**Table S3:** **List of the exclusively downregulated proteins in *S. aureus* biofilm in comparison to planktonic culture (fold change >-2, p <0.05).** \* CM denotes Cytoplasmic Membrane.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Accession ID** | **Protein Name** | **Gene Names** | **Fold Change** | **Protein Pathways** | **Subcellular Localisation** |
| AIO21667.1 | delta-hemolysin | hld SA1841.1 SAS065 | -34.02 | Quorum sensing | Cytoplasmic |
| AIO20700.1 | spermidine/putrescine ABC transporter substrate-binding protein | potD | -22.04 | ABC transporters | Unknown |
| AIO20763.1 | alpha-hemolysin | SA1007 | -13.83 |  | Extracellular |
| AIO22369.1 | phosphodiesterase | hlb SACOL2003 | -12.33 |  | Extracellular |
| OOC90902.1 | calcium-binding protein | SACOL1846 | -11.77 |  | Unknown |
| AIO20644.1 | cysteine protease | sspB SACOL1056 | -11.44 |  | Extracellular |
| AIO22207.1 | transglycosylase | isaA SACOL2584 | -10.14 |  | Extracellular |
| AIO20556.1 | hypothetical protein KQ76\_04470 | SA0841 | -9.46 |  | CM\* |
| AIO19942.1 | peptidase M23 | lytM SACOL0263 | -9.30 |  | Extracellular |
| AIO20056.1 | hypothetical protein KQ76\_01725 |  | -8.47 |  | CM |
| AIO20660.1 | chitinase | SA0914 | -8.44 |  | Unknown |
| AIO19870.1 | peptidase M23 | SA0205 | -8.28 |  | Extracellular |
| AIO21024.1 | cold-shock protein | cspA SA1234 | -8.08 |  | Cytoplasmic |
| AIO19947.1 | staphyloxanthin biosynthesis protein | SACOL0270 | -7.54 |  | Extracellular |
| AIO21349.1 | DNA-3-methyladenine glycosylase | tag | -7.16 | Base excision repair | Unknown |
| AIO21509.1 | serine protease | splC SACOL1867 | -6.98 |  | Extracellular |
| AIO20463.1 | thermonuclease | nuc SACOL0860 | -6.97 |  | Extracellular |
| AIO20332.1 | peptidase M23B | SA0620 | -6.86 |  | Cell wall |
| AIO20645.1 | glutamyl endopeptidase | sspA SACOL1057 | -6.52 | Quorum sensing | Extracellular |
| AIO20716.1 | SCP-like extracellular protein | SA0967 | -6.49 |  | Unknown |
| AIO19770.1 | 1-phosphatidylinositol phosphodiesterase | plc | -5.85 | Inositol phosphate metabolism | Extracellular |
| AIO20387.1 | glycerol phosphate lipoteichoic acid synthase | ltaS SA0674 | -5.84 | Metabolic pathways, Glycerolipid metabolism | CM |
| AIO22290.1 | N-acetylmuramoyl-L-alanine amidase | SACOL2666 | -5.80 |  | Extracellular |
|  |  |  |  |  |  |
| AIO21492.1 | hypothetical protein KQ76\_09365 | SACOL1852 | -5.35 |  | Unknown |
| AIO20326.1 | response regulator GraR | graR SACOL0716 | -5.34 | Two-component system, Cationic antimicrobial peptide (CAMP) resistance | Cytoplasmic |
| AIO21221.1 | acetyl-CoA carboxylase | accB | -5.16 | Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Pyruvate metabolism, Carbon metabolism, Fatty acid metabolism, Propanoate metabolism, Fatty acid biosynthesis | Cytoplasmic |
| AIO19779.1 | peptigoglycan-binding protein LysM | spa SACOL0095 | -4.71 | *Staphylococcus aureus* infection | Cell wall |
