**Table S4.** Genes up-regulated in late log phase by Ax21

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  |  | **Fold up-regulated** | | |
| **Locus ID** | **Common name** | **COG ID** | **Early log** | **Mid log** | **Late log** |
| PXO\_00005 | PDZ domain family protein | COG3975R |  |  | 1.81 |
| PXO\_00059 | beta-ketoadipate enol-lactone hydrolase | COG0596R |  |  | 1.98 |
| PXO\_00106 | conserved hypothetical protein |  |  |  | 1.74 |
| PXO\_00128 | conserved hypothetical protein |  |  |  | 1.92 |
| PXO\_00136 | transcriptional regulator | COG0583K |  |  | 3.37 |
| PXO\_00159 | ribosomal RNA large subunit methyltransferase J | COG0293J |  |  | 1.75 |
| PXO\_00399 | major cold shock protein | COG1278K |  | 1.93 | 2.00 |
| PXO\_00467 | metabolite transport protein |  |  | 2.75 | 7.69 |
| PXO\_00524 | preprotein translocase, (YajC) | COG1862U |  |  | 1.77 |
| PXO\_00526 | S-adenosylmethionine:tRNA ribosyltransferase-isomerase | COG0809J |  |  | 15.25 |
| PXO\_00602 | succinate dehydrogenase, flavoprotein subunit | COG1053C |  |  | 1.82 |
| PXO\_00605 | conserved hypothetical protein | COG5508S |  |  | 1.76 |
| PXO\_00696 | N-acetylmuramoyl-L-alanine amidase | COG0860M |  |  | 1.78 |
| PXO\_00853 | oxidoreductase | COG0277C |  |  | 2.54 |
| PXO\_00872 | segregation and condensation protein B, putative | COG1386K |  |  | 2.39 |
| PXO\_00873 | segregation and condensation protein A | COG1354S |  |  | 2.38 |
| PXO\_00929 | poly-beta-hydroxybutyrate PHB polymerase | COG3243I |  |  | 3.01 |
| PXO\_01121 | outer membrane antigen | COG4775M |  |  | 2.16 |
| PXO\_01151 | bacterioferritin | COG2193P |  |  | 2.59 |
| PXO\_01156 | multidrug resistance efflux pump | COG1566V |  |  | 1.80 |
| PXO\_01181 | ferric uptake regulator (Fur) | COG0735P |  |  | 1.87 |
| PXO\_01184 | heat shock protein (GrpE) | COG0576O |  |  | 2.07 |
| PXO\_01274 | phosphoglucosamine mutase (GlmM) | COG1109G |  |  | 1.79 |
| PXO\_01295 | NADH-quinone oxidoreductase chain 9 | COG1143C |  |  | 1.91 |
| PXO\_01296 | NADH-ubiquinone oxidoreductase Nqo10 subunit | COG0839C |  | 2.33 | 1.99 |
| PXO\_01299 | NADH dehydrogenase subunit M | COG1008C |  | 2.06 | 2.29 |
| PXO\_01301 | YhbC | COG0779S |  |  | 1.83 |
| PXO\_01303 | translation initiation factor IF-2 | COG0532J |  |  | 1.82 |
| PXO\_01353 | P2 phage tail completion protein R (GprR) |  |  |  | 3.65 |
| PXO\_01373 | fimbrial biogenesis protein |  |  |  | 1.78 |
| PXO\_01386 | ribosomal protein L20 | COG0292J |  |  | 1.74 |
| PXO\_01524 | GntY | COG0694O |  |  | 1.80 |
| PXO\_01552 | aspartyl-tRNA synthetase | COG0173J |  |  | 1.97 |
| PXO\_01631 | membrane-fusion protein | COG1566V |  |  | 2.21 |
| PXO\_01654 | glycine cleavage system T protein | COG0404E |  |  | 2.85 |
| PXO\_01772 | conserved hypothetical protein |  |  |  | 1.90 |
| PXO\_01779 | dehydrogenase | COG2907R |  |  | 2.05 |
| PXO\_01820 | acetyl-CoA carboxylase, carboxyl transferase, alpha subunit | COG0825I |  |  | 1.83 |
| PXO\_01908 | peptidyl-prolyl cis-trans isomerase | COG1047O |  |  | 1.86 |
