

Table 1: Kinetic of the glucose starvation repressed genes of *B. licheniformis*. Listed are such genes, whose mRNA levels showed a more than threefold repression during at least one sampling point throughout the growth curve. Genes the expresion of which is also repressed under nitrogen starvation conditions are labelled with “**”. Trans. ph. = transient phase, Transcript. = Transcriptional , SD = standard deviation

Gene name	Trans. ph.	SD	10 min	SD	20 min	SD	30 min	SD	60 min	SD	120 min	SD	Transcriptional organisation	Function
Cell wall														
<i>tuaB</i>	1.2 ± 0.1		3.9 ± 0.1		3.1 ± 0.2		3.1 ± 0.5		5.0 ± 0.1		4.2 ± 0.8		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaC</i>	1.2 ± 0.1		4.4 ± 0.2		3.8 ± 0.1		4.0 ± 0.2		4.4 ± 0.1		3.5 ± 0.8		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaD</i>	1.2 ± 0.3		4.9 ± 0.8		3.6 ± 0.4		3.4 ± 0.7		5.9 ± 0.1		6.3 ± 2.0		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaG</i>	1.2 ± 0.1		4.3 ± 0.1		4.0 ± 0.1		3.6 ± 0.1		7.3 ± 1.3		7.1 ± 3.5		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>BLi03767</i>	1.2 ± 0.1		5.7 ± 1.1		3.9 ± 0.1		4.1 ± 0.1		10.8 ± 2.4		9.1 ± 1.4			putative cell wall-binding protein
Transport/binding proteins and lipoproteins														
<i>yclN</i>	1.0 ± 0.1		12.9 ± 0.6		7.7 ± 2.9		10.8 ± 1.0		11.3 ± 3.7		9.3 ± 1.7		<i>yclN-O-P-Q</i>	similar to ferrichrome ABC transporter
<i>yclO</i>	1.0 ± 0.2		6.0 ± 1.2		6.9 ± 2.2		11.8 ± 3.9		4.5 ± 0.4		3.1 ± 1.2		<i>yclN-O-P-Q</i>	similar to ferrichrome ABC transporter
<i>yclP</i>	1.2 ± 0.2		9.1 ± 3.2		7.5 ± 1.7		5.9 ± 0.1		7.3 ± 3.8		7.2 ± 1.3		<i>yclN-O-P-Q</i>	similar to ferrichrome ABC transporter
<i>yclQ</i>	1.2 ± 0.2		6.3 ± 1.3		3.9 ± 0.3		4.1 ± 0.9		4.1 ± 0.3		2.2 ± 0.4		<i>yclN-O-P-Q</i>	similar to ferrichrome ABC transporter
<i>yhcJ</i>	2.4 ± 0.3		6.5 ± 1.8		5.9 ± 1.2		6.7 ± 0.1		5.9 ± 3.3		5.5 ± 0.1		<i>yhcJ-N</i>	similar to ABC transporter
<i>yhcL</i>	1.9 ± 0.1		8.2 ± 1.0		4.7 ± 0.6		7.3 ± 1.5		5.4 ± 0.5		4.9 ± 0.2		<i>yhc operon</i>	similar to sodium-glutamate symporter
<i>yxdl</i>	3.3 ± 0.2		9.3 ± 1.2		9.9 ± 1.4		12.5 ± 0.1		12.5 ± 5.6		7.7 ± 0.1		<i>yxdl-K-L-M</i>	similar to ABC transporter
<i>yxdm</i>	4.8 ± 0.5		5.3 ± 1.2		4.5 ± 1.9		10.6 ± 0.8		5.6 ± 0.1		7.9 ± 2.6		<i>yxdm-K-L-M</i>	similar to ABC transporter
<i>cysP</i>	1.7 ± 0.3		4.1 ± 1.0		5.0 ± 1.2		7.3 ± 2.2		4.7 ± 0.8		5.8 ± 0.6		<i>cysP</i>	sulfate permease
<i>feuA</i>	0.8 ± 0.3		4.7 ± 0.8		3.1 ± 0.8		2.9 ± 0.8		8.8 ± 2.0		4.0 ± 0.4		<i>feuA-B-C</i>	iron-uptake system
<i>fhuB</i>	1.1 ± 0.2		2.6 ± 0.9		1.5 ± 1.0		2.5 ± 0.6		3.5 ± 1.9		2.7 ± 1.0		<i>fhuB-G-C</i>	ferrichrome transport system permease protein
<i>fhuC</i>	1.1 ± 0.1		4.6 ± 1.4		3.2 ± 1.0		3.5 ± 0.5		4.4 ± 1.0		3.2 ± 0.3		<i>fhuB-G-C</i>	ferrichrome transport ATP-binding protein
<i>fhuD</i>	1.3 ± 0.2		5.1 ± 0.6		3.1 ± 1.3		3.1 ± 0.2		4.5 ± 0.3		4.2 ± 1.4		<i>fhuD</i>	ferrichrome-binding periplasmic protein
<i>fhuG</i>	1.6 ± 0.3		3.5 ± 1.1		3.1 ± 0.8		3.9 ± 1.4		2.3 ± 1.0		1.7 ± 0.5		<i>fhuB-G-C</i>	ferrichrome transport system permease protein
<i>opuAA</i>	1.3 ± 0.2		2.8 ± 0.3		2.2 ± 0.8		1.8 ± 0.1		2.3 ± 0.7		2.5 ± 0.6		<i>opuAA-AB-AC</i>	glycine betaine transport ATP-binding protein
<i>opuAB</i>	1.0 ± 0.2		5.0 ± 0.5		2.8 ± 0.1		2.3 ± 0.1		4.6 ± 1.0		4.3 ± 1.0		<i>opuAA-AB-AC</i>	glycine betaine transport system permease
<i>opuAC</i>	1.4 ± 0.3		5.3 ± 1.4		3.5 ± 0.8		2.1 ± 0.1		5.7 ± 3.3		5.0 ± 1.5		<i>opuAA-AB-AC</i>	glycine betaine-binding protein
<i>opuE</i>	1.4 ± 0.3		2.3 ± 0.4		2.8 ± 0.2		2.8 ± 0.2		1.7 ± 0.5		1.5 ± 0.1		<i>opuE</i>	proline transporter

<i>pbuX</i>	1.8 ± 0.1	5.4 ± 0.4	4.2 ± 0.2	5.1 ± 0.3	4.2 ± 1.7	3.0 ± 0.5	<i>pbuX</i>	xanthine permease
<i>ssuA</i>	0.7 ± 0.1	3.7 ± 0.7	4.4 ± 1.6	5.4 ± 0.8	4.0 ± 0.2	4.4 ± 0.9	<i>ssuB-A-C</i>	aliphatic sulfonate binding protein
<i>ssuB</i>	0.7 ± 0.1	2.3 ± 0.2	3.9 ± 0.7	3.6 ± 0.8	2.4 ± 0.1	3.8 ± 0.9	<i>ssuB-A-C</i>	sulfonate ABC transporter
<i>ssuC</i>	1.1 ± 0.1	2.7 ± 0.3	3.4 ± 0.6	4.0 ± 0.9	2.2 ± 0.4	3.1 ± 0.4	<i>ssuB-A-C</i>	aliphatic sulfonates transport
<i>ybaE</i>	1.3 ± 0.2	3.7 ± 0.1	3.7 ± 0.5	3.6 ± 0.2	4.9 ± 1.1	2.1 ± 1.0	<i>ybaE</i>	permease protein similar to ABC transporter
<i>ycdH</i>	1.0 ± 0.5	2.0 ± 0.3	1.9 ± 0.3	1.7 ± 0.5	3.1 ± 0.5	3.3 ± 0.6	<i>ycdH</i>	ATP-binding protein similar to ABC transporter
<i>ykoD</i>	1.4 ± 0.2	4.8 ± 1.3	5.1 ± 2.5	4.8 ± 0.6	3.7 ± 1.1	4.1 ± 0.5	<i>yko operon</i>	ATP-binding protein similar to ABC transporter
<i>yqiX</i>	1.1 ± 0.2	8.8 ± 1.0	7.5 ± 1.5	12.6 ± 1.6	4.8 ± 1.0	2.8 ± 0.8	<i>yqi operon</i>	probable amino-acid ABC transporter
<i>yqiY</i>	1.1 ± 0.0	6.1 ± 1.8	6.5 ± 1.0	8.5 ± 3.9	5.3 ± 1.3	3.1 ± 1.6	<i>yqi operon</i>	probable amino-acid ABC transporter
<i>yqiZ</i>	0.8 ± 0.1	4.8 ± 0.7	3.8 ± 0.9	4.0 ± 0.3	4.3 ± 0.6	3.8 ± 0.8	<i>yqi operon</i>	probable amino-acid ABC transporter
<i>yvrG</i>	1.2 ± 0.3	2.9 ± 0.7	1.7 ± 0.4	1.9 ± 0.3	8.1 ± 2.2	8.2 ± 1.8	<i>yvrH-G</i>	similar to two-component sensor histidine kinase homolog
<i>yvrH</i>	1.2 ± 0.1	2.9 ± 0.9	2.1 ± 0.3	2.3 ± 0.5	5.2 ± 1.3	5.3 ± 2.4	<i>yvrH-G</i>	histidine kinase homolog similar to two-component sensor
<i>BLi00972</i>	3.3 ± 0.7	9.5 ± 1.7	12.9 ± 2.8	8.3 ± 0.1	9.5 ± 2.3	7.3 ± 1.0		putative ABC transporter ATP-binding protein
<i>BLi00973</i>	2.6 ± 0.4	6.9 ± 0.5	6.3 ± 1.8	7.7 ± 0.1	5.5 ± 1.8	4.6 ± 0.9		putative ABC transporter permease
<i>BLi03178</i>	1.2 ± 0.1	3.0 ± 0.5	3.0 ± 0.4	3.5 ± 0.1	2.6 ± 0.4	2.5 ± 0.4		putative ABC transporter
<i>BLi03767</i>	1.2 ± 0.1	5.7 ± 1.1	3.3 ± 0.8	4.1 ± 0.5	10.8 ± 3.9	8.5 ± 1.4		putative cell wall-binding protein
<i>BLi02528</i>	1.2 ± 0.1	2.2 ± 0.5	2.1 ± 0.5	1.3 ± 0.2	4.0 ± 0.1	3.4 ± 0.6		putative ABC transporter periplasmic binding protein
Motility and chemotaxis								
<i>ylxH</i>	1.4 ± 0.1	5.6 ± 0.1	6.5 ± 2.3	3.7 ± 0.1	6.1 ± 0.1	7.3 ±	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i>	similar to flagellar biosynthesis
							<i>fliD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i>	switch protein
							<i>flihB-A-F-ylxH</i>	
<i>cheD</i>	1.0 ± 0.3	3.2 ± 0.9	4.3 ± 2.0	3.0 ± 0.4	3.9 ± 0.8	3.5 ± 1.2	<i>cheA-W-C-D-fliA</i>	required for methylation
<i>flgE</i>	1.0 ± 0.1	3.3 ± 1.3	2.8 ± 0.5	3.0 ± 0.2	8.2 ± 2.3	8.0 ± 2.1	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i>	flagellar hook protein
							<i>fliD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i>	
							<i>flihB-A-F-ylxH</i>	
<i>flihB</i>	1.1 ± 0.1	4.9 ± 0.1	3.6 ± 0.7	4.7 ± 0.5	9.1 ± 2.1	6.7 ± 2.2	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i>	flagellar biosynthetic protein
							<i>fliD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i>	
							<i>flihB-A-F-ylxH</i>	
<i>flihO</i>	1.1 ± 0.3	1.6 ± 0.2	1.4 ± 0.2	2.1 ± 0.6	3.5 ± 0.4	3.7 ± 0.8	<i>flihO-P</i>	flagellar hook-basal body complex protein

<i>fliP</i>	1.0 ± 0.2	1.7 ± 0.2	2.0 ± 0.2	2.3 ± 0.5	4.5 ± 0.6	6.2 ± 0.3	<i>fliO-P</i>	flagellar hook-basal body complex protein
<i>fliD</i>	1.0 ± 0.1	1.3 ± 0.1	1.7 ± 0.1	1.9 ± 0.2	5.3 ± 0.7	5.8 ± 2.0	<i>fliD-S-T</i>	flagellar hook-associated protein 2
<i>fliE</i>	1.3 ± 0.2	1.8 ± 0.3	1.5 ± 0.3	1.9 ± 0.6	5.7 ± 2.3	4.4 ± 1.2	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellar hook-basal body complex protein
<i>fliG</i>	1.3 ± 0.1	2.3 ± 0.8	2.8 ± 0.4	2.3 ± 0.7	6.2 ± 0.9	5.7 ± 2.2	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellar motor switch protein
<i>fliH</i>	0.9 ± 0.3	2.6 ± 0.6	2.3 ± 0.6	2.7 ± 0.7	1.1 ± 1.7	7.3 ± 2.4	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	frobable flagellar assembly protein
<i>fliI</i>	1.0 ± 0.1	3.4 ± 1.4	2.1 ± 0.4	2.3 ± 1.4	4.9 ± 1.0	6.2 ± 0.8	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellum-specific ATP synthase
<i>fliJ</i>	0.8 ± 0.2	3.7 ± 0.6	1.7 ± 0.6	3.1 ± 0.5	11.1 ± 2.8	6.7 ± 0.6	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellar protein
<i>fliK</i>	1.1 ± 0.6	3.7 ± 1.2	2.4 ± 0.1	3.0 ± 0.9	5.3 ± 1.9	4.5 ± 0.8	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellar hook-length control protein
<i>fliM</i>	1.0 ± 0.2	3.9 ± 0.8	2.0 ± 0.2	3.1 ± 0.5	6.4 ± 2.5	5.3 ± 0.6	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellar motor switch protein
<i>fliP</i>	1.0 ± 0.1	3.4 ± 0.8	3.3 ± 0.9	3.1 ± 0.7	5.0 ± 1.2	5.3 ± 1.5	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellar biosynthetic protein
<i>fliR</i>	1.0 ± 0.1	5.3 ± 1.5	4.3 ± 1.7	4.8 ± 1.3	5.3 ± 0.2	6.3 ± 2.9	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellar biosynthetic protein
<i>fliZ</i>	1.0 ± 0.1	4.2 ± 0.8	4.1 ± 1.3	3.7 ± 1.4	7.0 ± 1.0	10.3 ± 4.6	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>fliB-A-F-ylxH</i>	flagellar biosynthetic protein
<i>motA</i>	1.0 ± 0.2	1.7 ± 0.2	1.6 ± 0.1	2.1 ± 0.3	4.0 ± 0.7	3.8 ± 0.5	<i>motA-B</i>	strong similarity to motility protein
<i>tlpB</i>	0.9 ± 0.1	2.7 ± 0.5	2.3 ± 0.3	3.9 ± 0.5	4.0 ± 1.2	4.3 ± 0.6	<i>tlpB</i>	methyl-accepting chemotaxis protein
<i>ylxG</i>	1.0 ± 0.2	2.5 ± 0.2	2.6 ± 0.4	2.5 ± 0.4	4.3 ± 1.2	5.4 ± 1.0	<i>ylxG</i>	mcpB similar to flagellar hook assembly

<i>yvyF</i>	1.0 ± 0.1	1.3 ± 0.1	1.1 ± 0.6	1.4 ± 0.4	4.4 ± 0.7	6.0 ± 0.8	<i>yvyF-flgM-yvyG</i>	protein flgD
<i>yvyG</i>	0.9 ± 0.1	1.2 ± 0.1	1.5 ± 0.2	1.8 ± 0.3	3.2 ± 0.8	4.3 ± 0.6	<i>yvyF-flgM-yvyG</i>	similar to flagellar protein homolog <i>yvyF</i>
Protein secretion								hypothetical protein
<i>secY</i>	1.1 ± 0.1	8.4 ± 2.1	9.9 ± 2.7	5.4 ± 1.7	10.6 ± 2.7	17.7 ± 3.2	<i>rplR-secY-adk-map</i>	preprotein translocase subunit
Specific pathways								
<i>ackA</i>	1.0 ± 0.1	5.9 ± 1.7	6.5 ± 1.0	6.7 ± 1.3	4.8 ± 0.7	4.2 ± 1.4	<i>ackA</i>	acetate kinase
Main glycolytic pathways								
<i>eno</i> *	1.1 ± 0.2	3.7 ± 0.7	3.9 ± 1.0	3.4 ± 0.3	5.5 ± 0.3	6.1 ± 0.5	<i>gapA-pgk-tpiA-pgm-eno</i>	enolase
<i>gapA</i> *	1.4 ± 0.1	8.9 ± 0.3	16.2 ± 2.7	18.3 ± 2.3	11.4 ± 1.2	9.2 ± 2.5	<i>gapA-pgk-tpiA-pgm-eno</i>	glyceraldehyde-3-phosphat
<i>pdhC</i> *	0.4 ± 0.1	3.8 ± 0.8	3.8 ± 0.1	4.1 ± 0.8	4.3 ± 0.3	4.6 ± 0.9	<i>pdhA-B-C-D</i>	pyruvate dehydrogenase
<i>pdhD</i> *	0.5 ± 0.1	4.1 ± 0.1	2.6 ± 0.1	2.7 ± 0.1	12.6 ± 3.7	7.1 ± 0.1	<i>pdhA-B-C-D</i>	pyruvate dehydrogenase/ 2-oxoglutarate dehydrogenase
<i>pgk</i>	1.1 ± 0.1	5.6 ± 0.6	4.6 ± 1.1	4.2 ± 1.1	11.0 ± 3.2	11.0 ± 2.3	<i>gapA-pgk-tpiA-pgm-eno</i>	phosphoglycerate kinase
<i>pgm</i>	1.1 ± 0.1	5.4 ± 0.8	4.6 ± 0.1	3.8 ± 0.5	7.3 ± 0.1	9.5 ± 3.2	<i>gapA-pgk-tpiA-pgm-eno</i>	phosphoglycerate mutase
<i>ptsG</i>	0.7 ± 0.2	5.3 ± 1.6	10.0 ± 0.1	8.7 ± 0.1	8.3 ± 2.0	9.5 ± 2.1	<i>ptsG-I</i>	PTS glucose-specific enzyme IICBA component
Metabolism of amino acids and related molecules								
<i>argB</i>	1.2 ± 0.1	7.8 ± 0.3	5.4 ± 0.1	3.0 ± 0.1	0.9 ± 0.1	0.8 ± 0.1	<i>argC-J-B-D-carA-B-argF</i>	N-acetylglutamate 5-phototransferase
<i>argC</i>	0.8 ± 0.1	6.2 ± 1.0	5.8 ± 0.1	5.6 ± 0.1	3.6 ± 0.7	2.6 ± 0.2	<i>argC-J-B-D-carA-B-argF</i>	N-acetylglutamate gamma-semialdehyde dehydrogenase
<i>argD</i>	0.9 ± 0.1	5.8 ± 1.2	4.5 ± 0.8	9.8 ± 2.5	3.3 ± 0.1	1.9 ± 0.1	<i>argC-J-B-D-carA-B-argF</i>	N-acetylornithine aminotransferase
<i>argF</i>	1.1 ± 0.1	7.9 ± 0.2	11.1 ± 3.7	7.9 ± 0.7	5.9 ± 0.0	7.1 ± 0.1	<i>argC-J-B-D-carA-B-argF</i>	ornithine carbamoyltransferase
<i>argG</i>	1.2 ± 0.1	12.5 ± 4.1	7.6 ± 2.6	16.3 ± 8.7	5.8 ± 0.9	3.5 ± 0.6	<i>argG-H</i>	argininosuccinate synthase
<i>argH</i>	1.4 ± 0.4	14.2 ± 7.9	13.3 ± 0.1	14.3 ± 0.2	5.1 ± 0.6	3.4 ± 0.7	<i>argG-H</i>	argininosuccinate lyase
<i>argJ</i>	0.8 ± 0.1	7.6 ± 1.0	8.2 ± 1.4	12.5 ± 0.2	3.7 ± 0.1	4.4 ± 0.1	<i>argC-J-B-D-carA-B-argF</i>	ornithine acetyltransferase
<i>carA</i>	1.0 ± 0.1	15.0 ± 2.3	9.5 ± 3.0	6.1 ± 0.1	4.3 ± 2.0	2.9 ± 0.1	<i>argC-J-B-D-carA-B-argF</i>	carbamoyl-phosphate transferase- arginine (subunit A)
<i>carB</i>	1.0 ± 0.1	7.5 ± 1.2	6.9 ± 0.1	13.4 ± 2.8	3.7 ± 0.7	4.8 ± 0.1	<i>argC-J-B-D-carA-B-argF</i>	carbamoyl-phosphate transferase- arginine (subunit B)
<i>leuA</i>	1.1 ± 0.1	4.5 ± 1.2	3.6 ± 0.1	4.0 ± 0.1	9.6 ± 1.8	9.9 ± 0.5	<i>ilvB-H-C-leuA-B-C-D</i>	2-isopropylmalate synthase
<i>leuB</i>	1.1 ± 0.1	4.2 ± 0.3	3.4 ± 0.8	3.2 ± 0.1	7.9 ± 4.3	10.2 ± 2.2	<i>ilvB-H-C-leuA-B-C-D</i>	3-isopropylmalate dehydrogenase
<i>leuD</i>	1.2 ± 0.1	4.9 ± 0.1	4.0 ± 0.1	3.5 ± 0.5	4.9 ± 0.4	4.8 ± 0.7	<i>ilvB-H-C-leuA-B-C-D</i>	3-isopropylmalate dehydrase
<i>yjcI</i>	2.3 ± 0.1	6.6 ± 1.6	9.0 ± 2.2	12.5 ± 1.1	13.8 ± 2.3	9.8 ± 1.5	<i>yjcI-J</i>	similar to cystathionine gamma-synthase
<i>yjcJ</i>	2.2 ± 0.2	5.5 ± 0.5	6.9 ± 0.1	10.8 ± 2.4	5.8 ± 1.3	5.4 ± 1.1	<i>yjcI-J</i>	similar to cystathionine beta-lyase
<i>hisB</i>	1.2 ± 0.2	1.8 ± 0.2	5.2 ± 2.0	4.7 ± 0.3	4.1 ± 1.7	5.0 ± 1.0	<i>hisIE-F-A-H-B-D-G-Z</i>	imidazoleglycerol-phospho