| AIO20739.1 | ribonuclease HIII | rnhC SACOL1150 | -4.61 | DNA replication | Unknown |
| AIO20228.1 | hydrolase | sdrD SA0520 | -4.49 | *Staphylococcus aureus* infection | Cell wall |
| AIO20762.1 | hypothetical protein KQ76\_05550 | SA1005 | -4.44 |  | Unknown |
| AIO20126.1 | N-acetylmuramoyl-L-alanine amidase | sle1 aaa SA0423 | -4.42 |  | Cell wall |
| AIO20637.1 | acetyltransferase | SA0893 | -4.41 |  | Cytoplasmic |
| AIO21273.1 | molecular chaperone DnaJ | dnaJ SA1408 | -4.24 |  | Cytoplasmic |
| AIO20577.1 | competence negative regulator MecA | mecA SA0857 | -4.19 |  | Cytoplasmic |
| AIO20418.1 | ABC transporter | SACOL0811 | -4.18 |  | Cytoplasmic |
| AIO21353.1 | delta-aminolevulinic acid dehydratase | hemB SA1492 | -4.18 | Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Porphyrin and chlorophyll metabolism | Cytoplasmic |
| AIO21508.1 | serine protease | splE SACOL1865 | -4.18 | Quorum sensing | Extracellular |
| AIO19905.1 | nucleoside hydrolase | SACOL0225 | -4.17 |  | Cytoplasmic |
| AIO20630.1 | hypothetical protein KQ76\_04865 | SACOL1575 | -4.12 |  | Unknown |
| AIO19987.1 | lipase | lip2 geh SA0309 | -4.12 | Metabolic pathways, Glycerolipid metabolism | Extracellular |
| AIO20479.1 | arsenate reductase | SA0759 | -4.06 |  | Cytoplasmic |
|  |  |  |  |  |  |
| AIO20651.1 | mannosyl-glycoprotein endo-beta-N-acetylglucosamidase | atl nag SACOL1062 | -4.01 |  | Extracellular |
| AIO21549.1 | Fur family transcriptional regulator | perR SACOL1919 | -4.00 |  | Cytoplasmic |
| AIO22042.1 | glutathione S-transferase | SACOL2402 | -3.94 |  | Unknown |
| AIO21406.1 | Free methionine-(R)-sulfoxide reductase | SACOL1768 | -3.85 | Cysteine and methionine metabolism | Cytoplasmic |
| AIO20229.1 | bis(5'-nucleosyl)-tetraphosphatase | sdrE SACOL0610 | -3.82 | *Staphylococcus aureus* infection | Cell wall |
| AIO22060.1 | gamma-hemolysin subunit A | hlgC SA2208 | -3.79 | *Staphylococcus aureus* infection | Extracellular |
| AIO20738.1 | phenylalanyl-tRNA synthase subunit beta | pheT SA0986 | -3.75 | Aminoacyl-tRNA biosynthesis | Cytoplasmic |
| AIO21601.1 | cysteine protease | sspP scpA SA1725 | -3.73 |  | Extracellular |
| AIO20874.1 | 50S ribosomal protein L7 | SA1111 | -3.73 |  | Unknown |
| AIO21505.1 | serine protease | splF SA1627 | -3.71 | Quorum sensing | Extracellular |
| AIO22081.1 | sodium:proton antiporter | SA2228 | -3.68 |  | CM |
| AIO20884.1 | zinc protease | SA1121 | -3.66 |  | Cytoplasmic |
| AIO20093.1 | superantigen-like protein | set11 | -3.63 | *Staphylococcus aureus* infection | Extracellular |
| AIO21182.1 | transcriptional regulator | srrA SA1323 | -3.63 | Two-component system | Cytoplasmic |
| AIO20960.1 | secretion protein | SACOL1373 | -3.63 |  | Unknown |
| AIO22350.1 | peptidase |  | -3.61 |  | Extracellular |
| AIO21805.1 | uridylyltransferase | SA1974 | -3.60 |  | Cytoplasmic |
| AIO21491.1 | hypothetical protein KQ76\_09360 | SACOL1851 | -3.58 |  | Cytoplasmic |
