Additional file 2: Genes differentially expressed at 2 and/or 6 post internalization

	Common	Organism	2h fold change	6h fold change	Protein name	GO*	class	Annot
SA0033	*aadD*	N315	3.69		kanamycin nucleotidyltransferase			-
SA1519	*aapA*	N315	0.17	0.17	Dserine/Dalanine/glycine transporter	**COG1113E**	**E**	Amino acid transport and metabolism
SA1522	*accA*	N315	0.09	0.11	acetylCoA carboxylase carboxyl transferase subunit alpha	**COG0825I**	**I**	Lipid transport and metabolism
SA1357	*accC*	N315	0.04	0.09	acetylCoA carboxylase accC	**COG0439I**	**I**	Lipid transport and metabolism
SA0562	*adh1*	N315	0.14	0.14	alcohol dehydrogenase I	**COG1064R**	**R**	General function prediction only
SA2027	*adk*	N315	0.01	0.15	adenylate kinase	**COG0563F**	**F**	Nucleotide transport and metabolism
SA1844	*agrA*	N315	0.10	0.12	AgrA	**COG3279KT**	**t**	Signal transduction mechanisms
SA1843	*agrC*	N315	0.01	0.02	AgrC	**COG2972T**	**T**	Signal transduction mechanisms
SA0366	*ahpC*	N315	0.11	0.11	alkyl hydroperoxide reductase subunit C	**COG0450O**	**O**	Posttranslational modification, protein turnover, chaperones
SA0365	*ahpF*	N315	0.11	0.30	alkyl hydroperoxide reductase subunit F	**COG3634O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1531	*ald*	N315	3.07		alanine dehydrogenase	**COG0686E**	**E**	Amino acid transport and metabolism
SA0162	*aldA*	N315	3.70		aldehyde dehydrogenase homologue	**COG1012C**	**C**	Energy production and conversion
SA1874	*alr*	N315	0.21	0.23	alanine racemase	**COG0787M**	**M**	Cell wall/membrane/envelope biogenesis
SA1190	*alsT*	N315	0.18		amino acid carrier protein	**COG1115E**	**E**	Amino acid transport and metabolism
SA1695	*ampS*	N315	0.17	0.18	aminopeptidase ampS	**COG2309E**	**E**	Amino acid transport and metabolism
SA0822	*argG*	N315	0.30		argininosuccinate synthase	**COG0137E**	**E**	Amino acid transport and metabolism
SA0564	*argS*	N315	0.19	0.17	arginyltRNA synthetase	**COG0018J**	**J**	Translation, ribosomal structure and biogenesis
SA1246	*arlS*	N315	0.33		putative protein histidine kinase ArlS	**COG0642T**	**T**	Signal transduction mechanisms
SA1297	*aroA*	N315	0.08	0.17	3phosphoshikimate 1carboxyvinyltransferase	**COG0128E**	**E**	Amino acid transport and metabolism
SA1298	*aroB*	N315	0.27		3dehydroquinate synthase	**COG0337E**	**E**	Amino acid transport and metabolism
SA1424	*aroE*	N315	0.03	0.04	shikimate dehydrogenease	**COG0169E**	**E**	Amino acid transport and metabolism
SA1226	*asd*	N315	0.13	0.23	aspartate semialdehyde dehydrogenase	**COG0136E**	**E**	Amino acid transport and metabolism
SA1984	*asp23*	N315	0.04	0.06	alkaline shock protein 23, ASP23			-
SA1456	*aspS*	N315	0.10	0.06	aspartyltRNA synthetase	**COG0173J**	**J**	Translation, ribosomal structure and biogenesis
SA0905	*atl*	N315	0.04	0.20	autolysin	**COG4193G,COG5632M**	**G**	Carbohydrate transport and metabolism
SA1907	*atpA*	N315	0.08	0.25	ATP synthase alpha chain	**COG0056C**	**C**	Energy production and conversion
SA1911	*atpB*	N315	0.01	0.03	ATP synthase A chain			-
SA1904	*atpC*	N315	0.19	0.24	FoF1ATP synthase epsilon subunit			-
SA1905	*atpD*	N315	0.02	0.09	ATP synthase beta chain	**COG0055C**	**C**	Energy production and conversion
SA1910	*atpE*	N315	0.01	0.10	ATP synthase C chain	**COG0636C**	**C**	Energy production and conversion
SA1909	*atpF*	N315	0.01	0.12	ATP synthase B chain	**COG0711C**	**C**	Energy production and conversion
SA1906	*atpG*	N315	0.05	0.15	ATP synthase gamma chain	**COG0224C**	**C**	Energy production and conversion
SA1908	*atpH*	N315	0.08	0.20	ATP synthase delta chain	**COG0712C**	**C**	Energy production and conversion
SA2430	*aur*	N315	3.91		zinc metalloproteinase aureolysin	**COG3227E**	**E**	Amino acid transport and metabolism
SA2405	*betA*	N315	0.24	0.30	choline dehydrogenase	**COG2303E**	**E**	Amino acid transport and metabolism
SA1396	*bex*	N315	0.16	0.18	GTPbinding protain Era homolog	**COG1159R**	**R**	General function prediction only
SA1347	*bfmBAB*	N315	0.23	0.28	branchedchain alphaketo acid dehydrogenase E1	**COG0022C**	**C**	Energy production and conversion
SA2213	*bioB*	N315	0.08	0.14	biotin synthase	**COG0502H**	**H**	Coenzyme transport and metabolism
SA1346	*bmfBB*	N315	0.31		branchedchain alphaketo acid dehydrogenase E2	**COG0508C**	**C**	Energy production and conversion
MW1766	*bsaA1*	MW2	3.51		gallidermin precursor [Genomic island nu Sa beta2]			-
MW1764	*bsaB*	MW2	3.89	3.83	lantibiotic epidermin biosynthesis protein EpiB [Genomic island nu Sa beta2]			-
MW0136	*cap8M*	MW2	0.07	0.23	capsular polysaccharide synthesis enzyme Cap8M	**COG2148M**	**M**	Cell wall/membrane/envelope biogenesis
SA0149	*capF*	N315	0.23	0.25	capsular polysaccharide synthesis enzyme Cap5F	**COG1898M,COG0451MG**	**g**	Carbohydrate transport and metabolism
SA0150	*capG*	N315	0.15	0.24	capsular polysaccharide synthesis enzyme Cap5G	**COG0381M**	**M**	Cell wall/membrane/envelope biogenesis
SA0152	*capI*	N315	3.16		capsular polysaccharide synthesis enzyme Cap5I	**COG0438M**	**M**	Cell wall/membrane/envelope biogenesis
SA0157	*capN*	N315	0.18	0.32	capsular polysaccharide synthesis enzyme Cap5N	**COG0451MG**	**g**	Carbohydrate transport and metabolism
SA1557	*ccpA*	N315	0.29	0.29	catabolite control protein A	**COG1609K**	**K**	Transcription
SA1397	*cdd*	N315	0.15	0.19	cytidine deaminase	**COG0295F**	**F**	Nucleotide transport and metabolism
SA0831	*cdr*	N315	0.31	0.33	coenzyme A disulfide reductase	**COG0446R**	**R**	General function prediction only
SA1065	*cfxE*	N315	0.28	0.31	ribulose5phosphate 3epimerase homolog	**COG0036G**	**G**	Carbohydrate transport and metabolism
SA1184	*citB*	N315	0.01	0.01	aconitate hydratase	**COG1048C**	**C**	Energy production and conversion
SA1517	*citC*	N315	0.16	0.19	isocitrate dehyrogenase	**COG0538C**	**C**	Energy production and conversion
SA1518	*citZ*	N315	0.18	0.17	citrate synthase II	**COG0372C**	**C**	Energy production and conversion
SA2423	*clfB*	N315	0.17	0.19	Clumping factor B			-
SA0483	*clpC*	N315	0.23		endopeptidase	**COG0542O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1498	*clpX*	N315	0.29	0.33	protease ClpX	**COG1219O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1097	*clpY*	N315	0.14	0.28	heat shock protein HslU	**COG1220O**	**O**	Posttranslational modification, protein turnover, chaperones
SA2349	*crtM*	N315	0.22	0.27	squalene synthase	**COG1562I**	**I**	Lipid transport and metabolism
SA2494	*cspB*	N315	5.24		cold shock protein cspB			-
SA0965	*ctaB*	N315	0.16	0.16	cytochrome caa3 oxidase (assembly factor) homolog	**COG0109O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1929	*ctrA*	N315	0.10	0.11	CTP synthase	**COG0504F**	**F**	Nucleotide transport and metabolism
SA0480	*ctsR*	N315	0.16		transcription repressor of class III stress genes homologue			-
SA0487	*cysE*	N315	0.32		Serine acetyltransferase homologue	**COG1045E**	**E**	Amino acid transport and metabolism
SA0471	*cysK*	N315	0.19	0.12	cysteine synthase (oacetylserine sulfhydrylase) homologue	**COG0031E**	**E**	Amino acid transport and metabolism
SA0418	*cysM*	N315	3.39	3.69	cysteine synthase homologue	**COG0031E**	**E**	Amino acid transport and metabolism
SA0488	*cysS*	N315	0.09	0.13	cysteinyltRNA synthetase	**COG0215J**	**J**	Translation, ribosomal structure and biogenesis
SA1948	*czrB*	N315		0.33	cationefflux system membrane protein homolog	**COG1230P**	**P**	Inorganic ion transport and metabolism
SA1227	*dapA*	N315	0.08	0.14	dihydrodipicolinate synthase	**COG0329EM**	**e**	Amino acid transport and metabolism
MW1284	*dapB*	MW2	0.31	0.29	dihydrodipicolinate reductase	**COG0289E**	**E**	Amino acid transport and metabolism
SA1887	*ddlA*	N315	0.33		DalanineDalanine ligase	**COG1181M**	**M**	Cell wall/membrane/envelope biogenesis
SA1259	*dfrA*	N315	0.03	0.20	dihydrofolate reductase	**COG0262H**	**H**	Coenzyme transport and metabolism
SA1164	*dhoM*	N315	0.28		homoserine dehydrogenase	**COG0460E**	**E**	Amino acid transport and metabolism
SA1288	*dinG*	N315	0.29	0.25	probable ATPdependent DNA helicase dinG	**COG0847L,COG1199KL**	**L**	Replication, recombination and repair
SA1027	*div1b*	N315	0.05	0.11	cell division protein, FtsQ homolog	**COG1589M**	**M**	Cell wall/membrane/envelope biogenesis
SA0793	*dltA*	N315	0.07	0.17	DalanineDalanyl carrier protein ligase	**COG1020Q**	**Q**	Secondary metabolites biosynthesis, transport and catabolism
SA0794	*dltB*	N315	0.04	0.10	DltB membrane protein	**COG1696M**	**M**	Cell wall/membrane/envelope biogenesis
SA0795	*dltC*	N315	0.06	0.10	Dalanyl carrier protein	**COG0236IQ**	**i**	Lipid transport and metabolism
SA0796	*dltD*	N315	0.16	0.18	poly Dalanine transfer protein	**COG3966M**	**M**	Cell wall/membrane/envelope biogenesis
SA1508	*dnaB*	N315	0.04	0.05	chromosome replication initiation/membrane attachment protei	**COG3611L**	**L**	Replication, recombination and repair
SA0015	*dnaC*	N315	0.23	0.26	replicative DNA helicase	**COG0305L**	**L**	Replication, recombination and repair
SA1525	*dnaE*	N315	0.14	0.15	DNA polymerase III, alpha chain	**COG0587L**	**L**	Replication, recombination and repair
SA1391	*dnaG*	N315	0.15	0.25	DNA primase	**COG0358L**	**L**	Replication, recombination and repair
SA1507	*dnaI*	N315	0.07	0.07	primosomal protein	**COG1484L**	**L**	Replication, recombination and repair
SA1408	*dnaJ*	N315	0.31		DnaJ protein	**COG0484O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1409	*dnaK*	N315	0.22		DnaK protein	**COG0443O**	**O**	Posttranslational modification, protein turnover, chaperones
SA0002	*dnaN*	N315	0.12	0.14	DNA polymerase III, beta chain	**COG0592L**	**L**	Replication, recombination and repair
SA1875	*dpj*	N315	0.14	0.22	holoACP synthase	**COG0736I**	**I**	Lipid transport and metabolism
SA1941	*dps*	N315	3.40	3.66	general stress protein 20U	**COG0783P**	**P**	Inorganic ion transport and metabolism
MW0113	*drm*	MW2		0.18	phosphopentomutase	**COG1015G**	**G**	Carbohydrate transport and metabolism
SA0134	*drm*	N315	0.32		phosphopentomutase	**COG1015G**	**G**	Carbohydrate transport and metabolism
SA2480	*drp35*	N315	3.25	3.47	Drp35	**COG3386G**	**G**	Carbohydrate transport and metabolism
SA1267	*ebhA*	N315	3.23	3.41	streptococcal adhesin emb	**COG0419L**	**L**	Replication, recombination and repair
SA0731	*eno*	N315	0.04	0.13	enolase	**COG0148G**	**G**	Carbohydrate transport and metabolism
SA0843	*fab*	N315	0.30	0.31	3oxoacyl synthase	**COG0304IQ**	**i**	Lipid transport and metabolism
SA1073	*fabD*	N315	0.18	0.27	malonyl CoAacyl carrier protein transacylase	**COG0331I**	**I**	Lipid transport and metabolism
SA1074	*fabG*	N315	0.31	0.33	3oxoacyl reductase	**COG1028IQR**	**r**	General function prediction only
SA0842	*FabH*	N315	0.10	0.08	FabH	**COG0332I**	**I**	Lipid transport and metabolism
SA0869	*fabI*	N315	0.13	0.18	trans2enoylACP reductase	**COG0623I**	**I**	Lipid transport and metabolism
SA1927	*fbaA*	N315	0.14	0.15	fructosebisphosphate aldolase	**COG0191G**	**G**	Carbohydrate transport and metabolism
SA1206	*femA*	N315	0.33	0.28	factor essential for expression of methicillin resistance	**COG2348V**	**V**	Defense mechanisms
SA1207	*femB*	N315	0.14	0.10	FemB protein	**COG2348V**	**V**	Defense mechanisms
SA1080	*ffh*	N315	0.17	0.15	signal recognition particle homolog	**COG0541U**	**U**	Intracellular trafficking, secretion, and vesicular transport
SA1553	*fhs*	N315	0.14	0.19	formyltetrahydrofolate synthetase	**COG2759F**	**F**	Nucleotide transport and metabolism
SA0602	*fhuA*	N315	0.28		ferrichrome transport ATPbinding protein	**COG1120PH**	**h**	Coenzyme transport and metabolism
SA0603	*fhuB*	N315	0.16	0.24	ferrichrome transport permease	**COG0609P**	**P**	Inorganic ion transport and metabolism
SA1193	*fmtC*	N315	0.07	0.16	oxacillin resistancerelated FmtC protein	**COG0392S,COG2898S**	**S**	Function unknown
SA2291	*fnb*	N315	3.23		fibronectinbinding protein homolog			-
SA2290	*fnbB*	N315		3.83	fibronectinbinding protein homolog			-
SA1487	*folC*	N315	0.12	0.33	folylpolyglutamate synthase	**COG0285H**	**H**	Coenzyme transport and metabolism
SA0915	*folD*	N315	0.05	0.08	FolD bifunctional protein	**COG0190H**	**H**	Coenzyme transport and metabolism
SA0472	*folP*	N315	3.52		dihydropteroate synthase chain A synthetase	**COG0294H**	**H**	Coenzyme transport and metabolism
SA2124	*fosB*	N315		3.45	fosfomycin resistance protein fofB	**COG0346E**	**E**	Amino acid transport and metabolism
SA1102	*frr*	N315	0.08	0.23	ribosome recycling factor			-
SA0655	*fruA*	N315	3.47	3.65	fructose specific permease	**COG1762GT,COG1299G**	**g**	Carbohydrate transport and metabolism
SA0469	*ftsH*	N315	0.11	0.16	celldivision protein	**COG0465O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1029	*ftsZ*	N315	0.05	0.07	cell division protein	**COG0206D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA0505	*fus*	N315	0.07	0.25	translational elongation factor G	**COG0480J**	**J**	Translation, ribosomal structure and biogenesis
SA0727	*gap*	N315	0.10	0.27	glyceraldehyde3phosphate dehydrogenase	**COG0057G**	**G**	Carbohydrate transport and metabolism
SA0726	*gapR*	N315	0.31		glycolytic operon regulator	**COG2390K**	**K**	Transcription
SA0309	*geh*	N315	0.04	0.07	glycerol ester hydrolase	**COG1075R**	**R**	General function prediction only
SA1302	*gerCC*	N315	0.32	0.22	heptaprenyl diphosphate syntase component II	**COG0142H**	**H**	Coenzyme transport and metabolism
