

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
1-phosphatidylinositol phosphodiesterase precursor, putative	SAOUHSC_00051	plc	Fatty acid and phospholipid metabolism	Degradation	S	0	Extracellular		1				2
1-pyrroline-5-carboxylate dehydrogenase	SAOUHSC_02869	rocA	Energy metabolism	Amino acids and amines		0	Cytoplasmic				11	12	11
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	SAOUHSC_01398	dapD	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		2	Cytoplasmic		1	2	6	3	5
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	SAOUHSC_02703	gpmA	Energy metabolism	Glycolysis/ gluconeogenesis		0	Unknown	13	8	13	9	10	10
2',3'-cyclic-nucleotide 2'-phosphodiesterase	SAOUHSC_01263		Unclassified	Role category not yet assigned	S	1	Cytoplasmic	4	4	10	7	10	7
2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	SAOUHSC_00225		Biosynthesis of cofactors, prosthetic groups, and carriers	Other		0	Unknown	6	4	10	11	11	11
2-oxoglutarate dehydrogenase E1 component	SAOUHSC_01418	sucA,odhA	Energy metabolism	TCA cycle		0	Cytoplasmic	1			4	5	8
2-oxoisovalerate dehydrogenase, E1 component, alpha subunit, putative	SAOUHSC_01613	bfmBAA	Energy metabolism	Amino acids and amines		0	Cytoplasmic		2	2	2	3	2
2-oxoisovalerate dehydrogenase, E1 component, beta subunit, putative	SAOUHSC_01612	bfmBAB	Energy metabolism	Amino acids and amines		1	Cytoplasmic	3	1	3	4	3	3
2-oxoisovalerate dehydrogenase, E2 component, dihydroipoamide acetyltransferase, putative	SAOUHSC_01611	bmfBB	Energy metabolism	Pyruvate dehydrogenase		1	Cytoplasmic	1				2	2
30S ribosomal protein S1, putative	SAOUHSC_01493	rpsA	Protein synthesis	Ribosomal proteins: synthesis and modification		2	Cytoplasmic	12	11	14	13	15	16
30S ribosomal protein S11	SAOUHSC_02486	rpsK	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	3	6	3	3	3
30S ribosomal protein S12	SAOUHSC_00527	rpsL	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	5	4	4	2	2	5
30S ribosomal protein S13	SAOUHSC_02487	rpsM	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	7	4	8	6	6	6
30S ribosomal protein S15	SAOUHSC_01250	rpsO	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	1	1	2	1	2	2
30S ribosomal protein S16	SAOUHSC_01208	rpsP	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	2	4	4	4	4

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
30S ribosomal protein S17	SAOUHSC_02503	rpsQ	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	1		1	1	1	2
30S ribosomal protein S18	SAOUHSC_00350	rpsR	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	2		5	2	1	1
30S ribosomal protein S19	SAOUHSC_02508	rpsS	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	5	2	4	3	4	4
30S ribosomal protein S20	SAOUHSC_01689	rpsT	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	1	1	4	3	1	1
30S ribosomal protein S21	SAOUHSC_01678	rpsU	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	2		4	3	2	2
30S ribosomal protein S3	SAOUHSC_02506	rpsC	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	11	3	11	12	12	14
30S ribosomal protein S4	SAOUHSC_01829	rpsD	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	1	10	6	7	8
30S ribosomal protein S5	SAOUHSC_02494	rpsE	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	8	6	10	8	9	11
30S ribosomal protein S6	SAOUHSC_00348	rpsF	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	8	8	9	6	7	8
30S ribosomal protein S7	SAOUHSC_00528	rpsG	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	5	3	7	5	6	7
30S ribosomal protein S8	SAOUHSC_02498	rpsH	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	2	7	3	3	5
30S ribosomal protein S9	SAOUHSC_02477	rpsI	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	2	2	3	2	2	3
33 kDa chaperonin	SAOUHSC_00487		Protein fate	Protein folding and stabilization		0	Cytoplasmic	3	1	3	2	2	3
3-hexulose-6-phosphate synthase	SAOUHSC_00553		Energy metabolism	Other		1	Cytoplasmic	6	2	3	3	5	5
3-ketoacyl-acyl carrier protein reductase, putative	SAOUHSC_00086	butA	Energy metabolism	Fermentation		0	Cytoplasmic	1	2	1	6	7	5
3-methyl-2-oxobutanoate hydroxymethyltransferase	SAOUHSC_02919	panB	Biosynthesis of cofactors, prosthetic groups, and carriers	Pantothenate and coenzyme A		2	Unknown			2	2	1	3

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
3-oxoacyl- synthase, putative	SAOUHSC_00921	fabF,fab	Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic Membrane	7	8	9	5	9	7
3-oxoacyl-(acyl-carrier-protein) reductase, putative	SAOUHSC_01199	fabG	Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic	10	4	12	10	10	8
3-oxoacyl-[acyl-carrier-protein] synthase 3	SAOUHSC_00920	fabH	Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic	6	5	7	5	5	8
50S ribosomal protein L1	SAOUHSC_00519	rplA	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	8	4	9	9	10	10
50S ribosomal protein L10	SAOUHSC_00520	rplJ	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	6	3	5	7	5	5
50S ribosomal protein L11	SAOUHSC_00518	rplK	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	2	5	5	4	4
50S ribosomal protein L13	SAOUHSC_02478	rplM	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Unknown	9	5	13	7	8	7
50S ribosomal protein L14	SAOUHSC_02502	rplN	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic			2	4	1	2
50S ribosomal protein L15	SAOUHSC_02492	rplO	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Unknown	6	5	9	5	5	9
50S ribosomal protein L16	SAOUHSC_02505	rplP	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	1	1	3	1	2	3
50S ribosomal protein L17	SAOUHSC_02484	rplQ	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	3	3	3	4	4
50S ribosomal protein L18	SAOUHSC_02495	rplR	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	2	6	6	4	5
50S ribosomal protein L19	SAOUHSC_01211	rplS	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	2	8	5	5	7
50S ribosomal protein L2	SAOUHSC_02509	rplB	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	7	5	9	7	7	9
50S ribosomal protein L20	SAOUHSC_01784	rplT	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	3	1	5	3	4	4

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
50S ribosomal protein L21	SAOUHSC_01757	rplU	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Unknown	5	4	6	5	5	5
50S ribosomal protein L22	SAOUHSC_02507	rplV	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	5	3	7	5	4	4
50S ribosomal protein L23	SAOUHSC_02510	rplW	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Unknown	4	2	4	4	4	3
50S ribosomal protein L24	SAOUHSC_02501	rplX	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	2	1	4	2	2	2
50S ribosomal protein L27	SAOUHSC_01755	rpmA	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	2	2	4	3	3	2
50S ribosomal protein L28	SAOUHSC_01191	rpmB	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	2		2	2	2	2
50S ribosomal protein L29	SAOUHSC_02504	rpmC	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	2	4	3	4	4
50S ribosomal protein L3	SAOUHSC_02512	rplC	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	5	2	5	4	4	5
50S ribosomal protein L30	SAOUHSC_02493	rpmD	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	4	2	6	4	6	4
50S ribosomal protein L31 type B	SAOUHSC_02361	rpmE	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	3	3	2	2	2	3
50S ribosomal protein L35	SAOUHSC_01785	rpmI	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic			2	1	1	2
50S ribosomal protein L4	SAOUHSC_02511	rplD	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Unknown	4	5	5	3	4	5
50S ribosomal protein L5	SAOUHSC_02500	rplE	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	9	5	18	10	11	10
50S ribosomal protein L6	SAOUHSC_02496	rplF	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	10	5	12	9	8	9
50S ribosomal protein L7/L12	SAOUHSC_00521	rplL	Protein synthesis	Ribosomal proteins: synthesis and modification	S	0	Cytoplasmic	8	6	8	4	5	7

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
50S ribosomal protein L9	SAOUHSC_00017	rplI	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	1	1	4	2	1	2
6,7-dimethyl-8-ribityllumazine synthase	SAOUHSC_01886	ribH	Biosynthesis of cofactors, prosthetic groups, and carriers	Riboflavin, FMN, and FAD		0	Cytoplasmic			2	1	2	2
60 kDa chaperonin	SAOUHSC_02254	groL,groEL	Protein fate	Protein folding and stabilization		1	Cytoplasmic	20	13	19	20	18	19
6-phosphofructokinase, putative	SAOUHSC_01807	pfkA	Energy metabolism	Glycolysis/ gluconeogenesis		0	Cytoplasmic	6	3	10	6	6	8
6-phosphogluconate dehydrogenase, decarboxylating	SAOUHSC_01605	gnd	Energy metabolism	Pentose phosphate pathway		2	Cytoplasmic	13	12	19	16	18	14
ABC transporter periplasmic binding protein, putative	SAOUHSC_02430	htsA	Transport and binding proteins	Amino acids, peptides and amines	S	0	Cytoplasmic Membrane	10	5	12	3	10	12
ABC transporter, ATP-binding protein, putative	SAOUHSC_00847	sufC	Biosynthesis of cofactors, prosthetic groups, and carriers	Other		0	Cytoplasmic	4	4	6	5	3	6
ABC transporter, ATP-binding protein, putative	SAOUHSC_01392		Transport and binding proteins	Unknown substrate		0	Cytoplasmic	9	5	16	11	11	11
ABC transporter, ATP-binding protein, putative	SAOUHSC_02152		Transport and binding proteins	Unknown substrate		0	Cytoplasmic Membrane		2	3	5	5	4
ABC transporter, substrate-binding protein, putative	SAOUHSC_00634	mntC	Transport and binding proteins	Unknown substrate	S	0	Cytoplasmic Membrane	18	11	18	10	10	11
accessory gene regulator protein A	SAOUHSC_02265	agrA	Cellular processes	Pathogenesis		0	Cytoplasmic	1	2	2	1	2	4
Acetate kinase	SAOUHSC_01820	ackA	Energy metabolism	Fermentation		1	Cytoplasmic	9	7	14	7	10	11
acetolactate synthase, large subunit, biosynthetic type	SAOUHSC_02282	ilvB	Amino acid biosynthesis	Pyruvate family		0	Cytoplasmic				2	1	1
acetyl-CoA acetyltransferase, putative	SAOUHSC_00195	fadA	Fatty acid and phospholipid metabolism	Other		0	Cytoplasmic				2	2	2
acetyl-CoA carboxylase, biotin carboxyl carrier protein	SAOUHSC_01624	accB	Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic	2	1		2	2	3
acetyl-CoA carboxylase, biotin carboxylase	SAOUHSC_01623	accC	Fatty acid and phospholipid metabolism	Biosynthesis		1	Cytoplasmic	5	4	2	2	4	3
acetyl-CoA synthetase, putative	SAOUHSC_01846	acsA	Central intermediary metabolism	Other		1	Cytoplasmic				6	3	8
acetyl-CoA synthetase, putative	SAOUHSC_02929		Protein synthesis	tRNA aminoacylation		2	Cytoplasmic	1	4	4	4	3	4
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	SAOUHSC_01808	accA	Fatty acid and phospholipid metabolism	Biosynthesis		1	Cytoplasmic	3	1	2	3	6	4
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	SAOUHSC_01809	accD	Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic	3	3	3	4	5	4

