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Production and secretion stress caused by overexpression of heterologous alpha-amylase leads to inhibition of sporulation and a prolonged motile phase in *Bacillus subtilis*

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Table S1. Differentially expressed genes in response to AmyQ overproduction in the late exponential phase of growth. ⁽¹⁾Fold represents relative change in expression levels between the stressed and non-stressed cells.

Gene	Fold ¹	Function	Functional Group
<i>htrA</i>	22.72	serine protease Do (heat-shock protein)	Adaptation To Atypical Conditions
<i>htrB</i>	7.76	serine protease Do (heat-shock protein)	Adaptation To Atypical Conditions
<i>rpsB</i>	4.99	30S ribosomal protein S2	Protein Synthesis; Ribosomal Proteins
<i>ahpF</i>	2.55	alkyl hydroperoxide reductase (large subunit)and NADH dehydrogenase	Detoxification
<i>citB</i>	2.45	aconitate hydratase (aconitase)	Metabolism Of Carbohydrates And Related Molecules; Tca Cycle
<i>groEL</i>	2.42	class I heat-shock protein (chaperonin)	Protein Folding
<i>acpA</i>	2.30	acyl carrier protein	Metabolism Of Lipids
<i>ftsZ</i>	2.17	cell-division initiation protein	Cell Diision
<i>sodA</i>	2.12	superoxide dismutase	Detoxification
<i>cssR</i>	1.97	two-component response regulator involved in the control of cellular responses to protein secretion stress. cognate sensor kinase is cssS	Sensors (Signal Transduction)
<i>cssS</i>	1.89	two-component sensor histidine kinase nvolved in the control of cellular responses to protein secretion stress. cognate response regulator is cssR	Sensors (Signal Transduction)
<i>accC</i>	1.87	acetyl-CoA carboxylase subunit (biotincarboxylase subunit)	Metabolism Of Lipids
<i>yerP/swrc</i>	1.86	involved in the efflux of surfactin	Detoxification
<i>mrgA</i>	1.81	DNA-binding stress protein	Adaptation To Atypical Conditions
<i>dnaK</i>	1.72	class I heat-shock protein (chaperone)	Protein Folding
<i>pycA</i>	1.65	pyruvate carboxylase	Metabolism Of Carbohydrates And Related Molecules; Main Glycolytic Pathways
<i>dltA</i>	1.52	D-alanyl-D-alanine carrier protein ligase (Dcl)	Cell Wall
<i>trxA</i>	1.50	Thioredoxin	Membrane Bioenergetics (Electron Transport Chain And Atp Synthase)
<i>spIB</i>	-1.96	spore photoproduct (thymine dimer) lyase	Sporulation
<i>xpaC</i>	-2.03	hydrolysis of 5-bromo 4-chloroindolyl phosphate(X-phos)	Metabolism Of Phosphate
<i>tenI</i>	-2.07	transcriptional activator of extracellular enzyme genes	Rna Synthesis; Regulation
<i>nasC</i>	-2.11	assimilatory nitrate reductase (catalyticsubunit)	Metabolism Of Amino Acids And Related Molecules
<i>purE</i>	-2.12	phosphoribosylaminoimidazole carboxylase I	Metabolism Of Nucleotides And Nucleic Acids
<i>glpT</i>	-2.15	glycerol-3-phosphate permease	Transport/Binding Proteins And Lipoproteins
<i>bioD</i>	-2.17	dethiobiotin synthetase	Metabolism Of Coenzymes And Prosthetic Groups
<i>spoIVFA</i>	-2.19	inhibition of SpoIVFB (negative regulation) andhypothesised to stabilize the thermolabile spoIVFB product(positive regulation) (stage IV sporulation)	Sporulation
<i>sqhC</i>	-2.26	squalene-hopene cyclase	Metabolism Of Lipids
<i>ribR</i>	-2.27	monofunctional riovflavin kinase	Rna Synthesis; Regulation
<i>pps</i>	-2.27	phosphoenolpyruvate synthase	Metabolism Of Carbohydrates And Related Molecules; Specific Pathways
<i>lipB</i>	-2.29	extracellular lipase	Metabolism Of Lipids
<i>gerM</i>	-2.30	germination (cortex hydrolysis) and sporulation(stage II, multiple polar septa)	Germination
<i>nucA/comI</i>	-2.34	membrane-associated nuclease	Metabolism Of Nucleotides And Nucleic Acids
<i>spoVFB</i>	-2.40	Sporulation operon spoIVF and the characterization of mutations that uncouple mother-cell from forespore gene expression	Sporulation
<i>mmgD</i>	-2.40	citrate synthase III	Metabolism Of Carbohydrates And Related Molecules; Tca Cycle
<i>cwlJ</i>	-2.41	cell wall hydrolase	Cell Wall
<i>hisP / mdgS</i>	-2.47	methionine - methionine sulfoxide transport system ATP-binding protein	Transport/Binding Proteins And Lipoproteins
<i>mmgA</i>	-2.49	acetyl-CoA acetyltransferase	Metabolism Of Lipids
<i>blyA</i>	-2.61	N-acetylmuramoyl-L-alanine amidase, peptidoglycan hydrolase, SP-beta protein	Phage-Related Functions
<i>ebrB</i>	-2.63	SMR-type multidrug efflux transporte	Transport/Binding Proteins And Lipoproteins
<i>thyB</i>	-2.66	thymidylate synthase B	Metabolism Of Nucleotides And Nucleic Acids
<i>licH</i>	-2.68	6-phospho-beta-glucosidase	Metabolism Of Carbohydrates And Related Molecules; Specific Pathways