SA1094	*gid*	N315	0.04	0.07	glucoseinhibited division protein gid	**COG1206J**	**J**	Translation, ribosomal structure and biogenesis
SA2500	*gidA*	N315	0.08	0.29	glucose inhibited division protein A	**COG0445D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA2499	*gidB*	N315	0.12	0.32	glucose inhibited division protein B	**COG0357M**	**M**	Cell wall/membrane/envelope biogenesis
SA0183	*glcA*	N315	0.15	0.14	PTS enzyme II (EC 2.7.1.69), glucosespecific, factor IIA homol	**COG1263G**	**G**	Carbohydrate transport and metabolism
SA1377	*glcK*	N315	0.19	0.16	glucokinase	**COG1940KG**	**g**	Carbohydrate transport and metabolism
SA1965	*glmM(femD)*	N315	0.32	0.28	phosphoglucosaminemutase	**COG1109G**	**G**	Carbohydrate transport and metabolism
SA1150	*glnA*	N315	0.22		glutamineammonia ligase			-
SA1140	*glpF*	N315	3.37	3.16	glycerol uptake facilitator			-
SA1139	*glpP*	N315	0.15	0.12	glycerol uptake operon antiterminator regulatory protein	**COG1954K**	**K**	Transcription
SA0820	*glpQ*	N315	3.16		glycerophosphoryl diester phosphodiesterase	**COG0584C**	**C**	Energy production and conversion
SA0325	*glpT*	N315	4.74	4.10	glycerol3phosphate transporter	**COG2271G**	**G**	Carbohydrate transport and metabolism
SA0486	*gltX*	N315	0.18	0.18	glutamyltRNA synthetase	**COG0008J**	**J**	Translation, ribosomal structure and biogenesis
SA1915	*glyA*	N315	0.03	0.06	serine hydroxymethyl transferase	**COG0112E**	**E**	Amino acid transport and metabolism
SA1342	*gnd*	N315	0.09	0.09	phosphogluconate dehydrogenase	**COG0362G**	**G**	Carbohydrate transport and metabolism
SA2294	*gntK*	N315	3.51		gluconokinase	**COG1070G**	**G**	Carbohydrate transport and metabolism
SA2293	*gntP*	N315	3.13		gluconate permease	**COG2610GE**	**e**	Amino acid transport and metabolism
SA1306	*gpsA*	N315	0.05	0.08	glycerol3phosphate dehydrogenase	**COG0240C**	**C**	Energy production and conversion
SA1836	*groEL*	N315	0.20	0.24	GroEL protein	**COG0459O**	**O**	Posttranslational modification, protein turnover, chaperones
SA0376	*guaA*	N315	0.11	0.12	GMP synthase	**COG0518F,COG0519F**	**F**	Nucleotide transport and metabolism
SA0375	*guaB*	N315	0.06	0.09	inositolmonophosphate dehydrogenase	**COG0517R,COG0516F**	**R**	General function prediction only
SA0819	*gudB*	N315		0.33	NADspecific glutamate dehydrogenase	**COG0334E**	**E**	Amino acid transport and metabolism
SA0006	*gyrA*	N315	0.13	0.11	DNA gyrase subunit A	**COG0188L**	**L**	Replication, recombination and repair
SA0005	*gyrB*	N315	0.13	0.12	DNA gyrase subunit B	**COG0187L**	**L**	Replication, recombination and repair
SA1496	*hemA*	N315	0.15	0.28	glutamyltRNA reductase	**COG0373H**	**H**	Coenzyme transport and metabolism
SA1492	*hemB*	N315	0.06	0.14	deltaaminolevulinic acid dehydratase			-
SA1494	*hemC*	N315	0.20		porphobilinogen deaminase			-

SA1493	*hemD*	N315	0.24		uroporphyrinogen III synthase	**COG1587H**	**H**	Coenzyme transport and metabolism
SA1652	*hemE*	N315	0.14		uroporphyrinogen decarboxylase	**COG0407H**	**H**	Coenzyme transport and metabolism
SA1651	*hemH*	N315	0.32		ferrochelatase homolog			-
SA1491	*hemL*	N315	0.03	0.03	glutamate1semialdehyde 2,1aminomutase	**COG0001H**	**H**	Coenzyme transport and metabolism
SA1495	*hemX*	N315	0.05	0.26	hemA concentration negative effector hemX	**COG0755O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1650	*hemY*	N315	0.15	0.23	protoporphyrinogen oxidase	**COG1232H**	**H**	Coenzyme transport and metabolism
MW1940	*hlb*	MW2	3.08		truncated betahemolysin			-
SAS065	*hld*	N315	3.05		deltahemolysin			-
SA2209	*hlgB*	N315		3.12	gammahemolysin component B			-
SA0055	HP	N315	4.18	4.74	Hypothetical protein			-
SA0213	HP	N315	9.31	3.91	Hypothetical protein			-
SA0301	HP	N315	7.24	3.14	Hypothetical protein			-
SA0360	HP	N315	3.34	3.55	Hypothetical protein			-
SA0554	HP	N315	5.02	4.31	Hypothetical protein			-
SA0630	HP	N315	4.04	3.91	Hypothetical protein			-
SA0632	HP	N315	4.29	3.70	Hypothetical protein			-
SA0906	HP	N315	3.96	3.25	Hypothetical protein			-
SA1744	HP	N315	3.64	4.61	Hypothetical protein			-
SA2478	HP	N315	3.82	3.55	Hypothetical protein			-
SA2479	HP	N315	18.60	9.90	Hypothetical protein			-
SA0024	HP	N315	3.83		Hypothetical protein			-
SA0025	HP	N315	12.89		Hypothetical protein			-
SA0030	HP	N315	4.05		Hypothetical protein			-
SA0031	HP	N315	4.42		Hypothetical protein			-
SA0072	HP	N315	4.95		Hypothetical protein			-
SA0074	HP	N315	50.25		Hypothetical protein			-
SA0076	HP	N315	8.15		Hypothetical protein			-
SA0080	HP	N315	3.21		Hypothetical protein			-
SA0096	HP	N315	3.19		Hypothetical protein			-
SA0101	HP	N315	5.97		Hypothetical protein			-
SA0103	HP	N315	3.10		Hypothetical protein			-
SA0105	HP	N315	3.15		Hypothetical protein			-
SA0188	HP	N315	4.11		Hypothetical protein			-
SA0203	HP	N315	4.45		Hypothetical protein			-
SA0269	HP	N315	3.09		Hypothetical protein			-
SA0292	HP	N315	6.71		Hypothetical protein			-
SA0355	HP	N315	4.02		Hypothetical protein			-
SA0358	HP	N315	3.70		Hypothetical protein			-
SA0377	HP	N315	3.12		Hypothetical protein			-
SA0378	HP	N315	5.20		Hypothetical protein			-
SA0394	HP	N315	3.43		Hypothetical protein			-
SA0399	HP	N315	3.92		Hypothetical protein			-
SA0400	HP	N315	4.19		Hypothetical protein			-
SA0402	HP	N315	3.21		Hypothetical protein			-
SA0403	HP	N315	4.25		Hypothetical protein			-
SA0532	HP	N315	4.17		Hypothetical protein			-
SA0575	HP	N315	3.70		Hypothetical protein			-
SA0651	HP	N315	4.93		Hypothetical protein			-
SA0751	HP	N315	4.49		Hypothetical protein			-
SA0752	HP	N315	26.47		Hypothetical protein			-
SA0798	HP	N315	5.77		Hypothetical protein			-
SA0844	HP	N315	5.73		Hypothetical protein			-
SA0883	HP	N315	4.05		Hypothetical protein			-
SA0889	HP	N315	3.09		Hypothetical protein			-
SA0930	HP	N315	4.71		Hypothetical protein			-
SA1002	HP	N315	4.38		Hypothetical protein			-
SA1179	HP	N315	3.33		Hypothetical protein			-
SA1208	HP	N315	3.67		Hypothetical protein			-
SA1284	HP	N315	3.42		Hypothetical protein			-
SA1320	HP	N315	4.87		Hypothetical protein			-
SA1437	HP	N315	4.71		Hypothetical protein			-
SA1477	HP	N315	3.33		Hypothetical protein			-
SA1567	HP	N315	3.72		Hypothetical protein			-
SA1600	HP	N315	4.24		Hypothetical protein			-
SA1610	HP	N315	4.67		Hypothetical protein			-
SA1616	HP	N315	4.66		Hypothetical protein			-
SA1619	HP	N315	3.22		Hypothetical protein			-
SA1621	HP	N315	3.58		Hypothetical protein			-
SA1670	HP	N315	5.42		Hypothetical protein			-
SA1706	HP	N315	15.00		Hypothetical protein			-
SA1767	HP	N315	3.37		Hypothetical protein			-
SA1778	HP	N315	3.33		Hypothetical protein			-
SA1782	HP	N315	3.00		Hypothetical protein			-
SA1786	HP	N315	4.05		Hypothetical protein			-
SA1788	HP	N315	4.56		Hypothetical protein			-
SA1797	HP	N315	4.08		Hypothetical protein			-
SA1802	HP	N315	4.36		Hypothetical protein			-
SA1809	HP	N315	3.33		Hypothetical protein			-
SA1821	HP	N315	3.33		Hypothetical protein			-
SA1825	HP	N315	4.03		Hypothetical protein			-
SA1826	HP	N315	3.29		Hypothetical protein			-
SA1832	HP	N315	22.41		Hypothetical protein			-
SA1928	HP	N315	3.81		Hypothetical protein			-
SA1971	HP	N315	3.09		Hypothetical protein			-
SA2015	HP	N315	3.57		Hypothetical protein			-
SA2107	HP	N315	3.21		Hypothetical protein			-
SA2249	HP	N315	6.49		Hypothetical protein			-
SA2263	HP	N315	3.04		Hypothetical protein			-
SA2267	HP	N315	4.59		Hypothetical protein			-
SA2292	HP	N315	4.22		Hypothetical protein			-
SA2321	HP	N315	3.91		Hypothetical protein			-
SA2338	HP	N315	4.02		Hypothetical protein			-
SA2398	HP	N315	3.39		Hypothetical protein			-
SA2432	HP	N315	3.04		Hypothetical protein			-
SA2444	HP	N315	3.83		Hypothetical protein			-
SA2485	HP	N315	8.39		Hypothetical protein			-
SA2488	HP	N315	3.74		Hypothetical protein			-
SAS002	HP	N315	4.37		Hypothetical protein			-
SAS003	HP	N315	3.51		Hypothetical protein			-
SAS009	HP	N315	3.13		Hypothetical protein			-
SAS013	HP	N315	3.31		Hypothetical protein			-
SAS015	HP	N315	3.45		Hypothetical protein			-
SAS017	HP	N315	3.31		Hypothetical protein			-
SAS019	HP	N315	4.61		Hypothetical protein			-
SAS024	HP	N315	5.00		Hypothetical protein			-
SAS030	HP	N315	3.47		Hypothetical protein			-
SAS031	HP	N315	3.25		Hypothetical protein			-
SAS034	HP	N315	3.65		Hypothetical protein			-
SAS036	HP	N315	3.93		Hypothetical protein			-
SAS040	HP	N315	3.78		Hypothetical protein			-
SAS048	HP	N315	3.06		Hypothetical protein			-
SAS060	HP	N315	4.74		Hypothetical protein			-
SAS073	HP	N315	5.04		Hypothetical protein			-
SAS090	HP	N315	3.25		Hypothetical protein			-
SA0019	HP	N315	0.15	0.07	Hypothetical protein			-
SA0287	HP	N315	0.27	0.27	Hypothetical protein			-
SA0289	HP	N315	0.26	0.25	Hypothetical protein			-
SA0290	HP	N315	0.10	0.26	Hypothetical protein			-
SA0314	HP	N315	0.13	0.12	Hypothetical protein			-
SA0350	HP	N315	0.18	0.24	Hypothetical protein			-
SA0407	HP	N315	0.26	0.27	Hypothetical protein			-
SA0624	HP	N315	0.16	0.16	Hypothetical protein			-
SA0718	HP	N315	0.02	0.02	Hypothetical protein			-
SA0721	HP	N315	0.10	0.09	Hypothetical protein			-
SA0739	HP	N315	0.32	0.27	Hypothetical protein			-
SA0775	HP	N315	0.07	0.23	Hypothetical protein			-
SA0778	HP	N315	0.14	0.22	Hypothetical protein			-
SA0783	HP	N315	0.21	0.13	Hypothetical protein			-
SA0941	HP	N315	0.23	0.12	Hypothetical protein			-
SA0954	HP	N315	0.07	0.21	Hypothetical protein			-
SA1068	HP	N315	0.15	0.16	Hypothetical protein			-
SA1124	HP	N315	0.04	0.04	Hypothetical protein			-
SA1135	HP	N315	0.04	0.07	Hypothetical protein			-
SA1256	HP	N315	0.18	0.17	Hypothetical protein			-
SA1293	HP	N315	0.16	0.18	Hypothetical protein			-
SA1295	HP	N315	0.21	0.23	Hypothetical protein			-
SA1296	HP	N315	0.14	0.10	Hypothetical protein			-
SA1325	HP	N315	0.23	0.30	Hypothetical protein			-
SA1356	HP	N315	0.03	0.07	Hypothetical protein			-
SA1376	HP	N315	0.20	0.19	Hypothetical protein			-
SA1378	HP	N315	0.03	0.04	Hypothetical protein			-
SA1392	HP	N315	0.24	0.31	Hypothetical protein			-
SA1423	HP	N315	0.01	0.03	Hypothetical protein			-
SA1445	HP	N315	0.07	0.04	Hypothetical protein			-
SA1509	HP	N315	0.21	0.21	Hypothetical protein			-
SA1867	HP	N315	0.16	0.18	Hypothetical protein			-
SA1916	HP	N315	0.07	0.10	Hypothetical protein			-
SA2130	HP	N315	0.10	0.08	Hypothetical protein			-
SA2355	HP	N315	0.17	0.15	Hypothetical protein			-

SA0277	HP	N315	0.01		Hypothetical protein			-
SA0278	HP	N315	0.06		Hypothetical protein			-
SA0279	HP	N315	0.15		Hypothetical protein			-
SA0280	HP	N315	0.19		Hypothetical protein			-
SA0283	HP	N315	0.09		Hypothetical protein			-
SA0284	HP	N315	0.16		Hypothetical protein			-
SA0363	HP	N315	0.29		Hypothetical protein			-
SA0364	HP	N315	0.28		Hypothetical protein			-
SA0371	HP	N315	0.32		Hypothetical protein			-
SA0401	HP	N315	0.11		Hypothetical protein			-
SA0491	HP	N315	0.30		Hypothetical protein			-
SA0539	HP	N315	0.20		Hypothetical protein			-
SA0662	HP	N315	0.10		Hypothetical protein			-
SA0663	HP	N315	0.19		Hypothetical protein			-
SA0664	HP	N315	0.27		Hypothetical protein			-
SA0671	HP	N315	0.13		Hypothetical protein			-
SA0684	HP	N315	0.26		Hypothetical protein			-
SA0931	HP	N315	0.29		Hypothetical protein			-
SA0933	HP	N315	0.33		Hypothetical protein			-
SA1049	HP	N315	0.19		Hypothetical protein			-
SA1210	HP	N315	0.25		Hypothetical protein			-
SA1242	HP	N315	0.31		Hypothetical protein			-
SA1420	HP	N315	0.29		Hypothetical protein			-
SA1514	HP	N315	0.10		Hypothetical protein			-
SA1573	HP	N315	0.14		Hypothetical protein			-
SA1594	HP	N315	0.32		Hypothetical protein			-
SA1740	HP	N315	0.14		Hypothetical protein			-
SA1746	HP	N315	0.10		Hypothetical protein			-
SA1768	HP	N315	0.20		Hypothetical protein			-
SA1771	HP	N315	0.20		Hypothetical protein			-
SA1912	HP	N315	0.02		Hypothetical protein			-
SA1985	HP	N315	0.05		Hypothetical protein			-
SA1986	HP	N315	0.09		Hypothetical protein			-
SA2058	HP	N315	0.07		Hypothetical protein			-
SA2076	HP	N315	0.12		Hypothetical protein			-
SA2264	HP	N315	0.06		Hypothetical protein			-
SA2273	HP	N315	0.18		Hypothetical protein			-
SA2440	HP	N315	0.11		Hypothetical protein			-
SA2445	HP	N315	0.30		Hypothetical protein			-
SAS016	HP	N315	0.05		Hypothetical protein			-
SAS026	HP	N315	0.23		Hypothetical protein			-
SA1154	HP	N315	5.39	5.85	Hypothetical protein	**COG2008E**	**E**	Amino acid transport and metabolism
SA0345	HP	N315	3.91		Hypothetical protein	**COG0646E,COG0685E**	**E**	Amino acid transport and metabolism
SA2229	HP	N315	3.60		Hypothetical protein	**COG0531E**	**E**	Amino acid transport and metabolism
SA0212	HP	N315	4.05	3.05	Hypothetical protein	**COG1082G**	**G**	Carbohydrate transport and metabolism
SA0319	HP	N315	3.72		Hypothetical protein	**COG3414G**	**G**	Carbohydrate transport and metabolism
SA1737	HP	N315	3.33		Hypothetical protein	**COG2706G**	**G**	Carbohydrate transport and metabolism
SA0865	HP	N315	0.14	0.13	Hypothetical protein	**COG0061G**	**G**	Carbohydrate transport and metabolism
SA1593	HP	N315	0.07	0.20	Hypothetical protein	**COG4193G**	**G**	Carbohydrate transport and metabolism
SA1601	HP	N315	3.95	3.82	Hypothetical protein	**COG0239D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA2196	HP	N315	4.35		Hypothetical protein	**COG2161D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA0467	HP	N315	0.14	0.23	Hypothetical protein	**COG0037D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA0191	HP	N315	4.81	3.34	Hypothetical protein	**COG0845M**	**M**	Cell wall/membrane/envelope biogenesis