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
aconitate hydratase 1	SAOUHSC_01347	citB,acnA	Energy metabolism	TCA cycle		2	Cytoplasmic	8	2	5	3	7	5
Acyl carrier protein	SAOUHSC_01201	hmrB,acpP	Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic	4	6	6	5	5	6
adenosylmethionine-8-amino-7-oxononoate aminotransferase	SAOUHSC_02715	bioA	Biosynthesis of cofactors, prosthetic groups, and carriers	Biotin		0	Cytoplasmic	3		5	3	6	7
adenylate kinase, putative	SAOUHSC_02490	adk	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions		0	Cytoplasmic	7	4	8	5	6	5
Adenylosuccinate lyase	SAOUHSC_02126	purB	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		2	Cytoplasmic	13	4	18	11	16	17
adenylosuccinate synthetase	SAOUHSC_00019	purA	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	11	4	13	7	9	10
Aerobic glycerol-3-phosphate dehydrogenase	SAOUHSC_01278	glpD	Energy metabolism	Other		0	Cytoplasmic	8	2	9	8	9	7
Alanyl-tRNA synthetase	SAOUHSC_01722	alaS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	20	10	20	11	15	13
aldehyde dehydrogenase, putative	SAOUHSC_02142	aldH,aldA2	Energy metabolism	Fermentation		1	Cytoplasmic	3	1	4	9	9	10
Alkaline shock protein 23	SAOUHSC_02441	asp23	Cellular processes	Adaptations to atypical conditions		0	Unknown	8	7	10	5	6	11
Alkyl hydroperoxide reductase subunit C	SAOUHSC_00365	ahpC	Cellular processes	Detoxification		0	Cytoplasmic	8	5	9	7	8	8
Alkyl hydroperoxide reductase subunit F	SAOUHSC_00364	ahpF	Energy metabolism	Electron transport		2	Cytoplasmic Membrane	11	8	12	7	12	11
amidophosphoribosyltransferase	SAOUHSC_01014	purF	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	3	1	3	1		2
amino acid ABC transporter, permease protein, putative	SAOUHSC_00732		Transport and binding proteins	Unknown substrate		6	Cytoplasmic Membrane	3	1		1	2	
Aminoacyltransferase femA	SAOUHSC_01373	femA	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		2	Cytoplasmic	2	3	5	6	5	4
Aminoacyltransferase femB	SAOUHSC_01374	femB	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		0	Cytoplasmic	5	1	6	5	6	6
Aminoacyltransferase femX	SAOUHSC_02527	fmhB	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		1	Cytoplasmic	3	2	3	6	3	6
Aminomethyltransferase	SAOUHSC_01634	gcvT	Energy metabolism	Amino acids and amines		0	Cytoplasmic	3	3	4	5	5	3

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
aminopeptidase PepS, putative	SAOUHSC_02092	pepS,ampS	Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Cytoplasmic	7	6	10	9	9	7
aminotransferase, class V superfamily, putative	SAOUHSC_00849	sufS,csdB	Central intermediary metabolism	Sulfur metabolism		1	Cytoplasmic	2	3	4	1	3	5
anti-sigma B factor, putative	SAOUHSC_02299	rsbW	Regulatory functions	Protein interactions		0	Cytoplasmic	2	1	3	1	2	3
Anti-sigma-B factor antagonist	SAOUHSC_02300	rsbV	Transcription	Transcription factors		0	Cytoplasmic	3	2	3	2	2	3
Arginine repressor	SAOUHSC_01617	argR,ahrC	Amino acid biosynthesis	Glutamate family		0	Cytoplasmic	1		2	3	3	1
Arginyl-tRNA synthetase	SAOUHSC_00611	argS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	13	5	15	8	10	13
Asparaginyl-tRNA synthetase	SAOUHSC_01471	asnS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	6	5	10	5	8	10
aspartate-semialdehyde dehydrogenase	SAOUHSC_01395	asd	Amino acid biosynthesis	Aspartate family		0	Cytoplasmic				15	12	14
aspartokinase II, putative	SAOUHSC_01394	lysC	Amino acid biosynthesis	Aspartate family		0	Cytoplasmic			2	4	4	2
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	SAOUHSC_02116	gatB	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	17	12	18	14	18	18
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	SAOUHSC_02118		Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	3	1	1		2	2
Aspartyl-tRNA synthetase	SAOUHSC_01737	aspS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	14	7	15	11	10	12
ATP synthase epsilon chain	SAOUHSC_02340	atpC	Energy metabolism	ATP-proton motive force interconversion		0	Cytoplasmic	2	1	1	1	2	2
ATP synthase F1, gamma subunit	SAOUHSC_02343	atpG	Energy metabolism	ATP-proton motive force interconversion		0	Unknown	4	4	2	5	5	4
ATP synthase subunit alpha	SAOUHSC_02345	atpA	Energy metabolism	ATP-proton motive force interconversion		1	Cytoplasmic	13	11	19	14	16	17
ATP synthase subunit b	SAOUHSC_02347	atpF	Energy metabolism	ATP-proton motive force interconversion		1	Cytoplasmic Membrane	3	3	4	2	3	3
ATP synthase subunit beta	SAOUHSC_02341	atpD	Energy metabolism	ATP-proton motive force interconversion		0	Cytoplasmic Membrane	17	13	22	21	23	23
ATP synthase subunit delta	SAOUHSC_02346	atpH	Energy metabolism	ATP-proton motive force interconversion		0	Unknown	4	4	5	7	6	6
ATP-dependent Clp protease ATP-binding subunit clpC	SAOUHSC_00505	clpC	Cellular processes	DNA transformation		0	Cytoplasmic	17	8	16	14	20	18
ATP-dependent Clp protease ATP-binding subunit clpL	SAOUHSC_02862	clpL	Unknown function	General		0	Cytoplasmic	1		1			2

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
ATP-dependent Clp protease ATP-binding subunit clpX	SAOUHSC_01778	clpX	Protein fate	Protein folding and stabilization		1	Cytoplasmic	7	5	6	5	8	9
ATP-dependent Clp protease proteolytic subunit	SAOUHSC_00790	clpP	Protein fate	Degradation of proteins, peptides, and glycopeptides		1	Cytoplasmic	4	3	6	4	5	5
ATP-dependent Clp protease, ATP-binding subunit ClpB	SAOUHSC_00912	clpB	Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Cytoplasmic	6	5	4	8	12	17
ATP-dependent DNA helicase pcrA	SAOUHSC_02123	pcrA	DNA metabolism	DNA replication, recombination, and repair		1	Cytoplasmic	5	2	5	1	3	4
ATP-dependent hsl protease ATP-binding subunit hslU	SAOUHSC_01226	hslU,clpY	Protein fate	Protein folding and stabilization		0	Cytoplasmic	4	3	3	4	5	5
Bifunctional protein foldD	SAOUHSC_01007	foldD	Biosynthesis of cofactors, prosthetic groups, and carriers	Folic acid		0	Cytoplasmic	9	6	12	10	10	9
Bifunctional protein pyrR	SAOUHSC_01164	pyrR	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides		0	Cytoplasmic	2		3	1	1	2
Bifunctional purine biosynthesis protein purH	SAOUHSC_01017	purH	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	13	6	19	10	17	14
Biofilm operon icaADBC HTH-type negative transcriptional regulator icaR	SAOUHSC_03001	tetR,icaR	Unknown function	General		0	Cytoplasmic		1	1	1	2	1
Biotin synthase	SAOUHSC_02714	bioB	Biosynthesis of cofactors, prosthetic groups, and carriers	Biotin		0	Cytoplasmic	1	2	4	3	3	2
branched-chain amino acid aminotransferase	SAOUHSC_00536	ilvE	Amino acid biosynthesis	Pyruvate family		0	Cytoplasmic	7	5	9	13	10	9
Carbamoyl-phosphate synthase large chain	SAOUHSC_01170	pyrAB,carB	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis		3	Cytoplasmic	16	10	25	13	14	15
carbamoyl-phosphate synthase, small subunit	SAOUHSC_01169	pyrAA,carA	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis		1	Cytoplasmic	7	5	4		5	3
catabolite control protein A	SAOUHSC_01850	ccpA	Regulatory functions	DNA interactions		0	Cytoplasmic	5	1	6	5	4	6
catalase	SAOUHSC_01327	katA	Cellular processes	Detoxification		0	Cytoplasmic	7	5	12	13	15	17
Cell cycle protein gpsB	SAOUHSC_01462		Cellular processes	Cell division		0	Cytoplasmic	5	5	6	4	4	4
Cell division protein ftsA	SAOUHSC_01149	ftsA	Cellular processes	Cell division		0	Cytoplasmic	6	4	7	5	8	6
Cell division protein ftsZ	SAOUHSC_01150	ftsZ	Cellular processes	Cell division		0	Cytoplasmic	13	12	16	14	13	13
Cell division protein sepF	SAOUHSC_01154		Unknown function	General		0	Unknown	1	1	2	1	1	2
Chaperone protein dnaJ	SAOUHSC_01682	dnaJ	Protein fate	Protein folding and stabilization		0	Cytoplasmic	4	2	2	4	5	4
Chaperone protein dnaK	SAOUHSC_01683	dnaK	Protein fate	Protein folding and stabilization		0	Cytoplasmic	28	22	33	23	23	28



description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
Chaperone protein hchA	SAOUHSC_00533		Protein fate	Protein folding and stabilization		0	Cytoplasmic	6	3	9	5	5	6
Chromosomal replication initiator protein dnaA	SAOUHSC_00001	dnaA	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	1		1	2	3	3
coenzyme A disulfide reductase, putative	SAOUHSC_00908	cdr	Energy metabolism	Electron transport		0	Cytoplasmic	3	3	8	6	8	9
Cold shock protein cspA	SAOUHSC_01403	cspA	Hypothetical proteins	Domain		0	Cytoplasmic	1	2	2	2	2	1
cold shock protein, putative	SAOUHSC_03045	cspB	Hypothetical proteins	Domain		0	Cytoplasmic	3	1	1	1	2	3
conserved hypothetical phage protein	SAOUHSC_01583		Hypothetical proteins	Conserved		0	Unknown	1	1		2		
conserved hypothetical phage protein	SAOUHSC_01547		Cellular processes	Pathogenesis		0	Cytoplasmic		1				2
conserved hypothetical phage protein	SAOUHSC_02218		Hypothetical proteins	Conserved		0	Unknown	4		3	2	4	2
conserved hypothetical phage protein	SAOUHSC_02031		Hypothetical proteins	Conserved	S	0	Cytoplasmic		1		2		
conserved hypothetical protein	SAOUHSC_00003		DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	2	1	2	1	2	2
conserved hypothetical protein	SAOUHSC_00015		Unknown function	General		1	Cytoplasmic	2	1	1	1	2	1
conserved hypothetical protein	SAOUHSC_00075		Amino acid biosynthesis	Serine family		2	Cytoplasmic	7	3	7		3	
conserved hypothetical protein	SAOUHSC_00080		Transport and binding proteins	Cations and iron carrying compounds		2	Cytoplasmic	13	9	15	3	9	6
conserved hypothetical protein	SAOUHSC_00196	fadB	Fatty acid and phospholipid metabolism	Degradation		3	Unknown				11	8	11
conserved hypothetical protein	SAOUHSC_00197	fadD	Fatty acid and phospholipid metabolism	Degradation		1	Cytoplasmic	1			5	5	6
conserved hypothetical protein	SAOUHSC_00226		Energy metabolism	Fermentation		0	Cytoplasmic	3	1	2	3	4	4
conserved hypothetical protein	SAOUHSC_00227		Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic Membrane	7	3	7	6	8	7
conserved hypothetical protein	SAOUHSC_00228		Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		0	Cytoplasmic	5		6	5	2	7
conserved hypothetical protein	SAOUHSC_00257		Cellular processes	Pathogenesis		0	Extracellular	1		2	4	3	2
conserved hypothetical protein	SAOUHSC_00346	ychF	Unknown function	General		0	Cytoplasmic	4	6	5	8	7	8
conserved hypothetical protein	SAOUHSC_00356		Cellular processes	Chemotaxis and motility	S	0	Unknown	10	2	6	4	3	4
conserved hypothetical protein	SAOUHSC_00362		Cell envelope	Other	S	0	Unknown	7	3	5	1	4	4

