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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 S2. Differentially expressed genes in response to AmyQ overproduction in the stationary phase of growth.  
<sup>(1)</sup>Fold represents relative change in expression levels between the stressed and non-stressed cells.

Gene	Fold <sup>1</sup>	Product	Functional Group
<i>htrA</i>	8.81	serine protease Do (heat-shock protein)	Adaptation To Atypical Conditions
<i>citM</i>	6.12	2-oxoglutarate dehydrogenase (dihydrolipoamide transsuccinylase, E2 subunit)	Transport/Binding Proteins And Lipoproteins
<i>htrB</i>	4.70	serine protease Do (heat-shock protein)	Adaptation To Atypical Conditions
<i>fliF</i>	4.25	flagellar basal-body M-ring protein	Motility And Chemotaxis
<i>flgB</i>	3.83	flagellar basal-body rod protein	Motility And Chemotaxis
<i>flgC</i>	3.61	flagellar basal-body rod protein	Motility And Chemotaxis
<i>fliJ</i>	3.26	flagellar protein	Motility And Chemotaxis
<i>fliG</i>	2.94	flagellar motor switch protein	Motility And Chemotaxis
<i>fliZ</i>	2.93	flagellar protein	Motility And Chemotaxis
<i>fliE</i>	2.89	flagellar hook-basal body protein	Motility And Chemotaxis
<i>fliY</i>	2.80	flagellar motor switch protein	Motility And Chemotaxis
<i>PrpC/yloO</i>	2.76	PP2C protein phosphatase	Protein Modification
<i>ilvD</i>	2.73	dihydroxy-acid dehydratase	Metabolism Of Amino Acids And Related Molecules
<i>fliI</i>	2.72	flagellar-specific ATP synthase	Motility And Chemotaxis
<i>fliL</i>	2.66	flagellar protein	Motility And Chemotaxis
<i>sucC</i>	2.52	succinyl-CoA synthetase (beta subunit)	Metabolism Of Carbohydrates And Related Molecules; Tca Cycle
<i>serA</i>	2.49	phosphoglycerate dehydrogenase	Metabolism Of Amino Acids And Related Molecules
<i>alsT</i>	2.48	amino acid carrier protein	Transport/Binding Proteins And Lipoproteins
<i>flgE</i>	2.45	flagellar hook protein	Motility And Chemotaxis
<i>soj/spo0JA</i>	2.42	centromere-like function involved in forespore chromosome partitioning / negative regulation of sporulation initiation	Sporulation
<i>fliK</i>	2.39	flagellar hook-length control	Motility And Chemotaxis
<i>fliH</i>	2.38	flagellar assembly protein	Motility And Chemotaxis
<i>dppA</i>	2.35	D-alanyl-aminopeptidase	Transport/Binding Proteins And Lipoproteins
<i>cheV</i>	2.28	modulation of CheA activity in response to attractants (chemotaxis)	Motility And Chemotaxis
<i>TatAd/yczB</i>	2.26	component of the twin-arginine pre-protein translocation pathway	Protein Secretion
<i>flhA</i>	2.23	flagella-associated protein	Motility And Chemotaxis
<i>uxaC/yjmA</i>	2.19	glucuronate isomerase, hexuronate utilization	Metabolism Of Carbohydrates And Related Molecules / Specific Pathways
<i>sigD</i>	2.14	RNA polymerase flagella, motility, chemotaxis and autolysis sigma factor	Rna Synthesis; initiation
<i>flhP</i>	2.12	flagellar hook-basal body protein	Motility And Chemotaxis
<i>spo0E</i>	2.11	negative sporulation regulatory phosphatase	Sporulation
<i>dltA</i>	2.08	D-alanyl-D-alanine carrier protein ligase (Dcl)	Cell Wall
<i>rpsP</i>	2.06	ribosomal protein S16 (BS17)	Protein Synthesis; Ribosomal Proteins
<i>mcpB</i>	2.04	methyl-accepting chemotaxis protein	Motility And Chemotaxis
<i>smf</i>	2.04	DNA processing Smf protein homolog	Dna Packaging And Segregation
<i>nprE</i>	2.04	extracellular neutral metalloprotease	Metabolism Of Amino Acids And Related Molecules
<i>fliD</i>	2.04	flagellar hook-associated protein 2 (HAP2)	Motility And Chemotaxis
<i>fhuC</i>	2.01	errichrome transport system ATP-binding protein	Transport/Binding Proteins And Lipoproteins
<i>flgL</i>	1.98	flagellar hook-associated protein 3 (HAP3)	Motility And Chemotaxis
<i>motB</i>	1.97	motility protein B	Motility And Chemotaxis
<i>htpG</i>	1.97	class III heat-shock protein (molecular chaperone)	Adaptation To Atypical Conditions
<i>mcpA</i>	1.97	methyl-accepting chemotaxis protein	Motility And Chemotaxis
<i>qoxA</i>	1.96	cytochrome aa3 quinol oxidase subunit II	Membrane Bioenergetics (Electron Transport Chain And Atp Synthase)
<i>qoxB</i>	1.93	cytochrome aa3 quinol oxidase (subunit I)	Membrane Bioenergetics (Electron Transport Chain And Atp Synthase)
<i>flgK</i>	1.93	flagellar hook-associated protein 1 (HAP1)	Motility And Chemotaxis
<i>ffh</i>	1.86	signal recognition particle-like (SRP) component	Protein Secretion
<i>recA</i>	1.69	multifunctional SOS repair regulator	Dna Recombination