<i>hisD</i>	1.0 ± 0.1	2.0 ± 0.1	4.0 ± 0.4	5.1 ± 0.9	6.6 ± 2.5	5.2 ± 1.8	<i>hisIE-F-A-H-B-D-G-Z</i>	histidinol dehydrogenase
<i>hisF</i>	1.3 ± 0.1	0.7 ± 0.1	2.3 ± 0.4	3.9 ± 1.0	2.4 ± 0.3	2.3 ± 0.4	<i>hisIE-F-A-H-B-D-G-Z</i>	cyclase-like protein
<i>hisG</i>	1.1 ± 0.2	1.7 ± 0.5	1.7 ± 0.4	4.2 ± 1.3	2.2 ± 0.7	2.3 ± 0.1	<i>hisIE-F-A-H-B-D-G-Z</i>	ATP phosphoribosyltransfe
<i>hisH</i>	1.1 ± 0.1	1.0 ± 0.1	3.3 ± 0.5	4.3 ± 0.7	2.7 ± 0.5	3.0 ± 0.4	<i>hisIE-F-A-H-B-D-G-Z</i>	amidotransferase
<i>ilvB</i>	0.9 ± 0.3	2.1 ± 1.1	1.7 ± 0.5	2.1 ± 0.7	4.8 ± 1.0	4.8 ± 0.8	<i>ilvB-H-C-leuA-B-C-D</i>	acetolactate synthase large subunit
<i>ilvC</i>	1.0 ± 0.2	1.4 ± 0.1	1.4 ± 0.3	1.3 ± 0.3	1.8 ± 0.3	2.9 ± 2.0	<i>ilvB-H-C-leuA-B-C-D</i>	ketol-acid reductoisomerase
<i>ilvH</i>	1.1 ± 0.3	3.5 ± 0.6	1.7 ± 0.5	1.9 ± 0.4	4.3 ± 0.8	3.5 ± 0.3	<i>ilvB-H-C-leuA-B-C-D</i>	acetolactate synthase small subunit
<i>serA</i>	1.1 ± 0.1	3.2 ± 0.7	2.7 ± 0.2	4.1 ± 1.0	4.2 ± 0.7	3.8 ± 0.9	<i>serA</i>	phosphoglycerate dehydrogenase
<i>ykrV</i>	1.1 ± 0.4	3.8 ± 0.9	5.5 ± 2.3	5.3 ± 0.4	5.1 ± 1.1	5.5 ± 0.9	<i>ykrV</i>	similar to aspartate aminotransferase
<i>yrhB</i>	1.2 ± 0.1	4.1 ± 0.5	5.0 ± 0.7	6.1 ± 1.1	4.5 ± 1.0	3.3 ± 0.1	<i>yrhB</i>	similar to cystathionine beta-lyase or gamma-lyase
<i>yrrN</i>	1.3 ± 0.3	2.6 ± 0.3	2.7 ± 0.5	2.5 ± 0.6	1.9 ± 0.6	2.0 ± 0.1	<i>yrrN-O</i>	similar to collagenase family protease
<i>yrrO</i>	1.0 ± 0.1	3.1 ± 0.6	4.0 ± 1.9	3.1 ± 0.3	3.1 ± 0.6	2.2 ± 1.2	<i>yrrN-O</i>	putative protease
Metabolism of nucleotides and nucleic acids								
<i>adk</i>	1.3 ± 0.3	11.1 ± 0.9	6.6 ± 1.3	7.5 ± 2.3	10.0 ± 0.7	9.6 ± 3.8	<i>rplR-secY-adk-map</i>	adenylate kinase
<i>guaA</i>	1.3 ± 0.2	7.7 ± 2.0	4.7 ± 1.5	5.1 ± 0.3	11.8 ± 0.1	11.1 ± 2.3	<i>guaA</i>	GMP synthetase
<i>nrdE</i>	1.5 ± 0.3	4.7 ± 0.8	3.1 ± 0.1	2.9 ± 0.1	9.0 ± 2.3	6.0 ± 1.0	<i>nrdE-nrdF</i>	ribonucleoside-diphosphate reductase (major subunit)
<i>nrdF</i>	1.5 ± 0.3	5.0 ± 0.4	3.9 ± 1.2	3.2 ± 0.1	4.8 ± 0.6	4.3 ± 1.1	<i>nrdE-nrdF</i>	ribonucleoside-diphosphate reductase (minor subunit)
<i>purA</i>	0.6 ± 0.1	1.8 ± 0.1	4.2 ± 1.3	3.1 ± 0.1	6.1 ± 1.4	5.3 ± 0.6	<i>purA</i>	adenylosuccinate synthetase
<i>purB</i>	0.8 ± 0.1	6.7 ± 2.7	8.3 ± 1.2	6.4 ± 0.1	8.0 ± 0.8	7.5 ± 0.2	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	adenylosuccinate lyase
<i>purC</i>	0.8 ± 0.1	9.5 ± 3.4	10.4 ± 4.2	15.6 ± 6.3	12.9 ± 0.6	10.0 ± 0.2	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole succinocarboxamide synthetase
<i>purD</i>	0.8 ± 0.1	6.8 ± 1.7	5.1 ± 0.6	19.4 ± 3.9	5.4 ± 1.3	5.3 ± 0.1	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylglycinamide synthetase
<i>purE</i>	0.8 ± 0.1	4.3 ± 0.5	3.9 ± 0.0	9.3 ± 2.5	2.9 ± 0.1	3.8 ± 0.1	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole carboxylase I
<i>purF</i>	0.9 ± 0.2	7.7 ± 1.7	6.6 ± 0.2	8.3 ± 0.1	9.6 ± 1.3	7.9 ± 4.5	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	glutamine phosphoribosylpyrophosphate amidotransferase
<i>purH</i>	1.0 ± 0.2	11.8 ± 5.3	8.0 ± 1.9	15.5 ± 1.7	10.3 ± 1.1	7.9 ± 1.5	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole carboxy formyl formyltransferase
<i>purK</i>	0.9 ± 0.1	7.1 ± 1.5	7.0 ± 3.5	14.3 ± 0.1	8.8 ± 2.4	7.6 ± 1.3	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole carboxylase II
<i>purL</i>	0.8 ± 0.2	8.0 ± 1.8	5.6 ± 1.5	16.0 ± 0.9	7.8 ± 1.3	6.3 ± 1.1	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylformylglycinamidine synthetase II
<i>purM</i>	0.8 ± 0.2	5.6 ± 1.0	4.0 ± 0.5	12.1 ± 3.0	4.7 ± 0.1	3.3 ± 0.4	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole synthetase

<i>purN</i>	1.1 ± 0.2	10.5 ± 2.4	10.6 ± 0.8	16.0 ± 0.9	10.6 ± 5.2	9.2 ± 0.2	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylglycinamide formyltransferase
<i>purQ</i>	0.9 ± 0.1	10.2 ± 4.3	8.7 ± 3.4	12.1 ± 1.5	10.5 ± 0.1	8.4 ± 2.8	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylformylglycinamidine synthetase I
<i>pyrAA</i>	0.5 ± 0.1	6.3 ± 3.0	5.7 ± 0.5	6.3 ± 0.1	5.1 ± 0.5	4.3 ± 0.1	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	carbamoyl-phosphate synthetase (glutaminase subunit)
<i>pyrAB</i>	0.6 ± 0.2	4.5 ± 0.7	4.3 ± 1.0	5.8 ± 0.7	3.5 ± 0.4	3.2 ± 0.2	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	carbamoyl-phosphate synthetase (catalytic subunit)
<i>pyrC</i>	0.5 ± 0.1	4.1 ± 0.6	3.4 ± 0.7	5.4 ± 0.9	3.0 ± 0.1	3.1 ± 0.1	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	dihydroorotate
<i>pyrD</i>	0.8 ± 0.2	5.7 ± 0.7	3.8 ± 0.1	5.6 ± 0.2	3.1 ± 0.1	3.4 ± 0.1	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	dihydroorotate dehydrogenase (catalytic subunit)
<i>pyrE</i>	0.7 ± 0.2	4.2 ± 0.8	6.1 ± 0.1	8.4 ± 1.0	4.1 ± 0.3	3.0 ± 0.3	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	orotate phosphoribosyltransferase
<i>pyrF</i>	0.8 ± 0.1	5.7 ± 1.9	7.7 ± 0.1	7.0 ± 1.0	5.2 ± 1.1	3.9 ± 0.1	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	orotidine 5'-phosphate decarboxylase
<i>pyrG</i>	1.1 ± 0.2	2.9 ± 0.1	3.3 ± 0.1	2.0 ± 0.1	1.1 ± 0.1	1.2 ± 0.1	<i>pyrG-rpoE</i>	CTP synthetase
<i>pyrH</i>	0.9 ± 0.1	8.2 ± 1.2	4.2 ± 0.8	3.5 ± 0.3	5.0 ± 0.1	5.0 ± 0.3	<i>pyrH-frr</i>	uridylate kinase
<i>pyrK</i>	0.6 ± 0.1	7.5 ± 2.9	6.1 ± 1.2	8.4 ± 3.8	4.5 ± 0.7	3.3 ± 0.1	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	dihydroorotate dehydrogenase (electron transfer subunit)
<i>pyrP</i>	0.6 ± 0.2	4.4 ± 1.6	3.5 ± 0.2	5.8 ± 0.7	1.8 ± 0.1	2.2 ± 0.1	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	uracil permease
Metabolism of lipids								
<i>cdsA</i>	1.0 ± 0.1	5.6 ± 1.2	3.1 ± 0.2	3.6 ± 1.2	7.8 ± 1.9	7.4 ± 0.3	<i>uppS-cdsA-dxr</i>	phosphatidate cytidylyltransferase
<i>fabD</i>	1.1 ± 0.2	6.2 ± 1.0	5.1 ± 1.3	4.3 ± 0.9	7.4 ± 0.9	5.9 ± 0.8	<i>plsX-fabD-fabG</i>	strong similarity to malonyl CoA-acyl carrier protein transacylase
<i>fabG</i>	1.0 ± 0.1	4.6 ± 1.1	2.7 ± 0.3	4.1 ± 1.5	5.3 ± 0.6	3.0 ± 1.5	<i>plsX-fabD-fabG</i>	strong similarity to beta-ketoacyl-acyl carrier protein reductase
<i>fabI</i>	1.1 ± 0.2	1.8 ± 0.5	1.3 ± 0.2	1.4 ± 1.0	1.4 ± 0.7	1.3 ± 0.5	<i>yjbV-fabI-yjbX</i>	enoyl-[acyl-carrier-protein] reductase
<i>fabL</i>	0.8 ± 0.2	4.0 ± 0.5	2.3 ± 1.9	2.9 ± 0.5	4.2 ± 1.0	3.5 ± 1.0	<i>fabL</i>	weak similarity to 3-oxoacyl-[acyl-carrier-protein] reductase
<i>yqiD</i>	1.1 ± 0.1	1.8 ± 0.4	2.3 ± 0.8	1.7 ± 0.3	3.6 ± 0.6	3.2 ± 0.9	<i>yqiD</i>	similar to geranyltransterase
Metabolism of coenzymes and prosthetic groups								
<i>bioA</i>	1.1 ± 0.4	3.5 ± 0.8	4.4 ± 0.5	3.6 ± 0.1	4.1 ± 0.6	4.5 ± 2.0	<i>bioA-F-D-B-I</i>	adenosylmethionine-8-amino-7-oxononanoate aminotransferase
<i>bioB</i>	1.1 ± 0.2	4.6 ± 0.1	3.4 ± 0.6	5.6 ± 0.1	7.4 ± 1.3	6.6 ± 3.3	<i>bioA-F-D-B-I</i>	biotin synthetase
<i>bioD</i>	1.1 ± 0.2	5.6 ± 0.4	5.1 ± 2.1	6.0 ± 0.4	18.2 ± 2.9	33.3 ± 16.0	<i>bioA-F-D-B-I</i>	dethiobiotin synthetase
<i>bioF</i>	1.2 ± 0.3	5.7 ± 0.1	5.3 ± 0.1	7.8 ± 4.5	11.1 ± 2.9	29.8 ± 18.3	<i>bioA-F-D-B-I</i>	8-amino-7-oxononanoate sythase
<i>biol</i>	1.1 ± 0.1	4.1 ± 1.1	4.6 ± 0.1	3.9 ± 0.2	8.7 ± 3.5	8.3 ± 0.9	<i>bioA-F-D-B-I</i>	cytochrome P450 enzyme
<i>nadA</i>	1.2 ± 0.3	8.4 ± 0.4	10.5 ± 2.6	10.8 ± 3.5	4.8 ± 2.2	7.4 ± 1.3	<i>nadB-C-A</i>	quinolinate synthetase

<i>nadB</i>	1.2 ± 0.1	6.7 ± 0.4	7.0 ± 1.8	9.4 ± 2.4	4.7 ± 1.0	4.2 ± 0.3	<i>nadB-C-A</i>	L-aspartate oxidase
<i>nadC</i>	1.2 ± 0.3	7.7 ± 0.5	11.5 ± 1.4	9.8 ± 1.8	6.0 ± 2.8	8.1 ± 0.1	<i>nadB-C-A</i>	nicotinate-nucleotide pyrophosphorylase
<i>menH</i>	1.2 ± 0.4	2.3 ± 0.6	2.0 ± 0.4	1.5 ± 0.3	4.0 ± 0.4	5.0 ± 2.3	<i>menH</i>	menaquinone biosynthesis methyltransferase
<i>nifS</i>	1.0 ± 0.2	7.1 ± 1.7	6.5 ± 0.9	6.2 ± 2.4	5.5 ± 1.4	5.1 ± 1.2	<i>nifS</i>	required for NAD biosynthesis
<i>thiF</i>	0.9 ± 0.1	2.0 ± 0.3	1.8 ± 0.2	1.6 ± 0.3	4.3 ± 0.9	8.3 ± 1.2	<i>thiG-F</i>	hydroxyethylthiazole phosphate biosynthesis
<i>thiG</i>	1.3 ± 0.2	1.4 ± 0.1	1.5 ± 0.3	1.8 ± 0.7	2.1 ± 0.7	4.0 ± 0.5	<i>thiG-F</i>	thiazole biosynthesis protein
DNA replication								
<i>ssb</i>	1.1 ± 0.1	9.3 ± 0.9	5.3 ± 0.1	6.0 ± 1.2	15.1 ± 6.1	11.4 ± 0.1	<i>ssb</i>	single-strand DNA-binding protein
Protein modification								
<i>map</i>	1.2 ± 0.1	9.3 ± 2.6	10.3 ± 5.0	6.3 ± 1.6	12.9 ± 1.8	13.3 ± 2.6	<i>rplR-secY-adk-map</i>	methionine aminopeptidase
<i>yqeT</i>	0.9 ± 0.2	4.0 ± 0.3	2.2 ± 0.6	2.5 ± 0.3	4.4 ± 0.8	3.4 ± 1.1	<i>yqe operon</i>	probable methyltransferase
<i>yqhT</i>	1.0 ± 0.1	1.8 ± 0.4	1.6 ± 0.2	1.7 ± 0.2	3.2 ± 0.3	3.4 ± 0.5	<i>yqhT-V</i>	putative peptidase
Translation initiation								
<i>ykrS</i>	1.1 ± 0.1	6.3 ± 1.1	6.3 ± 2.0	6.0 ± 1.7	5.8 ± 0.5	5.0 ± 0.1	<i>ykr operon</i>	similar to initiation factor eIF-2B (alpha subunit)
Translation elongation								
<i>tsf</i>	1.0 ± 0.1	8.2 ± 2.7	4.7 ± 1.5	3.8 ± 0.1	8.2 ± 1.8	7.7 ± 0.1	<i>tsf</i>	elongation factor Ts
<i>lepA</i>	1.0 ± 0.1	3.0 ± 0.4	3.1 ± 0.3	2.9 ± 0.7	5.7 ± 2.0	2.7 ± 0.6	<i>lepA</i>	GTP-binding protein
<i>ylaG</i>	1.2 ± 0.2	2.7 ± 0.6	2.6 ± 0.1	2.6 ± 0.8	3.8 ± 0.1	3.2 ± 0.4	<i>yla operon</i>	similar to GTP-binding elongation factor
Translation termination								
<i>frr</i>	1.2 ± 0.1	5.6 ± 1.7	3.4 ± 0.2	2.9 ± 0.5	4.3 ± 0.7	3.8 ± 0.5	<i>pyrH-frr</i>	ribosome recycling factor
Ribosomal proteins								
<i>rplA</i>	1.2 ± 0.1	8.2 ± 0.2	4.9 ± 0.3	4.2 ± 0.1	10.0 ± 2.4	10.6 ± 0.8	<i>rpl operon</i>	ribosomal protein L1 (BL1)
<i>rplB</i>	1.1 ± 0.2	12.1 ± 3.0	7.3 ± 2.0	6.8 ± 1.3	12.3 ± 0.8	12.9 ± 0.1	<i>rpl operon</i>	ribosomal protein L2 (BL2)
<i>rplC</i>	1.1 ± 0.1	8.9 ± 0.3	5.5 ± 0.7	4.7 ± 0.8	6.8 ± 1.5	6.7 ± 0.1	<i>rpl operon</i>	ribosomal protein L3 (BL3)
<i>rplD</i>	1.2 ± 0.3	13.4 ± 1.3	8.9 ± 0.3	6.1 ± 1.4	10.9 ± 4.1	13.7 ± 1.6	<i>rpl operon</i>	ribosomal protein L4
<i>rplE</i>	1.3 ± 0.2	16.0 ± 0.9	13.2 ± 3.0	7.5 ± 1.7	13.9 ± 3.0	20.0 ± 0.1	<i>rpl operon</i>	ribosomal protein L5 (BL6)
<i>rplF</i>	1.0 ± 0.1	9.3 ± 0.3	7.7 ± 0.1	6.2 ± 1.3	7.0 ± 4.6	10.9 ± 2.3	<i>rpl operon</i>	ribosomal protein L6 (BL8)
<i>rplJ</i>	1.3 ± 0.1	25.0 ± 11.8	21.4 ± 10.1	10.4 ± 2.9	31.8 ± 11.6	54.1 ± 31.0	<i>rpl operon</i>	ribosomal protein L10 (BL5)
<i>rplK</i>	1.3 ± 0.1	5.6 ± 1.0	3.9 ± 0.2	5.7 ± 0.1	6.3 ± 1.5	2.4 ± 1.2	<i>rpl operon</i>	ribosomal protein L11 (BL11)
<i>rplL</i>	1.3 ± 0.2	17.7 ± 3.3	8.9 ± 0.8	8.9 ± 0.3	15.4 ± 0.1	12.6 ± 2.9	<i>rpl operon</i>	ribosomal protein L12 (BL9)
<i>rplM</i>	1.2 ± 0.0	4.2 ± 0.7	4.4 ± 0.3	3.8 ± 0.4	4.7 ± 0.8	6.3 ± 0.2	<i>rpl operon</i>	ribosomal protein L13
<i>rplN</i>	0.9 ± 0.3	16.7 ± 0.1	11.8 ± 0.1	7.7 ± 0.1	14.2 ± 1.2	1.9 ± 0.1	<i>rpl operon</i>	ribosomal protein L14
<i>rplO</i>	1.1 ± 0.1	8.0 ± 4.4	7.1 ± 0.0	8.0 ± 5.3	6.5 ± 1.3	12.7 ± 7.7	<i>rpl operon</i>	ribosomal protein L15