SA1764	HP	N315	3.71		Hypothetical protein	**COG3064M**	**M**	Cell wall/membrane/envelope biogenesis
SA1822	HP	N315	4.57		Hypothetical protein	**COG5577M**	**M**	Cell wall/membrane/envelope biogenesis
SA0349	HP	N315	0.29	0.22	Hypothetical protein	**COG0668M**	**M**	Cell wall/membrane/envelope biogenesis
SA0529	HP	N315	0.32		Hypothetical protein	**COG0794M**	**M**	Cell wall/membrane/envelope biogenesis
SA1105	HP	N315	0.15		Hypothetical protein	**COG0750M**	**M**	Cell wall/membrane/envelope biogenesis
SA2157	HP	N315	0.18		Hypothetical protein	**COG1887M**	**M**	Cell wall/membrane/envelope biogenesis
SA2350	HP	N315	0.32		Hypothetical protein	**COG0463M**	**M**	Cell wall/membrane/envelope biogenesis
SA1363	HP	N315	3.12		Hypothetical protein	**COG0095H**	**H**	Coenzyme transport and metabolism
SA0174	HP	N315	0.04	0.08	Hypothetical protein	**COG2091H**	**H**	Coenzyme transport and metabolism
SA0546	HP	N315	0.22	0.20	Hypothetical protein	**COG0095H**	**H**	Coenzyme transport and metabolism
SA0666	HP	N315	0.06	0.09	Hypothetical protein	**COG0720H**	**H**	Coenzyme transport and metabolism
SA1066	HP	N315	0.29	0.23	Hypothetical protein	**COG1564H**	**H**	Coenzyme transport and metabolism
SA1421	HP	N315	0.14	0.20	Hypothetical protein	**COG1713H**	**H**	Coenzyme transport and metabolism
SA1422	HP	N315	0.04	0.06	Hypothetical protein	**COG1057H**	**H**	Coenzyme transport and metabolism
SA0323	HP	N315	3.40	3.22	Hypothetical protein	**COG0534V**	**V**	Defense mechanisms
SA2150	HP	N315	3.01		Hypothetical protein	**COG0577V**	**V**	Defense mechanisms
SA1683	HP	N315	0.27	0.29	Hypothetical protein	**COG1132V**	**V**	Defense mechanisms
SA0581	HP	N315	0.13	4.59	Hypothetical protein	**COG0651CP**	**c**	Energy production and conversion
SA1236	HP	N315	0.29	0.22	Hypothetical protein	**COG1254C**	**C**	Energy production and conversion
SA0578	HP	N315	0.27		Hypothetical protein	**COG2111P,COG1009CF**	**c**	Energy production and conversion
SA2156	HP	N315	0.03		Hypothetical protein	**COG1620C**	**C**	Energy production and conversion
SA0081	HP	N315	5.28	4.67	Hypothetical protein	**COG1937S**	**S**	Function unknown
SA0170	HP	N315	3.71	3.64	Hypothetical protein	**COG5609S**	**S**	Function unknown
SA0574	HP	N315	3.30	3.04	Hypothetical protein	**COG3238S**	**S**	Function unknown
SA0801	HP	N315	5.92	4.57	Hypothetical protein	**COG0316S**	**S**	Function unknown
SA1130	HP	N315	3.57	4.27	Hypothetical protein	**COG1692S**	**S**	Function unknown
SA1265	HP	N315	4.11	3.29	Hypothetical protein	**COG1738S**	**S**	Function unknown
SA2238	HP	N315	3.36	3.18	Hypothetical protein	**COG4430S**	**S**	Function unknown
SA1344	HP	N315	5.43	0.11	Hypothetical protein	**COG4129S**	**S**	Function unknown
SA0054	HP	N315	3.35		Hypothetical protein	**COG4333S**	**S**	Function unknown
SA0102	HP	N315	3.30		Hypothetical protein	**COG4716S**	**S**	Function unknown
SA0324	HP	N315	3.84		Hypothetical protein	**COG4815S**	**S**	Function unknown
SA0428	HP	N315	3.28		Hypothetical protein	**COG5438S**	**S**	Function unknown
SA0892	HP	N315	3.85		Hypothetical protein	**COG2314S**	**S**	Function unknown
SA1014	HP	N315	3.30		Hypothetical protein	**COG1288S**	**S**	Function unknown
SA1020	HP	N315	3.17		Hypothetical protein	**COG4365S**	**S**	Function unknown
SA1050	HP	N315	4.01		Hypothetical protein	**COG3865S**	**S**	Function unknown
SA1057	HP	N315	4.48		Hypothetical protein	**COG2314S**	**S**	Function unknown
SA1937	HP	N315	3.86		Hypothetical protein	**COG4270S**	**S**	Function unknown
SA2133	HP	N315	3.66		Hypothetical protein	**COG3152S**	**S**	Function unknown
SA2219	HP	N315	3.39		Hypothetical protein	**COG2246S**	**S**	Function unknown
SA2299	HP	N315	3.17		Hypothetical protein	**COG1289S**	**S**	Function unknown
SA2378	HP	N315	3.17		Hypothetical protein	**COG2764S**	**S**	Function unknown
SA0012	HP	N315	0.28	0.33	Hypothetical protein	**COG4241S**	**S**	Function unknown
SA0020	HP	N315	0.13	0.11	Hypothetical protein	**COG4853S**	**S**	Function unknown
SA0489	HP	N315	0.10	0.17	Hypothetical protein	**COG1939S**	**S**	Function unknown
SA0636	HP	N315	0.21	0.14	Hypothetical protein	**COG1671S**	**S**	Function unknown
SA0722	HP	N315	0.27	0.30	Hypothetical protein	**COG1481S**	**S**	Function unknown
SA0789	HP	N315	0.25	0.18	Hypothetical protein	**COG2445S**	**S**	Function unknown
SA1021	HP	N315	0.28	0.30	Hypothetical protein	**COG2001S**	**S**	Function unknown
SA1079	HP	N315	0.08	0.08	Hypothetical protein	**COG2739S**	**S**	Function unknown
SA1125	HP	N315	0.04	0.05	Hypothetical protein	**COG1426S**	**S**	Function unknown
SA1173	HP	N315	0.09	0.04	Hypothetical protein	**COG2340S**	**S**	Function unknown
SA1258	HP	N315	0.21	0.27	Hypothetical protein	**COG1307S**	**S**	Function unknown
SA1314	HP	N315	0.20	0.22	Hypothetical protein	**COG4955S**	**S**	Function unknown
SA1326	HP	N315	0.13	0.20	Hypothetical protein	**COG1354S**	**S**	Function unknown
SA1402	HP	N315	0.02	0.03	Hypothetical protein	**COG4864S**	**S**	Function unknown
SA1661	HP	N315	0.06	0.05	Hypothetical protein	**COG4717S**	**S**	Function unknown
SA1702	HP	N315	0.25	0.20	Hypothetical protein	**COG4758S**	**S**	Function unknown
SA1723	HP	N315	0.27	0.29	Hypothetical protein	**COG4496S**	**S**	Function unknown
SA1727	HP	N315	0.11	0.15	Hypothetical protein	**COG4843S**	**S**	Function unknown
SA1741	HP	N315	0.07	0.15	Hypothetical protein	**COG4709S**	**S**	Function unknown
SA1876	HP	N315	0.17	0.19	Hypothetical protein	**COG3402S**	**S**	Function unknown
SA1877	HP	N315	0.21	0.29	Hypothetical protein	**COG3428S**	**S**	Function unknown
SAS001	HP	N315	0.22	0.19	Hypothetical protein	**COG4392S**	**S**	Function unknown
SA1388	HP	N315	0.26		Hypothetical protein	**COG0327S,COG3323S**	**S**	Function unknown
SA0275	HP	N315	0.21		Hypothetical protein	**COG4499S**	**S**	Function unknown
SA0481	HP	N315	0.18		Hypothetical protein	**COG3880S**	**S**	Function unknown
SA0680	HP	N315	0.28		Hypothetical protein	**COG4502S**	**S**	Function unknown
SA0966	HP	N315	0.32		Hypothetical protein	**COG2322S**	**S**	Function unknown
SA1030	HP	N315	0.23		Hypothetical protein	**COG1496S**	**S**	Function unknown
SA1406	HP	N315	0.30		Hypothetical protein	**COG1385S**	**S**	Function unknown
SA1966	HP	N315	0.25		Hypothetical protein	**COG4856S**	**S**	Function unknown
SA1209	HP	N315	4.55	3.37	Hypothetical protein	**COG0561R**	**R**	General function prediction only
SA1840	HP	N315	4.47	3.52	Hypothetical protein	**COG3560R**	**R**	General function prediction only
SA0425	HP	N315	3.03		Hypothetical protein	**COG0494LR**	**r**	General function prediction only
SA2383	HP	N315	5.07		Hypothetical protein	**COG0500QR**	**r**	General function prediction only
SA0840	HP	N315	4.17		Hypothetical protein	**COG1881R**	**R**	General function prediction only
SA1335	HP	N315	3.13		Hypothetical protein	**COG1234R**	**R**	General function prediction only
SA1649	HP	N315	3.53		Hypothetical protein	**COG3545R**	**R**	General function prediction only
SA1692	HP	N315	3.78		Hypothetical protein	**COG0693R**	**R**	General function prediction only
SA1739	HP	N315	3.10		Hypothetical protein	**COG4927R**	**R**	General function prediction only
SA2225	HP	N315	3.31		Hypothetical protein	**COG1409R**	**R**	General function prediction only
SA2313	HP	N315	3.93		Hypothetical protein	**COG0561R**	**R**	General function prediction only
SA0485	HP	N315	0.22	0.26	Hypothetical protein	**COG4956R**	**R**	General function prediction only
SA0560	HP	N315	0.15	0.14	Hypothetical protein	**COG1078R**	**R**	General function prediction only
SA0667	HP	N315	0.09	0.08	Hypothetical protein	**COG0603R**	**R**	General function prediction only
SA0720	HP	N315	0.06	0.08	Hypothetical protein	**COG1660R**	**R**	General function prediction only
SA0932	HP	N315	0.28	0.24	Hypothetical protein	**COG1092R**	**R**	General function prediction only
SA0940	HP	N315	0.11	0.03	Hypothetical protein	**COG0595R**	**R**	General function prediction only
SA0975	HP	N315	0.17	0.14	Hypothetical protein	**COG1399R**	**R**	General function prediction only
SA0999	HP	N315	0.15	0.16	Hypothetical protein	**COG0622R**	**R**	General function prediction only
SA1031	HP	N315	0.23	0.26	Hypothetical protein	**COG0325R**	**R**	General function prediction only
SA1061	HP	N315	0.12	0.16	Hypothetical protein	**COG0820R**	**R**	General function prediction only
SA1064	HP	N315	0.21	0.20	Hypothetical protein	**COG1162R**	**R**	General function prediction only
SA1224	HP	N315	0.11	0.11	Hypothetical protein	**COG0488R**	**R**	General function prediction only

SA1379	HP	N315	0.11	0.13	Hypothetical protein	COG0705R	R	General function prediction only
SA1393	HP	N315	0.24	0.32	Hypothetical protein	COG0517R	R	General function prediction only
SA1399	HP	N315	0.08	0.13	Hypothetical protein	COG0319R	R	General function prediction only
SA1425	HP	N315	0.02	0.05	Hypothetical protein	COG1161R	R	General function prediction only
SA1426	HP	N315	0.10	0.21	Hypothetical protein	COG2179R	R	General function prediction only
SA1526	HP	N315	0.14	0.11	Hypothetical protein	COG0618R	R	General function prediction only
SA1536	HP	N315	0.08	0.08	Hypothetical protein	COG0730R	R	General function prediction only
SA1576	HP	N315	0.22	0.24	Hypothetical protein	COG2081R	R	General function prediction only
SA1892	HP	N315	0.20	0.20	Hypothetical protein	COG1418R	R	General function prediction only
SA2050	HP	N315	0.32	0.27	Hypothetical protein	COG2252R	R	General function prediction only
SA0621	HP	N315	0.21		Hypothetical protein	COG0670R	R	General function prediction only
SA1185	HP	N315	0.32		Hypothetical protein	COG0824R	R	General function prediction only
SA1274	HP	N315	0.24		Hypothetical protein	COG0699R	R	General function prediction only
SA1389	HP	N315	0.25		Hypothetical protein	COG2384R	R	General function prediction only
SA0581	HP	N315	0.13	4.59	Hypothetical protein	COG0651CP	p	Inorganic ion transport and metabolism
SA0806	HP	N315	3.69		Hypothetical protein	COG2072P	P	Inorganic ion transport and metabolism
SA0868	HP	N315	0.06	0.13	Hypothetical protein	COG0569P,COG0475F	P	Inorganic ion transport and metabolism
SA0585	HP	N315	0.14	0.11	Hypothetical protein	COG0025P	P	Inorganic ion transport and metabolism
SA0588	HP	N315	0.11	0.06	Hypothetical protein	COG1108P	P	Inorganic ion transport and metabolism
SA0872	HP	N315	0.30	0.23	Hypothetical protein	COG2382P	P	Inorganic ion transport and metabolism
SA1240	HP	N315	0.33	0.28	Hypothetical protein	COG4548P	P	Inorganic ion transport and metabolism
SA1578	HP	N315	0.21	0.13	Hypothetical protein	COG0607P	P	Inorganic ion transport and metabolism
SA2019	HP	N315	0.11	0.18	Hypothetical protein	COG0619P	P	Inorganic ion transport and metabolism
SA0578	HP	N315	0.27		Hypothetical protein	COG2111P,COG1009CF	P	Inorganic ion transport and metabolism
SA0939	HP	N315	0.05		Hypothetical protein	COG0569P	P	Inorganic ion transport and metabolism
SA0335	HP	N315	3.89		Hypothetical protein	COG1826U	U	Intracellular trafficking, secretion, and vesicular transport
SA0406	HP	N315	0.24		Hypothetical protein	COG5153UI	u	Intracellular trafficking, secretion, and vesicular transport
SA0227	HP	N315	6.56	4.24	Hypothetical protein	COG4670I	I	Lipid transport and metabolism
SA1694	HP	N315	0.17	0.18	Hypothetical protein	COG1607I	I	Lipid transport and metabolism
SA0406	HP	N315	0.24		Hypothetical protein	COG5153UI	i	Lipid transport and metabolism
SA0784	HP	N315	0.11	0.09	Hypothetical protein	COG0737F	F	Nucleotide transport and metabolism
SA0919	HP	N315	0.03	0.02	Hypothetical protein	COG1828F	F	Nucleotide transport and metabolism
SA1849	HP	N315	3.33		Hypothetical protein	COG0425O	O	Posttranslational modification, protein turnover, chaperones
SA2370	HP	N315	11.71		Hypothetical protein	COG0492O	O	Posttranslational modification, protein turnover, chaperones
SA1403	HP	N315	0.02	0.02	Hypothetical protein	COG1030O	O	Posttranslational modification, protein turnover, chaperones
SA0425	HP	N315	3.03		Hypothetical protein	COG0494LR	l	Replication, recombination and repair
SA1415	HP	N315	3.01		Hypothetical protein	COG1466L	L	Replication, recombination and repair
SA1093	HP	N315	0.09	0.18	Hypothetical protein	COG0550L,COG0551L	L	Replication, recombination and repair
SA0449	HP	N315	0.18	0.11	Hypothetical protein	COG0084L	L	Replication, recombination and repair
SA0450	HP	N315	0.09	0.09	Hypothetical protein	COG1658L	L	Replication, recombination and repair
SA1277	HP	N315	0.22	0.13	Hypothetical protein	COG0116L	L	Replication, recombination and repair
SA1454	HP	N315	0.14	0.14	Hypothetical protein	COG2256L	L	Replication, recombination and repair
SA1534	HP	N315	0.16	0.11	Hypothetical protein	COG0827L	L	Replication, recombination and repair
SA1662	HP	N315	0.21	0.25	Hypothetical protein	COG0420L	L	Replication, recombination and repair
SA0972	HP	N315	0.31		Hypothetical protein	COG0742L	L	Replication, recombination and repair
SA2383	HP	N315	5.07		Hypothetical protein	COG0500QR	q	Secondary metabolites biosynthesis, transport and catabolism
SA1071	HP	N315	0.20	0.16	Hypothetical protein	COG2050Q	Q	Secondary metabolites biosynthesis, transport and catabolism
SA0959	HP	N315	0.13	0.26	Hypothetical protein	COG1217T	T	Signal transduction mechanisms
