 | 1.15 E+7 | 2.42 E+7 | -1.0788 | 25.0883 | G 🟢 |
| *PGN1078* | *PG1134* | *gmd GDP-mannose 46-dehydratase* | | | | | | | | | | | | |
| PG1289 | | 3.57 E-3 | 1.7 | 14 | -3.0323 | 3.9737 | Y 🟡 | 🟢 G | 2.05 E-7 | 5.5 E+5 | 3.45 E+6 | -2.6495 | 21.9321 | G 🟢 |
| *PGN1079* | *PG1135* | *fcl GDP-fucose synthetase* | | | | | | | | | | | | |
| PG1290 | | 4.75 E-1 | 516.8 | 539.5 | -0.0620 | 10.0448 | Y 🟡 | 🟡 Y | 2.15 E-2 | 3.43 E+8 | 4.73 E+8 | -0.4652 | 29.6044 | Y 🟡 |
| *PGN1080* | *PG1136* | *ilvE branched-chain amino acid aminotransferase* | | | | | | | | | | | | |
| PG1291 | | 1.3 E-3 | 21.4 | 4 | 2.4190 | 4.6663 | R 🔴 | 🔴 R | 1.04 E-12 | 8.14 E+6 | 9.67 E+5 | 3.0730 | 23.1188 | R 🔴 |
| *PGN1081* | *PG1137* | *hypothetical protein PG_1291* | | | | | | | | | | | | |
| PG1294 | | 3.5 E-1 | 4.3 | 8 | -0.9030 | 3.6180 | Y 🟡 | 🔴 R | 5.04 E-4 | 1.52 E+6 | 7.22 E+5 | 1.0755 | 21.0966 | Y 🟡 |
| *PGN1085* | *PG1138* | *feoB-2 ferrous iron transport protein B* | | | | | | | | | | | | |
| PG1297 | | 0 | 350.8 | 117.5 | 1.5781 | 8.8713 | R 🔴 | 🔴 R | 2.26 E-10 | 3.27 E+8 | 1.5 E+8 | 1.1240 | 28.8315 | R 🔴 |
| *PGN1088* | *PG1140* | *rpsA ribosomal protein S1* | | | | | | | | | | | | |
| PG1300 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 9.21 E+4 | -5.6372 | 16.5196 | Y 🟡 |
| *PGN1089* | *PG1141* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG1301 | | 5.43 E-1 | 2.6 | 1.5 | 0.7751 | 2.0240 | Y 🟡 | 🔴 R | 0 | 8.98 E+5 | 3.06 E+5 | 1.5543 | 20.1984 | R 🔴 |
| *PGN1090* | *PG1142* | *hypothetical protein PG_1301* | | | | | | | | | | | | |
| PG1302 | | 8.78 E-3 | 73.6 | 41.5 | 0.8263 | 6.8466 | R 🔴 | 🟡 Y | 8.7 E-2 | 7.57 E+7 | 6.12 E+7 | 0.3066 | 27.0293 | R 🔴 |
| *PGN1091* | *PG1143* | *hypothetical protein PG_1302* | | | | | | | | | | | | |
| PG1304 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y 🟡 | 🟡 Y | 5.41 E-2 | 8.81 E+5 | 1.89 E+6 | -1.0994 | 21.4010 | Y 🟡 |
| *PGN1093* | *PG1145* | *hypothetical protein PG_1304* | | | | | | | | | | | | |
| PG1305 | | 2.13 E-1 | 426.1 | 471 | -0.1445 | 9.8091 | Y 🟡 | 🟢 G | 1.2 E-5 | 3.84 E+8 | 5.51 E+8 | -0.5220 | 29.7992 | G 🟢 |
| *PGN1094* | *PG1146* | *gcvP glycine cleavage system P protein* | | | | | | | | | | | | |
| PG1306 | | 3.85 E-1 | 5.1 | 2.5 | 1.0381 | 2.9324 | Y 🟡 | 🔴 R | 6.7 E-6 | 3.58 E+6 | 1.06 E+6 | 1.7588 | 22.1431 | R 🔴 |
| *PGN1095* | *PG1147* | *metallo-beta-lactamase family protein* | | | | | | | | | | | | |
| PG1307 | | 1.32 E-1 | 7.7 | 16.5 | -1.0994 | 4.5970 | Y 🟡 | 🟡 Y | 1.42 E-1 | 2.43 E+6 | 2.09 E+6 | 0.2192 | 22.1090 | Y 🟡 |
| *PGN1096* | *PG1148* | *gidB glucose-inhibited division protein B* | | | | | | | | | | | | |
| PG1308 | | 2.74 E-1 | 10.3 | 17 | -0.7274 | 4.7691 | Y 🟡 | 🟢 G | 5.03 E-5 | 2.24 E+6 | 5.9 E+6 | -1.3945 | 22.9564 | G 🟢 |
| *PGN1097* | *PG1149* | *hypothetical protein PG_1308* | | | | | | | | | | | | |
| PG1310 | | 2 E-1 | 4.3 | 10 | -1.2249 | 3.8357 | Y 🟡 | 🟡 Y | 1.12 E-1 | 1.29 E+6 | 1.48 E+6 | -0.1998 | 21.4041 | Y 🟡 |
| *PGN1098* | *PG1150* | *exsB protein* | | | | | | | | | | | | |
| PG1311 | | 2.22 E-2 | 1.7 | 10.5 | -2.6172 | 3.6101 | Y 🟡 | 🟢 G | 6.39 E-8 | 2.85 E+5 | 1.2 E+6 | -2.0783 | 20.5063 | G 🟢 |
| *PGN1099* | *PG1151* | *conserved hypothetical protein* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | q-value | PP (Norm) | PPC (Norm) | $log_2$Ratio | $log_2$Sum | Regulation | | q-value | PP (Norm) | PPC (Norm) | $log_2$Ratio | $log_2$Sum | Consensus |
| PG1312 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y 🟡 | 🔴 R | 0 | 9.18 E+5 | 1 E+3 | 9.8416 | 19.8090 | R 🔴 |
| *PGN1100* | *PG1152* | *capA protein putative* | | | | | | | | | | | | |
| PG1313 | | 5.73 E-5 | 110.4 | 54 | 1.0314 | 7.3609 | R 🔴 | 🔴 R | 5.24 E-11 | 8.82 E+7 | 4.23 E+7 | 1.0606 | 26.9594 | R 🔴 |
| *PGN1103* | *PG1153* | *dipeptidase-related protein* | | | | | | | | | | | | |
| PG1315 | | 6.56 E-1 | 33.4 | 35.5 | -0.0892 | 6.1058 | Y 🟡 | 🟡 Y | 1.71 E-1 | 2.64 E+7 | 2.78 E+7 | -0.0751 | 25.6905 | Y 🟡 |
| *PGN1105* | *PG1155* | *slyD peptidyl-prolyl cis-trans isomerase SlyD FKBP-type* | | | | | | | | | | | | |
| PG1321 | | 1.85 E-1 | 185.7 | 217.5 | -0.2282 | 8.6553 | Y 🟡 | 🟡 Y | 1.17 E-3 | 6.51 E+7 | 1.02 E+8 | -0.6491 | 27.3166 | Y 🟡 |
| *PGN1111* | *PG1160* | *fhs formate--tetrahydrofolate ligase* | | | | | | | | | | | | |
| PG1323 | | 2.18 E-7 | 40.2 | 5 | 3.0078 | 5.4988 | R 🔴 | 🔴 R | 0 | 2.18 E+7 | 2.58 E+6 | 3.0811 | 24.5422 | R 🔴 |
| *PGN1112* | *PG1161* | *PhoH family protein* | | | | | | | | | | | | |
| PG1324 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 5.04 E-6 | 1.85 E+3 | 5.38 E+5 | -8.1826 | 19.0413 | G 🟢 |
| *PGN1113* | *PG1162* | *ruvC crossover junction endodeoxyribonuclease RuvC* | | | | | | | | | | | | |
| PG1325 | | 6.69 E-1 | 2.6 | 3 | -0.2249 | 2.4769 | Y 🟡 | 🟡 Y | 5.31 E-2 | 3.18 E+5 | 1.12 E+6 | -1.8196 | 20.4582 | Y 🟡 |
| *PGN1114* | *PG1163* | *hypothetical protein PG_1325* | | | | | | | | | | | | |
| PG1326 | | 8.79 E-2 | 6.8 | 16.5 | -1.2693 | 4.5451 | Y 🟡 | 🟡 Y | 1.67 E-3 | 2.97 E+6 | 6.31 E+6 | -1.0867 | 23.1469 | Y 🟡 |
| *PGN1115* | *PG1164* | *hemagglutinin putative* | | | | | | | | | | | | |
| PG1327 | | 3.49 E-1 | 220.8 | 244 | -0.1444 | 8.8603 | Y 🟡 | 🟢 G | 3.09 E-6 | 1.56 E+8 | 2.76 E+8 | -0.8260 | 28.6874 | G 🟢 |
| *PGN1116* | *PG1165* | *aminotransferase putative* | | | | | | | | | | | | |
| PG1328 | | 3.06 E-9 | 146.3 | 57.5 | 1.3475 | 7.6711 | R 🔴 | 🔴 R | 0 | 1.36 E+8 | 5.13 E+7 | 1.4108 | 27.4836 | R 🔴 |
| *PGN1117* | *PG1166* | *CoA ligase family protein* | | | | | | | | | | | | |
| PG1330 | | 1.04 E-4 | 5.1 | 29 | -2.4979 | 5.0931 | G 🟢 | 🟢 G | 4.27 E-5 | 2.87 E+6 | 1.26 E+7 | -2.1276 | 23.8790 | G 🟢 |
| *PGN1119* | *PG1167* | *mscL large conductance mechanosensitive channel protein* | | | | | | | | | | | | |
| | | 2.77 E-3 | 722.2 | 599 | 0.2698 | 10.3676 | R 🔴 | 🟡 Y | 5.43 E-2 | 9.62 E+8 | 8.59 E+8 | 0.1636 | 30.7617 | R 🔴 |
| *PGN1120* | | | | | | | | | | | | | | |
| PG1332 | | 5.2 E-1 | 20.5 | 24.5 | -0.2547 | 5.4930 | Y 🟡 | 🟡 Y | 7.14 E-3 | 1.94 E+7 | 4.07 E+7 | -1.0657 | 25.8420 | Y 🟡 |
| *PGN1122* | *PG1170* | *pntB NAD(P) transhydrogenase beta subunit* | | | | | | | | | | | | |
| PG1333 | | 9.48 E-2 | 1.7 | 7.5 | -2.1318 | 3.2034 | Y 🟡 | 🟢 G | 3.65 E-10 | 1.85 E+3 | 1.33 E+6 | -9.4908 | 20.3465 | G 🟢 |
| *PGN1123* | *PG1171* | *hypothetical protein PG_1333* | | | | | | | | | | | | |
| PG1334 | | 1.47 E-2 | 63.3 | 35.5 | 0.8348 | 6.6267 | Y 🟡 | 🔴 R | 5.29 E-7 | 3.86 E+7 | 1.96 E+7 | 0.9766 | 25.7936 | R 🔴 |
| *PGN1124* | *PG1172* | *band 7/Mec-2 family protein* | | | | | | | | | | | | |
| PG1335 | | 1.6 E-1 | 11.1 | 20.5 | -0.8820 | 4.9829 | Y 🟡 | 🟡 Y | 1.38 E-2 | 7.71 E+6 | 1.47 E+7 | -0.9343 | 24.4190 | Y 🟡 |
| *PGN1125* | *PG1173* | *membrane protein putative* | | | | | | | | | | | | |
| PG1340 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y 🟡 | 🟡 Y | 3.09 E-3 | 1.85 E+3 | 8.35 E+5 | -8.8175 | 19.6744 | Y 🟡 |
| *PGN1128* | *PG1176* | *L-lactate permease* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1341 | | 1.32 E-10 | 109.5 | 31 | 1.8209 | 7.1347 | R | 🔴 | 🔴 | R | 4.37 E-15 | 2.21 E+8 | 5.72 E+7 | 1.9481 | 28.0508 | R | 🔴 |
| *PGN1129* | *PG1177* | *hypothetical protein PG_1341* | | | | | | | | | | | | | | | |
| PG1342 | | 5.43 E-1 | 2.6 | 1.5 | 0.7751 | 2.0240 | Y | 🟡 | 🔴 | R | 0 | 1.03 E+6 | 2.18 E+5 | 2.2357 | 20.2453 | R | 🔴 |
| *PGN1130* | *PG1178* | *murB UDP-N-acetylenolpyruvoylglucosamine reductase* | | | | | | | | | | | | | | | |
| PG1343 | | 1.5 E-1 | 1.7 | 6.5 | -1.9253 | 3.0376 | Y | 🟡 | 🟢 | G | 6.34 E-7 | 1.85 E+3 | 7.6 E+5 | -8.6812 | 19.5384 | G | 🟢 |
| *PGN1131* | *PG1179* | *lipB lipoate-protein ligase B* | | | | | | | | | | | | | | | |
| PG1345 | | 7.79 E-2 | 6.0 | 15.5 | -1.3717 | 4.4256 | Y | 🟡 | 🟡 | Y | 2.15 E-2 | 1.07 E+6 | 3.06 E+6 | -1.5140 | 21.9772 | Y | 🟡 |
| *PGN1134* | *PG1180* | *glycosyl transferase group 1 family protein* | | | | | | | | | | | | | | | |
| PG1346 | | 6.7 E-1 | 5.1 | 5.5 | -0.0994 | 3.4106 | Y | 🟡 | 🟡 | Y | 1.49 E-2 | 1.24 E+6 | 7.45 E+5 | 0.7384 | 20.9228 | Y | 🟡 |
| *PGN1135* | *PG1181* | *glycosyl transferase group 1 family protein* | | | | | | | | | | | | | | | |
| PG1347 | | 5.77 E-2 | 5.1 | 15 | -1.5468 | 4.3316 | Y | 🟡 | 🟢 | G | 3.6 E-4 | 2.13 E+6 | 6.87 E+6 | -1.6882 | 23.1016 | G | 🟢 |
| *PGN1136* | *PG1182* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1348 | | 1.56 E-1 | 6.0 | 1.5 | 1.9975 | 2.9049 | Y | 🟡 | 🟡 | Y | 5.04 E-2 | 2.14 E+6 | 2.51 E+6 | -0.2343 | 22.1478 | Y | 🟡 |
| *PGN1137* | *PG1183* | *conserved hypothetical protein TIGR00147* | | | | | | | | | | | | | | | |
| PG1351 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 2.33 E-4 | 1.85 E+3 | 1.4 E+6 | -9.5583 | 20.4139 | G | 🟢 |
| *PGN1138* | *PG1186* | *hypothetical protein PG_1351* | | | | | | | | | | | | | | | |
| PG1352 | | 4.1 E-2 | 21.4 | 8.5 | 1.3315 | 4.9017 | Y | 🟡 | 🔴 | R | 8.92 E-4 | 1.35 E+7 | 5.97 E+6 | 1.1790 | 24.2162 | R | 🔴 |
| *PGN1139* | *PG1187* | *hypothetical protein PG_1352* | | | | | | | | | | | | | | | |
| PG1353 | | 3.11 E-2 | 65.0 | 39.5 | 0.7192 | 6.7078 | Y | 🟡 | 🔴 | R | 2.33 E-4 | 4.19 E+7 | 2.41 E+7 | 0.8012 | 25.9757 | R | 🔴 |
| *PGN1140* | *PG1188* | *pyrE orotate phosphoribosyltransferase* | | | | | | | | | | | | | | | |
| PG1354 | | 2.25 E-1 | 1.7 | 5.5 | -1.6843 | 2.8503 | Y | 🟡 | 🟡 | Y | 8.62 E-3 | 1.85 E+3 | 1.06 E+6 | -9.1576 | 20.0138 | Y | 🟡 |
| *PGN1141* | *PG1189* | *hydrolase carbon-nitrogen family* | | | | | | | | | | | | | | | |
| PG1356 | | 2.99 E-1 | 38.5 | 50 | -0.3769 | 6.4677 | Y | 🟡 | 🟡 | Y | 3.49 E-3 | 3 E+7 | 1.71 E+7 | 0.8125 | 25.4882 | Y | 🟡 |
| *PGN1143* | *PG1191* | *hypothetical protein PG_1356* | | | | | | | | | | | | | | | |
| PG1360 | | 6 E-1 | 62.5 | 67 | -0.1012 | 7.0164 | Y | 🟡 | 🟡 | Y | 1.11 E-2 | 3.94 E+7 | 5.05 E+7 | -0.3593 | 26.4222 | Y | 🟡 |
| *PGN1148* | *PG1195* | *purD phosphoribosylamine--glycine ligase* | | | | | | | | | | | | | | | |
| PG1361 | | 3.21 E-1 | 111.2 | 129 | -0.2138 | 7.9083 | Y | 🟡 | 🟡 | Y | 2.21 E-3 | 6.9 E+7 | 9.21 E+7 | -0.4154 | 27.2637 | Y | 🟡 |
| *PGN1149* | *PG1196* | *dipeptidyl aminopeptidase IV putative* | | | | | | | | | | | | | | | |
| PG1362 | | 6.69 E-1 | 6.8 | 7.5 | -0.1318 | 3.8425 | Y | 🟡 | 🔴 | R | 2.6 E-7 | 4.57 E+6 | 9.76 E+5 | 2.2270 | 22.4031 | Y | 🟡 |
| *PGN1150* | *PG1197* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1364 | | 4.4 E-1 | 5.1 | 8 | -0.6399 | 3.7152 | Y | 🟡 | 🟡 | Y | 1.15 E-1 | 1.39 E+6 | 1.76 E+6 | -0.3372 | 21.5856 | Y | 🟡 |
| *PGN1151* | *PG1199* | *dxr 1-deoxy-D-xylulose 5-phosphate reductoisomerase* | | | | | | | | | | | | | | | |
| PG1365 | | 3.21 E-1 | 1.7 | 4.5 | -1.3948 | 2.6349 | Y | 🟡 | 🟢 | G | 1.22 E-6 | 1.85 E+3 | 6.23 E+5 | -8.3956 | 19.2536 | G | 🟢 |
| *PGN1152* | *PG1200* | *16S rRNA processing protein RimM putative* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Regulation** | | | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Consensus** | |
| PG1366 | | 4.41 E-1 | 34.2 | 28 | 0.2897 | 5.9594 | Y | 🟡 | 🟡 | Y | 1.66 E-1 | 1.93 E+7 | 2.01 E+7 | -0.0608 | 25.2293 | Y | 🟡 |
| *PGN1153* | *PG1201* | *murA UDP-N-acetylglucosamine 1-carboxyvinyltransferase* | | | | | | | | | | | | | | | |
| PG1367 | | 2.27 E-2 | 18.0 | 5.5 | 1.7080 | 4.5527 | Y | 🟡 | 🔴 | R | 2.66 E-6 | 6.74 E+6 | 1.1 E+6 | 2.6099 | 22.9034 | R | 🔴 |
| *PGN1154* | *PG1202* | *hypothetical protein PG_1367* | | | | | | | | | | | | | | | |
| PG1368 | | 6.54 E-1 | 34.2 | 36.5 | -0.0928 | 6.1442 | Y | 🟡 | 🟡 | Y | 2.82 E-3 | 9.17 E+6 | 1.32 E+7 | -0.5255 | 24.4148 | Y | 🟡 |
| *PGN1155* | *PG1203* | *pgi glucose-6-phosphate isomerase* | | | | | | | | | | | | | | | |
| PG1369 | | 3.76 E-1 | 6.0 | 3 | 0.9975 | 3.1683 | Y | 🟡 | 🟢 | G | 0 | 1.86 E+6 | 3.18 E+6 | -0.7727 | 22.2636 | Y | 🟡 |
| *PGN1156* | *PG1204* | *gpsA glycerol-3-phosphate dehydrogenase (NAD(P)+)* | | | | | | | | | | | | | | | |
| PG1370 | | 1.88 E-1 | 54.8 | 72.5 | -0.4048 | 6.9917 | Y | 🟡 | 🟢 | G | 5.47 E-4 | 2.92 E+7 | 5.15 E+7 | -0.8196 | 26.2649 | G | 🟢 |
| *PGN1157* | *PG1205* | *lysS lysyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG1371 | | 7.24 E-2 | 47.1 | 70 | -0.5728 | 6.8711 | Y | 🟡 | 🟡 | Y | 1.48 E-1 | 1.71 E+7 | 1.82 E+7 | -0.0900 | 25.0748 | Y | 🟡 |
| *PGN1158* | *PG1206* | *phosphorylase family protein* | | | | | | | | | | | | | | | |
| PG1372 | | 2.67 E-1 | 9.4 | 4.5 | 1.0646 | 3.7983 | Y | 🟡 | 🔴 | R | 1.67 E-4 | 6.14 E+6 | 2.13 E+6 | 1.5305 | 22.9797 | R | 🔴 |
| *PGN1159* | *PG1207* | *hypothetical protein PG_1372* | | | | | | | | | | | | | | | |
| PG1066 | | 5.36 E-1 | 24.8 | 21 | 0.2408 | 5.5177 | Y | 🟡 | 🟡 | Y | 9.62 E-2 | 3.47 E+7 | 4.06 E+7 | -0.2267 | 26.1644 | Y | 🟡 |
| *PGN1162* | *PG0948* | *ctfA butyrate-acetoacetate CoA-transferase subunit A* | | | | | | | | | | | | | | | |
| PG1067 | | 3.99 E-1 | 20.5 | 15 | 0.4532 | 5.1512 | Y | 🟡 | 🟡 | Y | 1.6 E-1 | 1.52 E+7 | 1.42 E+7 | 0.0997 | 24.8099 | Y | 🟡 |
| *PGN1163* | *PG0949* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1068 | | 3.82 E-1 | 80.4 | 93.5 | -0.2172 | 7.4424 | Y | 🟡 | 🟢 | G | 3.58 E-5 | 3.88 E+7 | 7.33 E+7 | -0.9195 | 26.7405 | G | 🟢 |
| *PGN1164* | *PG0950* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1069 | | 2.18 E-7 | 111.2 | 43 | 1.3712 | 7.2690 | R | 🔴 | 🔴 | R | 1.11 E-12 | 7.63 E+7 | 2.82 E+7 | 1.4337 | 26.6393 | R | 🔴 |
| *PGN1165* | *PG0951* | *alcohol dehydrogenase zinc-containing putative* | | | | | | | | | | | | | | | |
| PG1070 | | 6.69 E-1 | 33.4 | 35 | -0.0688 | 6.0953 | Y | 🟡 | 🟡 | Y | 1.13 E-1 | 1.31 E+7 | 1.73 E+7 | -0.4076 | 24.8572 | Y | 🟡 |
| *PGN1166* | *PG0952* | *kamA L-lysine 23-aminomutase* | | | | | | | | | | | | | | | |
| PG1071 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 4.51 E+5 | 5.38 E+5 | -0.2553 | 19.9161 | Y | 🟡 |
| *PGN1167* | *PG0953* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1072 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.1 E+5 | -5.8885 | 16.7663 | Y | 🟡 |
| *PGN1168* | *PG0954* | *MutS family protein* | | | | | | | | | | | | | | | |
| PG1073 | | 5.77 E-2 | 8.6 | 20.5 | -1.2605 | 4.8608 | Y | 🟡 | 🟡 | Y | 3.32 E-3 | 5.91 E+6 | 9.76 E+6 | -0.7246 | 23.9019 | Y | 🟡 |
| *PGN1169* | *PG0955* | *kamD D-lysine 56-aminomutase alpha subunit* | | | | | | | | | | | | | | | |
| PG1074 | | 6.64 E-1 | 13.7 | 12.5 | 0.1312 | 4.7110 | Y | 🟡 | 🟡 | Y | 5.2 E-2 | 5.22 E+6 | 7.11 E+6 | -0.4448 | 23.5562 | Y | 🟡 |
| *PGN1170* | *PG0956* | *kamE D-lysine 56-aminomutase beta subunit* | | | | | | | | | | | | | | | |
| PG1075 | | 3.93 E-1 | 10.3 | 15 | -0.5468 | 4.6592 | Y | 🟡 | 🟡 | Y | 3.48 E-3 | 6.92 E+6 | 1.17 E+7 | -0.7557 | 24.1498 | Y | 🟡 |
| *PGN1171* | *PG0957* | *coenzyme A transferase beta subunit* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Regulation** | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Consensus** |
| PG1076 | | 3.14 E-4 | 397.9 | 519 | -0.3834 | 9.8406 | G 🟢 | 🟡 Y | 4.32 E-3 | 2.66 E+8 | 3.44 E+8 | -0.3717 | 29.1853 | G 🟢 |
| *PGN1172* | *PG0958* | *acdA acyl-CoA dehydrogenase short-chain specific* | | | | | | | | | | | | |
| PG1077 | | 1.72 E-2 | 338.0 | 413.5 | -0.2909 | 9.5536 | Y 🟡 | 🟡 Y | 5.28 E-2 | 3.16 E+8 | 3.78 E+8 | -0.2591 | 29.3706 | Y 🟡 |
| *PGN1173* | *PG0959* | *etfB-2 electron transfer flavoprotein beta subunit* | | | | | | | | | | | | |
| PG1078 | | 6.74 E-1 | 611.8 | 615.5 | -0.0087 | 10.2613 | Y 🟡 | 🟡 Y | 3.13 E-2 | 3.45 E+8 | 3.13 E+8 | 0.1433 | 29.2933 | Y 🟡 |
| *PGN1174* | *PG0960* | *etfA-2 electron transfer flavoprotein alpha subunit* | | | | | | | | | | | | |
| PG1079 | | 4.02 E-1 | 24.0 | 18 | 0.4125 | 5.3909 | Y 🟡 | 🟡 Y | 1.62 E-1 | 1.7 E+7 | 1.82 E+7 | -0.0919 | 25.0691 | Y 🟡 |
| *PGN1175* | *PG0961* | *enoyl-CoA hydratase/isomerase family protein* | | | | | | | | | | | | |
| PG1080 | | 4.82 E-1 | 46.2 | 53 | -0.1979 | 6.6323 | Y 🟡 | 🟡 Y | 2.1 E-2 | 3.14 E+7 | 4.96 E+7 | -0.6595 | 26.2719 | Y 🟡 |
| *PGN1176* | *PG0962* | *3-hydroxyacyl-CoA dehydrogenase family protein* | | | | | | | | | | | | |
| PG1081 | | 2.7 E-1 | 99.3 | 81.5 | 0.2843 | 7.4979 | Y 🟡 | 🟡 Y | 1.46 E-1 | 6.37 E+7 | 6.02 E+7 | 0.0827 | 26.8843 | Y 🟡 |
| *PGN1178* | *PG0963* | *ackA acetate kinase* | | | | | | | | | | | | |
| PG1082 | | 0 | 274.7 | 62 | 2.1473 | 8.3952 | R 🔴 | 🔴 R | 5.28 E-12 | 2.24 E+8 | 8.88 E+7 | 1.3337 | 28.2202 | R 🔴 |
| *PGN1179* | *PG0964* | *pta phosphotransacetylase* | | | | | | | | | | | | |
| PG1083 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 2.26 E+6 | -10.2524 | 21.1072 | G 🟢 |
| *PGN1180* | *PG0965* | *hypothetical protein PG_1083* | | | | | | | | | | | | |
| PG1084 | | 3.36 E-2 | 251.6 | 199 | 0.3381 | 8.8156 | Y 🟡 | 🔴 R | 3.22 E-15 | 3.07 E+8 | 1.4 E+8 | 1.1329 | 28.7368 | R 🔴 |
| *PGN1181* | *PG0966* | *thioredoxin family protein* | | | | | | | | | | | | |
| PG1085 | | 1.18 E-9 | 70.2 | 13.5 | 2.3778 | 6.3865 | R 🔴 | 🔴 R | 3.48 E-4 | 1.78 E+8 | 7.21 E+7 | 1.3031 | 27.8982 | R 🔴 |
| *PGN1182* | *PG0967* | *hypothetical protein PG_1085* | | | | | | | | | | | | |
| PG1087 | | 6.69 E-1 | 3.4 | 4 | -0.2249 | 2.8919 | Y 🟡 | 🟡 Y | 1.87 E-1 | 7.01 E+5 | 7.16 E+5 | -0.0302 | 20.4346 | Y 🟡 |
| *PGN1184* | *PG0968* | *radical SAM protein TIGR01212 family* | | | | | | | | | | | | |
| PG1089 | | 9.91 E-3 | 61.6 | 33 | 0.9006 | 6.5639 | R 🔴 | 🔴 R | 5.67 E-4 | 3.62 E+7 | 2.21 E+7 | 0.7135 | 25.7961 | R 🔴 |
