

TABLE S3. Expression ratios ($\log_2FC \geq 1.0$ or $\log_2FC \leq -1.0$) of 7-h developing biofilm genes exhibiting statistically significant ($p < 0.05$) change in expression compared to planktonic culture

peg ID	Subsystem	Role	Mean (biofilm/plank) ^c at 7-h
<i>Amino Acids and Derivatives</i>			
23630.peg.441	Alanine biosynthesis	Iron binding protein IscA for iron-sulfur cluster assembly	1.6
23630.peg.439	Alanine biosynthesis	Chaperone protein HscA	1.5
23630.peg.1669	Arginine and Ornithine Degradation	Ornithine cyclodeaminase (EC 4.3.1.12)	-1.2
23630.peg.4722	Branched-Chain Amino Acid Biosynthesis	Leucine dehydrogenase (EC 1.4.1.9)	1.7
23630.peg.482	Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.	Isochorismatase (EC 3.3.2.1)	-1.0
23630.peg.1373	Cysteine Biosynthesis	Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)	1.7
23630.peg.504	Glutamate and Aspartate uptake in Bacteria	Glutamate Aspartate periplasmic binding protein precursor GltI (TC 3.A.1.3.4)	1.9
23630.peg.3683	Glutamate dehydrogenases	NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	1.5
23630.peg.1752	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Aspartate ammonia-lyase (EC 4.3.1.1)	-1.1
23630.peg.754	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	-1.2
23630.peg.4143	Glycine and Serine Utilization	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)	1.9
23630.peg.2011	Glycine cleavage system	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)	1.3
23630.peg.2179	Histidine Biosynthesis	Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	-1.5
23630.peg.1084	Histidine Degradation	Urocanate hydratase (EC 4.2.1.49)	1.8
23630.peg.1083	Histidine Degradation	Histidine ammonia-lyase (EC 4.3.1.3)	1.0
23630.peg.2884	HMG CoA Synthesis	Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family	2.9
23630.peg.2880	HMG CoA Synthesis	Methylglutaconyl-CoA hydratase (EC 4.2.1.18)	1.3
23630.peg.2883	Leucine Degradation and HMG-CoA Metabolism	Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)	2.7
23630.peg.1904	Lysine degradation	Glutarate-semialdehyde dehydrogenase (EC 1.2.1.20); Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)	2.3
23630.peg.1909	Lysine degradation	Glutarate-semialdehyde dehydrogenase (EC 1.2.1.20); Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)	1.6
23630.peg.2842	Methionine Biosynthesis	Methionine ABC transporter permease protein	-2.0
23630.peg.2027	Polyamine Metabolism	Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)	1.5
23630.peg.1546	Proline, 4-hydroxyproline uptake and utilization	Predicted regulator PutR for proline utilization, GntR family	1.7
23630.peg.1905	Putrescine utilization pathways	5-aminovalerate aminotransferase (EC 2.6.1.48) / Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.6.1.19)	1.8
23630.peg.2423	Urea decomposition	Urea ABC transporter, ATPase protein UrtE	-1.2
23630.peg.2539	Urea decomposition	Urea ABC transporter, permease protein UrtB	-1.4
23630.peg.2426	Urea decomposition	Urea ABC transporter, permease protein UrtB	-1.9
<i>Carbohydrates</i>			
23630.peg.2153	Acetyl-CoA fermentation to Butyrate	Electron transfer flavoprotein, alpha subunit	-1.3
23630.peg.726	Entner-Doudoroff Pathway	Gluconolactonase (EC 3.1.1.17)	-1.5
23630.peg.2532	Fructose utilization	1-phosphofructokinase (EC 2.7.1.56)	1.3
23630.peg.2611	Fructose utilization	Phosphotransferase system, phosphocarrier protein HPr	-1.7
23630.peg.2897	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate ABC transporter, permease protein UgpA (TC 3.A.1.1.3)	2.0