Gene	Fold ¹	Function	Functional Group
<i>hmp</i>	-2.77	Flavo-hemoglobin	Membrane Bioenergetics (Electron Transport Chain And Atp Synthase)
<i>csfB</i>	-2.89	sigma-F transcribed gene	Miscellaneous
<i>cotJC</i>	-2.97	polypeptide composition of the spore coat	Sporulation
<i>fabHB/yhfB</i>	-3.22	beta-ketoacyl-acyl carrier protein synthase III	Metabolism Of Lipids
<i>cotE</i>	-3.60	spore coat protein (outer)	Sporulation
<i>spoIIIAH</i>	-3.64	mutants block sporulation after engulfmen	Sporulation
<i>bceB /ytsd</i>	-3.76	bacitracine efflux ABC transport system permease	Transport/Binding Proteins And Lipoproteins
<i>Genes with unknown function</i>			
<i>yvfW</i>	3.19	iron-sulfur-binding protein	Similar To Unknown Proteins; From Other Organisms
<i>yvqH</i>	2.56	similar to phage shock protein	Similar To Unknown Proteins; From BSubtilis
<i>ykoJ</i>	2.09	conserved protein	Similar To Unknown Proteins; From BSubtilis
<i>ydbK</i>	2.03	probable ABC transport system permease protein	Similar To Unknown Proteins; From BSubtilis
<i>ywjD</i>	-2.29	similar to UV-endonuclease	Dna Restriction/Modification And Repair
<i>yhfC</i>	-2.51	conserved membrane protein, probably involved in fatty acid synthesis	No Similarity To Other Proteins
<i>ywdL</i>	-2.52	Bacterial regulatory helix-turn-helix protein, lysR family	No Similarity To Other Proteins
<i>yomC</i>	-2.61	N-acetylmuramoyl-L-alanine amidase, peptidoglycan hydrolase, SP-beta protein	Cell Wall
<i>yxjO</i>	-2.61	probable transcriptional regulator (LysR family)	Rna Synthesis; Regulation
<i>yckI</i>	-2.75	probable polar amino acid transport system ATP-binding protein	Transport/Binding Proteins And Lipoproteins
<i>yhfU</i>	-2.75	Flavo-hemoglobin	Metabolism Of Coenzymes And Prosthetic Groups
<i>ytnJ</i>	-2.79	probable methionine sulfoxide oxidase	Detoxification
<i>yvbA</i>	-2.87	Transcriptional regulator (ArsR family), inducing the atp and yusLKJ operon	Rna Synthesis; Regulation
<i>yhcN</i>	-2.90	inner spore membrane protein; Characterization of yhcN, a new forespore-specific gene of <i>Bacillus subtilis</i>	Similar To Unknown Proteins; From Other Organisms
<i>yuiF</i>	-2.96	unknown; putative transporter	Similar To Unknown Proteins; From Other Organisms
<i>ycdA</i>	-3.02	Unknown	No Similarity To Other Proteins
<i>yjhA</i>	-3.04	Unknown	No Similarity To Other Proteins
<i>yngI</i>	-4.07	long-chain fatty-acid-CoA ligase	Metabolism Of Lipids
<i>ysxE</i>	-5.15	conserved protein	No Similarity To Other Proteins
<i>yosA</i>	-6.23	SP-beta protein	No Similarity To Other Proteins