

| PMC Strains |     |     |     | Gene   | Encoding Protein Function   | COG category   |
|-------------|-----|-----|-----|--------|---|--|
| 627         | 638 | 644 | -   | glsF   | PFAM Conserved region in glutamate synthase                           | C - Energy production and conversion                           |
| 627         | -   | -   | -   | ntaA_2 | Nitrilotriacetate monooxygenase component A                           | C - Energy production and conversion                           |
| 627         | -   | -   | -   | ssuD   | Alkanesulfonate monooxygenase   | C - Energy production and conversion                           |
| -           | 638 | -   | -   | parA   | chromosome partitioning   | D - Cell cycle control, cell division, chromosome partitioning |
| 627         | 638 | -   | 649 | aroQ   | 3-dehydroquinate dehydratase  | E - Amino acid transport and metabolism                        |
| 627         | 638 | -   | -   | cdd    | Cytidine deaminase  | F - Nucleotide transport and metabolism                        |
| -           | 638 | -   | -   | tktC   | Transketolase   | G - Carbohydrate transport and metabolism                      |
| 627         | 638 | -   | 649 | fdtB   | Aminotransferase  | H - Coenzyme transport and metabolism                          |
| 627         | 638 | 644 | -   | rpaB   | Two-component response regulator                                      | K - Transcription  |
| -           | 638 | 644 | -   | nblR   | Response regulator receiver domain                                    | K - Transcription  |
| 627         | -   | 644 | -   | cmr4   | CRISPR system Cmr endoribonuclease                                    | L - Replication, recombination and repair                      |
| 627         | -   | 644 | -   | xerC   | Tyrosine recombinase  | L - Replication, recombination and repair                      |
| 627         | -   | -   | -   | cmr6   | CRISPR system Cmr subunit   | L - Replication, recombination and repair                      |
| -           | 638 | 644 | 649 | mrr    | Type IV methyl-directed restriction enzyme                            | L - Replication, recombination and repair                      |
| -           | 638 | 644 | -   | hup    | DNA-binding protein   | L - Replication, recombination and repair                      |
| -           | 638 | -   | -   | res    | Type III restriction enzyme, res subunit                              | L - Replication, recombination and repair                      |
| -           | -   | -   | 649 | rnhC   | Ribonuclease HIII   | L - Replication, recombination and repair                      |
| 627         | 638 | 644 | -   | murB   | UDP-N-acetylenolpyruvoylglucosamine reductase                         | M - Cell wall/membrane/envelope biogenesis                     |
| 627         | 638 | 644 | -   | murC   | UDP-N-acetylmuramate--L-alanine ligase                                | M - Cell wall/membrane/envelope biogenesis                     |
| 627         | 638 | -   | 649 | wbsE   | Putative glycosyl transferase   | M - Cell wall/membrane/envelope biogenesis                     |
| 627         | -   | 644 | -   | kdsA   | 2-dehydro-3-deoxyphosphooctonate aldolase                             | M - Cell wall/membrane/envelope biogenesis                     |
| 627         | -   | 644 | -   | kdsB   | 3-deoxy-manno-octulosonate cytidyltransferase                         | M - Cell wall/membrane/envelope biogenesis                     |
| 627         | -   | 644 | -   | kpsF   | Arabinose 5-phosphate isomerase                                       | M - Cell wall/membrane/envelope biogenesis                     |
| -           | 638 | -   | 649 | gumK   | UDP-glucuronate:glycolipid 2-beta-glucuronosyltransferase             | M - Cell wall/membrane/envelope biogenesis                     |
| -           | -   | 644 | 649 | mtfB   | Glycosyl transferases group 1   | M - Cell wall/membrane/envelope biogenesis                     |