23630.peg.2893	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3)	1.8
23630.peg.2895	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)	1.7
23630.peg.2113	Glycolysis and Gluconeogenesis	Phosphoglycerate kinase (EC 2.7.2.3)	-1.3
23630.peg.2957	Glyoxylate bypass	Citrate synthase (si) (EC 2.3.3.1)	1.9

23630.peg.1827	Glyoxylate bypass	Malate synthase G (EC 2.3.3.9)	1.1
23630.peg.1826	Lactate utilization	L-lactate permease	1.6
23630.peg.2154	Lactate utilization	Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF	-1.3
23630.peg.1856	Malonate decarboxylase	Phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.-)	2.0
23630.peg.1855	Malonate decarboxylase	Malonate decarboxylase gamma subunit	1.6
23630.peg.1851	Malonate decarboxylase	Malonate decarboxylase alpha subunit	1.6
23630.peg.3002	Methylcitrate cycle	2-methylcitrate synthase (EC 2.3.3.5)	-1.4
23630.peg.4416	Pentose phosphate pathway	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	1.7
23630.peg.128	Pentose phosphate pathway	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	1.1
23630.peg.72	Peripheral Glucose Catabolism Pathways	Glucose ABC transport system, inner membrane component 2	1.1
23630.peg.235	Pyruvate metabolism I: anaplerotic reactions, PEP	Pyruvate kinase (EC 2.7.1.40)	2.1
23630.peg.1507	Pyruvate metabolism I: anaplerotic reactions, PEP	Pyruvate carboxyl transferase subunit A (EC 6.4.1.1)	1.3
23630.peg.2964	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) / Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)	1.4
23630.peg.63	TCA Cycle	Malate:quinone oxidoreductase (EC 1.1.99.16)	-1.2
Cell Division and Cell Cycle			
23630.peg.2603	Bacterial Cytoskeleton	Rod shape-determining protein MreD	1.9
23630.peg.3275	Bacterial Cytoskeleton	Cell division protein FtsK	-1.7
Cell Wall and Capsule			
23630.peg.4702	Alginate metabolism	Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)	-2.0
23630.peg.2289	Core Oligosaccharide Glycosylation in Pseudomonas	Glycosyl transferase in large core OS assembly cluster	-1.3
23630.peg.2296	Core Oligosaccharide Glycosylation in Pseudomonas	Hypothetical protein FIG015671 in large core OS assembly cluster	-1.3
23630.peg.24	KDO2-Lipid A biosynthesis	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-)	-1.8
23630.peg.2458	Peptidoglycan Biosynthesis	Penicillin-insensitive transglycosylase (EC 2.4.2.-) & transpeptidase PBP-1C	1.1
23630.peg.286	Rhamnose containing glycans	UDP-glucose 4-epimerase (EC 5.1.3.2)	2.4
23630.peg.1702	Rhamnose containing glycans	UDP-glucose 4-epimerase (EC 5.1.3.2)	1.0
Cofactors, Vitamins, Prosthetic Groups, Pigments			
23630.peg.299	5-FCL-like protein	Formyltetrahydrofolate deformylase (EC 3.5.1.10)	1.2
23630.peg.4727	Biotin biosynthesis	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	-1.7
23630.peg.3122	NAD and NADP cofactor biosynthesis global	Ribosyl nicotinamide transporter, PnuC-like	1.3
23630.peg.2308	NAD and NADP cofactor biosynthesis global	ADP-ribose pyrophosphatase (EC 3.6.1.13)	-1.2
23630.peg.3744	Pterin carbinolamine dehydratase	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)	2.9
23630.peg.3742	Pterin carbinolamine dehydratase	Fumarylacetoacetase (EC 3.7.1.2)	1.9
23630.peg.3743	Pterin carbinolamine dehydratase	Homogentisate 1,2-dioxygenase (EC 1.13.11.5)	1.4
23630.peg.3678	Pyridoxin (Vitamin B6) Biosynthesis	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	-1.3
23630.peg.875	Riboflavin, FMN and FAD metabolism	Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)	1.3