<i>rplP</i>	1.0 ± 0.9	13.3 ± 0.0	10.0 ± 2.4	6.3 ± 1.9	12.5 ± 1.1	13.5 ± 0.2	<i>rpl operon</i>	ribosomal protein L16
<i>rplQ</i>	1.1 ± 0.2	4.6 ± 1.2	6.7 ± 0.3	4.2 ± 0.8	6.0 ± 1.6	7.3 ± 0.9	<i>rpl operon</i>	ribosomal protein L17 (BL15)
<i>rplR</i>	1.3 ± 0.2	14.4 ± 5.4	6.9 ± 0.3	5.7 ± 0.5	8.8 ± 3.7	11.8 ± 0.1	<i>rpl operon</i>	ribosomal protein L18
<i>rplT</i>	1.2 ± 0.1	6.2 ± 0.4	5.1 ± 0.2	5.0 ± 0.9	8.7 ± 0.5	12.1 ± 0.1	<i>rpl operon</i>	ribosomal protein L20
<i>rplV</i>	1.0 ± 0.2	7.9 ± 1.1	5.8 ± 2.6	5.5 ± 1.3	6.8 ± 0.7	6.0 ± 2.4	<i>rpl operon</i>	ribosomal protein L22 (BL17)
<i>rpoA</i>	1.3 ± 0.1	1.3 ± 0.1	6.3 ± 0.3	5.0 ± 0.4	8.1 ± 1.3	13.8 ± 0.9	<i>rpoA</i>	RNA polymerase (alpha subunit)
<i>rpoB</i>	1.3 ± 0.2	4.1 ± 0.4	3.0 ± 0.1	3.2 ± 0.1	4.7 ± 0.1	5.1 ± 1.4	<i>rpoB-C</i>	RNA polymerase (beta subunit)
<i>rpoC</i>	1.3 ± 0.2	4.8 ± 0.3	3.0 ± 0.1	3.4 ± 0.1	6.5 ± 0.3	5.3 ± 0.1	<i>rpoB-C</i>	RNA polymerase (beta' subunit)
<i>rpsB</i>	1.1 ± 0.2	10.6 ± 0.8	5.3 ± 0.1	5.1 ± 1.6	8.7 ± 0.1	6.3 ± 0.1	<i>rps operon</i>	ribosomal protein S2
<i>rpsC</i>	1.3 ± 0.1	5.4 ± 0.1	3.6 ± 0.1	5.1 ± 1.6	5.7 ± 0.2	3.6 ± 1.4	<i>rps operon</i>	ribosomal protein S3 (BS3)
<i>rpsE</i>	1.2 ± 0.3	10.6 ± 0.8	8.5 ± 2.2	7.0 ± 1.9	8.2 ± 2.5	11.7 ± 2.1	<i>rps operon</i>	ribosomal protein S5
<i>rpsG</i>	1.1 ± 0.1	5.6 ± 1.3	4.1 ± 0.1	3.3 ± 0.1	5.4 ± 1.0	5.8 ± 2.2	<i>rps operon</i>	ribosomal protein S7 (BS7)
<i>rpsI</i>	1.1 ± 0.1	4.1 ± 0.4	4.4 ± 1.3	3.8 ± 0.4	4.9 ± 0.3	5.1 ± 0.6	<i>rps operon</i>	ribosomal protein S9
<i>rpsK</i>	1.0 ± 0.2	9.3 ± 2.6	8.7 ± 0.1	5.8 ± 0.9	10.4 ± 4.1	12.1 ± 3.0	<i>rps operon</i>	ribosomal protein S11 (BS11)
<i>rpsL</i>	1.2 ± 0.2	6.3 ± 2.8	3.8 ± 0.1	3.5 ± 0.7	5.0 ± 0.4	4.1 ± 1.5	<i>rps operon</i>	ribosomal protein S12 (BS12)
<i>rpsM</i>	1.2 ± 0.2	8.7 ± 0.1	8.6 ± 2.0	5.8 ± 0.1	13.4 ± 1.3	13.3 ± 2.7	<i>rps operon</i>	ribosomal protein S13
Aminoacyl-tRNA synthetases								
<i>asnS</i>	1.0 ± 0.1	3.3 ± 0.1	2.1 ± 0.1	1.9 ± 0.1	9.5 ± 0.5	7.8 ± 0.1	<i>asnS</i>	asparaginyl-tRNA synthetase
<i>gatA</i>	1.2 ± 0.1	3.2 ± 0.7	2.6 ± 1.0	2.4 ± 0.4	4.7 ± 0.7	5.2 ± 1.8	<i>gatC-A-B</i>	glutamyl-tRNA(Gln) amidotransferase subunit A
<i>gatB</i>	1.2 ± 0.2	2.9 ± 0.6	2.3 ± 0.7	2.1 ± 0.4	3.9 ± 1.1	2.7 ± 0.4	<i>gatC-A-B</i>	glutamyl-tRNA(Gln) amidotransferase subunit B
<i>gatC</i>	1.2 ± 0.1	2.9 ± 1.0	2.6 ± 0.4	2.2 ± 0.3	4.2 ± 1.3	3.8 ± 0.4	<i>gatC-A-B</i>	glutamyl-tRNA(Gln) amidotransferase subunit C
<i>hisS</i>	1.0 ± 0.1	2.4 ± 0.4	1.8 ± 0.3	2.6 ± 0.4	4.2 ± 1.1	3.8 ± 0.5	<i>hisS</i>	histidyl-tRNA synthetase
<i>hisZ</i>	1.0 ± 0.2	1.9 ± 0.2	3.8 ± 0.5	4.0 ± 0.1	3.4 ± 0.4	4.0 ± 0.2	<i>hisIE-F-A-H-B-D-G-Z</i>	histidyl-tRNA synthetase
Unknown function								
<i>BLi00156</i>	1.0 ± 0.2	8.9 ± 0.8	7.9 ± 1.4	6.2 ± 0.3	12.4 ± 3.9	9.1 ± 2.2		conserved hypothetical
<i>BLi01945</i>	1.2 ± 0.1	1.2 ± 0.2	1.3 ± 0.4	1.5 ± 0.3	3.7 ± 0.9	4.1 ± 0.6		hypothetical
<i>BLi00764</i>	1.2 ± 0.2	3.7 ± 0.8	3.8 ± 0.6	1.5 ± 1.2	4.5 ± 2.0	3.4 ± 0.7		hypothetical
<i>BLi03803</i>	1.1 ± 0.5	3.4 ± 0.5	3.3 ± 0.8	1.5 ± 0.5	4.6 ± 1.2	3.2 ± 0.2		putative NDP-sugar epimerase (EC 5.1.3.2)
<i>BLi00763</i>	1.1 ± 0.2	2.8 ± 0.6	1.9 ± 0.5	3.0 ± 0.1	3.6 ± 1.2	2.8 ± 0.6		putative oxidoreductase
<i>BLi01778</i>	1.0 ± 0.2	3.5 ± 0.5	3.2 ± 0.2	5.0 ± 0.9	3.5 ± 0.7	2.9 ± 0.8		putative phosphoadenosine phosphosulfate reductase
<i>BLi04205</i>	1.0 ± 0.4	4.1 ± 1.0	3.4 ± 0.7	3.7 ± 0.4	3.0 ± 0.6	3.2 ± 0.2		putative transcriptional regulator

<i>ybxB</i>	0.9 ± 0.2	5.8 ± 0.6	3.6 ± 0.6	4.9 ± 1.2	5.2 ± 0.8	4.6 ± 0.7	<i>ybxB</i>	unknown
<i>ycdA</i>	1.2 ± 0.5	5.7 ± 1.0	4.0 ± 0.4	3.1 ± 0.4	3.9 ± 0.4	2.5 ± 0.6	<i>ycdA</i>	unknown
<i>yerB</i>	0.8 ± 0.1	1.1 ± 0.1	1.2 ± 0.1	1.2 ± 0.1	3.6 ± 0.4	3.9 ± 0.7	<i>yerB</i>	unknown
<i>ygaE</i>	1.1 ± 0.1	3.1 ± 0.1	3.2 ± 0.1	1.6 ± 0.3	3.7 ± 0.5	2.4 ± 0.6	<i>ygaE</i>	unknown
<i>yitJ</i>	1.1 ± 0.0	2.9 ± 0.5	3.9 ± 0.2	4.8 ± 0.3	4.0 ± 1.6	4.1 ± 0.6	<i>yit operon</i>	unknown
<i>yjbL</i>	1.1 ± 0.1	2.3 ± 0.1	2.6 ± 0.3	2.3 ± 0.3	3.7 ± 1.4	4.2 ± 1.2	<i>yjb operon</i>	unknown
<i>yjlC</i>	1.1 ± 0.2	5.3 ± 1.4	3.1 ± 1.0	3.4 ± 0.5	7.2 ± 2.4	3.1 ± 1.2	<i>yjl operon</i>	unknown
<i>ykoC</i>	1.1 ± 0.1	4.7 ± 1.4	4.8 ± 0.7	5.8 ± 1.3	4.1 ± 0.6	4.1 ± 0.9	<i>yko operon</i>	unknown
<i>ykoE</i>	1.2 ± 0.3	4.4 ± 1.3	3.6 ± 0.4	5.4 ± 1.4	3.9 ± 0.9	3.3 ± 1.2	<i>yko operon</i>	unknown
<i>ykqC</i>	1.0 ± 0.1	1.6 ± 0.4	1.4 ± 0.1	1.3 ± 0.4	3.9 ± 0.7	3.6 ± 1.2	<i>YkqC</i>	unknown
<i>ykrT</i>	0.9 ± 0.3	5.6 ± 0.6	5.8 ± 1.2	6.9 ± 1.9	4.2 ± 0.8	2.5 ± 1.1	<i>ykr operon</i>	unknown
<i>ykrY</i>	0.9 ± 0.6	4.2 ± 1.5	5.3 ± 2.2	8.3 ± 1.6	6.1 ± 2.6	6.0 ± 1.3	<i>ykr operon</i>	unknown
<i>ykrZ</i>	0.9 ± 0.2	4.7 ± 0.7	6.3 ± 1.0	6.6 ± 1.9	6.1 ± 2.3	6.0 ± 0.9	<i>ykr operon</i>	unknown
<i>ykyA</i>	0.8 ± 0.2	1.5 ± 0.3	2.3 ± 0.7	2.1 ± 0.7	3.1 ± 0.6	2.2 ± 0.1	<i>ykyA</i>	unknown
<i>yloN</i>	1.2 ± 0.1	2.3 ± 0.2	2.3 ± 0.7	1.6 ± 0.3	3.7 ± 0.2	2.9 ± 0.3	<i>ylo operon</i>	unknown
<i>yloQ</i>	1.1 ± 0.0	3.3 ± 0.3	3.1 ± 1.2	1.8 ± 0.3	3.4 ± 0.5	2.7 ± 1.0	<i>ylo operon</i>	unknown
<i>ylpC</i>	1.3 ± 0.2	3.9 ± 0.8	3.2 ± 1.3	2.9 ± 0.4	3.9 ± 0.9	3.4 ± 0.9	<i>YlpC</i>	unknown
<i>ylxF</i>	1.1 ± 0.1	3.6 ± 0.6	3.1 ± 0.8	4.1 ± 0.1	10.1 ± 3.6	7.1 ± 4.7	<i>cotY-flgB-C-fliE-F-G-H-I-J-ylxF-fliK-</i> <i>flgD-E-fliL-M-Y-cheY-fliZ-P-Q-R-</i> <i>flhB-A-F-ylxH</i>	unknown
<i>ylxS</i>	1.1 ± 0.2	2.9 ± 0.3	3.1 ± 0.8	3.1 ± 0.3	4.8 ± 0.7	2.8 ± 0.5	<i>ylx operon</i>	unknown
<i>yoaZ</i>	1.1 ± 0.2	3.7 ± 1.0	2.9 ± 0.6	3.3 ± 0.1	4.2 ± 1.0	3.5 ± 0.9	<i>yoa operon</i>	unknown
<i>ytnM</i>	1.1 ± 0.2	3.4 ± 1.2	2.8 ± 0.7	3.7 ± 0.5	2.6 ± 0.6	2.7 ± 0.6	<i>ytnM</i>	unknown
<i>ytpQ</i>	0.9 ± 0.1	2.1 ± 0.3	2.2 ± 0.2	2.1 ± 0.1	3.5 ± 0.8	3.3 ± 0.9	<i>ytpQ</i>	unknown
<i>yuil</i>	0.9 ± 0.2	7.5 ± 2.4	6.3 ± 0.2	8.3 ± 2.7	9.3 ± 3.0	5.4 ± 0.8	<i>yui operon</i>	unknown
<i>yukC</i>	1.0 ± 0.3	3.3 ± 0.4	2.5 ± 0.6	2.2 ± 0.4	4.5 ± 1.6	3.0 ± 1.1	<i>yuk operon</i>	unknown
<i>yunG</i>	1.2 ± 0.1	3.7 ± 0.8	2.6 ± 0.9	2.9 ± 0.8	3.8 ± 1.1	3.1 ± 0.7	<i>yunG</i>	unknown
<i>yusA</i>	1.1 ± 0.1	5.5 ± 0.9	3.8 ± 0.1	5.3 ± 0.1	5.0 ± 1.5	3.7 ± 0.5	<i>yus operon</i>	unknown
<i>yusB</i>	2.9 ± 0.1	4.8 ± 1.5	5.6 ± 0.1	11.1 ± 2.6	5.5 ± 1.0	6.7 ± 1.9	<i>yus operon</i>	unknown
<i>yvbl</i>	1.3 ± 0.1	3.6 ± 1.0	3.4 ± 0.1	3.6 ± 0.4	4.5 ± 1.4	4.2 ± 1.0	<i>yvb operon</i>	unknown
<i>yvsG</i>	0.8 ± 0.2	2.8 ± 0.8	2.0 ± 0.8	2.3 ± 0.3	3.4 ± 0.6	3.5 ± 1.5	<i>yvs operon</i>	unknown
<i>ywkF</i>	0.9 ± 0.1	3.2 ± 0.5	3.3 ± 1.2	4.0 ± 0.9	3.4 ± 1.0	2.0 ± 0.6	<i>ywk operon</i>	unknown
<i>yxjG</i>	1.1 ± 0.1	5.5 ± 0.4	5.6 ± 1.2	7.0 ± 0.9	3.6 ± 0.7	4.2 ± 1.2	<i>yxj operon</i>	unknown

Table 2: Kinetic of the glucose starvation inducible genes of *B. licheniformis*. Listed are such genes, the mRNA level of which showed a more than threefold induction during at least one sampling point throughout the growth curve. Genes the expression of which is also induced under nitrogen starvation conditions are labelled with “*”. Trans. ph. = transient phase, SD = standard deviation

Gene name	Trans. ph.	SD	10min	SD	20min	SD	30min	SD	60min	SD	120min	SD	Transcriptional organisation	Function
Cell wall														
<i>dltE</i>	0.8 ± 0.1		1.5 ± 0.1		1.2 ± 0.1		5.3 ± 0.3		5.2 ± 1.1		5.2 ± 0.8		<i>dltE</i>	involved in lipoteichoic acid biosynthesis
<i>BLi00494</i>	1.0 ± 0.1		7.8 ± 0.1		10.8 ± 2.2		36.3 ± 8.8		28.5 ± 14.1		21.7 ± 4.7			putative membrane protein
Transport/binding proteins and lipoproteins														
<i>bglP</i>	1.5 ± 0.1		6.0 ± 1.6		2.6 ± 0.1		4.5 ± 1.5		6.3 ± 1.1		6.4 ± 0.6		<i>bglP-H</i>	PTS beta-glucoside-specific enzyme IIIBCA component
<i>cydC*</i>	1.5 ± 0.1		4.5 ± 1.1		4.9 ± 0.1		4.8 ± 0.7		4.1 ± 1.2		4.3 ± 0.8		<i>cydA-B-C-D</i>	ABC transporter
<i>cydD*</i>	1.0 ± 0.1		3.0 ± 0.1		3.3 ± 0.2		3.4 ± 0.5		4.2 ± 0.9		4.0 ± 0.2		<i>cydA-B-C-D</i>	ABC transporter
<i>dctB</i>	1.2 ± 0.1		2.7 ± 0.2		3.8 ± 0.1		4.0 ± 0.1		4.7 ± 1.3		4.7 ± 0.5		<i>dctB</i>	possible C4-dicarboxylate binding protein
<i>dppA</i>	1.1 ± 0.1		1.7 ± 0.1		2.1 ± 0.1		4.1 ± 4.2		2.4 ± 0.1		1.6 ± 0.1		<i>dppA-B-C-D-E</i>	dipeptide ABC transporter
<i>dppB*</i>	1.0 ± 0.1		1.4 ± 0.2		1.9 ± 0.1		3.4 ± 0.1		1.5 ± 0.1		1.1 ± 0.1		<i>dppA-B-C-D-E</i>	dipeptide ABC transporter
<i>dppC*</i>	1.0 ± 0.1		2.0 ± 0.1		3.3 ± 0.1		3.8 ± 0.4		2.8 ± 0.1		2.0 ± 0.1		<i>dppA-B-C-D-E</i>	dipeptide ABC transporter
<i>dppD*</i>	0.9 ± 0.1		1.7 ± 0.1		4.3 ± 0.7		3.7 ± 0.3		4.0 ± 0.2		2.1 ± 0.1		<i>dppA-B-C-D-E</i>	dipeptide ABC transporter
<i>exuT</i>	0.9 ± 0.1		4.4 ± 0.1		2.0 ± 0.1		4.0 ± 0.1		3.4 ± 0.1		3.0 ± 0.1		<i>exuT</i>	hexuronate transporter
<i>fruA</i>	1.1 ± 0.2		2.9 ± 0.1		2.8 ± 0.1		2.3 ± 0.1		4.1 ± 0.2		3.8 ± 0.1		<i>fruA-K-R</i>	close homolog to FruA: PTS fructose-specific enzyme IIABC component
<i>fruA</i>	1.1 ± 0.2		6.1 ± 0.7		2.6 ± 0.1		2.8 ± 0.1		5.1 ± 1.3		6.2 ± 0.7		<i>fruA-K-R</i>	PTS fructose-specific enzyme IIABC component
<i>levE</i>	1.7 ± 0.2		5.4 ± 0.4		3.7 ± 0.1		3.1 ± 0.1		3.2 ± 0.1		1.1 ± 0.1		<i>levR-D-E-F-G</i>	PTS fructose-specific enzyme IIB component
<i>levG</i>	1.3 ± 0.1		4.6 ± 0.6		2.6 ± 0.1		3.3 ± 0.1		3.2 ± 0.1		2.5 ± 0.3		<i>levR-D-E-F-G</i>	PTS fructose-specific enzyme IID component
<i>levR</i>	1.9 ± 0.1		1.6 ± 0.1		1.2 ± 0.1		1.5 ± 0.2		2.6 ± 0.6		3.2 ± 0.1		<i>levR-D-E-F-G</i>	transcriptional activator
<i>licA</i>	1.0 ± 0.1		12.1 ± 0.3		8.6 ± 1.1		6.2 ± 0.2		3.3 ± 0.1		3.6 ± 0.4		<i>licA</i>	PTS lichenan-specific enzyme IIA component
<i>licC</i>	1.1 ± 0.1		8.1 ± 0.4		7.2 ± 0.3		6.2 ± 1.6		3.3 ± 0.2		3.5 ± 0.6		<i>licH-C-R</i>	PTS lichenan-specific enzyme IIC component
<i>licR</i>	1.1 ± 0.2		5.3 ± 0.2		4.4 ± 0.2		3.4 ± 0.2		3.1 ± 0.2		3.3 ± 0.1		<i>licH-C-R</i>	transcriptional activator
<i>lpIC</i>	1.0 ± 0.2		4.4 ± 0.1		2.5 ± 0.1		4.3 ± 0.3		3.4 ± 0.1		2.3 ± 0.1		<i>lpI A-B-C</i>	transmembrane lipoprotein
<i>manP</i>	1.1 ± 0.1		6.1 ± 0.2		4.3 ± 0.1		6.0 ± 0.3		5.3 ± 0.8		4.2 ± 0.1		<i>manA-P-R</i>	phosphotransferase system (PTS) mannose-specific enzyme IIIBCA component
<i>msmE</i>	1.1 ± 0.1		2.4 ± 0.1		2.6 ± 0.1		3.0 ± 0.1		4.2 ± 1.0		4.2 ± 0.1		<i>msmR-E-amyD-C-melA</i>	multiple sugar-binding protein
<i>amyC</i>	1.1 ± 0.2		2.3 ± 0.3		2.6 ± 0.1		2.4 ± 0.1		3.4 ± 0.1		2.9 ± 0.1		<i>msmR-E-amyD-C-melA</i>	maltose transport protein
<i>amyD</i>	1.1 ± 0.1		2.7 ± 0.1		3.3 ± 0.4		4.7 ± 1.4		3.8 ± 0.2		3.1 ± 0.1		<i>msmR-E-amyD-C-melA</i>	sugar transport