SA1062	HP	N315	0.20	0.19	Hypothetical protein	COG0631T	T	Signal transduction mechanisms
SA1873	HP	N315	0.21		Hypothetical protein	COG2337T	T	Signal transduction mechanisms
SA2181	HP	N315	0.24		Hypothetical protein	COG2203T	T	Signal transduction mechanisms
SA2105	HP	N315	3.44	3.68	Hypothetical protein	COG2378K	K	Transcription
SA0908	HP	N315	3.24	0.27	Hypothetical protein	COG1316K	K	Transcription
SA0120	HP	N315	3.07		Hypothetical protein	COG1475K	K	Transcription
SA0492	HP	N315	4.60		Hypothetical protein	COG1595K	K	Transcription
SA1110	HP	N315	0.01	0.01	Hypothetical protein	COG2740K	K	Transcription
SA1868	HP	N315	0.28	0.21	Hypothetical protein	COG2183K	K	Transcription
SA1925	HP	N315	0.23	0.22	Hypothetical protein	COG1733K	K	Transcription
SA0873	HP	N315	3.58	3.95	Hypothetical protein	COG1514J	J	Translation, ribosomal structure and biogenesis
SA1684	HP	N315	3.15	3.52	Hypothetical protein	COG3557J	J	Translation, ribosomal structure and biogenesis
SA0838	HP	N315	0.08	6.58	Hypothetical protein	COG0009J	J	Translation, ribosomal structure and biogenesis
SA0707	HP	N315	3.23		Hypothetical protein	COG1544J	J	Translation, ribosomal structure and biogenesis
SA0464	HP	N315	0.18	0.06	Hypothetical protein	COG1188J	J	Translation, ribosomal structure and biogenesis
SA1040	HP	N315	0.04	0.04	Hypothetical protein	COG0564J	J	Translation, ribosomal structure and biogenesis
SA1134	HP	N315	0.15	0.05	Hypothetical protein	COG0621J	J	Translation, ribosomal structure and biogenesis
SA1668	HP	N315	0.09	0.21	Hypothetical protein	COG0564J	J	Translation, ribosomal structure and biogenesis
SA1405	HP	N315	0.18		Hypothetical protein	COG0621J	J	Translation, ribosomal structure and biogenesis
SA0715	*hprK*	N315	0.16	0.16	HPr kinase/phosphatase	COG1493T	T	Signal transduction mechanisms
SA0391	*hsdM*	N315	0.20	0.30	probable type I sitespecific deoxyribonuclease LldI chain hsdM	COG0286V	V	Defense mechanisms
SA0879	*htrA*	N315	0.24	0.24	serine protease HtrA	COG0265O	O	Posttranslational modification, protein turnover, chaperones
SA2459	*icaA*	N315	3.92	3.64	intercellular adhesion protein A	COG1215M	M	Cell wall/membrane/envelope biogenesis
SA2461	*icaB*	N315	3.75		intercellular adhesion protein B			-
SA2462	*icaC*	N315	3.91	5.18	intercellular adhesion protein C	COG3936G	G	Carbohydrate transport and metabolism
MW1076	*ileS*	MW2	0.26	0.18	IletRNA synthetase	COG0060J	J	Translation, ribosomal structure and biogenesis
SA1859	*ilvB*	N315	0.08	0.08	acetolactate synthase large subunit	COG0028EH	e	Amino acid transport and metabolism
SA1858	*ilvD*	N315	4.39		dihydroxyacid dehydratase			-
SA2026	*infA*	N315	0.01	0.16	translation initiation factor IF1	COG0361J	J	Translation, ribosomal structure and biogenesis
SA1112	*infB*	N315	0.02	0.14	translation initiation factor IF2	COG0532J	J	Translation, ribosomal structure and biogenesis
SA1504	*infC*	N315	0.33		translation initiation factor IF3	COG0290J	J	Translation, ribosomal structure and biogenesis
SAV0847	*int*	Mu50		3.48	integrase			-
SA2431	*isaB*	N315	5.05	3.52	immunodominant antigen B			-
SA0981	*isdF*	N315	3.34		ferrichrome ABC transporter	COG0609P	P	Inorganic ion transport and metabolism
SA1170	*katA*	N315	0.25	0.32	Catalase	COG0753P	P	Inorganic ion transport and metabolism
SA0067	*kdpD*	N315	5.81	3.91	kdp operon sensor protein	COG2205T	T	Signal transduction mechanisms
SA1882	*kdpD*	N315	0.05	0.21	sensor protein KdpD	COG2205T	T	Signal transduction mechanisms
SA1997	*lacA*	N315	3.37		galactose6phosphate isomerase LacA subunit	COG0698G	G	Carbohydrate transport and metabolism
SA1996	*lacB*	N315	62.50	65.36	galactose6phosphate isomerase LacB subunit	COG0698G	G	Carbohydrate transport and metabolism
SA1995	*lacC*	N315	3.22	3.14	tagatose6phosphate kinase	COG1105G	G	Carbohydrate transport and metabolism
SA1994	*lacD*	N315	3.30	3.82	tagatose 1,6diphosphate aldolase	COG3684G	G	Carbohydrate transport and metabolism
SA0232	*lctE*	N315	0.29	0.20	Llactate dehydrogenase	COG0039C	C	Energy production and conversion
SA1413	*lepA*	N315	0.26	0.27	GTPbinding protein	COG0481M	M	Cell wall/membrane/envelope biogenesis
SA1579	*leuS*	N315	0.05	0.15	leucyltRNA synthetase	COG0495J	J	Translation, ribosomal structure and biogenesis
SA0716	*lgt*	N315	0.29	0.24	prolipoprotein diacylglyceryl transferase			-
SA1720	*lig*	N315	0.17	0.31	DNA ligase	COG0272L	L	Replication, recombination and repair
SA1638	*lukE*	N315	3.06		leukotoxin LukE			-
SA1232	*lysA*	N315	0.07	0.12	diaminopimelate decarboxylase	COG0019E	E	Amino acid transport and metabolism
SA1225	*lysC*	N315	0.09	0.11	aspartokinase II	COG0527E	E	Amino acid transport and metabolism
MW1625	*lysP*	MW2	0.32		lysinespecific permease	COG0833E	E	Amino acid transport and metabolism
SA0475	*lysS*	N315	0.05	0.13	lysyltRNA synthetase	COG1190J	J	Translation, ribosomal structure and biogenesis
SA1757	*lytA*	N315	3.69	3.24	truncated amidase			-
SA0265	*lytM*	N315	14.88		peptidoglycan hydrolase	COG0739M	M	Cell wall/membrane/envelope biogenesis
SA1338	*malA*	N315	3.21		alphaD1,4glucosidase			-
SA1704	*map*	N315	3.98	3.72	methionyl aminopeptidase map	COG0024J	J	Translation, ribosomal structure and biogenesis
SA1751	*mapW*	N315	0.23		truncated mapw protein			-
SA0038	*mecA*	N315	3.32	3.50	penicillin binding protein 2'	COG0768M	M	Cell wall/membrane/envelope biogenesis
SA1614	*menC*	N315		0.23	osuccinylbenzoic acid synthetase	COG4948MR	m	Cell wall/membrane/envelope biogenesis
SA0896	*menD*	N315	0.23	0.26	menaquinone biosynthesis protein	COG1165H	H	Coenzyme transport and metabolism
SA0461	*mfd*	N315	0.29		transcriptionrepair coupling factor	COG1197LK	l	Replication, recombination and repair
SA1913	*mnaA*	N315	0.01	0.07	UDPGlcNAc 2epimerase	COG0381M	M	Cell wall/membrane/envelope biogenesis
SA0813	*mnhA*	N315	0.32		Na+/H+ antiporter subunit	COG2111P,COG1009CF	c	Energy production and conversion
SA0810	*mnhD*	N315	0.05	0.07	Na+/H+antiporter subunit	COG0651CP	c	Energy production and conversion
SA0808	*mnhF*	N315		0.21	Na+/H+ antiporter subunit	COG2212P	P	Inorganic ion transport and metabolism
SA2063	*moaA*	N315	0.32		molybdenum cofactor biosynthesis protein A	COG2896H	H	Coenzyme transport and metabolism
SA2070	*moaB*	N315	0.22	0.19	molybdopterin precursor biosynthesis moaB			-
MW2192	*moaC*	MW2	0.21		molybdenum cofactor biosynthesis protein C			-
SA2065	*moaD*	N315	0.31	0.28	probable molybdopterin synthase small subunit	COG1977H	H	Coenzyme transport and metabolism
SA2066	*moaE*	N315	0.09	0.11	molybdopterin converting factor moa			-
SA2064	*mobA*	N315	0.15	0.24	molybdopteringuanine dinucleotide biosynthesis mobA	COG0746H	H	Coenzyme transport and metabolism
SA2067	*mobB*	N315	0.06	0.14	probable molybdopteringuanine dinucleotide biosynthesis mob	COG1763H	H	Coenzyme transport and metabolism
SA2073	*modB*	N315	0.31		probable molybdenum transport permease	COG4149P	P	Inorganic ion transport and metabolism
SA2072	*modC*	N315	0.20		molybdenum transport ATPbinding protein ModC	COG4148P	P	Inorganic ion transport and metabolism
SA2068	*moeA*	N315	0.16	0.28	molybdopterin biosynthesis protein moeA	COG0303H	H	Coenzyme transport and metabolism
SA2071	*moeB*	N315	0.16	0.24	molybdopterin biosynthesis protein moeB	COG0476H	H	Coenzyme transport and metabolism
SA0583	*mprF*	N315		0.22	Na+/H+ antiporter	COG2212P	P	Inorganic ion transport and metabolism
SA2400	*mqo2*	N315	0.11	0.06	malate:quinone oxidoreductase	COG0579R	R	General function prediction only
SA1025	*mraY*	N315	0.22	0.26	phosphoNmuramic acidpentapeptide translocase	COG0472M	M	Cell wall/membrane/envelope biogenesis
SA1902	*murA*	N315	0.04	0.23	UDPNacetylglucosamine 1carboxyvinyl transferase 1	COG0766M	M	Cell wall/membrane/envelope biogenesis
SA1561	*murC*	N315	0.10	0.19	UDPNAacerylmuramatealanine ligase	COG0773M	M	Cell wall/membrane/envelope biogenesis
SA1026	*murD*	N315	0.04	0.08	UDPNacetylmuramoylalanineDglutamate ligase	COG0771M	M	Cell wall/membrane/envelope biogenesis
SA1886	*murF*	N315	0.07	0.08	UDPNacetylmuramoylalanylDglutamyl2, 6diaminopimelateDala	COG0770M	M	Cell wall/membrane/envelope biogenesis
SA1251	*murG*	N315	0.28	0.31	undecaprenylPPMurNAcpentapeptideUDPGlcNAc GlcNAc tran	COG0707M	M	Cell wall/membrane/envelope biogenesis
SA0997	*murI*	N315	0.09	0.11	glutamate racemase	COG0796M	M	Cell wall/membrane/envelope biogenesis
SA1926	*murZ*	N315	0.14	0.17	UDPNacetylglucosamine 1carboxylvinyl transferase 2	COG0766M	M	Cell wall/membrane/envelope biogenesis
SA1137	*mutS*	N315	0.04	0.17	DNA mismatch repair protein	COG0249L	L	Replication, recombination and repair
SA0991	*mutS2*	N315	0.29		MutSlike protein	COG1193L	L	Replication, recombination and repair
SA0549	*mvaK2*	N315	0.22		phosphomevalonate kinase	COG1577I	I	Lipid transport and metabolism
MW0020	MW0020	MW2		0.12	hypothetical protein			-
MW0115	MW0115	MW2		0.28	phosphonates transport permease	COG3639P	P	Inorganic ion transport and metabolism
MW0200	MW0200	MW2	45.05	25.06	periplasmicironbinding protein BitC	COG1840P	P	Inorganic ion transport and metabolism
MW0263	MW0263	MW2		0.26	conserved diarrheal toxin	COG1674D	D	Cell cycle control, cell division, chromosome partitioning
MW0318	MW0318	MW2		3.30	ribosomalproteinserine Nacetyltransferase	COG1670J	J	Translation, ribosomal structure and biogenesis
MW0327	MW0327	MW2		0.32	ABC transporter ATPbinding protein	COG1131V	V	Defense mechanisms
MW0379	MW0379	MW2		3.98	hypothetical protein	COG1432S	S	Function unknown
MW0381	MW0381	MW2		4.63	hypothetical protein	COG0702MG	g	Carbohydrate transport and metabolism
MW0446	MW0446	MW2		0.22	hypothetical protein	COG0084L	L	Replication, recombination and repair
MW0539	MW0539	MW2	0.23	0.26	cationic amino acid transporter	COG0531E	E	Amino acid transport and metabolism
MW0751	MW0751	MW2	8.93	10.65	putative primase	COG3378R,COG4983S	s	Function unknown
MW0761	MW0761	MW2		0.24	hypothetical protein			-
MW0778	MW0778	MW2		3.75	phosphoglycerate mutase	COG0406G	G	Carbohydrate transport and metabolism

MW0812	MW0812	MW2		0.26	glycerate dehydrogenase	**COG1052CHR**	**h**	Coenzyme transport and metabolism
MW0820	MW0820	MW2	0.20		NADH dehydrogenase	**COG1252C**	**C**	Energy production and conversion
MW0967	MW0967	MW2		3.04	hypothetical protein	**COG0695O**	**O**	Posttranslational modification, protein turnover, chaperones
MW1034	MW1034	MW2		0.13	hypothetical protein	**COG0127F**	**F**	Nucleotide transport and metabolism
MW1071	MW1071	MW2		0.20	hypothetical protein	**COG0325R**	**R**	General function prediction only
MW1173	MW1173	MW2		0.25	2oxoacid ferredoxin oxidoreductase, beta subunit	**COG1013C**	**C**	Energy production and conversion
MW1225	MW1225	MW2		0.11	hypothetical protein	**COG2340S**	**S**	Function unknown
MW1351	MW1351	MW2		0.12	hypothetical protein			-
MW1399	MW1399	MW2		5.41	protease	**COG0740OU**	**u**	Intracellular trafficking, secretion, and vesicular transport
MW1518	MW1518	MW2	0.13	0.23	DNA repair protein RecO	**COG1381L**	**L**	Replication, recombination and repair
MW1657	MW1657	MW2		0.10	hypothetical protein	**COG0730R**	**R**	General function prediction only
MW1680	MW1680	MW2	3.37	4.67	chorismate mutase homolog	**COG2876E,COG1605E**	**E**	Amino acid transport and metabolism
MW1696	MW1696	MW2		0.11	16S pseudouridylate synthase	**COG1187J**	**J**	Translation, ribosomal structure and biogenesis
MW1714	MW1714	MW2	0.30		arsenical pump membrane protein homolog	**COG1055P**	**P**	Inorganic ion transport and metabolism
MW1818	MW1818	MW2		0.31	hypothetical protein	**COG1607I**	**I**	Lipid transport and metabolism
MW1932	MW1932	MW2	3.05		phage anti repressor	**COG3561K,COG3645S**	**s**	Function unknown
MW1975	MW1975	MW2	0.19	0.27	glycoprotein endopeptidase	**COG1214O**	**O**	Posttranslational modification, protein turnover, chaperones
MW2102	MW2102	MW2		0.09	ferrichrome ABC transporter (permease)	**COG0609P**	**P**	Inorganic ion transport and metabolism
MW2217	MW2217	MW2		0.16	secretory antigen precursor SsaA homolog	**COG3942R**	**R**	General function prediction only
MW2317	MW2317	MW2	0.10	0.09	nitrate reductase delta chain	**COG2180C**	**C**	Energy production and conversion
SA1728	*nadE*	N315	0.08	0.08	NAD synthetase, prefers NH3 over glutamine	**COG0171H**	**H**	Coenzyme transport and metabolism
MW1853	*nadE*	MW2	0.12	0.08	NAD synthetase	**COG0171H**	**H**	Coenzyme transport and metabolism
SA0304	*nanA*	N315	3.30		Nacetylneuraminate lyase subunit	**COG0329EM**	**e**	Amino acid transport and metabolism
SA2182	*narI*	N315	0.33	0.33	nitrate reductase gamma chain	**COG2181C**	**C**	Energy production and conversion
SA2188	*nasD*	N315		0.33	nitrite reductase	**COG1251C**	**C**	Energy production and conversion
SA0686	*nrdE*	N315	0.28	0.29	ribonucleoside diphosphate reductase major subunit	**COG0209F**	**F**	Nucleotide transport and metabolism
SA1285	*nth*	N315	3.44		endonucleaselike protein	**COG0177L**	**L**	Replication, recombination and repair
SA1109	*nusA*	N315	0.05	0.20	transcription terminationantitermination factor	**COG0195K**	**K**	Transcription
SA0494	*nusG*	N315	0.23	0.26	transcription antitermination protein	**COG0250K**	**K**	Transcription
SA0717	*OatA*	N315		0.23	Oacetyltransferase	**COG0110R**	**R**	General function prediction only
SA1470	*obg*	N315	0.29		Spo0Bassociated GTPbinding protein	**COG0536R**	**R**	General function prediction only