| *PGN1186* | *PG0970* | *rprY DNA-binding response regulator RprY* | | | | | | | | | | | | |
| PG1091 | | 2.74 E-1 | 15.4 | 9 | 0.7751 | 4.6089 | Y 🟡 | 🟡 Y | 2.95 E-2 | 2.64 E+6 | 4.12 E+6 | -0.6404 | 22.6897 | Y 🟡 |
| *PGN1187* | *PG0971* | *DHH subfamily 1 protein* | | | | | | | | | | | | |
| PG1093 | | 5.46 E-4 | 8.6 | 32.5 | -1.9253 | 5.3595 | G 🟢 | 🟢 G | 2.22 E-5 | 6.73 E+6 | 2.11 E+7 | -1.6508 | 24.7311 | G 🟢 |
| *PGN1188* | *PG0972* | *hypothetical protein PG_1093* | | | | | | | | | | | | |
| PG1094 | | 1.62 E-1 | 65.0 | 85.5 | -0.3948 | 7.2339 | Y 🟡 | 🟡 Y | 1.98 E-2 | 4.29 E+7 | 5.78 E+7 | -0.4291 | 26.5864 | Y 🟡 |
| *PGN1189* | *PG0973* | *pgm phosphomannomutase* | | | | | | | | | | | | |
| PG1095 | | 3.64 E-1 | 14.5 | 9.5 | 0.6146 | 4.5877 | Y 🟡 | 🟡 Y | 4.25 E-3 | 3.15 E+6 | 1.75 E+6 | 0.8447 | 22.2239 | Y 🟡 |
| *PGN1190* | *PG0974* | *RNA methyltransferase TrmA family* | | | | | | | | | | | | |
| PG1096 | | 6.49 E-1 | 4.3 | 3.5 | 0.2897 | 2.9594 | Y 🟡 | 🟡 Y | 1.4 E-1 | 6.49 E+5 | 8.48 E+5 | -0.3846 | 20.5140 | Y 🟡 |
| *PGN1193* | *PG0975* | *hypothetical protein PG_1096* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1097 | | 4.4 E-1 | 5.1 | 8 | -0.6399 | 3.7152 | Y | 🟡 | 🟡 | Y | 4.36 E-2 | 9.17 E+5 | 1.45 E+6 | -0.6611 | 21.1750 | Y | 🟡 |
| *PGN1194* | *PG0976* | *Mur ligase domain protein/alanine racemase* | | | | | | | | | | | | | | | |
| PG1098 | | 4.65 E-1 | 2.6 | 4.5 | -0.8099 | 2.8211 | Y | 🟡 | 🟡 | Y | 1.32 E-3 | 2.3 E+5 | 1.88 E+5 | 0.2896 | 18.6758 | Y | 🟡 |
| *PGN1195* | *PG0977* | *hypothetical protein PG_1098* | | | | | | | | | | | | | | | |
| PG1100 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.06 E+6 | -9.1593 | 20.0156 | G | 🟢 |
| *PGN1197* | *PG0979* | *hypothetical protein PG_1100* | | | | | | | | | | | | | | | |
| PG1497 | | 6.69 E-1 | 3.4 | 4 | -0.2249 | 2.8919 | Y | 🟡 | 🟡 | Y | 5.33 E-2 | 5.54 E+5 | 4.67 E+5 | 0.2458 | 19.9622 | Y | 🟡 |
| *PGN1199* | *PG1312* | *DNA-binding protein histone-like family* | | | | | | | | | | | | | | | |
| PG1103 | | 6.64 E-1 | 6.8 | 6 | 0.1901 | 3.6832 | Y | 🟡 | 🟡 | Y | 1.5 E-1 | 2.55 E+6 | 2.25 E+6 | 0.1824 | 22.1952 | Y | 🟡 |
| *PGN1200* | *PG0982* | *ATPase AAA family* | | | | | | | | | | | | | | | |
| PG1105 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟡 | Y | 6.1 E-3 | 1.85 E+3 | 7.49 E+5 | -8.6617 | 19.5190 | Y | 🟡 |
| *PGN1202* | *PG0984* | *rpoN RNA polymerase sigma-54 factor* | | | | | | | | | | | | | | | |
| PG1106 | | 1.16 E-2 | 12.8 | 32 | -1.3180 | 5.4865 | Y | 🟡 | 🟡 | Y | 2.64 E-2 | 4.09 E+6 | 7.88 E+6 | -0.9459 | 23.5134 | Y | 🟡 |
| *PGN1203* | *PG0985* | *murF UDP-N-acetylmuramoylalanyl-D-glutamyl-26-diaminopimelate--D-alanyl-D-alanyl ligase* | | | | | | | | | | | | | | | |
| PG1114 | | 4.67 E-3 | 1.7 | 13.5 | -2.9798 | 3.9271 | Y | 🟡 | 🟡 | Y | 1.24 E-3 | 8.71 E+5 | 1.08 E+7 | -3.6359 | 23.4799 | Y | 🟡 |
| *PGN1204* | *PG0995* | *panD aspartate-1-decarboxylase* | | | | | | | | | | | | | | | |
| PG1115 | | 6.16 E-4 | 41.9 | 14 | 1.5825 | 5.8055 | R | 🔴 | 🔴 | R | 4.14 E-15 | 1.84 E+7 | 8.32 E+6 | 1.1470 | 24.6724 | R | 🔴 |
| *PGN1205* | *PG0996* | *ffh signal recognition particle protein* | | | | | | | | | | | | | | | |
| PG1116 | | 2.35 E-10 | 118.1 | 36.5 | 1.6938 | 7.2722 | R | 🔴 | 🔴 | R | 0 | 8.31 E+7 | 2.37 E+7 | 1.8102 | 26.6707 | R | 🔴 |
| *PGN1206* | *PG0997* | *folD methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase* | | | | | | | | | | | | | | | |
| PG1118 | | 3.96 E-7 | 91.6 | 32 | 1.5166 | 6.9490 | R | 🔴 | 🔴 | R | 0 | 3.76 E+7 | 9.97 E+6 | 1.9155 | 25.5034 | R | 🔴 |
| *PGN1208* | *PG1000* | *clpB clpB protein* | | | | | | | | | | | | | | | |
| PG1119 | | 3.79 E-4 | 30.8 | 70 | -1.1843 | 6.6554 | G | 🟢 | 🟢 | G | 4.4 E-5 | 1.4 E+7 | 4.18 E+7 | -1.5732 | 25.7345 | G | 🟢 |
| *PGN1209* | *PG1001* | *flavodoxin putative* | | | | | | | | | | | | | | | |
| | | 6.54 E-1 | 2.6 | 2 | 0.3601 | 2.1912 | Y | 🟡 | 🟡 | Y | 8.41 E-2 | 7.54 E+5 | 5.45 E+5 | 0.4671 | 20.3091 | Y | 🟡 |
| *PGN1211* | | | | | | | | | | | | | | | | | |
| | | 3.06 E-1 | 4.3 | 1.5 | 1.5121 | 2.5306 | Y | 🟡 | 🔴 | R | 2.58 E-16 | 5.46 E+5 | 3.96 E+5 | 0.4612 | 19.8456 | R | 🔴 |
| *PGN1212* | | | | | | | | | | | | | | | | | |
| | | 6.69 E-1 | 8.6 | 8 | 0.0970 | 4.0493 | Y | 🟡 | 🟡 | Y | 1.23 E-2 | 4.12 E+6 | 2.51 E+6 | 0.7165 | 22.6608 | Y | 🟡 |
| *PGN1213* | | | | | | | | | | | | | | | | | |
| | | 2.74 E-1 | 1.7 | 5 | -1.5468 | 2.7466 | Y | 🟡 | 🟡 | Y | 2.48 E-3 | 1.85 E+3 | 9.1 E+5 | -8.9420 | 19.7986 | Y | 🟡 |
| *PGN1214* | | | | | | | | | | | | | | | | | |
| PG1121 | | 1.76 E-2 | 165.1 | 119 | 0.4727 | 8.1505 | Y | 🟡 | 🟡 | Y | 2.89 E-3 | 1.17 E+8 | 8.29 E+7 | 0.4924 | 27.5718 | Y | 🟡 |
| *PGN1218* | *PG1002* | *asnS asparaginyl-tRNA synthetase* | | | | | | | | | | | | | | | |

| **TIGR** | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1122 | | 6.02 E-5 | 48.8 | 14.5 | 1.7500 | 5.9835 | R | 🔴 | 🔴 | R | 0 | 2.4 E+7 | 3.83 E+6 | 2.6481 | 24.7324 | R | 🔴 |
| *PGN1219* | *PG1003* | | | | | | | | | | | | | | | | |
| PG1123 | | 6.85 E-1 | 98.4 | 99.5 | -0.0160 | 7.6286 | Y | 🟡 | 🟡 | Y | 1.76 E-2 | 4.94 E+7 | 6.33 E+7 | -0.3562 | 26.7484 | Y | 🟡 |
| *PGN1220* | *PG1004* | *purB adenylosuccinate lyase* | | | | | | | | | | | | | | | |
| PG1124 | | 2.15 E-1 | 13.7 | 7 | 0.9677 | 4.3709 | Y | 🟡 | 🟡 | Y | 6.66 E-2 | 2.05 E+6 | 1.51 E+6 | 0.4482 | 21.7638 | Y | 🟡 |
| *PGN1221* | *PG1005* | *ATP:cob(I)alamin adenosyltransferase putative* | | | | | | | | | | | | | | | |
| PG1125 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 0 | 2.72 E+5 | 1 E+3 | 8.0880 | 18.0591 | R | 🔴 |
| *PGN1222* | *PG1006* | *hypothetical protein PG_1125* | | | | | | | | | | | | | | | |
| PG1126 | | 4.75 E-1 | 3.4 | 5.5 | -0.6843 | 3.1575 | Y | 🟡 | 🟡 | Y | 5.14 E-2 | 1.67 E+6 | 5.12 E+6 | -1.6201 | 22.6948 | Y | 🟡 |
| *PGN1223* | *PG1007* | *uraA uracil permease* | | | | | | | | | | | | | | | |
| PG1127 | | 2.15 E-3 | 12.8 | 1 | 3.6820 | 3.7902 | Y | 🟡 | 🔴 | R | 0 | 5.27 E+6 | 1 E+3 | 12.3644 | 22.3305 | R | 🔴 |
| *PGN1224* | *PG1008* | *transcriptional regulator AsnC Family* | | | | | | | | | | | | | | | |
| PG1128 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟡 | Y | 1.29 E-3 | 1.85 E+3 | 4.27 E+5 | -7.8515 | 18.7115 | Y | 🟡 |
| *PGN1225* | *PG1009* | *xseA exodeoxyribonuclease VII large subunit* | | | | | | | | | | | | | | | |
| PG1129 | | 0 | 239.6 | 46 | 2.3808 | 8.1578 | R | 🔴 | 🔴 | R | 0 | 9.05 E+7 | 1.88 E+7 | 2.2654 | 26.7041 | R | 🔴 |
| *PGN1226* | *PG1010* | *nrd ribonucleotide reductase* | | | | | | | | | | | | | | | |
| PG1130 | | 4.23 E-1 | 9.4 | 6 | 0.6496 | 3.9460 | Y | 🟡 | 🟡 | Y | 2.51 E-2 | 1.98 E+6 | 1.21 E+6 | 0.7077 | 21.6030 | Y | 🟡 |
| *PGN1227* | *PG1011* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG1132 | | 9.4 E-6 | 99.3 | 42.5 | 1.2237 | 7.1473 | R | 🔴 | 🔴 | R | 0 | 7.12 E+7 | 2.26 E+7 | 1.6547 | 26.4842 | R | 🔴 |
| *PGN1229* | *PG1013* | *valS valyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG1133 | | 3.87 E-2 | 7.7 | 1 | 2.9450 | 3.1212 | Y | 🟡 | 🔴 | R | 0 | 1.96 E+6 | 1 E+3 | 10.9386 | 20.9051 | R | 🔴 |
| *PGN1230* | *PG1014* | *hypothetical protein PG_1133* | | | | | | | | | | | | | | | |
| PG1134 | | 1.27 E-2 | 35.9 | 64.5 | -0.8438 | 6.6502 | Y | 🟡 | 🟡 | Y | 5.9 E-2 | 3.85 E+7 | 5.29 E+7 | -0.4606 | 26.4456 | Y | 🟡 |
| *PGN1232* | *PG1016* | *trxB thioredoxin reductase* | | | | | | | | | | | | | | | |
| PG1135 | | 2.55 E-1 | 10.3 | 5 | 1.0381 | 3.9324 | Y | 🟡 | 🟡 | Y | 1.5 E-1 | 2.94 E+6 | 2.44 E+6 | 0.2681 | 22.3592 | Y | 🟡 |
| *PGN1233* | *PG1017* | *bacterial sugar transferase* | | | | | | | | | | | | | | | |
| PG1137 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 4.92 E+5 | -8.0541 | 18.9133 | Y | 🟡 |
| *PGN1235* | *PG1019* | *porS porS protein* | | | | | | | | | | | | | | | |
| PG1138 | | 6 E-1 | 3.4 | 4.5 | -0.3948 | 2.9860 | Y | 🟡 | 🟡 | Y | 4.74 E-2 | 5.85 E+5 | 1.15 E+6 | -0.9710 | 20.7232 | Y | 🟡 |
| *PGN1236* | *PG1020* | *porR pigmentation and extracellular proteinase regulator* | | | | | | | | | | | | | | | |
| PG1139 | | 8.55 E-2 | 11.1 | 3.5 | 1.6682 | 3.8702 | Y | 🟡 | 🟡 | Y | 6.61 E-2 | 2 E+6 | 2.95 E+6 | -0.5584 | 22.2380 | Y | 🟡 |
| *PGN1238* | *PG1021* | *hypothetical protein PG_1139* | | | | | | | | | | | | | | | |
| PG1140 | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y | 🟡 | 🔴 | R | 1.93 E-4 | 8.72 E+5 | 4.96 E+5 | 0.8130 | 20.3832 | R | 🔴 |
| *PGN1239* | *PG1022* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1141 | | 4.45 E-2 | 18.0 | 6.5 | 1.4670 | 4.6129 | Y | 🟡 | 🟡 | Y | 6.43 E-3 | 3.48 E+6 | 1.91 E+6 | 0.8692 | 22.3618 | Y | 🟡 |
| *PGN1240* | *PG1023* | *glycosyl transferase group 1 family protein* | | | | | | | | | | | | | | | |
| PG1143 | | 6.77 E-1 | 4.3 | 4 | 0.0970 | 3.0493 | Y | 🟡 | 🟡 | Y | 3.21 E-3 | 1.56 E+6 | 1.23 E+6 | 0.3455 | 21.4144 | Y | 🟡 |
| *PGN1243* | *PG1026* | *sugar dehydrogenase UDP-glucose/GDP-mannose dehydrogenase family* | | | | | | | | | | | | | | | |
| PG1144 | | 2.52 E-1 | 5.1 | 10.5 | -1.0323 | 3.9666 | Y | 🟡 | 🟡 | Y | 7 E-2 | 1.33 E+6 | 2.09 E+6 | -0.6498 | 21.7047 | Y | 🟡 |
| *PGN1244* | *PG1027* | | | | | | | | | | | | | | | | |
| PG1145 | | 6.94 E-1 | 10.3 | 10.5 | -0.0323 | 4.3763 | Y | 🟡 | 🟡 | Y | 6.5 E-3 | 4.19 E+6 | 6.92 E+6 | -0.7220 | 23.4057 | Y | 🟡 |
| *PGN1245* | *PG1028* | *long-chain-fatty-acid--CoA ligase putative* | | | | | | | | | | | | | | | |
| | | 4.8 E-1 | 4.3 | 2.5 | 0.7751 | 2.7609 | Y | 🟡 | 🔴 | R | 3.27 E-13 | 2.67 E+6 | 1.2 E+5 | 4.4767 | 21.4143 | R | 🔴 |
| *PGN1246* | | | | | | | | | | | | | | | | | |
| PG1149 | | 6.7 E-1 | 5.1 | 5.5 | -0.0994 | 3.4106 | Y | 🟡 | 🔴 | R | 0 | 2.45 E+6 | 6.26 E+5 | 1.9708 | 21.5540 | Y | 🟡 |
| *PGN1251* | *PG1029* | *glycosyl transferase group 1 family protein* | | | | | | | | | | | | | | | |
| PG1151 | | 3.24 E-3 | 35.1 | 12.5 | 1.4888 | 5.5723 | R | 🔴 | 🔴 | R | 1.01 E-15 | 1.74 E+7 | 4.5 E+6 | 1.9540 | 24.3877 | R | 🔴 |
| *PGN1252* | *PG1031* | *alcohol dehydrogenase iron-containing* | | | | | | | | | | | | | | | |
| | | 1.41 E-1 | 69.3 | 50 | 0.4711 | 6.8985 | Y | 🟡 | 🟡 | Y | 5.05 E-3 | 2.75 E+7 | 4.87 E+7 | -0.8234 | 26.1844 | Y | 🟡 |
| *PGN1254* | | | | | | | | | | | | | | | | | |
| PG1155 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟡 | Y | 9.35 E-3 | 1.85 E+3 | 9.13 E+5 | -8.9458 | 19.8024 | Y | 🟡 |
| *PGN1255* | *PG1034* | *ADP-heptose--LPS heptosyltransferase putative* | | | | | | | | | | | | | | | |
| PG1156 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟡 | Y | 6.01 E-3 | 1.85 E+3 | 1.43 E+6 | -9.5918 | 20.4473 | Y | 🟡 |
| *PGN1256* | *PG1035* | *S4 domain protein* | | | | | | | | | | | | | | | |
| PG1160 | | 6.54 E-1 | 2.6 | 2 | 0.3601 | 2.1912 | Y | 🟡 | 🟡 | Y | 9.55 E-3 | 6.76 E+4 | 7.16 E+4 | -0.0840 | 17.0865 | Y | 🟡 |
| *PGN1259* | *PG1037* | *L-threonine-O-3-phosphate decarboxylase putative* | | | | | | | | | | | | | | | |
| PG1163 | | 2.67 E-1 | 2.6 | 6.5 | -1.3404 | 3.1806 | Y | 🟡 | 🟡 | Y | 1.14 E-2 | 1.45 E+6 | 9.85 E+5 | 0.5601 | 21.2161 | Y | 🟡 |
| *PGN1262* | *PG1040* | *cbiA cobyrinic acid ac-diamide synthase* | | | | | | | | | | | | | | | |
| PG1164 | | 3.82 E-1 | 19.7 | 14 | 0.4913 | 5.0738 | Y | 🟡 | 🟡 | Y | 1.98 E-1 | 4.18 E+6 | 4.21 E+6 | -0.0103 | 23.0010 | Y | 🟡 |
| *PGN1263* | *PG1041* | *hypothetical protein PG_1164* | | | | | | | | | | | | | | | |
| PG1165 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.56 E+5 | -6.3995 | 17.2702 | G | 🟢 |
| *PGN1264* | *PG1042* | *hypothetical protein PG_1165* | | | | | | | | | | | | | | | |
| PG1171 | | 4.89 E-1 | 35.9 | 30.5 | 0.2367 | 6.0539 | Y | 🟡 | 🟡 | Y | 6.11 E-3 | 1.66 E+7 | 9.96 E+6 | 0.7414 | 24.6649 | Y | 🟡 |
| *PGN1268* | *PG1044* | *oxidoreductase putative* | | | | | | | | | | | | | | | |
| PG1172 | | 2.25 E-4 | 3.4 | 23.5 | -2.7795 | 4.7507 | G | 🟢 | 🟢 | G | 3.1 E-8 | 1.97 E+6 | 9.27 E+6 | -2.2320 | 23.4221 | G | 🟢 |
| *PGN1269* | *PG1045* | *iron-sulfur cluster binding protein putative* | | | | | | | | | | | | | | | |
| PG1173 | | 2.96 E-1 | 18.8 | 12 | 0.6496 | 4.9460 | Y | 🟡 | 🟡 | Y | 1.13 E-1 | 9.14 E+6 | 7.77 E+6 | 0.2357 | 24.0113 | Y | 🟡 |
| *PGN1270* | *PG1046* | *YkgG family protein* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG1174 | | 2.8 E-1 | 11.1 | 18 | -0.6944 | 4.8641 | Y | 🟡 | 🟡 | Y | 3.45 E-3 | 2.08 E+6 | 3.3 E+6 | -0.6674 | 22.3596 | Y | 🟡 |
| *PGN1271* | *PG1047* | *thioesterase family protein* | | | | | | | | | | | | | | | |
| PG1058 | | 1.46 E-2 | 6.8 | 21.5 | -1.6512 | 4.8250 | Y | 🟡 | 🟡 | Y | 2.35 E-3 | 5.3 E+6 | 8.98 E+6 | -0.7603 | 23.7679 | Y | 🟡 |
| *PGN1296* | *PG0941* | *OmpA family protein* | | | | | | | | | | | | | | | |
| PG1057 | | 6.55 E-1 | 5.1 | 6 | -0.2249 | 3.4769 | Y | 🟡 | 🟡 | Y | 1.04 E-1 | 1.86 E+6 | 1.22 E+6 | 0.6019 | 21.5557 | Y | 🟡 |
| *PGN1297* | *PG0940* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1056 | | 4.75 E-1 | 3.4 | 5.5 | -0.6843 | 3.1575 | Y | 🟡 | 🟡 | Y | 3.63 E-2 | 1.02 E+6 | 1.78 E+6 | -0.8099 | 21.4180 | Y | 🟡 |
| *PGN1298* | *PG0939* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1050 | | 1.49 E-2 | 12.0 | 2 | 2.5825 | 3.8052 | Y | 🟡 | 🔴 | R | 0 | 2.99 E+6 | 7.99 E+4 | 5.2262 | 21.5501 | R | 🔴 |
| *PGN1303* | *PG0934* | *hypothetical protein PG_1050* | | | | | | | | | | | | | | | |
| PG1049 | | 1.6 E-1 | 18.0 | 29.5 | -0.7152 | 5.5689 | Y | 🟡 | 🟢 | G | 8.5 E-8 | 7.44 E+6 | 2.06 E+7 | -1.4691 | 24.7408 | G | 🟢 |
| *PGN1304* | *PG0933* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1048 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 0 | 3.92 E+5 | 7.32 E+5 | -0.9010 | 20.0993 | G | 🟢 |
| *PGN1305* | *PG0932* | *N-acetylmuramoyl-L-alanine amidase family 3* | | | | | | | | | | | | | | | |
| PG1044 | | 9.48 E-2 | 1.7 | 7.5 | -2.1318 | 3.2034 | Y | 🟡 | 🟢 | G | 6.6 E-6 | 1.85 E+3 | 2.34 E+6 | -10.3030 | 21.1579 | G | 🟢 |
| *PGN1308* | *PG0931* | *iron dependent repressor putative* | | | | | | | | | | | | | | | |
| PG1042 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.32 E+5 | -6.1601 | 17.0338 | Y | 🟡 |
| *PGN1310* | *PG0929* | *glycogen synthase putative* | | | | | | | | | | | | | | | |
| PG1041 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 2.1 E+6 | -10.1462 | 21.0012 | Y | 🟡 |
| *PGN1311* | *PG0928* | *K+-dependent Na+/Ca+ exchanger related-protein* | | | | | | | | | | | | | | | |
| PG1039 | | 5.43 E-1 | 3.4 | 5 | -0.5468 | 3.0743 | Y | 🟡 | 🟡 | Y | 1.6 E-1 | 1.11 E+6 | 1.19 E+6 | -0.1029 | 21.1349 | Y | 🟡 |
| *PGN1313* | *PG0926* | *integral membrane protein* | | | | | | | | | | | | | | | |
| PG1038 | | 1.53 E-1 | 2.6 | 8 | -1.6399 | 3.4015 | Y | 🟡 | 🟡 | Y | 1.76 E-2 | 6.84 E+5 | 1.55 E+6 | -1.1791 | 21.0913 | Y | 🟡 |
| *PGN1314* | *PG0925* | *ATP-dependent DNA helicase UvrD/PcrA/Rep Family* | | | | | | | | | | | | | | | |
| PG1037 | | 0 | 298.6 | 107.5 | 1.4740 | 8.6658 | R | 🔴 | 🔴 | R | 0 | 2.47 E+8 | 9.1 E+7 | 1.4385 | 28.3314 | R | 🔴 |
| *PGN1315* | *PG0924* | *hypothetical protein PG_1037* | | | | | | | | | | | | | | | |
| PG1036 | | 6.97 E-1 | 5.1 | 5 | 0.0381 | 3.3411 | Y | 🟡 | 🟡 | Y | 6.54 E-3 | 9.28 E+5 | 1.65 E+6 | -0.8342 | 21.2999 | Y | 🟡 |
| *PGN1316* | *PG0923* | *uvrA-1 excinuclease ABC A subunit* | | | | | | | | | | | | | | | |
| PG1035 | | 1.42 E-1 | 6.8 | 15 | -1.1318 | 4.4492 | Y | 🟡 | 🟢 | G | 8.08 E-6 | 2.35 E+6 | 7.45 E+6 | -1.6636 | 23.2237 | G | 🟢 |
| *PGN1317* | *PG0922* | *hypothetical protein PG_1035* | | | | | | | | | | | | | | | |
| PG1034 | | 4.65 E-1 | 2.6 | 4.5 | -0.8099 | 2.8211 | Y | 🟡 | 🔴 | R | 8.69 E-8 | 1.72 E+6 | 5.92 E+5 | 1.5355 | 21.1387 | Y | 🟡 |
| *PGN1318* | *PG0921* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG1030 | | 4.28 E-1 | 25.7 | 32 | -0.3180 | 5.8497 | Y | 🟡 | 🟡 | Y | 2.87 E-2 | 1.22 E+7 | 2.05 E+7 | -0.7472 | 24.9626 | Y | 🟡 |
| *PGN1321* | *PG0917* | *hypothetical protein PG_1030* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG1029 | | 5.89 E-3 | 11.1 | 1 | 3.4755 | 3.5997 | Y 🟡 | 🔴 R | 2.77 E-14 | 5.24 E+5 | 1 E+3 | 9.0343 | 19.0028 | R 🔴 |
| *PGN1322* | | *hypothetical protein PG_1029* | | | | | | | | | | | | |
| PG1028 | | 4.61 E-3 | 199.4 | 140 | 0.5100 | 8.4067 | R 🔴 | 🟡 Y | 1.5 E-1 | 1.65 E+8 | 1.72 E+8 | -0.0574 | 28.3278 | Y 🟡 |
| *PGN1323* | *PG0916* | *TPR domain protein* | | | | | | | | | | | | |
| | | 1.59 E-1 | 8.6 | 17 | -0.9904 | 4.6756 | Y 🟡 | 🟡 Y | 2.94 E-2 | 2.82 E+6 | 5.08 E+6 | -0.8505 | 22.9126 | Y 🟡 |
| *PGN1326* | | | | | | | | | | | | | | |
| | | 2.8 E-2 | 31.7 | 14.5 | 1.1266 | 5.5285 | Y 🟡 | 🔴 R | 5.01 E-9 | 1.27 E+7 | 3.6 E+6 | 1.8181 | 23.9586 | R 🔴 |
| *PGN1327* | | | | | | | | | | | | | | |
| | | 6.41 E-1 | 73.6 | 70 | 0.0721 | 7.1658 | Y 🟡 | 🟡 Y | 3.8 E-2 | 3.83 E+7 | 3.08 E+7 | 0.3144 | 26.0414 | Y 🟡 |
| *PGN1328* | | | | | | | | | | | | | | |
| PG0685 | | 6.97 E-1 | 2.6 | 2.5 | 0.0381 | 2.3411 | Y 🟡 | 🟢 G | 0 | 8.52 E+5 | 1 E+6 | -0.2386 | 20.8242 | Y 🟡 |
| *PGN1329* | *PG0618* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | |
| PG0628 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y 🟡 | 🔴 R | 0 | 1.96 E+6 | 1 E+3 | 10.9341 | 20.9006 | R 🔴 |
| *PGN1330* | *PG0566* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | |
| PG1022 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟡 Y | 6.86 E-2 | 1.85 E+3 | 1.35 E+6 | -9.5127 | 20.3684 | Y 🟡 |
| *PGN1334* | *PG0911* | *hypothetical protein PG_1022* | | | | | | | | | | | | |
| PG1020 | | 5.43 E-1 | 6.8 | 5 | 0.4532 | 3.5662 | Y 🟡 | 🟡 Y | 2.89 E-3 | 1.52 E+6 | 9.58 E+5 | 0.6683 | 21.2423 | Y 🟡 |