| AIO20144.1 | hypothetical protein KQ76\_02220 | SA0441 | -3.57 |  | Unknown |
| AIO21160.1 | single-stranded DNA-binding protein | ssb | -3.53 | Homologous recombination, Mismatch repair, DNA replication | Unknown |
| AIO22099.1 | peptidase M28 | SA2244 | -3.47 |  | Cytoplasmic |
| AIO22349.1 | hypothetical protein KQ76\_14165 |  | -3.46 |  | Unknown |
| AIO20756.1 | formyl peptide receptor-like 1 inhibitory protein | flr SA1001 | -3.39 | *Staphylococcus aureus* infection | Unknown |
| AIO20951.1 | HAD family hydrolase | SA1167 | -3.34 |  | Cytoplasmic |
| AIO22292.1 | adhesin | sasF SACOL2668 | -3.28 |  | Cell wall |
| AIO19988.1 | alpha/beta hydrolase | SACOL0391 | -3.27 |  | Cytoplasmic |
| AIO20737.1 | phenylalanine--tRNA ligase | pheS SA0985 | -3.27 | Aminoacyl-tRNA biosynthesis | Cytoplasmic |
| AIO21246.1 | penicillin-binding protein | pbp3 | -3.24 | Metabolic pathways, beta-Lactam resistance, Peptidoglycan biosynthesis | CM |
| OOC94232.1 | aureolysin | aur SACOL2659 | -3.22 | *Staphylococcus aureus* infection, Cationic antimicrobial peptide (CAMP) resistance | Extracellular |
| AIO21853.1 | 50S ribosomal protein L17 | rplQ SA2022 | -3.19 | Ribosome | Cytoplasmic |
| AIO21391.1 | oligoribonuclease | SA1526 | -3.17 | Metabolic pathways, Microbial metabolism in diverse environments, Sulfur metabolism | Cytoplasmic |
| AIO21842.1 | toxin | SACOL2197 | -3.14 |  | CM |
| AIO22206.1 | acetyltransferase | oatA SA2354 | -3.12 |  | CM |
| AIO21365.1 | 50S ribosomal protein L20 | rplT SA1502 | -3.09 | Ribosome | Cytoplasmic |
| AIO21565.1 | hypothetical protein KQ76\_09970 | SAS054 | -3.08 |  | Cytoplasmic |
| AIO22160.1 | lactate dehydrogenase | ldhD ddh SACOL2535 | -3.04 | Pyruvate metabolism, Microbial metabolism in diverse environments | Cytoplasmic |
| AIO20515.1 | hypothetical protein KQ76\_04260 | SACOL0943 | -3.00 |  | Cytoplasmic |
| OOC94758.1 | alpha/beta hydrolase | SA1990 | -2.98 |  | Unknown |
| AIO22074.1 | glycerate kinase | SA2220 | -2.97 | Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of antibiotics, Glycerolipid metabolism, Glyoxylate and dicarboxylate metabolism, Glycine, serine and threonine metabolism | Cytoplasmic |
| AIO21275.1 | heat shock protein GrpE | grpE SA1410 | -2.97 |  | Cytoplasmic |
| AIO22275.1 | clumping factor B | clfB SA2423 | -2.96 | *Staphylococcus aureus* infection | Cell wall |
| AIO20071.1 | NADPH-dependent oxidoreductase | nfrA SACOL0453 | -2.92 | Metabolic pathways, Riboflavin metabolism | Cytoplasmic |
| AIO22317.1 | lipase | lip1 SA2463 | -2.89 | Metabolic pathways, Glycerolipid metabolism | Extracellular |
| AIO19780.1 | MarR family transcriptional regulator | sarS sarH1 SA0108 | -2.87 |  | Cytoplasmic |
| AIO21530.1 | peptidylprolyl isomerase | prsA SA1659 | -2.86 |  | CM |
| AIO21602.1 | staphostatin A | SA1726 | -2.86 |  | Unknown |
| AIO20100.1 | hypothetical protein KQ76\_01960 | SA0395 | -2.85 |  | Unknown |