23630.peg.212	Riboflavin, FMN and FAD metabolism in plants	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61) / FAD-dependent cmnm(5)s(2)U34 oxidoreductase	1.7
DNA Metabolism			
23630.peg.4861	DNA Repair Base Excision	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)	1.2
23630.peg.420	DNA repair, bacterial	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	1.2
23630.peg.1123	DNA repair, bacterial DinG and relatives	DinG family ATP-dependent helicase CPE1197	-1.2
23630.peg.4301	DNA repair, UvrABC system	Excinuclease cho (excinuclease ABC alternative C subunit)	-1.1
Fatty Acids, Lipids, and Isoprenoids			
23630.peg.2061	Fatty acid metabolism cluster	Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)	1.4
23630.peg.3260	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	1.1

23630.peg.4561	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Diacylglycerol kinase (EC 2.7.1.107)	-1.3
23630.peg.28	Nonmevalonate Branch of Isoprenoid Biosynthesis	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	-1.4
23630.peg.3616	Phospholipid and Fatty acid biosynthesis related cluster	FIG027190: Putative transmembrane protein	1.1
23630.peg.2244	Phospholipid and Fatty acid biosynthesis related cluster	FIG027190: Putative transmembrane protein	-1.0
23630.peg.2241	Phospholipid and Fatty acid biosynthesis related cluster	FIG022199: FAD-binding protein	-1.0
Iron acquisition and metabolism			
23630.peg.1579	ABC transporter [iron.B12.siderophore.hemin]	ABC transporter (iron.B12.siderophore.hemin) , permease component	1.4
23630.peg.4736	Heme, hemin uptake and utilization systems in GramNegatives	Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)	1.5
23630.peg.4646	Siderophore Pyoverdine	FIG139991: Putative thiamine pyrophosphate-requiring enzyme	-1.3
23630.peg.4641	Siderophore Pyoverdine	ABC transporter in pyoverdin gene cluster, permease component	-1.5
Membrane Transport			
23630.peg.3767	ABC transporter alkylphosphonate (TC 3.A.1.9.1)	Phosphonate ABC transporter permease protein phnE (TC 3.A.1.9.1)	-1.3
23630.peg.2585	ABC transporter dipeptide (TC 3.A.1.5.2)	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)	2.0
23630.peg.4056	Multi-subunit cation antiporter	Na(+) H(+) antiporter subunit G	-1.3
23630.peg.354	Ton and Tol transport systems	Outer membrane lipoprotein omp16 precursor	2.0
23630.peg.106	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, periplasmic component	1.6
23630.peg.4677	TRAP Transporter unknown substrate 5	TRAP transporter solute receptor, unknown substrate 5	-2.2
23630.peg.4474	Type IV pilus	Type IV pilus biogenesis protein Pile	-1.4
23630.peg.1726	Type VI secretion systems	Uncharacterized protein ImpJ/VasE	1.8
23630.peg.625	Type VI secretion systems	ClpB protein	-1.2
23630.peg.1716	Type VI secretion systems	Uncharacterized protein similar to VCA0109	-1.3
Metabolism of Aromatic Compounds			
23630.peg.3983	n-Phenylalkanoic acid degradation	enoyl-CoA hydratase, R-specific	1.8
Motility and Chemotaxis			
23630.peg.1228	Bacterial Chemotaxis	Chemotaxis response regulator protein-glutamate methyltransferase CheB (EC 3.1.1.61)	-1.6
23630.peg.4750	Flagellum	Flagellar basal-body rod protein FlgF	2.0
23630.peg.4780	Flagellum	Flagellar motor switch protein FliN	1.7
23630.peg.4743	Flagellum	Flagellar basal-body P-ring formation protein FlgA	1.2
23630.peg.1819	Flagellum	RNA polymerase sigma factor for flagellar operon	-1.0
23630.peg.4768	Flagellum in Campylobacter	Flagellar hook-basal body complex protein FlIE	1.9