<i>rbsA</i>	0.9 ± 0.1	1.7 ± 0.1	1.8 ± 0.1	3.2 ± 0.1	5.3 ± 0.5	4.3 ± 0.1	<i>rbs operon</i>	close homolog to RbsA: ribose ABC transporter
<i>ycgO*</i>	1.1 ± 0.1	3.9 ± 0.5	4.5 ± 0.3	4.2 ± 1.3	12.5 ± 2.7	3.3 ± 0.1	<i>ycg operon</i>	similar to proline permease
<i>yesO</i>	1.0 ± 0.1	2.5 ± 0.1	1.7 ± 0.1	2.3 ± 0.1	4.9 ± 1.8	4.4 ± 1.9	<i>yes operon</i>	similar to sugar-binding protein
<i>yvdG</i>	1.2 ± 0.1	6.1 ± 0.1	16.1 ± 0.2	41.2 ± 11.8	41.5 ± 16.3	28.2 ± 6.3	<i>yvd operon</i>	maltose/maltodextrin-binding protein
<i>yvdH*</i>	1.1 ± 0.1	3.4 ± 0.2	4.1 ± 1.0	6.8 ± 0.9	11.1 ± 1.1	10.4 ± 0.5	<i>yvd operon</i>	similar to maltodextrin transport system permease
<i>yvdl</i>	1.4 ± 0.3	5.9 ± 1.2	12.1 ± 2.6	27.7 ± 5.2	50.6 ± 4.9	27.1 ± 4.3	<i>yvd operon</i>	similar to maltodextrin transport system permease
<i>yvfH</i>	1.3 ± 0.1	4.0 ± 1.0	3.7 ± 0.1	3.6 ± 0.1	4.9 ± 1.6	5.0 ± 0.1	<i>yvf operon</i>	similar to L-lactate permease
<i>yvfK</i>	1.2 ± 0.1	9.6 ± 0.1	6.3 ± 1.2	4.7 ± 0.1	6.6 ± 1.7	7.3 ± 0.2	<i>yvf operon</i>	similar to maltose/maltodextrin-binding protein
<i>yvfl</i>	1.2 ± 0.3	4.5 ± 0.1	2.0 ± 0.1	3.2 ± 0.2	2.5 ± 0.1	2.1 ± 0.1	<i>yvf operon</i>	similar to maltodextrin transport system permease
<i>yvfm</i>	1.1 ± 0.1	3.6 ± 0.1	2.8 ± 0.1	3.8 ± 0.1	2.6 ± 0.1	2.6 ± 0.1	<i>yvf operon</i>	similar to maltodextrin transport system permease
<i>BLi04097</i>	1.1 ± 0.1	3.7 ± 0.2	4.4 ± 0.1	3.3 ± 0.3	3.2 ± 0.1	3.6 ± 0.5		putative chromate transport protein
<i>BLi03990*</i>	1.3 ± 0.1	8.3 ± 1.4	18.2 ± 3.5	35.3 ± 1.2	13.8 ± 2.2	12.5 ± 1.4		putative benzoate transport protein
<i>BLi02118</i>	1.0 ± 0.1	3.5 ± 0.1	3.4 ± 0.2	4.6 ± 0.1	6.3 ± 1.4	5.3 ± 0.4		putative C4-dicarboxylate transport protein
<i>BLi04117</i>	1.2 ± 0.2	4.3 ± 0.2	4.7 ± 1.6	4.2 ± 0.1	6.2 ± 0.7	13.8 ± 2.7		putative ABC transporter ATP-binding protein
<i>BLi04125</i>	0.9 ± 0.2	3.2 ± 0.1	3.5 ± 0.1	4.2 ± 0.8	7.8 ± 1.3	6.7 ± 0.7		putative ABC-transporter
<i>BLi03551</i>	1.6 ± 0.1	2.4 ± 0.2	2.1 ± 0.1	2.5 ± 0.1	8.5 ± 3.0	9.7 ± 0.7		putative phosphotransferase system enzyme II
<i>BLi03917</i>	1.0 ± 0.1	4.2 ± 1.6	3.2 ± 0.1	4.4 ± 0.2	5.2 ± 0.6	5.2 ± 2.1		putative oxalateformate antiporter
<i>BLi01465*</i>	1.0 ± 0.2	3.6 ± 0.1	3.9 ± 0.9	6.6 ± 1.3	4.3 ± 0.1	3.7 ± 0.2		putative portal protein
Signal transduction								
<i>ycbA</i>	1.0 ± 0.1	1.1 ± 0.1	1.4 ± 0.1	2.7 ± 0.1	4.2 ± 0.3	3.4 ± 0.1	<i>ycb operon</i>	similar to two-component sensor histidine kinase
<i>ycbL</i>	1.0 ± 0.1	2.0 ± 0.1	1.8 ± 0.1	1.8 ± 0.2	2.9 ± 0.1	2.6 ± 0.1	<i>ycb operon</i>	similar to two-component sensor histidine kinase
<i>yesM</i>	0.8 ± 0.2	3.9 ± 0.9	2.4 ± 0.1	3.3 ± 0.1	3.0 ± 0.1	2.5 ± 0.1	<i>yes operon</i>	similar to two-component sensor histidine kinase
<i>yesN</i>	0.9 ± 0.2	3.2 ± 0.1	1.9 ± 0.1	3.4 ± 0.3	4.0 ± 0.6	3.2 ± 0.1	<i>yes operon</i>	similar to two-component sensor histidine kinase
Electron transport chain and ATP synthase								
<i>ctaB</i>	0.9 ± 0.1	3.2 ± 0.1	3.7 ± 0.3	3.2 ± 0.1	2.2 ± 0.1	1.9 ± 0.1	<i>ctaA-B-C-D-E-F-G</i>	cytochrome c aa3 oxidase(assembly factor)
<i>ctaC</i>	1.1 ± 0.2	5.8 ± 1.0	7.9 ± 0.3	7.6 ± 1.0	4.0 ± 0.3	3.4 ± 0.1	<i>ctaA-B-C-D-E-F-G</i>	cytochrome c aa3 oxidase(subunit II)
<i>ctaD</i>	1.0 ± 0.2	3.4 ± 0.1	4.9 ± 1.2	4.0 ± 0.1	3.2 ± 0.1	2.5 ± 0.1	<i>ctaA-B-C-D-E-F-G</i>	cytochrome c aa3 oxidase(subunit I)
<i>ctaE</i>	1.0 ± 0.1	3.6 ± 0.3	5.4 ± 0.6	6.2 ± 0.9	3.2 ± 0.1	2.6 ± 0.1	<i>ctaA-B-C-D-E-F-G</i>	cytochrome c aa3 oxidase(subunit III)
<i>ctaF</i>	1.0 ± 0.1	4.0 ± 0.1	2.9 ± 0.1	4.7 ± 0.8	1.9 ± 0.1	1.7 ± 0.1	<i>ctaA-B-C-D-E-F-G</i>	cytochrome c aa3 oxidase(subunit IV)
<i>ctaG</i>	1.0 ± 0.1	3.7 ± 0.1	5.6 ± 0.9	6.1 ± 2.2	3.3 ± 0.1	2.4 ± 0.1	<i>ctaA-B-C-D-E-F-G</i>	function unknown
<i>cydA*</i>	0.8 ± 0.1	5.9 ± 0.3	3.8 ± 0.4	3.5 ± 0.2	4.5 ± 0.4	2.9 ± 0.2	<i>cydA-B-C-D</i>	cytochrome bd ubiquinol oxidase (subunit I)
<i>cydB*</i>	1.1 ± 0.3	3.9 ± 0.1	3.6 ± 0.1	3.4 ± 0.1	3.9 ± 0.5	2.2 ± 0.1	<i>cydA-B-C-D</i>	cytochrome bd ubiquinol oxidase (subunit II)

<i>etfA</i>	1.0 ± 0.1	10.7 ± 0.9	10.3 ± 2.6	10.3 ± 1.0	42.5 ± 4.6	20.4 ± 1.8	<i>etfA-B</i>	electron transfer flavoprotein (alpha subunit)
<i>etfB</i>	0.8 ± 0.2	12.3 ± 2.7	10.3 ± 0.3	13.5 ± 1.2	44.2 ± 0.5	17.2 ± 1.5	<i>etfA-B</i>	electron transfer flavoprotein (beta subunit)
<i>narG</i>	1.1 ± 0.2	2.3 ± 0.1	2.2 ± 0.1	1.9 ± 0.1	4.7 ± 2.0	4.2 ± 1.3	<i>narG-H-I-J</i>	nitrate reductase (alpha subunit)
<i>narH</i>	1.4 ± 0.1	1.7 ± 0.3	1.9 ± 0.1	3.5 ± 0.1	4.1 ± 0.1	2.5 ± 0.1	<i>narG-H-I-J</i>	nitrate reductase (beta subunit)
<i>ndhF</i>	1.4 ± 0.2	1.2 ± 0.1	1.4 ± 0.2	3.8 ± 0.3	7.7 ± 1.5	6.1 ± 0.4	<i>ndhF</i>	NADH dehydrogenase (subunit)
<i>qcrA</i>	1.0 ± 0.1	4.4 ± 0.5	4.6 ± 0.6	5.2 ± 0.6	3.9 ± 0.2	3.4 ± 0.3	<i>qcrA-B-C</i>	menaquinol:cytochrome c oxidoreductase (iron-sulfur subunit)
<i>qcrB</i>	0.9 ± 0.1	5.1 ± 1.0	4.1 ± 0.5	6.4 ± 0.9	4.0 ± 0.4	2.4 ± 0.1	<i>qcrA-B-C</i>	menaquinol:cytochrome c oxidoreductase (cytochrome b subunit)
<i>qcrC</i>	1.0 ± 0.1	4.8 ± 0.2	4.7 ± 0.1	6.2 ± 0.7	3.5 ± 0.1	1.5 ± 0.1	<i>qcrA-B-C</i>	menaquinol:cytochrome c oxidoreductase (cytochrome b/c subunit)
<i>ywjF</i>	1.0 ± 0.1	14.6 ± 4.1	11.2 ± 1.5	9.7 ± 3.1	44.3 ± 2.2	20.1 ± 1.0	<i>ywjE-F</i>	similar to iron-sulphur-binding reductase
<i>BLi03918</i>	0.9 ± 0.1	11.2 ± 0.4	10.6 ± 2.2	3.8 ± 0.2	15.5 ± 2.6	15.7 ± 0.7		putative formate dehydrogenase alpha chain
Sporulation								
<i>sigF</i>	1.3 ± 0.2	3.3 ± 0.1	3.5 ± 0.1	3.3 ± 0.1	3.5 ± 0.1	1.6 ± 0.1	<i>dacF-spollAA-spollAB-sigF</i>	known RNA polymerase sigma factor
<i>spollAA*</i>	1.1 ± 0.1	3.5 ± 0.1	2.4 ± 0.1	3.4 ± 0.1	3.5 ± 0.1	1.7 ± 0.1	<i>dacF-spollAA-spollAB-sigF</i>	anti-sigma F factor antagonist
<i>spollAB*</i>	1.2 ± 0.1	5.3 ± 0.2	4.6 ± 1.3	5.1 ± 0.8	4.6 ± 1.1	4.3 ± 0.8	<i>dacF-spollAA-spollAB-sigF</i>	known anti-sigma F factor
<i>cotE</i>	1.0 ± 0.2	3.7 ± 0.1	3.8 ± 0.7	3.5 ± 0.1	2.3 ± 0.1	2.1 ± 0.1	<i>cotE</i>	spore coat protein (outer)
<i>kipI</i>	1.0 ± 0.1	2.1 ± 0.2	1.8 ± 0.1	2.0 ± 0.1	4.1 ± 0.3	4.1 ± 1.1	<i>kipI-A-R</i>	inhibitor of KinA
Germination								
<i>gerAB</i>	0.9 ± 0.1	3.6 ± 0.2	4.8 ± 1.7	4.9 ± 1.8	3.6 ± 0.1	3.4 ± 0.1	<i>gerAA-AB-AC</i>	germination response to L-alanine
Specific pathway								
<i>acoA</i>	1.1 ± 0.1	2.0 ± 0.2	6.7 ± 1.9	37.3 ± 6.6	88.8 ± 12.0	84.0 ± 15.6	<i>acoA-B-C-L-R</i>	acetoin dehydrogenase E1
<i>acoB</i>	1.2 ± 0.1	2.3 ± 0.3	6.6 ± 0.9	47.1 ± 24.6	104.0 ± 39.1	88.5 ± 16.3	<i>acoA-B-C-L-R</i>	acetoin dehydrogenase E1
<i>acoC</i>	1.0 ± 0.2	0.9 ± 0.1	3.4 ± 0.4	8.4 ± 0.2	51.0 ± 5.7	41.2 ± 8.6	<i>acoA-B-C-L-R</i>	acetoin dehydrogenase E2
<i>acoL</i>	1.0 ± 0.1	2.6 ± 0.2	3.7 ± 0.1	18.4 ± 1.0	51.7 ± 13.9	39.7 ± 5.7	<i>acoA-B-C-L-R</i>	acetoin dehydrogenase E3
<i>acoR</i>	1.1 ± 0.1	3.9 ± 0.8	4.1 ± 0.2	9.1 ± 1.5	22.2 ± 13.5	25.1 ± 3.7	<i>acoA-B-C-L-R</i>	transcriptional activator
<i>acsA</i>	1.1 ± 0.1	21.7 ± 2.3	21.1 ± 4.8	19.3 ± 0.1	14.6 ± 3.8	17.0 ± 1.2	<i>acuC-A-acsA</i>	acetyl-CoA synthetase
<i>acuA</i>	1.2 ± 0.2	21.7 ± 0.7	17.9 ± 1.0	17.1 ± 2.7	15.8 ± 2.1	11.6 ± 2.7	<i>acuC-A-acsA</i>	acetoin dehydrogenase
<i>acuC</i>	0.8 ± 0.2	6.1 ± 2.0	4.9 ± 0.7	5.8 ± 0.4	4.6 ± 1.1	2.9 ± 0.1	<i>acuC-A-acsA</i>	acetoin dehydrogenase
<i>alsD</i>	9.2 ± 1.6	4.7 ± 1.5	2.0 ± 0.1	1.6 ± 0.1	1.7 ± 0.1	1.4 ± 0.1	<i>alsR-S-D</i>	alpha-acetolactate decarboxylase
<i>alsR</i>	1.6 ± 0.1	2.3 ± 0.2	1.2 ± 0.1	1.1 ± 0.1	1.3 ± 0.1	1.3 ± 0.1	<i>alsR-S-D</i>	transcriptional regulator
<i>alsS</i>	13.0 ± 1.5	5.9 ± 0.5	3.4 ± 1.1	2.0 ± 0.1	2.3 ± 0.1	2.4 ± 0.1	<i>alsR-S-D</i>	alpha-acetolactate synthase
<i>bglH</i>	1.1 ± 0.2	4.0 ± 0.9	2.5 ± 0.1	4.0 ± 0.1	3.8 ± 0.1	4.1 ± 0.1	<i>bglP-H</i>	beta-glucosidase
<i>fruK</i>	1.1 ± 0.1	9.7 ± 4.6	3.9 ± 0.6	4.1 ± 0.1	8.3 ± 2.6	10.3 ± 1.8	<i>fruA-K-R</i>	fructose 1-phosphate kinase