| AIO20776.1 | phenol soluble modulin | SACOL1186 | -2.85 | Quorum sensing | Unknown |
| AIO20863.1 | elongation factor Ts | tsf SACOL1276 | -2.82 |  | Cytoplasmic |
| OOC93971.1 | phosphoglucomutase | pgcA SA2279 | -2.81 | Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Purine metabolism, Amino sugar and nucleotide sugar metabolism, Starch and sucrose metabolism, Streptomycin biosynthesis, Glycolysis / Gluconeogenesis, Pentose phosphate pathway, Galactose metabolism | Cytoplasmic |
| AIO21506.1 | serine protease | splE SACOL1865 | -2.81 |  | Extracellular |
| AIO20279.1 | hypothetical protein KQ76\_03005 | SA0570 | -2.80 |  | Unknown |
| AIO21343.1 | membrane protein | SA1476 | -2.76 |  | Unknown |
|  |  |  |  |  |  |
| AIO20368.1 | PTS fructose transporter subunit IIC | fruA | -2.73 | Metabolic pathways, Microbial metabolism in diverse environments, Fructose and mannose metabolism, Phosphotransferase system (PTS) | CM |
| AIO20534.1 | glycerophosphodiester phosphodiesterase | glpQ | -2.73 | Glycerophospholipid metabolism | Unknown |
| AIO20049.1 | pathogenicity island protein | SA1824 | -2.72 |  | Unknown |
| AIO21274.1 | molecular chaperone DnaK | dnaK SA1409 | -2.68 | RNA degradation | Cytoplasmic |
| AIO21449.1 | leucyl-tRNA synthetase | leuS SA1579 | -2.67 | Aminoacyl-tRNA biosynthesis | Cytoplasmic |
| AIO21282.1 | competence protein ComE | comEB | -2.67 | Metabolic pathways, Pyrimidine metabolism | Cytoplasmic |
| AIO21436.1 | peptidase M28 | SA1566 | -2.66 |  | Cytoplasmic |
| AIO20170.1 | hypothetical protein KQ76\_02355 | SA0464 | -2.65 |  | Cytoplasmic |
| AIO21073.1 | hypothetical protein KQ76\_07205 | SACOL1491 | -2.65 |  | Unknown |
| AIO21788.1 | HAD family hydrolase | SA1957 | -2.64 |  | Cytoplasmic |
| AIO22136.1 | fibronectin-binding protein | fnbA SA2291 | -2.60 | Bacterial invasion of epithelial cells | Cell wall |
| AIO21371.1 | primosomal protein DnaI | dnaI | -2.59 |  | Cytoplasmic |
| AIO20579.1 | oligopeptidase PepB | SA0859 | -2.58 |  | Cytoplasmic |
| AIO20152.1 | methionine--tRNA ligase | metG metS SA0448 | -2.58 | Selenocompound metabolism, Aminoacyl-tRNA biosynthesis | Cytoplasmic |
| AIO20286.1 | recombinase | SA0577 | -2.58 |  | Cytoplasmic |
| OOC92415.1 | sphingomyelin phosphodiesterase | hlb SACOL2003 | -2.56 | Quorum sensing, Metabolic pathways, Inositol phosphate metabolism, Glycerophospholipid metabolism, Biosynthesis of secondary metabolites | Extracellular |
| AIO20439.1 | Clp protease | clpP SA0723 | -2.55 |  | Cytoplasmic |
| AIO21970.1 | ribose 5-phosphate isomerase | rpiA SA2127 | -2.54 | Metabolic pathways, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Pentose phosphate pathway | Cytoplasmic |
|  |  |  |  |  |  |
| AIO20435.1 | thioredoxin reductase | trxB SA0719 | -2.54 | Selenocompound metabolism | Cytoplasmic |