Nitrogen Metabolism			
23630.peg.3021	Nitrate and nitrite ammonification	Nitrate/nitrite transporter	-1.1
23630.peg.979	Nitrate and nitrite ammonification	Nitrate/nitrite sensor protein (EC 2.7.3.-)	-1.5
23630.peg.3017	Nitrate and nitrite ammonification	Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4)	-1.5
Nucleosides and Nucleotides			
23630.peg.3285	Nudix proteins (nucleoside triphosphate hydrolases)	Nudix-like NDP and NTP phosphohydrolase YmfB	1.7
23630.peg.3746	pyrimidine conversions	CTP synthase (EC 6.3.4.2)	-1.2
23630.peg.4526	Xanthine dehydrogenase subunits	Xanthine-uracil permease	1.0
23630.peg.1791	Xanthine Metabolism in Bacteria	Xanthine permease	1.6
Phosphorus Metabolism			
23630.peg.3762	Alkylphosphonate utilization	PhnJ protein	-1.0
23630.peg.4436	Phosphate metabolism	Predicted ATPase related to phosphate starvation-inducible protein PhoH	1.4
23630.peg.825	Phosphate metabolism	Inorganic pyrophosphatase (EC 3.6.1.1)	1.0
23630.peg.1811	Phosphate metabolism	Phosphate transport system regulatory protein PhoU	-1.2
23630.peg.4237	Phosphate metabolism	Inorganic pyrophosphatase (EC 3.6.1.1)	-1.4
23630.peg.4239	Phosphate metabolism	Pyrophosphate-specific outer membrane porin OprO	-1.8
23630.peg.1807	Phosphate metabolism	Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1)	-2.1

Protein Metabolism			
23630.peg.1395	Ribosome LSU bacterial	LSU ribosomal protein L33p @ LSU ribosomal protein L33p, zinc-independent	1.9
23630.peg.938	Ribosome LSU bacterial	LSU ribosomal protein L11p (L12e)	1.7
23630.peg.925	Ribosome LSU bacterial	LSU ribosomal protein L23p (L23Ae)	1.6
23630.peg.922	Ribosome LSU bacterial	LSU ribosomal protein L22p (L17e)	1.6
23630.peg.911	Ribosome LSU bacterial	LSU ribosomal protein L18p (L5e)	1.4
23630.peg.1390	Selenocysteine metabolism	NADH dehydrogenase-like protein / Selenide,water dikinase (EC 2.7.9.3)	-1.0
23630.peg.2196	tRNA aminoacylation, Arg	Arginyl-tRNA synthetase (EC 6.1.1.19)	2.2
23630.peg.1655	tRNA aminoacylation, Gly	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)	1.7
Regulation and Cell signaling			
23630.peg.4193	DNA-binding regulatory proteins, strays	LysR family transcriptional regulator PA3398	-1.1
23630.peg.2592	Global Two-component Regulator PrrBA in Proteobacteria	Dna binding response regulator PrrA (RegA)	1.8
Respiration			
23630.peg.4804	Biogenesis of c-type cytochromes	ABC transporter involved in cytochrome c biogenesis, CcmB subunit	1.6
23630.peg.2068	Formate hydrogenase	Putative formate dehydrogenase oxidoreductase protein	2.0
23630.peg.3882	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Na(+)-translocating NADH-quinone reductase subunit C (EC 1.6.5.-)	1.0
23630.peg.179	Quinone oxidoreductase family	Putative oxidoreductase SMc00968	2.2
23630.peg.3310	Respiratory Complex I	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)	-1.5
23630.peg.2754	Soluble cytochromes and functionally related electron carriers	Cytochrome C550 (Soluble cytochrome C)	1.8
23630.peg.4963	Soluble cytochromes and functionally related electron carriers	Cytochrome C550 (Soluble cytochrome C)	1.8
23630.peg.1775	Terminal cytochrome C oxidases	Cytochrome c oxidase polypeptide III (EC 1.9.3.1)	2.5
23630.peg.3423	Terminal cytochrome C oxidases	Cytochrome c oxidase subunit CcoO (EC 1.9.3.1)	-1.1
23630.peg.3964	Terminal cytochrome oxidases	Cytochrome O ubiquinol oxidase subunit I (EC 1.10.3.-)	1.7
RNA Metabolism			