<i>glpD</i>	1.1 ± 0.1	20.2 ± 5.2	18.5 ± 3.3	42.4 ± 3.0	4.1 ± 0.3	3.6 ± 0.1	<i>glpD</i>	glycerol-3-phosphate dehydrogenase
<i>glpF</i>	1.1 ± 0.1	9.2 ± 2.5	8.4 ± 1.9	16.4 ± 3.0	3.5 ± 0.1	3.3 ± 0.1	<i>glpF-P</i>	glycerol uptake facilitator
<i>glpT</i>	1.1 ± 0.1	2.7 ± 0.1	2.4 ± 0.1	5.6 ± 0.1	1.9 ± 0.1	1.6 ± 0.1	<i>glpQ-T</i>	glycerol-3-phosphate permease
<i>glpQ</i>	1.1 ± 0.1	3.9 ± 0.2	3.5 ± 0.2	8.8 ± 2.2	1.7 ± 0.1	1.4 ± 0.1	<i>glpQ-T</i>	glycerophosphoryl diester phosphodiesterase
<i>hxIA</i>	2.6 ± 0.4	11.0 ± 2.3	8.8 ± 0.4	7.5 ± 0.9	9.9 ± 2.9	6.9 ± 0.8	<i>hxIA-B</i>	3-hexulose-6-phosphate synthase
<i>hxIB</i>	1.7 ± 0.2	6.4 ± 1.4	4.4 ± 1.7	5.6 ± 0.8	6.0 ± 1.5	3.4 ± 0.1	<i>hxIA-B</i>	6-phospho-3-hexulose isomerase
<i>iolB</i>	1.1 ± 0.1	4.4 ± 0.9	3.1 ± 0.1	2.9 ± 0.1	3.3 ± 0.1	1.9 ± 0.1	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	myo-inositol catabolism
<i>iolC</i>	0.9 ± 0.2	7.2 ± 0.2	9.0 ± 0.8	8.2 ± 2.9	4.6 ± 0.5	4.5 ± 0.1	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	myo-inositol catabolism
<i>iolD</i>	0.9 ± 0.1	15.8 ± 0.3	8.7 ± 0.2	12.8 ± 2.6	5.3 ± 0.1	5.4 ± 0.1	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	myo-inositol catabolism
<i>iolE</i>	0.9 ± 0.1	13.6 ± 6.5	8.5 ± 0.1	8.0 ± 1.0	5.1 ± 1.5	4.5 ± 1.3	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	myo-inositol catabolism
<i>iolF</i>	1.1 ± 0.1	5.3 ± 0.2	2.3 ± 0.1	2.8 ± 0.1	2.3 ± 0.1	1.3 ± 0.1	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	inositol transport protein
<i>iolH</i>	0.7 ± 0.2	5.1 ± 0.3	5.5 ± 0.2	7.8 ± 2.8	3.4 ± 0.1	4.0 ± 0.1	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	myo-inositol catabolism
<i>ioll</i>	0.8 ± 0.1	3.4 ± 0.1	2.6 ± 0.1	2.3 ± 0.1	1.7 ± 0.1	1.7 ± 0.1	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	myo-inositol catabolism
<i>iolR</i>	1.1 ± 0.1	5.2 ± 1.2	3.5 ± 0.2	4.3 ± 0.2	3.3 ± 0.1	3.0 ± 0.1	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	transcriptional repressor
<i>iolS</i>	1.1 ± 0.1	3.5 ± 0.1	3.3 ± 0.1	3.9 ± 0.1	1.8 ± 0.1	1.7 ± 0.1	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	myo-inositol catabolism
<i>idh</i>	0.8 ± 0.1	9.5 ± 6.5	3.6 ± 0.1	6.9 ± 0.2	4.3 ± 0.3	3.4 ± 0.2	<i>iolB-C-D-E-F-idh-iolH-I-fbab</i>	myo-inositol 2-dehydrogenase
<i>lacA</i>	1.3 ± 0.2	3.4 ± 0.1	2.7 ± 0.1	2.4 ± 0.1	2.2 ± 0.1	2.3 ± 0.1	<i>lacA</i>	beta-galactosidase
<i>lacA</i>	1.1 ± 0.2	4.2 ± 0.2	4.4 ± 0.2	3.9 ± 0.2	3.9 ± 0.1	3.4 ± 0.1	<i>lacA</i>	close homolog to LacA:beta-galactosidase
<i>malA</i>	1.3 ± 0.2	1.5 ± 0.1	2.0 ± 0.1	2.3 ± 0.1	39.7 ± 19.6	41.2 ± 0.4	<i>malA-yfiA-malP</i>	6-phospho-alpha-glucosidase
<i>mall</i>	1.0 ± 0.1	7.0 ± 0.7	15.7 ± 4.6	43.0 ± 7.1	65.6 ± 7.4	80.8 ± 21.6	<i>mall-pgcM</i>	maltose-inducible alpha-glucosidase
<i>pgcM</i>	1.0 ± 0.1	3.7 ± 0.7	5.8 ± 1.7	16.0 ± 3.3	22.4 ± 9.2	18.9 ± 0.1	<i>mall-pgcM</i>	beta-phosphoglucomutase
<i>malP</i>	1.0 ± 0.1	1.9 ± 0.1	1.4 ± 0.1	4.5 ± 1.1	24.2 ± 4.9	38.0 ± 2.3	<i>malA-yfiA-malP</i>	PTS maltose-specific enzyme
<i>yqiQ*</i>	1.1 ± 0.1	11.5 ± 0.1	10.3 ± 2.7	12.8 ± 1.8	12.4 ± 2.9	12.7 ± 2.1	<i>mmgD-E-yqiQ</i>	similar to phosphoenolpyruvate mutase
<i>melA</i>	1.0 ± 0.1	2.9 ± 0.2	2.9 ± 0.1	3.9 ± 1.0	4.4 ± 0.1	4.3 ± 0.1	<i>melA-amY-C-D</i>	alpha-D-galactoside galactohydrolase
<i>pmi</i>	1.1 ± 0.2	1.9 ± 0.1	2.7 ± 0.2	3.0 ± 0.1	6.0 ± 0.1	2.7 ± 0.1	<i>pmi</i>	mannose-6-phosphate isomerase
<i>rbsK</i>	1.5 ± 0.3	10.9 ± 0.5	2.3 ± 0.1	2.8 ± 0.1	4.0 ± 0.8	4.3 ± 1.1	<i>rbs operon</i>	ribokinase
<i>sacX</i>	1.2 ± 0.1	1.2 ± 0.1	1.0 ± 0.1	1.8 ± 0.1	6.0 ± 2.4	7.1 ± 0.6	<i>sacX-Y</i>	negative regulatory protein
<i>uxuA</i>	1.0 ± 0.1	5.8 ± 3.0	3.5 ± 0.1	5.0 ± 1.5	3.4 ± 0.7	3.1 ± 0.1	<i>yjmD-uxuA-yjmF</i>	D-mannonate hydrolase
<i>yjmD</i>	0.9 ± 0.1	4.4 ± 0.1	3.9 ± 0.2	3.6 ± 0.1	2.1 ± 0.1	1.4 ± 0.1	<i>yjmD-uxuA-yjmF</i>	similar to alcohol dehydrogenase
<i>yjmF</i>	0.9 ± 0.2	4.2 ± 0.2	3.7 ± 0.1	3.8 ± 0.2	4.1 ± 0.1	2.4 ± 0.1	<i>yjmD-uxuA-yjmF</i>	similar to D-mannonate oxidoreductase
<i>BLi04208</i>	1.0 ± 0.1	20.4 ± 3.6	19.8 ± 9.0	19.4 ± 3.7	76.7 ± 18.1	95.2 ± 7.3		putative malate synthase
<i>BLi02105</i>	1.5 ± 0.2	20.6 ± 0.3	25.6 ± 1.3	27.1 ± 0.5	55.6 ± 12.1	41.5 ± 11.9		putative 2-hydroxy-3-oxopropionate reductase
<i>BLi02116</i>	0.7 ± 0.1	3.7 ± 0.1	3.9 ± 0.1	5.0 ± 0.1	6.1 ± 1.1	6.0 ± 0.5		putative D-mannonate dehydratase
<i>BLi01109</i>	0.8 ± 0.1	7.2 ± 1.1	5.6 ± 1.6	5.9 ± 2.4	14.2 ± 1.1	20.3 ± 1.8		known subtilisin carlsberg precursor

<i>BLi00658</i>	1.0 ± 0.1	3.2 ± 0.1	4.6 ± 1.2	6.3 ± 0.2	11.4 ± 1.6	9.4 ± 0.2		known maltogenic alpha-amylase
<i>BLi00828*</i>	1.4 ± 0.1	5.0 ± 2.0	3.6 ± 0.1	3.8 ± 0.5	6.4 ± 1.0	5.1 ± 0.6		putative glycerol dehydrogenase
<i>BLi04129</i>	0.6 ± 0.1	2.6 ± 0.2	3.3 ± 0.2	4.2 ± 0.1	3.6 ± 0.6	3.0 ± 0.1		putative pectate lyase
<i>BLi03549</i>	1.4 ± 0.1	1.8 ± 0.1	1.8 ± 0.1	2.3 ± 0.1	6.1 ± 1.1	6.3 ± 0.4		putative fructose 1-phosphate kinase
<i>BLi00656</i>	1.3 ± 0.1	3.3 ± 0.3	3.8 ± 0.5	4.4 ± 1.3	9.0 ± 1.4	8.3 ± 1.0		known alpha-amylase precursor
<i>BLi04207</i>	1.6 ± 0.1	7.4 ± 1.7	6.5 ± 1.0	4.3 ± 0.4	24.5 ± 2.3	33.0 ± 3.6		putative isocitrate lyase
Main glycolytic pathways								
<i>gapB</i>	1.2 ± 0.1	8.3 ± 1.8	7.4 ± 1.7	4.5 ± 1.2	11.6 ± 1.7	9.2 ± 0.9	<i>gapB-speD</i>	glyceraldehyde-3-phosphate dehydrogenase
<i>pckA*</i>	1.0 ± 0.1	24.9 ± 8.2	16.3 ± 3.9	11.7 ± 1.2	21.9 ± 3.4	18.2 ± 1.9	<i>pfkA-pyk</i>	6-phosphofructokinase
<i>fbaB</i>	1.2 ± 0.1	4.8 ± 2.0	3.3 ± 0.1	3.4 ± 0.3	2.4 ± 0.1	2.2 ± 0.5	<i>lolB-C-D-E-F-idh-iolH-l-fbab</i>	fructose-1,6-bisphosphate aldolase
<i>BLi00496</i>	1.3 ± 0.1	5.3 ± 0.2	25.0 ± 0.5	112.0 ± 10.7	57.8 ± 7.2	55.9 ± 8.1		putative transketolase
<i>BLi00495</i>	1.1 ± 0.3	3.7 ± 0.2	8.7 ± 1.0	27.9 ± 3.9	18.5 ± 5.5	24.8 ± 0.6		putative transketolase
TCA cycles								
<i>citA*</i>	0.9 ± 0.1	3.9 ± 0.1	3.8 ± 0.1	1.9 ± 0.1	7.8 ± 1.4	9.5 ± 3.2	<i>citA-R</i>	citrate synthase I
<i>citB</i>	1.2 ± 0.2	4.1 ± 0.4	3.7 ± 0.1	2.4 ± 0.1	2.0 ± 0.1	1.4 ± 0.1	<i>citB</i>	aconitate hydratase
<i>citG</i>	1.7 ± 0.1	3.1 ± 0.1	3.4 ± 0.1	3.3 ± 0.3	3.3 ± 0.1	2.4 ± 0.1	<i>citG</i>	fumarate hydratase
<i>mmgD</i>	1.2 ± 0.1	17.0 ± 6.0	11.8 ± 0.4	28.0 ± 6.5	28.1 ± 6.0	30.0 ± 3.9	<i>mmgD-E-yqiQ</i>	citrate synthase III
Metabolism of amino acids								
<i>bpr*</i>	1.1 ± 0.1	4.7 ± 0.3	7.8 ± 1.5	12.9 ± 6.3	19.9 ± 2.5	16.5 ± 0.6	<i>bpr</i>	bacillopeptidase F
<i>ispA*</i>	1.1 ± 0.3	3.8 ± 0.1	3.0 ± 0.1	4.1 ± 0.1	7.4 ± 0.2	11.4 ± 4.3	<i>ispA</i>	major intracellular serine protease
<i>mmsA</i>	1.2 ± 0.1	25.6 ± 4.9	24.4 ± 1.8	41.8 ± 10.3	51.8 ± 28.7	27.3 ± 0.9	<i>mmsA</i>	methylmalonate-semialdehyde dehydrogenase
<i>nasC*</i>	1.1 ± 0.1	2.1 ± 0.2	1.8 ± 0.1	1.9 ± 0.1	3.4 ± 0.1	3.2 ± 0.1	<i>nasB-C-D-E-F</i>	assimilatory nitrate reductase
<i>nasD*</i>	1.3 ± 0.1	3.1 ± 0.1	4.0 ± 0.1	1.8 ± 0.1	3.6 ± 0.1	3.5 ± 0.1	<i>nasB-C-D-E-F</i>	assimilatory nitrate reductase
<i>nasE*</i>	1.0 ± 0.1	3.5 ± 0.4	4.9 ± 0.6	5.3 ± 0.7	4.1 ± 0.5	3.3 ± 0.1	<i>nasB-C-D-E-F</i>	assimilatory nitrate reductase
<i>nasF*</i>	1.1 ± 0.2	3.1 ± 0.1	3.7 ± 0.2	4.6 ± 0.1	3.5 ± 0.1	2.1 ± 0.1	<i>nasB-C-D-E-F</i>	uroporphyrin-III C-methyltransferase
<i>BLi00198</i>	1.1 ± 0.2	5.77 ± 0.7	6.31 ± 0.3	6.27 ± 0.2	6.42 ± 0.5	3.81 ± 0.1	<i>rocR-D-E-F</i>	close homolog to RocF: arginase
<i>rocD</i>	1.3 ± 0.1	7.8 ± 2.3	6.3 ± 1.6	12.7 ± 0.9	4.7 ± 0.9	1.5 ± 0.1	<i>rocR-D-E-F</i>	ornithine aminotransferase
<i>rocE</i>	1.2 ± 0.1	5.1 ± 2.3	4.1 ± 0.3	8.8 ± 0.8	3.5 ± 0.1	1.2 ± 0.1	<i>rocR-D-E-F</i>	amino acid permease
<i>rocF</i>	1.1 ± 0.1	3.9 ± 0.7	3.6 ± 0.4	5.7 ± 0.2	5.0 ± 0.5	3.1 ± 0.1	<i>rocR-D-E-F</i>	arginase
<i>kbl</i>	1.1 ± 0.2	50.3 ± 11.5	45.8 ± 0.3	56.8 ± 13.0	18.1 ± 2.1	14.3 ± 1.6	<i>tdh-kbl</i>	2-amino-3-ketobutyrate CoA ligase
<i>tdh</i>	1.2 ± 0.2	23.6 ± 1.1	23.5 ± 3.1	27.5 ± 6.0	8.7 ± 0.2	9.3 ± 1.2	<i>tdh-kbl</i>	threonine 3-dehydrogenase
<i>trpB*</i>	1.3 ± 0.1	4.6 ± 0.8	4.1 ± 0.9	3.1 ± 0.1	3.1 ± 0.1	1.8 ± 0.1	<i>trpA-B-F-C-D-E</i>	tryptophan synthase
<i>trpC*</i>	1.2 ± 0.1	6.0 ± 1.7	4.3 ± 0.2	3.6 ± 0.1	3.4 ± 0.3	2.1 ± 0.1	<i>trpA-B-F-C-D-E</i>	indol-3-glycerol phosphate synthase
<i>trpD*</i>	1.2 ± 0.1	4.8 ± 0.9	3.8 ± 0.5	3.0 ± 0.2	3.1 ± 0.1	1.9 ± 0.1	<i>trpA-B-F-C-D-E</i>	anthranilate phosphoribosyltransferase

<i>trpE*</i>	1.5 ± 0.2	7.0 ± 1.0	4.1 ± 0.1	4.1 ± 0.1	3.6 ± 0.1	1.7 ± 0.1	<i>trpA-B-F-C-D-E</i>	anthranilate synthase
<i>trpF*</i>	1.5 ± 0.1	5.9 ± 2.8	3.4 ± 0.1	2.5 ± 0.1	3.5 ± 0.1	1.8 ± 0.1	<i>trpA-B-F-C-D-E</i>	phosphoribosyl anthranilate isomerase
<i>ggt*</i>	0.8 ± 0.1	3.8 ± 0.1	4.1 ± 0.1	4.2 ± 1.0	5.2 ± 0.2	5.2 ± 0.1	<i>ggt</i>	gamma-glutamyltranspeptidase
<i>ycgM*</i>	1.2 ± 0.1	16.4 ± 3.5	10.1 ± 2.8	22.1 ± 1.7	51.7 ± 19.6	14.7 ± 0.2	<i>ycgL-M-N-O-P-Q-R</i>	similar to proline oxidase
<i>ycgN*</i>	1.2 ± 0.1	12.4 ± 3.4	12.3 ± 2.6	19.8 ± 10.2	55.3 ± 4.7	24.0 ± 5.4	<i>ycgL-M-N-O-P-Q-R</i>	similar to 1-pyrroline-5-carboxylate dehydrogenase
<i>yjbG</i>	1.2 ± 0.1	3.5 ± 0.4	3.4 ± 0.1	4.4 ± 0.2	6.5 ± 1.1	3.9 ± 0.3	<i>yjb operon</i>	YjbG: unknown; similar to oligoendopeptidase
<i>BLi01747*</i>	1.1 ± 0.1	3.0 ± 0.2	3.5 ± 0.1	3.4 ± 0.1	5.2 ± 0.4	5.8 ± 0.5		putative bacillopeptidase F
<i>BLi00301*</i>	0.9 ± 0.1	9.5 ± 0.8	5.8 ± 0.3	9.8 ± 2.8	19.2 ± 4.1	20.0 ± 2.0		putative serine protease
<i>BLi04275</i>	2.6 ± 0.3	10.2 ± 2.4	3.2 ± 0.1	1.6 ± 0.1	1.7 ± 0.1	1.6 ± 0.1		close homolog to Ald: L-alanine dehydrogenase
<i>BLi04251</i>	1.3 ± 0.2	10.7 ± 3.9	6.4 ± 0.5	9.5 ± 1.5	4.9 ± 0.2	3.5 ± 0.1		putative methylmalonate-semialdehyde dehydrogenase
Metabolism of lipids								
<i>acdA</i>	0.9 ± 0.1	3.9 ± 0.3	5.5 ± 0.1	7.9 ± 1.3	19.6 ± 3.8	11.7 ± 1.9	<i>acdA-mmgA-B-C</i>	acyl-CoA dehydrogenase
<i>lcfa</i>	0.9 ± 0.1	3.6 ± 0.1	2.9 ± 0.1	4.6 ± 1.6	5.1 ± 0.9	3.7 ± 0.4	<i>ysiA-lcfA-etcB-A</i>	long chain acyl-CoA synthetase
<i>mmgA</i>	1.5 ± 0.1	7.0 ± 0.6	8.1 ± 2.8	8.7 ± 3.0	35.8 ± 6.3	23.0 ± 3.4	<i>acdA-mmgA-B-C</i>	acetyl-CoA acetyltransferase
<i>mmgB</i>	1.0 ± 0.1	5.0 ± 0.7	6.3 ± 0.9	7.6 ± 3.0	27.5 ± 4.3	14.5 ± 0.1	<i>mmgA-B-C</i>	3-hydroxybutyryl-CoA dehydrogenase
<i>mmgC</i>	1.0 ± 0.1	4.3 ± 0.1	7.8 ± 0.3	7.2 ± 2.0	30.4 ± 7.9	11.4 ± 3.4	<i>mmgA-B-C</i>	acyl-CoA dehydrogenase
<i>mmgE*</i>	1.0 ± 0.2	11.5 ± 0.4	11.1 ± 0.2	9.7 ± 4.0	12.8 ± 1.5	14.0 ± 0.8	<i>mmgD-E-yqiQ</i>	function unknown
<i>yhaR</i>	1.0 ± 0.1	7.7 ± 1.7	4.7 ± 0.4	7.7 ± 1.1	6.8 ± 0.6	4.8 ± 0.2	<i>yha operon</i>	similar to enoyl CoA hydratase
<i>ytkK</i>	1.0 ± 0.1	2.0 ± 0.1	2.3 ± 0.1	2.5 ± 0.1	6.9 ± 0.8	3.4 ± 0.2	<i>ytkK-L</i>	similar to 3-oxoacyl- acyl-carrier protein reductase
<i>yusJ</i>	1.0 ± 0.1	8.3 ± 1.8	12.4 ± 3.1	7.1 ± 0.6	40.2 ± 7.1	16.3 ± 1.4	<i>yusJ-K-L</i>	similar to butyryl-CoA dehydrogenase
<i>yusK</i>	0.9 ± 0.1	6.7 ± 0.6	5.2 ± 0.6	6.1 ± 0.9	21.3 ± 2.0	10.0 ± 0.7	<i>yusJ-K-L</i>	similar to acetyl-CoA C-acyltransferase
<i>yusL</i>	1.1 ± 0.1	18.7 ± 8.0	13.0 ± 2.9	15.3 ± 7.3	51.2 ± 3.7	14.0 ± 4.2	<i>yusJ-K-L</i>	similar to 3-hydroxyacyl-CoA dehydrogenase
<i>ywjE</i>	1.0 ± 0.1	3.1 ± 0.2	2.8 ± 0.1	2.1 ± 0.1	7.5 ± 1.9	4.9 ± 0.4	<i>ywj operon</i>	similar to cardiolipin synthetase
<i>BLi02102</i>	0.9 ± 0.1	8.9 ± 1.2	10.3 ± 0.6	15.9 ± 0.5	17.5 ± 5.8	16.0 ± 0.8		putative enoyl (3-hydroxyisobutyrate dehydrogenase)
<i>BLi02103</i>	0.9 ± 0.1	15.0 ± 6.0	16.9 ± 2.3	34.2 ± 8.6	29.2 ± 8.4	22.8 ± 2.0		putative enoyl-CoA hydratase
<i>BLi02106</i>	1.0 ± 0.1	48.4 ± 5.9	50.8 ± 8.7	60.1 ± 11.8	90.6 ± 33.7	78.3 ± 4.0		putative butyryl-CoA dehydrogenase
Metabolism of coenzymes								
<i>BLi03994*</i>	1.7 ± 0.3	11.3 ± 0.8	23.9 ± 0.5	31.2 ± 11.5	12.0 ± 0.2	9.7 ± 0.3		close homolog to DhaS: aldehyde dehydrogenase
<i>dhaS*</i>	1.2 ± 0.3	7.0 ± 0.7	10.8 ± 1.2	14.3 ± 1.5	16.5 ± 2.1	9.9 ± 1.3	<i>dhaS</i>	aldehyde dehydrogenase
<i>hemA</i>	1.1 ± 0.1	4.0 ± 1.0	3.3 ± 0.2	3.0 ± 0.1	1.6 ± 0.1	1.5 ± 0.1	<i>hemA-X-C-D-B-L-spoVID</i>	glutamyl-tRNA reductase
<i>hemH</i>	1.7 ± 0.1	2.7 ± 0.2	2.3 ± 0.1	4.2 ± 0.1	4.4 ± 0.1	5.3 ± 0.2	<i>hemE-H-Y</i>	close homolog to HemH: ferrochelatase