| PXO\_01927 | diaminopimelate decarboxylase (LysA) | COG0019E |  |  | 2.07 |
| PXO\_01945 | transcriptional regulator, LysR family | COG0583K |  | 2.86 | 2.29 |
| PXO\_01948 | xylanase | COG0657I |  | 4.17 | 5.43 |
| PXO\_01988 | bacterial DNA-binding protein |  |  | 1.80 | 1.93 |
| PXO\_02037 | conserved hypothetical protein |  |  |  | 2.30 |
| PXO\_02047 | Hcp family protein | COG3157S |  | 2.02 | 1.99 |
| PXO\_02088 | LexA repressor | COG1974KT |  |  | 1.76 |
| PXO\_02106 | transcriptional regulator AraC/XylS family | COG2207K |  |  | 1.95 |
| PXO\_02108 | conserved hypothetical protein |  |  | 1.90 | 2.08 |
| PXO\_02124 | siroheme synthase (CysG) | COG0007H |  |  | 3.62 |
| PXO\_02158 | ATP-dependent chaperone (ClpB) | COG0542O |  |  | 1.86 |
| PXO\_02159 | conserved hypothetical protein |  |  |  | 1.75 |
| PXO\_02189 | lipoprotein, putative | COG5463S |  |  | 3.10 |
| PXO\_02229 | conserved hypothetical protein | COG1934S |  |  | 1.76 |
| PXO\_02236 | conserved hypothetical protein |  |  |  | 2.05 |
| PXO\_02237 | conserved hypothetical protein |  |  |  | 1.89 |
| PXO\_02249 | succinyl-diaminopimelate desuccinylase | COG0624E |  |  | 1.90 |
| PXO\_02250 | DNA transport competence protein | COG1555L | 3.93 | 2.06 | 4.65 |
| PXO\_02262 | putative cytochrome C assembly protein | COG4137R |  |  | 9.49 |
| PXO\_02286 | TdcF | COG0251J |  |  | 1.76 |
| PXO\_02303 | two-component system regulatory protein | COG0745TK |  |  | 1.99 |
| PXO\_02305 | two-component system sensor protein | COG0642T |  |  | 1.74 |
| PXO\_02338 | ErfK/YbiS/YcfS/YnhG | COG1376S |  |  | 1.81 |
| PXO\_02364 | guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase ((ppGpp)ase) | COG0317TK |  |  | 1.86 |
| PXO\_02380 | conserved hypothetical protein |  |  |  | 1.86 |
| PXO\_02433 | peptide deformylase | COG0242J |  |  | 2.33 |
| PXO\_02469 | RNase H | COG0328L |  |  | 1.83 |
| PXO\_02552 | TonB-dependent outer membrane receptor | COG1629P |  |  | 1.89 |
| PXO\_02597 | conserved hypothetical protein |  |  |  | 1.98 |
| PXO\_02600 | TonB-dependent receptor | COG4206H |  | 1.86 | 3.84 |
| PXO\_02637 | regulatory protein (PilH) | COG0745TK |  |  | 1.80 |
| PXO\_02662 | putative permease, YjgP/YjgQ family | COG0795R |  |  | 2.15 |
| PXO\_02698 | crispr-associated protein, Csd2 family | COG3649L |  |  | 1.89 |
| PXO\_02700 | crispr-associated protein Cas5, subtype |  |  |  | 1.81 |
| PXO\_02802 | tryptophan halogenase |  |  |  | 12.02 |
| PXO\_02898 | ribonucleoside-diphosphate reductase, beta subunit | COG0208F | 1.75 | 2.08 | 1.81 |
| PXO\_02951 | conserved hypothetical protein | COG1506E |  |  | 1.86 |
| PXO\_02996 | DNA-binding protein (Fis) | COG2901KL |  |  | 2.08 |
| PXO\_03116 | conserved hypothetical protein |  |  |  | 12.12 |
| PXO\_03130 | lactoylglutathione lyase | COG0346E |  |  | 3.78 |
| PXO\_03158 | putative methyltransferase |  |  | 2.48 | 2.38 |
| PXO\_03161 | putative glycosyltransferase | COG0438M |  | 2.18 | 2.35 |
| PXO\_03168 | electron transfer flavoprotein beta subunit | COG2086C |  |  | 1.85 |
