

Table A-7: Prioritised rank (*amss* scoring function) on SA-2603 genes

The rank position, rank fraction (in *pct*), cluster of orthologous groups (COG), and loci of the prioritised rank by *amss* scoring function in the SA-2603 genome.

Rank	<i>pct</i>	Score	COG	Valid. Set	Gene	Locus	Function
1	0.05	0.97	M	M	<i>pbp2A</i>	SAG2066	penicillin-binding protein 2A
2	0.09	0.97	O		<i>groES</i>	SAG2075	co-chaperonin GroES
3	0.14	0.96			<i>aroC</i>	SAG1377	chorismate synthase
3	0.14	0.96	M	B,M	<i>alr</i>	SAG1684	alanine racemase
5	0.24	0.96	M	B,M	<i>ddl</i>	SAG0767	D-alanylalanine synthetase
6	0.28	0.96	M	M	<i>pbp1A</i>	SAG0298	penicillin-binding protein 1A
7	0.33	0.96	M	M		SAG0159	penicillin-binding protein 1B, putative
7	0.33	0.96	E		<i>aroB</i>	SAG1378	3-dehydroquinate synthase
9	0.42	0.96	M	C,B,M	<i>murD</i>	SAG0475	UDP- <i>N</i> -acetylmuramoyl-L-alanyl-D-glutamate synthetase
9	0.42	0.96			<i>ftsW</i>	SAG0761	cell division protein, FtsW/RodA/SpoVE family
9	0.42	0.96	M	C,B,M	<i>murF</i>	SAG0768	UDP- <i>N</i> -acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanyl ligase
9	0.42	0.96	M	C,B,M	<i>murA-1</i>	SAG0843	UDP- <i>N</i> -acetylglucosamine 1-carboxyvinyltransferase
9	0.42	0.96	M	C,B,M	<i>murA-2</i>	SAG0866	UDP- <i>N</i> -acetylglucosamine 1-carboxyvinyltransferase
14	0.66	0.96	M		<i>pbpX</i>	SAG0287	penicillin-binding protein 2X
14	0.66	0.96	M	B,M	<i>mraY</i>	SAG0288	phospho- <i>N</i> -acetylmuramoyl-pentapeptide-transferase
14	0.66	0.96	M	C,B,M	<i>murC</i>	SAG1615	UDP- <i>N</i> -acetylmuramate-L-alanine ligase
17	0.8	0.95	M			SAG0140	glycosyl transferase, group 4 family protein
18	0.85	0.95	E		<i>aroE</i>	SAG1680	shikimate 5-dehydrogenase
19	0.89	0.95	TK			SAG0322	DNA-binding response regulator
20	0.94	0.95	E		<i>cysK</i>	SAG0334	cysteine synthase A
21	0.99	0.95	M	B,M	<i>murE</i>	SAG1391	UDP- <i>N</i> -acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase
22	1.04	0.95	T			SAG1507	phoH family protein

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Rank	<i>pct</i>	Score	COG	Valid. Set	Gene	Locus	Function
23	1.08	0.94	M	B,M	<i>glmU</i>	SAG1538	UDP- <i>N</i> -acetylglucosamine pyrophosphorylase
24	1.13	0.94	R			SAG0480	ylmE protein, putative
25	1.18	0.94	O		<i>radA</i>	SAG0110	DNA repair protein RadA
26	1.22	0.94	Q		<i>dltA</i>	SAG1790	D-alanine-D-alanyl carrier protein ligase
27	1.27	0.94			<i>rodA</i>	SAG0621	rod shape-determining protein RodA, putative
28	1.32	0.94	EH			SAG1528	chorismate binding enzyme
29	1.37	0.94	O		<i>clpX</i>	SAG1312	ATP-dependent protease ATP-binding subunit
29	1.37	0.94	OU		<i>clpP</i>	SAG1585	ATP-dependent Clp protease proteolytic subunit
31	1.46	0.94	J		<i>rpsA</i>	SAG1150	30S ribosomal protein S1
32	1.51	0.94	H			SAG0498	geranyltranstransferase, putative
32	1.51	0.94	H			SAG1738	polyprenyl synthetase family protein
34	1.6	0.94	E			SAG0339	aspartate kinase
35	1.65	0.94	O			SAG1530	peptidyl-prolyl cis-trans isomerase, cyclophilin-type
36	1.69	0.94	I		<i>accC</i>	SAG0352	acetyl-CoA carboxylase
37	1.74	0.93	M	B,M	<i>murI</i>	SAG1600	glutamate racemase
38	1.79	0.93	L		<i>nth</i>	SAG0468	endonuclease III
							⋮
Remaining peptidoglycan genes							
43	2.02	0.93	I	B,M	<i>uppS</i>	SAG1916	undecaprenyl diphosphate synthase
56	2.64	0.92	M	B,M	<i>glmS</i>	SAG0944	D-fructose-6-phosphate amidotransferase
62	2.92	0.92		B,M	<i>uppP</i>	SAG0138	undecaprenyl pyrophosphate phosphatase
73	3.44	0.92	M	C,B,M	<i>murG</i>	SAG0476	<i>N</i> -acetylglucosaminyl transferase
90	4.24	0.91	M	M		SAG0765	penicillin-binding protein 2b
108	5.08	0.90		B,M	<i>glnA</i>	SAG1763	glutamine synthetase, type I
159	7.49	0.86	M	C,B,M	<i>murB</i>	SAG1112	UDP- <i>N</i> -acetylenolpyruvoylglucosamine reductase
264	12.43	0.81	G	B,M		SAG0887	phosphoglucomutase/phosphomannomutase family protein
276	12.99	0.81	M	M		SAG0146	penicillin-binding protein 4, putative
566	26.65	0.66	NU	M		SAG0094	<i>N</i> -acetylmuramoyl-L-alanine amidase, family 4 protein

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