| AIO21298.1 | acetyl-CoA carboxylase biotin carboxylase subunit | SA1434 | -2.52 | Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Pyruvate metabolism, Carbon metabolism, Fatty acid metabolism, Propanoate metabolism, Fatty acid biosynthesis | Cytoplasmic |
| AIO21363.1 | DNA mismatch repair protein MutT | SA1501 | -2.50 |  | Cytoplasmic |
| AIO20575.1 | tryptophanyl-tRNA synthetase | trpS SA0855 | -2.50 | Aminoacyl-tRNA biosynthesis | Cytoplasmic |
| AIO21606.1 | nicotinate phosphoribosyltransferase | SA1729 | -2.49 | Metabolic pathways, Nicotinate and nicotinamide metabolism | Cytoplasmic |
| AIO22387.1 | replication-associated protein (plasmid) | SAP031 | -2.49 |  | Unknown |
| AIO20282.1 | transcriptional regulator | sarA SA0573 | -2.48 |  | Cytoplasmic |
|  |  |  |  |  |  |
| AIO20202.1 | antitermination protein NusG | nusG SA0494 | -2.48 |  | Cytoplasmic |
| AIO21595.1 | lipoprotein | SA1719 | -2.46 |  | Unknown |
| AIO22291.1 | isochorismatase | SA2438 | -2.45 |  | Unknown |
| AIO21531.1 | 3'-5' exonuclease | cbf1 | -2.44 |  | Cytoplasmic |
| AIO20398.1 | 7-cyano-7-deazaguanine reductase | queF SA0683 | -2.44 | Metabolic pathways, Folate biosynthesis | Cytoplasmic |
| AIO21033.1 | hypothetical protein KQ76\_06965 | SA1242 | -2.44 |  | Unknown |
| AIO19802.1 | cell wall surface anchor family protein | sasD SACOL0119 | -2.43 |  | Cell wall |
| AIO21623.1 | thioredoxin | SA1743 | -2.41 |  | Unknown |
| AIO20231.1 | glycosyl transferase family 1 | SACOL0612 | -2.41 |  | Cytoplasmic |
| AIO20885.1 | zinc protease | SACOL1298 | -2.40 |  | Unknown |
| AIO21583.1 | ferritin | ftnA SA1709 | -2.39 |  | Cytoplasmic |
| AIO22235.1 | 3-methyl-2-oxobutanoate hydroxymethyltransferase | panB SA2392 | -2.37 | Metabolic pathways, Biosynthesis of secondary metabolites, Pantothenate and CoA biosynthesis | Unknown |
|  |  |  |  |  |  |
| AIO20406.1 | iron ABC transporter substrate-binding protein | SA0691 | -2.37 | ABC transporters | CM |
| AIO20712.1 | pyruvate carboxylase | pyc SACOL1123 | -2.35 | Metabolic pathways, Pyruvate metabolism, Microbial metabolism in diverse environments, Biosynthesis of amino acids, Carbon metabolism, Citrate cycle (TCA cycle) | Cytoplasmic |
| AIO22158.1 | glyoxalase | SA2310 | -2.35 | Metabolic pathways, Microbial metabolism in diverse environments, Benzoate degradation, Xylene degradation, Degradation of aromatic compounds | Unknown |
| AIO20704.1 | hypothetical protein KQ76\_05255 | SA0957 | -2.34 |  | Cytoplasmic |
| AIO21607.1 | nitric oxide synthase | nos SA1730 | -2.34 | Metabolic pathways, Biosynthesis of secondary metabolites, Arginine biosynthesis, Arginine and proline metabolism | Cytoplasmic |
| AIO22191.1 | TetR family transcriptional regulator | SA2340 | -2.33 |  | Cytoplasmic |
| AIO22006.1 | acetyltransferase | SA2159 | -2.33 |  | Cytoplasmic |
| AIO20913.1 | glutamine synthetase | glnA SACOL1329 | -2.32 | Metabolic pathways, Two-component system, Biosynthesis of amino acids, Glyoxylate and dicarboxylate metabolism, Arginine biosynthesis, Microbial metabolism in diverse environments, Alanine, aspartate and glutamate metabolism, Nitrogen metabolism | Cytoplasmic |
