

SOM Table 8. Genes with homologues involved in peptidoglycan biosynthesis and cell division

cell division/cell wall proteins	enzyme	orf	hit start ³	e-value
	D-alanine-D-alanine ligase (ddlA)	kuste2386	Escherichia coli (b0092:306/334 3-320 (40%))	Geobacter_sulfurreducens (gsu:GSU3066:316/334 1-323 (42%))
	alanine racemase 1, PLP-binding, biosynthetic	kuste2410	Escherichia coli (b4053:359/374 9-371 (33%))	Thermoanaerobacter_tengcongensis (tte:TTE2168:388/374 3-370 (42%))
	L-glutamine:D-fructose-6-phosphate aminotransferase (glmS)	kustd1383	Thermus thermophilus (U17352:604/608 1-608 (49%))	Chlorobium_tepidum_TLS (cte:CT0130:614/608 1-608 (57%))
	bifunctional multimodular glmU: N-acetyl glucosamine-1-phosphate uridylyltransferase (glmU)	kusta0024	Escherichia coli (b3730:456/323 4-311 (32%))	Clostridium_perfringens (cpe:CPE2490:454/323 6-315 (40%))
	L-glutamine:D-fructose-6-phosphate aminotransferase (glmS)	kuste3187	Thermus thermophilus (U17352:604/608 1-608 (49%))	Chlorobium_tepidum_TLS (cte:CT0130:614/608 1-608 (57%))
	phosphoglucosamine mutase (mrsA,glmM)	kustc0508	Escherichia coli (b0688:546/541 34-541 (27%))	Desulfotalea_psychrophila_LV54 (dps:DP2231:581/541 30-535 (42%))
	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	kuste3313	Escherichia coli (b3189:419/431 8-429 (43%))	Geobacter_sulfurreducens (gsu:GSU3102:417/431 8-431 (53%))
	UDP-N-acetyl(enol)pyruvoylglucosamine reductase (FAD-binding)	kuste3330	Escherichia coli (b3972:342/300 11-298 (24%))	Thermoanaerobacter_tengcongensis (tte:TTE1836:302/300 2-299 (39%))
	L-alanine adding enzyme, UDP-N-acetyl-muramate:alanine ligase (murC)	kustc0684	Escherichia coli (b0091:491/471 15-448 (31%))	Geobacter_sulfurreducens (gsu:GSU3068:462/471 17-448 (35%))
	UDP-N-acetylmuramoylalanine-D-glutamate ligase	kuste3480	Escherichia coli (b0088:438/476 80-476 (27%))	Clostridium_tetani_E88 (ctc:CTC00213:464/476 9-476 (39%))
	glutamate racemase	kustd1506	Bacillus subtilis (Z75208:272/266 3-198 (31%))	Clostridium_tetani_E88 (ctc:CTC00259:266/266 1-259 (31%))
	cell division protein mraZ	kuste2373	Escherichia coli (b0081:152/146 1-126 (33%))	Staphylococcus_saprophyticus (ssp:SSP1593:143/146 1-144 (50%))
	S-adenosyl-dependent methyl transferase mraW	kuste2374	Escherichia coli (b0082:313/299 6-298 (38%))	Aquifex_aeolicus (aae:aq_1875:294/299 8-299 (47%))
	division specific transpeptidase, penicillin-binding protein 3	kuste2376	Bacillus subtilis (Z25865:645/571 19-565 (33%))	Geobacter_sulfurreducens (gsu:GSU3075:657/571 14-563 (41%))
	UDP-N-acetylmuramoylalanine-D-glutamate 2,6-diaminopimelate ligase (murE)	kuste2378	Escherichia coli (b0085:495/489 26-481 (36%))	Thermoanaerobacter_tengcongensis (tte:TTE1649:492/489 23-482 (45%))
	D-alanine:D-alanine-adding enzyme	kuste2379	Escherichia coli (b0086:452/484 3-474 (30%))	Desulfotalea_psychrophila_LV54 (dps:DP2901:1014/484 9-318 (25%))
	phospho-N-acetylmuramoyl-pentapeptide transferase	kuste2380	Escherichia coli (b0087:360/358 24-350 (41%))	Pasteurella_multocida (pmu:PM0139:360/358 12-358 (46%))
	cell division protein ftsW, stabilizes FtsZ ring, cytoplasmic membrane required for PBP2 expression	kuste2381	Escherichia coli (b0089:414/399 93-329 (32%))	Bacillus_thuringiensis_konkukian (btk:BT9727_3653:363/399 7-358 (44%))
	UDP-N-acetylglucosamine:N-acetylmuramyl-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (murG)	kuste2383	Escherichia coli (b0090:355/374 32-361 (24%))	Thermoanaerobacter_tengcongensis (tte:TTE1645:364/374 1-361 (36%))
	L-alanine adding enzyme, UDP-N-acetyl-muramate:alanine ligase (murC)	kuste2385	Escherichia coli (b0091:491/500 23-475 (33%))	Thermoanaerobacter_tengcongensis (tte:TTE2575:460/500 26-475 (43%))
	membrane-bound lytic murein transglycosylase A	kusta0010	Escherichia coli (U32224:365/381 125-378 (33%))	Thermosynechococcus_elongatus (tel:tlr0969:390/381 59-381 (41%))
	rod shape determining protein rodA	kustd1894	Escherichia coli (b0634:370/363 89-358 (38%))	Geobacter_sulfurreducens (gsu:GSU2078:366/363 9-355 (40%))
	penicillin binding protein mrdA	kustd1895	Escherichia coli (b0635:633/642 24-621 (26%))	Geobacter_sulfurreducens (gsu:GSU2079:639/642 7-631 (29%))
	rod shape-determining protein mreD	kustd1896	Escherichia coli (b3249:162/165 2-155 (21%))	Thermoanaerobacter_tengcongensis (tte:TTE0900:172/165 1-148 (22%))
	rod shape-determining protein	kustd1897	Escherichia coli (b3250:367/288 186-286 (28%))	Vibrio_parahaemolyticus (vpa:VP2690:298/288 33-286 (27%))
	rod shape-determining protein	kustd1898	Escherichia coli (b3251:367/351 9-348 (51%))	Geobacter_sulfurreducens (gsu:GSU2089:347/351 5-343 (59%))
	murein lipoprotein, links outer and inner membranes	no hit		
	penicillin binding protein I	no hit		

2) length of validated gene/length of orf in K. stuttgartiensis

3) start and ends refer to positions in the orf of K. stuttgartiensis

Blast hits are indicated for each gene. Genes were blasted against a database of proteins with experimentally validated functions (www.cmbi.kun.nl/exprot)

and against the KEGG genes database (www.genome.jp). The best Blast hits of each orf are summarized in the following notation: organism name

(id of database entry: length of protein in the dababase/length of orf in Kuenenia stuttgartiensis start of Blast hit in K. stuttgartiensis - end of Blast hit

in K. stuttgartiensis (percentage of amino acids identical)).