| 627         | -   | -   | -   | ssuB   | Aliphatic sulfonates import ATP-binding protein                       | P - Inorganic ion transport and metabolism                     |
| 627         | -   | -   | -   | ssuC   | Putative aliphatic sulfonates transport permease protein              | P - Inorganic ion transport and metabolism                     |
| -           | -   | 644 | 649 | cutA   | Divalent-cation tolerance protein                                     | P - Inorganic ion transport and metabolism                     |
| 627         | 638 | 644 | -   | psaX   | Photosystem I 4.8 kDa protein   | S - Function unknown   |
| 627         | 638 | -   | 649 | wbpD   | UDP-2-acetamido-3-amino-2,3-dideoxy-D-glucuronate N-acetyltransferase | S - Function unknown   |
| 627         | 638 | -   | -   | yqcl   | Uncharacterized protein   | S - Function unknown   |
| 627         | -   | 644 | 649 | crm2-2 | CRISPR-associated protein Cas10 Cmr2, subtype III-B                   | S - Function unknown   |
| -           | -   | 644 | -   | yxal   | Uncharacterized protein   | S - Function unknown   |
| -           | 638 | -   | 649 | hsdM   | Type I restriction system adenine methylase                           | V - Defense mechanisms   |
| -           | -   | 644 | -   | hsdS   | Type I restriction modification DNA specificity domain (methylase)    | V - Defense mechanisms   |

| PMC Strains |     |     |     | Gene   | Biological process / Pathway (from Uniprot)  |
|-------------|-----|-----|-----|--------|--|
| 627         | 638 | 644 | -   | glsF   | Amino-acid biosynthesis; Glutamate biosynthesis  |
| 627         | -   | -   | -   | ntaA_2 | -  |
| 627         | -   | -   | -   | ssuD   | Cellular response to sulfur starvation; Response to heat   |
| -           | 638 | -   | -   | parA   | Plasmid partitioning   |
| 627         | 638 | -   | 649 | aroQ   | Amino-acid biosynthesis; Aromatic amino acid biosynthesis  |
| 627         | 638 | -   | -   | cdd    | Cytidine deamination; deoxycytidine catabolic process; nucleobase-containing small molecule interconversion  |
| -           | 638 | -   | -   | tktC   | Pentose-phosphate shunt, oxidative branch; reductive pentose-phosphate cycle   |
| 627         | 638 | -   | 649 | fdtB   | -  |
| 627         | 638 | 644 | -   | rpaB   | Phosphorelay signal transduction system  |
| -           | 638 | 644 | -   | nblR   | Phosphorelay signal transduction system; Biological Process; Regulation of DNA-templated transcription   |
| 627         | -   | 644 | -   | cmr4   | -  |
| 627         | -   | 644 | -   | xerC   | -  |
| 627         | -   | -   | -   | cmr6   | -  |
| -           | 638 | 644 | 649 | mrr    | Restriction system   |
| -           | 638 | 644 | -   | hup    | DNA condensation   |
| -           | 638 | -   | -   | res    | Toxin-antitoxin system   |
| -           | -   | -   | 649 | rnhC   | DNA replication, removal of RNA primer; Mismatch repair  |
| 627         | 638 | 644 | -   | murB   | Cell wall biogenesis; peptidoglycan biosynthesis.  |
| 627         | 638 | 644 | -   | murC   | Cell wall biogenesis; peptidoglycan biosynthesis.  |
| 627         | 638 | -   | 649 | wbsE   | -  |
| 627         | -   | 644 | -   | kdsA   | Carbohydrate biosynthesis; 3-deoxy-D-manno-octulosonate biosynthesis; 3-deoxy-D-manno-octulosonate from D-ribulose 5-phosphate: step 2/3.<br>Bacterial outer membrane biogenesis; lipopolysaccharide biosynthesis.                           |
| 627         | -   | 644 | -   | kdsB   | Nucleotide-sugar biosynthesis; CMP-3-deoxy-D-manno-octulosonate biosynthesis; CMP-3-deoxy-D-manno-octulosonate from 3-deoxy-D-manno-octulosonate and CTP: step 1/1.<br>Bacterial outer membrane biogenesis; lipopolysaccharide biosynthesis. |
| 627         | -   | 644 | -   | kpsF   | Lipopolysaccharide biosynthesis  |
| -           | 638 | -   | 649 | gumK   | Glycan biosynthesis; xanthan biosynthesis.   |
| -           | -   | 644 | 649 | mtfB   | Methylation  |
| 627         | -   | -   | -   | ssuB   | Cellular response to sulfur starvation   |
