**Table S7.** Genes down-regulated in late log phase by Ax21

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|  |  |  | **Fold down-regulated** |
| **Locus ID** | **Common name** | **COG ID** | **Early log** | **Mid log** | **Late log** |
| PXO\_00062 | PIN domain, putative | COG1487R |  |  | 2.23 |
| PXO\_00098 | ferrous iron transport protein B | COG0370P |  |  | 1.94 |
| PXO\_00256 | Rhs-family protein | COG3501S |  |  | 1.84 |
| PXO\_00301 | putative phytase | COG4247I |  |  | 1.87 |
| PXO\_00383 | lysine 2,3-aminomutase | COG1509E |  |  | 2.03 |
| PXO\_00430 | ATP-dependent DNA helicase (Ihr) |  |  |  | 1.75 |
| PXO\_00434 | conserved hypothetical protein |  |  |  | 1.80 |
| PXO\_00438 | stringent starvation protein A (SspA) | COG0625O |  |  | 1.82 |
| PXO\_00471 | omega-amino acid-pyruvate aminotransferase | COG0161H |  |  | 1.96 |
| PXO\_00481 | multidrug resistance protein | COG0845M |  |  | 1.78 |
| PXO\_00542 | phosphate ABC transporter, permease protein (PstC) | COG0573P |  |  | 1.84 |
| PXO\_00656 | ABC transporter ATP-binding protein | COG1132V |  |  | 1.93 |
| PXO\_00666 | putative DNA-directed RNA polymerase specialized sigma subunit, sigma24-like protein | COG1595K | 2.62 | 1.79 | 3.45 |
| PXO\_00684 | alkaline phosphatase | COG3211R |  |  | 2.34 |
| PXO\_00721 | putative polyhydroxyalkanoic acid system protein |  |  |  | 1.86 |
| PXO\_00723 | conserved hypothetical protein |  |  |  | 1.77 |
| PXO\_00772 | acetyltransferase | COG3153R |  |  | 1.85 |
| PXO\_00779 | peptidyl-prolyl cis-trans isomerase | COG0545O |  |  | 1.85 |
| PXO\_00789 | phosphate ABC transporter, phosphate-binding protein (PstS) | COG0226P |  |  | 1.92 |
| PXO\_00831 | putative TrpR-like protein YerC/YecD | COG4496S | 1.92 |  | 2.37 |
| PXO\_00832 | ATP phosphoribosyltransferase (HisG) | COG0040E | 1.87 |  | 1.95 |
| PXO\_00904 | bifunctional protein (FolD) | COG0190H |  |  | 1.77 |
| PXO\_01126 | phosphatidate cytidylyltransferase | COG0575I |  |  | 1.88 |
| PXO\_01235 | acyl-CoA dehydrogenase, short-chain specific | COG1960I |  |  | 1.76 |
| PXO\_01288 | NADH-ubiquinone oxidoreductase 20 kda subunit | COG0377C |  |  | 1.81 |
| PXO\_01414 | conserved hypothetical protein | COG5340K |  |  | 1.76 |
| PXO\_01517 | ribonuclease E | COG1530J |  |  | 1.90 |
| PXO\_01558 | potassium uptake protein (Kup) | COG3158P |  |  | 2.14 |
| PXO\_01664 | hydrolase, alpha/beta fold family, putative | COG0596R |  |  | 4.23 |
| PXO\_01755 | conserved hypothetical protein |  |  |  | 2.05 |
| PXO\_01794 | S-methylmethionine permease | COG0833E |  |  | 1.86 |
| PXO\_01796 | conserved hypothetical protein | COG4805S |  | 1.87 | 2.14 |
| PXO\_01840 | tRNA (guanine-N(7)-)-methyltransferase | COG0220R |  |  | 1.84 |
| PXO\_01841 | thiazole biosynthesis protein (ThiG) | COG2022H |  |  | 1.76 |
| PXO\_01992 | conserved hypothetical protein | COG0325R |  |  | 1.86 |
| PXO\_01995 | conserved hypothetical protein | COG1284S |  |  | 1.84 |
| PXO\_02042 | conserved hypothetical protein | COG3522S | 1.83 |  | 2.00 |
| PXO\_02335 | conserved hypothetical protein |  |  |  | 2.09 |
| PXO\_02406 | two-component system sensor protein | COG0642T |  |  | 1.76 |