| PXO\_03208 | toluene tolerance protein (Ttg2D) | COG2854Q |  |  | 1.87 |
| PXO\_03211 | ABC transporter ATP-binding protein | COG1127Q |  |  | 1.82 |
| PXO\_03322 | lipoprotein, putative |  |  |  | 1.85 |
| PXO\_03344 | acriflavin resistance protein | COG1566V |  |  | 2.13 |
| PXO\_03430 | conserved hypothetical protein |  |  |  | 1.76 |
| PXO\_03437 | conserved hypothetical protein |  |  |  | 10.45 |
| PXO\_03477 | tetratricopeptide repeat domain protein | COG4783R |  |  | 2.30 |
| PXO\_03481 | DNA replication and repair (RecF) | COG1195L |  |  | 1.80 |
| PXO\_03547 | carboxyl-terminal protease | COG0793M |  |  | 1.77 |
| PXO\_03585 | transcriptional regulator | COG1476K |  | 1.82 | 2.99 |
| PXO\_03586 | HipA | COG3550R |  |  | 2.00 |
| PXO\_03595 | conserved hypothetical protein | COG2013S |  |  | 2.59 |
| PXO\_03613 | PrnA |  |  |  | 1.90 |
| PXO\_03614 | orotidine 5'-phosphate decarboxylase | COG0284F |  |  | 4.36 |
| PXO\_03631 | aspartyl-asparaginyl beta-hydroxylase | COG3555O |  |  | 1.92 |
| PXO\_03643 | conserved hypothetical protein |  |  |  | 2.45 |
| PXO\_03717 | thioredoxin (TrxA) | COG3118O |  |  | 2.06 |
| PXO\_03746 | conserved hypothetical protein |  |  |  | 1.87 |
| PXO\_03861 | glycosyl hydrolase family 10 | COG3693G |  | 2.12 | 1.94 |
| PXO\_03972 | conserved hypothetical protein |  |  |  | 1.86 |
| PXO\_04004 | indole-3-glycerol phosphate synthase (TrpC) | COG0134E |  |  | 2.11 |
| PXO\_04013 | bacterioferritin | COG2193P |  |  | 2.37 |
| PXO\_04053 | DNA protecting protein (DprA) | COG0758LU |  |  | 1.75 |
| PXO\_04097 | DNA primase | COG0358L |  |  | 1.80 |
| PXO\_04101 | ribosomal protein S21 | COG0828J |  |  | 2.91 |
| PXO\_04112 | membrane protein | COG4682S |  |  | 3.81 |
| PXO\_04132 | prolyl oligopeptidase family protein | COG1505E |  |  | 2.11 |
| PXO\_04279 | heat shock protein, ATPase subunit (HslU) | COG1220O |  |  | 1.86 |
| PXO\_04299 | rickettsia 17 kDa surface antigen family |  |  |  | 2.11 |
| PXO\_04305 | two-component system regulatory protein | COG0745TK |  |  | 2.20 |
| PXO\_04442 | isrso16-transposase orfa protein |  |  |  | 2.28 |
| PXO\_04495 | ribosomal protein L17 | COG0203J |  | 1.85 | 2.19 |
| PXO\_04570 | pyridine nucleotide transhydrogenase subunit beta | COG1282C |  |  | 2.02 |
| PXO\_04657 | ISXoo8 transposase |  |  |  | 1.94 |
| PXO\_04662 | oxidoreductase | COG3127Q |  |  | 8.27 |
| PXO\_04672 | conserved hypothetical protein | COG4256P | 1.82 |  | 2.69 |
| PXO\_04745 | transcription-repair coupling factor | COG1197LK |  |  | 3.24 |
| PXO\_04752 | chemotaxis protein | COG0835NT | 1.92 | 2.31 | 16.55 |
| PXO\_04757 | metallopeptidase | COG3590O |  |  | 1.92 |
| PXO\_04763 | pirin, N-terminal:Pirin, C-terminal | COG1741R |  | 2.01 | 8.19 |
| PXO\_04786 | conserved hypothetical protein |  |  |  | 2.09 |
| PXO\_04825 | ATP-dependent RNA helicase | COG0513LKJ |  |  | 1.77 |
| PXO\_05411 | putative glycosyl transferase | COG1216R |  | 2.83 | 3.07 |
| PXO\_06135 | translation initiation factor IF-1 | COG0361J |  |  | 4.68 |