| *PGN1335* | *PG0910* | *hypothetical protein PG_1020* | | | | | | | | | | | | |
| PG1017 | | 1.11 E-8 | 559.6 | 373.5 | 0.5833 | 9.8659 | R 🔴 | 🔴 R | 0 | 4.87 E+8 | 1.35 E+8 | 1.8526 | 29.2117 | R 🔴 |
| *PGN1338* | *PG0907* | *ppdK pyruvate phosphate dikinase* | | | | | | | | | | | | |
| PG1014 | | 6 E-1 | 39.4 | 36 | 0.1287 | 6.2357 | Y 🟡 | 🟡 Y | 1.03 E-1 | 1.39 E+7 | 1.21 E+7 | 0.1995 | 24.6366 | Y 🟡 |
| *PGN1340* | *PG0906* | *TPR domain protein* | | | | | | | | | | | | |
| PG1013 | | 6.54 E-7 | 199.4 | 321.5 | -0.6894 | 9.0248 | G 🟢 | 🟡 Y | 1.25 E-2 | 2.34 E+8 | 3 E+8 | -0.3581 | 28.9931 | G 🟢 |
| *PGN1341* | *PG0905* | *acetyl-CoA hydrolase/transferase family protein* | | | | | | | | | | | | |
| PG1012 | | 1.05 E-1 | 8.6 | 18.5 | -1.1124 | 4.7579 | Y 🟡 | 🟡 Y | 7.65 E-2 | 3.92 E+6 | 6.02 E+6 | -0.6170 | 23.2450 | Y 🟡 |
| *PGN1342* | *PG0904* | *tRNA-i(6)A37 modification enzyme MiaB* | | | | | | | | | | | | |
| PG1010 | | 6.69 E-1 | 12.0 | 13 | -0.1180 | 4.6427 | Y 🟡 | 🟡 Y | 2.7 E-3 | 6.08 E+6 | 1.43 E+7 | -1.2319 | 24.2791 | Y 🟡 |
| *PGN1343* | *PG0903* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | |
| PG1006 | | 0 | 12.0 | 200 | -4.0614 | 7.7278 | G 🟢 | 🟢 G | 0 | 1.9 E+6 | 6.65 E+7 | -5.1296 | 26.0275 | G 🟢 |
| *PGN1347* | *PG0899* | *hypothetical protein PG_1006* | | | | | | | | | | | | |
| PG1004 | | 4.33 E-1 | 325.1 | 304.5 | 0.0947 | 9.2984 | Y 🟡 | 🟡 Y | 1.61 E-1 | 2.88 E+8 | 2.95 E+8 | -0.0368 | 29.1185 | Y 🟡 |
| *PGN1349* | *PG0897* | *prolyl oligopeptidase family protein* | | | | | | | | | | | | |
| PG1003 | | 6.05 E-2 | 1.7 | 8.5 | -2.3124 | 3.3521 | Y 🟡 | 🟢 G | 3.34 E-5 | 1.85 E+3 | 1.59 E+6 | -9.7430 | 20.5984 | G 🟢 |
| *PGN1350* | *PG0896* | *conserved hypothetical protein* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1001 | | 4.75 E-1 | 6.8 | 4.5 | 0.6052 | 3.5040 | Y | 🟡 | 🟡 | Y | 7.29 E-2 | 1.4 E+6 | 8.21 E+6 | -2.5553 | 23.1961 | Y | 🟡 |
| *PGN1352* | *PG0894* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1215 | | 3.5 E-1 | 7.7 | 12.5 | -0.6988 | 4.3363 | Y | 🟡 | 🟡 | Y | 2.18 E-3 | 2.33 E+6 | 4.08 E+6 | -0.8107 | 22.6113 | Y | 🟡 |
| *PGN1354* | *PG1076* | *lipoprotein protein putative* | | | | | | | | | | | | | | | |
| PG1217 | | 2.52 E-6 | 27.4 | 2 | 3.7751 | 4.8768 | R | 🔴 | 🔴 | R | 1.31 E-9 | 2.26 E+7 | 4.88 E+5 | 5.5336 | 24.4614 | R | 🔴 |
| *PGN1356* | *PG1077* | *hypothetical protein PG_1217* | | | | | | | | | | | | | | | |
| PG1219 | | 3.93 E-1 | 42.8 | 34.5 | 0.3104 | 6.2721 | Y | 🟡 | 🟡 | Y | 9.75 E-2 | 4.34 E+7 | 5.27 E+7 | -0.2822 | 26.5181 | Y | 🟡 |
| *PGN1358* | *PG1079* | *hypothetical protein PG_1219* | | | | | | | | | | | | | | | |
| PG1220 | | 4.94 E-3 | 2.6 | 15.5 | -2.5941 | 4.1753 | G | 🟢 | 🟢 | G | 3.05 E-5 | 1.57 E+6 | 5.42 E+6 | -1.7833 | 22.7376 | G | 🟢 |
| *PGN1359* | *PG1081* | *erythronate-4-phosphate dehydrogenase putative* | | | | | | | | | | | | | | | |
| PG1224 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 8.9 E-10 | 1.85 E+3 | 1.72 E+5 | -6.5412 | 17.4103 | G | 🟢 |
| *PGN1362* | *PG1083* | | | | | | | | | | | | | | | | |
| PG1225 | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y | 🟡 | 🔴 | R | 0 | 3.1 E+5 | 1 E+3 | 8.2764 | 18.2469 | R | 🔴 |
| *PGN1363* | *PG1084* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG1226 | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y | 🟡 | 🟡 | Y | 3.48 E-2 | 7.49 E+5 | 1.11 E+6 | -0.5637 | 20.8237 | Y | 🟡 |
| *PGN1364* | *PG1085* | *peptidyl-prolyl cis-trans isomerase cyclophilin-type* | | | | | | | | | | | | | | | |
| PG1230 | | 7 E-1 | 36.8 | 37 | -0.0081 | 6.2054 | Y | 🟡 | 🟡 | Y | 1.55 E-1 | 1.72 E+7 | 1.85 E+7 | -0.1043 | 25.0871 | Y | 🟡 |
| *PGN1366* | *PG1089* | *hypothetical protein PG_1230* | | | | | | | | | | | | | | | |
| PG1232 | | 1.3 E-9 | 2892.1 | 3405 | -0.2355 | 12.6205 | G | 🟢 | 🟡 | Y | 1.42 E-2 | 4.72 E+9 | 5.38 E+9 | -0.1904 | 33.2331 | G | 🟢 |
| *PGN1367* | *PG1090* | *gdh glutamate dehydrogenase NAD-specific* | | | | | | | | | | | | | | | |
| PG1235 | | 3.42 E-7 | 166.0 | 80.5 | 1.0441 | 7.9454 | R | 🔴 | 🔴 | R | 0 | 1.34 E+8 | 5.42 E+7 | 1.3060 | 27.4866 | R | 🔴 |
| *PGN1370* | *PG1091* | *epimerase/reductase putative* | | | | | | | | | | | | | | | |
| PG1236 | | 5.25 E-3 | 51.3 | 24 | 1.0970 | 6.2353 | R | 🔴 | 🔴 | R | 8.23 E-9 | 1.35 E+7 | 5.87 E+6 | 1.2074 | 24.2103 | R | 🔴 |
| *PGN1372* | *PG1092* | *hypothetical protein PG_1236* | | | | | | | | | | | | | | | |
| PG1237 | | 6.85 E-1 | 4.3 | 4.5 | -0.0729 | 3.1339 | Y | 🟡 | 🟡 | Y | 1.25 E-1 | 1.44 E+6 | 1.86 E+6 | -0.3709 | 21.6520 | Y | 🟡 |
| *PGN1373* | *PG1093* | *transcriptional regulator LuxR family* | | | | | | | | | | | | | | | |
| PG1239 | | 7.32 E-8 | 106.1 | 38 | 1.4814 | 7.1709 | R | 🔴 | 🔴 | R | 4.07 E-11 | 1 E+8 | 3.3 E+7 | 1.6034 | 26.9912 | R | 🔴 |
| *PGN1375* | *PG1095* | *fabG 3-oxoacyl-(acyl-carrier-protein) reductase* | | | | | | | | | | | | | | | |
| PG1240 | | 5.17 E-1 | 7.7 | 5.5 | 0.4856 | 3.7226 | Y | 🟡 | 🟡 | Y | 6.1 E-3 | 2.39 E+6 | 1.35 E+6 | 0.8292 | 21.8350 | Y | 🟡 |
| *PGN1376* | *PG1096* | *transcriptional regulator tetR family* | | | | | | | | | | | | | | | |
| PG1241 | | 4.07 E-2 | 12.0 | 3 | 1.9975 | 3.9049 | Y | 🟡 | 🔴 | R | 0 | 7.46 E+6 | 7.81 E+5 | 3.2555 | 22.9748 | R | 🔴 |
| *PGN1377* | *PG1097* | *lepA GTP-binding protein Lepa* | | | | | | | | | | | | | | | |
| PG1242 | | 9.44 E-2 | 6.0 | 1 | 2.5825 | 2.8052 | Y | 🟡 | 🔴 | R | 0 | 1.44 E+6 | 1 E+3 | 10.4938 | 20.4606 | R | 🔴 |
| *PGN1378* | *PG1098* | *dnaB replicative DNA helicase* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG1246 | | 1.13 E-4 | 178.8 | 107 | 0.7410 | 8.1590 | R 🔴 | 🔴 R | 9.96 E-11 | 1.14 E+8 | 6.31 E+7 | 0.8558 | 27.4016 | R 🔴 |
| *PGN1381* | *PG1101* | *alaS alanyl-tRNA synthetase* | | | | | | | | | | | | |
| PG1247 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y 🟡 | 🟢 G | 2.67 E-7 | 1.85 E+3 | 2.98 E+5 | -7.3331 | 18.1957 | G 🟢 |
| *PGN1382* | *PG1102* | *aroB 3-dehydroquinate synthase* | | | | | | | | | | | | |
| PG1248 | | 6.54 E-1 | 8.6 | 7.5 | 0.1901 | 4.0051 | Y 🟡 | 🟡 Y | 1.53 E-2 | 2.48 E+6 | 1.47 E+6 | 0.7539 | 21.9141 | Y 🟡 |
| *PGN1383* | *PG1103* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG1249 | | 4.21 E-1 | 3.4 | 1.5 | 1.1901 | 2.2994 | Y 🟡 | 🔴 R | 0 | 1.93 E+6 | 1.51 E+5 | 3.6762 | 20.9920 | R 🔴 |
| *PGN1384* | *PG1104* | *1-acyl-sn-glycerol-3-phosphate acetyltransferase putative* | | | | | | | | | | | | |
| PG1252 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 7.65 E+4 | -5.3694 | 16.2576 | Y 🟡 |
| *PGN1387* | *PG1106* | *membrane protein putative* | | | | | | | | | | | | |
| PG1253 | | 5.43 E-1 | 3.4 | 5 | -0.5468 | 3.0743 | Y 🟡 | 🟡 Y | 6.08 E-3 | 2.31 E+5 | 1.05 E+6 | -2.1830 | 20.2874 | Y 🟡 |
| *PGN1388* | *PG1107* | *ligA DNA ligase NAD-dependent* | | | | | | | | | | | | |
| PG1255 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 1.12 E+5 | -5.9249 | 16.8021 | Y 🟡 |
| *PGN1390* | *PG1109* | *recR recombination protein RecR* | | | | | | | | | | | | |
| PG1256 | | 7.01 E-1 | 17.1 | 17 | 0.0096 | 5.0923 | Y 🟡 | 🔴 R | 2.2 E-4 | 6.47 E+6 | 3.09 E+6 | 1.0679 | 23.1876 | R 🔴 |
| *PGN1391* | *PG1110* | *ribonuclease Rne/Rng family* | | | | | | | | | | | | |
| PG1258 | | 3.25 E-1 | 34.2 | 25.5 | 0.4246 | 5.9003 | Y 🟡 | 🟡 Y | 1.73 E-1 | 5.37 E+7 | 5.07 E+7 | 0.0847 | 26.6371 | Y 🟡 |
| *PGN1393* | *PG1111* | *hup-2 DNA-binding protein HU* | | | | | | | | | | | | |
| PG1260 | | 1.67 E-1 | 292.6 | 254 | 0.2043 | 9.0944 | Y 🟡 | 🟡 Y | 9.02 E-3 | 1.97 E+8 | 2.48 E+8 | -0.3301 | 28.7278 | Y 🟡 |
| *PGN1396* | *PG1113* | *anaerobic ribonucleoside-triphosphate reductase putative* | | | | | | | | | | | | |
| PG1269 | | 6.69 E-1 | 309.7 | 315 | -0.0243 | 9.2871 | Y 🟡 | 🟡 Y | 1.34 E-2 | 4 E+8 | 5 E+8 | -0.3237 | 29.7450 | Y 🟡 |
| *PGN1401* | *PG1120* | *pruA delta-1-pyrroline-5-carboxylate dehydrogenase* | | | | | | | | | | | | |
| PG1270 | | 4.62 E-3 | 29.1 | 9.5 | 1.6146 | 5.2702 | R 🔴 | 🔴 R | 0 | 2.36 E+7 | 3.07 E+6 | 2.9445 | 24.6687 | R 🔴 |
| *PGN1402* | *PG1121* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG1271 | | 1.55 E-3 | 325.1 | 422.5 | -0.3779 | 9.5462 | G 🟢 | 🟡 Y | 8.93 E-3 | 2.8 E+8 | 3.64 E+8 | -0.3794 | 29.2632 | G 🟢 |
| *PGN1403* | *PG1122* | *acetylornithine aminotransferase putative* | | | | | | | | | | | | |
| PG0562 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y 🟡 | 🔴 R | 0 | 7.42 E+5 | 1 E+3 | 9.5344 | 19.5021 | R 🔴 |
| *PGN1408* | *PG0508* | *potassium uptake protein TrkA putative* | | | | | | | | | | | | |
| PG0561 | | 5.8 E-1 | 182.3 | 173.5 | 0.0710 | 8.4747 | Y 🟡 | 🟡 Y | 2.95 E-2 | 1.65 E+8 | 2.02 E+8 | -0.2949 | 28.4534 | Y 🟡 |
| *PGN1409* | *PG0507* | *peptidase M20/M25/M40 family* | | | | | | | | | | | | |
| PG0559 | | 1.53 E-1 | 2.6 | 8 | -1.6399 | 3.4015 | Y 🟡 | 🟢 G | 4.39 E-6 | 1 E+6 | 6.45 E+6 | -2.6859 | 22.8292 | G 🟢 |
| *PGN1411* | *PG0506* | *chlorohydrolase family protein* | | | | | | | | | | | | |
| PG0558 | | 1.21 E-5 | 67.6 | 135 | -0.9979 | 7.6625 | G 🟢 | 🟡 Y | 1.81 E-3 | 3.32 E+7 | 6.1 E+7 | -0.8758 | 26.4901 | G 🟢 |
| *PGN1412* | *PG0505* | *purine nucleoside phosphorylase I inosine and guanosine-specific* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0555 | | 5.47 E-3 | 4.3 | 19 | -2.1509 | 4.5409 | G | 🟢 | 🟡 | Y | 2.65 E-2 | 7.41 E+5 | 1.15 E+6 | -0.6364 | 20.8531 | G | 🟢 |
| *PGN1415* | *PG0502* | *DNA-binding protein histone-like family* | | | | | | | | | | | | | | | |
| PG0553 | | 5.63 E-4 | 312.3 | 416 | -0.4136 | 9.5084 | G | 🟢 | 🟡 | Y | 1.59 E-3 | 1.89 E+8 | 2.67 E+8 | -0.4976 | 28.7643 | G | 🟢 |
| *PGN1416* | *PG0501* | *extracellular protease putative* | | | | | | | | | | | | | | | |
| PG0548 | | 1.1 E-1 | 328.6 | 281.5 | 0.2231 | 9.2528 | Y | 🟡 | 🔴 | R | 5.48 E-4 | 2.27 E+8 | 1.62 E+8 | 0.4895 | 28.5337 | R | 🔴 |
| *PGN1418* | *PG0498* | *pyruvate ferredoxin/flavodoxin oxidoreductase family protein* | | | | | | | | | | | | | | | |
| PG0547 | | 1.34 E-7 | 53.1 | 10 | 2.4074 | 5.9784 | R | 🔴 | 🔴 | R | 3.5 E-6 | 3.56 E+7 | 5.8 E+6 | 2.6176 | 25.3031 | R | 🔴 |
| *PGN1419* | *PG0497* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟡 | Y | 5.45 E-3 | 1.85 E+3 | 8.99 E+5 | -8.9245 | 19.7812 | Y | 🟡 |
| *PGN1426* | | | | | | | | | | | | | | | | | |
| PG0541 | | 6.94 E-1 | 7.7 | 7.5 | 0.0381 | 3.9261 | Y | 🟡 | 🟡 | Y | 1.93 E-1 | 3.56 E+6 | 3.42 E+6 | 0.0568 | 22.7352 | Y | 🟡 |
| *PGN1429* | *PG0494* | *hypothetical protein PG_0541* | | | | | | | | | | | | | | | |
| | | 3.05 E-1 | 18.0 | 11.5 | 0.6439 | 4.8811 | Y | 🟡 | 🟡 | Y | 1.49 E-1 | 9.48 E+6 | 8.52 E+6 | 0.1540 | 24.1020 | Y | 🟡 |
| *PGN1430* | | | | | | | | | | | | | | | | | |
| PG0539 | | 1.98 E-1 | 15.4 | 8 | 0.9450 | 4.5485 | Y | 🟡 | 🔴 | R | 8.61 E-5 | 7.47 E+6 | 3.69 E+6 | 1.0155 | 23.4123 | R | 🔴 |
| *PGN1431* | *PG0492* | *efflux transporter MFP component RND family* | | | | | | | | | | | | | | | |
| PG0538 | | 1.86 E-2 | 10.3 | 26.5 | -1.3679 | 5.2004 | Y | 🟡 | 🟢 | G | 3.38 E-4 | 3.93 E+6 | 8.69 E+6 | -1.1472 | 23.5890 | G | 🟢 |
| *PGN1432* | *PG0490* | *outer membrane efflux protein* | | | | | | | | | | | | | | | |
| PG0537 | | 2.5 E-13 | 616.1 | 917 | -0.5738 | 10.5822 | G | 🟢 | 🟡 | Y | 1.06 E-2 | 5.45 E+8 | 6.53 E+8 | -0.2614 | 30.1571 | G | 🟢 |
| *PGN1434* | *PG0489* | *pepD-2 aminoacyl-histidine dipeptidase* | | | | | | | | | | | | | | | |
| PG0535 | | 4.23 E-1 | 6.8 | 4 | 0.7751 | 3.4390 | Y | 🟡 | 🟡 | Y | 3.5 E-2 | 6.05 E+6 | 3.28 E+6 | 0.8844 | 23.1522 | Y | 🟡 |
| *PGN1436* | *PG0488* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0534 | | 1.76 E-5 | 8.6 | 40 | -2.2249 | 5.6016 | G | 🟢 | 🟢 | G | 1.62 E-12 | 3.3 E+6 | 1.49 E+7 | -2.1780 | 24.1202 | G | 🟢 |
| *PGN1437* | *PG0487* | *hypothetical protein PG_0534* | | | | | | | | | | | | | | | |
| PG0532 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟡 | Y | 2.84 E-2 | 1.85 E+3 | 1.15 E+6 | -9.2795 | 20.1355 | Y | 🟡 |
| *PGN1440* | *PG0486* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG0531 | | 7.86 E-5 | 82.1 | 35.5 | 1.2103 | 6.8783 | R | 🔴 | 🟡 | Y | 6.61 E-2 | 3.18 E+7 | 2.34 E+7 | 0.4388 | 25.7181 | R | 🔴 |
| *PGN1441* | *PG0485* | *nadE glutamine-dependent NAD+ synthetase* | | | | | | | | | | | | | | | |
| PG0530 | | 7.93 E-2 | 26.5 | 13.5 | 0.9744 | 5.3228 | Y | 🟡 | 🔴 | R | 5.58 E-5 | 1.82 E+7 | 7.72 E+6 | 1.2355 | 24.6259 | R | 🔴 |
| *PGN1443* | *PG0484* | *carB carbamoyl-phosphate synthase large subunit* | | | | | | | | | | | | | | | |
| PG0529 | | 1.04 E-2 | 2.6 | 14 | -2.4473 | 4.0502 | Y | 🟡 | 🟢 | G | 6.88 E-6 | 9.86 E+5 | 7.82 E+6 | -2.9879 | 23.0700 | G | 🟢 |
| *PGN1444* | *PG0482* | *carA carbamoyl-phosphate synthase small subunit* | | | | | | | | | | | | | | | |
| PG0528 | | 5.08 E-2 | 28.2 | 13.5 | 1.0646 | 5.3832 | Y | 🟡 | 🔴 | R | 3.1 E-5 | 1.04 E+7 | 4.24 E+6 | 1.2882 | 23.7996 | R | 🔴 |
| *PGN1445* | *PG0481* | *amidophosphoribosyltransferase putative* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0526 | | 1.41 E-6 | 24.8 | 1 | 4.6331 | 4.6901 | R | 🔴 | 🔴 | R | 0 | 9.83 E+6 | 1 E+3 | 13.2635 | 23.2294 | R | 🔴 |
| *PGN1446* | *PG0480* | *membrane protein putative* | | | | | | | | | | | | | | | |
| PG0525 | | 4.5 E-1 | 29.1 | 23.5 | 0.3080 | 5.7168 | Y | 🟡 | 🔴 | R | 1.33 E-6 | 1.33 E+7 | 5.2 E+6 | 1.3581 | 24.1441 | R | 🔴 |
| *PGN1447* | *PG0479* | *pyrG CTP synthase* | | | | | | | | | | | | | | | |
| PG0523 | | 1.21 E-2 | 127.5 | 85.5 | 0.5764 | 7.7347 | Y | 🟡 | 🟡 | Y | 8.93 E-3 | 4.09 E+7 | 5.47 E+7 | -0.4212 | 26.5107 | Y | 🟡 |
| *PGN1449* | *PG0477* | *guaB inosine-5'-monophosphate dehydrogenase* | | | | | | | | | | | | | | | |
| PG0521 | | 3.86 E-1 | 70.2 | 82 | -0.2249 | 7.2495 | Y | 🟡 | 🟡 | Y | 1.46 E-1 | 1.5 E+8 | 1.64 E+8 | -0.1314 | 28.2279 | Y | 🟡 |
| *PGN1451* | *PG0475* | *groES chaperonin 10 kDa* | | | | | | | | | | | | | | | |
| PG0520 | | 0 | 779.5 | 384.5 | 1.0196 | 10.1849 | R | 🔴 | 🔴 | R | 1.01 E-15 | 5.51 E+8 | 2.76 E+8 | 1.0004 | 29.6230 | R | 🔴 |
| *PGN1452* | *PG0474* | *groEL chaperonin 60 kDa* | | | | | | | | | | | | | | | |
| PG0517 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 0 | 7.61 E+5 | 1 E+3 | 9.5712 | 19.5389 | R | 🔴 |
| *PGN1455* | *PG0471* | *hypothetical protein PG_0517* | | | | | | | | | | | | | | | |
| PG0516 | | 1.45 E-1 | 5.1 | 1 | 2.3601 | 2.6168 | Y | 🟡 | 🔴 | R | 0 | 9.33 E+5 | 1 E+3 | 9.8654 | 19.8327 | R | 🔴 |
| *PGN1456* | *PG0470* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0515 | | 6.22 E-1 | 18.0 | 16 | 0.1674 | 5.0861 | Y | 🟡 | 🔴 | R | 3.86 E-4 | 1.2 E+7 | 3.61 E+6 | 1.7289 | 23.8942 | R | 🔴 |
| *PGN1457* | *PG0469* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0514 | | 2.95 E-10 | 160.9 | 62.5 | 1.3639 | 7.8032 | R | 🔴 | 🔴 | R | 0 | 8.47 E+7 | 2.1 E+7 | 2.0100 | 26.6555 | R | 🔴 |
| *PGN1458* | *PG0468* | *secA preprotein translocase SecA subunit* | | | | | | | | | | | | | | | |
| PG0513 | | 9.48 E-2 | 1.7 | 7.5 | -2.1318 | 3.2034 | Y | 🟡 | 🟢 | G | 1.34 E-4 | 1.85 E+3 | 1.11 E+6 | -9.2318 | 20.0879 | G | 🟢 |
| *PGN1459* | *PG0467* | *conserved hypothetical protein TIGR00255* | | | | | | | | | | | | | | | |
| PG0510 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 2 E+5 | -6.7581 | 17.6250 | Y | 🟡 |
| *PGN1462* | *PG0464* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0506 | | 6.68 E-1 | 1976.6 | 1962.5 | 0.0103 | 11.9436 | Y | 🟡 | 🟡 | Y | 3.96 E-2 | 1.11 E+9 | 1.29 E+9 | -0.2168 | 31.1552 | Y | 🟡 |
| *PGN1466* | *PG0461* | *prtRII arginine-specific cysteine proteinase* | | | | | | | | | | | | | | | |
| PG0504 | | 3.21 E-1 | 1.7 | 4.5 | -1.3948 | 2.6349 | Y | 🟡 | 🟢 | G | 3.01 E-4 | 1.85 E+3 | 6.86 E+5 | -8.5348 | 19.3924 | G | 🟢 |
| *PGN1468* | *PG0460* | *lipA lipoate synthase* | | | | | | | | | | | | | | | |
| PG0503 | | 5.76 E-5 | 39.4 | 89 | -1.1771 | 7.0041 | G | 🟢 | 🟢 | G | 1.33 E-4 | 2.26 E+7 | 4.65 E+7 | -1.0434 | 26.0422 | G | 🟢 |
| *PGN1469* | *PG0459* | *dpp dipeptidyl aminopeptidase IV* | | | | | | | | | | | | | | | |
| PG0502 | | 1.45 E-1 | 5.1 | 1 | 2.3601 | 2.6168 | Y | 🟡 | 🔴 | R | 1.44 E-5 | 4.13 E+5 | 1 E+3 | 8.6913 | 18.6606 | R | 🔴 |
| *PGN1470* | *PG0458* | *smpB SsrA-binding protein* | | | | | | | | | | | | | | | |
| PG0500 | | 1.7 E-1 | 14.5 | 7 | 1.0552 | 4.4294 | Y | 🟡 | 🟡 | Y | 5.26 E-2 | 4.2 E+6 | 2.77 E+6 | 0.6012 | 22.7333 | Y | 🟡 |
| *PGN1472* | *PG0456* | *tgt queuine tRNA-ribosyltransferase* | | | | | | | | | | | | | | | |
| PG0498 | | 6.69 E-1 | 5.1 | 4.5 | 0.1901 | 3.2681 | Y | 🟡 | 🟡 | Y | 1.85 E-1 | 1.27 E+6 | 1.3 E+6 | -0.0435 | 21.2933 | Y | 🟡 |
| *PGN1474* | *PG0454* | *luxS autoinducer-2 production protein LuxS* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG0497 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 1.57 E-7 | 1.85 E+3 | 2.51 E+5 | -7.0840 | 17.9483 | G | 🟢 |
| *PGN1475* | *PG0453* | *mtn 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase* | | | | | | | | | | | | | | | |
| PG0495 | | 8.44 E-2 | 4.3 | 12.5 | -1.5468 | 4.0685 | Y | 🟡 | 🟢 | G | 2.09 E-5 | 1.15 E+6 | 3.85 E+6 | -1.7364 | 22.2534 | G | 🟢 |
| *PGN1476* | *PG0452* | *hypothetical protein PG_0495* | | | | | | | | | | | | | | | |
| PG0491 | | 2.44 E-1 | 353.4 | 391.5 | -0.1478 | 9.5409 | Y | 🟡 | 🟡 | Y | 1.81 E-1 | 3.53 E+8 | 3.47 E+8 | 0.0230 | 29.3819 | Y | 🟡 |
| *PGN1479* | *PG0449* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0490 | | 1.45 E-1 | 5.1 | 1 | 2.3601 | 2.6168 | Y | 🟡 | 🔴 | R | 0 | 3.37 E+6 | 1 E+3 | 11.7167 | 21.6829 | R | 🔴 |
