**Table S2: List of the significantly upregulated 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** |
| AIO20486.1 | hypothetical protein KQ76\_04110 | SA0772 | 5.09 |  | Unknown |
| AIO21910.1 | molybdenum ABC transporter permease | modB | 4.68 | ABC transporters | CM\* |
| AIO20812.1 | DNA-directed RNA polymerase subunit omega | rpoZ SA1053 | 4.52 | Metabolic pathways, Pyrimidine metabolism, RNA polymerase, Purine metabolism | Unknown |
| AIO20306.1 | glycosyltransferase | tagX SA0596 | 4.32 |  | Unknown |
| AIO19852.1 | branched-chain amino acid transporter II carrier protein | SA0180 | 4.04 |  | CM |
| AIO21307.1 | hypothetical protein KQ76\_08425 | SA1443 | 3.57 |  | Cytoplasmic |
| AIO20635.1 | hypothetical protein KQ76\_04890 | SACOL1046 | 3.43 |  | Unknown |
| AIO21316.1 | hypothetical protein KQ76\_08470 | SAS049 | 3.38 |  | Unknown |
| AIO21773.1 | membrane protein | SA1937 | 3.32 |  | CM |
| AIO21982.1 | hypothetical protein KQ76\_12230 | SACOL2344 | 3.30 |  | Cytoplasmic |
| AIO21211.1 | 2-oxoisovalerate dehydrogenase | bfmBAA | 3.19 | Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Propanoate metabolism, Valine, leucine and isoleucine degradation | Cytoplasmic |
| AIO20267.1 | NAD(P)H-dependent oxidoreductase | SA0558 | 3.17 |  | Unknown |
| AIO21660.1 | DNA-binding protein |  | 3.12 |  | Cytoplasmic |
| AIO22226.1 | fructosamine kinase | SA2374 | 2.97 |  | Cytoplasmic |
| AIO19750.1 | transposase | SA0379 | 2.91 |  | Cytoplasmic |
| AIO19867.1 | peptide ABC transporter substrate-binding protein | SACOL0187 | 2.91 | Quorum sensing | Unknown |
| AIO21786.1 | lytic regulatory protein | truncated-SA | 2.89 |  | CM |
| AIO22040.1 | formate/nitrite transporter | SACOL2401 | 2.84 |  | CM |
| AIO22234.1 | pantoate--beta-alanine ligase | panC SACOL2614 | 2.82 | Metabolic pathways, Biosynthesis of secondary metabolites, beta-Alanine metabolism, Pantothenate and CoA biosynthesis | Cytoplasmic |
|  |  |  |  |  |  |
| AIO20180.1 | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase | folK SACOL0560 | 2.78 | Metabolic pathways, Folate biosynthesis | Cytoplasmic |
| AIO20754.1 | fibrinogen-binding protein | SA1000 | 2.78 |  | Extracellular |
| AIO21317.1 | hypothetical protein KQ76\_08475 | SA1452 | 2.76 |  | Extracellular |
| AIO20178.1 | dihydropteroate synthase | folP SA0472 | 2.76 | Metabolic pathways, Folate biosynthesis | Cytoplasmic |
| AIO20957.1 | 30S ribosomal protein S14 | rpsN rpsN2 SA1171 | 2.76 | Ribosome | Cytoplasmic |
| AIO20787.1 | cell division protein FtsA | ftsA SA1028 | 2.74 |  | Cytoplasmic |
| AIO20718.1 | glycerophosphodiester phosphodiesterase | SA0969 | 2.72 | Glycerophospholipid metabolism | Cytoplasmic |
| AIO21337.1 | 50S ribosomal protein L27 | rpmA SA1471 | 2.64 | Ribosome | Cytoplasmic |
| AIO21082.1 | zinc metallopeptidase | SACOL1500 | 2.59 |  | CM |
| AIO21503.1 | restriction endonuclease subunit S | hsdS | 2.57 |  | Unknown |
| AIO21727.1 | membrane protein | yidC SA1893 | 2.53 | Quorum sensing, Protein export, Bacterial secretion system | CM |
| AIO21819.1 | hypothetical protein KQ76\_11385 | SA1986 | 2.52 |  | CM |
| AIO21839.1 | hyaluronate lyase | hysA | 2.50 |  | Extracellular |