SA1245	*odhA*	N315	0.02	0.31	2oxoglutarate dehydrogenase E1	**COG0567C**	**C**	Energy production and conversion
MW1303	*odhA*	MW2	0.30		oxoglutarate dehydrogenase	**COG0567C**	**C**	Energy production and conversion
SA1244	*odhB*	N315	0.05	0.09	dihydrolipoamide succinyltransferase	**COG0508C**	**C**	Energy production and conversion
MW1267	*opp2F*	MW2	0.06	0.09	oligopeptide transporter putative ATPase domain	**COG4608E**	**E**	Amino acid transport and metabolism
SA0845	*oppB*	N315	0.16	0.14	oligopeptide transport system permease protein	**COG0601EP**	**e**	Amino acid transport and metabolism
SA0847	*oppD*	N315	0.05	0.05	oligopeptide transport system ATPbinding protein OppD homol	**COG0444EP**	**e**	Amino acid transport and metabolism
SA0848	*oppF*	N315	0.01	0.02	oligopeptide transport system ATPbinding protein OppF homol	**COG4608E**	**E**	Amino acid transport and metabolism
SA2234	*opuCD*	N315		3.10	probable glycine betaine/carnitine/choline ABC transporter opu	**COG1174E**	**E**	Amino acid transport and metabolism
SA1183	*opuD*	N315	0.30	0.32	glycine betaine transporter	**COG1292M**	**M**	Cell wall/membrane/envelope biogenesis
SA2392	*panB*	N315	0.14	0.21	3methyl2oxobutanoate hydroxymethyltransferase	**COG0413H**	**H**	Coenzyme transport and metabolism
SA2391	*panC*	N315	0.22	0.29	pantoate betaalanine ligase			-
SA1189	*parC*	N315	0.21	0.31	topoisomerase IV subunit A	**COG0188L**	**L**	Replication, recombination and repair
SA1283	*pbp2*	N315	0.15	0.17	PBP2	**COG0744M**	**M**	Cell wall/membrane/envelope biogenesis
SA1381	*pbp3*	N315	0.23	0.31	penicillinbinding protein 3	**COG0768M**	**M**	Cell wall/membrane/envelope biogenesis
SA0374	*pbuX*	N315	0.03	0.05	xanthine permease	**COG2233F**	**F**	Nucleotide transport and metabolism
SA2482	*pcp*	N315	5.00		pyrrolidonecarboxylate peptidase	**COG2039O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1721	*pcrA*	N315	0.13	0.15	ATPdepentend DNA helicase	**COG0210L**	**L**	Replication, recombination and repair
SA09431	*pdhA*	N315	0.09	0.09	pyruvate dehydrogenase E1 component alpha subunit	**COG1071C**	**C**	Energy production and conversion
SA0944	*pdhB*	N315	0.01	0.04	pyruvate dehydrogenase E1 component beta subunit	**COG0022C**	**C**	Energy production and conversion
SA0945	*pdhC*	N315	0.01	0.03	dihydrolipoamide Sacetyltransferase component of pyruvate de	**COG0508C**	**C**	Energy production and conversion
SA0946	*pdhD*	N315	0.04	0.12	dihydrolipoamide dehydrogenase component of pyruvate dehy	**COG1249C**	**C**	Energy production and conversion
SA1938	*pdp*	N315	0.24	0.25	pyrimidine nucleoside phosphorylase	**COG0213F**	**F**	Nucleotide transport and metabolism
SA0698	*pepT*	N315	3.46		aminotripeptidase	**COG2195E**	**E**	Amino acid transport and metabolism
SA1521	*pfk*	N315	0.23	0.32	6phosphofructokinase	**COG0205G**	**G**	Carbohydrate transport and metabolism
SA0219	*pflA*	N315	0.22		formate acetyltransferase activating enzyme	**COG1180O**	**O**	Posttranslational modification, protein turnover, chaperones
SA0218	*pflB*	N315	0.23	0.29	formate acetyltransferase	**COG1882C**	**C**	Energy production and conversion
SA0823	*pgi*	N315	0.02	0.04	glucose6phosphate isomerase A	**COG0166G**	**G**	Carbohydrate transport and metabolism
SA0728	*pgk*	N315	0.06	0.16	phosphoglycerate kinase			-
SA0730	*pgm*	N315	0.08	0.22	2, 3diphosphoglycerateindependentphosphoglycer ate mutase	**COG0696G**	**G**	Carbohydrate transport and metabolism
SA0985	*pheS*	N315	0.13	0.19	PhetRNA synthetase alpha chain	**COG0016J**	**J**	Translation, ribosomal structure and biogenesis
SA0986	*pheT*	N315	0.04	0.06	PhetRNA synthetase beta chain	**COG0072J,COG0073R**	**r**	General function prediction only
SA2420	*phoB*	N315	3.58		alkaline phosphatase III precursor			-
SA1400	*phoH*	N315	0.18	0.21	phosphate starvationinduced protein phoH homolog	**COG1702T**	**T**	Signal transduction mechanisms
SA0131	*pnp*	N315		3.05	purine nucleoside phosphorylase	**COG0813F**	**F**	Nucleotide transport and metabolism
SA1117	*pnpA*	N315	0.15	0.18	polyribonucleotide nucleotidyltransferase	**COG1185J**	**J**	Translation, ribosomal structure and biogenesis
SA1107	*polC*	N315	0.25	0.33	DNA polymerase III, alpha chain PolCtype	**COG2176L**	**L**	Replication, recombination and repair
SA0950	*potA*	N315	0.27		spermidine/putrescine ABC transporter, ATPbinding protein ho	**COG3842E**	**E**	Amino acid transport and metabolism
SA0951	*potB*	N315	0.20	0.22	potB	**COG1176E**	**E**	Amino acid transport and metabolism
SA0953	*potD*	N315	0.20	0.29	spermidine/putrescinebinding protein precursor homolog	**COG0687E**	**E**	Amino acid transport and metabolism
SA1920	*prfA*	N315	0.25		peptide chain release factor 1	**COG0216J**	**J**	Translation, ribosomal structure and biogenesis
SA0877	*prfC*	N315	0.11	0.27	peptide chain release factor 3	**COG4108J**	**J**	Translation, ribosomal structure and biogenesis
SA1055	*priA*	N315	0.22	0.19	PriA, primosomal protein	**COG1198L**	**L**	Replication, recombination and repair
SA1106	*proS*	N315	0.22	0.29	prolinetRNA ligase	**COG0442J**	**J**	Translation, ribosomal structure and biogenesis
SA0458	*prs*	N315	0.32	0.26	ribosephosphate pyrophosphokinase	**COG0462FE**	**e**	Amino acid transport and metabolism
SA1218	*pstB*	N315	3.12	4.22	phosphate ABC transporter, ATPbinding protein	**COG1117P**	**P**	Inorganic ion transport and metabolism
SA1547	*ptaA*	N315	0.19	0.23	PTS system, Nacetylglucosaminespecific IIABC component	**COG1263G**	**G**	Carbohydrate transport and metabolism
SA2326	*ptsG*	N315	0.13	0.17	PTS system, glucosespecific IIABC component	**COG1263G**	**G**	Carbohydrate transport and metabolism
SA0934	*ptsH*	N315	0.09	0.13	phophocarrier protein HPR	**COG1925G**	**G**	Carbohydrate transport and metabolism
SA0935	*ptsI*	N315	0.07	0.07	phosphoenolpyruvateprotein phosphatase	**COG1080G**	**G**	Carbohydrate transport and metabolism
SA1724	*purB*	N315	0.21	0.21	adenylosuccinate lyase	**COG0015F**	**F**	Nucleotide transport and metabolism
SA0918	*purC*	N315	0.04	0.04	phosphoribosylaminoimidazolesuccinocarboxamide synthetase homolog			-
SA0926	*purD*	N315	0.01	0.01	phosphoribosylamineglycine ligase PurD	**COG0151F**	**F**	Nucleotide transport and metabolism
SA0922	*purF*	N315	0.04	0.06	phosphoribosylpyrophosphate amidotransferase PurF	**COG0034F**	**F**	Nucleotide transport and metabolism
SA0925	*purH*	N315	0.03	0.04	bifunctional purine biosynthesis protein PurH			-
SA0917	*purK*	N315	0.00	0.02	phosphoribosylaminoimidazole carboxylase carbon dioxidefixa	**COG0026F**	**F**	Nucleotide transport and metabolism
SA0921	*purL*	N315	0.01	0.02	phosphoribosylformylglycinamidine synthetase PurL	**COG0046F**	**F**	Nucleotide transport and metabolism
SA0923	*purM*	N315	0.02	0.03	phosphoribosylformylglycinamidine cycloligase PurM	**COG0150F**	**F**	Nucleotide transport and metabolism
SA0924	*purN*	N315	0.03	0.04	phosphoribosylglycinamide formyltransferase			-
SA0920	*purQ*	N315	0.01	0.02	phosphoribosylformylglycinamidine synthase I PurQ	**COG0047F**	**F**	Nucleotide transport and metabolism
SA0454	*purR*	N315	0.05	0.11	pur operon repressor homologue	**COG0503F**	**F**	Nucleotide transport and metabolism
SA0963	*pycA*	N315	0.27	0.22	pyruvate carboxylase	**COG1038C**	**C**	Energy production and conversion
SA1520	*pykA*	N315	0.01	0.07	pyruvate kinase			-
SA1045	*pyrAA*	N315	0.03	0.20	carbamoylphosphate synthase small chain	**COG0505EF**	**e**	Amino acid transport and metabolism
SA1046	*pyrAB*	N315	0.09	0.21	carbamoylphosphate synthase large chain	**COG0458EF**	**e**	Amino acid transport and metabolism
SA1043	*pyrB*	N315	0.03	0.08	aspartate transcarbamoylase chain A	**COG0540F**	**F**	Nucleotide transport and metabolism
SA1044	*pyrC*	N315	0.03	0.10	dihydroorotase	**COG0044F**	**F**	Nucleotide transport and metabolism
SA1048	*pyrE*	N315	0.01	0.03	orotate phosphoribosyltransferase	**COG0461F**	**F**	Nucleotide transport and metabolism
SA1047	*pyrF*	N315	0.05	0.07	orotidine5phosphate decarboxylase	**COG0284F**	**F**	Nucleotide transport and metabolism
SA1042	*pyrP*	N315	0.08	0.24	uracil permease	**COG2233F**	**F**	Nucleotide transport and metabolism
SA0912	*qoxB*	N315	0.02	0.06	Quinol oxidase polypeptide I QoxB	**COG0843C**	**C**	Energy production and conversion
SA0911	*qoxC*	N315	0.06	0.09	Quinol oxidase polypeptide III QoxC	**COG1845C**	**C**	Energy production and conversion
SA1466	*queA*	N315	0.05	0.24	Sadenosylmethionine tRNA ribosyltransferase			-
SA0484	*radA*	N315	0.10	0.13	radA	**COG1066O**	**O**	Posttranslational modification, protein turnover, chaperones
SA0053	*radC*	N315	3.28	3.19	truncated DNA repair protein	**COG2003L**	**L**	Replication, recombination and repair
SA1113	*rbfA*	N315	0.33		ribosomebinding factor A	**COG0858J**	**J**	Translation, ribosomal structure and biogenesis
SA0259	*rbsD*	N315	0.27	0.22	ribose permease	**COG1869G**	**G**	Carbohydrate transport and metabolism
SA1128	*recA*	N315	0.27	0.32	RecA protein	**COG0468L**	**L**	Replication, recombination and repair
SA0004	*recF*	N315	0.20	0.18	DNA repair and genetic recombination protein	**COG1195L**	**L**	Replication, recombination and repair
MW1110	*recG*	MW2	0.31		ATPdependent DNA helicase	**COG1200LK**	**l**	Replication, recombination and repair
SA1350	*recN*	N315	0.12	0.15	DNA repair protein	**COG0497L**	**L**	Replication, recombination and repair
SA0676	*recQ*	N315	0.26	0.30	probable DNA helicase	**COG0514L**	**L**	Replication, recombination and repair
SA1282	*recU*	N315	0.22		recombination protein U homolog	**COG3331R**	**R**	General function prediction only
SA0028	*repB*	N315	4.41	3.39	truncated replication protein for pUB110 plasmid	**COG5655L**	**L**	Replication, recombination and repair
SA1923	*rho*	N315	0.23	0.14	transcription termination factor Rho	**COG1158K**	**K**	Transcription
SA1587	*ribA*	N315	3.44		riboflavin biosynthesis protein	**COG0807H**	**H**	Coenzyme transport and metabolism
SA1586	*ribH*	N315	3.13	3.12	6,7dimethyl8ribityllumazine synthase			-
SA1082	*rimM*	N315	0.33		probable 16S rRNA processing protein	**COG0806J**	**J**	Translation, ribosomal structure and biogenesis
SA0201	*rlp*	N315	3.83	3.52	RGDcontaining lipoprotein	**COG0747E**	**E**	Amino acid transport and metabolism
SA1324	*rluB*	N315	0.16	0.31	ribosomal large subunit pseudouridine synthase B	**COG1187J**	**J**	Translation, ribosomal structure and biogenesis
SA0735	*rnr*	N315	0.17	0.23	ribonuclease R	**COG0557K**	**K**	Transcription
SA0818	*rocD*	N315	0.27	0.16	ornithine aminotransferase	**COG4992E**	**E**	Amino acid transport and metabolism
SA2044	*rplB*	N315	0.13		50S Protein synthesis L2	**COG0090J**	**J**	Translation, ribosomal structure and biogenesis
SA2047	*rplC*	N315	0.10	0.20	50S Protein synthesis L3			-
SA2046	*rplD*	N315	0.20	0.20	50S Protein synthesis L4			-
SA2035	*rplE*	N315	0.03	0.26	50S Protein synthesis L5	**COG0094J**	**J**	Translation, ribosomal structure and biogenesis
SA2033	*rplF*	N315	0.04		50S Protein synthesis L6	**COG0097J**	**J**	Translation, ribosomal structure and biogenesis
SA0014	*rplI*	N315	0.18	0.16	50S Protein synthesis L9	**COG0359J**	**J**	Translation, ribosomal structure and biogenesis
SA0498	*rplL*	N315	0.16		50S Protein synthesis L7/L12	**COG0222J**	**J**	Translation, ribosomal structure and biogenesis
SA2017	*rplM*	N315	0.14	0.22	50S Protein synthesis L13			-
SA2037	*rplN*	N315	0.08	0.23	50S Protein synthesis L14			-
SA2029	*rplO*	N315	0.04	0.32	50S Protein synthesis L15	**COG0200J**	**J**	Translation, ribosomal structure and biogenesis
SA2040	*rplP*	N315	0.06	0.21	50S Protein synthesis L16	**COG0197J**	**J**	Translation, ribosomal structure and biogenesis
SA2022	*rplQ*	N315	0.12		50S Protein synthesis L17	**COG0203J**	**J**	Translation, ribosomal structure and biogenesis
SA2032	*rplR*	N315	0.06	0.33	50S Protein synthesis L18	**COG0256J**	**J**	Translation, ribosomal structure and biogenesis
SA1473	*rplU*	N315	0.16	0.24	50S Protein synthesis L21			-
SA2042	*rplV*	N315	0.07	0.23	50S Protein synthesis L22			-
SA2045	*rplW*	N315	0.15	0.23	50S Protein synthesis L23	**COG0089J**	**J**	Translation, ribosomal structure and biogenesis
SA2036	*rplX*	N315	0.04	0.22	50S Protein synthesis L24	**COG0198J**	**J**	Translation, ribosomal structure and biogenesis
SA1471	*rpmA*	N315	0.29		50S Protein synthesis L27			-
SA2039	*rpmC*	N315	0.03	0.26	50S Protein synthesis L29			-
SA2030	*rpmD*	N315	0.05		50S Protein synthesis L30	**COG1841J**	**J**	Translation, ribosomal structure and biogenesis
SA1922	*rpmE*	N315	3.75		Protein synthesis L31	**COG0254J**	**J**	Translation, ribosomal structure and biogenesis
SAS042	*rpmG*	N315	0.11	0.30	50S Protein synthesis L33	**COG0267J**	**J**	Translation, ribosomal structure and biogenesis
SAS078	*rpmJ*	N315	0.01	0.17	50S Protein synthesis L36	**COG0257J**	**J**	Translation, ribosomal structure and biogenesis
SA2023	*rpoA*	N315	0.10		DNAdirected RNA polymerase alpha chain	**COG0202K**	**K**	Transcription
SA0500	*rpoB*	N315	0.07	0.32	RNA polymerase beta chain	**COG0085K**	**K**	Transcription
SA0501	*rpoC*	N315	0.16	0.27	RNA polymerase betaprime chain	**COG0086K**	**K**	Transcription
SA1099	*rpsB*	N315	0.11	0.26	30S Protein synthesis S2			-

SA2041	*rpsC*	N315	0.03	0.21	30S Protein synthesis S3	**COG0092J**	**J**	Translation, ribosomal structure and biogenesis
SA2031	*rpsE*	N315	0.14	0.30	30S Protein synthesis S5	**COG0098J**	**J**	Translation, ribosomal structure and biogenesis