| *PGN1480* | *PG0448* | *membrane protein putative* | | | | | | | | | | | | | | | |
| PG0488 | | 6.61 E-1 | 9.4 | 10.5 | -0.1578 | 4.3156 | Y | 🟡 | 🟡 | Y | 2.06 E-2 | 2.38 E+6 | 4.17 E+6 | -0.8069 | 22.6447 | Y | 🟡 |
| *PGN1482* | *PG0446* | *ruvB Holliday junction DNA helicase RuvB* | | | | | | | | | | | | | | | |
| PG0486 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 1.28 E-4 | 1.85 E+3 | 1.84 E+6 | -9.9579 | 20.8131 | G | 🟢 |
| *PGN1484* | *PG0444* | *ogt methylated-DNA--protein-cysteine S-methyltransferase* | | | | | | | | | | | | | | | |
| PG0485 | | 2.32 E-1 | 42.8 | 57 | -0.4139 | 6.6407 | Y | 🟡 | 🟡 | Y | 9.87 E-2 | 1.51 E+7 | 1.77 E+7 | -0.2363 | 24.9667 | Y | 🟡 |
| *PGN1485* | *PG0443* | *yajC preprotein translocase YajC subunit* | | | | | | | | | | | | | | | |
| PG0484 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 1.87 E-7 | 8.48 E+5 | 1 E+3 | 9.7284 | 19.6959 | R | 🔴 |
| *PGN1486* | *PG0442* | *hypothetical protein PG_0484* | | | | | | | | | | | | | | | |
| PG0482 | | 6.64 E-1 | 13.7 | 12.5 | 0.1312 | 4.7110 | Y | 🟡 | 🟡 | Y | 3.9 E-2 | 7.17 E+6 | 3.71 E+6 | 0.9482 | 23.3750 | Y | 🟡 |
| *PGN1488* | *PG0440* | *hypothetical protein PG_0482* | | | | | | | | | | | | | | | |
| PG0481 | | 0 | 367.9 | 122 | 1.5926 | 8.9364 | R | 🔴 | 🔴 | R | 1.84 E-6 | 1.9 E+8 | 1.01 E+8 | 0.9065 | 28.1189 | R | 🔴 |
| *PGN1489* | *PG0439* | *kbl 2-amino-3-ketobutyrate CoA ligase* | | | | | | | | | | | | | | | |
| PG0477 | | 4.14 E-1 | 36.8 | 29.5 | 0.3187 | 6.0508 | Y | 🟡 | 🔴 | R | 1.42 E-5 | 1.63 E+7 | 8.82 E+6 | 0.8862 | 24.5830 | R | 🔴 |
| *PGN1492* | *PG0436* | *panC pantoate--beta-alanine ligase* | | | | | | | | | | | | | | | |
| PG0476 | | 4.75 E-1 | 18.0 | 22.5 | -0.3244 | 5.3387 | Y | 🟡 | 🟡 | Y | 9.88 E-2 | 9.27 E+6 | 7.61 E+6 | 0.2832 | 24.0089 | Y | 🟡 |
| *PGN1493* | *PG0435* | *yngK-2 yngK protein* | | | | | | | | | | | | | | | |
| PG0474 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟡 | Y | 1.05 E-1 | 4.32 E+5 | 6.36 E+5 | -0.5581 | 20.0267 | Y | 🟡 |
| *PGN1495* | *PG0433* | *low-specificity L-threonine aldolase* | | | | | | | | | | | | | | | |
| PG0471 | | 6.69 E-1 | 2.6 | 3 | -0.2249 | 2.4769 | Y | 🟡 | 🟡 | Y | 1.8 E-2 | 1.04 E+6 | 3.99 E+6 | -1.9438 | 22.2600 | Y | 🟡 |
| *PGN1498* | *PG0429* | *hypothetical protein PG_0471* | | | | | | | | | | | | | | | |
| PG0468 | | 3.09 E-1 | 9.4 | 5 | 0.9126 | 3.8492 | Y | 🟡 | 🟡 | Y | 2.19 E-3 | 4.31 E+6 | 2.38 E+6 | 0.8548 | 22.6749 | Y | 🟡 |
| *PGN1501* | *PG0427* | *manA mannose-6-phosphate isomerase class I* | | | | | | | | | | | | | | | |
| PG0466 | | 1.16 E-1 | 5.1 | 13 | -1.3404 | 4.1806 | Y | 🟡 | 🟡 | Y | 1.57 E-2 | 1.98 E+6 | 5.16 E+6 | -1.3814 | 22.7667 | Y | 🟡 |
| *PGN1502* | *PG0426* | *hypothetical protein PG_0466* | | | | | | | | | | | | | | | |
| PG0465 | | 6.05 E-2 | 6.8 | 1 | 2.7751 | 2.9718 | Y | 🟡 | 🔴 | R | 4.08 E-8 | 2.08 E+6 | 1 E+3 | 11.0250 | 20.9915 | R | 🔴 |
| *PGN1503* | *PG0425* | *fur ferric uptake transcriptional regulator* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG0464 | | 3.01 E-1 | 82.1 | 98.5 | -0.2620 | 7.4970 | Y | 🟡 | 🟡 | Y | 1.36 E-1 | 6.39 E+7 | 6.77 E+7 | -0.0832 | 26.9720 | Y | 🟡 |
| *PGN1504* | *PG0424* | *purA adenylosuccinate synthetase* | | | | | | | | | | | | | | | |
| PG0463 | | 6 E-1 | 8.6 | 7 | 0.2897 | 3.9594 | Y | 🟡 | 🔴 | R | 6.37 E-4 | 2.67 E+6 | 9.68 E+5 | 1.4649 | 21.7955 | R | 🔴 |
| *PGN1505* | *PG0423* | *folC folylpolyglutamate synthase* | | | | | | | | | | | | | | | |
| PG0462 | | 2.51 E-6 | 13.7 | 54.5 | -1.9931 | 6.0915 | G | 🟢 | 🟢 | G | 6.92 E-6 | 8.87 E+6 | 2.4 E+7 | -1.4365 | 24.9709 | G | 🟢 |
| *PGN1506* | *PG0422* | *transporter putative* | | | | | | | | | | | | | | | |
| PG0452 | | 3.11 E-4 | 243.0 | 162.5 | 0.5805 | 8.6636 | R | 🔴 | 🔴 | R | 0 | 3.08 E+8 | 1.36 E+8 | 1.1782 | 28.7261 | R | 🔴 |
| *PGN1510* | *PG0414* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0451 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.18 E+5 | -5.9917 | 16.8679 | Y | 🟡 |
| *PGN1511* | *PG0413* | *CBS domain protein* | | | | | | | | | | | | | | | |
| PG0450 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 1.28 E-5 | 1.85 E+3 | 4.43 E+5 | -7.9019 | 18.7616 | G | 🟢 |
| *PGN1512* | *PG0412* | *hypothetical protein PG_0450* | | | | | | | | | | | | | | | |
| PG0449 | | 2.61 E-9 | 187.4 | 84 | 1.1576 | 8.0842 | R | 🔴 | 🔴 | R | 1.16 E-11 | 1.79 E+8 | 7.28 E+7 | 1.2966 | 27.9076 | R | 🔴 |
| *PGN1513* | *PG0411* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG0448 | | 2.24 E-8 | 39.4 | 111.5 | -1.5022 | 7.2371 | G | 🟢 | 🟢 | G | 5.49 E-14 | 1.13 E+7 | 5.32 E+7 | -2.2400 | 25.9432 | G | 🟢 |
| *PGN1514* | *PG0410* | *hypothetical protein PG_0448* | | | | | | | | | | | | | | | |
| PG0447 | | 2.26 E-1 | 6.0 | 2 | 1.5825 | 2.9981 | Y | 🟡 | 🔴 | R | 3.51 E-5 | 2.54 E+6 | 5.3 E+5 | 2.2611 | 21.5487 | R | 🔴 |
| *PGN1515* | *PG0409* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0446 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 3.8 E+5 | 1 E+3 | 8.5708 | 18.5404 | R | 🔴 |
| *PGN1516* | *PG0408* | *thiF thiF protein* | | | | | | | | | | | | | | | |
| PG0445 | | 2.52 E-1 | 57.3 | 73 | -0.3486 | 7.0260 | Y | 🟡 | 🟡 | Y | 3.17 E-3 | 5.66 E+7 | 9.71 E+7 | -0.7788 | 27.1950 | Y | 🟡 |
| *PGN1517* | *PG0407* | *pepT peptidase T* | | | | | | | | | | | | | | | |
| PG0444 | | 6.06 E-1 | 10.3 | 12 | -0.2249 | 4.4769 | Y | 🟡 | 🟡 | Y | 7.97 E-2 | 8.14 E+6 | 6.97 E+6 | 0.2251 | 23.8488 | Y | 🟡 |
| *PGN1518* | *PG0406* | *oligopeptide transporter OPT family* | | | | | | | | | | | | | | | |
| PG0443 | | 3.68 E-1 | 92.4 | 79 | 0.2262 | 7.4213 | Y | 🟡 | 🟡 | Y | 1.76 E-2 | 6.76 E+7 | 4.84 E+7 | 0.4830 | 26.7902 | Y | 🟡 |
| *PGN1519* | *PG0405* | *hemagglutinin-related protein* | | | | | | | | | | | | | | | |
| PG0441 | | 1.34 E-2 | 1.7 | 11.5 | -2.7485 | 3.7237 | Y | 🟡 | 🟢 | G | 3.96 E-8 | 1.85 E+3 | 1.89 E+6 | -9.9958 | 20.8509 | G | 🟢 |
| *PGN1520* | *PG0404* | *hypothetical protein PG_0441* | | | | | | | | | | | | | | | |
| PG0438 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 3.53 E+5 | -7.5771 | 18.4383 | Y | 🟡 |
| *PGN1522* | *PG0401* | *hypothetical protein PG_0438* | | | | | | | | | | | | | | | |
| PG0437 | | 7.69 E-2 | 8.6 | 2 | 2.0970 | 3.4001 | Y | 🟡 | 🔴 | R | 4.86 E-5 | 7.6 E+6 | 6.01 E+5 | 3.6611 | 22.9674 | R | 🔴 |
| *PGN1523* | *PG0400* | *polysaccharide export protein BexD/CtrA/VexA family* | | | | | | | | | | | | | | | |
| PG0436 | | 1.18 E-1 | 31.7 | 18.5 | 0.7751 | 5.6484 | Y | 🟡 | 🟡 | Y | 8.37 E-2 | 1.31 E+7 | 1.62 E+7 | -0.3082 | 24.8042 | Y | 🟡 |
| *PGN1524* | *PG0399* | *capsular polysaccharide transport protein putative* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | q-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | q-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0435 | | 1.5 E-1 | 1.7 | 6.5 | -1.9253 | 3.0376 | Y | 🟡 | 🟢 | G | 8 E-4 | 1.85 E+3 | 2.44 E+6 | -10.3676 | 21.2224 | G | 🟢 |
| *PGN1525* | *PG0398* | *capsular polysaccharide biosythesis protein putative* | | | | | | | | | | | | | | | |
| PG0434 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟡 | Y | 1 E-2 | 1.85 E+3 | 3.77 E+5 | -7.6692 | 18.5300 | Y | 🟡 |
| *PGN1526* | *PG0397* | *hypothetical protein PG_0434* | | | | | | | | | | | | | | | |
| PG0433 | | 5.72 E-1 | 12.8 | 10.5 | 0.2897 | 4.5444 | Y | 🟡 | 🟡 | Y | 1.45 E-2 | 2.63 E+6 | 3.64 E+6 | -0.4697 | 22.5809 | Y | 🟡 |
| *PGN1527* | *PG0396* | *tetrapyrrole methylase family protein* | | | | | | | | | | | | | | | |
| PG0432 | | 6 E-1 | 3.4 | 4.5 | -0.3948 | 2.9860 | Y | 🟡 | 🟡 | Y | 8.66 E-2 | 6.49 E+5 | 4.77 E+5 | 0.4438 | 20.1021 | Y | 🟡 |
| *PGN1528* | *PG0395* | *NOL1/NOP2/sun family protein* | | | | | | | | | | | | | | | |
| PG0430 | | 1.75 E-3 | 112.9 | 66 | 0.7751 | 7.4834 | R | 🔴 | 🔴 | R | 2.27 E-4 | 7.77 E+7 | 4.92 E+7 | 0.6599 | 26.9188 | R | 🔴 |
| *PGN1529* | *PG0394* | *oxidoreductase putative* | | | | | | | | | | | | | | | |
| PG0429 | | 0 | 326.9 | 104 | 1.6521 | 8.7511 | R | 🔴 | 🔴 | R | 1.13 E-4 | 1.47 E+8 | 8.77 E+7 | 0.7447 | 27.8058 | R | 🔴 |
| *PGN1530* | *PG0393* | *pyruvate synthase* | | | | | | | | | | | | | | | |
| | | 4 E-3 | 23.1 | 6 | 1.9450 | 4.8631 | R | 🔴 | 🔴 | R | 5.6 E-7 | 2.32 E+7 | 8.24 E+6 | 1.4941 | 24.9073 | R | 🔴 |
| *PGN1533* | | | | | | | | | | | | | | | | | |
| | | 5.43 E-1 | 6.8 | 5 | 0.4532 | 3.5662 | Y | 🟡 | 🟡 | Y | 1.97 E-3 | 1.19 E+6 | 5.44 E+5 | 1.1304 | 20.7255 | Y | 🟡 |
| *PGN1534* | | | | | | | | | | | | | | | | | |
| | | 1.6 E-1 | 11.1 | 20.5 | -0.8820 | 4.9829 | Y | 🟡 | 🟡 | Y | 1.61 E-1 | 5.83 E+6 | 5.48 E+6 | 0.0885 | 23.4308 | Y | 🟡 |
| *PGN1535* | | | | | | | | | | | | | | | | | |
| | | 6.97 E-1 | 3.4 | 3.5 | -0.0323 | 2.7913 | Y | 🟡 | 🟡 | Y | 3.32 E-2 | 1.33 E+6 | 7.66 E+5 | 0.7915 | 20.9971 | Y | 🟡 |
| *PGN1536* | | | | | | | | | | | | | | | | | |
| | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟢 | G | 1.85 E-8 | 1.85 E+3 | 3.5 E+5 | -7.5614 | 18.4227 | G | 🟢 |
| *PGN1538* | | | | | | | | | | | | | | | | | |
| | | 2.04 E-2 | 4.3 | 16 | -1.9030 | 4.3419 | Y | 🟡 | 🟡 | Y | 1.69 E-3 | 2.2 E+6 | 4.73 E+6 | -1.1033 | 22.7236 | Y | 🟡 |
| *PGN1539* | | | | | | | | | | | | | | | | | |
| PG0540 | | 5.43 E-1 | 2.6 | 1.5 | 0.7751 | 2.0240 | Y | 🟡 | 🔴 | R | 0 | 2.31 E+6 | 3.39 E+5 | 2.7728 | 21.3395 | R | 🔴 |
| *PGN1540* | *PG0493* | *AcrB/AcrD/AcrF family protein* | | | | | | | | | | | | | | | |
| PG0423 | | 3.52 E-1 | 12.8 | 8 | 0.6820 | 4.3809 | Y | 🟡 | 🔴 | R | 4.53 E-8 | 1.17 E+7 | 4.62 E+6 | 1.3422 | 23.9607 | R | 🔴 |
| *PGN1544* | *PG0388* | *hypothetical protein PG_0423* | | | | | | | | | | | | | | | |
| PG0421 | | 1.32 E-4 | 28.2 | 5 | 2.4976 | 5.0547 | R | 🔴 | 🔴 | R | 6.33 E-11 | 1.14 E+7 | 2.03 E+6 | 2.4893 | 23.6810 | R | 🔴 |
| *PGN1547* | *PG0386* | *hypothetical protein PG_0421* | | | | | | | | | | | | | | | |
| PG0418 | | 2.8 E-1 | 40.2 | 52.5 | -0.3846 | 6.5347 | Y | 🟡 | 🟡 | Y | 1.83 E-2 | 2.81 E+7 | 3.94 E+7 | -0.4877 | 26.0076 | Y | 🟡 |
| *PGN1549* | *PG0384* | *clpP ATP-dependent Clp protease proteolytic subunit* | | | | | | | | | | | | | | | |
| PG0417 | | 4.45 E-1 | 6.0 | 9 | -0.5875 | 3.9059 | Y | 🟡 | 🟡 | Y | 2.59 E-2 | 1.74 E+6 | 2.92 E+6 | -0.7454 | 22.1537 | Y | 🟡 |
| *PGN1550* | *PG0382* | *clpX ATP-dependent Clp protease ATP-binding subunit ClpX* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus |
| PG0416 | | 8.91 E-2 | 34.2 | 19.5 | 0.8116 | 5.7476 | Y 🟡 | 🟡 Y | 4.97 E-3 | 1.34 E+7 | 6.83 E+6 | 0.9689 | 24.2683 | Y 🟡 |
| *PGN1551* | *PG0381* | *recQ-1 ATP-dependent DNA helicase RecQ* | | | | | | | | | | | | |
| PG0415 | | 1.63 E-8 | 48.8 | 6.5 | 2.9075 | 5.7885 | R 🔴 | 🔴 R | 0 | 2.15 E+7 | 3.49 E+6 | 2.6203 | 24.5729 | R 🔴 |
| *PGN1552* | *PG0380* | *peptidyl-prolyl cis-trans isomerase PPIC-type* | | | | | | | | | | | | |
| PG0414 | | 9.48 E-2 | 1.7 | 7.5 | -2.1318 | 3.2034 | Y 🟡 | 🟢 G | 1.72 E-8 | 1.85 E+3 | 1.52 E+6 | -9.6863 | 20.5417 | G 🟢 |
| *PGN1553* | *PG0379* | *hypothetical protein PG_0414* | | | | | | | | | | | | |
| PG0413 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 1.79 E-13 | 1.85 E+3 | 2.31 E+5 | -6.9630 | 17.8282 | G 🟢 |
| *PGN1554* | *PG0378* | *hypothetical protein PG_0413* | | | | | | | | | | | | |
| PG0412 | | 2.74 E-1 | 1.7 | 5 | -1.5468 | 2.7466 | Y 🟡 | 🟢 G | 6.76 E-5 | 3.93 E+4 | 1.34 E+6 | -5.0912 | 20.3963 | G 🟢 |
| *PGN1555* | *PG0377* | *mutL DNA mismatch repair protein MutL* | | | | | | | | | | | | |
| PG0411 | | 6.33 E-1 | 12.8 | 14.5 | -0.1760 | 4.7727 | Y 🟡 | 🟡 Y | 1.21 E-1 | 4.61 E+6 | 5.26 E+6 | -0.1903 | 23.2344 | Y 🟡 |
| *PGN1556* | *PG0376* | *hemagglutinin putative* | | | | | | | | | | | | |
| PG0409 | | 3.53 E-6 | 38.5 | 96 | -1.3180 | 7.0715 | G 🟢 | 🟢 G | 2.24 E-5 | 1.81 E+7 | 4.87 E+7 | -1.4268 | 25.9934 | G 🟢 |
| *PGN1557* | *PG0373* | *hypothetical protein PG_0409* | | | | | | | | | | | | |
| PG0401 | | 6.35 E-1 | 65.0 | 61.5 | 0.0805 | 6.9833 | Y 🟡 | 🟡 Y | 9.98 E-2 | 3.6 E+7 | 2.96 E+7 | 0.2830 | 25.9681 | Y 🟡 |
| *PGN1564* | *PG0368* | *KH/HDIG domain protein* | | | | | | | | | | | | |
| PG0400 | | 2.22 E-1 | 7.7 | 3 | 1.3601 | 3.4197 | Y 🟡 | 🔴 R | 8.86 E-8 | 1.01 E+6 | 4.82 E+5 | 1.0731 | 20.5124 | R 🔴 |
| *PGN1565* | *PG0367* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG0398 | | 5.17 E-1 | 7.7 | 5.5 | 0.4856 | 3.7226 | Y 🟡 | 🔴 R | 9.34 E-6 | 1.14 E+6 | 3.37 E+5 | 1.7623 | 20.4985 | R 🔴 |
| *PGN1567* | *PG0365* | *recF recF protein* | | | | | | | | | | | | |
| PG0395 | | 0 | 348.3 | 103.5 | 1.7505 | 8.8194 | R 🔴 | 🔴 R | 0 | 2.69 E+8 | 5.1 E+7 | 2.3992 | 28.2542 | R 🔴 |
| *PGN1570* | *PG0361* | *rpoC DNA-directed RNA polymerase beta' subunit* | | | | | | | | | | | | |
| PG0394 | | 0 | 262.7 | 68.5 | 1.9392 | 8.3715 | R 🔴 | 🔴 R | 0 | 1.82 E+8 | 2.99 E+7 | 2.6101 | 27.6620 | R 🔴 |
| *PGN1571* | *PG0360* | *rpoB DNA-directed RNA polymerase beta subunit* | | | | | | | | | | | | |
| PG0393 | | 2.04 E-1 | 432.1 | 388.5 | 0.1535 | 9.6805 | Y 🟡 | 🟡 Y | 2.02 E-1 | 8.05 E+8 | 8.05 E+8 | -0.0005 | 30.5839 | Y 🟡 |
| *PGN1572* | *PG0359* | *rplL ribosomal protein L7/L12* | | | | | | | | | | | | |
| PG0392 | | 6.8 E-2 | 251.6 | 205.5 | 0.2918 | 8.8362 | Y 🟡 | 🔴 R | 2.37 E-4 | 1.88 E+8 | 1.2 E+8 | 0.6434 | 28.2008 | R 🔴 |
| *PGN1573* | *PG0358* | *rplJ ribosomal protein L10* | | | | | | | | | | | | |
| PG0391 | | 0 | 308.9 | 65.5 | 2.2375 | 8.5484 | R 🔴 | 🔴 R | 3.98 E-11 | 1.87 E+8 | 7.24 E+7 | 1.3675 | 27.9499 | R 🔴 |
| *PGN1574* | *PG0357* | *rplA ribosomal protein L1* | | | | | | | | | | | | |
| PG0390 | | 1.89 E-3 | 87.3 | 47 | 0.8929 | 7.0691 | R 🔴 | 🟡 Y | 1.12 E-2 | 1.36 E+8 | 9.63 E+7 | 0.5028 | 27.7947 | R 🔴 |
| *PGN1575* | *PG0356* | *rplK ribosomal protein L11* | | | | | | | | | | | | |
| PG0389 | | 3.11 E-4 | 52.2 | 19 | 1.4579 | 6.1537 | R 🔴 | 🔴 R | 1.87 E-12 | 2.54 E+7 | 6.38 E+6 | 1.9944 | 24.9235 | R 🔴 |
| *PGN1576* | *PG0355* | *nusG transcription antitermination protein NusG* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| | | 4.02 E-1 | 10.3 | 6.5 | 0.6596 | 4.0676 | Y | 🟡 | 🟡 | Y | 3.87 E-2 | 9.35 E+6 | 6.31 E+6 | 0.5680 | 23.9003 | Y | 🟡 |
| *PGN1577* | | | | | | | | | | | | | | | | | |
| PG0387 | | 0 | 1491.4 | 695.5 | 1.1005 | 11.0947 | R | 🔴 | 🔴 | R | 0 | 2.28 E+9 | 9.23 E+8 | 1.3054 | 31.5780 | R | 🔴 |
| *PGN1578* | *PG0353* | *tuf translation elongation factor Tu* | | | | | | | | | | | | | | | |
| PG0386 | | 1.34 E-4 | 38.5 | 10 | 1.9450 | 5.6000 | R | 🔴 | 🔴 | R | 3.13 E-13 | 4.37 E+7 | 4.62 E+6 | 3.2413 | 25.5253 | R | 🔴 |
| *PGN1579* | *PG0352* | *site-specific recombinase phage integrase family/ribosomal subunit interface protein* | | | | | | | | | | | | | | | |
| PG0384 | | 6 E-1 | 4.3 | 5.5 | -0.3624 | 3.2896 | Y | 🟡 | 🟡 | Y | 1.95 E-1 | 1.32 E+6 | 1.3 E+6 | 0.0278 | 21.3202 | Y | 🟡 |
| *PGN1581* | *PG0350* | *MutS2 family protein* | | | | | | | | | | | | | | | |
| PG0383 | | 1.52 E-2 | 9.4 | 1 | 3.2345 | 3.3802 | Y | 🟡 | 🔴 | R | 0 | 2.6 E+6 | 1 E+3 | 11.3440 | 21.3103 | R | 🔴 |
| *PGN1582* | *PG0349* | *membrane-associated zinc metalloprotease putative* | | | | | | | | | | | | | | | |
| PG0380 | | 1.26 E-1 | 2.6 | 8.5 | -1.7274 | 3.4682 | Y | 🟡 | 🟡 | Y | 1.67 E-1 | 8.98 E+5 | 8.38 E+5 | 0.0996 | 20.7269 | Y | 🟡 |
| *PGN1585* | *PG0346* | *uvrB excinuclease ABC B subunit* | | | | | | | | | | | | | | | |
| PG0378 | | 0 | 195.9 | 38 | 2.3664 | 7.8700 | R | 🔴 | 🔴 | R | 0 | 1.8 E+8 | 3.34 E+7 | 2.4337 | 27.6704 | R | 🔴 |
| *PGN1587* | *PG0345* | *tsf translation elongation factor Ts* | | | | | | | | | | | | | | | |
| PG0377 | | 0 | 276.4 | 106 | 1.3826 | 8.5788 | R | 🔴 | 🔴 | R | 0 | 2.15 E+8 | 4.12 E+7 | 2.3839 | 27.9312 | R | 🔴 |
| *PGN1588* | *PG0344* | *rpsB ribosomal protein S2* | | | | | | | | | | | | | | | |
| PG0376 | | 5.43 E-1 | 21.4 | 25 | -0.2249 | 5.5358 | Y | 🟡 | 🟡 | Y | 2.84 E-2 | 1.78 E+7 | 1.28 E+7 | 0.4727 | 24.8652 | Y | 🟡 |
| *PGN1589* | *PG0343* | *rpsI ribosomal protein S9* | | | | | | | | | | | | | | | |
| PG0375 | | 2.87 E-1 | 81.3 | 66 | 0.3006 | 7.2025 | Y | 🟡 | 🔴 | R | 1.84 E-5 | 4.32 E+7 | 1.84 E+7 | 1.2322 | 25.8751 | R | 🔴 |
| *PGN1590* | *PG0342* | *rplM ribosomal protein L13* | | | | | | | | | | | | | | | |
| PG0373 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟡 | Y | 1.5 E-3 | 1.85 E+3 | 1.04 E+6 | -9.1288 | 19.9851 | Y | 🟡 |
| *PGN1591* | *PG0341* | *hypothetical protein PG_0373* | | | | | | | | | | | | | | | |
| PG0369 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 5.58 E+5 | -8.2351 | 19.0935 | G | 🟢 |
| *PGN1593* | *PG0340* | *coaD phosphopantetheine adenylyltransferase* | | | | | | | | | | | | | | | |
| PG0368 | | 1.4 E-1 | 14.5 | 6.5 | 1.1621 | 4.3955 | Y | 🟡 | 🟡 | Y | 2.5 E-3 | 6.44 E+6 | 2 E+6 | 1.6860 | 23.0088 | Y | 🟡 |
| *PGN1594* | *PG0339* | *DNA topoisomerase IV B subunit putative* | | | | | | | | | | | | | | | |
| PG0366 | | 2.74 E-1 | 8.6 | 4 | 1.0970 | 3.6504 | Y | 🟡 | 🔴 | R | 6.45 E-7 | 3.29 E+6 | 1.01 E+6 | 1.7055 | 22.0364 | R | 🔴 |
| *PGN1595* | *PG0338* | *hypothetical protein PG_0366* | | | | | | | | | | | | | | | |
| PG0365 | | 5.39 E-1 | 5.1 | 3.5 | 0.5527 | 3.1100 | Y | 🟡 | 🔴 | R | 2.92 E-4 | 1.66 E+6 | 5.2 E+5 | 1.6763 | 21.0567 | R | 🔴 |
| *PGN1596* | *PG0337* | *3'-5' exonuclease domain protein* | | | | | | | | | | | | | | | |
| PG0364 | | 2.14 E-1 | 3.4 | 8.5 | -1.3124 | 3.5756 | Y | 🟡 | 🟡 | Y | 1.68 E-2 | 1.63 E+6 | 3.35 E+6 | -1.0406 | 22.2484 | Y | 🟡 |