| AIO22003.1 | L-lactate permease | SACOL2363 | 2.47 |  | CM |
| AIO21769.1 | hypothetical protein KQ76\_11075 | SA1933 | 2.47 |  | Cytoplasmic |
| AIO20806.1 | orotidine 5'-phosphate decarboxylase | pyrF SA1047 | 2.42 | Metabolic pathways, Pyrimidine metabolism | Cytoplasmic |
| AIO20697.1 | spermidine/putrescine ABC transporter ATP-binding protein | potA SA0950 | 2.39 | ABC transporters | CM |
| AIO21790.1 | glucosamine--fructose-6-phosphate aminotransferase | glmS SACOL2145 | 2.37 | Metabolic pathways, Amino sugar and nucleotide sugar metabolism, Alanine, aspartate and glutamate metabolism, Biosynthesis of antibiotics | Cytoplasmic |
| AIO20817.1 | peptide deformylase | SA1058 | 2.35 |  | Cytoplasmic |
| AIO21826.1 | PTS system lactose-specific transporter subunit IIA | lacF SA1993 | 2.34 | Metabolic pathways, Galactose metabolism, Phosphotransferase system (PTS) | Cytoplasmic |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| AIO20444.1 | glyceraldehyde-3-phosphate dehydrogenase | gapA1 gap gapA SA0727 | 2.34 | Metabolic pathways, Biosynthesis of antibiotics, Biosynthesis of amino acids, Microbial metabolism in diverse environments, Carbon metabolism, Biosynthesis of secondary metabolites, Glycolysis / Gluconeogenesis | Cytoplasmic |
| AIO21863.1 | 30S ribosomal protein S5 | rpsE SA2031 | 2.33 | Ribosome | Cytoplasmic |
| AIO21333.1 | ATP-dependent DNA helicase RuvB | ruvB SACOL1696 | 2.33 | Homologous recombination | Cytoplasmic |
| AIO20122.1 | cystathionine gamma-synthase | metB | 2.33 | Metabolic pathways, Biosynthesis of antibiotics, Biosynthesis of amino acids, Cysteine and methionine metabolism, Glycine, serine and threonine metabolism, Sulfur metabolism | Cytoplasmic |
| OOC89123.1 | heme ABC transporter ATP-binding protein | SACOL0779 | 2.32 |  | Cytoplasmic |
| AIO22129.1 | helicase | SACOL2499 | 2.28 |  | Unknown |
| AIO20958.1 | guanosine 5'-monophosphate oxidoreductase | guaC SACOL1371 | 2.28 | Purine metabolism | Cytoplasmic |
| AIO21372.1 | helicase DnaB | SACOL1732 | 2.27 |  | Cytoplasmic |
| AIO20949.1 | threonine synthase | thrC SACOL1363 | 2.27 | Metabolic pathways, Biosynthesis of secondary metabolites, Microbial metabolism in diverse environments, Vitamin B6 metabolism, Glycine, serine and threonine metabolism, Biosynthesis of amino acids | Cytoplasmic |
| AIO21528.1 | hypothetical protein KQ76\_09615 | SA1657 | 2.26 |  | Unknown |
| AIO19973.1 | 5'-nucleotidase | SA0295 | 2.23 |  | Unknown |
| AIO20535.1 | argininosuccinate lyase | argH SA0821 | 2.21 | Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Alanine, aspartate and glutamate metabolism, Arginine biosynthesis | Cytoplasmic |
|  |  |  |  |  |  |
| AIO21844.1 | acetolactate synthase | alsS | 2.21 | Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Pantothenate and CoA biosynthesis, 2-Oxocarboxylic acid metabolism, C5-Branched dibasic acid metabolism, Butanoate metabolism, Valine, leucine and isoleucine biosynthesis | CM |
| AIO21768.1 | pantothenate kinase | coaW SA1932 | 2.17 | Metabolic pathways, Pantothenate and CoA biosynthesis | Unknown |
| AIO21133.1 | capsid protein |  | 2.17 |  | Extracellular |