| AIO20225.1 | HAD family hydrolase | SA0517 | -2.32 |  | Cytoplasmic |
| AIO22285.1 | hypothetical protein KQ76\_13835 | SACOL2661 | -2.31 |  | Extracellular |
| AIO19949.1 | type VII secretion protein EsaA | esaA SA0272 | -2.29 |  | CM |
| AIO21929.1 | transcriptional regulator | SA2091 | -2.28 |  | Unknown |
| AIO21020.1 | hydrolase | SACOL1433 | -2.28 |  | Cytoplasmic |
| AIO21157.1 | replication protein |  | -2.28 |  | Cytoplasmic |
|  |  |  |  |  |  |
| AIO22336.1 | pyrrolidone-carboxylate peptidase | pcp SACOL2714 | -2.27 |  | Cytoplasmic |
| AIO22054.1 | phosphoglyceromutase | gpmA SA2204 | -2.24 | Metabolic pathways, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Methane metabolism, Glycolysis / Gluconeogenesis, Glycine, serine and threonine metabolism | Unknown |
| OOC89529.1 | dUTP pyrophosphatase | dut SACOL0357 | -2.23 | Metabolic pathways, Pyrimidine metabolism | Cytoplasmic |
| AIO21679.1 | ABC transporter ATP-binding protein | vga | -2.23 |  | Cytoplasmic |
| AIO21204.1 | hypothetical protein KQ76\_07895 | SACOL1555 | -2.22 |  | Cytoplasmic |
|  |  |  |  |  |  |
| AIO21459.1 | riboflavin synthase subunit alpha | ribE SACOL1819 | -2.22 | Metabolic pathways, Riboflavin metabolism, Biosynthesis of secondary metabolites | Cytoplasmic |
| AIO20749.1 | succinate dehydrogenase | sdhB | -2.21 | Metabolic pathways, Microbial metabolism in diverse environments, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Carbon metabolism, Citrate cycle (TCA cycle), Oxidative phosphorylation, Butanoate metabolism | Cytoplasmic |
| AIO20507.1 | alanine-phosphoribitol ligase | dltA SACOL0935 | -2.20 | Two-component system, Cationic antimicrobial peptide (CAMP) resistance, D-Alanine metabolism, *Staphylococcus aureus* infection | Cytoplasmic |
| AIO21007.1 | oligoendopeptidase F | SA1216 | -2.19 |  | Cytoplasmic |
| AIO21222.1 | elongation factor P | efp SA1359 | -2.19 |  | Cytoplasmic |
| AIO22338.1 | adhesin |  | -2.18 |  | Cell wall |
| AIO20422.1 | sigma-54 modulation protein | hpf SA0707 | -2.16 |  | Cytoplasmic |
| AIO20857.1 | ATP-dependent protease subunit HslV | hslV clpQ SA1096 | -2.16 |  | Cytoplasmic |
| AIO21536.1 | Cro/Cl family transcriptional regulator | SA1665 | -2.15 |  | Cytoplasmic |
| AIO20783.1 | penicillin-binding protein | pbpA | -2.15 | Metabolic pathways, beta-Lactam resistance, Peptidoglycan biosynthesis | CM |
| AIO20880.1 | polynucleotide phosphorylase | pnp pnpA SA1117 | -2.14 | Purine metabolism, Pyrimidine metabolism, RNA degradation | Cytoplasmic |
| AIO19900.1 | nitric oxide dioxygenase | SA0231 | -2.14 |  | Cytoplasmic |
| AIO21401.1 | peroxidase | tpx SACOL1762 | -2.14 |  | Unknown |
| AIO20237.1 | 6-phospho 3-hexuloisomerase | SA0529 | -2.13 | Metabolic pathways, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of amino acids, Pentose phosphate pathway, Methane metabolism | Unknown |