| *PGN1597* | *PG0336* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0362 | | 1.48 E-4 | 6.8 | 32 | -2.2249 | 5.2797 | G | 🟢 | 🟡 | Y | 5.91 E-3 | 5.32 E+6 | 1.03 E+7 | -0.9605 | 23.9008 | G | 🟢 |
| *PGN1599* | *PG0334* | *hypothetical protein PG_0362* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0361 | | 4.23 E-1 | 3.4 | 6 | -0.8099 | 3.2361 | Y | 🟡 | 🟡 | Y | 7.19 E-3 | 8 E+5 | 1.83 E+6 | -1.1907 | 21.3238 | Y | 🟡 |
| *PGN1600* | *PG0333* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG0360 | | 5.84 E-4 | 47.9 | 17.5 | 1.4532 | 6.0316 | R | 🔴 | 🔴 | R | 5.19 E-10 | 2.92 E+7 | 9.06 E+6 | 1.6899 | 25.1910 | R | 🔴 |
| *PGN1601* | *PG0332* | *lemA protein* | | | | | | | | | | | | | | | |
| PG0359 | | 3.21 E-1 | 1.7 | 4.5 | -1.3948 | 2.6349 | Y | 🟡 | 🟢 | G | 4.4 E-8 | 1.85 E+3 | 4.86 E+6 | -11.3588 | 22.2131 | G | 🟢 |
| *PGN1602* | *PG0331* | *flavin reductase domain protein* | | | | | | | | | | | | | | | |
| PG0358 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 2.64 E+5 | 1 E+3 | 8.0465 | 18.0177 | R | 🔴 |
| *PGN1603* | *PG0330* | *pyrI aspartate carbamoyltransferase regulatory subunit* | | | | | | | | | | | | | | | |
| PG0357 | | 1.56 E-1 | 28.2 | 42.5 | -0.5899 | 6.1444 | Y | 🟡 | 🟡 | Y | 8.6 E-3 | 9.98 E+6 | 1.63 E+7 | -0.7087 | 24.6485 | Y | 🟡 |
| *PGN1604* | *PG0329* | *pyrB aspartate carbamoyltransferase catalytic subunit* | | | | | | | | | | | | | | | |
| PG0356 | | 2.15 E-1 | 6.8 | 13.5 | -0.9798 | 4.3466 | Y | 🟡 | 🟡 | Y | 2.89 E-2 | 3.77 E+6 | 6.35 E+6 | -0.7500 | 23.2710 | Y | 🟡 |
| *PGN1605* | *PG0328* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0352 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 7.01 E-4 | 1.85 E+3 | 1.3 E+6 | -9.4527 | 20.3085 | G | 🟢 |
| *PGN1608* | *PG0324* | *sialidase putative* | | | | | | | | | | | | | | | |
| PG0350 | | 3.49 E-1 | 24.0 | 32 | -0.4175 | 5.8063 | Y | 🟡 | 🟡 | Y | 1.85 E-1 | 2.15 E+7 | 2.1 E+7 | 0.0324 | 25.3431 | Y | 🟡 |
| *PGN1611* | *PG0322* | *internalin-related protein* | | | | | | | | | | | | | | | |
| PG0348 | | 5.43 E-1 | 2.6 | 1.5 | 0.7751 | 2.0240 | Y | 🟡 | 🟡 | Y | 1.83 E-2 | 6.35 E+5 | 4.17 E+5 | 0.6058 | 20.0047 | Y | 🟡 |
| *PGN1613* | *PG0320* | *recG ATP-dependent DNA helicase RecG* | | | | | | | | | | | | | | | |
| PG0347 | | 3.52 E-1 | 32.5 | 24.5 | 0.4083 | 5.8333 | Y | 🟡 | 🔴 | R | 2.31 E-6 | 1.76 E+7 | 7.7 E+6 | 1.1894 | 24.5901 | R | 🔴 |
| *PGN1614* | *PG0319* | *galE UDP-glucose 4-epimerase* | | | | | | | | | | | | | | | |
| PG0346 | | 5.76 E-2 | 10.3 | 2.5 | 2.0381 | 3.6744 | Y | 🟡 | 🟡 | Y | 5.66 E-3 | 3.04 E+6 | 1.2 E+6 | 1.3382 | 22.0165 | Y | 🟡 |
| *PGN1615* | *PG0318* | *GTP-binding protein* | | | | | | | | | | | | | | | |
| PG0345 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 1.12 E-11 | 1.39 E+6 | 1 E+3 | 10.4407 | 20.4075 | R | 🔴 |
| *PGN1616* | *PG0316* | *hypothetical protein PG_0345* | | | | | | | | | | | | | | | |
| PG0344 | | 6.54 E-3 | 6.8 | 23.5 | -1.7795 | 4.9234 | G | 🟢 | 🟡 | Y | 8.76 E-3 | 4.21 E+6 | 8.04 E+6 | -0.9310 | 23.5464 | G | 🟢 |
| *PGN1617* | *PG0315* | *purple acid phosphatase* | | | | | | | | | | | | | | | |
| PG0343 | | 1.63 E-11 | 531.4 | 789.5 | -0.5712 | 10.3673 | G | 🟢 | 🟡 | Y | 5.6 E-2 | 2.73 E+8 | 3.18 E+8 | -0.2194 | 29.1384 | G | 🟢 |
| *PGN1618* | *PG0314* | *megL methionine gamma-lyase* | | | | | | | | | | | | | | | |
| PG0339 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y | 🟡 | 🟡 | Y | 5.42 E-2 | 1.85 E+3 | 9.95 E+6 | -12.3929 | 23.2469 | Y | 🟡 |
| *PGN1622* | *PG0313* | *hypothetical protein PG_0339* | | | | | | | | | | | | | | | |
| PG0338 | | 4.23 E-1 | 8.6 | 12.5 | -0.5468 | 4.3962 | Y | 🟡 | 🟡 | Y | 1.13 E-1 | 1.61 E+6 | 2.02 E+6 | -0.3295 | 21.7905 | Y | 🟡 |
| *PGN1623* | *PG0312* | *hypothetical protein PG_0338* | | | | | | | | | | | | | | | |
| PG0336 | | 5.43 E-1 | 13.7 | 11 | 0.3157 | 4.6259 | Y | 🟡 | 🔴 | R | 8.93 E-9 | 5.17 E+6 | 2.03 E+6 | 1.3476 | 22.7790 | R | 🔴 |
| *PGN1625* | *PG0311* | *hypothetical protein PG_0336* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| | | 4.55 E-1 | 5.1 | 3 | 0.7751 | 3.0240 | Y | 🟡 | 🔴 | R | 7.82 E-5 | 1.89 E+6 | 2.81 E+5 | 2.7497 | 21.0498 | R | 🔴 |
| *PGN1627* | | | | | | | | | | | | | | | | | |
| PG0334 | | 2.66 E-1 | 8.6 | 15 | -0.8099 | 4.5581 | Y | 🟡 | 🟡 | Y | 1.34 E-1 | 4.2 E+6 | 3.68 E+6 | 0.1903 | 22.9111 | Y | 🟡 |
| *PGN1628* | *PG0309* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | | | | |
| PG0332 | | 1.89 E-3 | 80.4 | 42 | 0.9374 | 6.9358 | R | 🔴 | 🔴 | R | 0 | 5.58 E+7 | 2.28 E+7 | 1.2919 | 26.2289 | R | 🔴 |
| *PGN1630* | *PG0307* | *rho transcription termination factor Rho* | | | | | | | | | | | | | | | |
| PG0330 | | 6.21 E-2 | 62.5 | 89.5 | -0.5189 | 7.2476 | Y | 🟡 | 🟡 | Y | 1.17 E-1 | 1.32 E+8 | 1.49 E+8 | -0.1755 | 28.0687 | Y | 🟡 |
| *PGN1631* | *PG0306* | *DNA-binding protein histone-like family* | | | | | | | | | | | | | | | |
| | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 0 | 1.77 E+5 | 1 E+3 | 7.4705 | 17.4444 | R | 🔴 |
| *PGN1632* | | | | | | | | | | | | | | | | | |
| PG0329 | | 2.52 E-1 | 160.0 | 185.5 | -0.2133 | 8.4326 | Y | 🟡 | 🟡 | Y | 3.35 E-3 | 2.03 E+8 | 1.48 E+8 | 0.4601 | 28.3874 | Y | 🟡 |
| *PGN1633* | *PG0305* | *formiminotransferase-cyclodeaminase-related protein* | | | | | | | | | | | | | | | |
| PG0328 | | 3.82 E-1 | 41.9 | 51.5 | -0.2967 | 6.5458 | Y | 🟡 | 🟡 | Y | 8.61 E-3 | 1.86 E+7 | 2.57 E+7 | -0.4680 | 25.3990 | Y | 🟡 |
| *PGN1634* | *PG0304* | *hutI imidazolonepropionase* | | | | | | | | | | | | | | | |
| PG0327 | | 2.78 E-1 | 12.0 | 6.5 | 0.8820 | 4.2078 | Y | 🟡 | 🔴 | R | 3.96 E-4 | 4.29 E+6 | 2.1 E+6 | 1.0315 | 22.6055 | R | 🔴 |
| *PGN1635* | *PG0303* | *hypothetical protein PG_0327* | | | | | | | | | | | | | | | |
| PG0326 | | 4.57 E-3 | 21.4 | 48 | -1.1660 | 6.1167 | G | 🟢 | 🟢 | G | 1.14 E-7 | 6.69 E+6 | 1.75 E+7 | -1.3890 | 24.5294 | G | 🟢 |
| *PGN1636* | *PG0302* | *hypothetical protein PG_0326* | | | | | | | | | | | | | | | |
| PG0325 | | 1.96 E-12 | 100.1 | 234 | -1.2249 | 8.3842 | G | 🟢 | 🟡 | Y | 1.66 E-1 | 5.76 E+7 | 5.55 E+7 | 0.0524 | 26.7537 | Y | 🟡 |
| *PGN1637* | *PG0301* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0324 | | 5.87 E-2 | 118.1 | 155 | -0.3925 | 8.0932 | Y | 🟡 | 🟡 | Y | 2.44 E-2 | 7.46 E+7 | 9.83 E+7 | -0.3986 | 27.3655 | Y | 🟡 |
| *PGN1638* | *PG0299* | *hutH histidine ammonia-lyase* | | | | | | | | | | | | | | | |
| PG0323 | | 8.6 E-7 | 30.8 | 87.5 | -1.5062 | 6.8863 | G | 🟢 | 🟡 | Y | 1.07 E-2 | 1.47 E+7 | 2.63 E+7 | -0.8390 | 25.2897 | G | 🟢 |
| *PGN1639* | *PG0297* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0321 | | 7.53 E-2 | 18.0 | 7.5 | 1.2605 | 4.6707 | Y | 🟡 | 🟡 | Y | 2.25 E-3 | 4.9 E+6 | 2.51 E+6 | 0.9675 | 22.8202 | Y | 🟡 |
| *PGN1641* | *PG0295* | *LAO/AO transport system ATPase* | | | | | | | | | | | | | | | |
| PG0320 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.47 E+6 | -9.6371 | 20.4927 | G | 🟢 |
| *PGN1642* | *PG0294* | *hypothetical protein PG_0320* | | | | | | | | | | | | | | | |
| PG0319 | | 6.36 E-5 | 57.3 | 19.5 | 1.5558 | 6.2636 | R | 🔴 | 🔴 | R | 0 | 4.27 E+7 | 1.29 E+7 | 1.7282 | 25.7267 | R | 🔴 |
| *PGN1643* | *PG0293* | *hypothetical protein PG_0319* | | | | | | | | | | | | | | | |
| PG0317 | | 1.1 E-1 | 16.3 | 29 | -0.8350 | 5.5001 | Y | 🟡 | 🟡 | Y | 2.15 E-2 | 6.05 E+6 | 1.64 E+7 | -1.4393 | 24.4218 | Y | 🟡 |
| *PGN1645* | *PG0291* | *peptidase M49 family* | | | | | | | | | | | | | | | |
| PG0316 | | 1.76 E-1 | 58.2 | 42 | 0.4702 | 6.6465 | Y | 🟡 | 🟡 | Y | 1.37 E-1 | 2.92 E+7 | 2.69 E+7 | 0.1185 | 25.7400 | Y | 🟡 |
| *PGN1646* | *PG0290* | *serS seryl-tRNA synthetase* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG0315 | | 1.18 E-1 | 10.3 | 3.5 | 1.5527 | 3.7832 | Y | 🟡 | 🟡 | Y | 4.06 E-3 | 7.8 E+6 | 2.82 E+6 | 1.4694 | 23.3396 | Y | 🟡 |
| *PGN1647* | *PG0289* | *rpmA ribosomal protein L27* | | | | | | | | | | | | | | | |
| PG0314 | | 5.1 E-2 | 35.9 | 19 | 0.9195 | 5.7797 | Y | 🟡 | 🟡 | Y | 1.44 E-1 | 2.74 E+7 | 2.52 E+7 | 0.1200 | 25.6508 | Y | 🟡 |
| *PGN1648* | *PG0288* | *rplU ribosomal protein L21* | | | | | | | | | | | | | | | |
| PG0311 | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y | 🟡 | 🔴 | R | 0 | 2.43 E+5 | 1 E+3 | 7.9231 | 17.8949 | R | 🔴 |
| *PGN1651* | *PG0285* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | | | | |
| PG0310 | | 6 E-1 | 31.7 | 35 | -0.1447 | 6.0587 | Y | 🟡 | 🟡 | Y | 5.72 E-2 | 1.47 E+7 | 1.95 E+7 | -0.4039 | 25.0296 | Y | 🟡 |
| *PGN1652* | *PG0284* | *nitroreductase family protein* | | | | | | | | | | | | | | | |
| PG0308 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 6.77 E+6 | -11.8360 | 22.6901 | Y | 🟡 |
| *PGN1654* | *PG0281* | *electron transport complex RnfABCDGE type A subunit* | | | | | | | | | | | | | | | |
| PG0307 | | 4.67 E-3 | 1.7 | 13.5 | -2.9798 | 3.9271 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 3.47 E+5 | -7.5502 | 18.4116 | G | 🟢 |
| *PGN1655* | *PG0280* | *electron transport complex RnfABCDGE type E subunit* | | | | | | | | | | | | | | | |
| PG0306 | | 6.07 E-3 | 47.9 | 22 | 1.1230 | 6.1276 | R | 🔴 | 🔴 | R | 5.99 E-12 | 6.07 E+7 | 1.51 E+7 | 2.0103 | 26.1750 | R | 🔴 |
| *PGN1656* | *PG0279* | *electron transport complex RnfABCDGE type G subunit* | | | | | | | | | | | | | | | |
| PG0305 | | 1.42 E-1 | 6.8 | 15 | -1.1318 | 4.4492 | Y | 🟡 | 🟡 | Y | 1.37 E-3 | 3.17 E+6 | 7.51 E+6 | -1.2436 | 23.3486 | Y | 🟡 |
| *PGN1657* | *PG0278* | *electron transport complex RnfABCDGE type D subunit* | | | | | | | | | | | | | | | |
| PG0304 | | 6.69 E-1 | 50.5 | 49 | 0.0430 | 6.6364 | Y | 🟡 | 🟡 | Y | 3.2 E-2 | 3.62 E+7 | 2.98 E+7 | 0.2835 | 25.9755 | Y | 🟡 |
| *PGN1658* | *PG0277* | *electron transport complex RnfABCDGE type C subunit* | | | | | | | | | | | | | | | |
| PG0303 | | 1.37 E-1 | 30.8 | 46.5 | -0.5941 | 6.2725 | Y | 🟡 | 🟡 | Y | 6.66 E-2 | 9.27 E+6 | 1.06 E+7 | -0.1932 | 24.2438 | Y | 🟡 |
| *PGN1659* | *PG0276* | *electron transport complex RnfABCDGE type B subunit* | | | | | | | | | | | | | | | |
| PG0302 | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y | 🟡 | 🔴 | R | 3.82 E-8 | 1.04 E+6 | 1 E+3 | 10.0267 | 19.9939 | R | 🔴 |
| *PGN1660* | *PG0275* | *hypothetical protein PG_0302* | | | | | | | | | | | | | | | |
| PG0300 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 1.55 E+6 | 1 E+3 | 10.6017 | 20.5684 | R | 🔴 |
| *PGN1661* | *PG0274* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG0296 | | 7 E-1 | 138.6 | 139 | -0.0040 | 8.1169 | Y | 🟡 | 🟡 | Y | 1.21 E-1 | 9.8 E+7 | 9.24 E+7 | 0.0852 | 27.5048 | Y | 🟡 |
| *PGN1666* | *PG0272* | *phosphoribosylformylglycinamidine synthase putative* | | | | | | | | | | | | | | | |
| PG0295 | | 4.75 E-1 | 3.4 | 5.5 | -0.6843 | 3.1575 | Y | 🟡 | 🟡 | Y | 2.16 E-2 | 1.74 E+6 | 1.13 E+6 | 0.6244 | 21.4495 | Y | 🟡 |
| *PGN1667* | *PG0271* | *dprA DNA processing protein DprA putative* | | | | | | | | | | | | | | | |
| PG0294 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟡 | Y | 1.54 E-2 | 1.85 E+3 | 4.27 E+5 | -7.8513 | 18.7112 | Y | 🟡 |
| *PGN1668* | *PG0270* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | | | | |
| PG0293 | | 0 | 247.3 | 72.5 | 1.7701 | 8.3210 | R | 🔴 | 🔴 | R | 0 | 2.68 E+8 | 7.93 E+7 | 1.7574 | 28.3719 | R | 🔴 |
| *PGN1670* | *PG0269* | *secretion activator protein putative* | | | | | | | | | | | | | | | |
| PG0291 | | 2.99 E-1 | 6.0 | 11 | -0.8770 | 4.0866 | Y | 🟡 | 🟡 | Y | 1.29 E-2 | 3.15 E+6 | 6.4 E+6 | -1.0233 | 23.1868 | Y | 🟡 |
| *PGN1673* | *PG0266* | *hypothetical protein PG_0291* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus |
| PG0290 | | 3.55 E-2 | 25.7 | 11 | 1.2226 | 5.1965 | Y 🟡 | 🟡 Y | 5.41 E-2 | 1.34 E+7 | 1.05 E+7 | 0.3460 | 24.5100 | Y 🟡 |
| *PGN1674* | *PG0265* | *hypothetical protein PG_0290* | | | | | | | | | | | | |
| PG0289 | | 1.47 E-2 | 36.8 | 16.5 | 1.1570 | 5.7359 | Y 🟡 | 🔴 R | 9.86 E-10 | 3.29 E+7 | 9.4 E+6 | 1.8084 | 25.3344 | R 🔴 |
| *PGN1675* | *PG0264* | *hypothetical protein PG_0289* | | | | | | | | | | | | |
| PG0288 | | 2.82 E-1 | 20.5 | 29.5 | -0.5226 | 5.6449 | Y 🟡 | 🟡 Y | 7.1 E-2 | 1.42 E+7 | 1.7 E+7 | -0.2593 | 24.8989 | Y 🟡 |
| *PGN1676* | *PG0263* | *lipoprotein putative* | | | | | | | | | | | | |
| PG0287 | | 1.55 E-3 | 1.7 | 15.5 | -3.1791 | 4.1053 | G 🟢 | 🟢 G | 1.9 E-5 | 1.85 E+3 | 3.65 E+6 | -10.9460 | 21.8004 | G 🟢 |
| *PGN1677* | *PG0262* | *hypothetical protein PG_0287* | | | | | | | | | | | | |
| PG0286 | | 4.53 E-1 | 9.4 | 13 | -0.4659 | 4.4862 | Y 🟡 | 🟢 G | 2.34 E-4 | 6.5 E+6 | 2.07 E+7 | -1.6701 | 24.6974 | G 🟢 |
| *PGN1678* | *PG0260* | *hypothetical protein PG_0286* | | | | | | | | | | | | |
| PG0279 | | 1.24 E-1 | 80.4 | 105.5 | -0.3914 | 7.5386 | Y 🟡 | 🟡 Y | 1.4 E-3 | 4.3 E+7 | 6.48 E+7 | -0.5909 | 26.6839 | Y 🟡 |
| *PGN1685* | *PG0251* | *maeB NADP-dependent malic enzyme* | | | | | | | | | | | | |
| PG0278 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 6.13 E+5 | -8.3706 | 19.2287 | Y 🟡 |
| *PGN1687* | *PG0250* | *hypothetical protein PG_0278* | | | | | | | | | | | | |
| PG1747 | | 1.21 E-1 | 4.3 | 11.5 | -1.4265 | 3.9799 | Y 🟡 | 🟡 Y | 1.39 E-1 | 4.16 E+6 | 4.56 E+6 | -0.1346 | 23.0557 | Y 🟡 |
| *PGN1688* | *PG1523* | *ribose 5-phosphate isomerase B putative* | | | | | | | | | | | | |
| PG1748 | | 2.21 E-3 | 150.6 | 96.5 | 0.6421 | 7.9489 | R 🔴 | 🔴 R | 2.85 E-5 | 1.33 E+8 | 8.38 E+7 | 0.6637 | 27.6909 | R 🔴 |
| *PGN1689* | *PG1524* | *tkt transketolase* | | | | | | | | | | | | |
| PG1750 | | 1.84 E-1 | 1.7 | 6 | -1.8099 | 2.9470 | Y 🟡 | 🟢 G | 2.58 E-16 | 1.85 E+3 | 7.03 E+5 | -8.5685 | 19.4260 | G 🟢 |
| *PGN1690* | *PG1525* | *alpha-13/4-fucosidase putative* | | | | | | | | | | | | |
| PG1751 | | 4.4 E-1 | 1.7 | 3.5 | -1.0323 | 2.3816 | Y 🟡 | 🟡 Y | 1.07 E-2 | 1.85 E+3 | 1.19 E+6 | -9.3325 | 20.1885 | Y 🟡 |
| *PGN1691* | *PG1526* | *aminotransferase class V* | | | | | | | | | | | | |
| PG1753 | | 6.97 E-1 | 2.6 | 2.5 | 0.0381 | 2.3411 | Y 🟡 | 🔴 R | 0 | 8.4 E+5 | 4.51 E+5 | 0.8957 | 20.2998 | R 🔴 |
| *PGN1693* | *PG1527* | *selD selenide water dikinase* | | | | | | | | | | | | |
| PG1754 | | 6.14 E-1 | 43.6 | 47 | -0.1071 | 6.5020 | Y 🟡 | 🟡 Y | 8.83 E-2 | 2.17 E+7 | 2.45 E+7 | -0.1754 | 25.4585 | Y 🟡 |
| *PGN1694* | *PG1528* | *conserved domain protein* | | | | | | | | | | | | |
| PG1755 | | 1.97 E-4 | 298.6 | 206 | 0.5357 | 8.9791 | R 🔴 | 🟡 Y | 4.09 E-3 | 5.15 E+8 | 3.93 E+8 | 0.3911 | 29.7569 | R 🔴 |
| *PGN1695* | *PG1529* | *fbaB fructose-bisphosphate aldolase class I* | | | | | | | | | | | | |
| PG1757 | | 5.88 E-10 | 18.0 | 81 | -2.1724 | 6.6289 | G 🟢 | 🟢 G | 5.03 E-5 | 1.05 E+7 | 6.37 E+7 | -2.5968 | 26.1444 | G 🟢 |
| *PGN1697* | *PG1530* | *hypothetical protein PG_1757* | | | | | | | | | | | | |
| PG1758 | | 2.8 E-1 | 43.6 | 32.5 | 0.4252 | 6.2506 | Y 🟡 | 🟡 Y | 1.84 E-1 | 6.29 E+7 | 6.1 E+7 | 0.0442 | 26.8842 | Y 🟡 |
| *PGN1698* | *PG1531* | *rpsO ribosomal protein S15* | | | | | | | | | | | | |
| PG1759 | | 3.05 E-1 | 6.8 | 12 | -0.8099 | 4.2361 | Y 🟡 | 🟡 Y | 2.67 E-2 | 2.78 E+6 | 5.16 E+6 | -0.8929 | 22.9205 | Y 🟡 |
| *PGN1699* | *PG1532* | *adhesion protein putative* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1760 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 1.09 E+6 | 1 E+3 | 10.0844 | 20.0515 | R | 🔴 |
| *PGN1700* | *PG1533* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG1762 | | 0 | 288.4 | 87.5 | 1.7205 | 8.5540 | R | 🔴 | 🔴 | R | 0 | 2.17 E+8 | 9.17 E+7 | 1.2400 | 28.1992 | R | 🔴 |
| *PGN1702* | *PG1536* | *secDF protein-export membrane protein SecD/protein-export membrane protein SecF* | | | | | | | | | | | | | | | |
| PG1763 | | 9.44 E-2 | 6.0 | 1 | 2.5825 | 2.8052 | Y | 🟡 | 🔴 | R | 1.74 E-15 | 1.7 E+6 | 1 E+3 | 10.7321 | 20.6987 | R | 🔴 |
| *PGN1703* | *PG1537* | *rnc ribonuclease III* | | | | | | | | | | | | | | | |
| PG1764 | | 9.32 E-3 | 288.4 | 221 | 0.3838 | 8.9925 | R | 🔴 | 🟡 | Y | 1.68 E-2 | 1.22 E+8 | 1.55 E+8 | -0.3461 | 28.0478 | Y | 🟡 |
| *PGN1704* | *PG1538* | *fabF 3-oxoacyl-(acyl-carrier-protein) synthase II* | | | | | | | | | | | | | | | |
| PG1765 | | 0 | 476.6 | 149.5 | 1.6726 | 9.2902 | R | 🔴 | 🟡 | Y | 1.74 E-1 | 4.62 E+8 | 4.8 E+8 | -0.0553 | 29.8123 | Y | 🟡 |
| *PGN1705* | | *acpP acyl carrier protein* | | | | | | | | | | | | | | | |
| PG1766 | | 6.69 E-1 | 10.3 | 9.5 | 0.1121 | 4.3051 | Y | 🟡 | 🟡 | Y | 8.63 E-2 | 1.56 E+6 | 2.12 E+6 | -0.4482 | 21.8113 | Y | 🟡 |
| *PGN1706* | *PG1539* | *purN phosphoribosylglycinamide formyltransferase* | | | | | | | | | | | | | | | |
| PG1767 | | 1.53 E-1 | 2.6 | 8 | -1.6399 | 3.4015 | Y | 🟡 | 🟡 | Y | 8.54 E-2 | 1.47 E+6 | 3.02 E+6 | -1.0390 | 22.0988 | Y | 🟡 |
| *PGN1707* | *PG1540* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG1768 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 8.3 E+5 | 1 E+3 | 9.6970 | 19.6645 | R | 🔴 |
| *PGN1708* | *PG1541* | *magnesium chelatase subunit D/I family* | | | | | | | | | | | | | | | |
| PG1771 | | 1.72 E-2 | 50.5 | 26.5 | 0.9298 | 6.2665 | Y | 🟡 | 🟡 | Y | 3.72 E-2 | 1.48 E+7 | 1.18 E+7 | 0.3324 | 24.6665 | Y | 🟡 |
| *PGN1711* | *PG1545* | *pheS phenylalanyl-tRNA synthetase alpha subunit* | | | | | | | | | | | | | | | |
| PG1772 | | 3.05 E-1 | 5.1 | 2 | 1.3601 | 2.8347 | Y | 🟡 | 🔴 | R | 0 | 4.01 E+5 | 6 E+4 | 2.7409 | 18.8146 | R | 🔴 |
| *PGN1712* | *PG1547* | *nth endonuclease III* | | | | | | | | | | | | | | | |
| PG1774 | | 4.23 E-1 | 6.8 | 4 | 0.7751 | 3.4390 | Y | 🟡 | 🔴 | R | 2.64 E-5 | 3.53 E+6 | 8.19 E+5 | 2.1082 | 22.0530 | R | 🔴 |