| AIO20460.1 | coagulase | SACOL0857 | 2.17 |  | Extracellular |
| AIO21800.1 | chromosome partitioning protein ParA | SA1969 | 2.16 |  | Cytoplasmic |
| AIO21846.1 | ATP-dependent DNA helicase RecG |  | 2.15 |  | Cytoplasmic |
| AIO21327.1 | adenine phosphoribosyltransferase | apt SA1461 | 2.15 | Metabolic pathways, Purine metabolism | Cytoplasmic |
| AIO20536.1 | argininosuccinate synthase | argG SA0822 | 2.15 | Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Alanine, aspartate and glutamate metabolism, Arginine biosynthesis | Cytoplasmic |
| AIO20205.1 | 50S ribosomal protein L10 | rplJ SA0497 | 2.15 | Ribosome | Cytoplasmic |
| AIO21502.1 | NTPase |  | 2.13 |  | Unknown |
| AIO19985.1 | N-acetylmannosamine-6-phosphate 2-epimerase | nanE SACOL0315 | 2.13 | Amino sugar and nucleotide sugar metabolism | Cytoplasmic |
| AIO21111.1 | lipoprotein | SACOL1528 | 2.12 |  | Unknown |
| AIO20869.1 | prolyl-tRNA synthetase | proS SA1106 | 2.12 | Aminoacyl-tRNA biosynthesis | Cytoplasmic |
| AIO21190.1 | aldo/keto reductase | SACOL1543 | 2.11 |  | Cytoplasmic |
| AIO22278.1 | amino acid APC transporter | arcD | 2.10 |  | CM |
| AIO19888.1 | coagulase | coa | 2.10 |  | Extracellular |
| AIO20778.1 | hypothetical protein KQ76\_05635 | SA1019 | 2.09 |  | Unknown |
| AIO21086.1 | 3-phosphoshikimate 1-carboxyvinyltransferase | aroA SACOL1504 | 2.09 | Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Phenylalanine, tyrosine and tryptophan biosynthesis | Cytoplasmic |
| AIO21153.1 | hypothetical protein KQ76\_07625 | SACOL0347 | 2.08 |  | Cytoplasmic |
| AIO20531.1 | NADH-dependent flavin oxidoreductase | SACOL0959 | 2.08 |  | Cytoplasmic |
| AIO20985.1 | LytR family transcriptional regulator | msrR SA1195 | 2.08 |  | CM |
| AIO20616.1 | glycosyl transferase family 1 | SACOL1043 | 2.08 |  | Cytoplasmic |
| AIO20898.1 | (dimethylallyl)adenosine tRNA methylthiotransferase | miaB SA1134 | 2.06 |  | Cytoplasmic |
| AIO22086.1 | epimerase | SA2231 | 2.06 |  | Cytoplasmic |
| OOC90965.1 | glutamine ABC transporter ATP-binding protein | SA1674 | 2.05 |  | CM |
| AIO20143.1 | thymidylate kinase | tmk SA0440 | 2.03 | Metabolic pathways, Pyrimidine metabolism | Cytoplasmic |
| AIO20221.1 | HAD family hydrolase | SACOL0602 | 2.02 | Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Glyoxylate and dicarboxylate metabolism | Cytoplasmic |
| AIO19823.1 | UDP-N-acetylglucosamine 2-epimerase | capG | 2.02 | Metabolic pathways, Amino sugar and nucleotide sugar metabolism | Cytoplasmic |
| AIO21443.1 | hypothetical protein KQ76\_09120 | SA1573 | 2.01 |  | Unknown |
| AIO22323.1 | histidinol-phosphate aminotransferase | SACOL2701 | 2.01 | Metabolic pathways, Biosynthesis of secondary metabolites, Biosynthesis of antibiotics, Biosynthesis of amino acids, Phenylalanine, tyrosine and tryptophan biosynthesis, Novobiocin biosynthesis, Tyrosine metabolism, Histidine metabolism, Phenylalanine metabolism | Cytoplasmic |
| AIO21737.1 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | murA1 murA SA1902 | 2.01 | Metabolic pathways, Peptidoglycan biosynthesis, Amino sugar and nucleotide sugar metabolism | Cytoplasmic |