23630.peg.2661	16S rRNA modification within P site of ribosome	rRNA small subunit methyltransferase H	-1.4
23630.peg.2096	ATP-dependent RNA helicases, bacterial	ATP-dependent RNA helicase RhlE	1.5
23630.peg.577	Polyadenylation bacterial	Poly(A) polymerase (EC 2.7.7.19)	1.5
23630.peg.2092	RNA methylation	Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-)	-1.3
23630.peg.4026	RNA pseudouridine syntheses	Similar to ribosomal large subunit pseudouridine synthase A	1.9
23630.peg.4256	tRNA modification Bacteria	Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)	2.1
Stress Response			
23630.peg.59	Bacterial hemoglobins	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	1.8
23630.peg.528	Bacterial hemoglobins	Hemoglobin-like protein HbO	1.1
23630.peg.2146	Choline and Betaine Uptake and Betaine Biosynthesis	Glycine betaine ABC transport system, permease protein OpuAB	1.2
23630.peg.2724	Choline and Betaine Uptake and Betaine Biosynthesis	GbcA Glycine betaine demethylase subunit A	-2.0
23630.peg.2174	D-tyrosyl-tRNA(Tyr) deacylase	D-tyrosyl-tRNA(Tyr) deacylase	1.5
23630.peg.2017	Protection from Reactive Oxygen Species	Cytochrome c551 peroxidase (EC 1.11.1.5)	-1.5
23630.peg.3193	Synthesis of osmoregulated periplasmic glucans	Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)	-1.5
23630.peg.3398	Universal stress protein family	Universal stress protein family 7	-1.5
23630.peg.234	Universal stress protein family	Universal stress protein E	-1.6
Sulfur Metabolism			
23630.peg.1337	Alkanesulfonate assimilation	Alkanesulfonate monooxygenase (EC 1.14.14.5)	-1.8
23630.peg.79	Galactosylceramide and Sulfatide metabolism	Arylsulfatase (EC 3.1.6.1)	1.4
23630.peg.4166	Thioredoxin-disulfide reductase	Alkyl hydroperoxide reductase protein C (EC 1.6.4.-)	1.8
Virulence, Disease and Defense			
23630.peg.2827	Adaptation to d-cysteine	D-cysteine desulfhydrase (EC 4.4.1.15)	-1.3

23630.peg.747	Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein	1.8
23630.peg.1008	Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA	-1.4
23630.peg.1006	Cobalt-zinc-cadmium resistance	Heavy metal RND efflux outer membrane protein, CzcC family	-1.4
23630.peg.3320	Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA	-1.5
23630.peg.1007	Cobalt-zinc-cadmium resistance	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	-2.0
23630.peg.2567	Copper homeostasis	Copper chaperone	-1.4
23630.peg.4812	Copper homeostasis	Cytochrome c heme lyase subunit CcmH	-1.5
23630.peg.2565	Copper homeostasis	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)	-1.6
23630.peg.1045	Copper homeostasis	Copper chaperone	-1.7
23630.peg.1705	Lysozyme inhibitors	Inhibitor of vertebrate lysozyme precursor	1.3
23630.peg.3114	MexE-MexF-OprN Multidrug Efflux System	Multidrug efflux transporter MexF	-1.3
23630.peg.2445	Multidrug Resistance Efflux Pumps	Type I secretion outer membrane protein, TolC precursor	-1.2
DEGs non classified in RAST Category			
23630.peg.4130		(R)-3-hydroxydecanoyl-ACP:CoA transacylase PhaG (3-hydroxyacyl-CoA-acyl carrier protein transferase) (EC 2.4.1.-)	-1.2
23630.peg.4535		2-Oxobutyrate oxidase, putative	-1.3
23630.peg.3904		ABC transporter ATP-binding protein	1.8
23630.peg.834		ABC transporter ATP-binding protein	1.4
23630.peg.2978		ABC transporter ATP-binding protein YvcR	1.0
23630.peg.2227		acyl carrier protein	1.3
23630.peg.2062		Acyl-CoA dehydrogenase (EC 1.3.99.3)	1.7
23630.peg.254		Acyl-CoA long-chain enzyme transcriptional related heme family	-1.0
23630.peg.4621		Aerobic C4-dicarboxylate transporter for fumarate, L-malate, D-malate, succinate	-1.6
