

SAA6008_01027	2.8	0.00072	2.82	0.00026	COG0150F	<i>purM</i>	phosphoribosylaminoimidazole synthetase
SAA6008_01028	2.57	0.0021	2.18	0.00075	COG0299F	<i>purN</i>	phosphoribosylglycinamide formyltransferase
SAA6008_01029	3.14	0.000096	1.68	0.042	COG0138F	<i>purH</i>	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
SAA6008_01030	2.68	0.000014	2.7	0.0025	COG0151F	<i>purD</i>	phosphoribosylamine-glycine ligase
SAA6008_01041	3.21	0.0007	4.77	0.0034	COG1271C		cytochrome ubiquinol oxidase
SAA6008_01043	1.7	0.0016	2.26	0.00018	COG0569P		NAD ⁺ binding potassium transporter
SAA6008_01053	1.69	0.044	7.73	0.02	COG1476K	<i>trkA</i>	transcriptional regulator Cro/C family
SAA6008_01111	4.58	0.0011	5.49	0.0061		<i>efb</i>	fibrinogen-binding protein precursor
SAA6008_01112	4.79	0.001	7.5	0.00099		<i>scc</i>	fibrinogen-binding protein precursor-related protein
SAA6008_01152	3.16	0.00042	6.98	0.0018	COG2065F	<i>pyrR</i>	pyrimidine regulatory protein
SAA6008_01153	2.58	0.0043	10.34	0.0000039	COG2233F	<i>pyrP</i>	uracil permease
SAA6008_01154	3.29	0.0029	10.5	0.00053	COG0540F	<i>pyrB</i>	aspartate carbamoyltransferase catalytic subunit
SAA6008_01155	2.92	0.0077	8.61	0.00013	COG0044F	<i>pyrC</i>	dihydroorotase
SAA6008_01156	2.86	0.039	15.38	0.0000075	COG0505EF	<i>pyrAA</i>	carbamoyl-phosphate synthase small subunit
SAA6008_01234	1.83	0.00029	1.97	0.0037	COG0612R		zinc-dependent peptidase, M16 family
SAA6008_01264	4.47	0.00066	3.13	0.012			conserved hypothetical protein
SAA6008_01287	2.1	0.0016	2.97	0.044			conserved hypothetical protein
SAA6008_01318	2.27	0.00053	4.12	0.016	COG0344S	<i>plsY</i>	glycerol-3-phosphate acyltransferase PlsY
SAA6008_01321	2.07	0.00003	2.96	0.00084	COG1115E	<i>alsT</i>	amino acid carrier protein (sodium/alanine symporter)
SAA6008_01373	1.95	0.00042	1.57	0.023	COG1114E	<i>braB</i>	branched-chain amino acid carrier protein
SAA6008_01405	13.76	0.02	4.99	0.014	COG0531E	<i>frtA</i>	fructoselysine transporter
SAA6008_01407	3.61	0.0012	3.98	0.018	COG0686E	<i>ald1</i>	alanine dehydrogenase
SAA6008_01410	3.37	0.00017	4.1	0.0066	COG3182S	<i>piuB</i>	putative iron-regulated membrane protein
SAA6008_01785	1.59	0.007	1.82	0.00081			conserved hypothetical protein
SAA6008_01799	1.86	0.014	1.58	0.0012	COG3481R	<i>cbf1</i>	3'-5' exoribonuclease YhaM / cmp-binding-factor 1
SAA6008_01815	3.71	0.0065	11.6	0.016	COG0765E		polar amino acid ABC transporter, inner membrane subunit
SAA6008_01835	6.96	0.000069	4.12	0.015	COG5546S		phage holin
SAA6008_02155	1.74	0.00013	2.41	0.00015	COG2890J		modification methylase HemK family protein
SAA6008_02156	2.51	0.000093	3.3	0.0017	COG0216J	<i>prfA</i>	peptide chain release factor RF1 / peptide chain release factor 1
SAA6008_02157	1.77	0.00036	2.62	0.00056	COG1435F	<i>tdk</i>	thymidine kinase
SAA6008_02174	1.68	0.006	1.56	0.039	COG0213F	<i>pdp</i>	putative pyrimidine-nucleoside phosphorylase / pyrimidine-nucleoside phosphorylase
SAA6008_02336	1.58	0.0061	3.59	0.0017	COG1757C	<i>nhaC</i>	putative Na ⁺ /H ⁺ antiporter
SAA6008_02342	2.06	0.00017	2.78	0.00013	COG193G	<i>lytA</i>	Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase
SAA6008_02398	2.76	0.034	2.3	0.0073	COG0577V		hemin ABC superfamily ATP binding cassette transporter, permease component
SAA6008_02432	1.79	0.023	3.07	0.00075	COG2197TK		two component transcriptional regulator, LuxR family
SAA6008_02433	3.5	0.0019	4.01	0.0063	COG4585T	<i>nreB</i>	oxygen sensor histidine kinase
SAA6008_02607	2.33	0.00054	6.22	0.011		<i>isaB</i>	immunodominant antigen A, transglycosylase IsaA
SAA6008_02751	1.91	0.015	2.26	0.0056	COG4932M	<i>can</i>	collagen adhesin domain protein