|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **COG description** | **COG** | **Gen #** | **Fr Gen** | **Expect S3** | **Actual S3 #** | **Fr Actual S3** | **RR S3/**  **Gen** | **G** |
| **Information storage and processing** |  |  |  |  |  |  |  |  |
| Translation, ribosomal structure and biogenesis | J | 172 | 0.045 | 14.9 | 35 | 0.106 | + 2.36 | 21.03\*\* |
| Transcription | K | 264 | 0.069 | 22.8 | 21 | 0.064 | - 1.08 | 0.15 |
| Replication, recombination and repair | L | 296 | 0.077 | 25.4 | 21 | 0.064 | - 1.21 | 0.88 |
| **Cellular processes and signaling** |  |  |  |  |  |  |  |  |
| Cell cycle control, cell division, chrom. partitioning | D | 21 | 0.006 | 2.0 | 4 | 0.012 | + 2.02 | 1.60 |
| Defense mechanisms | V | 70 | 0.018 | 5.9 | 5 | 0.015 | - 1.19 | 0.16 |
| Signal transduction mechanisms | T | 162 | 0.042 | 13.9 | 3 | 0.009 | - 4.62 | 12.91\* |
| Cell wall/membrane/envelope biogenesis | M | 97 | 0.025 | 8.3 | 12 | 0.036 | + 1.45 | 1.54 |
| Cell motility | N | 56 | 0.015 | 5.0 | 1 | 0.003 | - 4.95 | 4.75 |
| Intracell. trafficking, secretion & vesicular transport | U | 20 | 0.005 | 1.7 | 0 | 0 | - inf. | 3.31 |
| Posttransl. Mod., protein turnover, chaperones | O | 114 | 0.030 | 9.9 | 17 | 0.052 | + 1.72 | 4.34 |
| **Metabolism** |  |  |  |  |  |  |  |  |
| Energy production and conversion | C | 221 | 0.058 | 19.1 | 27 | 0.082 | + 1.41 | 3.06 |
| Carbohydrate transport and metabolism | G | 154 | 0.040 | 13.2 | 17 | 0.052 | + 1.29 | 1.05 |
| Amino acid transport and metabolism | E | 360 | 0.094 | 31.0 | 48 | 0.145 | + 1.55 | 8.93 |
| Nucleotide transport and metabolism | F | 79 | 0.021 | 6.9 | 5 | 0.015 | - 1.39 | 0.61 |
| Coenzyme transport and metabolism | H | 128 | 0.033 | 10.9 | 25 | 0.076 | + 2.30 | 13.96\* |
| Lipid transport and metabolism | I | 82 | 0.021 | 6.9 | 22 | 0.067 | + 3.17 | 21.40\*\* |
| Inorganic ion transport and metabolism | P | 177 | 0.046 | 15.2 | 13 | 0.039 | - 1.17 | 0.34 |
| Secondary metabol., biosyn. transp. & catabolism | Q | 53 | 0.014 | 4.6 | 8 | 0.024 | + 1.73 | 2.06 |
| **Poorly characterized** |  |  |  |  |  |  |  |  |
| General function prediction only | R | 416 | 0.108 | 35.6 | 21 | 0.064 | - 1.70 | 7.78 |
| Unknown | S | 900 | 0.234 | 77.2 | 25 | 0.076 | - 3.09 | 58.13\*\* |
| **Total classified** |  | **3842** |  |  | **330** |  |  |  |
| **unclassified** | **-** | **442** |  |  | **1** |  |  |  |
| **Total** |  | **4284** |  |  | **331** |  |  |  |

Table 5-3. Relative representation (RR) of COG groupings of proteins found to co-purify with SAMP3 in the presence of UbaA compared to the proteins deduced from genome sequencea.

aFunctional categories of clusters of orthologous genes (COGs) (http://www.ncbi.nlm.nih.gov/COG), as updated for Archaea by Wolf *et al.* (Wolf *et al*., 2012). Gen #, COG groupings of proteins deduced from the *Hfx. volcanii* DS2 genome sequence (Hartman *et al.*, 2010) according to Wolf *et al.* (Wolf *et al*., 2012). Fr Gen, fraction of the total number of deduced proteins classified. Expect S3, COG distribution of SAMP3 A90K associated proteins enriched in wild-type (compared to *ΔubaA*) predicted based on the number of SAMP3 A90K associated proteins identified by MS that were classified to COGs (330 proteins) compared to Fr Gen. Actual S3 # and Fr Actual S3, COG distribution and fraction of the total number of classified proteins identified by MS to be SAMP3 A90K associated, respectively. RR S3/Gen, relative ratio of fractions of proteins identified by MS of SAMP3 samples (S3) and deduced from genome sequence (Gen), indicated as S3/Gen if S3 > Gen (S3 over-represented), and as –Gen/S3 if Gen > S3 (S3 under-represented). G, G-test on RR of S3 compared to Gen (where \* designates p < 0.001, \*\* designates p < 0.0001).