23630.peg.642		AraC-type DNA-binding domain-containing proteins	1.7
23630.peg.2496		ATPase (PilT family)	-1.2
23630.peg.851		Auxin Efflux Carrier	-1.3
23630.peg.339		Bacterioferritin	-1.8
23630.peg.538		Carboxynorspermidine dehydrogenase	1.8
23630.peg.2719		chemotaxis protein MotB-related protein	-1.2
23630.peg.4185		Chloramphenicol-sensitive protein rarD	1.8
23630.peg.4894		Chromosome segregation ATPases	-1.1
23630.peg.4401		COG2907: Amine oxidase, flavin-containing	2.0
23630.peg.2853		COG5430: Uncharacterized secreted protein	1.1
23630.peg.2984		Conserved domain protein	-1.3
23630.peg.4508		CopG domain-containing protein	-1.6
23630.peg.2473		Cyanide insensitive terminal oxidase, putative subunit III	-1.2
23630.peg.1036		Cytochrome c family protein	-1.5
23630.peg.3619		Dolichol-phosphate mannosyltransferase (EC 2.4.1.83) in lipid-linked oligosaccharide synthesis cluster	-1.0
23630.peg.4399		FIG002994: Putative transcriptional regulator	1.6
23630.peg.3236		FIG00457034: hypothetical protein	1.9
23630.peg.2156		FIG00953113: hypothetical protein	1.1
23630.peg.952		FIG00953184: hypothetical protein	1.4
23630.peg.353		FIG00953405: hypothetical protein	1.9
23630.peg.3894		FIG00954079: hypothetical protein	-1.4
23630.peg.3990		FIG00954516: hypothetical protein	-2.1
23630.peg.3676		FIG00954807: hypothetical protein	1.6

23630.peg.1040	FIG00955197: hypothetical protein	-1.5
23630.peg.4594	FIG00955360: hypothetical protein	1.3
23630.peg.3259	FIG00956188: hypothetical protein	-1.4
23630.peg.1033	FIG00958355: hypothetical protein	-1.3
23630.peg.4602	FIG00958722: hypothetical protein	1.5
23630.peg.3189	FIG00959020: hypothetical protein	-2.1
23630.peg.2121	FIG00960943: hypothetical protein	2.3
23630.peg.2747	FIG00963224: hypothetical protein	1.4
23630.peg.4970	FIG00963224: hypothetical protein	1.4
23630.peg.168	FIG00964654: hypothetical protein	-1.1
23630.peg.2720	FIG00964765: hypothetical protein	-1.2
23630.peg.2816	FMN-dependent NADH-azoreductase	-1.2
23630.peg.3069	FOG: CBS domain	-1.1
23630.peg.318	GCN5-related N-acetyltransferase	1.6
23630.peg.3810	Gfa-like protein	1.7
23630.peg.554	Glycosyltransferase	-1.3
23630.peg.1997	HlyD family secretion protein	-1.8
23630.peg.1707	hypothetical protein	2.3
23630.peg.1359	hypothetical protein	2.2
23630.peg.3523	hypothetical protein	1.9
23630.peg.1748	hypothetical protein	1.9
23630.peg.2563	hypothetical protein	1.9
23630.peg.767	hypothetical protein	1.9
23630.peg.3814	hypothetical protein	1.7
23630.peg.458	hypothetical protein	1.7
23630.peg.116	hypothetical protein	1.5
23630.peg.3808	hypothetical protein	1.5
23630.peg.4283	hypothetical protein	1.4
23630.peg.3348	hypothetical protein	1.3
23630.peg.1062	hypothetical protein	1.1
23630.peg.3367	hypothetical protein	1.0
23630.peg.1041	hypothetical protein	-1.2
23630.peg.2141	hypothetical protein	-1.2
23630.peg.4523	hypothetical protein	-1.2
23630.peg.1061	hypothetical protein	-1.3
23630.peg.2225	hypothetical protein	-1.3
23630.peg.2903	hypothetical protein	-1.4
23630.peg.3410	hypothetical protein	-1.4
23630.peg.412	hypothetical protein	-1.5
23630.peg.3384	hypothetical protein	-1.5
23630.peg.2701	hypothetical protein	-1.6
23630.peg.712	hypothetical protein	-1.7
23630.peg.410	hypothetical protein	-1.7
23630.peg.1512	hypothetical protein	-1.9
23630.peg.371	hypothetical protein	-2.0
23630.peg.4432	hypothetical protein	-2.3
23630.peg.1044	hypothetical protein	-2.7

23630.peg.3329	Integral membrane protein TerC	1.5