DNA restriction/modification and repair								
<i>dinB</i> *	1.3 ± 0.1	4.2 ± 0.2	3.8 ± 0.6	3.6 ± 0.3	3.3 ± 0.3	3.2 ± 0.1	<i>dinB</i>	nuclease inhibitor
<i>yxlJ</i>	1.0 ± 0.1	5.7 ± 1.0	4.3 ± 0.5	5.0 ± 1.1	4.7 ± 0.8	5.0 ± 0.6	<i>yxlJ</i>	similar to DNA-3-methyladenine glycosidase
Aminoacyl-tRNA synthetases								
<i>tyrZ</i>	1.5 ± 0.1	1.3 ± 0.1	1.4 ± 0.2	4.0 ± 0.4	4.8 ± 0.4	4.9 ± 0.1	<i>tyrZ</i>	tyrosyl-tRNA synthetase
Adaptation to atypical conditions								
<i>cstA</i>	1.1 ± 0.1	8.9 ± 1.1	6.1 ± 0.5	6.5 ± 0.4	6.2 ± 1.2	5.8 ± 0.6	<i>cstA</i>	carbon starvation-induced protein
<i>clpC</i> *	1.1 ± 0.2	3.9 ± 0.3	2.5 ± 0.1	3.6 ± 0.2	3.8 ± 0.5	3.9 ± 0.1	<i>ctsR-mcsA-B-clpC-radA</i>	class III stress response
<i>mrgA</i> *	1.1 ± 0.1	3.8 ± 0.2	3.3 ± 0.3	3.8 ± 0.1	2.8 ± 0.1	1.9 ± 0.1	<i>mrgA</i>	metalloregulation DNA-binding stress protein
<i>ywqC</i> *	1.2 ± 0.1	3.9 ± 0.1	2.1 ± 0.1	4.3 ± 0.1	3.0 ± 0.1	1.3 ± 0.1	<i>ywqE-C-B-A</i>	similar to capsular polysaccharide biosynthesis
<i>ywsC</i>	1.5 ± 0.2	4.0 ± 0.2	3.8 ± 0.2	2.9 ± 0.1	2.8 ± 0.1	2.8 ± 0.1	<i>ywsC</i>	similar to capsular polysaccharide biosynthesis
<i>BLi04126</i> *	0.8 ± 0.1	3.4 ± 0.1	3.3 ± 0.1	3.7 ± 0.7	5.2 ± 0.4	6.8 ± 0.1		putative bacteriocin formation
<i>BLi04128</i> *	0.9 ± 0.1	3.5 ± 0.2	3.4 ± 0.1	3.6 ± 0.4	5.1 ± 0.8	4.0 ± 0.4		putative bacteriocin formation
Detoxification								
<i>katA</i>	1.3 ± 0.2	0.7 ± 0.1	3.2 ± 0.1	4.3 ± 0.1	4.0 ± 0.1	3.8 ± 0.1	<i>katA-X</i>	vegetative catalase 1
<i>katX</i>	1.4 ± 0.2	3.7 ± 0.1	2.2 ± 0.1	2.9 ± 0.1	3.7 ± 0.2	2.6 ± 0.1	<i>katA-X</i>	major catalase in spores
<i>yfIM</i>	1.0 ± 0.2	1.3 ± 0.1	2.4 ± 0.1	6.3 ± 1.4	5.0 ± 0.8	6.9 ± 3.2	<i>yfI operon</i>	similar to nitric-oxide synthase
<i>yxel</i>	1.1 ± 0.1	5.4 ± 0.7	4.7 ± 1.0	4.7 ± 0.1	10.1 ± 3.1	10.8 ± 1.2	<i>yxe operon</i>	unknown; similar to penicillin amidase
Transcription regulation								
<i>sacY</i>	1.4 ± 0.2	0.7 ± 0.1	0.7 ± 0.1	1.1 ± 0.1	5.0 ± 0.2	4.3 ± 0.9	<i>sacX-Y</i>	transcriptional antiterminator
<i>BLi01063</i>	0.9 ± 0.1	6.2 ± 1.5	6.6 ± 2.0	7.4 ± 1.8	6.2 ± 1.1	4.4 ± 0.1		putative response regulator aspartate phosphatase A
<i>ydhQ</i>	1.2 ± 0.1	2.3 ± 0.2	2.5 ± 0.1	1.6 ± 0.1	5.2 ± 0.1	5.4 ± 0.5	<i>ydhP-Q</i>	similar to transcriptional regulator
<i>ykoM</i> *	1.0 ± 0.1	6.7 ± 1.6	6.5 ± 0.6	7.2 ± 2.0	5.0 ± 0.3	3.6 ± 0.1	<i>yko operon</i>	similar to transcriptional regulator
<i>ysiA</i>	0.9 ± 0.1	10.3 ± 0.6	8.9 ± 2.4	8.7 ± 1.4	25.7 ± 1.6	4.4 ± 0.1	<i>lcfA-ysiA</i>	similar to transcriptional regulator
<i>ytrA</i>	4.4 ± 0.8	2.6 ± 0.2	2.3 ± 0.1	3.7 ± 0.1	4.8 ± 0.4	4.3 ± 0.1	<i>ytrA-B-C-E-F</i>	similar to transcriptional regulator
<i>yvdE</i>	1.1 ± 0.1	4.1 ± 1.0	4.3 ± 0.5	9.5 ± 0.2	10.8 ± 2.3	8.3 ± 1.6	<i>yvd operon</i>	similar to transcriptional regulator
<i>ywaE</i> *	1.1 ± 0.1	1.3 ± 0.1	1.8 ± 0.1	3.3 ± 0.1	4.3 ± 0.1	4.7 ± 0.1	<i>ywaE</i>	similar to transcriptional regulator
<i>BLi00492</i>	1.6 ± 0.1	7.2 ± 2.3	18.3 ± 3.2	33.0 ± 8.3	18.8 ± 3.5	20.6 ± 3.7		putative transcriptional regulation
<i>BLi04093</i> *	1.6 ± 0.1	6.1 ± 1.4	6.9 ± 1.6	10.4 ± 6.7	6.7 ± 0.6	8.4 ± 0.1		putative transcriptional regulation
<i>BLi03995</i> *	1.3 ± 0.1	3.5 ± 0.2	4.8 ± 1.8	4.7 ± 0.5	4.7 ± 0.5	3.9 ± 0.2		putative transcriptional regulation
<i>BLi03548</i> *	1.6 ± 0.1	4.3 ± 0.1	3.4 ± 0.1	3.3 ± 0.1	5.8 ± 1.2	4.6 ± 0.2		putative transcriptional regulation
Transcription initiation								
<i>yvyD</i> *	2.4 ± 0.3	11.4 ± 1.9	6.8 ± 1.7	3.8 ± 0.3	9.1 ± 0.6	8.5 ± 2.9	<i>yvyD</i>	similar to sigma-54
<i>sigG</i>	1.1 ± 0.1	1.5 ± 0.1	2.8 ± 0.1	3.4 ± 0.2	3.8 ± 0.1	3.3 ± 0.1	<i>spoIIGA-sigE-sigG</i>	RNA polymerase sporulation

<i>sigX*</i>	1.2 ± 0.1	4.4 ± 1.0	5.7 ± 1.1	5.6 ± 0.9	9.6 ± 0.4	12.7 ± 1.7	<i>sigX</i>	RNA polymerase ECF-type sigma factor
Unknown function								
<i>BLi00227</i>	1.3 ± 0.3	4.3 ± 0.4	3.6 ± 0.3	3.5 ± 0.2	3.4 ± 0.1	3.0 ± 0.1		putative carboxylase
<i>BLi00235*</i>	1.0 ± 0.1	8.5 ± 0.8	11.7 ± 5.3	9.3 ± 1.6	8.7 ± 1.2	6.6 ± 0.6		hypothetical
<i>BLi00236*</i>	0.9 ± 0.1	5.9 ± 0.1	7.6 ± 1.9	8.2 ± 1.7	4.7 ± 1.2	3.8 ± 0.7		hypothetical
<i>BLi00303*</i>	1.1 ± 0.1	3.9 ± 0.2	3.0 ± 0.1	5.4 ± 0.2	7.8 ± 2.5	6.2 ± 1.4		hypothetical
<i>BLi00654*</i>	0.9 ± 0.1	5.2 ± 0.7	5.7 ± 2.6	3.6 ± 0.1	4.0 ± 1.0	6.8 ± 0.6		conserved hypothetical
<i>BLi00829</i>	1.1 ± 0.2	3.7 ± 0.4	3.8 ± 0.1	4.4 ± 0.1	3.4 ± 0.6	2.4 ± 0.1		hypothetical
<i>BLi00858</i>	1.0 ± 0.2	1.4 ± 0.1	1.8 ± 0.1	2.4 ± 0.1	7.6 ± 2.4	8.6 ± 0.6		conserved hypothetical
<i>BLi00930</i>	1.1 ± 0.1	3.8 ± 0.2	3.6 ± 0.1	3.3 ± 0.1	3.6 ± 0.1	3.4 ± 0.1		conserved hypothetical
<i>BLi01011</i>	1.5 ± 0.1	2.7 ± 0.1	3.3 ± 0.2	3.5 ± 0.1	3.8 ± 0.1	3.3 ± 0.5		putative oxidoreductase
<i>BLi01171</i>	1.2 ± 0.1	2.1 ± 0.1	2.4 ± 0.1	2.5 ± 0.1	3.6 ± 0.6	4.0 ± 0.1		conserved hypothetical
<i>BLi01466*</i>	1.0 ± 0.1	4.0 ± 0.3	6.6 ± 1.0	9.1 ± 0.2	3.7 ± 0.6	3.4 ± 0.1		putative phage protein
<i>BLi02008</i>	0.9 ± 0.1	2.2 ± 0.1	3.6 ± 0.2	4.0 ± 0.9	3.5 ± 0.1	4.7 ± 0.1		hypothetical
<i>BLi02101</i>	0.8 ± 0.1	3.6 ± 0.1	4.4 ± 0.2	7.6 ± 0.5	8.6 ± 2.0	5.9 ± 0.6		hypothetical
<i>BLi03498</i>	1.0 ± 0.1	14.1 ± 1.4	10.0 ± 1.7	15.7 ± 7.7	11.8 ± 4.2	10.2 ± 1.9		putative pectin methylesterase
<i>BLi03560</i>	1.4 ± 0.2	3.1 ± 0.1	3.0 ± 0.1	3.0 ± 0.1	3.3 ± 0.1	2.9 ± 0.1		hypothetical
<i>BLi03989*</i>	1.0 ± 0.1	5.0 ± 0.1	10.7 ± 1.6	15.8 ± 4.7	6.8 ± 0.8	8.5 ± 1.3		putative hydroxybenzoate hydroxylase
<i>BLi03991*</i>	1.0 ± 0.1	11.2 ± 1.0	19.3 ± 4.8	40.4 ± 6.2	12.2 ± 3.5	13.2 ± 5.0		putative aromatic compounds specific dioxygenase
<i>BLi03993*</i>	0.9 ± 0.1	14.2 ± 1.6	30.4 ± 2.6	45.2 ± 8.6	16.5 ± 1.7	13.4 ± 1.5		putative decarboxylase
<i>BLi03996*</i>	0.9 ± 0.2	3.1 ± 0.1	3.7 ± 0.2	4.7 ± 0.1	4.0 ± 0.8	2.9 ± 0.1		conserved hypothetical
<i>BLi04116*</i>	1.8 ± 0.1	3.6 ± 0.8	4.1 ± 0.6	4.2 ± 0.4	7.8 ± 1.0	14.3 ± 5.0		hypothetical
<i>BLi04118</i>	1.0 ± 0.1	3.6 ± 0.1	3.9 ± 0.1	4.5 ± 0.1	6.6 ± 2.2	6.9 ± 3.0		hypothetical
<i>BLi04119*</i>	0.7 ± 0.1	4.9 ± 0.2	4.1 ± 0.2	3.7 ± 0.7	6.8 ± 2.3	7.7 ± 1.7		hypothetical
<i>BLi04120*</i>	1.1 ± 0.1	3.5 ± 0.2	3.8 ± 0.1	3.9 ± 1.2	5.4 ± 1.0	7.2 ± 2.2		conserved hypothetical
<i>BLi04124*</i>	1.2 ± 0.1	3.0 ± 0.1	3.7 ± 0.1	4.4 ± 0.5	6.6 ± 0.5	5.9 ± 1.4		conserved hypothetical
<i>BLi04185*</i>	0.9 ± 0.1	5.2 ± 0.8	5.9 ± 1.8	5.3 ± 0.1	10.6 ± 3.8	11.1 ± 1.9		hypothetical
<i>ybdN</i>	0.9 ± 0.1	4.0 ± 0.1	4.5 ± 0.1	4.6 ± 0.1	10.3 ± 0.3	6.2 ± 2.3	<i>ybdN</i>	unknown
<i>ybfA</i>	1.2 ± 0.1	5.9 ± 0.6	4.3 ± 0.3	4.8 ± 1.9	4.2 ± 0.2	4.6 ± 0.8	<i>ybfA-B</i>	unknown
<i>ycgF</i>	0.9 ± 0.1	0.7 ± 0.1	3.0 ± 0.1	4.9 ± 0.3	4.0 ± 0.6	2.8 ± 0.1	<i>ycg operon</i>	unknown
<i>ycgL</i>	0.9 ± 0.1	3.3 ± 0.1	2.5 ± 0.1	3.1 ± 0.1	3.7 ± 0.3	2.5 ± 0.1	<i>ycg operon</i>	unknown
<i>ycgP</i>	1.1 ± 0.1	3.2 ± 0.3	3.4 ± 0.4	3.5 ± 0.2	6.1 ± 1.1	3.2 ± 0.1	<i>ycg operon</i>	unknown
<i>ycgQ</i>	0.6 ± 0.1	2.4 ± 0.1	2.3 ± 0.1	2.9 ± 0.1	4.2 ± 0.1	3.3 ± 0.1	<i>ycg operon</i>	unknown
<i>ycgR</i>	0.8 ± 0.1	1.7 ± 0.1	2.2 ± 0.1	2.2 ± 0.1	3.6 ± 0.5	3.1 ± 0.1	<i>ycg operon</i>	unknown

<i>yceS</i>	1.3 ± 0.2	1.8 ± 0.1	3.5 ± 0.2	6.3 ± 1.2	5.9 ± 0.4	5.8 ± 0.5	<i>yceS</i>	unknown
<i>yeaA</i>	1.8 ± 0.3	2.6 ± 0.1	2.8 ± 0.1	2.6 ± 0.1	4.6 ± 0.4	4.3 ± 1.1	<i>yeaA</i>	unknown
<i>yesL</i>	1.6 ± 0.1	5.5 ± 1.4	4.4 ± 1.1	6.4 ± 0.5	7.3 ± 2.0	5.3 ± 1.6	<i>yes operon</i>	unknown
<i>yfiA</i>	1.1 ± 0.2	2.3 ± 0.1	2.3 ± 0.1	5.4 ± 0.1	68.1 ± 37.8	53.9 ± 11.9	<i>malA-yfiA-malP</i>	unknown
<i>yfmQ</i>	0.8 ± 0.1	9.0 ± 0.5	8.4 ± 0.7	3.9 ± 0.8	2.7 ± 0.1	2.5 ± 0.1	<i>yfmQ</i>	unknown
<i>yjbD</i>	1.0 ± 0.1	3.8 ± 0.1	4.8 ± 0.2	3.1 ± 0.1	3.9 ± 0.1	3.4 ± 0.1	<i>yjbC-D</i>	unknown
<i>ykyB</i>	0.9 ± 0.1	3.7 ± 0.6	3.4 ± 0.1	3.6 ± 0.1	4.2 ± 0.6	4.3 ± 0.1	<i>ykyB</i>	unknown
<i>ylbP</i>	1.1 ± 0.1	7.3 ± 0.4	6.4 ± 0.7	6.9 ± 1.4	7.9 ± 0.1	7.6 ± 0.6	<i>ylbO-P</i>	unknown
<i>ymcA</i>	0.9 ± 0.2	4.1 ± 0.3	4.9 ± 0.5	6.2 ± 0.1	3.4 ± 0.4	1.9 ± 0.1	<i>ymcA-B</i>	unknown
<i>ymcB</i>	1.0 ± 0.2	6.7 ± 0.2	6.4 ± 0.4	8.3 ± 1.4	2.0 ± 0.1	2.1 ± 0.1	<i>ymcA-B</i>	unknown
<i>yoEB</i>	1.0 ± 0.1	29.2 ± 4.4	30.6 ± 9.2	15.6 ± 1.9	37.1 ± 3.9	60.0 ± 0.4	<i>yoEB</i>	unknown
<i>ypiB*</i>	1.6 ± 0.1	8.3 ± 1.1	4.3 ± 0.6	5.2 ± 0.6	5.0 ± 1.2	3.3 ± 0.2	<i>ypiA-B-F</i>	unknown
<i>ypiF</i>	1.1 ± 0.1	4.3 ± 0.5	3.9 ± 0.7	4.8 ± 1.2	3.0 ± 0.1	2.9 ± 0.1	<i>ypiA-B-F</i>	unknown
<i>ysbA</i>	0.6 ± 0.1	17.8 ± 0.1	7.9 ± 0.4	2.1 ± 0.1	1.7 ± 0.1	1.2 ± 0.1	<i>ysbA-B</i>	unknown
<i>ytdl</i>	0.9 ± 0.2	3.3 ± 0.1	4.2 ± 0.1	4.3 ± 0.1	5.0 ± 0.1	4.2 ± 0.1	<i>ytdl</i>	unknown
<i>yuaB</i>	1.0 ± 0.1	3.1 ± 0.2	3.7 ± 0.1	3.5 ± 0.1	3.2 ± 0.2	3.0 ± 0.1	<i>yuaB</i>	unknown
<i>yvdJ</i>	1.3 ± 0.1	7.3 ± 0.2	13.0 ± 2.2	43.5 ± 14.8	63.4 ± 22.4	47.5 ± 7.5	<i>yvd operon</i>	unknown
<i>yvdK</i>	2.2 ± 0.3	9.5 ± 0.5	17.1 ± 2.4	36.5 ± 11.9	65.6 ± 17.0	65.0 ± 13.9	<i>yvd operon</i>	unknown
<i>yvfW</i>	1.5 ± 0.1	3.1 ± 0.3	3.9 ± 0.6	3.4 ± 0.1	3.2 ± 0.1	4.0 ± 0.1	<i>yvfl-V-W</i>	unknown
<i>yvIB*</i>	1.1 ± 0.1	2.4 ± 0.1	2.4 ± 0.1	2.3 ± 0.1	3.1 ± 0.1	3.8 ± 0.1	<i>yvIB-D</i>	unknown
<i>yvoA</i>	1.0 ± 0.1	1.9 ± 0.1	1.9 ± 0.1	9.0 ± 3.1	12.5 ± 1.6	19.6 ± 0.3	<i>yvoA</i>	unknown
<i>yvqH*</i>	1.2 ± 0.1	4.2 ± 0.1	6.5 ± 0.8	8.3 ± 2.1	18.0 ± 5.6	17.4 ± 5.5	<i>yvq operon</i>	unknown
<i>yvql*</i>	0.9 ± 0.1	4.6 ± 0.3	6.5 ± 1.1	9.4 ± 2.1	16.0 ± 6.9	15.1 ± 3.2	<i>yvq operon</i>	unknown
<i>ywfL*</i>	0.9 ± 0.1	3.6 ± 0.1	7.5 ± 0.7	11.2 ± 1.8	5.7 ± 0.2	6.1 ± 0.2	<i>ywfL</i>	unknown
<i>yxkO</i>	1.0 ± 0.1	3.3 ± 0.2	3.7 ± 0.1	3.3 ± 0.1	3.4 ± 0.3	3.3 ± 0.1	<i>yxkO</i>	unknown
<i>yycA</i>	0.8 ± 0.1	3.6 ± 0.1	3.4 ± 0.1	3.4 ± 0.1	5.1 ± 0.2	6.2 ± 0.1	<i>yycA</i>	unknown

