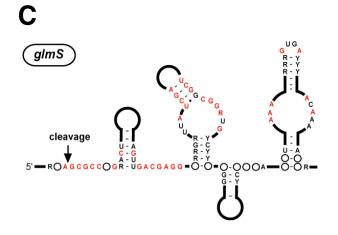
Abb Organism	Accession	P	osition		Genes	
Bacillus/Clostridia						
Ban Bacillus anthracis	NC_003997.3	+	157538	157672	glmS	COG0449
Bce Bacillus cereus	NC 004722.1	+	163187	163321	BC0190	COG0449
Bha Bacillus halodurans	NC_002570.1	+	288777	288923	glmS	COG0449
Bsu <i>Bacillus subtilis</i>	NC 000964.1	+	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 AAAW0000000.2	-	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	1mo0727	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, contair	ns a	amidotra	nsferase	and phosp	hosugar isomerase domair
COG0006 pepP Xaa-Pro aminopeptidase						

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Structure	·····	<
Consensus		
Ban glmS	UUAUAGAAGCGCCAG <mark>AACUACA</mark>	AGUAG
Bce BC0190	UUAUA <mark>G</mark> AAGCGCCAG <mark>AACUACA</mark>	Ū
Bha glmS		ACGGACGGUAAC
Bsu glmS		GCCCGGAAAAAGGCCCGGAAAAAGGCCCGGAAAAAG
Cac glmS		UAUAGU
Cpe glmS		UACAUUAAAAAUGCUUAAUUAAGAUUCUUAAUAAA_UU
Cte CTC02543	3 AUAAUAAAGCGCCAGGACUUAGGUGAUGAAAACUCAGACUAUGGUCUGAGUA	AGUU <mark>CG</mark> ACUAACCAAAUC <mark>ACA</mark> GAUUUGG——AGU <mark>AA</mark> GAUUAAUGAAACUCAGACUAUGGUCUGAGU <mark>AAGUUCCACCAACCAAAUCACAGAUUUGG——GGUG</mark> UCACU
Dha Desu0691		
Efa glmS		
Gst (glmS)		GGACGGAAG
Lpl glmS1	GCGGAAUAGCGCCAG <mark>GACUUUAG</mark>	
Lin <i>lin0734</i>		AAAGUGAAAUUCCUGGAAA <mark>CAA</mark>
Lmo <i>1mo0727</i>		GAAGGUGAAAUCCCUGAACCGA
Oih 0B0235		GGACGGAUAG
Sau glmS		<mark>UGGCCUUUA</mark> UA <mark>GAGUGCAAUAUAUGAG</mark>
Sep SE1751		
Tte glmS		GGCUU
Fnu FN0452	UAAAAGAAGCGCCAG <mark>AACUCU</mark>	

Structure	>>>>>>
Consensus	.aGuuGACGAGGrrgruuA.UCGA.rUCGgCGGRuGycyygg
Ban glmS	EUAGUUGACGAGGUUUA-UCGAGAUUUCGCGCGGAUGAC-UCCCG-GUUGUUCAUCACAACGCGCAA-GCUUUUACUUAAAUCAUUAAGGGGACGUUAGUGGACAAAGGUGAAAGUGUGAUGAGA
Bce BC0190	EUAGUUGACGAGGUUUA-UCGAGAUUUCGGCGGAUGGC-UUCGCGGAUGGC-EUUGUUCAUCAGAAGCGCGA-GCUUUUACUUAAAUCAUUAAGGGGACGUUAGUGGACAAAGGUGAAAGUGUGAUGAGA
Bha glmS	
Bsu glmS	
Cac glmS	UAAGUUGACGAGGA-UGGGG-AGAA-UCGA-AUCU-UCGGCGGAUGCCCCA-GCUAACCGCACUACCGUUGGUAAAAG-CCAGAAAGUGAUUUCUG-UCACAAAGCCAAUCUGGUGUUAA
Cpe glmS	UAAGUUGACGAGGU-UGGGG-AGUA-UCGA-AUUU-UCGGCGGAUGCCCCA-GCCUAAAGCACQACCCGUAAAA-GAUUGGUUAAAACUUAAAAGUGAUUUUAAGGACAAAGCCAAUUGGGUUUUA
Cte CTC02543	
Dha Desu0691	1 AGGUU GACGAGGA-CGAGAG-UUA-UCGA-AAGACUCGGCGGAUGCCCUCUCC-CGCUGUCUUCAAAACCCUUAUUACAAAACCCUGAAGUAAUUUGCGGGACAAAAGCUAAGCCCCAAGGAA
Efa glmS	
Gst (glmS)	
Lpl glmS1	
Lin <i>lin0734</i>	
Lmo <i>1mo0727</i>	UCAGUUGACGAGGAUUAA <mark>UCGA</mark> AGUU <mark>UCGG</mark> CGGGAG <mark>UCUCC-GCCUCU</mark> GCAU <mark>CCAGUCC</mark> UUAAG- <mark>UC-UUACU</mark> UACAAA <mark>UCAUUUGG</mark> GUGA <mark>CCAAGUGG</mark> ACAGAGU <mark>AGUAA</mark> UAUGCUU
Oih 0B0235	
Sau glmS	
Sep SE1751	UUUGUAGACGAGGA-CGAUAGUGA-UCGA-AUCAGA-UCGGCGGAUGCUAUCC-CGCAUGUGGCACUUAUCGUUAGCUUAUUAAGUUAAUCAUUAAGGUGACUUAGUGGACAAAGUUAAUAAGAUCGCCAAA
Tte glmS	
Fnu FN0452	AGAGUUGACGAGGA-UUGGAA-UUA-UCGAA-GUU-UUCGGCGGAUG-UUCCAAAGCU-UUCCAAAGCU-GGUUACAGGUUACA