| PXO\_02407 | two-component system regulatory protein | COG0745TK |  |  | 1.75 |
| PXO\_02492 | phosphate regulon transcriptional regulatory protein (PhoB) | COG0745TK | 1.95 |  | 1.99 |
| PXO\_02585 | conserved hypothetical protein | COG3781S |  |  | 1.95 |
| PXO\_02797 | helix-turn-helix, putative | COG1476K |  |  | 1.86 |
| PXO\_02823 | conserved hypothetical protein |  |  |  | 1.86 |
| PXO\_02834 | tRNA-dihydrouridine synthase A | COG0042J |  |  | 1.77 |
| PXO\_02860 | RarD | COG2962R |  |  | 1.83 |
| PXO\_02897 | ribonucleoside-diphosphate reductase, alpha subunit | COG0209F |  |  | 1.76 |
| PXO\_02937 | conserved hypothetical protein | COG2377O |  |  | 1.75 |
| PXO\_02954 | transmembrane protein |  |  |  | 1.81 |
| PXO\_03059 | protease | COG1404O |  |  | 1.87 |
| PXO\_03150 | pilus assembly protein (Tfp) | COG5008NU |  |  | 1.78 |
| PXO\_03244 | alkaline phosphatase D | COG3540P |  |  | 2.10 |
| PXO\_03245 | alkaline phosphatase | COG3540P |  |  | 1.75 |
| PXO\_03262 | oxidoreductase | COG0667C |  |  | 1.81 |
| PXO\_03309 | conserved hypothetical protein | COG3230P |  |  | 1.76 |
| PXO\_03490 | phosphatase | COG0671I |  |  | 1.97 |
| PXO\_03708 | conserved hypothetical protein |  |  |  | 1.92 |
| PXO\_03709 | NADH dehydrogenase | COG1252C |  |  | 1.79 |
| PXO\_03736 | ketosynthase |  |  |  | 1.88 |
| PXO\_03751 | phosphate-selective porin O and P |  |  |  | 1.80 |
| PXO\_03772 | MFS transporter | COG2814G |  |  | 1.81 |
| PXO\_03849 | sal operon transcriptional repressor | COG1609K |  |  | 1.83 |
| PXO\_03879 | oxidoreductase | COG1018C |  | 2.14 | 2.16 |
| PXO\_03963 | conserved hypothetical protein |  |  |  | 2.13 |
| PXO\_03964 | conserved hypothetical protein |  |  |  | 2.14 |
| PXO\_04355 | conserved hypothetical protein |  |  | 1.77 | 1.78 |
| PXO\_04500 | preprotein translocase subunit (SecY) | COG0201U |  |  | 1.93 |
| PXO\_04539 | GTP-binding protein (YchF) | COG0012J |  |  | 1.85 |
| PXO\_04558 | xylanase | COG5520M |  |  | 1.74 |
| PXO\_04559 | asparaginase | COG0252EJ |  |  | 2.17 |
| PXO\_04572 | ECF sigma factor | COG1595K |  |  | 4.66 |
| PXO\_04573 | conserved hypothetical protein |  |  |  | 3.68 |
| PXO\_04577 | conserved hypothetical protein |  |  |  | 1.76 |
| PXO\_04590 | alkyl hydroperoxide reductase subunit F | COG3634O |  |  | 2.11 |
| PXO\_04591 | oxidative stress transcriptional regulator (OxyR) | COG0583K |  |  | 2.32 |
| PXO\_04858 | EF hand domain protein |  | 2.16 |  | 3.34 |
| PXO\_04862 | inorganic anion transporter, sulfate permease (SulP) |  |  |  | 2.20 |
| PXO\_05561 | conserved hypothetical protein |  |  |  | 1.77 |
| PXO\_05616 | pyridoxal phosphate biosynthetic protein |  |  |  | 1.83 |
| PXO\_06060 | hydrolase, carbon-nitrogen family | COG0388R |  |  | 1.78 |
| PXO\_06063 | heme exporter protein (CcmB) | COG2386O |  |  | 1.86 |
| PXO\_06065 | conserved hypothetical protein |  |  |  | 1.79 |
| PXO\_06090 | molybdopterin biosynthesis protein | COG0476H |  |  | 1.78 |
| PXO\_06118 | Cl- channel, voltage gated | COG0038P |  |  | 1.87 |
| PXO\_06128 | DNA translocase (FtsK) | COG1674D |  |  | 1.78 |