| *PGN1714* | *PG1549* | *mfd transcription-repair coupling factor* | | | | | | | | | | | | | | | |
| PG1775 | | 3.31 E-1 | 26.5 | 19 | 0.4814 | 5.5086 | Y | 🟡 | 🟡 | Y | 1.08 E-1 | 1.59 E+7 | 1.77 E+7 | -0.1566 | 25.0039 | Y | 🟡 |
| *PGN1715* | *PG1550* | *grpE grpE protein* | | | | | | | | | | | | | | | |
| PG1776 | | 4.75 E-1 | 18.0 | 14 | 0.3601 | 4.9986 | Y | 🟡 | 🟡 | Y | 6.14 E-2 | 2.97 E+6 | 5.53 E+6 | -0.8945 | 23.0197 | Y | 🟡 |
| *PGN1716* | *PG1552* | *dnaJ dnaJ protein* | | | | | | | | | | | | | | | |
| PG1777 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.44 E+6 | -9.6029 | 20.4585 | G | 🟢 |
| *PGN1717* | *PG1553* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1778 | | 2.67 E-1 | 2.6 | 6.5 | -1.3404 | 3.1806 | Y | 🟡 | 🟡 | Y | 2.95 E-2 | 7.96 E+5 | 1.32 E+6 | -0.7310 | 21.0145 | Y | 🟡 |
| *PGN1718* | *PG1554* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1779 | | 6 E-1 | 14.5 | 12.5 | 0.2187 | 4.7573 | Y | 🟡 | 🟡 | Y | 1.73 E-1 | 7.5 E+6 | 8.16 E+6 | -0.1213 | 23.9006 | Y | 🟡 |
| *PGN1719* | *PG1555* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1780 | | 6 E-1 | 35.1 | 38.5 | -0.1341 | 6.2013 | Y | 🟡 | 🟡 | Y | 9.99 E-3 | 1.25 E+7 | 9.06 E+6 | 0.4639 | 24.3621 | Y | 🟡 |
| *PGN1721* | *PG1556* | *bioF-3 8-amino-7-oxononanoate synthase* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus |
| PG1781 | | 9.98 E-4 | 29.1 | 7.5 | 1.9557 | 5.1935 | R 🔴 | 🔴 R | 7.95 E-12 | 1.14 E+7 | 2.76 E+6 | 2.0504 | 23.7574 | R 🔴 |
| *PGN1722* | *PG1557* | *udk uridine kinase* | | | | | | | | | | | | |
| PG1782 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y 🟡 | 🟢 G | 7.18 E-9 | 1.85 E+3 | 3.56 E+5 | -7.5890 | 18.4502 | G 🟢 |
| *PGN1723* | *PG1558* | *hypothetical protein PG_1782* | | | | | | | | | | | | |
| PG1783 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 1.77 E-6 | 1.85 E+3 | 1.56 E+5 | -6.3995 | 17.2702 | G 🟢 |
| *PGN1724* | *PG1559* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | |
| | | 0 | 1853.3 | 3174 | -0.7762 | 12.2956 | G 🟢 | 🟡 Y | 1.25 E-2 | 2.18 E+9 | 2.63 E+9 | -0.2724 | 32.1611 | G 🟢 |
| *PGN1728* | | | | | | | | | | | | | | |
| PG1842 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 2.57 E+5 | -7.1198 | 17.9838 | Y 🟡 |
| *PGN1729* | *PG1604* | *acetyltransferase GNAT family* | | | | | | | | | | | | |
| PG1841 | | 3.21 E-1 | 1.7 | 4.5 | -1.3948 | 2.6349 | Y 🟡 | 🟢 G | 7.61 E-16 | 1.85 E+3 | 6.95 E+5 | -8.5525 | 19.4100 | G 🟢 |
| *PGN1730* | *PG1603* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG1837 | | 2.09 E-2 | 77.9 | 48 | 0.6979 | 6.9757 | Y 🟡 | 🟡 Y | 3.34 E-3 | 1.04 E+8 | 6.39 E+7 | 0.7084 | 27.3255 | Y 🟡 |
| *PGN1733* | *PG1602* | *hemagglutinin protein HagA* | | | | | | | | | | | | |
| PG1835 | | 4.76 E-1 | 30.8 | 36.5 | -0.2448 | 6.0726 | Y 🟡 | 🟡 Y | 5.08 E-3 | 2.04 E+7 | 3.37 E+7 | -0.7238 | 25.6890 | Y 🟡 |
| *PGN1735* | *PG1600* | *lipoprotein putative* | | | | | | | | | | | | |
| PG1834 | | 4.21 E-1 | 29.9 | 23.5 | 0.3498 | 5.7401 | Y 🟡 | 🟡 Y | 6.16 E-2 | 1.45 E+7 | 1.2 E+7 | 0.2748 | 24.6555 | Y 🟡 |
| *PGN1736* | *PG1598* | *glycogen synthase-related protein* | | | | | | | | | | | | |
| PG1831 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 9.39 E+5 | -8.9877 | 19.8443 | Y 🟡 |
| *PGN1737* | *PG1597* | *recQ-2 ATP-dependent DNA helicase RecQ* | | | | | | | | | | | | |
| PG1829 | | 2.32 E-1 | 8.6 | 15.5 | -0.8572 | 4.5884 | Y 🟡 | 🟢 G | 2.72 E-4 | 1.26 E+6 | 5.01 E+6 | -1.9951 | 22.5787 | G 🟢 |
| *PGN1738* | *PG1596* | *long-chain-fatty-acid--CoA ligase putative* | | | | | | | | | | | | |
| PG1824 | | 1.69 E-6 | 463.8 | 635.5 | -0.4545 | 10.1023 | G 🟢 | 🟢 G | 1.36 E-5 | 2.91 E+8 | 4.26 E+8 | -0.5510 | 29.4182 | G 🟢 |
| *PGN1743* | *PG1593* | *eno enolase* | | | | | | | | | | | | |
| PG1823 | | 5.13 E-5 | 1.7 | 21.5 | -3.6512 | 4.5368 | G 🟢 | 🟢 G | 5.96 E-5 | 1.85 E+3 | 1.06 E+7 | -12.4779 | 23.3318 | G 🟢 |
| *PGN1744* | *PG1592* | *hypothetical protein PG_1823* | | | | | | | | | | | | |
| PG1820 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 2.69 E-9 | 1.85 E+3 | 2.24 E+6 | -10.2441 | 21.0990 | G 🟢 |
| *PGN1746* | *PG1591* | *nrfA cytochrome c nitrite reductase catalytic subunit NrfA* | | | | | | | | | | | | |
| PG1816 | | 1.07 E-2 | 103.5 | 65.5 | 0.6605 | 7.4012 | Y 🟡 | 🟡 Y | 1.74 E-1 | 4.47 E+7 | 4.31 E+7 | 0.0518 | 26.3878 | Y 🟡 |
| *PGN1749* | *PG1587* | *NAD(P)H dehydrogenase quinone family putative* | | | | | | | | | | | | |
| PG1815 | | 6.52 E-2 | 6.0 | 16 | -1.4175 | 4.4587 | Y 🟡 | 🟢 G | 1.55 E-5 | 8.89 E+5 | 4.94 E+6 | -2.4733 | 22.4738 | G 🟢 |
| *PGN1750* | *PG1586* | *kdsB 3-deoxy-D-manno-octulosonate cytidylyltransferase* | | | | | | | | | | | | |
| PG1814 | | 1.86 E-1 | 6.8 | 14 | -1.0323 | 4.3816 | Y 🟡 | 🟡 Y | 1.88 E-1 | 2.49 E+6 | 2.54 E+6 | -0.0270 | 22.2619 | Y 🟡 |
| *PGN1751* | *PG1585* | *dnaG DNA primase* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG1813 | | 1.84 E-1 | 2.6 | 7.5 | -1.5468 | 3.3316 | Y | 🟡 | 🟡 | Y | 3.72 E-2 | 2.92 E+6 | 5.2 E+6 | -0.8333 | 22.9524 | Y | 🟡 |
| *PGN1752* | | *ferredoxin 4Fe-4S* | | | | | | | | | | | | | | | |
| PG1812 | | 0 | 651.2 | 321.5 | 1.0182 | 9.9258 | R | 🔴 | 🔴 | R | 0 | 4.33 E+8 | 1.88 E+8 | 1.1999 | 29.2111 | R | 🔴 |
| *PGN1753* | *PG1583* | *2-oxoglutarate oxidoreductase alpha subunit* | | | | | | | | | | | | | | | |
| PG1810 | | 2.35 E-7 | 155.7 | 72.5 | 1.1030 | 7.8343 | R | 🔴 | 🔴 | R | 4.17 E-10 | 1.19 E+8 | 4.89 E+7 | 1.2811 | 27.3205 | R | 🔴 |
| *PGN1755* | *PG1582* | *2-oxoglutarate oxidoreductase beta subunit* | | | | | | | | | | | | | | | |
| PG1809 | | 4.35 E-12 | 116.4 | 30.5 | 1.9318 | 7.1984 | R | 🔴 | 🔴 | R | 0 | 1.35 E+8 | 2.8 E+7 | 2.2716 | 27.2798 | R | 🔴 |
| *PGN1756* | *PG1581* | *2-oxoglutarate oxidoreductase gamma subunit* | | | | | | | | | | | | | | | |
| PG1808 | | 4.75 E-1 | 23.1 | 18.5 | 0.3205 | 5.3786 | Y | 🟡 | 🟡 | Y | 2.01 E-1 | 7.87 E+6 | 7.85 E+6 | 0.0028 | 23.9057 | Y | 🟡 |
| *PGN1757* | *PG1580* | *spoT guanosine-3'5'-bis(diphosphate) 3'-pyrophosphohydrolase* | | | | | | | | | | | | | | | |
| PG1806 | | 6.34 E-3 | 29.1 | 10 | 1.5406 | 5.2888 | R | 🔴 | 🔴 | R | 3.54 E-4 | 1.68 E+7 | 7.04 E+6 | 1.2539 | 24.5072 | R | 🔴 |
| *PGN1759* | *PG1578* | *atpI v-type ATPase subunit I* | | | | | | | | | | | | | | | |
| PG1805 | | 2.62 E-1 | 18.8 | 28 | -0.5728 | 5.5492 | Y | 🟡 | 🟡 | Y | 1.45 E-1 | 8.02 E+6 | 8.65 E+6 | -0.1089 | 23.9901 | Y | 🟡 |
| *PGN1760* | *PG1577* | *atpD v-type ATPase subunit D* | | | | | | | | | | | | | | | |
| PG1804 | | 5.28 E-6 | 246.4 | 369 | -0.5825 | 9.2654 | G | 🟢 | 🟡 | Y | 1.78 E-1 | 1.42 E+8 | 1.38 E+8 | 0.0350 | 28.0599 | Y | 🟡 |
| *PGN1761* | *PG1576* | *atpB v-type ATPase subunit B* | | | | | | | | | | | | | | | |
| PG1803 | | 5.89 E-1 | 159.2 | 151.5 | 0.0711 | 8.2792 | Y | 🟡 | 🟡 | Y | 7.53 E-2 | 1.15 E+8 | 1.29 E+8 | -0.1625 | 27.8589 | Y | 🟡 |
| *PGN1762* | *PG1575* | *atpA v-type ATPase subunit A* | | | | | | | | | | | | | | | |
| PG1802 | | 7.01 E-1 | 52.2 | 52 | 0.0054 | 6.7031 | Y | 🟡 | 🟡 | Y | 1.32 E-2 | 2.15 E+7 | 1.71 E+7 | 0.3277 | 25.2027 | Y | 🟡 |
| *PGN1763* | *PG1574* | *hypothetical protein PG_1802* | | | | | | | | | | | | | | | |
| PG1801 | | 5.11 E-6 | 58.2 | 16.5 | 1.8182 | 6.2227 | R | 🔴 | 🔴 | R | 0 | 4.85 E+7 | 6.74 E+6 | 2.8455 | 25.7181 | R | 🔴 |
| *PGN1764* | *PG1573* | *v-type ATPase subunit E putative* | | | | | | | | | | | | | | | |
| PG1798 | | 1.15 E-2 | 35.9 | 65 | -0.8550 | 6.6573 | Y | 🟡 | 🟡 | Y | 8.87 E-3 | 1.49 E+7 | 2.21 E+7 | -0.5742 | 25.1420 | Y | 🟡 |
| *PGN1767* | *PG1572* | *immunoreactive 46 kDa antigen PG99* | | | | | | | | | | | | | | | |
| PG1797 | | 6.05 E-2 | 16.3 | 6 | 1.4381 | 4.4762 | Y | 🟡 | 🔴 | R | 4.42 E-7 | 7.99 E+6 | 3.03 E+6 | 1.4007 | 23.3931 | R | 🔴 |
| *PGN1768* | *PG1571* | *DNA-binding response regulator/sensor histidine kinase* | | | | | | | | | | | | | | | |
| PG1794 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 2.88 E-6 | 1.85 E+3 | 1.94 E+6 | -10.0368 | 20.8919 | G | 🟢 |
| *PGN1771* | *PG1569* | *polA DNA polymerase type I* | | | | | | | | | | | | | | | |
| PG1793 | | 6.69 E-1 | 10.3 | 11 | -0.0994 | 4.4106 | Y | 🟡 | 🟡 | Y | 3.49 E-3 | 4.2 E+6 | 2.26 E+6 | 0.8921 | 22.6223 | Y | 🟡 |
| *PGN1772* | *PG1568* | *glgB 14-alpha-glucan branching enzyme* | | | | | | | | | | | | | | | |
| PG1792 | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 1.63 E+5 | 1 E+3 | 7.3492 | 17.3238 | R | 🔴 |
| *PGN1773* | *PG1567* | *sodium/hydrogen antiporter* | | | | | | | | | | | | | | | |
| PG1790 | | 1.5 E-1 | 1.7 | 6.5 | -1.9253 | 3.0376 | Y | 🟡 | 🟢 | G | 6.92 E-6 | 1.85 E+3 | 1.12 E+6 | -9.2375 | 20.0936 | G | 🟢 |
| *PGN1775* | *PG1566* | *hypothetical protein PG_1790* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | PP PPC/ Pg Protein Intensity | | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus |
| PG1789 | | 2.8 E-2 | 21.4 | 41.5 | -0.9561 | 5.9748 | Y 🟡 | 🟡 Y | 1.12 E-3 | 1.08 E+7 | 2.08 E+7 | -0.9478 | 24.9126 | Y 🟡 |
| *PGN1776* | *PG1565* | *dcp-2 peptidyl-dipeptidase Dcp* | | | | | | | | | | | | |
| PG1788 | | 6.11 E-3 | 283.2 | 213.5 | 0.4077 | 8.9563 | R 🔴 | 🟡 Y | 2.02 E-1 | 2.81 E+8 | 2.81 E+8 | 0.0006 | 29.0672 | R 🔴 |
| *PGN1777* | *PG1564* | *cysteine peptidase putative* | | | | | | | | | | | | |
| PG1847 | | 8.08 E-7 | 24.8 | 77.5 | -1.6430 | 6.6769 | G 🟢 | 🟢 G | 1.82 E-5 | 1.17 E+7 | 2.51 E+7 | -1.1049 | 25.1325 | G 🟢 |
| *PGN1780* | *PG1609* | *endoribonuclease L-PSP putative* | | | | | | | | | | | | |
| PG1848 | | 3.05 E-1 | 5.1 | 2 | 1.3601 | 2.8347 | Y 🟡 | 🔴 R | 0 | 2.85 E+6 | 1.68 E+5 | 4.0800 | 21.5248 | R 🔴 |
| *PGN1781* | *PG1610* | *RNA methyltransferase TrmH family* | | | | | | | | | | | | |
| PG1849 | | 6.69 E-1 | 2.6 | 3 | -0.2249 | 2.4769 | Y 🟡 | 🟡 Y | 3.41 E-2 | 1.15 E+6 | 6.07 E+5 | 0.9172 | 20.7418 | Y 🟡 |
| *PGN1782* | *PG1611* | *recN DNA repair protein RecN* | | | | | | | | | | | | |
| PG1850 | | 3.52 E-1 | 10.3 | 6 | 0.7751 | 4.0240 | Y 🟡 | 🔴 R | 0 | 3.07 E+6 | 7.52 E+5 | 2.0324 | 21.8674 | R 🔴 |
| *PGN1783* | *PG1612* | *hypothetical protein PG_1850* | | | | | | | | | | | | |
| PG1851 | | 3.9 E-1 | 9.4 | 14 | -0.5728 | 4.5492 | Y 🟡 | 🟡 Y | 1.3 E-2 | 4.08 E+6 | 8.88 E+6 | -1.1205 | 23.6281 | Y 🟡 |
| *PGN1784* | *PG1613* | *coaBC phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase* | | | | | | | | | | | | |
| PG1852 | | 1.38 E-2 | 38.5 | 17.5 | 1.1377 | 5.8075 | Y 🟡 | 🟡 Y | 1.27 E-3 | 1.33 E+7 | 7.12 E+6 | 0.8990 | 24.2820 | Y 🟡 |
| *PGN1785* | *PG1614* | *exonuclease* | | | | | | | | | | | | |
| PG1853 | | 3.23 E-2 | 85.6 | 56 | 0.6116 | 7.1453 | Y 🟡 | 🟡 Y | 1.96 E-1 | 4.13 E+7 | 4.1 E+7 | 0.0111 | 26.2943 | Y 🟡 |
| *PGN1786* | *PG1615* | *dnaN DNA polymerase III beta subunit* | | | | | | | | | | | | |
| PG1854 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 5.7 E+5 | -8.2658 | 19.1242 | Y 🟡 |
| *PGN1787* | *PG1616* | *5-formyltetrahydrofolate cyclo-ligase family protein* | | | | | | | | | | | | |
| PG1855 | | 2.25 E-1 | 5.1 | 1.5 | 1.7751 | 2.7299 | Y 🟡 | 🔴 R | 0 | 3.86 E+6 | 1.12 E+6 | 1.7911 | 22.2471 | R 🔴 |
| *PGN1788* | *PG1617* | *carboxyl-terminal protease* | | | | | | | | | | | | |
| PG1858 | | 6.45 E-2 | 37.6 | 59 | -0.6481 | 6.5947 | Y 🟡 | 🟡 Y | 6.64 E-2 | 2.43 E+7 | 3.44 E+7 | -0.4981 | 25.8068 | Y 🟡 |
| *PGN1791* | *PG1621* | *flavodoxin* | | | | | | | | | | | | |
| PG1860 | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y 🟡 | 🔴 R | 5.11 E-12 | 8.07 E+5 | 1 E+3 | 9.6568 | 19.6243 | R 🔴 |
| *PGN1793* | *PG1624* | *conserved hypothetical protein* | | | | | | | | | | | | |
| PG1862 | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y 🟡 | 🟡 Y | 1.83 E-1 | 9.54 E+5 | 1.03 E+6 | -0.1114 | 20.9201 | Y 🟡 |
| *PGN1795* | *PG1625* | *hypothetical protein PG_1862* | | | | | | | | | | | | |
| PG1864 | | 6.94 E-1 | 18.8 | 18.5 | 0.0251 | 5.2220 | Y 🟡 | 🔴 R | 3.3 E-4 | 4.28 E+6 | 2.5 E+6 | 0.7760 | 22.6925 | R 🔴 |
| *PGN1796* | *PG1626* | *leucine-rich protein* | | | | | | | | | | | | |
| PG1872 | | 7.07 E-13 | 394.5 | 636.5 | -0.6903 | 10.0098 | G 🟢 | 🟢 G | 9.75 E-6 | 1.46 E+8 | 2.73 E+8 | -0.9079 | 28.6427 | G 🟢 |
| *PGN1800* | *PG1630* | *hutU urocanate hydratase* | | | | | | | | | | | | |
| PG1875 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 1.39 E+5 | -6.2340 | 17.1067 | Y 🟡 |
| *PGN1802* | *PG1632* | *hemolysin* | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1876 | | 1.5 E-1 | 1.7 | 6.5 | -1.9253 | 3.0376 | Y | 🟡 | 🟢 | G | 1.37 E-4 | 1.85 E+3 | 1.39 E+6 | -9.5564 | 20.4121 | G | 🟢 |
| *PGN1803* | *PG1633* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1877 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 5.5 E+5 | -8.2152 | 19.0738 | Y | 🟡 |
| *PGN1804* | *PG1634* | *nhaA Na+/H+ antiporter* | | | | | | | | | | | | | | | |
| PG1878 | | 1.85 E-3 | 54.8 | 24 | 1.1901 | 6.2994 | R | 🔴 | 🟡 | Y | 1.69 E-3 | 1.52 E+7 | 9.87 E+6 | 0.6228 | 24.5792 | R | 🔴 |
| *PGN1805* | *PG1635* | *cysS cysteinyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG1879 | | 5.8 E-1 | 26.5 | 30 | -0.1776 | 5.8208 | Y | 🟡 | 🟡 | Y | 2.52 E-3 | 1.78 E+7 | 2.97 E+7 | -0.7373 | 25.5040 | Y | 🟡 |
| *PGN1806* | *PG1636* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1880 | | 5.17 E-1 | 3.4 | 2 | 0.7751 | 2.4390 | Y | 🟡 | 🔴 | R | 0 | 9.4 E+5 | 8.86 E+5 | 0.0842 | 20.8003 | R | 🔴 |
| *PGN1807* | *PG1637* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | | | | |
| PG1881 | | 1.67 E-12 | 2.6 | 52.5 | -4.3542 | 5.7831 | G | 🟢 | 🟢 | G | 0 | 8.22 E+5 | 3.81 E+7 | -5.5332 | 25.2133 | G | 🟢 |
| *PGN1808* | *PG1638* | *hypothetical protein PG_1881* | | | | | | | | | | | | | | | |
| PG1884 | | 4.53 E-1 | 25.7 | 20.5 | 0.3244 | 5.5289 | Y | 🟡 | 🔴 | R | 4.19 E-4 | 1.03 E+7 | 5.24 E+6 | 0.9701 | 23.8866 | R | 🔴 |
| *PGN1811* | *PG1639* | *alpha-L-fucosidase precursor putative* | | | | | | | | | | | | | | | |
| PG1885 | | 8.79 E-3 | 24.0 | 7.5 | 1.6756 | 4.9754 | R | 🔴 | 🔴 | R | 1.33 E-12 | 1.03 E+7 | 1.64 E+6 | 2.6500 | 23.5097 | R | 🔴 |
| *PGN1812* | *PG1640* | *ppk polyphosphate kinase* | | | | | | | | | | | | | | | |
| PG1886 | | 6.69 E-1 | 6.8 | 7.5 | -0.1318 | 3.8425 | Y | 🟡 | 🟡 | Y | 1.89 E-1 | 2.01 E+6 | 2.07 E+6 | -0.0384 | 21.9587 | Y | 🟡 |
| *PGN1813* | *PG1641* | *hflX GTP-binding protein HflX* | | | | | | | | | | | | | | | |
| PG1887 | | 6.69 E-1 | 3.4 | 3 | 0.1901 | 2.6832 | Y | 🟡 | 🔴 | R | 3.16 E-6 | 1.1 E+6 | 2.6 E+5 | 2.0811 | 20.3726 | R | 🔴 |
| *PGN1814* | *PG1642* | *rhodanese-like domain protein* | | | | | | | | | | | | | | | |
| PG1888 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 1.22 E-9 | 1.85 E+3 | 4.85 E+5 | -8.0350 | 18.8942 | G | 🟢 |
| *PGN1815* | *PG1643* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1889 | | 5.72 E-1 | 47.1 | 42.5 | 0.1471 | 6.4848 | Y | 🟡 | 🔴 | R | 9.56 E-9 | 1.54 E+7 | 8.17 E+6 | 0.9182 | 24.4928 | R | 🔴 |
| *PGN1816* | *PG1644* | *hypothetical protein PG_1889* | | | | | | | | | | | | | | | |
| | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y | 🟡 | 🔴 | R | 0 | 1.27 E+5 | 1 E+3 | 6.9893 | 16.9664 | R | 🔴 |
| *PGN1818* | | | | | | | | | | | | | | | | | |
| | | 5.95 E-1 | 12.0 | 10 | 0.2605 | 4.4581 | Y | 🟡 | 🟡 | Y | 1.32 E-2 | 3.33 E+6 | 2.1 E+6 | 0.6660 | 22.3726 | Y | 🟡 |
| *PGN1819* | | | | | | | | | | | | | | | | | |
| PG1896 | | 1.15 E-3 | 55.6 | 101 | -0.8607 | 7.2911 | G | 🟢 | 🟢 | G | 1.68 E-6 | 3.16 E+7 | 6.11 E+7 | -0.9491 | 26.4668 | G | 🟢 |
| *PGN1827* | *PG1652* | *metK S-adenosylmethionine synthase* | | | | | | | | | | | | | | | |
| PG1897 | | 2.74 E-1 | 1.7 | 5 | -1.5468 | 2.7466 | Y | 🟡 | 🟢 | G | 3.47 E-4 | 1.85 E+3 | 1.85 E+6 | -9.9666 | 20.8217 | G | 🟢 |
| *PGN1828* | *PG1653* | *thiamin pyrophosphokinase catalytic domain protein* | | | | | | | | | | | | | | | |
| PG1899 | | 2.31 E-4 | 77.9 | 137.5 | -0.8204 | 7.7506 | G | 🟢 | 🟢 | G | 1.83 E-4 | 5.56 E+7 | 1.05 E+8 | -0.9110 | 27.2558 | G | 🟢 |
| *PGN1830* | *PG1655* | *TonB-dependent receptor putative* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG1901 | | 2.34 E-3 | 47.9 | 20 | 1.2605 | 6.0857 | R | 🔴 | 🔴 | R | 7.06 E-14 | 7.89 E+7 | 1.82 E+7 | 2.1140 | 26.5335 | R | 🔴 |
| *PGN1832* | *PG1657* | *frr ribosome recycling factor* | | | | | | | | | | | | | | | |
| PG1902 | | 4.55 E-1 | 5.1 | 3 | 0.7751 | 3.0240 | Y | 🟡 | 🟡 | Y | 1.72 E-1 | 3.1 E+6 | 2.86 E+6 | 0.1149 | 22.5077 | Y | 🟡 |
| *PGN1833* | *PG1658* | *pyrH uridylate kinase* | | | | | | | | | | | | | | | |
| PG1903 | | 1.21 E-2 | 24.8 | 8.5 | 1.5456 | 5.0581 | Y | 🟡 | 🔴 | R | 8.73 E-11 | 6.18 E+6 | 1.89 E+6 | 1.7087 | 22.9443 | R | 🔴 |
| *PGN1834* | *PG1659* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG1910 | | 1.02 E-5 | 103.5 | 45.5 | 1.1862 | 7.2195 | R | 🔴 | 🟡 | Y | 5.07 E-3 | 7.64 E+7 | 4.94 E+7 | 0.6281 | 26.9063 | R | 🔴 |
| *PGN1840* | *PG1666* | *rplQ ribosomal protein L17* | | | | | | | | | | | | | | | |
| PG1911 | | 4.13 E-4 | 145.5 | 86 | 0.7582 | 7.8546 | R | 🔴 | 🔴 | R | 9.81 E-4 | 7.47 E+7 | 3.66 E+7 | 1.0271 | 26.7298 | R | 🔴 |
| *PGN1841* | *PG1667* | *rpoA DNA-directed RNA polymerase alpha subunit* | | | | | | | | | | | | | | | |
| PG1912 | | 1.04 E-4 | 149.7 | 84.5 | 0.8254 | 7.8718 | R | 🔴 | 🔴 | R | 1.04 E-13 | 1.72 E+8 | 6.79 E+7 | 1.3391 | 27.8356 | R | 🔴 |
| *PGN1842* | *PG1668* | *rpsD ribosomal protein S4* | | | | | | | | | | | | | | | |
| PG1913 | | 2.11 E-4 | 39.4 | 11 | 1.8392 | 5.6542 | R | 🔴 | 🟡 | Y | 9.55 E-3 | 1.82 E+7 | 1.03 E+7 | 0.8198 | 24.7664 | R | 🔴 |