| AIO21562.1 | RecX family transcriptional regulator | recX SA1690 | -2.13 |  | Cytoplasmic |
| AIO21223.1 | peptidase M24 | SACOL1588 | -2.12 |  | Cytoplasmic |
| AIO21854.1 | DNA-directed RNA polymerase subunit alpha | rpoA SA2023 | -2.12 | Metabolic pathways, Purine metabolism, Pyrimidine metabolism, RNA polymerase | Cytoplasmic |
| AIO20194.1 | glutamyl-tRNA synthetase | gltX SA0486 | -2.11 | Metabolic pathways, Aminoacyl-tRNA biosynthesis | Cytoplasmic |
| AIO20273.1 | arginine--tRNA ligase | argS SACOL0663 | -2.11 | Aminoacyl-tRNA biosynthesis | Cytoplasmic |
| AIO21926.1 | MarR family transcriptional regulator | sarR SA2089 | -2.10 |  | Cytoplasmic |
| AIO20259.1 | dihydrolipoamide dehydrogenase | SA0551 | -2.09 |  | Cytoplasmic |
| AIO20623.1 | conjugal transfer protein | SACOL1582 | -2.08 |  | Unknown |
| AIO22143.1 | hypothetical protein KQ76\_13105 | SACOL2519 | -2.08 |  | Cytoplasmic |
| AIO21116.1 | gamma-hemolysin subunit A | hlgC SA2208 | -2.06 |  | Extracellular |
| AIO21055.1 | membrane protein | SA1265 | -2.06 |  | CM |
| AIO21194.1 | ribonuclease Z | rnz SACOL1548 | -2.06 |  | Cytoplasmic |
| AIO20555.1 | phosphatidylethanolamine-binding protein | SACOL0984 | -2.06 |  | Unknown |
|  |  |  |  |  |  |
| AIO20895.1 | 2-oxoglutarate ferredoxin oxidoreductase subunit alpha | SA1131 | -2.06 | Metabolic pathways, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of antibiotics, Glycolysis / Gluconeogenesis, Butanoate metabolism, Pyruvate metabolism, Citrate cycle (TCA cycle) | Cytoplasmic |
| AIO20402.1 | ribonucleotide-diphosphate reductase subunit beta | nrdF | -2.06 | Metabolic pathways, Purine metabolism, Pyrimidine metabolism | Cytoplasmic |
| AIO19739.1 | 50S ribosomal protein L9 | rplI SA0014 | -2.05 | Ribosome | Cytoplasmic |
| AIO20584.1 | GTP pyrophosphokinase | SA0864 | -2.04 | Purine metabolism | Cytoplasmic |
| AIO21458.1 | GTP cyclohydrolase | ribBA SACOL1818 | -2.04 | Metabolic pathways, Riboflavin metabolism, Biosynthesis of secondary metabolites, Folate biosynthesis | Cytoplasmic |
| AIO20455.1 | hypothetical protein KQ76\_03935 | SACOL0851 | -2.04 |  | Unknown |
|  |  |  |  |  |  |
| AIO20695.1 | hypothetical protein KQ76\_05210 | SA0947 | -2.04 |  | Unknown |
| AIO20687.1 | hypothetical protein KQ76\_05170 | SA0941 | -2.04 |  | Cytoplasmic |
| AIO20819.1 | 16S rRNA methyltransferase | SA1060 | -2.03 |  | Cytoplasmic |
| AIO20413.1 | peptidase T | pepT SA0698 | -2.03 |  | Cytoplasmic |
| AIO20838.1 | cell division protein FtsY | ftsY SACOL1251 | -2.03 | Quorum sensing, Protein export, Bacterial secretion system | CM |
| AIO21057.1 | ribonuclease H | SACOL1471 | -2.03 | DNA replication | Cell wall |
| OOC91307.1 | hypothetical protein BWO94\_08325 | SA1008 | -2.02 |  | Unknown |
| AIO20835.1 | acyl carrier protein | acpP hmrB SA1075 | -2.01 |  | Cytoplasmic |