23630.peg.316	Iron-regulated protein A precursor	1.1
23630.peg.648	Medium-chain-fatty-acid--CoA ligase (EC 6.2.1.-)	1.8
23630.peg.656	Methyl-accepting chemotaxis protein	1.0
23630.peg.2102	Methyl-accepting chemotaxis protein	-1.0
23630.peg.3335	Methyl-accepting chemotaxis protein	-1.6
23630.peg.2718	Methyl-accepting chemotaxis protein	-1.8
23630.peg.4352	NADH:flavin oxidoreductases, Old Yellow Enzyme family	1.1
23630.peg.4527	Nucleoside-binding outer membrane protein	-1.8
23630.peg.2735	Outer membrane protein (porin)	-1.5
23630.peg.4616	outer membrane protein H1	1.7
23630.peg.1284	Oxalate/formate antiporter	-1.6
23630.peg.3457	Oxidoreductase (EC 1.1.1.-)	-1.8
23630.peg.3501	Oxidoreductase, short-chain dehydrogenase/reductase family	1.3
23630.peg.2365	Peptidase M50	-1.2
23630.peg.3833	Permease of the major facilitator superfamily	-1.2
23630.peg.110	Probable acyl-CoA dehydrogenase (EC 1.3.99.3)	1.0
23630.peg.1537	probable dioxygenase	1.7
23630.peg.2587	probable metallopeptidase	-1.5
23630.peg.2896	Probable transmembrane protein	1.1
23630.peg.3503	Probable two-component response regulator	-1.5
23630.peg.3097	Protease subunit of ATP-dependent Clp proteases	-1.4
23630.peg.2104	protein of unknown function DUF1090	-1.4
23630.peg.1912	protein of unknown function DUF1127	-1.6
23630.peg.4430	protein of unknown function DUF6, transmembrane	-1.0
23630.peg.3401	protein of unknown function DUF903	1.7
23630.peg.1638	Protein YidD	1.1
23630.peg.449	Protein-export membrane protein SecF (TC 3.A.5.1.1)	-1.9
23630.peg.48	putative cold-shock DNA-binding domain protein	-1.7
23630.peg.618	Putative oligoketide cyclase/dehydratase or lipid transport protein YfjG	1.6
23630.peg.3300	Putative phosphatase	-2.5
23630.peg.718	regulatory protein, TetR	-1.3
23630.peg.1320	Ribonucleotide reductase, alpha subunit	1.6
23630.peg.1649	Ser/Thr and Tyr protein phosphatase (dual specificity)	-1.2
23630.peg.2285	Serine/threonine protein kinase	-1.5
23630.peg.3948	short-chain dehydrogenase/reductase	1.0
23630.peg.4737	sodium:dicarboxylate symporter	1.1
23630.peg.3923	Spermidine/putrescine-binding periplasmic protein	1.6
23630.peg.905	SSU ribosomal protein S13p (S18e)	1.4
23630.peg.918	SSU ribosomal protein S17p (S11e)	2.0
23630.peg.910	SSU ribosomal protein S5p (S2e)	1.4
23630.peg.2088	still frameshift probable component of chemotactic signal transduction system	-1.1
23630.peg.1887	SUGAR TRANSPORTER	1.1
23630.peg.3684	Thiosulfate sulfurtransferase, rhodanese (EC 2.8.1.1)	1.9
23630.peg.1988	Transcriptional regulator, GntR family	1.6
23630.peg.197	Transcriptional regulator, LysR family	-1.5
23630.peg.3934	transcriptional regulator, LysR family	-1.6

23630.peg.4397	Transcriptional regulator, MerR family, associated with photolyase	1.9
23630.peg.4888	Transglutaminase-like enzymes, putative cysteine proteases	-1.2
23630.peg.2260	TrkA domain protein	1.3
23630.peg.4603	Trp repressor-binding protein	1.6
23630.peg.2083	twitching motility protein PilG	-1.5
23630.peg.3369	two-component system sensor protein	-1.6
23630.peg.3247	Type IV secretion system protein VirD4	1.5
23630.peg.2548	Uncharacterized iron-regulated membrane protein; Iron-uptake factor PiuB	-1.3
23630.peg.327	Uncharacterized protein ynbE; probable lipoprotein STY1424	-1.4
23630.peg.2538	Urea ABC transporter, urea binding protein	-1.8

^c Relative gene expression is presented as the mean ratio of the fluorescence intensity of 7-h developing biofilm to planktonic cells. Each gene showed significant differential expression ($p < 0.05$).