| *PGN1843* | *PG1669* | *rpsK ribosomal protein S11* | | | | | | | | | | | | | | | |
| PG1914 | | 5.43 E-1 | 31.7 | 27.5 | 0.2032 | 5.8865 | Y | 🟡 | 🟡 | Y | 1.22 E-2 | 3.33 E+7 | 1.96 E+7 | 0.7668 | 25.6579 | Y | 🟡 |
| *PGN1844* | *PG1670* | *rpsM ribosomal protein S13* | | | | | | | | | | | | | | | |
| PG1916 | | 5.43 E-1 | 15.4 | 12.5 | 0.3012 | 4.8023 | Y | 🟡 | 🔴 | R | 3.62 E-6 | 5.91 E+6 | 2.1 E+6 | 1.4957 | 22.9327 | R | 🔴 |
| *PGN1846* | | *infA translation initiation factor IF-1* | | | | | | | | | | | | | | | |
| PG1917 | | 2.6 E-2 | 10.3 | 25.5 | -1.3124 | 5.1606 | Y | 🟡 | 🟡 | Y | 1.87 E-1 | 4.59 E+6 | 4.46 E+6 | 0.0439 | 23.1094 | Y | 🟡 |
| *PGN1847* | *PG1672* | *map methionine aminopeptidase type I* | | | | | | | | | | | | | | | |
| PG1918 | | 4.75 E-1 | 25.7 | 31 | -0.2722 | 5.8245 | Y | 🟡 | 🟡 | Y | 2.1 E-2 | 2.89 E+7 | 1.88 E+7 | 0.6214 | 25.5060 | Y | 🟡 |
| *PGN1848* | *PG1673* | *secY preprotein translocase SecY subunit* | | | | | | | | | | | | | | | |
| PG1919 | | 4.58 E-5 | 62.5 | 22 | 1.5055 | 6.4002 | R | 🔴 | 🔴 | R | 2.58 E-16 | 3.49 E+7 | 1.05 E+7 | 1.7296 | 25.4383 | R | 🔴 |
| *PGN1849* | *PG1673* | *rplO ribosomal protein L15* | | | | | | | | | | | | | | | |
| PG1920 | | 1.94 E-2 | 40.2 | 19.5 | 1.0443 | 5.9000 | Y | 🟡 | 🔴 | R | 2.03 E-6 | 4.75 E+7 | 1.85 E+7 | 1.3615 | 25.9756 | R | 🔴 |
| *PGN1850* | | *rpmD ribosomal protein L30* | | | | | | | | | | | | | | | |
| PG1921 | | 2.82 E-2 | 40.2 | 20.5 | 0.9721 | 5.9240 | Y | 🟡 | 🟡 | Y | 1.72 E-2 | 4.76 E+7 | 2.71 E+7 | 0.8133 | 26.1544 | Y | 🟡 |
| *PGN1851* | *PG1674* | *rpsE ribosomal protein S5* | | | | | | | | | | | | | | | |
| PG1922 | | 6.85 E-1 | 24.0 | 24.5 | -0.0323 | 5.5987 | Y | 🟡 | 🟡 | Y | 9.2 E-2 | 2.9 E+7 | 2.38 E+7 | 0.2876 | 25.6533 | Y | 🟡 |
| *PGN1852* | *PG1675* | *rplR ribosomal protein L18* | | | | | | | | | | | | | | | |
| PG1923 | | 4.37 E-1 | 151.5 | 166 | -0.1323 | 8.3104 | Y | 🟡 | 🟡 | Y | 1.69 E-1 | 1.52 E+8 | 1.58 E+8 | -0.0542 | 28.2041 | Y | 🟡 |
| *PGN1853* | *PG1676* | *rplF ribosomal protein L6* | | | | | | | | | | | | | | | |
| PG1924 | | 5.89 E-2 | 24.8 | 11.5 | 1.1095 | 5.1825 | Y | 🟡 | 🟡 | Y | 1.83 E-1 | 3.49 E+7 | 3.3 E+7 | 0.0811 | 26.0167 | Y | 🟡 |
| *PGN1854* | *PG1677* | *rpsH ribosomal protein S8* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Regulation** | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Consensus** |
| PG1925 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 2.5 E+6 | -10.4023 | 21.2571 | Y 🟡 |
| *PGN1855* | *PG1678* | *rpsN ribosomal protein S14* | | | | | | | | | | | | |
| PG1926 | | 4.87 E-11 | 313.2 | 162.5 | 0.9465 | 8.8938 | R 🔴 | 🟡 Y | 1.23 E-1 | 1.12 E+8 | 1.03 E+8 | 0.1220 | 27.6845 | R 🔴 |
| *PGN1856* | *PG1679* | *rplE ribosomal protein L5* | | | | | | | | | | | | |
| PG1927 | | 7.93 E-2 | 26.5 | 13.5 | 0.9744 | 5.3228 | Y 🟡 | 🔴 R | 7.88 E-5 | 3.36 E+7 | 1.54 E+7 | 1.1269 | 25.5464 | R 🔴 |
| *PGN1857* | *PG1680* | *rplX ribosomal protein L24* | | | | | | | | | | | | |
| PG1928 | | 2.31 E-15 | 95.8 | 14 | 2.7751 | 6.7792 | R 🔴 | 🔴 R | 3.44 E-15 | 4.27 E+7 | 1.08 E+7 | 1.9854 | 25.6710 | R 🔴 |
| *PGN1858* | *PG1681* | *rplN ribosomal protein L14* | | | | | | | | | | | | |
| PG1929 | | 2.15 E-3 | 12.8 | 1 | 3.6820 | 3.7902 | Y 🟡 | 🔴 R | 3.24 E-7 | 6.65 E+6 | 1 E+3 | 12.7000 | 22.6660 | R 🔴 |
| *PGN1859* | *PG1682* | *rpsQ ribosomal protein S17* | | | | | | | | | | | | |
| PG1930 | | 6.05 E-2 | 6.8 | 1 | 2.7751 | 2.9718 | Y 🟡 | 🔴 R | 4.06 E-6 | 9.46 E+6 | 1 E+3 | 13.2080 | 23.1740 | R 🔴 |
| *PGN1860* | | *rpmC ribosomal protein L29* | | | | | | | | | | | | |
| PG1931 | | 6.69 E-1 | 13.7 | 13 | 0.0747 | 4.7383 | Y 🟡 | 🟡 Y | 1.45 E-1 | 1.89 E+7 | 1.75 E+7 | 0.1098 | 25.1143 | Y 🟡 |
| *PGN1861* | *PG1683* | *rplP ribosomal protein L16* | | | | | | | | | | | | |
| PG1932 | | 3.3 E-4 | 107.8 | 57 | 0.9195 | 7.3647 | R 🔴 | 🟡 Y | 2.88 E-3 | 7.26 E+7 | 4.93 E+7 | 0.5598 | 26.8614 | R 🔴 |
| *PGN1862* | *PG1684* | *rpsC ribosomal protein S3* | | | | | | | | | | | | |
| PG1933 | | 2.15 E-1 | 27.4 | 17.5 | 0.6458 | 5.4880 | Y 🟡 | 🟡 Y | 7.62 E-2 | 1.61 E+7 | 1.2 E+7 | 0.4212 | 24.7430 | Y 🟡 |
| *PGN1863* | *PG1685* | *rplV ribosomal protein L22* | | | | | | | | | | | | |
| PG1934 | | 1.74 E-3 | 24.0 | 5.5 | 2.1230 | 4.8806 | R 🔴 | 🔴 R | 2.61 E-14 | 2.12 E+7 | 1.98 E+6 | 3.4177 | 24.4654 | R 🔴 |
| *PGN1864* | *PG1686* | *rpsS ribosomal protein S19* | | | | | | | | | | | | |
| PG1935 | | 3.16 E-3 | 27.4 | 8 | 1.7751 | 5.1449 | R 🔴 | 🔴 R | 0 | 3.13 E+7 | 3.6 E+6 | 3.1205 | 25.0551 | R 🔴 |
| *PGN1865* | *PG1687* | *rplB ribosomal protein L2* | | | | | | | | | | | | |
| PG1936 | | 2.27 E-2 | 11.1 | 2 | 2.4755 | 3.7141 | Y 🟡 | 🔴 R | 0 | 4.1 E+6 | 6.89 E+5 | 2.5744 | 22.1923 | R 🔴 |
| *PGN1866* | *PG1688* | *rplW ribosomal protein L23* | | | | | | | | | | | | |
| PG1937 | | 0 | 177.1 | 28 | 2.6612 | 7.6803 | R 🔴 | 🔴 R | 0 | 1.11 E+8 | 1.55 E+7 | 2.8445 | 26.9177 | R 🔴 |
| *PGN1867* | *PG1689* | *rplD ribosomal protein L4* | | | | | | | | | | | | |
| PG1938 | | 7.31 E-2 | 93.3 | 66.5 | 0.4880 | 7.3198 | Y 🟡 | 🟡 Y | 1.16 E-2 | 7.4 E+7 | 5.08 E+7 | 0.5411 | 26.8949 | Y 🟡 |
| *PGN1868* | *PG1690* | *rplC ribosomal protein L3* | | | | | | | | | | | | |
| PG1939 | | 4.02 E-4 | 129.2 | 73.5 | 0.8138 | 7.6632 | R 🔴 | 🟡 Y | 2.48 E-3 | 8.12 E+7 | 4.64 E+7 | 0.8072 | 26.9266 | R 🔴 |
| *PGN1869* | *PG1691* | *rpsJ ribosomal protein S10* | | | | | | | | | | | | |
| PG1940 | | 0 | 634.0 | 89 | 2.8327 | 9.4979 | R 🔴 | 🔴 R | 0 | 4.8 E+8 | 8.95 E+7 | 2.4232 | 29.0853 | R 🔴 |
| *PGN1870* | *PG1692* | *fusA translation elongation factor G* | | | | | | | | | | | | |
| PG1941 | | 6.66 E-3 | 62.5 | 32.5 | 0.9426 | 6.5693 | R 🔴 | 🔴 R | 1.16 E-6 | 7.28 E+7 | 3.2 E+7 | 1.1844 | 26.6436 | R 🔴 |
| *PGN1871* | *PG1693* | *rpsG ribosomal protein S7* | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | **$q$-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Regulation** | | | | **$q$-value** | **PP (Norm)** | **PPC (Norm)** | **$\log_2$Ratio** | **$\log_2$Sum** | **Consensus** | |
| PG1942 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🟡 | Y | 1.42 E-3 | 2.77 E+6 | 1 E+3 | 11.4345 | 21.4008 | Y | 🟡 |
| *PGN1872* | *PG1694* | *rpsL ribosomal protein S12* | | | | | | | | | | | | | | | |
| PG1947 | | 4.41 E-1 | 10.3 | 7 | 0.5527 | 4.1100 | Y | 🟡 | 🟡 | Y | 1.38 E-1 | 2.46 E+6 | 2.19 E+6 | 0.1699 | 22.1497 | Y | 🟡 |
| *PGN1877* | *PG1699* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG1948 | | 3.82 E-3 | 169.4 | 235.5 | -0.4751 | 8.6615 | G | 🟢 | 🟡 | Y | 1.01 E-2 | 1.2 E+8 | 1.54 E+8 | -0.3531 | 28.0301 | G | 🟢 |
| *PGN1878* | *PG1700* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG1949 | | 2.8 E-2 | 206.2 | 157.5 | 0.3888 | 8.5067 | Y | 🟡 | 🟡 | Y | 2.72 E-2 | 1.34 E+8 | 1.94 E+8 | -0.5320 | 28.2922 | Y | 🟡 |
| *PGN1880* | *PG1701* | *mdh malate dehydrogenase* | | | | | | | | | | | | | | | |
| PG1950 | | 1.86 E-1 | 5.1 | 11.5 | -1.1635 | 4.0561 | Y | 🟡 | 🟡 | Y | 9.67 E-3 | 2.33 E+6 | 3.73 E+6 | -0.6799 | 22.5295 | Y | 🟡 |
| *PGN1882* | *PG1703* | *membrane protein putative* | | | | | | | | | | | | | | | |
| PG1951 | | 3.78 E-2 | 71.0 | 103 | -0.5364 | 7.4431 | Y | 🟡 | 🟡 | Y | 1.66 E-3 | 4.21 E+7 | 6.4 E+7 | -0.6040 | 26.6603 | Y | 🟡 |
| *PGN1883* | *PG1704* | *glnS glutaminyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG1952 | | 7.06 E-1 | 6.0 | 6 | -0.0025 | 3.5837 | Y | 🟡 | 🔴 | R | 1.24 E-4 | 6.07 E+6 | 2.84 E+6 | 1.0939 | 23.0865 | Y | 🟡 |
| *PGN1884* | *PG1705* | *DedA family protein* | | | | | | | | | | | | | | | |
| PG1953 | | 3.88 E-1 | 31.7 | 24.5 | 0.3698 | 5.8114 | Y | 🟡 | 🟡 | Y | 1.89 E-1 | 1.83 E+7 | 1.87 E+7 | -0.0316 | 25.1399 | Y | 🟡 |
| *PGN1885* | *PG1706* | *YitT family protein* | | | | | | | | | | | | | | | |
| PG1956 | | 2.02 E-1 | 51.3 | 37 | 0.4725 | 6.4650 | Y | 🟡 | 🔴 | R | 4.32 E-4 | 2.39 E+7 | 1.47 E+7 | 0.7033 | 25.2024 | R | 🔴 |
| *PGN1888* | *PG1708* | *abfT-2 4-hydroxybutyrate CoA-transferase* | | | | | | | | | | | | | | | |
| | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y | 🟡 | 🔴 | R | 0 | 2.99 E+6 | 1 E+3 | 11.5467 | 21.5130 | R | 🔴 |
| *PGN1889* | | | | | | | | | | | | | | | | | |
| PG1959 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y | 🟡 | 🟢 | G | 0 | 1.85 E+3 | 1.37 E+5 | -6.2097 | 17.0828 | Y | 🟡 |
| *PGN1890* | *PG1710* | *rpmG ribosomal protein L33* | | | | | | | | | | | | | | | |
| PG1960 | | 3.68 E-1 | 11.1 | 16.5 | -0.5689 | 4.7878 | Y | 🟡 | 🟡 | Y | 2.16 E-2 | 1.02 E+7 | 5.91 E+6 | 0.7878 | 23.9421 | Y | 🟡 |
| *PGN1891* | *PG1710* | *rpmB ribosomal protein L28* | | | | | | | | | | | | | | | |
| PG1961 | | 6.97 E-1 | 2.6 | 2.5 | 0.0381 | 2.3411 | Y | 🟡 | 🟡 | Y | 1.11 E-1 | 9.09 E+5 | 7.22 E+5 | 0.3328 | 20.6366 | Y | 🟡 |
| *PGN1892* | *PG1711* | *hypothetical protein PG_1961* | | | | | | | | | | | | | | | |
| | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 2.11 E-6 | 1.85 E+3 | 9.67 E+5 | -9.0300 | 19.8865 | G | 🟢 |
| *PGN1893* | | | | | | | | | | | | | | | | | |
| PG1964 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟡 | Y | 1.27 E-2 | 1.85 E+3 | 5.84 E+5 | -8.3009 | 19.1592 | Y | 🟡 |
| *PGN1896* | *PG1715* | *bacterial sugar transferase* | | | | | | | | | | | | | | | |
| PG1966 | | 5.17 E-1 | 1.7 | 3 | -0.8099 | 2.2361 | Y | 🟡 | 🟡 | Y | 1.52 E-3 | 1.85 E+3 | 1.34 E+6 | -9.5025 | 20.3582 | Y | 🟡 |
| *PGN1898* | *PG1717* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| | | 1.73 E-1 | 31.7 | 46 | -0.5390 | 6.2791 | Y | 🟡 | 🟢 | G | 1.01 E-5 | 1.45 E+7 | 3.09 E+7 | -1.0891 | 25.4379 | G | 🟢 |
| *PGN1903* | | | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus |
| PG1972 | | 5.8 E-4 | 200.2 | 284.5 | -0.5068 | 8.9210 | G 🟢 | 🟡 Y | 2.76 E-3 | 2.86 E+8 | 3.98 E+8 | -0.4743 | 29.3488 | G 🟢 |
| *PGN1904* | *PG1721* | *hemagglutinin protein HagB* | | | | | | | | | | | | |
| PG1977 | | 2.74 E-1 | 1.7 | 5 | -1.5468 | 2.7466 | Y 🟡 | 🟡 Y | 2.02 E-2 | 1.85 E+3 | 5.18 E+5 | -8.1292 | 18.9881 | Y 🟡 |
| *PGN1907* | *PG1726* | *hypothetical protein PG_1977* | | | | | | | | | | | | |
| | | 4.23 E-1 | 2.6 | 1 | 1.3601 | 1.8347 | Y 🟡 | 🔴 R | 0 | 1.69 E+6 | 1 E+3 | 10.7218 | 20.6885 | R 🔴 |
| *PGN1910* | | | | | | | | | | | | | | |
| PG1983 | | 3.05 E-1 | 18.0 | 11.5 | 0.6439 | 4.8811 | Y 🟡 | 🟡 Y | 3.02 E-2 | 1.01 E+7 | 6.9 E+6 | 0.5486 | 24.0194 | Y 🟡 |
| *PGN1928* | *PG1731* | *CRISPR-associated protein TM1791 family* | | | | | | | | | | | | |
| PG1984 | | 3.37 E-1 | 12.0 | 18 | -0.5875 | 4.9059 | Y 🟡 | 🟡 Y | 1.38 E-1 | 4.57 E+6 | 5.11 E+6 | -0.1624 | 23.2062 | Y 🟡 |
| *PGN1929* | *PG1732* | *hypothetical protein PG_1984* | | | | | | | | | | | | |
| PG1985 | | 3.85 E-1 | 15.4 | 10.5 | 0.5527 | 4.6950 | Y 🟡 | 🟡 Y | 3.98 E-2 | 1.09 E+7 | 1.56 E+7 | -0.5164 | 24.6620 | Y 🟡 |
| *PGN1930* | *PG1733* | *CRISPR-associated protein TM1792 family* | | | | | | | | | | | | |
| PG1986 | | 4.93 E-1 | 18.8 | 15 | 0.3276 | 5.0800 | Y 🟡 | 🔴 R | 3.28 E-9 | 6.75 E+6 | 2.66 E+6 | 1.3424 | 23.1665 | R 🔴 |
| *PGN1931* | *PG1734* | *CRISPR-associated protein TM1793 family* | | | | | | | | | | | | |
| PG1987 | | 2.8 E-1 | 11.1 | 18 | -0.6944 | 4.8641 | Y 🟡 | 🟡 Y | 7.67 E-3 | 3.07 E+6 | 5.6 E+6 | -0.8691 | 23.0470 | Y 🟡 |
| *PGN1932* | *PG1735* | *CRISPR-associated protein TM1811 family* | | | | | | | | | | | | |
| PG1988 | | 5.43 E-1 | 16.3 | 19.5 | -0.2624 | 5.1602 | Y 🟡 | 🟡 Y | 1.08 E-1 | 7.7 E+6 | 6.38 E+6 | 0.2708 | 23.7471 | Y 🟡 |
| *PGN1933* | *PG1736* | *hypothetical protein PG_1988* | | | | | | | | | | | | |
| | | 7.43 E-2 | 6.8 | 17 | -1.3124 | 4.5756 | Y 🟡 | 🟡 Y | 8.87 E-3 | 1.87 E+6 | 3.06 E+6 | -0.7107 | 22.2341 | Y 🟡 |
| *PGN1935* | | | | | | | | | | | | | | |
| PG1992 | | 4.21 E-1 | 3.4 | 1.5 | 1.1901 | 2.2994 | Y 🟡 | 🔴 R | 1.36 E-6 | 1.74 E+6 | 4.18 E+5 | 2.0619 | 21.0436 | R 🔴 |
| *PGN1937* | *PG1739* | *gidA glucose-inhibited division protein A* | | | | | | | | | | | | |
| PG1993 | | 6.69 E-1 | 1.7 | 1.5 | 0.1901 | 1.6832 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 1.19 E+5 | -6.0095 | 16.8854 | Y 🟡 |
| *PGN1938* | *PG1740* | *uvrC excinuclease ABC C subunit* | | | | | | | | | | | | |
| PG1994 | | 2.93 E-1 | 6.8 | 3 | 1.1901 | 3.2994 | Y 🟡 | 🔴 R | 2.63 E-5 | 5.2 E+6 | 1.82 E+6 | 1.5127 | 22.7447 | R 🔴 |
| *PGN1939* | *PG1741* | *dtd D-tyrosyl-tRNA(Tyr) deacylase* | | | | | | | | | | | | |
| PG1996 | | 2.66 E-1 | 68.5 | 85 | -0.3124 | 7.2616 | Y 🟡 | 🟡 Y | 3.62 E-2 | 3.48 E+7 | 5.47 E+7 | -0.6539 | 26.4147 | Y 🟡 |
| *PGN1941* | *PG1743* | *deoC deoxyribose-phosphate aldolase* | | | | | | | | | | | | |
| PG1998 | | 1.06 E-1 | 20.5 | 10 | 1.0381 | 4.9324 | Y 🟡 | 🔴 R | 7.32 E-7 | 7.75 E+6 | 3.21 E+6 | 1.2693 | 23.3858 | R 🔴 |
| *PGN1943* | *PG1744* | *polyprenyl synthetase* | | | | | | | | | | | | |
| PG2001 | | 4.4 E-1 | 18.0 | 13.5 | 0.4125 | 4.9758 | Y 🟡 | 🔴 R | 8.78 E-6 | 1.31 E+7 | 6.45 E+6 | 1.0257 | 24.2222 | R 🔴 |
| *PGN1946* | *PG1747* | *lepB signal peptidase I* | | | | | | | | | | | | |
| PG2002 | | 3.99 E-1 | 17.1 | 23 | -0.4265 | 5.3260 | Y 🟡 | 🟡 Y | 4.24 E-2 | 5.19 E+6 | 6.92 E+6 | -0.4146 | 23.5297 | Y 🟡 |
| *PGN1947* | *PG1748* | *dapB dihydrodipicolinate reductase* | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG2003 | | 4.02 E-1 | 7.7 | 4.5 | 0.7751 | 3.6089 | Y | 🟡 | 🟡 | Y | 7.74 E-2 | 1.82 E+6 | 2.56 E+6 | -0.4959 | 22.0617 | Y | 🟡 |
| *PGN1948* | *PG1749* | *dgt deoxyguanosinetriphosphate triphosphohydrolase* | | | | | | | | | | | | | | | |
| PG2008 | | 1.63 E-3 | 17.1 | 44.5 | -1.3787 | 5.9452 | G | 🟢 | 🟢 | G | 1.2 E-8 | 5.14 E+6 | 2.13 E+7 | -2.0541 | 24.6585 | G | 🟢 |
| *PGN1953* | *PG1752* | *TonB-dependent receptor putative* | | | | | | | | | | | | | | | |
| PG2010 | | 2.93 E-1 | 111.2 | 93.5 | 0.2506 | 7.6776 | Y | 🟡 | 🔴 | R | 4.24 E-5 | 7.65 E+7 | 4.96 E+7 | 0.6241 | 26.9096 | R | 🔴 |
| *PGN1955* | *PG1754* | *phosphomannomutase putative* | | | | | | | | | | | | | | | |
| PG2014 | | 5.8 E-1 | 7.7 | 6 | 0.3601 | 3.7762 | Y | 🟡 | 🟡 | Y | 1.74 E-3 | 1.62 E+6 | 8.9 E+5 | 0.8655 | 21.2597 | Y | 🟡 |
| *PGN1960* | *PG1758* | *cas1 CRISPR-associated protein Cas1* | | | | | | | | | | | | | | | |
| PG2015 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟡 | Y | 1.08 E-3 | 1.85 E+3 | 2.66 E+5 | -7.1660 | 18.0297 | Y | 🟡 |
| *PGN1961* | *PG1759* | *cas4 CRISPR-associated protein Cas4* | | | | | | | | | | | | | | | |
| | | 1.09 E-1 | 269.5 | 227 | 0.2478 | 8.9557 | Y | 🟡 | 🔴 | R | 3.5 E-6 | 1.36 E+8 | 9.16 E+7 | 0.5745 | 27.7647 | R | 🔴 |
| *PGN1962* | | | | | | | | | | | | | | | | | |
| | | 6.69 E-1 | 68.5 | 70.5 | -0.0425 | 7.1184 | Y | 🟡 | 🟡 | Y | 2.04 E-2 | 4.56 E+7 | 5.75 E+7 | -0.3362 | 26.6197 | Y | 🟡 |
| *PGN1963* | | | | | | | | | | | | | | | | | |
| PG2016 | | 1.73 E-2 | 1.7 | 11 | -2.6843 | 3.6680 | Y | 🟡 | 🟡 | Y | 2.64 E-3 | 1.85 E+3 | 3.54 E+6 | -10.9034 | 21.7579 | Y | 🟡 |
| *PGN1964* | *PG1760* | *cas3 CRISPR-associated helicase Cas3* | | | | | | | | | | | | | | | |
| | | 3.29 E-1 | 10.3 | 16 | -0.6399 | 4.7152 | Y | 🟡 | 🟡 | Y | 2.53 E-3 | 5.97 E+6 | 9.77 E+6 | -0.7114 | 23.9081 | Y | 🟡 |
| *PGN1965* | | | | | | | | | | | | | | | | | |
| PG2020 | | 3.78 E-1 | 25.7 | 19 | 0.4341 | 5.4812 | Y | 🟡 | 🟡 | Y | 1.01 E-1 | 1.9 E+7 | 1.62 E+7 | 0.2370 | 25.0692 | Y | 🟡 |
| *PGN1966* | *PG1764* | *CRISPR-associated protein TM1814 family* | | | | | | | | | | | | | | | |
| PG2021 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟡 | Y | 1.14 E-3 | 1.85 E+3 | 4.79 E+5 | -8.0154 | 18.8746 | Y | 🟡 |
| *PGN1967* | *PG1765* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG2022 | | 6.49 E-1 | 17.1 | 15.5 | 0.1428 | 5.0274 | Y | 🟡 | 🟡 | Y | 3.76 E-2 | 8.55 E+6 | 6.51 E+6 | 0.3942 | 23.8441 | Y | 🟡 |
| *PGN1968* | *PG1766* | *hypothetical protein PG_2022* | | | | | | | | | | | | | | | |
| PG2023 | | 1.57 E-2 | 40.2 | 19 | 1.0818 | 5.8879 | Y | 🟡 | 🔴 | R | 1.87 E-7 | 1.46 E+7 | 5.87 E+6 | 1.3153 | 24.2883 | R | 🔴 |
| *PGN1969* | *PG1767* | *fmt methionyl-tRNA formyltransferase* | | | | | | | | | | | | | | | |
| | | 4.89 E-2 | 519.4 | 597 | -0.2009 | 10.1246 | Y | 🟡 | 🟡 | Y | 2.79 E-2 | 4.61 E+8 | 5.62 E+8 | -0.2876 | 29.9298 | Y | 🟡 |
| *PGN1970* | | | | | | | | | | | | | | | | | |
| PG2026 | | 2.25 E-1 | 1.7 | 5.5 | -1.6843 | 2.8503 | Y | 🟡 | 🟡 | Y | 4.02 E-3 | 1.85 E+3 | 2.71 E+6 | -10.5186 | 21.3733 | Y | 🟡 |
| *PGN1973* | *PG1769* | *phosphoglycerate mutase family protein* | | | | | | | | | | | | | | | |
| PG2029 | | 4.23 E-1 | 191.7 | 209 | -0.1249 | 8.6463 | Y | 🟡 | 🟡 | Y | 4.45 E-2 | 1.7 E+8 | 1.9 E+8 | -0.1638 | 28.4251 | Y | 🟡 |
| *PGN1976* | *PG1772* | *hypothetical protein PG_2029* | | | | | | | | | | | | | | | |
| PG2031 | | 6.41 E-1 | 6.0 | 5 | 0.2605 | 3.4581 | Y | 🟡 | 🟡 | Y | 6.16 E-2 | 1.21 E+6 | 7.16 E+5 | 0.7569 | 20.8780 | Y | 🟡 |
| *PGN1978* | *PG1774* | *hypothetical protein PG_2031* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG2033 | | 4.93 E-1 | 8.6 | 11.5 | -0.4265 | 4.3260 | Y | 🟡 | 🟡 | Y | 1.01 E-1 | 3.49 E+6 | 2.79 E+6 | 0.3218 | 22.5826 | Y | 🟡 |
| *PGN1980* | *PG1776* | *gltD glutamate synthase small subunit* | | | | | | | | | | | | | | | |
| PG2034 | | 2.92 E-1 | 31.7 | 22.5 | 0.4927 | 5.7591 | Y | 🟡 | 🟡 | Y | 1.52 E-1 | 1.09 E+7 | 1.23 E+7 | -0.1780 | 24.4691 | Y | 🟡 |
| *PGN1981* | *PG1777* | *oxidoreductase FAD-binding putative* | | | | | | | | | | | | | | | |
| PG2036 | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y | 🟡 | 🟡 | Y | 2.02 E-3 | 5.73 E+6 | 1 E+3 | 12.4843 | 22.4504 | Y | 🟡 |