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
conserved hypothetical protein	SAOUHSC_00369		Hypothetical proteins	Conserved		0	Cytoplasmic	7	8	5	3	3	6
conserved hypothetical protein	SAOUHSC_00371		Hypothetical proteins	Conserved		0	Cytoplasmic	2		2	1	2	4
conserved hypothetical protein	SAOUHSC_00405		Cell envelope	Other		0	Unknown	3	1	1	3	1	
conserved hypothetical protein	SAOUHSC_00486	ftsH	Protein fate	Degradation of proteins, peptides, and glycopeptides		3	Cytoplasmic Membrane	21	12	22	17	16	17
conserved hypothetical protein	SAOUHSC_00488	cysK	Amino acid biosynthesis	Serine family		1	Cytoplasmic	7	3	9	10	11	10
conserved hypothetical protein	SAOUHSC_00508		Unknown function	General		4	Cytoplasmic Membrane	1	3	1	3	1	1
conserved hypothetical protein	SAOUHSC_00513	yacO	Protein synthesis	tRNA and rRNA base modification		1	Cytoplasmic	3	2	3	1	1	3
conserved hypothetical protein	SAOUHSC_00532	kbl	Energy metabolism	Amino acids and amines		1	Cytoplasmic	4	1	6	8	5	6
conserved hypothetical protein	SAOUHSC_00539		Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions		1	Cytoplasmic	4	2	4	2	3	6
conserved hypothetical protein	SAOUHSC_00542		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic	6	3	5	5	7	5
conserved hypothetical protein	SAOUHSC_00548		Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		0	Cytoplasmic	1			2		3
conserved hypothetical protein	SAOUHSC_00607		Unclassified	Role category not yet assigned		0	Cytoplasmic	2		2		3	
conserved hypothetical protein	SAOUHSC_00616		Central intermediary metabolism	Other		1	Cytoplasmic	2	1	3	1	3	1
conserved hypothetical protein	SAOUHSC_00637	mntA	Transport and binding proteins	Unknown substrate		0	Cytoplasmic Membrane	4	4	6	6	5	6
conserved hypothetical protein	SAOUHSC_00647		Transport and binding proteins	Unknown substrate		5	Cytoplasmic Membrane		1	4	7	8	8
conserved hypothetical protein	SAOUHSC_00686		Hypothetical proteins	Conserved		0	Cytoplasmic		1	3	1	2	2
conserved hypothetical protein	SAOUHSC_00690		Hypothetical proteins	Conserved		1	Cytoplasmic	1	1	1	1	2	2
conserved hypothetical protein	SAOUHSC_00712		Regulatory functions	Other		0	Cytoplasmic				1		2
conserved hypothetical protein	SAOUHSC_00717		Cell envelope	Other	S	0	Unknown	4		3	5	3	5
conserved hypothetical protein	SAOUHSC_00749		Transport and binding proteins	Amino acids, peptides and amines		1	Cytoplasmic Membrane	4		11	1	4	7
conserved hypothetical protein	SAOUHSC_00787		Unclassified	Role category not yet assigned		0	Cytoplasmic		1	1	3	2	2
conserved hypothetical protein	SAOUHSC_00819	cspC	Hypothetical proteins	Domain		0	Cytoplasmic	3	1	3	2	3	4
conserved hypothetical protein	SAOUHSC_00833		Energy metabolism	Electron transport		0	Cytoplasmic	1		2	2	2	2
conserved hypothetical protein	SAOUHSC_00835		Cellular processes	Detoxification		0	Cytoplasmic		1	1	1	1	2

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
conserved hypothetical protein	SAOUHSC_00848	sufD	Biosynthesis of cofactors, prosthetic groups, and carriers	Other		0	Cytoplasmic	5	2	5	2	5	3
conserved hypothetical protein	SAOUHSC_00890		Unknown function	General		0	Cellwall	2		1	3	1	2
conserved hypothetical protein	SAOUHSC_00909		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic	4	2	3	2	4	3
conserved hypothetical protein	SAOUHSC_01026		Unclassified	Role category not yet assigned		0	Cytoplasmic	1				1	2
conserved hypothetical protein	SAOUHSC_01027		Hypothetical proteins	Conserved		0	Unknown				1	1	2
conserved hypothetical protein	SAOUHSC_01039		Cell envelope	Other		1	Unknown	9	2	5	2	2	3
conserved hypothetical protein	SAOUHSC_01061		Hypothetical proteins	Conserved		0	Unknown	1		2	2	1	3
conserved hypothetical protein	SAOUHSC_01091		Protein synthesis	tRNA and rRNA base modification		0	Unknown	2		2	1	3	2
conserved hypothetical protein	SAOUHSC_01107		DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	2		2	3	2	2
conserved hypothetical protein	SAOUHSC_01138		Unknown function	Enzymes of unknown specificity		0	Unknown	1	1	1	1	3	2
conserved hypothetical protein	SAOUHSC_01153		Hypothetical proteins	Conserved		0	Cytoplasmic		1				2
conserved hypothetical protein	SAOUHSC_01158		Cellular processes	Cell division		0	Cytoplasmic	2	2	6	4	4	4
conserved hypothetical protein	SAOUHSC_01163		Protein synthesis	tRNA and rRNA base modification		0	Cytoplasmic	5	4	9	3	6	6
conserved hypothetical protein	SAOUHSC_01192		Unclassified	Role category not yet assigned		0	Unknown	2	3	2	1	2	2
conserved hypothetical protein	SAOUHSC_01214		Transport and binding proteins	Unknown substrate		0	Cytoplasmic	1		3		1	2
conserved hypothetical protein	SAOUHSC_01252		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic	8	2	11	9	12	13
conserved hypothetical protein	SAOUHSC_01253	spoIIIIE,ftsK	Protein fate	Protein and peptide secretion and trafficking		4	Cytoplasmic Membrane	4		3	1	2	
conserved hypothetical protein	SAOUHSC_01255		Protein fate	Degradation of proteins, peptides, and glycopeptides		1	Cytoplasmic	3	1	4	3	2	3
conserved hypothetical protein	SAOUHSC_01256		Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Unknown	5	2	3	3	4	4
conserved hypothetical protein	SAOUHSC_01264		Hypothetical proteins	Conserved		0	Cytoplasmic	1		3	2	2	3
conserved hypothetical protein	SAOUHSC_01282	bsaA	Cellular processes	Detoxification		0	Unknown					1	2
conserved hypothetical protein	SAOUHSC_01317		Hypothetical proteins	Conserved		1	Unknown			1	1	2	
conserved hypothetical protein	SAOUHSC_01323		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic	4	2	3	1	3	4

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
conserved hypothetical protein	SAOUHSC_01338		Hypothetical proteins	Domain		1	Cytoplasmic Membrane	1	1	1	1	2	1
conserved hypothetical protein	SAOUHSC_01376		Unknown function	General		0	Cytoplasmic						2
conserved hypothetical protein	SAOUHSC_01383		Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Cytoplasmic	4	1	7	6	5	6
conserved hypothetical protein	SAOUHSC_01415		Energy metabolism	Other		0	Cytoplasmic	3	3	3	4	3	5
conserved hypothetical protein	SAOUHSC_01433		Unknown function	General		0	Cytoplasmic	2	2	1	2	2	2
conserved hypothetical protein	SAOUHSC_01438		Unclassified	Role category not yet assigned		0	Unknown	1		1	2	3	4
conserved hypothetical protein	SAOUHSC_01460		Central intermediary metabolism	Other		1	Cytoplasmic	4		3	2	1	4
conserved hypothetical protein	SAOUHSC_01629		Protein fate	Protein modification and repair		0	Cytoplasmic	4	2	5	2	2	4
conserved hypothetical protein	SAOUHSC_01659		DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	2	2	3	1	2	
conserved hypothetical protein	SAOUHSC_01673	phoH	Unknown function	General		0	Cytoplasmic	1		3	2	2	1
conserved hypothetical protein	SAOUHSC_01695		Unknown function	General		0	Cytoplasmic	3	1	3	2	4	2
conserved hypothetical protein	SAOUHSC_01698		Hypothetical proteins	Conserved		0	Cytoplasmic	2		3	1	1	3
conserved hypothetical protein	SAOUHSC_01729		Hypothetical proteins	Conserved		0	Unknown	2	1	3	2	2	2
conserved hypothetical protein	SAOUHSC_01732		Unclassified	Role category not yet assigned		0	Cytoplasmic	1	1			3	3
conserved hypothetical protein	SAOUHSC_01734		Unknown function	General		0	Cytoplasmic	1	1			1	2
conserved hypothetical protein	SAOUHSC_01735		Transport and binding proteins	Unknown substrate		2	Cytoplasmic	4	1	3	4	3	2
conserved hypothetical protein	SAOUHSC_01782		DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	1	3	2		1	2
conserved hypothetical protein	SAOUHSC_01814		Unknown function	General		0	Unknown	1	2	4	4	5	5
conserved hypothetical protein	SAOUHSC_01822	tpx	Cellular processes	Detoxification		0	Unknown	4	3	4	4	4	4
conserved hypothetical protein	SAOUHSC_01838		DNA metabolism	DNA replication, recombination, and repair	S	0	Cytoplasmic Membrane	6	1	3	8	4	10
conserved hypothetical protein	SAOUHSC_01852		Amino acid biosynthesis	Aromatic amino acid family		0	Cytoplasmic	6	5	8	5	6	6
conserved hypothetical protein	SAOUHSC_01854		Hypothetical proteins	Conserved		1	Cellwall	4	3	2	4	5	3
conserved hypothetical protein	SAOUHSC_01858		Transport and binding proteins	Unknown substrate		0	Cytoplasmic	4	4	6	6	4	4
conserved hypothetical protein	SAOUHSC_01860		Energy metabolism	Electron transport		0	Cytoplasmic	3	3	4	3	4	4
conserved hypothetical protein	SAOUHSC_01861		Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Cytoplasmic		1		1	4	1
conserved hypothetical protein	SAOUHSC_01869		Hypothetical proteins	Conserved		1	Unknown	3	1	3	2	2	4

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
conserved hypothetical protein	SAOUHSC_01895		Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		1	Extracellular	6		7	2	3	4
conserved hypothetical protein	SAOUHSC_01901		Energy metabolism	Pentose phosphate pathway		0	Unknown	6	1	4	9	6	4
conserved hypothetical protein	SAOUHSC_01908		Hypothetical proteins	Conserved	S	0	Unknown	7	4	5	7	5	6
conserved hypothetical protein	SAOUHSC_01968	hit	Unclassified	Role category not yet assigned		0	Unknown	3	2		3	2	2
conserved hypothetical protein	SAOUHSC_01974		Hypothetical proteins	Conserved		1	Cytoplasmic	6		6	4	4	2
conserved hypothetical protein	SAOUHSC_01975		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic			2	3	2	3
conserved hypothetical protein	SAOUHSC_01987		Central intermediary metabolism	Amino sugars		0	Cytoplasmic	8	6	7	7	10	7
conserved hypothetical protein	SAOUHSC_01999		Cellular processes	Detoxification		0	Cytoplasmic	2	1	2	4	3	5
conserved hypothetical protein	SAOUHSC_02014		Hypothetical proteins	Conserved		0	Cytoplasmic	1	2	2	2	2	2
conserved hypothetical protein	SAOUHSC_02093		Hypothetical proteins	Domain		0	Unknown	3	1	4	3	2	3
conserved hypothetical protein	SAOUHSC_02096		Hypothetical proteins	Conserved		1	Cytoplasmic	2		3	3		2
conserved hypothetical protein	SAOUHSC_02121		Cell envelope	Other		1	Unknown	9	4	6	1	3	
conserved hypothetical protein	SAOUHSC_02150		Energy metabolism	Electron transport		0	Unknown	2	2	1	6	6	6
conserved hypothetical protein	SAOUHSC_02151		Transport and binding proteins	Unknown substrate	S	4	Cytoplasmic Membrane			1	1	2	1
conserved hypothetical protein	SAOUHSC_02158		Amino acid biosynthesis	Aspartate family		0	Cytoplasmic	2	2	3	4	1	5
conserved hypothetical protein	SAOUHSC_02366	fbaA,fba	Energy metabolism	Glycolysis/ gluconeogenesis		0	Cytoplasmic	7	4	8	9	8	9
conserved hypothetical protein	SAOUHSC_02381	dps	Cellular processes	Adaptations to atypical conditions		0	Cytoplasmic	3		1	6	5	3
conserved hypothetical protein	SAOUHSC_02383		Hypothetical proteins	Conserved		0	Unknown	3	1	2		1	2
conserved hypothetical protein	SAOUHSC_02434		Transport and binding proteins	Cations and iron carrying compounds		2	Cytoplasmic	1	1	6		2	4
conserved hypothetical protein	SAOUHSC_02436		Transport and binding proteins	Cations and iron carrying compounds		1	Cytoplasmic	4		4	4	5	3
conserved hypothetical protein	SAOUHSC_02443		Hypothetical proteins	Conserved		2	Cytoplasmic Membrane	3	1	6	4	2	2
conserved hypothetical protein	SAOUHSC_02460		Central intermediary metabolism	Other		0	Cytoplasmic	4		5	2		1
conserved hypothetical protein	SAOUHSC_02554	fhuD2	Transport and binding proteins	Amino acids, peptides and amines		1	Cytoplasmic Membrane	13	5	11	9	9	10
conserved hypothetical protein	SAOUHSC_02568		Hypothetical proteins	Conserved		0	Cytoplasmic	3	1	1	3	4	1