Table 3: Kinetic of the nitrogen starvation repressed genes of *B. licheniformis*. Listed are such genes, whose mRNA levels showed a more than threefold repression during at least one sampling point throughout the growth curve. Genes the expression of which is also repressed under glucose starvation conditions are labelled with “**”. Trans. ph. = transient phase, Transcript. = Transcriptional , SD = standard deviation

Gene name	Trans. ph.	SD	30 min	SD	60 min	SD	90 min	SD	120 min	SD	Transcriptional organisation	Function
Cell wall												
<i>dacA</i>	1.7 ± 0.1		3.4 ± 1.1		3.1 ± 0.7		4.8 ± 1.0		4.2 ± 0.4		<i>dacA-yaaD-E</i>	penicillin-binding protein
<i>gcaD</i>	1.1 ± 0.2		4.0 ± 1.0		3.6 ± 0.9		4.7 ± 0.5		3.3 ± 0.5		<i>gcaD</i>	UDP-N-acetylglucosamine pyrophosphorylase
<i>lytB</i>	0.9 ± 0.1		4.2 ± 0.1		3.5 ± 0.9		3.8 ± 0.9		4.2 ± 0.4		<i>lytC-B-R</i>	modifier protein of major autolysin LytC
<i>lytC</i>	1.6 ± 0.1		4.0 ± 1.7		4.4 ± 1.0		5.6 ± 0.9		4.6 ± 1.0		<i>lytC-B-R</i>	N-acetylmuramoyl-L-alanine amidase
<i>mreB</i>	1.1 ± 0.1		3.8 ± 0.3		2.8 ± 0.8		3.2 ± 0.6		3.0 ± 0.4		<i>radC-mreB-C-D-minC-D</i>	cell-shape determining protein
<i>mreC</i>	1.1 ± 0.1		3.4 ± 0.3		3.8 ± 0.7		7.0 ± 1.4		4.3 ± 0.8		<i>radC-mreB-C-D-minC-D</i>	cell-shape determining protein
<i>mreD</i>	1.2 ± 0.1		3.0 ± 0.2		3.3 ± 0.1		4.3 ± 0.5		2.3 ± 0.2		<i>radC-mreB-C-D-minC-D</i>	cell-shape determining protein
<i>murAA</i>	1.4 ± 0.2		3.1 ± 0.7		3.3 ± 0.4		6.3 ± 1.3		4.4 ± 1.1		<i>murAA-spoIIID</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
<i>tagG</i>	2.2 ± 0.2		2.5 ± 0.1		2.0 ± 0.5		2.0 ± 0.5		2.0 ± 0.6		<i>tagG-H</i>	teichoic acid translocation
<i>tagH</i>	1.5 ± 0.2		1.3 ± 0.7		3.2 ± 0.5		3.1 ± 0.1		2.9 ± 0.4		<i>tagG-H</i>	teichoic acid translocation
<i>tuaA</i>	1.7 ± 0.1		6.8 ± 0.6		6.7 ± 1.8		7.1 ± 0.7		6.9 ± 1.3		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaB</i>	2.1 ± 0.2		5.0 ± 0.4		6.7 ± 1.9		6.9 ± 1.1		5.4 ± 1.2		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaC</i>	2.2 ± 0.1		6.3 ± 0.5		6.7 ± 1.5		7.1 ± 1.1		6.0 ± 1.1		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaD</i>	2.1 ± 0.2		6.3 ± 1.4		6.7 ± 1.8		7.1 ± 2.1		6.2 ± 1.2		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaE</i>	2.2 ± 0.1		4.7 ± 0.7		4.6 ± 0.8		5.5 ± 0.9		4.5 ± 1.0		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaF</i>	1.7 ± 0.2		1.6 ± 0.3		2.9 ± 0.6		2.9 ± 0.2		3.0 ± 0.5		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaG</i>	2.1 ± 0.4		4.7 ± 0.5		4.7 ± 0.9		4.3 ± 0.8		3.8 ± 0.8		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>tuaH</i>	2.1 ± 0.3		3.3 ± 0.4		5.4 ± 1.7		3.2 ± 0.9		4.9 ± 0.8		<i>tuaA-B-C-D-E-F-G-H</i>	biosynthesis of teichuronic acid
<i>yodJ</i>	1.0 ± 0.1		3.7 ± 0.1		4.3 ± 0.8		3.1 ± 0.5		4.7 ± 0.7		<i>yodJ-H</i>	similar to D-alanyl-D-alanine carboxypeptidase
<i>yojL</i>	1.1 ± 0.1		3.3 ± 0.3		3.1 ± 0.7		3.1 ± 0.5		3.7 ± 0.4		<i>yoj operon</i>	cell wall-binding protein
<i>yrvJ</i>	1.2 ± 0.1		2.1 ± 0.1		3.1 ± 0.4		3.3 ± 0.3		3.8 ± 0.3		<i>YrvJ-I</i>	N-acetylmuramoyl-L-alanine amidase
<i>yvcE</i>	0.9 ± 0.1		4.9 ± 1.2		4.9 ± 1.4		4.2 ± 0.1		4.5 ± 1.0		<i>yvcE</i>	cell wall-binding protein
<i>BLi02850</i>	1.4 ± 0.2		2.9 ± 0.5		2.9 ± 0.5		4.2 ± 0.8		2.7 ± 0.5			putative cell wall-associated protein
<i>BLi03767</i>	1.7 ± 0.2		5.4 ± 0.7		7.3 ± 2.0		9.3 ± 0.7		9.1 ± 1.6			putative cell wall-binding protein
Transport/binding proteins and lipoproteins												
<i>cysP</i>	2.4 ± 0.3		4.8 ± 0.5		3.8 ± 0.8		4.5 ± 1.1		3.8 ± 0.6		<i>cysH-P-sat-cysC-ylnD-E-F</i>	sulfate permease

<i>feuA</i>	0.6 ± 0.1	2.6 ± 0.1	5.1 ± 1.2	4.9 ± 1.7	6.0 ± 1.3	<i>feuA-B-C</i>	iron-uptake system
<i>feuB</i>	0.8 ± 0.1	2.4 ± 0.1	4.2 ± 1.1	5.4 ± 0.8	4.1 ± 1.1	<i>feuA-B-C</i>	iron-uptake system
<i>feuC</i>	0.6 ± 0.1	1.8 ± 0.1	3.0 ± 0.7	3.7 ± 0.7	1.9 ± 0.5	<i>feuA-B-C</i>	iron-uptake system
<i>opuAA</i>	1.2 ± 0.4	3.7 ± 0.3	3.8 ± 0.7	3.4 ± 0.1	4.8 ± 1.3	<i>opuAA-AB-AC</i>	glycine betaine ABC transporter
<i>opuAB</i>	1.5 ± 0.4	6.3 ± 0.7	7.6 ± 1.2	9.5 ± 2.9	6.1 ± 1.5	<i>opuAA-AB-AC</i>	glycine betaine ABC transporter
<i>opuAC</i>	1.8 ± 0.1	6.6 ± 1.5	8.4 ± 0.9	11.3 ± 1.8	7.0 ± 1.3	<i>opuAA-AB-AC</i>	glycine betaine ABC transporter
<i>opuE</i>	1.4 ± 0.1	3.9 ± 1.0	2.3 ± 0.3	3.0 ± 0.2	2.0 ± 0.5	<i>opuE</i>	proline transporter
<i>ptsG</i>	2.0 ± 0.2	23.3 ± 6.7	26.1 ± 6.7	27.1 ± 4.2	24.6 ± 6.3	<i>ptsI-G-glcT</i>	PTS glucose-specific enzyme IICBA component
<i>ptsI</i>	1.9 ± 0.1	4.2 ± 0.9	10.4 ± 2.4	12.9 ± 2.2	11.6 ± 2.8	<i>ptsI-G-glcT</i>	PTS enzyme I
<i>BLi02977</i>	0.9 ± 0.1	1.7 ± 0.1	3.1 ± 0.3	3.7 ± 0.5	2.8 ± 0.6		putative ABC transporter
<i>BLi00972</i>	3.1 ± 0.1	4.9 ± 0.7	7.1 ± 1.0	10.3 ± 2.1	6.0 ± 1.0		putative ABC transporter ATP-binding protein
<i>BLi00973</i>	3.1 ± 0.3	3.1 ± 0.2	3.2 ± 0.9	2.6 ± 0.4	2.7 ± 0.7		putative ABC transporter permease
<i>BLi03540</i>	1.9 ± 0.2	3.5 ± 0.9	3.3 ± 0.5	3.3 ± 0.5	2.1 ± 0.4		putative ABC transporter sugar
<i>BLi03657</i>	0.5 ± 0.6	4.1 ± 0.7	2.6 ± 0.5	3.3 ± 0.7	4.5 ± 0.4		putative iron(III) transporter
<i>ssuA</i>	1.4 ± 0.2	3.1 ± 0.5	3.2 ± 0.4	5.1 ± 1.0	2.7 ± 0.8	<i>ssuB-A-C-D</i>	aliphatic sulfonate ABC transporter
<i>ssuB</i>	1.2 ± 0.3	3.4 ± 0.7	2.9 ± 0.7	3.4 ± 0.8	2.8 ± 0.6	<i>ssuB-A-C-D</i>	aliphatic sulfonate ABC transporter
<i>ybaE</i>	1.8 ± 0.2	4.9 ± 0.4	3.5 ± 0.8	4.1 ± 0.7	3.2 ± 0.6	<i>ybaA-ybaE-F</i>	similar to ABC transporter
<i>ybxA</i>	1.5 ± 0.2	4.0 ± 0.6	4.6 ± 0.6	4.6 ± 0.8	3.8 ± 0.2	<i>ybxA-ybaE-F</i>	similar to ABC transporter
<i>yckK</i>	1.6 ± 0.1	2.2 ± 0.3	2.1 ± 0.3	3.8 ± 0.7	2.8 ± 0.4	<i>yckI-J-K</i>	similar to glutamine ABC transporter
<i>yclN</i>	0.4 ± 0.1	5.6 ± 1.5	3.1 ± 0.1	4.5 ± 0.6	2.6 ± 0.7	<i>yclN-O-P-Q</i>	similar to ferrichrome ABC transporter
<i>yhcJ</i>	3.2 ± 0.3	4.0 ± 1.3	3.0 ± 0.3	3.5 ± 1.0	3.3 ± 1.0	<i>yhcJ-N</i>	similar to ferrichrome ABC transporter
<i>yhcL</i>	3.5 ± 0.3	3.6 ± 1.0	5.0 ± 0.8	4.8 ± 0.3	5.5 ± 1.0	<i>yhc operon</i>	similar to sodium-glutamate symporter
<i>ykoD</i>	1.7 ± 0.1	6.8 ± 1.0	4.1 ± 0.8	7.1 ± 1.4	6.8 ± 1.4	<i>ykoC-D-E</i>	similar to cation ABC transporter
<i>yqiX</i>	4.2 ± 0.4	6.1 ± 1.2	2.7 ± 0.8	1.2 ± 0.2	0.3 ± 0.1	<i>yqiX-W</i>	similar to amino acid ABC transporter
<i>yqiY</i>	3.0 ± 0.1	4.4 ± 1.0	2.8 ± 0.6	2.4 ± 0.3	0.7 ± 0.2	<i>yqiY-Z</i>	similar to amino acid ABC transporter
<i>ytrB</i>	0.5 ± 0.2	1.1 ± 0.1	5.4 ± 0.6	10.5 ± 1.5	6.7 ± 2.2	<i>ytrA-B-C-E-F</i>	similar to ABC transporter
<i>ytrE</i>	0.3 ± 0.1	1.6 ± 0.1	4.1 ± 0.7	8.3 ± 2.6	6.3 ± 0.7	<i>ytrA-B-C-E-F</i>	similar to ABC transporter
<i>yutK</i>	1.8 ± 0.1	4.0 ± 0.7	3.3 ± 0.2	4.5 ± 0.6	2.7 ± 0.2	<i>yutK</i>	similar to Na+/nucleoside cotransporter
<i>yvbW</i>	1.6 ± 0.2	4.5 ± 0.2	3.6 ± 0.8	2.7 ± 0.5	2.7 ± 0.4	<i>yvbT-W</i>	similar to amino acid permease
<i>yveA</i>	1.2 ± 0.2	1.6 ± 0.1	1.2 ± 0.2	3.1 ± 0.7	3.2 ± 0.3	<i>yveA</i>	similar to permease
<i>yxdl</i>	7.7 ± 0.2	8.0 ± 1.5	8.3 ± 1.2	11.1 ± 2.8	8.7 ± 1.7	<i>yxdkL-M</i>	similar to ABC transporter
<i>yxdm</i>	4.0 ± 0.1	2.7 ± 0.2	3.3 ± 0.4	2.6 ± 0.1	2.8 ± 0.2	<i>yxdkL-M</i>	similar to ABC transporter
Electron transport chain and ATP synthase							
<i>atpA</i>	1.4 ± 0.3	4.2 ± 0.8	5.6 ± 1.6	6.0 ± 1.4	7.5 ± 1.4	<i>atpB-F-H-A-G-D-C</i>	ATP synthase (subunit alpha)

<i>atpB</i>	1.6 ± 0.2	7.4 ± 0.7	8.3 ± 2.3	7.4 ± 0.8	9.1 ± 0.7	<i>atpB-F-H-A-G-D-C</i>	ATP synthase (subunit a)
<i>atpC</i>	1.4 ± 0.2	4.0 ± 0.6	4.7 ± 0.5	5.9 ± 1.8	4.3 ± 0.7	<i>atpB-F-H-A-G-D-C</i>	ATP synthase (subunit epsilon)
<i>atpD</i>	1.2 ± 0.2	5.3 ± 0.3	3.7 ± 1.8	5.3 ± 1.3	5.9 ± 1.5	<i>atpB-F-H-A-G-D-C</i>	ATP synthase (subunit beta)
<i>atpF</i>	1.3 ± 0.1	7.4 ± 1.2	7.8 ± 2.6	8.4 ± 0.7	8.6 ± 1.1	<i>atpB-F-H-A-G-D-C</i>	ATP synthase (subunit b)
<i>atpG</i>	1.4 ± 0.2	7.5 ± 1.5	11.0 ± 43.0	7.7 ± 1.2	12.4 ± 2.2	<i>atpB-F-H-A-G-D-C</i>	ATP synthase (subunit gamma)
<i>ykuU</i>	0.9 ± 0.1	2.6 ± 0.2	3.4 ± 0.3	4.0 ± 0.8	4.9 ± 0.7	<i>ykuU-V</i>	similar to 2-cys peroxiredoxin
Motility and chemotaxis							
<i>cheC</i>	1.8 ± 0.1	7.6 ± 0.8	6.3 ± 0.7	7.0 ± 1.2	6.6 ± 0.8	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	inhibition of CheR-mediated methylation of MCPs
<i>cheD</i>	1.5 ± 0.3	4.2 ± 1.0	5.1 ± 0.9	4.8 ± 1.1	4.2 ± 0.9	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	required for methylation of methyl-accepting chemotaxis proteins by CheR
<i>cheW</i>	1.5 ± 0.1	3.9 ± 0.8	4.5 ± 1.0	4.0 ± 0.7	4.8 ± 0.6	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	modulation of CheA activity in response to attractants
<i>BLi03295</i>	1.0 ± 0.6	1.3 ± 0.1	4.8 ± 1.2	10.4 ± 1.2	5.5 ± 1.1		close homolog to McpA methyl-accepting chemotaxis protein
<i>BLi03297</i>	1.0 ± 0.2	1.6 ± 0.2	3.2 ± 1.1	3.6 ± 1.2	3.4 ± 0.6		close homolog to McpA methyl-accepting chemotaxis protein
<i>flgB</i>	0.8 ± 0.2	1.9 ± 0.1	4.2 ± 0.2	6.6 ± 1.1	6.8 ± 0.9	<i>flgB-fliR</i>	flagellar basal-body rod protein
<i>flgE</i>	1.2 ± 0.1	4.8 ± 0.7	7.2 ± 1.6	10.9 ± 1.7	11.1 ± 2.0	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar hook protein
<i>flgK</i>	1.2 ± 0.4	1.1 ± 0.1	2.7 ± 0.2	6.2 ± 2.4	4.1 ± 0.1	<i>flgK-L</i>	flagellar hook-associated protein 1 (HAP1)
<i>flgL</i>	1.4 ± 0.3	1.2 ± 0.2	3.2 ± 0.6	4.1 ± 0.2	4.4 ± 1.3	<i>flgK-L</i>	flagellar hook-associated protein 3 (HAP3)
<i>flhB</i>	1.5 ± 0.5	7.7 ± 1.1	8.6 ± 1.1	11.4 ± 2.2	10.1 ± 0.8	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagella-associated protein
<i>flhF</i>	1.6 ± 0.4	4.4 ± 1.1	3.2 ± 0.8	4.4 ± 0.4	3.4 ± 0.7	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagella-associated protein
<i>flhO</i>	1.0 ± 0.1	1.7 ± 0.1	4.3 ± 0.2	4.9 ± 1.1	4.6 ± 0.7	<i>flhO-P</i>	flagellar basal-body rod protein
<i>flhP</i>	1.1 ± 0.1	1.6 ± 0.2	5.4 ± 1.6	7.5 ± 0.8	6.3 ± 1.1	<i>flhO-P</i>	flagellar hook-basal body protein
<i>fliD</i>	1.0 ± 0.1	1.8 ± 0.1	5.3 ± 1.1	6.8 ± 1.3	6.9 ± 1.2	<i>hag-fliD</i>	flagellar hook-associated protein 2 (HAP2)
<i>fliE</i>	0.9 ± 0.1	1.5 ± 0.6	1.8 ± 0.1	3.6 ± 0.2	3.4 ± 0.5	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar hook-basal body protein
<i>fliF</i>	1.1 ± 0.1	2.4 ± 0.1	3.6 ± 0.5	4.4 ± 1.1	4.8 ± 0.3	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar basal-body M-ring protein
<i>fliG</i>	1.1 ± 0.1	3.0 ± 0.5	5.0 ± 1.2	5.0 ± 0.7	5.3 ± 0.9	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar motor switch protein
<i>fliH</i>	1.2 ± 0.2	3.3 ± 1.3	4.8 ± 0.9	6.7 ± 1.4	7.8 ± 0.9	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar assembly protein