SA0352	*rpsF*	N315	0.24	0.28	30S Protein synthesis S6	**COG0360J**	**J**	Translation, ribosomal structure and biogenesis
SA0504	*rpsG*	N315	0.04	0.23	30S Protein synthesis S7	**COG0049J**	**J**	Translation, ribosomal structure and biogenesis
SA2034	*rpsH*	N315	0.03	0.25	30S Protein synthesis S8			-
SA2016	*rpsI*	N315	0.26	0.16	30S Protein synthesis S9			-
SA2048	*rpsJ*	N315	0.20	0.28	30S Protein synthesis S10	**COG0051J**	**J**	Translation, ribosomal structure and biogenesis
SA2024	*rpsK*	N315	0.21	0.26	30S Protein synthesis S11	**COG0100J**	**J**	Translation, ribosomal structure and biogenesis
SA0503	*rpsL*	N315	0.06	0.20	30S Protein synthesis S12			-
SA2025	*rpsM*	N315	0.01	0.12	30S Protein synthesis S13	**COG0099J**	**J**	Translation, ribosomal structure and biogenesis
SAS079	*rpsN*	N315	0.06	0.20	30S Protein synthesis S14	**COG0199J**	**J**	Translation, ribosomal structure and biogenesis
SA2038	*rpsQ*	N315	0.03	0.19	30S Protein synthesis S17	**COG0186J**	**J**	Translation, ribosomal structure and biogenesis
SA2043	*rpsS*	N315	0.08		30S Protein synthesis S19	**COG0185J**	**J**	Translation, ribosomal structure and biogenesis
SA1414	*rpsT*	N315	3.12		30S Protein synthesis S20	**COG0268J**	**J**	Translation, ribosomal structure and biogenesis
SA1872	*rsbU*	N315	0.05	0.25	sigmaB regulation protein RsbU	**COG2208TK**	**t**	Signal transduction mechanisms
SA1871	*rsbV*	N315	0.15	0.19	antisigmaB factor antagonist	**COG1366T**	**T**	Signal transduction mechanisms
SA1870	*rsbW*	N315	0.15	0.33	antisigmaB factor	**COG2172T**	**T**	Signal transduction mechanisms
SA1467	*ruvB*	N315	0.09	0.22	holliday junction DNA helicase	**COG2255L**	**L**	Replication, recombination and repair
SA0010	SA0010	N315	0.19	0.17	amino acid permease	**COG1296E**	**E**	Amino acid transport and metabolism
SA0036	SA0036	N315		3.05	glycerophosphoryldiester phosphodiesterase homologue	**COG0584C**	**C**	Energy production and conversion
SA0043	SA0043	N315		3.61	hypothetical protein	**COG0491R**	**R**	General function prediction only
SA0062	SA0062	N315	3.17		transposase	**COG2801L**	**L**	Replication, recombination and repair
SA0064	SA0064	N315		19.84	transposase			-
SA0077	SA0077	N315	4.05	3.34	serine/threonine protein kinase	**COG0515RTKL**	**r**	General function prediction only
SA0082	SA0082	N315		3.38	hypothetical protein	**COG0607P,COG2210S,COG0425**	**s**	Function unknown
SA0084	SA0084	N315	3.03	3.01	homo sapiens CGI44 protein, PRO1975 protein	**COG0446R**	**R**	General function prediction only
SA0089	SA0089	N315	0.18	0.11	DNA helicase	**COG1112L**	**L**	Replication, recombination and repair
SA0099	SA0099	N315		3.30	transmembrane efflux pump protein			-
SA0112	SA0112	N315	3.06	3.47	cysteine synthase	**COG0031E**	**E**	Amino acid transport and metabolism
SA0113	SA0113	N315	24.10	27.78	ornithine cyclodeaminase	**COG2423E**	**E**	Amino acid transport and metabolism
SA0117	SA0117	N315	3.66	4.67	rhizobactin siderophore biosynthesisprotein RhsF			-
SA0119	SA0119	N315		3.13	diaminopimelate decarboxylase	**COG0019E**	**E**	Amino acid transport and metabolism
SA0125	SA0125	N315	3.62		Eps(Exopolysaccharide)G	**COG0438M**	**M**	Cell wall/membrane/envelope biogenesis
SA0126	SA0126	N315	4.35	3.56	capsular polysaccharide synthesis protein 14H			-
SA0132	SA0132	N315		4.05	tetracyclin resistance protein			-
SA0136	SA0136	N315	0.25	0.29	phosphonates transport permease	**COG3639P**	**P**	Inorganic ion transport and metabolism
SA0137	SA0137	N315	0.25	0.18	transport system protein	**COG3638P**	**P**	Inorganic ion transport and metabolism
SA0165	SA0165	N315	3.44	3.03	alphahelical coiledcoil protein SrpF			-
SA0168	SA0168	N315	3.42	3.34	probable permease of ABC transporter	**COG0600P**	**P**	Inorganic ion transport and metabolism
SA0172	SA0172	N315	3.36		integral membrane protein LmrP			-
SA0173	SA0173	N315	0.13	0.29	surfactin synthetase	**COG3320Q,COG1020Q**	**Q**	Secondary metabolites biosynthesis, transport and catabolism
SA0180	SA0180	N315		0.30	branchedchain amino acid transport system carrier protein	**COG1114E**	**E**	Amino acid transport and metabolism
SA0181	SA0181	N315	0.31		isochorismatase	**COG1335Q**	**Q**	Secondary metabolites biosynthesis, transport and catabolism
SA0193	SA0193	N315	7.09	6.54	Enterococcus faecalis plasmid pPD1 bacI	**COG0577V**	**V**	Defense mechanisms
SA0207	SA0207	N315	4.42		maltose/maltodextrinbinding protein	**COG2182G**	**G**	Carbohydrate transport and metabolism
SA0211	SA0211	N315	6.33		NADHdependent dehydrogenase	**COG0673R**	**R**	General function prediction only
SA0215	SA0215	N315	3.60		twocomponent response regulator	**COG4753T**	**T**	Signal transduction mechanisms
SA0220	SA0220	N315	3.47	3.11	glycerophosphodiester phosphodiesterase	**COG0584C,COG4781C**	**C**	Energy production and conversion
SA0231	SA0231	N315	0.33		flavohemoprotein	**COG1017C,COG1018C**	**C**	Energy production and conversion
SA0234	SA0234	N315	3.76	3.55	inosineuridine preferring nucleoside hydrolase	**COG1957F**	**F**	Nucleotide transport and metabolism
SA0241	SA0241	N315	0.16	0.15	4diphosphocytidyl2CmethylDerythritol synthase	**COG1211I**	**I**	Lipid transport and metabolism
SA0242	SA0242	N315	0.04	0.04	xylitol dehydrogenase	**COG1063ER**	**e**	Amino acid transport and metabolism
SA0243	SA0243	N315	0.11		teichoic acid biosynthesis protein B	**COG1887M**	**M**	Cell wall/membrane/envelope biogenesis
SA0246	SA0246	N315	0.08	0.18	hypotheticl protein, similar to Dxylulose reductase	**COG1063ER**	**e**	Amino acid transport and metabolism
SA0247	SA0247	N315		0.09	teichoic acid biosynthesis protein B	**COG1887M**	**M**	Cell wall/membrane/envelope biogenesis
SA0248	SA0248	N315	0.13	0.17	betaglycosyltransferase	**COG0463M**	**M**	Cell wall/membrane/envelope biogenesis
SA0255	SA0255	N315	3.24		PTS betaglucosidespecific enzyme II, ABC component			-
SA0263	SA0263	N315	4.35	3.55	proton antiporter efflux pump			-
SA0266	SA0266	N315		0.27	hypothetical protein	**COG1131V**	**V**	Defense mechanisms
SA0276	SA0276	N315	0.28	0.23	Cdiarrheal toxin	**COG1674D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA0299	SA0299	N315	3.53	3.60	carbohydrate kinase, PfkB family	**COG0524G**	**G**	Carbohydrate transport and metabolism
SA0303	SA0303	N315	3.08		sodiumcoupled permease	**COG0591ER**	**e**	Amino acid transport and metabolism
SA0312	SA0312	N315	0.33		alkanal monooxygenase alpha chain	**COG2141C**	**C**	Energy production and conversion
SA0313	SA0313	N315	0.29	0.20	glycine cleavage system H protein	**COG0509E**	**E**	Amino acid transport and metabolism
SA0316	SA0316	N315	0.33		lipoateprotein ligase	**COG0095H**	**H**	Coenzyme transport and metabolism
SA0328	SA0328	N315	3.10		NADHdependent FMN reductase	**COG0431R**	**R**	General function prediction only
SA0330	SA0330	N315	4.78	4.41	ribosomalproteinserine Nacetyltransferase	**COG1670J**	**J**	Translation, ribosomal structure and biogenesis
SA0337	SA0337	N315	3.91		transcriptional repressor	**COG1476K**	**K**	Transcription
SA0341	SA0341	N315	3.82		low temperature requirement A protein			-
SA0355	SA0355	N315	4.02		HP virulence plasmid pXO138			-
SA0361	SA0361	N315	4.22	5.26	truncated phosphoglycerate mutase; Gpm3p	**COG0406G**	**G**	Carbohydrate transport and metabolism
SA0417	SA0417	N315	3.04		sodiumdependent transporter	**COG0733R**	**R**	General function prediction only
SA0422	SA0422	N315	3.69	3.64	lactococcal lipoprotein	**COG1464P**	**P**	Inorganic ion transport and metabolism
SA0453	SA0453	N315	0.13	0.18	4diphosphocytidyl2CmethylDerythritol kinase	**COG1947I**	**I**	Lipid transport and metabolism
SA0462	SA0462	N315	0.01	0.13	low temperature requirement B protein	**COG2244R**	**R**	General function prediction only
SA0463	SA0463	N315		0.32	hypothetical protein	**COG3956R**	**R**	General function prediction only
SA0465	SA0465	N315	0.18	0.26	celldivision initiation protein	**COG2919D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA0466	SA0466	N315		0.31	polyribonucleotide nucleotidyltransferase	**COG1098J**	**J**	Translation, ribosomal structure and biogenesis
SA0468	SA0468	N315	0.09	0.17	hypoxanthineguanine phosphoribosyltransferase homologue	**COG0634F**	**F**	Nucleotide transport and metabolism
SA0476	SA0476	N315	4.69	3.13	transcription regulator GntR family	**COG1167KE**	**e**	Amino acid transport and metabolism
SA0482	SA0482	N315	0.29		creatine kinase	**COG3869E**	**E**	Amino acid transport and metabolism
SA0492	SA0492	N315	0.07		HP	**COG1595K**	**K**	Transcription
SA0502	SA0502	N315	0.06	0.30	Protein synthesis	**COG1358J**	**J**	Translation, ribosomal structure and biogenesis
SA0528	SA0528	N315	0.07	0.06	hexulose6phosphate synthase	**COG0269G**	**G**	Carbohydrate transport and metabolism
SA0557	SA0557	N315		0.24	oxidoreductase, ion channel	**COG0667C**	**C**	Energy production and conversion
SA0565	SA0565	N315	3.04		endonuclease III	**COG2231L**	**L**	Replication, recombination and repair
SA0567	SA0567	N315	5.00		iron(III) ABC transporter permease protein	**COG0609P**	**P**	Inorganic ion transport and metabolism
SA0569	SA0569	N315	0.16		2hydroxy6oxo6phenylhexa2,4dienoic acid hydrolase	**COG0596R**	**R**	General function prediction only
SA0572	SA0572	N315	3.31	3.31	esterase/lipase	**COG0596R**	**R**	General function prediction only
SA0580	SA0580	N315	0.18		Na+/H+ antiporter	**COG1006P**	**P**	Inorganic ion transport and metabolism
SA0587	SA0587	N315	0.08	0.10	lipoprotein, Streptococcal adhesin PsaA homologue	**COG0803P**	**P**	Inorganic ion transport and metabolism
SA0589	SA0589	N315	0.15		ABC transporter ATPbinding protein	**COG1121P**	**P**	Inorganic ion transport and metabolism
SA0590	SA0590	N315	4.50	3.47	iron dependent repressor	**COG1321K**	**K**	Transcription
SA0600	SA0600	N315		0.33	pyrimidine nucleoside transporter			-
SA0605	SA0605	N315	0.24	0.27	dihydroxyacetone kinase	**COG2376G**	**G**	Carbohydrate transport and metabolism
SA0614	SA0614	N315		0.22	twocomponent response regulator	**COG0745TK**	**t**	Signal transduction mechanisms
SA0622	SA0622	N315	5.32		AraC/XylS family transcriptional regulator			-
SA0628	SA0628	N315	0.25	0.30	sugar efflux transpoter			-
SA0640	SA0640	N315	0.33	0.21	ABC transporter required for expression of cytochrome bd	**COG4987CO**	**c**	Energy production and conversion
SA0646	SA0646	N315	0.18	0.17	deoxyribodipyrimidine photolyase	**COG0415L**	**L**	Replication, recombination and repair
SA0670	SA0670	N315	0.10	0.29	paraaminobenzoate synthase component I	**COG0115EH**	**e**	Amino acid transport and metabolism
SA0672	SA0672	N315	0.09	0.12	urea amidolyase			-
SA0674	SA0674	N315	0.12	0.20	anionbinding protein	**COG1368M**	**M**	Cell wall/membrane/envelope biogenesis
SA0677	SA0677	N315	0.31		choline transport ATPbinding protein	**COG1125E**	**E**	Amino acid transport and metabolism
SA0678	SA0678	N315	0.22	0.25	choline transporter	**COG1174E,COG1732M**	**E**	Amino acid transport and metabolism
SA0679	SA0679	N315	0.25	0.17	histidinolphosphate aminotransferase	**COG0079E**	**E**	Amino acid transport and metabolism
SA0682	SA0682	N315	0.25	0.14	ditripepride ABC transporter	**COG3104E**	**E**	Amino acid transport and metabolism
SA0683	SA0683	N315		0.24	hypothetical protein	**COG0780R**	**R**	General function prediction only
SA0688	SA0688	N315	0.26		ferrichrome ABC transporter permease	**COG4606P**	**P**	Inorganic ion transport and metabolism
SA0690	SA0690	N315	0.28	0.24	ferrichrome ABC transporter ATPbinding protein	**COG4604P**	**P**	Inorganic ion transport and metabolism
SA0693	SA0693	N315	0.33		UDPNacetylenolpyruvoylglucosamine reductase	**COG0812M**	**M**	Cell wall/membrane/envelope biogenesis
SA0705	SA0705	N315	3.80		comF operon protein 1	**COG4098L**	**L**	Replication, recombination and repair
SA0724	SA0724	N315	3.29	3.11	celldivision inhibitor	**COG1090R**	**R**	General function prediction only
SA0734	SA0734	N315	0.31		carboxyesterase precursor homologue	**COG1647R**	**R**	General function prediction only
SA0746	SA0746	N315		3.64	staphylococcal nuclease	**COG1525L**	**L**	Replication, recombination and repair
SA0759	SA0759	N315	3.39		arsenate reductase	**COG1393P**	**P**	Inorganic ion transport and metabolism
SA0776	SA0776	N315	0.26		aminotransferase NifS homologue	**COG0520E**	**E**	Amino acid transport and metabolism
SA0777	SA0777	N315	0.10	0.19	nitrogen fixation protein NifU	**COG0822C**	**C**	Energy production and conversion
SA0790	SA0790	N315	0.12	0.17	Nacetylglucosamine catabolism homologue	**COG0647G**	**G**	Carbohydrate transport and metabolism
SA0791	SA0791	N315	0.25	0.20	glycerate dehydrogenase	**COG1052CHR**	**h**	Coenzyme transport and metabolism
SA0827	SA0827	N315	0.06	0.10	ATPdependent nuclease subunit B	**COG3857L**	**L**	Replication, recombination and repair
SA0828	SA0828	N315	0.19	0.26	ATPdependent nuclease subunit A	**COG1074L**	**L**	Replication, recombination and repair
SA0829	SA0829	N315	0.28	0.26	5oxo1,2,5tricarboxilic3penten acid decarboxylase	**COG0179Q**	**Q**	Secondary metabolites biosynthesis, transport and catabolism
SA0846	SA0846	N315	0.01	0.01	oligopeptide transport system permease protein OppC	**COG1173EP**	**e**	Amino acid transport and metabolism
SA0849	SA0849	N315	0.02	0.02	peptide binding protein OppA	**COG4166E**	**E**	Amino acid transport and metabolism