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
conserved hypothetical protein	SAOUHSC_02574		Unknown function	Enzymes of unknown specificity		2	Cytoplasmic	7	2	9	6	8	10
conserved hypothetical protein	SAOUHSC_02626		Hypothetical proteins	Conserved		0	Cytoplasmic	2		2	1	1	3
conserved hypothetical protein	SAOUHSC_02666		Hypothetical proteins	Conserved		1	Unknown	4		5	4	2	3
conserved hypothetical protein	SAOUHSC_02668		Hypothetical proteins	Conserved		1	Unknown	5	2	3		3	1
conserved hypothetical protein	SAOUHSC_02699		Transport and binding proteins	Unknown substrate	S	0	Unknown	6	3	7	6	6	8
conserved hypothetical protein	SAOUHSC_02724		Hypothetical proteins	Conserved		1	Unknown	3	2	2	5	6	6
conserved hypothetical protein	SAOUHSC_02747		Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Unknown	1	1	1	2	4	2
conserved hypothetical protein	SAOUHSC_02774		Unknown function	General		0	Cytoplasmic	2	1	3		4	3
conserved hypothetical protein	SAOUHSC_02811		Unknown function	General		1	Cytoplasmic	2			1	2	1
conserved hypothetical protein	SAOUHSC_02827		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic		1				2
conserved hypothetical protein	SAOUHSC_02844		Fatty acid and phospholipid metabolism	Degradation		1	Cytoplasmic	1		2	4	3	4
conserved hypothetical protein	SAOUHSC_02980		Biosynthesis of cofactors, prosthetic groups, and carriers	Other		0	Unknown	2	2	1	1	2	2
conserved hypothetical protein	SAOUHSC_00077	sbnC	Transport and binding proteins	Cations and iron carrying compounds		2	Cytoplasmic Membrane	6	2	5	2	4	4
conserved hypothetical protein	SAOUHSC_00079		Transport and binding proteins	Cations and iron carrying compounds		0	Cytoplasmic	5	4	9	3	5	3
conserved hypothetical protein	SAOUHSC_00083		Hypothetical proteins	Conserved		0	Cytoplasmic	6	1	6		3	2
conserved hypothetical protein	SAOUHSC_00144		Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		6	Cytoplasmic			1	1	4	2
conserved hypothetical protein	SAOUHSC_00198	fadE	Protein synthesis	tRNA aminoacylation		1	Cytoplasmic					1	2
conserved hypothetical protein	SAOUHSC_00261		Unclassified	Role category not yet assigned		1	Unknown					3	
conserved hypothetical protein	SAOUHSC_00367		Transport and binding proteins	Amino acids, peptides and amines		10	Cytoplasmic Membrane				3	1	2
conserved hypothetical protein	SAOUHSC_00617		Hypothetical proteins	Conserved	S	0	Unknown	3		1	1		3
conserved hypothetical protein	SAOUHSC_00655		Regulatory functions	Protein interactions		0	Cytoplasmic				2	2	
conserved hypothetical protein	SAOUHSC_00756		Energy metabolism	Glycolysis/ gluconeogenesis		0	Cytoplasmic		1	1	1	2	1
conserved hypothetical protein	SAOUHSC_00864		Unknown function	General		0	Cytoplasmic			1	2		1

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
conserved hypothetical protein	SAOUHSC_00934	spxA	Regulatory functions	Other		0	Unknown	1	1	1	4	3	6
conserved hypothetical protein	SAOUHSC_01050		Hypothetical proteins	Conserved	S	2	Cytoplasmic Membrane	1		1	2	1	2
conserved hypothetical protein	SAOUHSC_01187	pknB	Regulatory functions	Other		1	Cytoplasmic Membrane	6	1	1	1	2	2
conserved hypothetical protein	SAOUHSC_01239		Protein fate	Degradation of proteins, peptides, and glycopeptides		5	Cytoplasmic Membrane	3		1	1	2	1
conserved hypothetical protein	SAOUHSC_01265		Hypothetical proteins	Conserved		0	Cytoplasmic			3	1	3	2
conserved hypothetical protein	SAOUHSC_01324		Hypothetical proteins	Conserved		0	Cytoplasmic	1		1		2	3
conserved hypothetical protein	SAOUHSC_01425		Cellular processes	Toxin production and resistance		0	Cytoplasmic	4	2	1		1	2
conserved hypothetical protein	SAOUHSC_01454		DNA metabolism	DNA replication, recombination, and repair		0	Unknown	2	1			2	
conserved hypothetical protein	SAOUHSC_01594		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic	1			2	1	1
conserved hypothetical protein	SAOUHSC_01660		Hypothetical proteins	Conserved		0	Unknown				2		1
conserved hypothetical protein	SAOUHSC_01675		Hypothetical proteins	Conserved		1	Cytoplasmic	1				2	3
conserved hypothetical protein	SAOUHSC_01677		Unknown function	General		2	Cytoplasmic Membrane			1		2	2
conserved hypothetical protein	SAOUHSC_01696		Hypothetical proteins	Conserved		0	Cytoplasmic	1	1		2	1	1
conserved hypothetical protein	SAOUHSC_01787	lysP	Transport and binding proteins	Amino acids, peptides and amines	S	11	Cytoplasmic Membrane	1			2	1	1
conserved hypothetical protein	SAOUHSC_01907		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic				3	2	2
conserved hypothetical protein	SAOUHSC_00400		Transport and binding proteins	Amino acids, peptides and amines	S	0	Unknown					2	
conserved hypothetical protein	SAOUHSC_02125		Unknown function	General		0	Cytoplasmic			1	2		
conserved hypothetical protein	SAOUHSC_02404	fmtB	Hypothetical proteins	Conserved	S	0	Cellwall	2	1		2	1	2
conserved hypothetical protein	SAOUHSC_02585		Regulatory functions	Other		0	Cytoplasmic Membrane	1	1	1	1	3	1
conserved hypothetical protein	SAOUHSC_00844		Unclassified	Role category not yet assigned	S	0	Cytoplasmic Membrane				2		1
conserved hypothetical protein	SAOUHSC_01979		Mobile and extrachromosomal element functions	Transposon functions		0	Cytoplasmic	4	3	3	2	2	1
conserved hypothetical protein	SAOUHSC_02759		Cell envelope	Other	S	0	Unknown	2	1				2
conserved hypothetical protein	SAOUHSC_02790		DNA metabolism	DNA replication, recombination, and repair		0	Unknown		2		2		
conserved hypothetical protein	SAOUHSC_02793		Energy metabolism	Sugars		2	Cytoplasmic	2	2	2	3	1	1

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
conserved hypothetical protein	SAOUHSC_02828		Unknown function	Enzymes of unknown specificity		1	Unknown				2		
conserved hypothetical protein	SAOUHSC_02866		Unknown function	General		12	Cytoplasmic Membrane						2
conserved hypothetical protein	SAOUHSC_02913		Hypothetical proteins	Conserved		1	Cytoplasmic	1			2	1	
conserved hypothetical protein	SAOUHSC_02100		Hypothetical proteins	Conserved		2	Cytoplasmic Membrane					1	2
conserved hypothetical protein	SAOUHSC_02982		Cell envelope	Other		1	Cellwall	16	4	7	2	1	3
conserved hypothetical protein	SAOUHSC_02690		Unknown function	General		0	Cytoplasmic Membrane	5		2	1	3	1
conserved hypothetical protein	SAOUHSC_00973		Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		0	Cytoplasmic		1	1		1	2
Conserved virulence factor B	SAOUHSC_01391		Hypothetical proteins	Conserved		0	Cytoplasmic	5	2	8	4	4	5
CTP synthase	SAOUHSC_02368	pyrG,ctrA	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis		0	Cytoplasmic	10	5	11	12	9	10
CysteinyI-tRNA synthetase	SAOUHSC_00511	cysS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	3	4	7	4	4	8
cytidylate kinase	SAOUHSC_01496	cmk	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions		0	Cytoplasmic	1	2	2	1	1	2
cytochrome d ubiquinol oxidase, subunit I, putative	SAOUHSC_01031		Energy metabolism	Electron transport		9	Cytoplasmic Membrane	1	1	1		1	2
D-3-phosphoglycerate dehydrogenase	SAOUHSC_01833	serA	Amino acid biosynthesis	Serine family		0	Cytoplasmic		1				2
D-alanine--D-alanine ligase	SAOUHSC_02318	ddl	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		0	Cytoplasmic	3		5	3	2	4
D-alanine--poly(phosphoribitol) ligase subunit 1	SAOUHSC_00869	dltA	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		2	Cytoplasmic	9	4	8	8	7	9
D-alanine--poly(phosphoribitol) ligase subunit 2	SAOUHSC_00871	dltC	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		0	Cytoplasmic	2	1	2	2	2	2
D-amino acid aminotransferase	SAOUHSC_01867	dat	Energy metabolism	Amino acids and amines		0	Cytoplasmic	3	2	9	6	10	9
Delta-aminolevulinic acid dehydratase	SAOUHSC_01772	hemB	Biosynthesis of cofactors, prosthetic groups, and carriers	Heme, porphyrin, and cobalamin		0	Cytoplasmic	1	1	1		2	



description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
deoxyribose-phosphate aldolase	SAOUHSC_00100	deoC,deoC1, dra	Energy metabolism	Other		1	Cytoplasmic			5		4	5
deoxyribose-phosphate aldolase	SAOUHSC_02379	deoC2	Energy metabolism	Other		1	Cytoplasmic	3	3		3		
dephospho-CoA kinase	SAOUHSC_01795	coaE	Biosynthesis of cofactors, prosthetic groups, and carriers	Pantothenate and coenzyme A		0	Cytoplasmic	3	1	3	2	4	2
dethiobiotin synthase, putative	SAOUHSC_02716	bioD	Biosynthesis of cofactors, prosthetic groups, and carriers	Biotin		0	Cytoplasmic		1			1	2
diaminopimelate decarboxylase	SAOUHSC_01401	lysA	Amino acid biosynthesis	Aspartate family		0	Cytoplasmic	1	3	2	2	4	5
dihydrodipicolinate reductase	SAOUHSC_01397	dapB	Amino acid biosynthesis	Aspartate family		1	Cytoplasmic				3	3	3
Dihydrodipicolinate synthase	SAOUHSC_01396	dapA	Amino acid biosynthesis	Aspartate family		0	Cytoplasmic				9	8	7
dihydrolipoamide dehydrogenase	SAOUHSC_01043	pdhD,lpdA	Energy metabolism	Pyruvate dehydrogenase		0	Cytoplasmic	11	6	16	11	13	16
dihydrolipoamide S-acetyltransferase component of pyruvate dehydrogenase complex E2, putative	SAOUHSC_01042	pdhC	Energy metabolism	Pyruvate dehydrogenase		0	Cytoplasmic	11	7	19	12	12	12
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	SAOUHSC_01416	sucB,odhB	Energy metabolism	TCA cycle		0	Cytoplasmic		2	1	6	2	4
dihydroorotase	SAOUHSC_01168	pyrC	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis		0	Cytoplasmic	4	2	8	4	5	7
dihydroorotate dehydrogenase	SAOUHSC_02909	pyrD	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis		0	Cytoplasmic Membrane			1		1	2
D-lactate dehydrogenase, putative	SAOUHSC_02830	ddh	Energy metabolism	Fermentation		0	Cytoplasmic	1		3	2	1	1
DNA directed RNA polymerase beta-prime chain, putative	SAOUHSC_00525	rpoC	Transcription	DNA-dependent RNA polymerase		0	Cytoplasmic	26	17	46	39	43	44
DNA gyrase subunit A	SAOUHSC_00006	gyrA	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	7	2	3	2	6	5
DNA gyrase, B subunit	SAOUHSC_00005	gyrB	DNA metabolism	DNA replication, recombination, and repair		2	Cytoplasmic	3	3	7	3	6	8
DNA ligase	SAOUHSC_02122	dnlJ,lig,ligA	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	2	4	2	4	2	2
DNA mismatch repair protein MutS	SAOUHSC_01272	mutS	DNA metabolism	DNA replication, recombination, and repair		1	Cytoplasmic	1		2	1	2	

