A

Abb	Organism	Accession	Position		Genes
Bacillus/Clostridia					
Ban	*Bacillus anthracis*	NC_003997.3	+ 157538	157672	*glmS* COG0449
Bce	*Bacillus cereus*	NC_004722.1	+ 163187	163321	*BC0190* COG0449
Bha	*Bacillus halodurans*	NC_002570.1	+ 288777	288923	*glmS* COG0449
Bsu	*Bacillus subtilis*	NC_000964.1	+ 200017	200163	*glmS* COG0449
Cac	*Clostridium acetobutylicum*	NC_003030.1	+ 179926	180064	*glmS* COG0449
Cpe	*Clostridium perfringens*	NC_003366.1	− 2678977	2679173	*glmS* COG0449
Cte	*Clostridium tetani*	NC_004557.1	− 2702212	2702464	*CTC02543* COG0449
Dha	*Desulfitobacterium hafniense*	NZ_AAAW00000000.2	− 3522	3675	*Desu0691* COG0449
Efa	*Enterococcus faecalis*	NC_004668.1	− 2055323	2055449	*glmS* COG0449
Gst	Geobacillus stearothermophilus		+ 152	302	*(glmS)* COG0449
	gnl|OUACGT_1422|bstearo.fasta.screen.Contig138				
Lpl	*Lactobacillus plantarum*	NC_004567.1	+ 761460	761590	*glmS1* COG0449
Lin	*Listeria innocua*	NC_003212.1	+ 755745	755920	*lin0734* COG0449
Lmo	*Listeria monocytogenes*	NC_003210.1	+ 756469	756643	*lmo0727* COG0449
Oih	*Oceanobacillus iheyensis*	NC_004193.1	− 258887	259034	*OB0235* COG0449
Sau	*Staphylococcus aureus*	NC_002745.1	− 2212077	2212272	*glmS* COG0449
Sep	*Staphylococcus epidermidis*	NC_004461.1	− 1803993	1804189	*SE1751* COG0449
Tte	*Thermoanaerobacter tengcongensis*	NC_003869.1	+ 2101458	2101594	*GlmS* COG0449
Fusobacteria					
Fnu	*Fusobacterium nucleatum*	NC_003454.1	+ 1095667	1095791	*FN0452* COG0449 *FN0453* COG0006

COG	Gene	Description
COG0449	glmS	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains
COG0006	pepP	Xaa-Pro aminopeptidase

B

C