SA0851	SA0851	N315	5.26	4.72	oligopeptide ABC transporter ATPbinding protein homologue	**COG0444EP**	**e**	Amino acid transport and metabolism
SA0857	SA0857	N315	0.20	0.31	negative regulator of genetic competence MecA			-
SA0859	SA0859	N315	0.28	0.22	thimet oligopeptidase homologue	**COG1164E**	**E**	Amino acid transport and metabolism
SA0863	SA0863	N315		0.33	hypothetical protein			-
SA0864	SA0864	N315	0.17	0.24	GTP pyrophosphokinase	**COG2357S**	**S**	Function unknown
SA0880	SA0880	N315	0.05	0.04	Na+transporting ATP synthase	**COG0168P**	**P**	Inorganic ion transport and metabolism
SA0881	SA0881	N315	3.76	3.57	nucleotidase	**COG0737F**	**F**	Nucleotide transport and metabolism
SA0882	SA0882	N315	3.77	3.08	competence transcription factor			-
SA0895	SA0895	N315	3.40	4.07	menaquinonespecific isochorismate synthase	**COG1169HQ**	**h**	Coenzyme transport and metabolism
SA0910	SA0910	N315	0.05	0.13	quinol oxidase polypeptide IV QoxD	**COG3125C**	**C**	Energy production and conversion
SA0913	SA0913	N315	0.05	0.10	quinol oxidase polypeptide II QoxA	**COG1622C**	**C**	Energy production and conversion
SA0916	SA0916	N315	0.10	0.10	phosphoribosylaminoimidazole carboxylase PurE	**COG0041F**	**F**	Nucleotide transport and metabolism
SA0947	SA0947	N315		0.28	hypothetical protein			-
SA0956	SA0956	N315	0.28	0.32	Mn2+transport protein	**COG1914P**	**P**	Inorganic ion transport and metabolism
SA0969	SA0969	N315		3.31	glycerophosphoryl diester phosphodiesterase	**COG0584C**	**C**	Energy production and conversion
SA0990	SA0990	N315	0.25		DNAdependent DNA polymerase beta chain	**COG1796L,COG1387ER**	**e**	Amino acid transport and metabolism
SA1009	SA1009	N315	3.73		exotoxin 1			-
SA1011	SA1011	N315	5.00	4.69	exotoxin 3			-
SA1058	SA1058	N315	0.32		polypeptide deformylase			-
SA1059	SA1059	N315	0.23		methionyltRNA formyltransferase	**COG0223J**	**J**	Translation, ribosomal structure and biogenesis
SA1063	SA1063	N315	0.31		protein kinase	**COG2815S,COG0515RTKL**	**S**	Function unknown
SA1078	SA1078	N315	0.08	0.12	signal recognition particle	**COG0552U**	**U**	Intracellular trafficking, secretion, and vesicular transport
SA1100	SA1100	N315	0.26		elongation factor TS			-
SA1111	SA1111	N315	0.07	0.10	Protein synthesis L7AE family	**COG1358J**	**J**	Translation, ribosomal structure and biogenesis

SA1122	SA1122	N315	0.26		precessing proteinase	**COG0612R**	**R**	General function prediction only
SA1123	SA1123	N315	0.04	0.10	3oxoacyl acylcarrier protein reductase homolog ymfI	**COG1028IQR**	**r**	General function prediction only
SA1131	SA1131	N315	0.07	0.25	2oxoacid ferredoxin oxidoreductase, alpha subunit	**COG1014C,COG0674C**	**C**	Energy production and conversion
SA1132	SA1132	N315	0.12	0.18	2oxoacid ferredoxin oxidoreductase, beta subunit	**COG1013C**	**C**	Energy production and conversion
SA1143	SA1143	N315	4.15		lysophospholipase	**COG2267I**	**I**	Lipid transport and metabolism
SA1169	SA1169	N315	0.24	0.21	gammaaminobutyrate permease	**COG0833E**	**E**	Amino acid transport and metabolism
SA1172	SA1172	N315	0.16	0.27	GMP reductase	**COG0516F**	**F**	Nucleotide transport and metabolism
SA1180	SA1180	N315	5.00	5.10	exonuclease SbcD	**COG0420L**	**L**	Replication, recombination and repair
SA1216	SA1216	N315		0.24	oligoendopeptidase	**COG1164E**	**E**	Amino acid transport and metabolism
SA1220	SA1220	N315		3.03	phosphate ABC transporter	**COG0573P**	**P**	Inorganic ion transport and metabolism
SA1231	SA1231	N315		0.10	alanine racemase	**COG0787M**	**M**	Cell wall/membrane/envelope biogenesis
SA1237	SA1237	N315	0.16	0.15	5bromo4chloroindolyl phosphate hydrolysis protein xpaC			-
SA1238	SA1238	N315	0.23	0.20	tellurite resistance protein	**COG3853P**	**P**	Inorganic ion transport and metabolism
SA1241	SA1241	N315	0.25	0.29	nitricoxide reductase	**COG0714R**	**R**	General function prediction only
SA1252	SA1252	N315		0.28	hypothetical protein			-
SA1255	SA1255	N315	0.09	0.25	PTS system, glucosespecific enzyme II, A component			-
SA1257	SA1257	N315	0.11	0.10	peptide methionine sulfoxide reductase			-
SA1270	SA1270	N315	3.70	3.64	amino acid pearmease	**COG0531E**	**E**	Amino acid transport and metabolism
SA1273	SA1273	N315	0.15	0.15	5'3' exonuclease	**COG0258L**	**L**	Replication, recombination and repair
SA1280	SA1280	N315		0.32	conserved hyothetical protein			-
SA1289	SA1289	N315	0.32	0.33	bifunctional biotin ligase/biotin operon repressor	**COG0340H,COG1654K**	**H**	Coenzyme transport and metabolism
SA1290	SA1290	N315	0.09	0.33	poly(A) polymerase	**COG0617J**	**J**	Translation, ribosomal structure and biogenesis
SA1291	SA1291	N315		0.30	lipopolysaccharide biosynthesisrelated pr homolog	**COG0438M**	**M**	Cell wall/membrane/envelope biogenesis
SA1307	SA1307	N315	0.13	0.31	GTP binding protein	**COG1160R**	**R**	General function prediction only
SA1329	SA1329	N315	0.22	0.26	ferric uptake regulator homolog	**COG0735P**	**P**	Inorganic ion transport and metabolism
SA1336	SA1336	N315	0.14	0.16	glucose6phosphate 1dehydrogenase			-
SA1345	SA1345	N315		0.24	hypothetical protein			-
SA1349	SA1349	N315	0.18	0.21	dihydrolipoamide dehydrogenase	**COG1249C**	**C**	Energy production and conversion
SA1353	SA1353	N315	0.26	0.31	exodeoxyribonuclease, small subunit	**COG1722L**	**L**	Replication, recombination and repair
SA1354	SA1354	N315	0.17	0.33	exodeoxyribonuclease large subunit	**COG1570L**	**L**	Replication, recombination and repair
SA1355	SA1355	N315	0.08	0.14	transcription termination factor	**COG0781K**	**K**	Transcription
SA1365	SA1365	N315	0.06	0.08	glycine dehydrogenase (decarboxylating) subunit 2 homolog	**COG1003E**	**E**	Amino acid transport and metabolism
SA1366	SA1366	N315	0.10	0.12	glycine dehydrogenase subunit 1	**COG0403E**	**E**	Amino acid transport and metabolism
SA1367	SA1367	N315	0.09	0.12	aminomethyltransferase	**COG0404E**	**E**	Amino acid transport and metabolism
SA1374	SA1374	N315	3.08		late competence protein comGA	**COG2804NU**	**n**	Cell motility
SA1384	SA1384	N315	0.12		ABC transporter	**COG1108P**	**P**	Inorganic ion transport and metabolism
SA1385	SA1385	N315		0.30	ABC transporter ATPbinding protein	**COG1121P**	**P**	Inorganic ion transport and metabolism
SA1386	SA1386	N315	0.04	0.20	endonuclease IV	**COG0648L**	**L**	Replication, recombination and repair
SA1387	SA1387	N315	0.15		ATPdependent RNA helicase	**COG0513LKJ**	**l**	Replication, recombination and repair
SA1398	SA1398	N315	0.09	0.09	diacylglycerol kinase			-
SA1435	SA1435	N315	4.48	3.58	acetylCoA carboxylase (biotin carboxyl carrier subunit), accB h	**COG0511I**	**I**	Lipid transport and metabolism
SA1441	SA1441	N315	0.04	0.16	protease			-
SA1449	SA1449	N315	3.40		(5methylaminomethyl2thiouridylate)methyl transferase	**COG0482J**	**J**	Translation, ribosomal structure and biogenesis
SA1462	SA1462	N315	0.23	0.33	singlestrand DNAspecific exonuclease	**COG0608L**	**L**	Replication, recombination and repair
SA1469	SA1469	N315	0.09	0.28	chorismate mutase	**COG4492R**	**R**	General function prediction only
SA1512	SA1512	N315	0.11	0.13	formamidopyrimidineDNA glycosylase	**COG0266L**	**L**	Replication, recombination and repair
SA1523	SA1523	N315	0.11	0.11	acetylCoA carboxylase transferase beta subunit	**COG0777I**	**I**	Lipid transport and metabolism
SA1524	SA1524	N315	0.24	0.32	malate dehydrogenase homolog	**COG0281C**	**C**	Energy production and conversion
SA1529	SA1529	N315		3.57	hypothetical protein	**COG2220R**	**R**	General function prediction only
SA1537	SA1537	N315	0.01	0.12	thiamine biosynthesis protein ThiI	**COG0301H**	**H**	Coenzyme transport and metabolism
SA1538	SA1538	N315	0.24	0.23	ironsulfur cofactor synthesis protein nifZ	**COG1104E**	**E**	Amino acid transport and metabolism
SA1540	SA1540	N315		3.14	hypothetical protein	**COG1956T**	**T**	Signal transduction mechanisms
SA1559	SA1559	N315	0.19	0.20	smooth muscle caldesmon			-
SA1560	SA1560	N315	0.13	0.18	general stress protein homolog	**COG4768R**	**R**	General function prediction only
SA1571	SA1571	N315	0.26	0.24	Dalanine aminotransferase	**COG0115EH**	**e**	Amino acid transport and metabolism
SA1572	SA1572	N315	0.03	0.03	XaaHis dipeptidase homolog	**COG0624E**	**E**	Amino acid transport and metabolism
SA1574	SA1574	N315	0.14	0.11	16S pseudouridylate synthase	**COG1187J**	**J**	Translation, ribosomal structure and biogenesis
SA1575	SA1575	N315	0.28		spore cortex protein homolog	**COG2244R**	**R**	General function prediction only
SA1584	SA1584	N315	4.20	3.39	lysophospholipase homolog	**COG2267I**	**I**	Lipid transport and metabolism
SA1592	SA1592	N315	0.25	0.16	aesenical pump membrane protein homolog	**COG1055P**	**P**	Inorganic ion transport and metabolism
SA1617	SA1617	N315	0.16	0.15	latent nuclear antigen [Kaposi's sarcomaassociated herpesvirus]			-
SA1633	SA1633	N315	16.08	18.76	probable betalactamase			-
SA1667	SA1667	N315	0.11	0.23	twocomponent sensor histidine kinase	**COG2203T,COG4585T**	**T**	Signal transduction mechanisms
SA1678	SA1678	N315	3.50	3.03	transcription regulator Fur family homolog	**COG0735P**	**P**	Inorganic ion transport and metabolism
SA1688	SA1688	N315	0.17	0.33	teichoic acid translocation ATPbinding protein tagH	**COG1134GM**	**g**	Carbohydrate transport and metabolism
SA1708	SA1708	N315	0.24	0.20	UDPNacetylmuramyl tripeptide synthetase homolog	**COG0769M**	**M**	Cell wall/membrane/envelope biogenesis
SA1713	SA1713	N315	0.22	0.19	RNA methyltransferase homolog	**COG2265J**	**J**	Translation, ribosomal structure and biogenesis
SA1715	SA1715	N315	0.17	0.16	glutamyltRNAGln amidotransferase subunit B	**COG0064J**	**J**	Translation, ribosomal structure and biogenesis
SA1716	SA1716	N315	0.07	0.08	glutamyltRNAGln amidotransferase subunit A			-
SA1717	SA1717	N315		0.28	glutamyltRNAGln amidotransferase subunit C	**COG0721J**	**J**	Translation, ribosomal structure and biogenesis
SA1719	SA1719	N315		0.30	hypothetical protein			-
SA1725	SA1725	N315	0.27	0.21	Staphopain, Cysteine Proteinase			-
SA1729	SA1729	N315	0.01	0.04	nicotinate phosphoribosyltransferase homolog	**COG1488H**	**H**	Coenzyme transport and metabolism
SA1730	SA1730	N315		0.28	nitricoxide synthase homolog	**COG4362PE**	**e**	Amino acid transport and metabolism
SA1735	SA1735	N315	0.12	0.14	manganesedependent inorganic pyrophosphatase	**COG1227C**	**C**	Energy production and conversion
SA1747	SA1747	N315	0.31		ABC transporter, ATPbinding protein	**COG1131V**	**V**	Defense mechanisms
SA1748	SA1748	N315	0.12		transcription regulator, GntR family	**COG1725K**	**K**	Transcription
SA1749	SA1749	N315	3.22		aspartate transaminase protein	**COG0436E**	**E**	Amino acid transport and metabolism
SA1759	SA1759	N315	4.50		lytic enzyme			-
SA1760	SA1760	N315		3.82	holin homolog			-
SA1775	SA1775	N315	3.04	3.06	scaffolding protein	**COG0740OU**	**u**	Intracellular trafficking, secretion, and vesicular transport
SA1806	SA1806	N315	4.03	3.80	probable ATPdependent helicase	**COG0847L**	**L**	Replication, recombination and repair
SA1812	SA1812	N315	0.14	0.22	synergohymenotropic toxin precursor Staphylococcus intermedius			-
SA1813	SA1813	N315	0.27	0.33	leukocidin chain lukM precursor			-
SA1814	SA1814	N315	3.57		succinyldiaminopimelate desuccinylase	**COG0624E**	**E**	Amino acid transport and metabolism
SA1820	SA1820	N315		3.01	bacteriophage terminase small subunit	**COG3728L**	**L**	Replication, recombination and repair
SA1839	SA1839	N315	0.13	0.24	SdrH			-
SA1854	SA1854	N315	0.22		Osialoglycoprotein endopeptidase	**COG0533O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1855	SA1855	N315	0.15	0.20	ribosomalproteinalanine Nacetyltransfer	**COG0456R**	**R**	General function prediction only
SA1885	SA1885	N315		0.32	ATPdependent RNA helicase	**COG0513LKJ**	**l**	Replication, recombination and repair
SA1888	SA1888	N315	4.52		rod shape determining protein RodA			-
SA1893	SA1893	N315	3.14	3.52	lipoprotein precursor	**COG0706U**	**U**	Intracellular trafficking, secretion, and vesicular transport
SA1919	SA1919	N315	0.05	0.10	protoporphyrinogen oxidase (hemK)	**COG2890J**	**J**	Translation, ribosomal structure and biogenesis
SA1939	SA1939	N315	0.15	0.25	deoxyribosephosphate aldolase	**COG0274F**	**F**	Nucleotide transport and metabolism
SA1958	SA1958	N315		3.12	transposase for IS232	**COG1119P**	**P**	Inorganic ion transport and metabolism
SA1972	SA1972	N315	3.14	3.28	multidrug transporter			-
SA1975	SA1975	N315		0.24	conserved hypotehtical protein	**COG1988R**	**R**	General function prediction only
SA1978	SA1978	N315	0.33	0.31	ferrichrome ABC transporter (permease)	**COG0609P**	**P**	Inorganic ion transport and metabolism
SA1979	SA1979	N315	0.30	0.26	HP, similar toferrichrome ABC transporter (binding prote)	**COG4594P**	**P**	Inorganic ion transport and metabolism
SA1989	SA1989	N315	0.22	0.21	quinone oxidoreductase	**COG2130R**	**R**	General function prediction only
SA2002	SA2002	N315	3.16	4.33	transcription regulator MerR family	**COG0789K**	**K**	Transcription
SA2006	SA2006	N315	7.75	11.20	MHC class II analog			-
SA2010	SA2010	N315	4.83		RNAdirected DNA polymerase from retron EC86	**COG3344L**	**L**	Replication, recombination and repair
SA2056	SA2056	N315	0.12	0.13	acriflavin resistance protein	**COG0841V**	**V**	Defense mechanisms
SA2077	SA2077	N315	0.05	0.06	biotin biosynthesis protein	**COG1268R**	**R**	General function prediction only