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
DNA polymerase I	SAOUHSC_01797	polA	DNA metabolism	DNA replication, recombination, and repair		1	Cytoplasmic	6	4	9	10	6	13
DNA polymerase III polC-type	SAOUHSC_01241	polC	DNA metabolism	DNA replication, recombination, and repair		2	Cytoplasmic			1		3	
DNA polymerase III, beta subunit	SAOUHSC_00002	dnaN	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	6	3	7	9	9	8
DNA repair protein RecN	SAOUHSC_01615	recN	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	1			2	3	2
DNA topoisomerase 4 subunit A	SAOUHSC_01352	parC,grlA	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic		3			2	3
DNA topoisomerase 4 subunit B	SAOUHSC_01351	parE,grlB	DNA metabolism	DNA replication, recombination, and repair		1	Cytoplasmic	1	1	2	1	2	1
DNA-binding protein HU, putative	SAOUHSC_01490	hup,hu	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	9	7	10	6	6	6
DNA-binding response regulator VraR, putative	SAOUHSC_02098	vraR	Regulatory functions	DNA interactions		0	Cytoplasmic	2	1	2	5	4	3
DNA-directed RNA polymerase subunit alpha	SAOUHSC_02485	rpoA	Transcription	DNA-dependent RNA polymerase		0	Cytoplasmic	6	7	11	12	12	13
DNA-directed RNA polymerase subunit omega	SAOUHSC_01177	rpoZ	Transcription	DNA-dependent RNA polymerase		0	Unknown	2	1	4	1	2	3
D-tyrosyl-tRNA(Tyr) deacylase	SAOUHSC_01741	dtd	Protein synthesis	tRNA aminoacylation		0	Unknown	1	1		2	2	
Elastin-binding protein ebpS	SAOUHSC_01501	ebpS	Unknown function	General		2	Cytoplasmic Membrane	6	1	4	2	5	4
Elongation factor G	SAOUHSC_00529	fusA,fus	Protein synthesis	Translation factors		0	Cytoplasmic	21	19	33	20	23	26
Elongation factor P	SAOUHSC_01625	efp	Protein synthesis	Translation factors		0	Cytoplasmic	3		3	2	2	4
Elongation factor Ts	SAOUHSC_01234	tsf	Protein synthesis	Translation factors		0	Cytoplasmic	20	16	26	16	18	16
Elongation factor Tu	SAOUHSC_00530	tuf	Protein synthesis	Translation factors		0	Cytoplasmic	22	19	24	18	18	19
Enolase	SAOUHSC_00799	eno	Energy metabolism	Glycolysis/ gluconeogenesis		1	Cytoplasmic	18	16	23	14	18	18
enoyl-(acyl-carrier-protein) reductase	SAOUHSC_00947	fabI	Energy metabolism	Aerobic		0	Cytoplasmic Membrane	3	1	5	8	6	5
enoyl-CoA hydratase/isomerase family protein, putative	SAOUHSC_00985	menB	Biosynthesis of cofactors, prosthetic groups, and carriers	Menaquinone and ubiquinone		0	Cytoplasmic	8	7	7	6	7	9
Epimerase family protein SAOUHSC_00792	SAOUHSC_00792		Hypothetical proteins	Conserved		2	Unknown	2		2	3	1	
Extracellular matrix-binding protein ebh	SAOUHSC_01447		Unclassified	Role category not yet assigned	S	1	Cellwall	3	3	1	8	3	3

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
extramembranal protein	SAOUHSC_00872	dltD	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		1	Cytoplasmic	11	5	10	2	5	6
Ferritin	SAOUHSC_02108	ftn	Unknown function	General		0	Cytoplasmic	1		1	3	4	2
FMN-dependent NADPH-azoreductase	SAOUHSC_00543		Central intermediary metabolism	Other		1	Unknown	1	1	3	2	2	2
Foldase protein prsA	SAOUHSC_01972	prsA	Protein fate	Protein folding and stabilization	S	0	Cytoplasmic Membrane	12	5	9	14	13	17
Formate--tetrahydrofolate ligase	SAOUHSC_01845	fhs	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		2	Cytoplasmic	7	7	17	8	14	17
fructose specific permease, putative	SAOUHSC_00708	fruA	Signal transduction	PTS		9	Cytoplasmic Membrane	5	5	4	1	2	4
Fructose-bisphosphate aldolase class 1	SAOUHSC_02926		Energy metabolism	Glycolysis/ gluconeogenesis		0	Unknown	19	16	26	20	19	19
fumarate hydratase, class II	SAOUHSC_01983	fumC,citG	Energy metabolism	TCA cycle		0	Cytoplasmic	2	1	1	1	6	3
GAF domain protein	SAOUHSC_01828		Unknown function	General		0	Cytoplasmic	1	1	1	2	1	2
Globin domain protein	SAOUHSC_00204		Energy metabolism	Electron transport		2	Cytoplasmic	1				2	1
glucokinase, putative	SAOUHSC_01646	glcK,glk,glk A	Energy metabolism	Glycolysis/ gluconeogenesis		0	Cytoplasmic	3	1	5	5	4	4
glucosamine--fructose-6-phosphate aminotransferase, isomerizing	SAOUHSC_02399	glmS	Central intermediary metabolism	Amino sugars		2	Cytoplasmic	5	4	4	7	7	4
glucose-6-phosphate 1-dehydrogenase	SAOUHSC_01599	zwf	Energy metabolism	Pentose phosphate pathway		0	Cytoplasmic	7	2	7	9	12	10
Glucose-6-phosphate isomerase	SAOUHSC_00900	pgi	Energy metabolism	Pentose phosphate pathway		3	Cytoplasmic	4	4	9	7	9	9
Glutamate-1-semialdehyde 2,1-aminomutase 1	SAOUHSC_01771	hemL	Biosynthesis of cofactors, prosthetic groups, and carriers	Heme, porphyrin, and cobalamin		0	Cytoplasmic	4	2	8	5	6	7
glutamate-1-semialdehyde-2,1-aminomutase, putative	SAOUHSC_02000	gsaB	Biosynthesis of cofactors, prosthetic groups, and carriers	Heme, porphyrin, and cobalamin		0	Cytoplasmic	4	1	5	3	5	8
glutamine synthetase, type I	SAOUHSC_01287	glnA	Amino acid biosynthesis	Glutamate family		0	Cytoplasmic	12	6	16	11	12	12
Glutamyl-tRNA synthetase	SAOUHSC_00509	gltX	Protein synthesis	tRNA aminoacylation		1	Cytoplasmic	11	11	12	10	12	11
Glutamyl-tRNA(Gln) amidotransferase subunit A	SAOUHSC_02117	gatA	Protein synthesis	tRNA aminoacylation		1	Cytoplasmic	11	5	14	9	12	14
glyceraldehyde-3-phosphate dehydrogenase, type I	SAOUHSC_00795	gap1,gap	Energy metabolism	Glycolysis/ gluconeogenesis		0	Cytoplasmic	15	15	16	13	12	15
Glycerol kinase	SAOUHSC_01276	glpK	Energy metabolism	Other		1	Cytoplasmic	1		3	3	4	3
Glycerol phosphate lipoteichoic acid synthase	SAOUHSC_00728		Central intermediary metabolism	Sulfur metabolism		4	Cytoplasmic Membrane	13	5	7	3	3	1

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
glycerol uptake operon antiterminator regulatory protein, putative	SAOUHSC_01274	glpP	Energy metabolism	Sugars		0	Cytoplasmic	2		1	1	2	1
glycine betaine transporter, putative	SAOUHSC_01346	opuD1,opuD	Transport and binding proteins	Amino acids, peptides and amines		12	Cytoplasmic Membrane	1	1		1	2	1
Glycine cleavage system H protein	SAOUHSC_00836	gcvH	Energy metabolism	Amino acids and amines		0	Cytoplasmic	1	2	1	2		1
Glycyl-tRNA synthetase	SAOUHSC_01666	glyS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	7	7	19	11	17	15
GMP reductase	SAOUHSC_01330	guaC	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions	S	1	Cytoplasmic	1		5	3	4	2
GMP synthase [glutamine-hydrolyzing]	SAOUHSC_00375	guaA	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	7	6	14	9	8	9
GTP cyclohydrolase folE2	SAOUHSC_00549		Hypothetical proteins	Conserved		0	Cytoplasmic	5	2	6	1	1	4
GTP pyrophosphokinase	SAOUHSC_01742	relA	Cellular processes	Adaptations to atypical conditions		0	Cytoplasmic	2	1	1	2	1	2
GTP pyrophosphokinase, putative	SAOUHSC_00942		Unknown function	General		0	Cytoplasmic		1	1	1	2	
GTPase obg	SAOUHSC_01753	obg	Unknown function	General		0	Cytoplasmic	8	3	6	7	9	7
GTP-binding protein engA	SAOUHSC_01492	engA	Unknown function	General		0	Cytoplasmic Membrane	4	3	7	4	3	6
GTP-binding protein Era	SAOUHSC_01668	era,bex	Cellular processes	Cell division		0	Cytoplasmic Membrane	2	1	2	3	4	2
GTP-binding protein lepA	SAOUHSC_01688	lepA	Unknown function	General		0	Cytoplasmic Membrane	4	1	5	4	5	5
GTP-binding protein TypA, putative	SAOUHSC_01058	typA	Unknown function	General		0	Cytoplasmic Membrane	9	7	8	7	10	11
GTP-sensing transcriptional pleiotropic repressor codY	SAOUHSC_01228	codY	Regulatory functions	DNA interactions		0	Cytoplasmic	6	3	10	6	10	7
Guanylate kinase	SAOUHSC_01176	gmk	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions		0	Cytoplasmic			1		2	1
Helix-turn-helix domain protein	SAOUHSC_01575		Protein fate	Degradation of proteins, peptides, and glycopeptides	S	0	Cytoplasmic	2		1	3	3	2
Heme-degrading monooxygenase isdI	SAOUHSC_00130	isdI	Cellular processes	Toxin production and resistance		0	Cytoplasmic	2	2	4	3	5	4
histidine kinase, putative	SAOUHSC_02099	vraS	Regulatory functions	Protein interactions		2	Cytoplasmic Membrane					1	3
Histidine protein kinase saeS	SAOUHSC_00714	saeS	Regulatory functions	Protein interactions		2	Cytoplasmic Membrane	4				2	1
Histidinol-phosphate aminotransferase	SAOUHSC_00733	hisC	Amino acid biosynthesis	Histidine family		1	Unknown						2
Histidyl-tRNA synthetase	SAOUHSC_01738	hisS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	6	3	9	5	6	3

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
HMG-CoA synthase, putative	SAOUHSC_02860	mvaS	Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic	5	5	6	8	7	7
homoserine dehydrogenase, putative	SAOUHSC_01320	dhoM	Energy metabolism	Electron transport		1	Unknown	1			4	2	4
HTH-type transcriptional regulator mgrA	SAOUHSC_00694		Regulatory functions	Other		0	Cytoplasmic	4	3	6	2	5	5
HTH-type transcriptional regulator sarR	SAOUHSC_02566	sarR	Regulatory functions	Other		0	Cytoplasmic	1	1	4	2	4	5
hypoxanthine phosphoribosyltransferase	SAOUHSC_00485	hpt	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides		0	Cytoplasmic	1	2	3	4	4	4
Immunodominant staphylococcal antigen B	SAOUHSC_02972	isaB	Unknown function	General	S	0	Extracellular	1			1		2
Immunoglobulin-binding protein sbi	SAOUHSC_02706	sbi	Cellular processes	Pathogenesis	S	0	Unknown			4	2	4	
indolepyruvate decarboxylase, putative	SAOUHSC_00153	ipdC	Cellular processes	Pathogenesis		1	Cytoplasmic Membrane	1			1	2	2
Inosine-5'-monophosphate dehydrogenase	SAOUHSC_00374	guaB	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		1	Cytoplasmic	14	12	22	9	15	13
iron compound ABC transporter, ATP-binding protein	SAOUHSC_00652	fhuA	Transport and binding proteins	Cations and iron carrying compounds		0	Cytoplasmic Membrane	2	2	5	1	3	4
Iron-regulated surface determinant protein A	SAOUHSC_01081	isdA	Cell envelope	Other		1	Cellwall	7	3	7	2	4	2
Iron-regulated surface determinant protein B	SAOUHSC_01079	isdB	Transport and binding proteins	Amino acids, peptides and amines	S	0	Cellwall	20	4	22	1	2	2
isocitrate dehydrogenase, NADP-dependent	SAOUHSC_01801	icd,citC	Energy metabolism	TCA cycle		0	Cytoplasmic	3	2	4	6	4	6
Isoleucyl-tRNA synthetase	SAOUHSC_01159	ileS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	13	11	27	12	17	18
Leucyl-tRNA synthetase	SAOUHSC_01875	leuS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	9	10	14	10	9	11
Lipoyl synthase	SAOUHSC_00861	lipA	Biosynthesis of cofactors, prosthetic groups, and carriers	Lipoate		0	Cytoplasmic				2	1	
L-lactate dehydrogenase	SAOUHSC_00206	ldh1,ldhE	Energy metabolism	Anaerobic		0	Cytoplasmic			1	5	1	1
L-lactate dehydrogenase 2	SAOUHSC_02922	ldh2,ldh	Energy metabolism	Anaerobic		0	Cytoplasmic	4	2	4	4	4	3
Lysostaphin resistance protein A	SAOUHSC_02611		Mobile and extrachromosomal element functions	Prophage functions		8	Cytoplasmic Membrane	1				1	2
Lysyl-tRNA synthetase	SAOUHSC_00493	lysS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	20	12	23	18	25	20
lytic regulatory protein, putative	SAOUHSC_02390		Regulatory functions	Other		6	Cytoplasmic Membrane	2	1	2	2	1	1
malate:quinone-oxidoreductase	SAOUHSC_02927	mqa2	Energy metabolism	TCA cycle		0	Cellwall	14	8	17	14	17	18