<i>degU</i>	1.65	two-component response regulator involved in degradative enzyme and competence regulation. cognate sensor kinase is degS	Rna Synthesis; Regulation

Gene	Fold <sup>1</sup>	Product	Functional Group
<i>spoVC</i>	-1.99	peptidyl-tRNA hydrolase (stage V sporulation protein C)	Sporulation
<i>acoB</i>	-2.04	acetoin dehydrogenase E1 component(TPP-dependent beta subunit)	Metabolism Of Carbohydrates And Related Molecules; Specific Pathways
<i>opuBB</i>	-2.12	choline ABC transporter (membrane protein)	Transport/Binding Proteins And Lipoproteins
<i>spoIIE</i>	-2.27	serine phosphatase (sigma-F activation) / asymmetric septum formation	Sporulation
<i>spoIVFA</i>	-2.40	inhibitor of SpoIVFB	Sporulation
<i>glgA</i>	-2.45	glycogen synthase (starch (bacterial glycogen) synthase)	Metabolism Of Carbohydrates And Related Molecules; Specific Pathways
<i>sspF</i>	-2.61	small acid-soluble spore protein(alpha/beta-type SASP)	Sporulation
<i>scoB/yxjE</i>	-2.64	3-oxoacid CoA-transferase subunit B	Metabolism Of Lipids
<i>spoVM</i>	-2.93	equired for normal spore cortex and coat synthesi	Sporulation
<i>sspD</i>	-4.75	small acid-soluble spore protein(alpha/beta-type SASP)	Sporulation
<i>spoIIIC</i>	-4.95	RNA polymerase sporulation-specific sigma factor(sigma-K) (C-terminal half)	Rna Synthesis;nitiation
<i>spoIVCB</i>	-5.47	RNA polymerase sporulation mother cell-specific (late) sigma factor (sigma-K N-terminal half)	Rna Synthesis;nitiation
<i>sspL</i>	-5.63	small acid-soluble spore protein (minor)	Sporulation
<i>spoVAA</i>	-6.12	sporulation protein VAA	Sporulation
<i>cotK</i>	-6.23	small acid-soluble spore protein	Sporulation
<i>spoIVB</i>	-9.46	serine peptidase of the SA clan	Sporulation
<i>tlp</i>	-9.70	small acid-soluble spore protein(thioredoxin-like protein)	Membrane Bioenergetics (Electron Transport Chain And Atp Synthase)
<i>Unknown genes</i>			
<i>yloA</i>	11.15	unknown; similar to fibronectin-binding protein	Adaptation To Atypical Conditions
<i>ykoJ</i>	5.31	conserved protein	Similar To Unknown Proteins; From BSubtilis
<i>yheN</i>	2.96	similar to endo-1,4-beta-xylanase	Metabolism Of Carbohydrates And Related Molecules; Specific Pathways
<i>ylxF</i>	2.63	conserved protein	No Similarity To Other Proteins
<i>yfmT</i>	2.61	similar to benzaldehyde dehydrogenase	Metabolism Of Carbohydrates And Related Molecules; Specific Pathways
<i>yusS</i>	2.52	similar to 3-oxoacyl- acyl-carrier protein reductase	Metabolism Of Lipids
<i>yusQ</i>	2.29	similar to 4-oxalocrotonate tautomerase	Metabolism Of Lipids
<i>yqzH</i>	2.23	function unknown and unique	No Similarity To Other Proteins
<i>yxiL</i>	2.21	function unknown and unique	No Similarity To Other Proteins
<i>yopS</i>	2.21	possible transcriptional regulator, SP-beta protein	Similar To Unknown Proteins; From BSubtilis
<i>ylxH</i>	2.10	similar to flagellar biosynthesis switch protein	Motility And Chemotaxis
<i>yolA</i>	2.09	SP-beta protein	No Similarity To Other Proteins
<i>yybN</i>	2.05	function unknown and unique	No Similarity To Other Proteins
<i>yyzE</i>	2.03	putative PTS glucose-specific enzyme IIA component	Transport/Binding Proteins And Lipoproteins
<i>ymfC</i>	2.02	unknown; similar to transcriptional regulator (GntR family)	Rna Synthesis;Regulation
<i>yorD</i>	1.97	cold shock and salt stress induced protein, SP-beta protein	No Similarity To Other Proteins
<i>ycbP</i>	-2.14	conserved membrane protein	Similar To Unknown Proteins; From BSubtilis
<i>ybbC</i>	-2.15	unknown; similar to unknown proteins	No Similarity To Other Proteins
<i>yjmG/exuT</i>	-2.02	hexuronate transporter	Transport/Binding Proteins And Lipoproteins
<i>yjmF</i>	-2.13	similar to D-mannonate oxidoreductase, hexuronate utilization	Metabolism Of Carbohydrates And Related Molecules; Specific Pathways
<i>yjmE</i>	-2.34	mannonate dehydratase, hexuronate utilization	Metabolism Of Carbohydrates And Related Molecules; Specific Pathways
<i>yhfN</i>	-2.56	putative Zn-dependent protease	Similar To Unknown Proteins; From Other Organisms
<i>yjmC</i>	-2.77	similar to malate dehydrogenase, hexuronate utilization	Metabolism Of Carbohydrates And Related Molecules; Tca Cycle
<i>yxjC</i>	-2.95	conserved membrane protein	Similar To Unknown Proteins; From BSubtilis
<i>yoaR</i>	-3.21	unknown; similar to unknown proteins	No Similarity To Other Proteins
<i>yngG</i>	-4.45	similar to hydroxymethylglutaryl-CoA lyase	Metabolism Of Lipids