SA2081	SA2081	N315	3.02	4.18	urea transporter	**COG4413E**	**E**	Amino acid transport and metabolism
SA2102	SA2102	N315	0.28	0.31	formate dehydrogenase homolog	**COG3383R**	**R**	General function prediction only
SA2106	SA2106	N315	3.48	4.33	protein of pXO246			-
SA2108	SA2108	N315	0.28		transcription regulator, RpiR family	**COG1737K**	**K**	Transcription
SA2112	SA2112	N315		3.64	sodiumdependent transporter	**COG0385R**	**R**	General function prediction only
SA2125	SA2125	N315	0.13	0.14	formiminoglutamase	**COG0010E**	**E**	Amino acid transport and metabolism
SA2127	SA2127	N315	3.13	4.10	ribose 5phosphate isomerase (rpi)	**COG0120G**	**G**	Carbohydrate transport and metabolism
SA2129	SA2129	N315	0.06	0.04	aldose 1epimerase	**COG2017G**	**G**	Carbohydrate transport and metabolism
SA2137	SA2137	N315	0.08	0.31	divalent cation transport	**COG0598P**	**P**	Inorganic ion transport and metabolism
SA2140	SA2140	N315		0.25	esterase	**COG0657I**	**I**	Lipid transport and metabolism
SA2142	SA2142	N315	0.15	0.16	multidrug resistance protein			-
SA2149	SA2149	N315		4.39	ABC transporter, ATPbinding protein	**COG1136V**	**V**	Defense mechanisms
SA2158	SA2158	N315	0.11	0.10	TpgX protein			-
SA2164	SA2164	N315	3.86	3.88	phage infection protein precursor	**COG1511S**	**S**	Function unknown
SA2165	SA2165	N315	0.15	0.18	transcriptional regulator tetRfamily	**COG1309K**	**K**	Transcription
SA2169	SA2169	N315	0.15	0.27	transcription regulatory protein			-
SA2174	SA2174	N315	3.34	4.29	transcriptional regulator	**COG1846K**	**K**	Transcription
SA2179	SA2179	N315	0.20	0.22	response regulators of twocomponent regulatory	**COG2197TK**	**t**	Signal transduction mechanisms
SA2180	SA2180	N315	0.01	0.07	two component sensor histidine kinase	**COG4585T,COG0642T**	**T**	Signal transduction mechanisms
SA2200	SA2200	N315	0.31		ABC transporter, ATP binding subunit	**COG1126E**	**E**	Amino acid transport and metabolism
SA2201	SA2201	N315	0.20	0.24	ABC transporter, permease protein	**COG0765E**	**E**	Amino acid transport and metabolism
SA2212	SA2212	N315	0.05	0.28	8amino7oxononanoate synthase	**COG0156H**	**H**	Coenzyme transport and metabolism
SA2217	SA2217	N315	3.13	3.15	lipoprotein inner membrane ABCtransporter	**COG1132V**	**V**	Defense mechanisms
SA2228	SA2228	N315		3.13	NA(+)/H(+) exchanger	**COG0025P**	**P**	Inorganic ion transport and metabolism
SA2233	SA2233	N315	0.05	0.08	integral membrane efflux protein			-
SA2285	SA2285	N315	3.18	3.13	accumulationassociated protein			-
SA2296	SA2296	N315	3.32		transcriptional regulator, MerR family	**COG0789K**	**K**	Transcription
SA2311	SA2311	N315	3.36		NAD(P)Hflavin oxidoreductase	**COG0778C**	**C**	Energy production and conversion
SA2318	SA2318	N315	3.65	3.02	Lserine dehydratase	**COG1760E**	**E**	Amino acid transport and metabolism
SA2319	SA2319	N315	4.10	3.40	betasubunit of Lserine dehydratas	**COG1760E**	**E**	Amino acid transport and metabolism
SA2330	SA2330	N315	4.31	3.61	transcription regulator	**COG0583K**	**K**	Transcription
SA2342	SA2342	N315	4.81		Oacetyltransferase	**COG0110R**	**R**	General function prediction only
SA2353	SA2353	N315	3.41		secretory antigen precursor SsaA	**COG3942R**	**R**	General function prediction only
SA2354	SA2354	N315	0.25	0.33	acyltransferase	**COG1835I**	**I**	Lipid transport and metabolism
SA2358	SA2358	N315	4.26	3.57	transcriptional regulator (TetR/AcrR family)	**COG1309K**	**K**	Transcription
SA2367	SA2367	N315	3.00		conserevd HP	**COG0596R**	**R**	General function prediction only
SA2368	SA2368	N315	4.61	3.30	cobalamin synthesis related protein CobW	**COG0523R**	**R**	General function prediction only
SA2369	SA2369	N315	3.26		ferrous iron transporter protein B	**COG0370P**	**P**	Inorganic ion transport and metabolism
SA2412	SA2412	N315	4.18		uroporphyrinIII Cmethyltransferase	**COG1648H**	**H**	Coenzyme transport and metabolism
SA2414	SA2414	N315	3.83	3.82	glutathione peroxidase	**COG0386O**	**O**	Posttranslational modification, protein turnover, chaperones
SA2429	SA2429	N315	3.95		arginine repressor	**COG1438K**	**K**	Transcription
SA2434	SA2434	N315	3.09		fructose phosphotransferase system enzyme fruA homolog	**COG1762GT,COG1299G**	**g**	Carbohydrate transport and metabolism
SA2447	SA2447	N315	0.21	0.26	streptococcal hemagglutinin protein			-
SA2487	SA2487	N315	3.15	7.30	rarD protein	**COG2962R**	**R**	General function prediction only

SA2498	SA2498	N315	0.10	0.15	DNAbinding protein Spo0Jlike homolog	**COG1475K**	**K**	Transcription
SA0661	*saeR*	N315	0.04	0.24	response regulator	**COG0745TK**	**t**	Signal transduction mechanisms
SA0660	*saeS*	N315	0.04	0.12	histidine protein kinase	**COG0642T**	**T**	Signal transduction mechanisms
SA0108	*sarS*	N315	4.08	4.20	sarS	**COG1846K**	**K**	Transcription
SAS020	SAS020	N315	4.46	4.61	phosphoglycerate mutase	**COG0406G**	**G**	Carbohydrate transport and metabolism
SAV0394	SAV0394	Mu50	6.29	4.22	hHP			-
SAV0913	SAV0913	Mu50	6.29		amidase	**COG5632M**	**M**	Cell wall/membrane/envelope biogenesis
SAV1996	SAV1996	Mu50		3.50	hypothetical protein			-
SA2206	*sbi*	N315	0.17	0.33	IgGbinding protein SBI			-
SA0249	*scdA*	N315	4.03		cell division and morphogenesisrelated protein	**COG2846D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA0995	*sdhA*	N315	0.04	0.12	succinate dehydrogenase flavoprotein subunit	**COG1053C**	**C**	Energy production and conversion
SA0996	*sdhB*	N315	0.13	0.16	succinate dehydrogenase ironsulfur protein subunit	**COG0479C**	**C**	Energy production and conversion
SA0994	*sdhC*	N315	0.19	0.24	succinate dehydrogenase cytochrome b558	**COG2009C**	**C**	Energy production and conversion
SA0521	*sdrE*	N315	0.20	0.29	SerAsp rich fibrinogenbinding, bone sialoproteinbinding protein			-
SA1817	*sec3*	N315	3.41		enterotoxin typeC3			-
MW0759	*sec4*	MW2	3.60	4.76	enterotoxin C precursor protein			-
SA0708	*secA*	N315	0.17		preprotein translocase subunit	**COG0653U**	**U**	Intracellular trafficking, secretion, and vesicular transport
SA0493	*secE*	N315		0.19	preprotein translocase subunit	**COG0690U**	**U**	Intracellular trafficking, secretion, and vesicular transport
SA1463	*secF*	N315	0.11	0.10	proteinexport membrane protein SecDF	**COG0341U,COG0342U**	**U**	Intracellular trafficking, secretion, and vesicular transport
SA0733	*secG*	N315	0.23		probable proteinexport membrane protein	**COG1314U**	**U**	Intracellular trafficking, secretion, and vesicular transport
SA2028	*secY*	N315	0.07	0.28	preprotein translocase SecY subunit	**COG0201U**	**U**	Intracellular trafficking, secretion, and vesicular transport
SA1642	*seg*	N315	4.90	3.70	extracellular enterotoxin type G precursor			-
SA1816	*sel*	N315	3.46	3.09	extracellular enterotoxin L			-
SA1648	*seo*	N315	3.94	6.33	enterotoxin SeO			-
SA1545	*serA*	N315	0.25	0.32	D3phosphoglycerate dehydrogenase	**COG0111HE**	**e**	Amino acid transport and metabolism
SA0009	*serS*	N315	0.03	0.02	seryltRNA synthetase	**COG0172J**	**J**	Translation, ribosomal structure and biogenesis
SA0389	*set13*	N315	3.52	3.45	exotoxin 13			-
SA0390	*set14*	N315	3.77	3.73	exotoxin 14			-
MW0385	*set19*	MW2	3.97		exotoxin homolog [Genomic island nu Sa alpha2]			-
MW0394	*set26*	MW2		4.95	exotoxin homolog [Genomic island nu Sa alpha2]			-
SA1551	*sgtA*	N315	7.46	7.75	probable transglycosylase	**COG0744M**	**M**	Cell wall/membrane/envelope biogenesis
SA1869	*sigB*	N315	0.11	0.15	sigma factor B	**COG1191K**	**K**	Transcription
SA0111	*sirA*	N315	3.53		lipoprotein	**COG0614P**	**P**	Inorganic ion transport and metabolism
SA1101	*smbA*	N315	0.23	0.17	uridylate kinase	**COG0528F**	**F**	Nucleotide transport and metabolism
MW1117	*smc*	MW2	0.30		chromosome segregation SMC protein	**COG1196D**	**D**	Cell cycle control, cell division, chromosome partitioning
SA1382	*sodA*	N315	3.86	3.14	superoxide dismutase SodA	**COG0605P**	**P**	Inorganic ion transport and metabolism
SA0107	*spa*	N315	0.15	0.10	Immunoglobulin G binding protein A precursor			-
SA1631	*splA*	N315	5.78	6.25	serine protease SplA	**COG0265O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1629	*splC*	N315	3.82	4.67	serine protease SplC			-
SA1628	*splD*	N315	4.29	4.08	serine protease SplD	**COG0265O**	**O**	Posttranslational modification, protein turnover, chaperones
SA0456	*spoVG*	N315	5.95		stage V sporulation protein G homologue	**COG2088M**	**M**	Cell wall/membrane/envelope biogenesis
SA1323	*srrA*	N315	0.10	0.23	staphylococcal respiratory response protein SrrA	**COG0745TK**	**t**	Signal transduction mechanisms
SA1322	*srrB*	N315	0.10	0.14	staphylococcal respiratory response protein SrrB	**COG0642T**	**T**	Signal transduction mechanisms
SA2093	*ssaA*	N315	0.26	0.24	secretory antigen precursor SsaA homolog	**COG3942R**	**R**	General function prediction only
SA0353	*ssb*	N315	0.08	0.16	singlestrand DNAbinding protein of phage phi PVL	**COG0629L**	**L**	Replication, recombination and repair
SA0744	*ssp*	N315	5.65	3.97	extracellular ECM and plasma binding protein			-
SA0901	*sspA*	N315	0.14	0.11	serine protease; V8 protease; glutamyl endopeptidase			-
SA0899	*sspC*	N315	3.22		cysteine protease			-
SA1089	*sucD*	N315	0.18	0.13	succinylCoA synthetase	**COG0074C**	**C**	Energy production and conversion
SA0595	*tagB*	N315		0.15	teichoic acid biosynthesis protein B	**COG1887M**	**M**	Cell wall/membrane/envelope biogenesis
SA0596	*tagX*	N315	0.15	0.10	teichoic acid biosynthesis protein X			-
SA2146	*tcaA*	N315	0.24	0.25	TcaA protein	**COG4640S**	**S**	Function unknown
SA2501	*thdF*	N315	0.14		possible thiophene and furan oxidation protein	**COG0486R**	**R**	General function prediction only
SA1165	*thrC*	N315	0.08	0.22	threonine synthase	**COG0498E**	**E**	Amino acid transport and metabolism
SA1506	*thrS*	N315	0.33	0.31	threonyltRNA synthetase 1	**COG0441J**	**J**	Translation, ribosomal structure and biogenesis
SA1260	*thyA*	N315	0.32		thymidylate synthase			-
SA1499	*tig*	N315	0.23		trigger factor	**COG0544O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1177	*tkt*	N315	0.17	0.16	transketolase	**COG0021G**	**G**	Carbohydrate transport and metabolism
SA1038	*tnp*	N315	8.62	4.33	truncated transposase	**COG3666L**	**L**	Replication, recombination and repair
SA2289	*tnp*	N315		5.95	transposase	**COG3464L**	**L**	Replication, recombination and repair
SA2386	*tnpC*	N315	4.26	8.13	transposition regulatory protein tnpC			-
SA2051	*topB*	N315	0.32	0.28	DNA topoisomerase III topB	**COG0550L,COG0551L**	**L**	Replication, recombination and repair
SA0729	*tpi*	N315	0.02	0.10	triosephosphate isomerase	**COG0149G**	**G**	Carbohydrate transport and metabolism
SA0432	*treP*	N315	3.60		PTS enzyme II, phosphoenolpyruvatedependent, trehalosespe	**COG1263G**	**G**	Carbohydrate transport and metabolism
SA1204	*trpB*	N315	3.42	3.15	tryptophan synthase beta chain	**COG0133E**	**E**	Amino acid transport and metabolism
SA1203	*trpF*	N315	3.86	3.23	phosphoriborylanthranilate isomerase	**COG0135E**	**E**	Amino acid transport and metabolism
SA2018	*truA*	N315	0.13	0.21	tRNA pseudouridine synthase A	**COG0101J**	**J**	Translation, ribosomal structure and biogenesis
MW1154	*truB*	MW2	0.32		tRNA pseudouridine 5S synthase	**COG0130J**	**J**	Translation, ribosomal structure and biogenesis
SA1956	*truncatedSA*	N315	0.31	0.22	lytic regulatory protein truncated with Tn554			-
SA2227	*truncatedSA*	N315	3.40		truncatedSA	**COG1113E**	**E**	Amino acid transport and metabolism
SA0719	*trxB*	N315	0.04	0.23	thioredoxine reductase	**COG0492O**	**O**	Posttranslational modification, protein turnover, chaperones
SA1819	*tst*	N315	3.80	4.10	toxic shock syndrome toxin1			-
SA0506	*tufA*	N315	0.02	0.10	translational elongation factor TU	**COG0050J**	**J**	Translation, ribosomal structure and biogenesis
SA1439	*udk*	N315	0.11	0.27	uridine kinase	**COG0572F**	**F**	Nucleotide transport and metabolism
SA0214	*uhpT*	N315	4.05	4.29	hexose phosphate transport protein	**COG2271G**	**G**	Carbohydrate transport and metabolism
SA1914	*upp*	N315	0.02	0.06	uracil phosphoribosyl transferase	**COG0035F**	**F**	Nucleotide transport and metabolism
SA2083	*ureB*	N315	4.17	4.10	urease beta subunit			-
SA2088	*ureD*	N315	7.09	4.95	urease accessory protein			-
SA0714	*uvrA*	N315	0.12	0.19	exinuclease ABC subunit A	**COG0178L**	**L**	Replication, recombination and repair
SA0713	*uvrB*	N315	0.18	0.27	exinuclease ABC subunit B	**COG0556L**	**L**	Replication, recombination and repair
SA1488	*valS*	N315	0.18	0.26	valinetRNA ligase	**COG0525J**	**J**	Translation, ribosomal structure and biogenesis
SA2492	*vraD*	N315	4.37	4.10	ABC transporter vraD	**COG1136V**	**V**	Defense mechanisms
SA2493	*vraE*	N315	4.13		ABC transporter (permease)	**COG0577V**	**V**	Defense mechanisms
SA0617	*vraG*	N315	0.07	0.13	ABC transporter permease			-
SA1701	*vraS*	N315		0.19	twocomponent sensor histidine kinase	**COG4585T**	**T**	Signal transduction mechanisms
SA1328	*xerD*	N315	4.07	0.18	sitespecific recombinase	**COG4974L**	**L**	Replication, recombination and repair
SA0373	*xprT*	N315	0.11	0.11	xanthine phosphoribosyltransferase	**COG0503F**	**F**	Nucleotide transport and metabolism
SA0041	*xylR*	N315	3.75	4.72	xylose repressor homologue	**COG1940KG**	**g**	Carbohydrate transport and metabolism
SA1645	*yent1*	N315		3.18	enterotoxin Yent1			-