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
malonyl CoA-acyl carrier protein transacylase	SAOUHSC_01198	fabD	Fatty acid and phospholipid metabolism	Biosynthesis		0	Cytoplasmic	5	2	6	5	4	4
Mannitol-1-phosphate 5-dehydrogenase	SAOUHSC_02403	mtlD	Energy metabolism	Sugars		1	Cytoplasmic	2	1	1	2	1	1
Membrane protein oxaA	SAOUHSC_02327	oxaA	Cell envelope	Other		5	Cytoplasmic Membrane	1		1	2	1	1
membrane protein, putative	SAOUHSC_00200		Cell envelope	Other		7	Cytoplasmic Membrane		1			2	
menaquinone biosynthesis methyltransferase, putative	SAOUHSC_01487	gerCB,menH,ubiE	Protein synthesis	tRNA and rRNA base modification		1	Unknown	1	1	1		2	
methionine aminopeptidase, type I	SAOUHSC_02102	map	Protein fate	Protein modification and repair		0	Cytoplasmic	4	5	3	3	3	3
Methionyl-tRNA formyltransferase	SAOUHSC_01183		Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	5	1	2	4	4	2
methionyl-tRNA synthetase, putative	SAOUHSC_00461	metS,metG	Protein synthesis	tRNA aminoacylation		2	Cytoplasmic	8	7	12	12	11	17
Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase trmFO	SAOUHSC_01223	gid	Unknown function	General		1	Cytoplasmic	2	1	6	3	5	4
MHC class II analog protein	SAOUHSC_02161		Cell envelope	Other	S	0	Cytoplasmic Membrane	2	1			2	1
Monofunctional glycosyltransferase	SAOUHSC_02012	sgtB	Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		1	Cytoplasmic Membrane				2	2	2
MutS2 protein	SAOUHSC_01099	mutS2	DNA metabolism	Other		1	Cytoplasmic	2		1	3	1	1
N utilization substance protein B homolog	SAOUHSC_01621	nusB	Transcription	Transcription factors		0	Unknown	2	1	3	3	3	2
NADH dehydrogenase-like protein SAOUHSC_00878	SAOUHSC_00878		Central intermediary metabolism	Other		1	Cytoplasmic Membrane	5	4	5	6	9	9
NADP-dependent malic enzyme, putative	SAOUHSC_01810		Energy metabolism	TCA cycle		3	Cytoplasmic	4	4	7	7	7	6
NH(3)-dependent NAD(+) synthetase	SAOUHSC_02132	nadE	Biosynthesis of cofactors, prosthetic groups, and carriers	Pyridine nucleotides		0	Cytoplasmic	2	3	6	4	3	4
nicotinate phosphoribosyltransferase, putative	SAOUHSC_02133		Biosynthesis of cofactors, prosthetic groups, and carriers	Pyridine nucleotides		1	Cytoplasmic	2	3	4	4	4	4
O-acetyltransferase oatA	SAOUHSC_02885		Unknown function	Enzymes of unknown specificity		9	Cytoplasmic Membrane	1	1	1	1	2	2
oligoendopeptidase F	SAOUHSC_00937	pepF,pepB	Protein fate	Degradation of proteins, peptides, and glycopeptides		1	Cytoplasmic	7	4	13	9	7	12

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
oligopeptide ABC transporter, substrate-binding protein, putative	SAOUHSC_00927	oppA	Transport and binding proteins	Amino acids, peptides and amines		1	Cellwall	1				1	2
ornithine aminotransferase, putative	SAOUHSC_00150	rocD	Amino acid biosynthesis	Glutamate family		2	Cytoplasmic	1		1	4	5	5
ornithine cyclodeaminase, putative	SAOUHSC_00076		Energy metabolism	Amino acids and amines		0	Cytoplasmic	5	4	7	4	5	5
orotate phosphoribosyltransferase	SAOUHSC_01172	pyrE	Purines, pyrimidines, nucleosides, and nucleotides	Pyrimidine ribonucleotide biosynthesis		1	Cytoplasmic	3	1	4	1	1	3
penicillin-binding protein 1	SAOUHSC_01145	pbpA	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		1	Cytoplasmic Membrane	5	2	2	3	1	1
penicillin-binding protein 2	SAOUHSC_01467	pbp2	Protein fate	Degradation of proteins, peptides, and glycopeptides		1	Cytoplasmic Membrane	22	10	14	16	15	11
penicillin-binding protein 3	SAOUHSC_01652	pbpF,pbp3	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		1	Cytoplasmic Membrane	9	3	4	2	3	3
penicillin-binding protein 4, putative	SAOUHSC_00646	pbp4	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan	S	1	Cytoplasmic Membrane	5	1	4	1		4
Peptidase T	SAOUHSC_00757	pepT	Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Cytoplasmic	3	1	4	3	6	5
peptide ABC transporter, peptide-binding protein, putative	SAOUHSC_02767	opp-1A,opp1A	Transport and binding proteins	Cations and iron carrying compounds		1	Cellwall	17	6	13	3	3	3
Peptide chain release factor 1	SAOUHSC_02359	prfA	Protein synthesis	Translation factors		0	Cytoplasmic	4	5	5	4	3	2
Peptide chain release factor 3	SAOUHSC_00956	prfC	Protein synthesis	Translation factors		1	Cytoplasmic	2	2	4	5	5	2
Peptide methionine sulfoxide reductase msrA 2	SAOUHSC_01432	msrA2	Cellular processes	Adaptations to atypical conditions		0	Unknown		1	3	5	6	8
Peptide methionine sulfoxide reductase msrB	SAOUHSC_01431	msrB	Cellular processes	Adaptations to atypical conditions		0	Cytoplasmic	4	4	5	3	4	5
periplasmic binding protein, putative	SAOUHSC_00074	sirA	Cell envelope	Other	S	0	Cytoplasmic Membrane	17	12	13	8	6	10
Peroxide-responsive repressor perR	SAOUHSC_01997	perR	Regulatory functions	Other		0	Cytoplasmic	1		2	2	1	
petidoglycan hydrolase, putative	SAOUHSC_01515	ytA	Cellular processes	Toxin production and resistance	S	0	Unknown		1			2	2
phage infection protein, putative	SAOUHSC_02978		Mobile and extrachromosomal element functions	Prophage functions		6	Cytoplasmic Membrane	9	3	6	6	1	1

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
phage minor structural protein, N-terminal region domain protein	SAOUHSC_02180		Mobile and extrachromosomal element functions	Prophage functions		0	Cytoplasmic				2		
Phenylalanyl-tRNA synthetase alpha chain	SAOUHSC_01092	pheS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	3	1	3	4	3	4
phenylalanyl-tRNA synthetase, beta subunit	SAOUHSC_01093	pheT	Protein synthesis	tRNA aminoacylation		1	Cytoplasmic	10	6	12	5	8	6
phi PVL ORF 30-like protein	SAOUHSC_01580		Hypothetical proteins	Conserved	S	3	Cytoplasmic Membrane	2	1		1	2	1
phosphate acetyltransferase	SAOUHSC_00574	pta	Central intermediary metabolism	Other		0	Cytoplasmic	8	8	9	7	9	9
Phosphate acyltransferase	SAOUHSC_01197	plsX	Fatty acid and phospholipid metabolism	Biosynthesis		1	Cytoplasmic	3	2	4	3	2	1
Phosphate-binding protein pstS	SAOUHSC_01389	pstS	Unclassified	Role category not yet assigned	S	0	Cytoplasmic Membrane				5	5	3
phosphocarrier protein hpr, putative	SAOUHSC_01028	ptsH	Transport and binding proteins	Carbohydrates, organic alcohols, and acids		0	Cytoplasmic	1	1	1	1	2	2
Phosphoenolpyruvate carboxykinase [ATP]	SAOUHSC_01910	pckA	Energy metabolism	Glycolysis/ gluconeogenesis		1	Cytoplasmic				5	4	3
phosphoenolpyruvate-protein phosphotransferase	SAOUHSC_01029	ptsI	Transport and binding proteins	Carbohydrates, organic alcohols, and acids		1	Cytoplasmic	15	7	15	12	16	12
Phosphoglucosamine mutase	SAOUHSC_02405	glmM(femD),glmM	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		1	Cytoplasmic	6	4	6	6	9	5
Phosphoglycerate kinase	SAOUHSC_00796	pgk	Energy metabolism	Glycolysis/ gluconeogenesis		1	Cytoplasmic	11	4	16	10	12	12
phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	SAOUHSC_00798	pgm,gpml	Energy metabolism	Glycolysis/ gluconeogenesis		0	Cytoplasmic	6	2	9	5	10	7
phosphomethylpyrimidine kinase	SAOUHSC_00562	thiD	Biosynthesis of cofactors, prosthetic groups, and carriers	Thiamine		0	Unknown	5	1	4	5	5	6
phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	SAOUHSC_01178	coaBC	Biosynthesis of cofactors, prosthetic groups, and carriers	Pantothenate and coenzyme A		1	Cytoplasmic	1	1	1	3	1	2
Phosphopentomutase	SAOUHSC_00101	drm,deoB	Purines, pyrimidines, nucleosides, and nucleotides	Other		0	Cytoplasmic	8	4	11	6	7	11
phosphoribosylamine-glycine ligase	SAOUHSC_01018	purD	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		1	Cytoplasmic	5	3	5	5	5	6



description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
phosphoribosylaminoimidazole carboxylase, ATPase subunit	SAOUHSC_01009	purK	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		2	Cytoplasmic Membrane	2		4	3	1	1
phosphoribosylaminoimidazole carboxylase, catalytic subunit	SAOUHSC_01008	purE	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		2	Cytoplasmic Membrane	1	1	3		1	2
Phosphoribosylaminoimidazole-succinocarboxamide synthase	SAOUHSC_01010	purC	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	7	1	8	4	3	5
Phosphoribosylformylglycinamide cyclo-ligase	SAOUHSC_01015	purM	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	1		2	1	2	2
Phosphoribosylformylglycinamide synthase 1	SAOUHSC_01012	purQ	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	3	1	5	4	2	6
Phosphoribosylformylglycinamide synthase 2	SAOUHSC_01013	purL	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	11	7	10	9	9	9
phosphoribosylformylglycinamide synthase, PurS protein	SAOUHSC_01011	purS	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	3	2	3	1	3	3
phosphotransferase system enzyme IIA, putative	SAOUHSC_01430	crr	Regulatory functions	Protein interactions		0	Cytoplasmic	5	5	5	5	5	5
polypeptide deformylase	SAOUHSC_01038	def	Protein fate	Protein modification and repair		0	Cytoplasmic	5	2	4	4	5	4
Polyribonucleotide nucleotidyltransferase	SAOUHSC_01251	pnpA	Transcription	Degradation of RNA		1	Cytoplasmic	15	5	15	13	21	15
Preprotein translocase subunit secY	SAOUHSC_02491	secY	Protein fate	Protein and peptide secretion and trafficking		10	Cytoplasmic Membrane			1	1	1	2
preprotein translocase, YajC subunit	SAOUHSC_01747	yajC	Protein fate	Protein and peptide secretion and trafficking		1	Cytoplasmic Membrane	1	1	2	2	1	1
primosomal protein N	SAOUHSC_01179	priA	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	1		1		2	1
Probable acetyl-CoA acyltransferase	SAOUHSC_00336	thl	Fatty acid and phospholipid metabolism	Other		0	Cytoplasmic	6	5	8	5	8	9
Probable ATP-dependent helicase dinG homolog	SAOUHSC_01472	dinG	DNA metabolism	DNA replication, recombination, and repair		1	Cytoplasmic	1		1		4	1
probable cytosol aminopeptidase	SAOUHSC_00879	pepA,ampA	Protein fate	Degradation of proteins, peptides, and glycopeptides		1	Cytoplasmic	5	3	7		4	6