| *PGN1983* | *PG1779* | *ion transporter* | | | | | | | | | | | | | | | |
| PG2040 | | 3.82 E-1 | 1.7 | 4 | -1.2249 | 2.5138 | Y | 🟡 | 🟢 | G | 4.25 E-5 | 1.85 E+3 | 3.36 E+6 | -10.8246 | 21.6791 | G | 🟢 |
| *PGN1986* | *PG1781* | *DNA-binding protein histone-like family* | | | | | | | | | | | | | | | |
| PG2041 | | 6.05 E-2 | 1.7 | 8.5 | -2.3124 | 3.3521 | Y | 🟡 | 🟢 | G | 9.91 E-15 | 1.85 E+3 | 1.94 E+6 | -10.0330 | 20.8881 | G | 🟢 |
| *PGN1987* | *PG1782* | *hypothetical protein PG_2041* | | | | | | | | | | | | | | | |
| PG2042 | | 3.93 E-1 | 4.3 | 7.5 | -0.8099 | 3.5581 | Y | 🟡 | 🟢 | G | 8.96 E-4 | 1.94 E+6 | 3.33 E+6 | -0.7795 | 22.3293 | G | 🟢 |
| *PGN1988* | *PG1783* | *thioredoxin family protein* | | | | | | | | | | | | | | | |
| PG2043 | | 1.45 E-1 | 40.2 | 26 | 0.6292 | 6.0491 | Y | 🟡 | 🟡 | Y | 3.61 E-2 | 8.2 E+6 | 5.92 E+6 | 0.4701 | 23.7510 | Y | 🟡 |
| *PGN1989* | *PG1784* | *conserved hypothetical protein TIGR00486* | | | | | | | | | | | | | | | |
| PG2044 | | 8.62 E-3 | 49.6 | 24 | 1.0481 | 6.2022 | R | 🔴 | 🔴 | R | 6.97 E-4 | 2.88 E+7 | 1.58 E+7 | 0.8676 | 25.4109 | R | 🔴 |
| *PGN1990* | *PG1785* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG2050 | | 1.98 E-2 | 57.3 | 32 | 0.8412 | 6.4811 | Y | 🟡 | 🟡 | Y | 1.94 E-1 | 6.9 E+7 | 6.79 E+7 | 0.0240 | 27.0280 | Y | 🟡 |
| *PGN1995* | *PG1790* | *hypothetical protein PG_2050* | | | | | | | | | | | | | | | |
| PG2052 | | 6.41 E-1 | 16.3 | 18 | -0.1469 | 5.0983 | Y | 🟡 | 🟡 | Y | 1.74 E-1 | 1.35 E+7 | 1.41 E+7 | -0.0636 | 24.7139 | Y | 🟡 |
| *PGN1996* | *PG1791* | *dapA dihydrodipicolinate synthase* | | | | | | | | | | | | | | | |
| PG2053 | | 5.43 E-1 | 2.6 | 1.5 | 0.7751 | 2.0240 | Y | 🟡 | 🔴 | R | 0 | 1.25 E+6 | 1.08 E+6 | 0.2073 | 21.1561 | R | 🔴 |
| *PGN1997* | *PG1792* | *bioD dethiobiotin synthase* | | | | | | | | | | | | | | | |
| PG2054 | | 6.94 E-1 | 35.1 | 35.5 | -0.0171 | 6.1412 | Y | 🟡 | 🟡 | Y | 7.15 E-2 | 2.78 E+7 | 3.69 E+7 | -0.4078 | 25.9486 | Y | 🟡 |
| *PGN1998* | *PG1793* | *lipoprotein PG3* | | | | | | | | | | | | | | | |
| PG2055 | | 6.74 E-1 | 178.0 | 176 | 0.0161 | 8.4675 | Y | 🟡 | 🔴 | R | 1.26 E-6 | 9.21 E+7 | 5.63 E+7 | 0.7112 | 27.1448 | R | 🔴 |
| *PGN1999* | *PG1794* | *dihydroorotate dehydrogenase family protein* | | | | | | | | | | | | | | | |
| PG0052 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 0 | 1.14 E+6 | 1 E+3 | 10.1491 | 20.1161 | R | 🔴 |
| *PGN2001* | *PG0045* | *sensor histidine kinase* | | | | | | | | | | | | | | | |
| PG0054 | | 4.53 E-1 | 9.4 | 13 | -0.4659 | 4.4862 | Y | 🟡 | 🟡 | Y | 1.26 E-2 | 2.46 E+6 | 7.54 E+6 | -1.6130 | 23.2541 | Y | 🟡 |
| *PGN2003* | *PG0046* | *recJ single-stranded-DNA-specific exonuclease RecJ* | | | | | | | | | | | | | | | |
| PG0055 | | 1.06 E-1 | 6.8 | 1.5 | 2.1901 | 3.0610 | Y | 🟡 | 🔴 | R | 3.44 E-15 | 1.46 E+6 | 7.78 E+4 | 4.2320 | 20.5534 | R | 🔴 |
| *PGN2004* | *PG0047* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG0056 | | 5.89 E-1 | 83.0 | 77.5 | 0.0989 | 7.3264 | Y | 🟡 | 🟡 | Y | 1.5 E-1 | 3.04 E+7 | 3.87 E+7 | -0.3479 | 26.0430 | Y | 🟡 |
| *PGN2005* | *PG0048* | *hypothetical protein PG_0056* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PGN** | **LANL** | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0057 | | 7.53 E-2 | 18.0 | 7.5 | 1.2605 | 4.6707 | Y | 🟡 | 🔴 | R | 4.94 E-6 | 3.6 E+6 | 1.72 E+6 | 1.0612 | 22.3439 | R | 🔴 |
| *PGN2006* | *PG0049* | *pncB nicotinate phosphoribosyltransferase* | | | | | | | | | | | | | | | |
| PG0058 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟡 | Y | 3.03 E-2 | 2.92 E+5 | 3.83 E+5 | -0.3949 | 19.3648 | Y | 🟡 |
| *PGN2007* | *PG0050* | *nadD nicotinate (nicotinamide) nucleotide adenylyltransferase* | | | | | | | | | | | | | | | |
| PG0059 | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y | 🟡 | 🔴 | R | 0 | 2.4 E+6 | 1 E+3 | 11.2306 | 21.1970 | R | 🔴 |
| *PGN2008* | *PG0051* | *hypothetical protein PG_0059* | | | | | | | | | | | | | | | |
| PG0062 | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y | 🟡 | 🔴 | R | 0 | 1.77 E+5 | 1 E+3 | 7.4711 | 17.4450 | R | 🔴 |
| *PGN2011* | *PG0053* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG0063 | | 3.21 E-1 | 1.7 | 4.5 | -1.3948 | 2.6349 | Y | 🟡 | 🟡 | Y | 2.02 E-2 | 1.37 E+6 | 3.77 E+6 | -1.4570 | 22.2950 | Y | 🟡 |
| *PGN2012* | *PG0054* | *outer membrane efflux protein* | | | | | | | | | | | | | | | |
| PG0064 | | 3.55 E-1 | 8.6 | 13.5 | -0.6579 | 4.4631 | Y | 🟡 | 🟡 | Y | 2.6 E-2 | 2.19 E+6 | 3.66 E+6 | -0.7364 | 22.4803 | Y | 🟡 |
| *PGN2013* | *PG0055* | *heavy metal efflux pump CzcA family* | | | | | | | | | | | | | | | |
| PG0065 | | 5.89 E-1 | 1.7 | 1 | 0.7751 | 1.4390 | Y | 🟡 | 🔴 | R | 0 | 2.52 E+5 | 1 E+3 | 7.9797 | 17.9511 | R | 🔴 |
| *PGN2014* | *PG0056* | *efflux transporter RND family MFP subunit* | | | | | | | | | | | | | | | |
| PG0069 | | 6.28 E-3 | 11.1 | 31 | -1.4787 | 5.3966 | G | 🟢 | 🟢 | G | 1.49 E-6 | 2.8 E+6 | 6.57 E+6 | -1.2277 | 23.1600 | G | 🟢 |
| *PGN2017* | *PG0058* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0070 | | 8.78 E-3 | 82.1 | 48 | 0.7751 | 7.0240 | R | 🔴 | 🟡 | Y | 1.6 E-1 | 4.76 E+7 | 4.45 E+7 | 0.0974 | 26.4556 | R | 🔴 |
| *PGN2018* | *PG0059* | *lpxA acyl-(acyl-carrier-protein)-UDP-N-acetylglucosamine acyltransferase* | | | | | | | | | | | | | | | |
| PG0071 | | 3.37 E-1 | 123.2 | 106.5 | 0.2103 | 7.8437 | Y | 🟡 | 🟡 | Y | 1.38 E-1 | 8.89 E+7 | 8.37 E+7 | 0.0873 | 27.3629 | Y | 🟡 |
| *PGN2019* | *PG0060* | *UDP-3-O-acyl-GlcNAc deacetylase/beta-hydroxyacyl-[acyl carrier protein] dehydratase FabZ* | | | | | | | | | | | | | | | |
| PG0072 | | 1.21 E-3 | 40.2 | 14 | 1.5223 | 5.7606 | R | 🔴 | 🔴 | R | 3.24 E-7 | 1.75 E+7 | 5.53 E+6 | 1.6592 | 24.4552 | R | 🔴 |
| *PGN2020* | *PG0061* | *lpxD UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase* | | | | | | | | | | | | | | | |
| PG0073 | | 3.2 E-6 | 24.8 | 74 | -1.5764 | 6.6266 | G | 🟢 | 🟢 | G | 1.08 E-8 | 1.63 E+7 | 5.34 E+7 | -1.7128 | 26.0547 | G | 🟢 |
| *PGN2021* | *PG0062* | *orotidine 5'-monophosphate decarboxylase* | | | | | | | | | | | | | | | |
| PG0074 | | 6.05 E-2 | 6.8 | 1 | 2.7751 | 2.9718 | Y | 🟡 | 🔴 | R | 2.58 E-16 | 4.07 E+6 | 1 E+3 | 11.9904 | 21.9566 | R | 🔴 |
| *PGN2022* | *PG0063* | *prfA peptide chain release factor 1* | | | | | | | | | | | | | | | |
| PG0075 | | 2.04 E-4 | 31.7 | 7 | 2.1772 | 5.2727 | R | 🔴 | 🔴 | R | 0 | 8.78 E+6 | 2.08 E+6 | 2.0772 | 23.3731 | R | 🔴 |
| *PGN2023* | *PG0064* | *phosphoribosylformylglycinamidine cyclo-ligase putative* | | | | | | | | | | | | | | | |
| PG0076 | | 5.8 E-1 | 7.7 | 6 | 0.3601 | 3.7762 | Y | 🟡 | 🟡 | Y | 1.17 E-2 | 4.61 E+6 | 2.97 E+6 | 0.6343 | 22.8552 | Y | 🟡 |
| *PGN2024* | *PG0065* | *N-acetylmuramoyl-L-alanine amidase family 4* | | | | | | | | | | | | | | | |
| PG0078 | | 6 E-1 | 1.7 | 2.5 | -0.5468 | 2.0743 | Y | 🟡 | 🟢 | G | 9.28 E-6 | 1.85 E+3 | 4.9 E+5 | -8.0485 | 18.9077 | G | 🟢 |
| *PGN2025* | *PG0066* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG0079 | | 1.16 E-1 | 29.1 | 16.5 | 0.8182 | 5.5107 | Y | 🟡 | 🔴 | R | 1.34 E-6 | 2.24 E+7 | 2.86 E+6 | 2.9678 | 24.5875 | R | 🔴 |
| *PGN2026* | *PG0067* | *abortive infection protein putative* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | PP PPC/ Pg Protein Intensity | | | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PGN* | *LANL* | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | $\log_2$Ratio | $\log_2$Sum | Consensus | |
| PG0081 | | 3.21 E-1 | 1.7 | 4.5 | -1.3948 | 2.6349 | Y | 🟡 | 🟡 | Y | 4.63 E-2 | 1.85 E+3 | 2.67 E+6 | -10.4953 | 21.3501 | Y | 🟡 |
| *PGN2028* | *PG0069* | *hypothetical protein PG_0081* | | | | | | | | | | | | | | | |
| PG0082 | | 2.84 E-2 | 1.7 | 10 | -2.5468 | 3.5498 | Y | 🟡 | 🟢 | G | 8.43 E-6 | 1.85 E+3 | 2.31 E+6 | -10.2863 | 21.1412 | G | 🟢 |
| *PGN2029* | *PG0070* | *hypothetical protein PG_0082* | | | | | | | | | | | | | | | |
| PG0083 | | 1.84 E-1 | 1.7 | 6 | -1.8099 | 2.9470 | Y | 🟡 | 🟢 | G | 1.22 E-5 | 1.85 E+3 | 2.21 E+6 | -10.2189 | 21.0739 | G | 🟢 |
| *PGN2030* | *PG0071* | *hypothetical protein PG_0083* | | | | | | | | | | | | | | | |
| PG0084 | | 4.03 E-1 | 5.1 | 8.5 | -0.7274 | 3.7691 | Y | 🟡 | 🟡 | Y | 6.1 E-3 | 1.23 E+6 | 2.86 E+6 | -1.2224 | 21.9616 | Y | 🟡 |
| *PGN2031* | *PG0072* | *sda L-serine dehydratase iron-sulfur-dependent single chain form* | | | | | | | | | | | | | | | |
| PG0086 | | 1.24 E-1 | 24.8 | 13.5 | 0.8782 | 5.2598 | Y | 🟡 | 🟡 | Y | 2.79 E-2 | 1.01 E+7 | 6.53 E+6 | 0.6313 | 23.9894 | Y | 🟡 |
| *PGN2033* | *PG0074* | *ATP-dependent RNA helicase DEAD/DEAH box family* | | | | | | | | | | | | | | | |
| PG0087 | | 5.43 E-1 | 4.3 | 6 | -0.4879 | 3.3615 | Y | 🟡 | 🟡 | Y | 1.84 E-1 | 2.92 E+6 | 3.05 E+6 | -0.0637 | 22.5082 | Y | 🟡 |
| *PGN2034* | *PG0076* | *SIS domain protein* | | | | | | | | | | | | | | | |
| PG0090 | | 2.77 E-9 | 543.3 | 354 | 0.6181 | 9.8095 | R | 🔴 | 🟡 | Y | 4.61 E-2 | 6.15 E+8 | 5.27 E+8 | 0.2236 | 30.0893 | R | 🔴 |
| *PGN2037* | *PG0079* | *Dps family protein* | | | | | | | | | | | | | | | |
| PG0091 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y | 🟡 | 🟡 | Y | 1.37 E-3 | 1.85 E+3 | 4.37 E+5 | -7.8821 | 18.7419 | Y | 🟡 |
| *PGN2038* | *PG0080* | *transporter putative* | | | | | | | | | | | | | | | |
| PG0092 | | 3.05 E-1 | 3.4 | 1 | 1.7751 | 2.1449 | Y | 🟡 | 🔴 | R | 9.6 E-14 | 9.06 E+5 | 1 E+3 | 9.8241 | 19.7915 | R | 🔴 |
| *PGN2039* | *PG0081* | *transporter putative* | | | | | | | | | | | | | | | |
| PG0093 | | 5.94 E-2 | 11.1 | 3 | 1.8906 | 3.8200 | Y | 🟡 | 🟡 | Y | 2.98 E-3 | 4.75 E+6 | 1.62 E+6 | 1.5514 | 22.6038 | Y | 🟡 |
| *PGN2040* | *PG0082* | *HlyD family secretion protein* | | | | | | | | | | | | | | | |
| PG0094 | | 2.09 E-3 | 23.1 | 53 | -1.1979 | 6.2499 | G | 🟢 | 🟢 | G | 2.79 E-4 | 9.59 E+6 | 3.26 E+7 | -1.7666 | 25.3318 | G | 🟢 |
| *PGN2041* | *PG0083* | *outer membrane efflux protein putative* | | | | | | | | | | | | | | | |
| PG0095 | | 4.23 E-1 | 11.1 | 7.5 | 0.5686 | 4.2191 | Y | 🟡 | 🟡 | Y | 2.1 E-2 | 3.47 E+6 | 2.26 E+6 | 0.6164 | 22.4492 | Y | 🟡 |
| *PGN2042* | *PG0084* | *mutS DNA mismatch repair protein MutS* | | | | | | | | | | | | | | | |
| PG0097 | | 1.9 E-12 | 95.0 | 19 | 2.3216 | 6.8326 | R | 🔴 | 🔴 | R | 0 | 1.93 E+7 | 1.9 E+6 | 3.3446 | 24.3371 | R | 🔴 |
| *PGN2043* | *PG0085* | *conserved hypothetical protein TIGR01033* | | | | | | | | | | | | | | | |
| PG0099 | | 7.94 E-4 | 78.7 | 38.5 | 1.0319 | 6.8731 | R | 🔴 | 🔴 | R | 1.56 E-14 | 4.42 E+7 | 1.92 E+7 | 1.2013 | 25.9196 | R | 🔴 |
| *PGN2045* | *PG0086* | *pheT phenylalanyl-tRNA synthetase beta subunit* | | | | | | | | | | | | | | | |
| PG2072 | | 2.15 E-1 | 4.3 | 1 | 2.0970 | 2.4001 | Y | 🟡 | 🔴 | R | 5.72 E-6 | 1.88 E+6 | 1 E+3 | 10.8767 | 20.8432 | R | 🔴 |
| *PGN2050* | *PG1811* | *UvrD/REP helicase domain protein* | | | | | | | | | | | | | | | |
| PG2070 | | 3.64 E-1 | 5.1 | 9 | -0.8099 | 3.8211 | Y | 🟡 | 🟡 | Y | 3.45 E-2 | 1.05 E+6 | 2.02 E+6 | -0.9389 | 21.5508 | Y | 🟡 |
| *PGN2052* | *PG1809* | *hypothetical protein PG_2070* | | | | | | | | | | | | | | | |
| PG2069 | | 2.52 E-1 | 19.7 | 12 | 0.7137 | 4.9855 | Y | 🟡 | 🔴 | R | 9.57 E-4 | 9.71 E+6 | 4.67 E+6 | 1.0576 | 23.7775 | R | 🔴 |
| *PGN2053* | *PG1808* | *oxidoreductase short chain dehydrogenase/reductase family* | | | | | | | | | | | | | | | |

| TIGR | | PP PPC / Pg Spectral Count | | | | | | | | | PP PPC/ Pg Protein Intensity | | | | | 33277 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Regulation | | | | *q*-value | PP (Norm) | PPC (Norm) | log$_2$Ratio | log$_2$Sum | Consensus | |
| PG2068 | | 1.61 E-1 | 46.2 | 31.5 | 0.5527 | 6.2799 | Y | 🟡 | 🟡 | Y | 1.36 E-1 | 2.92 E+7 | 3.29 E+7 | -0.1717 | 25.8884 | Y | 🟡 |
| *PGN2054* | *PG1807* | *tagD glycerol-3-phosphate cytidylyltransferase* | | | | | | | | | | | | | | | |
| PG2067 | | 4.23 E-1 | 20.5 | 26.5 | -0.3679 | 5.5557 | Y | 🟡 | 🟡 | Y | 2.07 E-2 | 7.97 E+6 | 1.19 E+7 | -0.5766 | 24.2429 | Y | 🟡 |
| *PGN2055* | *PG1806* | *pdxA pyridoxal phosphate biosynthetic protein PdxA* | | | | | | | | | | | | | | | |
| PG2066 | | 2.09 E-1 | 41.1 | 28.5 | 0.5272 | 6.1204 | Y | 🟡 | 🟡 | Y | 1.42 E-3 | 1.95 E+7 | 1.25 E+7 | 0.6433 | 24.9290 | Y | 🟡 |
| *PGN2056* | *PG1805* | *lipoprotein putative* | | | | | | | | | | | | | | | |
| PG2065 | | 6.69 E-1 | 2.6 | 3 | -0.2249 | 2.4769 | Y | 🟡 | 🟢 | G | 0 | 4.9 E+5 | 9.16 E+5 | -0.9037 | 20.4230 | G | 🟢 |
| *PGN2057* | *PG1804* | *conserved hypothetical protein TIGR00048* | | | | | | | | | | | | | | | |
| PG2062 | | 2 E-2 | 39.4 | 19 | 1.0507 | 5.8669 | Y | 🟡 | 🔴 | R | 2.01 E-7 | 2.07 E+7 | 10 E+6 | 1.0484 | 24.8705 | R | 🔴 |
| *PGN2060* | *PG1801* | *hisS histidyl-tRNA synthetase* | | | | | | | | | | | | | | | |
| PG2061 | | 5.43 E-1 | 3.4 | 5 | -0.5468 | 3.0743 | Y | 🟡 | 🔴 | R | 5.28 E-4 | 1.25 E+6 | 7.29 E+5 | 0.7782 | 20.9166 | Y | 🟡 |
| *PGN2061* | *PG1800* | *folA dihydrofolate reductase* | | | | | | | | | | | | | | | |
| PG2060 | | 7.06 E-1 | 18.0 | 18 | -0.0025 | 5.1687 | Y | 🟡 | 🟡 | Y | 1.07 E-2 | 9.94 E+6 | 6.34 E+6 | 0.6493 | 23.9569 | Y | 🟡 |
| *PGN2062* | *PG1799* | *thyA thymidylate synthase* | | | | | | | | | | | | | | | |
| PG2197 | | 5.74 E-1 | 4.3 | 3 | 0.5121 | 2.8636 | Y | 🟡 | 🔴 | R | 1.77 E-4 | 1.44 E+6 | 1.47 E+5 | 3.2877 | 20.5953 | R | 🔴 |
| *PGN2064* | *PG1921* | *conserved hypothetical protein* | | | | | | | | | | | | | | | |
| PG2024 | | 4.23 E-1 | 3.4 | 6 | -0.8099 | 3.2361 | Y | 🟡 | 🟡 | Y | 6.09 E-3 | 1.45 E+7 | 1.79 E+6 | 3.0116 | 23.9537 | Y | 🟡 |
| *PGN2065* | *PG1768* | *hagE hemagglutinin protein HagE* | | | | | | | | | | | | | | | |
| PG2199 | | 4.02 E-1 | 4.3 | 2 | 1.0970 | 2.6504 | Y | 🟡 | 🔴 | R | 0 | 1.44 E+6 | 3.97 E+5 | 1.8628 | 20.8118 | R | 🔴 |
| *PGN2066* | *PG1923* | *ABC transporter ATP-binding protein putative* | | | | | | | | | | | | | | | |
| PG2200 | | 3.06 E-1 | 4.3 | 1.5 | 1.5121 | 2.5306 | Y | 🟡 | 🔴 | R | 0 | 1.33 E+6 | 1.86 E+5 | 2.8385 | 20.5338 | R | 🔴 |
| *PGN2067* | *PG1924* | *TPR domain protein* | | | | | | | | | | | | | | | |
| PG2201 | | 6.49 E-1 | 15.4 | 17 | -0.1424 | 5.0180 | Y | 🟡 | 🟡 | Y | 1.74 E-1 | 4.65 E+6 | 4.88 E+6 | -0.0699 | 23.1830 | Y | 🟡 |
| *PGN2068* | *PG1925* | *def polypeptide deformylase* | | | | | | | | | | | | | | | |
| PG2204 | | 1.55 E-3 | 63.3 | 110 | -0.7968 | 7.4373 | G | 🟢 | 🟡 | Y | 7.49 E-3 | 3.52 E+7 | 4.58 E+7 | -0.3799 | 26.2723 | G | 🟢 |
| *PGN2070* | *PG1927* | *hypothetical protein PG_2204* | | | | | | | | | | | | | | | |
| PG2205 | | 3.76 E-1 | 16.3 | 22.5 | -0.4688 | 5.2764 | Y | 🟡 | 🟡 | Y | 3.53 E-2 | 7.93 E+6 | 1.03 E+7 | -0.3817 | 24.1220 | Y | 🟡 |
| *PGN2071* | *PG1928* | *panE 2-dehydropantoate 2-reductase* | | | | | | | | | | | | | | | |
| PG2206 | | 2.52 E-4 | 29.1 | 6 | 2.2776 | 5.1331 | R | 🔴 | 🔴 | R | 0 | 1.39 E+7 | 2.66 E+6 | 2.3868 | 23.9838 | R | 🔴 |
| *PGN2072* | *PG1929* | *ABC transporter ATP-binding protein* | | | | | | | | | | | | | | | |
| PG2207 | | 2.62 E-2 | 71.0 | 43.5 | 0.7072 | 6.8394 | Y | 🟡 | 🟡 | Y | 1.67 E-3 | 5.2 E+7 | 3.01 E+7 | 0.7881 | 26.2909 | Y | 🟡 |
| *PGN2073* | *PG1931* | *conserved domain protein* | | | | | | | | | | | | | | | |
| PG2210 | | 4.75 E-1 | 14.5 | 11 | 0.4031 | 4.6750 | Y | 🟡 | 🔴 | R | 6.76 E-5 | 4.1 E+6 | 1.82 E+6 | 1.1718 | 22.4971 | R | 🔴 |
| *PGN2075* | *PG1934* | *uvrA-2 excinuclease ABC A subunit* | | | | | | | | | | | | | | | |

| **TIGR** | | **PP PPC / Pg Spectral Count** | | | | | | | **PP PPC/ Pg Protein Intensity** | | | | | **33277** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***PGN*** | ***LANL*** | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Regulation** | | ***q*-value** | **PP (Norm)** | **PPC (Norm)** | **log$_2$Ratio** | **log$_2$Sum** | **Consensus** |
| PG2215 | | 7.2 E-3 | 43.6 | 19.5 | 1.1621 | 5.9804 | R 🔴 | 🔴 R | 3.64 E-4 | 4.38 E+7 | 2.29 E+7 | 0.9377 | 25.9920 | R 🔴 |
| *PGN2079* | *PG1936* | *manC mannose-1-phosphate guanylyltransferase* | | | | | | | | | | | | |
| PG2216 | | 5.77 E-2 | 26.5 | 45.5 | -0.7785 | 6.1704 | Y 🟡 | 🟡 Y | 1.11 E-3 | 1.47 E+7 | 2.14 E+7 | -0.5369 | 25.1055 | Y 🟡 |
| *PGN2080* | *PG1938* | *hypothetical protein PG_2216* | | | | | | | | | | | | |
| PG2217 | | 4.23 E-1 | 17.1 | 12.5 | 0.4532 | 4.8882 | Y 🟡 | 🟡 Y | 1.13 E-1 | 7.09 E+6 | 5.96 E+6 | 0.2511 | 23.6374 | Y 🟡 |
| *PGN2081* | *PG1939* | *dxs deoxyxylulose-5-phosphate synthase* | | | | | | | | | | | | |
| PG2218 | | 4.75 E-1 | 3.4 | 5.5 | -0.6843 | 3.1575 | Y 🟡 | 🟡 Y | 2.23 E-2 | 1.98 E+6 | 1.38 E+6 | 0.5149 | 21.6807 | Y 🟡 |
| *PGN2082* | *PG1940* | *trkA potassium uptake protein TrkA* | | | | | | | | | | | | |
| PG2221 | | 6.46 E-4 | 1.7 | 17 | -3.3124 | 4.2258 | G 🟢 | 🟢 G | 8.33 E-7 | 1.85 E+3 | 3.01 E+6 | -10.6698 | 21.5244 | G 🟢 |
| *PGN2085* | *PG1942* | *MiaB-like tRNA modifying enzyme* | | | | | | | | | | | | |
| PG2222 | | 6.97 E-1 | 3.4 | 3.5 | -0.0323 | 2.7913 | Y 🟡 | 🔴 R | 1.05 E-5 | 2.63 E+6 | 6.66 E+5 | 1.9787 | 21.6506 | Y 🟡 |
| *PGN2086* | *PG1943* | *acyltransferase HtrB/MsbB family* | | | | | | | | | | | | |
| PG2223 | | 6.69 E-1 | 1.7 | 2 | -0.2249 | 1.8919 | Y 🟡 | 🟢 G | 0 | 1.85 E+3 | 9.43 E+4 | -5.6705 | 16.5523 | G 🟢 |
| *PGN2087* | *PG1944* | *glycosyl transferase group 2 family protein* | | | | | | | | | | | | |
| PG2227 | | 6.77 E-1 | 4.3 | 4 | 0.0970 | 3.0493 | Y 🟡 | 🟡 Y | 1.29 E-1 | 2.33 E+6 | 2.7 E+6 | -0.2109 | 22.2629 | Y 🟡 |
| *PGN2091* | | *hypothetical protein PG_2227* | | | | | | | | | | | | |