| 627         | -   | -   | -   | ssuC   | Transport  |
| -           | -   | 644 | 649 | cutA   | Response to copper ion   |
| 627         | 638 | 644 | -   | psaX   | Photosynthesis   |
| 627         | 638 | -   | 649 | wbpD   | Bacterial outer membrane biogenesis; LPS O-antigen biosynthesis.   |
| 627         | 638 | -   | -   | yqcl   | -  |
| 627         | -   | 644 | 649 | crm2-2 | -  |
| -           | -   | 644 | -   | yxal   | -  |
| -           | 638 | -   | 649 | hsdM   | DNA restriction-modification system  |
| -           | -   | 644 | -   | hsdS   | DNA restriction-modification system  |

| PMC Strains |     |     |     | Gene   | Comments   | Reference  |
|-------------|-----|-----|-----|--------|--|--|
| 627         | 638 | 644 | -   | glsF   | glutamate biosynthesis   |  |
| 627         | -   | -   | -   | ntaA_2 | long-chain alkane monooxygenase - Unclassified: metabolism   |  |
| 627         | -   | -   | -   | ssuD   | <b>cellular response to sulfur starvation</b>  |  |
| -           | 638 | -   | -   | parA   | -  |  |
| 627         | 638 | -   | 649 | aroQ   | chorismate biosynthesis  |  |
| 627         | 638 | -   | -   | cdd    | scavenges exogenous and endogenous cytidine and 2'-deoxycytidine for UMP synthesis                             |  |
| -           | 638 | -   | -   | tktC   | Carbohydrate biosynthesis  |  |
| 627         | 638 | -   | 649 | fdtB   | -  |  |
| 627         | 638 | 644 | -   | rpaB   | <b>OmpR/PhoB family - regulation of energy transfer of excitation from phycobilisomes to photosystems</b>      | Ashby MK, et al. FEMS Microbiol Lett. (2022) Aug 27;214(1):25-30.    |
| -           | 638 | 644 | -   | nblR   | <b>OmpR/PhoB family - phycobilisome degradation/acclimation responses after nutrient or high-light stress.</b> | R. Schwarz, A.R. Grossman. Proc. Natl. Acad. Sci. U. S. A. (1998) 95 |
| 627         | -   | 644 | -   | cmr4   | -  |  |
| 627         | -   | 644 | -   | xerC   | Phage integrase family   |  |
| 627         | -   | -   | -   | cmr6   | -  |  |
| -           | 638 | 644 | 649 | mrr    | Mrr is involved in the RecB-dependent high pressure induction of the SOS stress response in E. coli.           |  |
| -           | 638 | 644 | -   | hup    | -  |  |
| -           | 638 | -   | -   | res    | -  |  |
| -           | -   | -   | 649 | rnhC   | Endonuclease that specifically degrades the RNA of RNA-DNA hybrids.  |  |
| 627         | 638 | 644 | -   | murB   | peptidoglycan biosynthesis   |  |
| 627         | 638 | 644 | -   | murC   | peptidoglycan biosynthesis   |  |
| 627         | 638 | -   | 649 | wbsE   | -  |  |
| 627         | -   | 644 | -   | kdsA   | 3-deoxy-D-manno-octulosonate biosynthesis - Carbohydrate biosynthesis.   |  |
| 627         | -   | 644 | -   | kdsB   | CMP-3-deoxy-D-manno-octulosonate biosynthesis - Nucleotide-sugar biosynthesis.                                 |  |
| 627         | -   | 644 | -   | kpsF   | Involved in the biosynthesis of K-antigen capsules.  |  |
| -           | 638 | -   | 649 | gumK   | xanthan biosynthesis - Glycan biosynthesis.  |  |
| -           | -   | 644 | 649 | mtfB   | -  |  |
| 627         | -   | -   | -   | ssuB   | <b>cellular response to sulfur starvation</b>  |  |
| 627         | -   | -   | -   | ssuC   | <b>cellular response to sulfur starvation</b>  |  |
| -           | -   | 644 | 649 | cutA   | Involved in resistance toward heavy metals.  |  |
| 627         | 638 | 644 | -   | psaX   | <b>accessory protein potentially involved in chlorophyll stabilization</b>                                     | Çoruh O, et al. Commun Biol. 2021 Mar 8;4(1):304.                    |
| 627         | 638 | -   | 649 | wbpD   | LPS O-antigen biosynthesis and in Bacterial outer membrane biogenesis.   |  |
| 627         | 638 | -   | -   | yqcl   | -  |  |
| 627         | -   | 644 | 649 | crm2-2 | -  |  |
| -           | -   | 644 | -   | yxal   | -  |  |
| -           | 638 | -   | 649 | hsdM   | -  |  |
| -           | -   | 644 | -   | hsdS   | -  |  |