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
Probable DEAD-box ATP-dependent RNA helicase SAOUHSC_02316	SAOUHSC_02316		DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic	11	9	12	12	14	14
Probable DNA-directed RNA polymerase subunit delta	SAOUHSC_02369	rpoE	Transcription	DNA-dependent RNA polymerase		0	Cytoplasmic	5	4	6	6	6	7
Probable glycine dehydrogenase [decarboxylating] subunit 1	SAOUHSC_01633		Energy metabolism	Amino acids and amines		0	Cytoplasmic	4	1	4	2	6	3
Probable glycine dehydrogenase [decarboxylating] subunit 2	SAOUHSC_01632		Energy metabolism	Amino acids and amines		0	Cytoplasmic	5	1	7	1	5	4
Probable manganese-dependent inorganic pyrophosphatase	SAOUHSC_02140	ppaC	Central intermediary metabolism	Phosphorus compounds		1	Cytoplasmic	5	2	6	6	7	7
Probable quinol oxidase subunit 1	SAOUHSC_01001	qoxB	Energy metabolism	Electron transport		15	Cytoplasmic Membrane	1		3	2	3	2
Probable quinol oxidase subunit 2	SAOUHSC_01002	qoxA	Energy metabolism	Electron transport	S	2	Cytoplasmic Membrane	5	2	5	6	4	6
Probable transglycosylase isaA	SAOUHSC_02887	isaA	Hypothetical proteins	Conserved	S	0	Extracellular	4	1	3	2	2	1
Probable uridylyltransferase SAOUHSC_02423	SAOUHSC_02423		Cell envelope	Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides		2	Cytoplasmic	7	4	5	4	5	6
proline dipeptidase, putative	SAOUHSC_01626		Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Cytoplasmic	3	1	5	5	6	4
Prolyl-tRNA synthetase	SAOUHSC_01240	proS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	16	9	15	10	19	21
Protein fmtA	SAOUHSC_00998	fmtA,fmt	Cellular processes	Toxin production and resistance		1	Cytoplasmic Membrane			1	2	2	2
Protein grpE	SAOUHSC_01684	grpE	Protein fate	Protein folding and stabilization		0	Cytoplasmic	7	7	7	6	7	6
Protein nagD homolog	SAOUHSC_00865		Unknown function	Enzymes of unknown specificity		0	Unknown	4	2	6	2	5	6
Protein translocase subunit secA 1	SAOUHSC_00769	secA	Protein fate	Protein and peptide secretion and trafficking		0	Cytoplasmic	10	5	10	12	9	11
protein-export membrane protein SecDF	SAOUHSC_01746	secF	Cell envelope	Other		9	Cytoplasmic Membrane	8	4	5	4	3	5
PTS system glucoside-specific EIICBA component	SAOUHSC_02848	glcB	Transport and binding proteins	Carbohydrates, organic alcohols, and acids		8	Cytoplasmic Membrane	2		1	2	3	2
PTS system, glucose-specific component	SAOUHSC_00155	ptsG,glcA	Transport and binding proteins	Carbohydrates, organic alcohols, and acids		10	Cytoplasmic Membrane	4	2	6	4	6	7

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
pur operon repressor	SAOUHSC_00467	purR	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	1		2	2	1	1
purine nucleoside phosphorylase	SAOUHSC_00097	deoD,deoD1,pnp	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides		0	Cytoplasmic	5	3	7	2	5	6
Putative 2-hydroxyacid dehydrogenase SAOUHSC_02577	SAOUHSC_02577		Central intermediary metabolism	Other		2	Cytoplasmic	3		3	10	13	8
Putative aldehyde dehydrogenase SAOUHSC_02363	SAOUHSC_02363		Energy metabolism	Fermentation		0	Cytoplasmic	2	1	4	1	2	4
Putative dipeptidase SAOUHSC_01868	SAOUHSC_01868		Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Cytoplasmic	7	6	10	8	11	11
Putative peptidyl-prolyl cis-trans isomerase	SAOUHSC_00891		Central intermediary metabolism	Other		0	Cytoplasmic	2	3	4	3	5	3
Putative phosphotransferase SAOUHSC_01664	SAOUHSC_01664		Regulatory functions	Other		0	Cytoplasmic	1	1	2		3	1
Putative septation protein spoVG	SAOUHSC_00469	spoVG	Unknown function	General		0	Cytoplasmic	5	2	3	5	4	5
Putative thiaminase-2	SAOUHSC_02331		Biosynthesis of cofactors, prosthetic groups, and carriers	Thiamine		0	Cytoplasmic				1	2	
Putative universal stress protein SAOUHSC_01819	SAOUHSC_01819		Unknown function	General		0	Cytoplasmic	1	1	3	5	4	7
Pyrimidine-nucleoside phosphorylase	SAOUHSC_02377	pyn,pdp	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides		1	Unknown		1	4	1	6	1
pyrroline-5-carboxylate reductase	SAOUHSC_01597	proC	Amino acid biosynthesis	Glutamate family		0	Cytoplasmic		1	1	4	2	1
pyruvate carboxylase	SAOUHSC_01064	pycA,pyc	Energy metabolism	Glycolysis/ gluconeogenesis		1	Cytoplasmic	16	10	10	18	16	23
pyruvate dehydrogenase complex, E1 component, alpha subunit, putative	SAOUHSC_01040	pdhA	Energy metabolism	Pyruvate dehydrogenase		0	Cytoplasmic	9	6	16	10	12	14
pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	SAOUHSC_01041	phdB,pdhB	Unclassified	Role category not yet assigned		1	Cytoplasmic	12	11	13	12	14	15
Pyruvate kinase	SAOUHSC_01806	pykA,pyk	Energy metabolism	Glycolysis/ gluconeogenesis		1	Cytoplasmic	22	13	31	19	22	23
pyruvate oxidase, putative	SAOUHSC_02849	cidC	Energy metabolism	Other		1	Cytoplasmic Membrane	3	2	1	2	1	3
recombination protein RecA, putative	SAOUHSC_01262	recA	DNA metabolism	DNA replication, recombination, and repair		1	Cytoplasmic	4	2	3	4	3	3
Redox-sensing transcriptional repressor rex	SAOUHSC_02273	rex	Regulatory functions	Other		1	Cytoplasmic	2	1	3	4	7	4

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
Regulatory protein msrR	SAOUHSC_01361	msrR	Regulatory functions	Other		1	Cytoplasmic Membrane	2	2	1	2		1
replicative DNA helicase	SAOUHSC_00018	dnaC,dnaB	DNA metabolism	DNA replication, recombination, and repair		0	Cytoplasmic				1		2
riboflavin biosynthesis protein RibF	SAOUHSC_01249	ribF,ribC	Biosynthesis of cofactors, prosthetic groups, and carriers	Riboflavin, FMN, and FAD		0	Cytoplasmic	6	1	4	6	8	1
Ribonuclease J 1	SAOUHSC_01035		Unknown function	Enzymes of unknown specificity		1	Cytoplasmic	10	5	12	14	12	11
ribonuclease R, putative	SAOUHSC_00803	rnr	Transcription	Degradation of RNA		0	Cytoplasmic	1	1	1		1	2
ribonucleotide-diphosphate reductase alpha chain, putative	SAOUHSC_00742	rir1,nrdE	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism		1	Cytoplasmic	22	14	24	9	12	10
ribonucleotide-diphosphate reductase beta chain, putative	SAOUHSC_00743	rir2,nrdF	Purines, pyrimidines, nucleosides, and nucleotides	2'-Deoxyribonucleotide metabolism		1	Cytoplasmic	12	9	13	7	9	6
ribose-phosphate pyrophosphokinase, putative	SAOUHSC_00472	prs	Purines, pyrimidines, nucleosides, and nucleotides	Purine ribonucleotide biosynthesis		0	Cytoplasmic	3	2	7	3	4	5
ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5	SAOUHSC_00474	rplY	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	5	5	4	4	4	4
ribosomal large subunit pseudouridine synthase B, putative	SAOUHSC_01587	rluB	Protein synthesis	tRNA and rRNA base modification		0	Cytoplasmic	1	4	4	2	3	3
ribosomal large subunit pseudouridine synthase, RluD subfamily, putative	SAOUHSC_01982		Protein synthesis	tRNA and rRNA base modification		0	Cytoplasmic	1	1	2	1	3	2
ribosomal protein S2	SAOUHSC_01232	rpsB	Protein synthesis	Ribosomal proteins: synthesis and modification		0	Cytoplasmic	8	6	11	11	11	11
Ribosome-binding factor A	SAOUHSC_01247	rbfA	Transcription	RNA processing		0	Cytoplasmic		1	1	3	1	3
Ribosome-recycling factor	SAOUHSC_01236	rrf,frf	Protein synthesis	Translation factors		0	Cytoplasmic	10	2	6	4	5	9
RNA polymerase beta chain, putative	SAOUHSC_00524	rpoB	Transcription	DNA-dependent RNA polymerase		1	Cytoplasmic	24	13	30	18	25	26
RNA polymerase sigma factor rpoD	SAOUHSC_01662	sigA,rpoD	Transcription	Transcription factors		0	Cytoplasmic	8	4	6	7	7	6
S1 RNA binding domain protein	SAOUHSC_00483		Transport and binding proteins	Unknown substrate		0	Cytoplasmic	3		3	1	1	3
S1 RNA binding domain protein	SAOUHSC_02297		Transport and binding proteins	Unknown substrate		1	Cytoplasmic	6	4	9	5	6	5
S-adenosylmethionine synthase	SAOUHSC_01909	metK	Central intermediary metabolism	Other		0	Cytoplasmic	8	8	10	7	9	8
S-adenosylmethionine:tRNA ribosyltransferase-isomerase	SAOUHSC_01749	queA	Protein synthesis	tRNA and rRNA base modification		0	Cytoplasmic				2	1	1

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
S-adenosyl-methyltransferase MraW	SAOUHSC_01143	mraW	Unknown function	Enzymes of unknown specificity		0	Cytoplasmic	1			1	2	3
secretory antigen precursor, putative	SAOUHSC_02571	ssaA	Cell envelope	Other	S	0	Extracellular	3	2	3	3	3	2
Septation ring formation regulator ezrA	SAOUHSC_01827	ezrA	Cellular processes	Cell division		1	Cytoplasmic	9	4	5	2	6	6
Serine hydroxymethyltransferase	SAOUHSC_02354	glyA	Amino acid biosynthesis	Serine family		1	Cytoplasmic	5	2	10	10	9	9
serine protease HtrA, putative	SAOUHSC_00958	htrA	Protein fate	Degradation of proteins, peptides, and glycopeptides		1	Cellwall	4	3	2			2
Seryl-tRNA synthetase	SAOUHSC_00009	serS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	7	4	9	7	6	8
Signal peptidase IB, putative	SAOUHSC_00903	spsB	Protein fate	Protein and peptide secretion and trafficking		0	Cellwall	7	2	6	5	5	3
signal recognition particle protein	SAOUHSC_01207	ffh	Protein fate	Protein and peptide secretion and trafficking		0	Cytoplasmic Membrane	4	2	9	4	8	6
Signal transduction protein TRAP	SAOUHSC_01964	TRAP	Regulatory functions	Other		0	Cytoplasmic	5	2	8	8	7	9
S-ribosylhomocysteine lyase	SAOUHSC_02375	luxS	Cellular processes	Other		0	Cytoplasmic	2	1	2	2	2	2
succinate dehydrogenase, flavoprotein chain TC0881, putative	SAOUHSC_01104	sdhA	Energy metabolism	TCA cycle		2	Cytoplasmic			1	3		2
Succinyl-CoA ligase [ADP-forming] subunit beta	SAOUHSC_01216	sucC	Energy metabolism	TCA cycle		1	Cytoplasmic	10	3	10	9	11	12
succinyl-CoA synthetase, alpha subunit, putative	SAOUHSC_01218	sucD	Energy metabolism	TCA cycle		0	Cytoplasmic	4	2	5	6	7	6
sucrose-6-phosphate dehydrogenase, putative	SAOUHSC_02268	scrB	Energy metabolism	Biosynthesis and degradation of polysaccharides		0	Cytoplasmic	1		1	2	1	2
sun protein	SAOUHSC_01184	sun	Protein synthesis	tRNA and rRNA base modification		0	Cytoplasmic	2	1	2	2	1	2
Superoxide dismutase [Mn/Fe] 2	SAOUHSC_00093	sodM	Cellular processes	Detoxification		0	Extracellular	3	1	3	2	3	3
Superoxide dismutase [Mn] 1	SAOUHSC_01653	sodA	Cellular processes	Detoxification		0	Extracellular	1	1	3	3	3	5
tagB protein, putative	SAOUHSC_00222		Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		0	Cytoplasmic Membrane			2	2	3	1
teichoic acid biosynthesis protein F, putative	SAOUHSC_00223		Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		0	Cytoplasmic Membrane	1	1	2	2	3	1
TelA-like protein SAOUHSC_01408	SAOUHSC_01408		Unclassified	Role category not yet assigned		0	Unknown	1		1		2	2
Thioredoxin	SAOUHSC_01100	trxA,trx	Energy metabolism	Electron transport		0	Cytoplasmic	5	2	4	5	4	4

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
thioredoxin reductase	SAOUHSC_00785	trxB	Energy metabolism	Electron transport		1	Cytoplasmic	2	2	3	4	6	5
thioredoxin, putative	SAOUHSC_00834		Energy metabolism	Electron transport		0	Cytoplasmic	2	3	2	2	2	2
threonine synthase	SAOUHSC_01321	thrC	Amino acid biosynthesis	Aspartate family		0	Cytoplasmic				4	2	
Threonyl-tRNA synthetase	SAOUHSC_01788	thrS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	7	3	12	9	12	9
Thymidylate kinase	SAOUHSC_00451	tmk	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions		0	Cytoplasmic				1	1	2
Transcription antitermination protein nusG	SAOUHSC_00517	nusG	Transcription	Transcription factors		0	Cytoplasmic	5	4	8	6	5	6
Transcription elongation factor greA	SAOUHSC_01714	greA	Transcription	Transcription factors		0	Cytoplasmic	7	6	7	6	6	7
transcription termination factor Rho	SAOUHSC_02362	rho	Transcription	Transcription factors		0	Cytoplasmic	3	2	4	8	9	8
transcription termination-antitermination factor, putative	SAOUHSC_01243	nusA	Transcription	Transcription factors		0	Cytoplasmic	5	5	6	5	7	8
Transcriptional regulator sarA	SAOUHSC_00620	sarA	Regulatory functions	Other		0	Cytoplasmic	3	2	3	6	7	5
transcriptional regulator, Fur, putative	SAOUHSC_01592	fur	Regulatory functions	Other		0	Cytoplasmic	2			3	2	2
transcriptional regulator, putative	SAOUHSC_02583		Cell envelope	Other	S	0	Cytoplasmic Membrane	6		2	3	8	4
transcriptional regulator, Sir2 family, putative	SAOUHSC_02457		Central intermediary metabolism	Other		0	Cytoplasmic						2
Transcriptional regulatory protein srrA	SAOUHSC_01586	srrA	Regulatory functions	DNA interactions		0	Cytoplasmic	2	1	2	2	3	2
Transcriptional regulatory protein walR	SAOUHSC_00020	ycyF,vicR	Regulatory functions	DNA interactions		0	Cytoplasmic	3	1		4	5	2
transketolase	SAOUHSC_01337	tkt	Energy metabolism	Pentose phosphate pathway		1	Unknown	28	17	31	23	22	27
Translation initiation factor IF-1	SAOUHSC_02489	infA	Protein synthesis	Translation factors		0	Cytoplasmic	2	2	4	1	1	3
Translation initiation factor IF-2	SAOUHSC_01246	infB	Protein synthesis	Translation factors		1	Cytoplasmic	15	9	13	16	11	16
Translation initiation factor IF-3	SAOUHSC_01786	infC	Protein synthesis	Translation factors		0	Cytoplasmic	4	3	5	4	5	3
Trigger factor	SAOUHSC_01779	tig	Protein fate	Protein folding and stabilization		0	Cytoplasmic	15	16	21	16	17	16
Triosephosphate isomerase	SAOUHSC_00797	tpiA,tpi	Energy metabolism	Glycolysis/ gluconeogenesis		0	Cytoplasmic	11	10	13	7	9	7
tRNA methyl transferase, putative	SAOUHSC_01725	trmU	Protein synthesis	tRNA and rRNA base modification		0	Cytoplasmic	2		2			2
tRNA modification GTPase mnmE	SAOUHSC_03053	trmE,thdF	Protein synthesis	tRNA and rRNA base modification		0	Cytoplasmic		2	1	1	2	1
truncated MHC class II analog protein	SAOUHSC_02466		Unknown function	General	S	0	Cytoplasmic Membrane				2	1	3
tryptophanyl-tRNA synthetase	SAOUHSC_00933	trpS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	3	1	4		2	3

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
type I restriction-modification system, M subunit	SAOUHSC_01933		DNA metabolism	Restriction/modification		1	Cytoplasmic	1	1		1	2	
type I restriction-modification system, M subunit	SAOUHSC_00397	hsdM	DNA metabolism	Restriction/modification		1	Cytoplasmic			1			3
type I site-specific deoxyribonuclease, HsdR family, putative	SAOUHSC_00162	hsdR	DNA metabolism	Restriction/modification		1	Cytoplasmic			1	1	1	2
Tyrosyl-tRNA synthetase	SAOUHSC_01839	tyrS	Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	9	5	6	5	7	6
UDP-N-acetylenolpyruvoylglucosamine reductase	SAOUHSC_00752	murB	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		2	Cytoplasmic	5	2	4	2	2	1
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	SAOUHSC_02337	murA1,murA	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		3	Cytoplasmic	4	3	6	3	4	7
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	SAOUHSC_02365	murZ,murA2	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		3	Cytoplasmic	1		1	4	5	5
UDP-N-acetylmuramate--L-alanine ligase	SAOUHSC_01856	murC	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		2	Cytoplasmic	1	1	2	3	2	3
UDP-N-acetylmuramoylalanine--D-glutamate ligase	SAOUHSC_01147	murD	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		1	Cytoplasmic	5	2	4	3	4	7
UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase	SAOUHSC_02317	murF	Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		0	Cytoplasmic	3		2	1		3
UDP-N-acetylmuramyl tripeptide synthetase, putative	SAOUHSC_02107		Cell envelope	Biosynthesis and degradation of murein sacculus and peptidoglycan		0	Cytoplasmic		2	1	3	4	1
Uncharacterized epimerase/dehydratase SAOUHSC_00535	SAOUHSC_00535		Unknown function	Enzymes of unknown specificity		0	Unknown		1		4	3	3
Uncharacterized hydrolase SAOUHSC_01399	SAOUHSC_01399		Central intermediary metabolism	Other		0	Cytoplasmic				3	5	5
Uncharacterized leukocidin-like protein 1	SAOUHSC_02241		Transport and binding proteins	Carbohydrates, organic alcohols, and acids	S	0	Extracellular	6		4	3	2	1

description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
Uncharacterized leukocidin-like protein 2	SAOUHSC_02243		Cellular processes	Toxin production and resistance	S	0	Extracellular	9	1	3	4	2	1
Uncharacterized lipoprotein SAOUHSC_02650	SAOUHSC_02650		Unclassified	Role category not yet assigned	S	0	Unknown	2	2	1	2	1	
Uncharacterized peptidase SAOUHSC_01816	SAOUHSC_01816		Protein fate	Degradation of proteins, peptides, and glycopeptides		1	Cytoplasmic	1	2	2	2	3	3
Uncharacterized protein SAOUHSC_00767	SAOUHSC_00767	yfiA	Transcription	Transcription factors		0	Cytoplasmic	3	2	2	6	6	7
Uncharacterized protein SAOUHSC_00906	SAOUHSC_00906		Unknown function	Enzymes of unknown specificity		0	Cytoplasmic	10	8	11	10	11	10
Uncharacterized protein SAOUHSC_00997	SAOUHSC_00997		Regulatory functions	Other	S	0	Cytoplasmic Membrane	2		1	1	2	1
Uncharacterized protein SAOUHSC_01193	SAOUHSC_01193		Unknown function	Enzymes of unknown specificity		0	Unknown	5	3	9	7	7	8
Uncharacterized protein SAOUHSC_01349	SAOUHSC_01349		Cell envelope	Other		0	Cytoplasmic	1	1		2	1	1
Uncharacterized protein SAOUHSC_01413	SAOUHSC_01413		Unknown function	General		0	Cytoplasmic			2	2	2	1
Uncharacterized protein SAOUHSC_02143	SAOUHSC_02143		Energy metabolism	Pentose phosphate pathway		0	Cytoplasmic	4	2	6	3	3	6
UPF0051 protein SAOUHSC_00851	SAOUHSC_00851	sufB	Biosynthesis of cofactors, prosthetic groups, and carriers	Other		0	Cytoplasmic	7	2	11	8	10	9
UPF0082 protein SAOUHSC_00675	SAOUHSC_00675		Hypothetical proteins	Conserved		0	Cytoplasmic	5	5	5	3	5	6
UPF0133 protein SAOUHSC_00444	SAOUHSC_00444		Hypothetical proteins	Conserved		0	Unknown	1		4	2	1	2
UPF0297 protein SAOUHSC_01721	SAOUHSC_01721		Unclassified	Role category not yet assigned		0	Unknown	1	1	2	2	2	4
UPF0337 protein SAOUHSC_00845	SAOUHSC_00845		Hypothetical proteins	Conserved		0	Unknown	4		5	3	2	4
UPF0342 protein SAOUHSC_01977	SAOUHSC_01977		Unclassified	Role category not yet assigned		0	Cytoplasmic	8	7	13	8	9	10
UPF0356 protein SAOUHSC_01036	SAOUHSC_01036		Hypothetical proteins	Domain		0	Cytoplasmic	2	1	3	2	1	3
UPF0365 protein SAOUHSC_01676	SAOUHSC_01676		Protein fate	Degradation of proteins, peptides, and glycopeptides	S	0	Cytoplasmic	13	11	14	14	16	13
UPF0403 protein SAOUHSC_01436	SAOUHSC_01436		Unclassified	Role category not yet assigned	S	0	Cytoplasmic	1		2	1	3	2
UPF0403 protein SAOUHSC_01610	SAOUHSC_01610		Unclassified	Role category not yet assigned	S	0	Cytoplasmic	1		1	1	1	2
UPF0447 protein SAOUHSC_00573	SAOUHSC_00573		Cellular processes	Detoxification		0	Unknown	3	3	3	3	7	6
UPF0457 protein SAOUHSC_02425	SAOUHSC_02425		Hypothetical proteins	Conserved		0	Unknown	1		1	2	3	3
UPF0473 protein SAOUHSC_01719	SAOUHSC_01719		Unknown function	General		0	Cytoplasmic	1		1	1	2	2
UPF0477 protein SAOUHSC_00951	SAOUHSC_00951		Protein synthesis	tRNA aminoacylation		0	Cytoplasmic	2	1	3	7	6	6



description	locus tag	gene	CMR main role	CMR subrole	signal peptide	TMDs	PSORTdb localization	# peptides control exp. 1	# peptides control exp. 2	# peptides control exp. 3	# peptides exp. 1	# peptides exp. 2	# peptides exp. 3
UPF0478 protein SAOUHSC_01855	SAOUHSC_01855		Unclassified	Role category not yet assigned	S	0	Cytoplasmic	7	4	5	6	8	8
UPF0637 protein SAOUHSC_01054	SAOUHSC_01054		Protein fate	Degradation of proteins, peptides, and glycopeptides		0	Cytoplasmic	4		3	3	5	3
Uracil phosphoribosyltransferase	SAOUHSC_02353	upp	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides		1	Cytoplasmic	5	4	9	5	6	7
Uridine kinase	SAOUHSC_01715	udk	Purines, pyrimidines, nucleosides, and nucleotides	Salvage of nucleosides and nucleotides	S	0	Cytoplasmic	3	2	2		3	1
Uridylate kinase	SAOUHSC_01235	smbA,pyrH	Purines, pyrimidines, nucleosides, and nucleotides	Nucleotide and nucleoside interconversions		0	Cytoplasmic	2	3	6	4	4	5
Uroporphyrinogen decarboxylase	SAOUHSC_01962	hemE	Biosynthesis of cofactors, prosthetic groups, and carriers	Heme, porphyrin, and cobalamin		0	Cytoplasmic	1			2		1
Valyl-tRNA synthetase	SAOUHSC_01767	valS	Protein synthesis	tRNA aminoacylation		2	Cytoplasmic	14	8	26	12	15	18