<i>fliI</i>	1.1 ± 0.2	4.2 ± 0.7	5.4 ± 1.1	4.8 ± 1.0	6.5 ± 0.9	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar-specific ATP synthase
<i>fliJ</i>	1.1 ± 0.2	3.8 ± 0.8	7.4 ± 1.4	10.0 ± 2.2	10.1 ± 1.2	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar protein required for formation of basal body
<i>fliK</i>	1.1 ± 0.2	5.0 ± 0.5	5.8 ± 1.0	7.7 ± 1.5	7.3 ± 1.1	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar hook-length control
<i>fliM</i>	1.3 ± 0.1	4.1 ± 0.9	6.5 ± 1.3	9.8 ± 1.8	7.3 ± 1.4	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar motor switch protein
<i>fliP</i>	1.5 ± 0.1	4.9 ± 1.6	8.9 ± 2.7	5.9 ± 1.0	9.8 ± 2.8	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar protein required for flagellar formation
<i>fliR</i>	1.7 ± 0.2	6.1 ± 0.7	7.8 ± 2.3	6.2 ± 1.9	5.9 ± 1.3	<i>flgB-fliR</i>	flagellar protein required for flagellar formation
<i>fliY</i>	1.3 ± 0.1	4.1 ± 0.9	4.6 ± 0.8	4.1 ± 0.8	5.4 ± 0.8	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar motor switch protein
<i>fliZ</i>	1.6 ± 0.2	5.2 ± 1.5	8.2 ± 0.9	11.0 ± 1.7	12.1 ± 4.0	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	flagellar protein required for flagellar formation
<i>hag</i>	0.9 ± 0.1	1.5 ± 0.1	7.4 ± 1.1	12.3 ± 2.2	20.2 ± 4.8	<i>hag-fliD</i>	flagellin protein
<i>motA</i>	1.1 ± 0.1	1.5 ± 0.3	2.7 ± 0.3	2.4 ± 0.4	2.7 ± 0.3	<i>motA-B</i>	motility protein
<i>tlpB</i>	1.3 ± 0.1	2.3 ± 0.2	4.6 ± 0.5	4.7 ± 0.1	4.6 ± 0.3	<i>tlpB</i>	methyl-accepting chemotaxis protein
<i>ylxG</i>	1.1 ± 0.1	2.6 ± 0.1	4.9 ± 1.0	6.0 ± 0.2	6.7 ± 1.4	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	similar to flagellar hook assembly protein
<i>ylxH</i>	1.6 ± 0.3	8.9 ± 1.2	5.6 ± 1.3	5.3 ± 1.2	4.9 ± 0.6	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	similar to flagellar biosynthesis switch protein
<i>yvyG</i> signal transduction	1.2 ± 0.1	1.6 ± 1.0	1.9 ± 0.1	3.8 ± 0.7	3.5 ± 0.2	<i>yvyF-G</i>	similar to flagellar protein
<i>cheA</i>	1.5 ± 0.1	6.2 ± 1.3	7.9 ± 1.1	8.7 ± 1.4	9.3 ± 0.7	<i>cheD.ylxH-flhF.fliP.cheY-</i> <i>fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>	two-component sensor histidine kinase chemotactic signal modulator
Protein secretion							
<i>ffh</i>	1.7 ± 0.1	2.8 ± 0.1	3.3 ± 0.5	3.8 ± 0.1	4.3 ± 0.6	<i>ffh</i>	signal recognition particle-like (SRP) component
<i>secY</i>	1.8 ± 0.4	16.7 ± 2.3	14.8 ± 3.4	25.0 ± 0.3	15.7 ± 4.3	<i>rplR-secY-adk-map</i>	preprotein translocase subunit
Cell division							
<i>ftsX</i>	1.8 ± 0.1	3.1 ± 0.3	4.3 ± 1.1	6.5 ± 0.8	5.2 ± 0.6	<i>ftsE-X</i>	cell-division protein
<i>gid</i>	1.3 ± 0.1	3.6 ± 0.4	3.6 ± 0.6	3.4 ± 0.8	4.2 ± 0.8	<i>gid</i>	glucose-inhibited division protein
<i>maf</i>	1.1 ± 0.1	3.2 ± 0.1	2.7 ± 0.2	3.1 ± 0.9	2.8 ± 0.1	<i>maf-nifS</i>	septum formation
Sporulation							
<i>cotX</i>	1.3 ± 0.2	2.8 ± 0.3	2.0 ± 0.5	3.0 ± 0.4	2.2 ± 0.2	<i>cotX</i>	spore coat protein

<i>safA</i>	1.4 ± 0.1	5.4 ± 1.1	1.2 ± 0.3	9.8 ± 1.4	1.5 ± 0.2	<i>safA</i>	morphogenetic protein associated with SpoVID
<i>spolIID</i>	0.9 ± 0.2	3.0 ± 0.5	1.5 ± 0.1	2.9 ± 0.6	3.4 ± 0.4	<i>murAA-spolIID</i>	required for complete dissolution of the asymmetric septum
<i>spolIIAB</i>	1.4 ± 0.1	3.6 ± 0.5	3.4 ± 0.5	3.0 ± 0.4	3.4 ± 0.8	<i>spolIIAH-AG-AF-AE-AD-AB-AA</i>	mutants block sporulation after engulfment
<i>ytgP</i>	1.2 ± 0.2	3.6 ± 0.6	3.0 ± 0.6	3.6 ± 0.8	2.7 ± 0.2	<i>ytgP</i>	similar to spore cortex protein
Specific pathways							
<i>ackA*</i>	1.8 ± 0.2	2.7 ± 0.3	4.0 ± 0.8	5.2 ± 1.2	3.0 ± 0.9	<i>moaB-ackA</i>	acetate kinase
<i>dxr</i>	1.2 ± 0.2	3.9 ± 0.5	4.3 ± 0.7	3.2 ± 0.6	4.2 ± 0.8	<i>dxr-cdsA-uppS-frr</i>	probable 1-deoxy-D-xylulose-5-phosphate reductoisomerase
<i>mgsA</i>	1.1 ± 0.2	2.0 ± 0.1	2.2 ± 0.5	1.7 ± 0.1	2.0 ± 0.8	<i>mgsA</i>	probable methylglyoxal synthase
<i>yfmT</i>	1.1 ± 0.3	3.8 ± 0.7	6.2 ± 0.7	6.5 ± 1.3	3.9 ± 0.4	<i>yfmS-T</i>	similar to benzaldehyde dehydrogenase
<i>yheN</i>	1.4 ± 0.1	2.3 ± 0.9	3.3 ± 0.4	4.2 ± 0.9	3.9 ± 0.3	<i>yheN</i>	similar to endo-1,4-beta-xylanase
<i>ykrW</i>	3.6 ± 0.1	3.0 ± 0.5	5.3 ± 1.6	4.5 ± 0.1	5.2 ± 1.2	<i>ykr operon</i>	similar to ribulose-bisphosphate carboxylase
<i>ykuF</i>	1.3 ± 0.3	2.9 ± 0.6	2.6 ± 0.7	3.4 ± 0.6	2.8 ± 0.2	<i>yku operon</i>	similar to glucose 1-dehydrogenase
<i>yIxY</i>	1.3 ± 0.1	2.9 ± 0.4	3.3 ± 0.7	3.4 ± 0.6	3.7 ± 0.7	<i>yIxY</i>	similar to deacetylase
<i>yvgN</i>	0.8 ± 0.1	1.7 ± 0.1	2.1 ± 0.5	3.2 ± 1.5	2.9 ± 0.5	<i>yvg operon</i>	similar to dehydrogenase
<i>ywjL</i>	1.1 ± 0.1	2.8 ± 0.7	2.7 ± 0.1	2.6 ± 0.8	2.6 ± 0.4	<i>ywjL-J</i>	similar to glycerol-inducible protein
<i>BLi02851</i>	0.6 ± 0.3	2.0 ± 0.1	4.1 ± 1.0	3.9 ± 0.6	2.8 ± 0.5		putative methyltransferase
<i>BLi03803</i>	1.6 ± 0.1	4.1 ± 0.3	4.5 ± 0.8	6.1 ± 1.0	4.7 ± 0.5		putative NDP-sugar epimerase
Main glycolytic pathways							
<i>eno*</i>	1.2 ± 0.2	16.7 ± 3.9	20.3 ± 3.0	25.0 ± 0.1	22.5 ± 2.7	<i>gapA-pgk-tpiA-pgm-eno</i>	enolase
<i>gapA*</i>	1.2 ± 0.1	10.5 ± 1.8	26.7 ± 4.9	26.1 ± 6.0	25.7 ± 4.8	<i>gapA-pgk-tpiA-pgm-eno</i>	glyceraldehyde-3-phosphate dehydrogenase
<i>pdhA</i>	1.6 ± 0.1	18.0 ± 8.1	11.8 ± 2.2	11.3 ± 1.8	12.0 ± 2.9	<i>pdhA-B-C-D</i>	pyruvate dehydrogenase
<i>pdhB</i>	1.6 ± 0.1	7.9 ± 2.5	11.2 ± 2.0	9.5 ± 1.4	11.2 ± 1.9	<i>pdhA-B-C-D</i>	pyruvate dehydrogenase
<i>pdhC*</i>	1.3 ± 0.2	5.1 ± 0.7	7.0 ± 1.8	10.7 ± 2.7	13.5 ± 1.6	<i>pdhA-B-C-D</i>	pyruvate dehydrogenase
<i>pdhD*</i>	1.2 ± 0.3	6.0 ± 0.6	7.1 ± 1.1	5.9 ± 0.6	8.8 ± 0.8	<i>pdhA-B-C-D</i>	pyruvate dehydrogenase
<i>pgk*</i>	1.1 ± 0.2	25.8 ± 8.8	26.3 ± 6.7	33.3 ± 0.2	25.7 ± 4.8	<i>gapA-pgk-tpiA-pgm-eno</i>	phosphoglycerate kinase
<i>pgm*</i>	1.4 ± 0.1	24.6 ± 6.3	19.2 ± 1.7	23.3 ± 6.7	18.7 ± 5.0	<i>gapA-pgk-tpiA-pgm-eno</i>	phosphoglycerate mutase
<i>tkt</i>	0.6 ± 0.1	3.7 ± 0.4	4.0 ± 0.3	5.1 ± 0.2	5.4 ± 0.7	<i>tkt</i>	transketolase
<i>tpiA</i>	1.2 ± 0.2	13.6 ± 3.6	14.8 ± 1.6	21.7 ± 2.9	18.2 ± 7.5	<i>gapA-pgk-tpiA-pgm-eno</i>	triose phosphate isomerase
TCA cycle							
<i>icd</i>	0.6 ± 0.1	2.8 ± 0.6	1.8 ± 0.1	4.1 ± 1.3	3.1 ± 0.3	<i>icd</i>	isocitrate dehydrogenase
<i>sdhA</i>	0.5 ± 0.1	3.6 ± 0.3	2.0 ± 0.1	3.3 ± 0.1	2.8 ± 0.2	<i>sdhA-B-C</i>	succinate dehydrogenase
<i>sdhB</i>	0.6 ± 0.1	3.5 ± 0.5	2.6 ± 0.2	3.3 ± 0.3	2.7 ± 0.3	<i>sdhA-B-C</i>	succinate dehydrogenase
<i>sdhC</i>	0.6 ± 0.1	3.7 ± 0.2	2.8 ± 0.1	4.6 ± 0.5	3.9 ± 0.7	<i>sdhA-B-C</i>	succinate dehydrogenase

<i>sucC</i>	0.7 ± 0.1	2.3 ± 0.2	3.0 ± 0.8	3.1 ± 0.4	3.8 ± 0.8	<i>sucC-D</i>	succinyl-CoA synthetase
<i>sucD</i>	0.9 ± 0.6	2.7 ± 0.2	3.4 ± 0.2	3.3 ± 0.3	4.2 ± 0.7	<i>sucC-D</i>	succinyl-CoA synthetase
Metabolism of amino acids and related molecules							
<i>alr</i>	1.4 ± 0.1	2.9 ± 0.6	3.0 ± 0.8	6.3 ± 1.5	2.7 ± 1.0	<i>alr</i>	D-alanine racemase
<i>ampS</i>	0.6 ± 0.1	4.3 ± 0.9	4.0 ± 1.0	6.3 ± 1.0	5.7 ± 0.7	<i>ampS</i>	aminopeptidase
<i>argB</i>	4.8 ± 0.6	4.5 ± 1.2	5.5 ± 0.9	5.0 ± 1.9	0.6 ± 0.2	<i>argC-J-B-D-carA-B-argF</i>	N-acetylglutamate 5-phosphotransferase
<i>argC</i>	3.7 ± 0.2	4.7 ± 0.3	4.0 ± 0.6	3.5 ± 0.3	0.6 ± 0.3	<i>argC-J-B-D-carA-B-argF</i>	N-acetylglutamate gamma-semialdehyde dehydrogenase
<i>argD</i>	3.6 ± 0.7	5.1 ± 1.6	5.1 ± 1.2	4.0 ± 1.1	0.8 ± 0.4	<i>argC-J-B-D-carA-B-argF</i>	N-acetylornithine aminotransferase
<i>argF</i>	4.9 ± 0.2	3.2 ± 0.2	4.8 ± 0.6	3.8 ± 0.8	1.1 ± 0.4	<i>argC-J-B-D-carA-B-argF</i>	ornithine carbamoyltransferase
<i>argG</i>	5.0 ± 1.0	6.1 ± 0.8	6.8 ± 1.7	2.1 ± 0.7	0.2 ± 0.2	<i>argG-H</i>	argininosuccinate synthase
<i>argH</i>	6.0 ± 0.5	12.1 ± 2.2	10.4 ± 2.8	3.3 ± 0.4	0.3 ± 0.1	<i>argG-H</i>	argininosuccinate lyase
<i>argJ</i>	5.6 ± 1.1	8.7 ± 2.2	5.0 ± 0.9	5.4 ± 1.2	0.6 ± 0.2	<i>argC-J-B-D-carA-B-argF</i>	ornithine acetyltransferase
<i>carA</i>	6.3 ± 0.7	8.7 ± 1.1	9.4 ± 2.0	9.1 ± 1.2	1.2 ± 0.1	<i>argC-J-B-D-carA-B-argF</i>	carbamoyl-phosphate transferase-arginine
<i>carB</i>	4.7 ± 0.8	11.8 ± 1.1	10.5 ± 1.8	9.5 ± 2.3	1.5 ± 0.3	<i>argC-J-B-D-carA-B-argF</i>	carbamoyl-phosphate transferase-arginine
<i>cysC</i>	2.4 ± 0.3	3.5 ± 0.4	3.9 ± 0.6	4.3 ± 1.2	1.1 ± 0.1	<i>cysH-P-sat-cysC-ylnD-E-F</i>	probable adenylsulfate kinase
<i>gcvPA</i>	1.4 ± 0.2	2.9 ± 0.6	4.7 ± 1.0	3.4 ± 0.7	4.3 ± 0.3	<i>gcvT-gcvPA-PB</i>	probable glycine decarboxylase
<i>gcvPB</i>	1.6 ± 0.1	2.7 ± 0.6	4.0 ± 1.8	5.2 ± 0.6	7.3 ± 1.1	<i>gcvT-gcvPA-PB</i>	probable glycine decarboxylase
<i>goxB</i>	1.0 ± 0.1	2.9 ± 0.4	1.7 ± 0.1	5.2 ± 1.0	3.7 ± 1.0	<i>goxB</i>	glycine oxidase
<i>ilvB</i>	1.9 ± 0.3	8.5 ± 0.5	7.4 ± 1.4	9.8 ± 0.5	9.4 ± 1.9	<i>ilvB-H-C-leuA-B-C-D</i>	acetolactate synthase (large subunit)
<i>ilvC</i>	1.4 ± 0.1	6.5 ± 1.5	6.6 ± 1.1	9.5 ± 1.4	8.3 ± 1.7	<i>ilvB-H-C-leuA-B-C-D</i>	ketol-acid reductoisomerase
<i>ilvH</i>	1.8 ± 0.2	7.0 ± 1.6	7.6 ± 1.6	7.7 ± 0.1	6.7 ± 1.3	<i>ilvB-H-C-leuA-B-C-D</i>	acetolactate synthase (small subunit)
<i>leuA</i>	1.8 ± 0.1	8.5 ± 0.4	9.3 ± 2.0	15.1 ± 2.4	3.6 ± 2.7	<i>ilvB-H-C-leuA-B-C-D</i>	2-isopropylmalate synthase
<i>leuB</i>	1.9 ± 0.3	8.9 ± 0.8	9.8 ± 1.1	14.3 ± 2.1	11.0 ± 1.9	<i>ilvB-H-C-leuA-B-C-D</i>	3-isopropylmalate dehydrogenase
<i>leuC</i>	1.9 ± 0.2	2.0 ± 0.4	4.7 ± 0.9	2.2 ± 0.7	5.2 ± 1.3	<i>ilvB-H-C-leuA-B-C-D</i>	3-isopropylmalate dehydratase (large subunit)
<i>leuD</i>	2.5 ± 0.1	4.7 ± 0.3	6.2 ± 0.2	6.0 ± 1.7	3.1 ± 1.2	<i>ilvB-H-C-leuA-B-C-D</i>	3-isopropylmalate dehydratase (small subunit)
<i>yjcl</i>	6.5 ± 1.2	6.8 ± 0.8	12.5 ± 1.5	17.8 ± 1.9	9.1 ± 0.5	<i>yjcl-J-L</i>	similar to cystathione gamma-synthase
<i>yjcJ</i>	5.6 ± 0.3	5.0 ± 0.6	6.5 ± 1.1	7.4 ± 1.5	6.0 ± 1.1	<i>yjcl-J-L</i>	similar to cystathione beta-lyase
<i>ykrV</i>	3.2 ± 0.3	3.1 ± 0.9	3.2 ± 0.6	3.2 ± 0.1	1.8 ± 0.2	<i>ykrV-W..</i>	similar to aspartate aminotransferase
<i>ykuQ</i>	1.3 ± 0.1	3.0 ± 0.4	4.5 ± 0.7	5.4 ± 0.3	4.7 ± 1.0	<i>ykuP-Q</i>	similar to tetrahydrodipicolinate succinylase
<i>yrhB</i>	2.9 ± 0.3	4.2 ± 0.2	5.3 ± 0.5	5.4 ± 1.3	3.6 ± 1.0	<i>yrhA-B</i>	similar to cystathione gamma-synthase
Metabolism of nucleotides and nucleic acids							
<i>adk</i>	2.7 ± 0.3	25.8 ± 5.5	31.9 ± 3.4	29.2 ± 4.8	25.6 ± 4.3	<i>rplR-secY-adk-map</i>	adenylate kinase
<i>guaA</i>	1.4 ± 0.1	5.3 ± 0.6	5.3 ± 1.3	8.7 ± 1.3	4.8 ± 1.0	<i>guaA</i>	GMP synthetase
<i>nrdE</i>	1.2 ± 0.3	3.5 ± 0.4	1.9 ± 0.4	4.3 ± 0.8	2.6 ± 0.8	<i>nrdE-nrdF</i>	ribonucleoside-diphosphate reductase

<i>nrdF</i>	1.5 ± 0.1	3.2 ± 0.5	1.9 ± 0.3	3.3 ± 1.0	3.3 ± 0.7	<i>nrdE-nrdF</i>	ribonucleoside-diphosphate reductase
<i>prs</i>	1.2 ± 0.2	3.1 ± 0.5	3.0 ± 0.3	3.8 ± 0.7	3.4 ± 0.5	<i>prs</i>	phosphoribosylpyrophosphate synthetase
<i>purB</i>	0.9 ± 0.1	10.1 ± 3.6	4.9 ± 1.5	6.4 ± 1.0	4.8 ± 0.4	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	adenylosuccinate lyase
<i>purC</i>	0.7 ± 0.1	7.7 ± 1.4	8.0 ± 0.7	8.3 ± 2.0	9.3 ± 2.1	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole succinocarboxamide synthetase
<i>purD</i>	1.0 ± 0.1	11.6 ± 2.1	5.2 ± 1.8	10.5 ± 1.8	6.4 ± 1.2	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylglycinamide synthetase
<i>purE</i>	1.0 ± 0.2	4.5 ± 1.6	2.9 ± 0.6	2.7 ± 0.3	2.3 ± 0.6	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole carboxylase I
<i>purF</i>	1.0 ± 0.2	11.7 ± 1.4	11.7 ± 1.4	10.3 ± 0.6	11.4 ± 1.0	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	glutamine phosphoribosylpyrophosphate amidotransferase
<i>purH</i>	1.0 ± 0.2	15.2 ± 4.2	10.3 ± 3.0	13.3 ± 1.0	14.8 ± 1.5	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole carboxy formyl formyltransferase
<i>purK</i>	0.8 ± 0.2	5.6 ± 0.7	3.9 ± 0.5	3.0 ± 0.1	3.9 ± 0.6	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole carboxylase II
<i>purL</i>	1.1 ± 0.1	12.9 ± 2.5	9.5 ± 1.4	8.2 ± 0.3	10.3 ± 0.6	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylformylglycinamide synthetase II
<i>purM</i>	1.0 ± 0.1	12.5 ± 3.6	6.9 ± 0.5	5.6 ± 0.6	5.5 ± 0.9	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylaminoimidazole synthetase
<i>purN</i>	1.1 ± 0.3	15.9 ± 4.8	9.7 ± 1.4	11.4 ± 2.2	12.3 ± 2.7	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylglycinamide formyltransferase
<i>purQ</i>	1.0 ± 0.1	6.6 ± 1.7	7.8 ± 1.7	6.1 ± 1.1	8.2 ± 1.1	<i>purE-K-B-C-Q-L-F-M-N-H-D</i>	phosphoribosylformylglycinamide synthetase I
<i>pyrAA</i>	0.9 ± 0.1	8.9 ± 0.4	6.0 ± 2.4	7.3 ± 1.5	7.0 ± 0.7	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	carbamoyl-phosphate synthetase
<i>pyrAB</i>	1.1 ± 0.1	5.4 ± 1.4	4.0 ± 1.3	5.5 ± 1.7	3.8 ± 0.8	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	carbamoyl-phosphate synthetase
<i>pyrB</i>	0.9 ± 0.2	4.2 ± 0.4	5.4 ± 0.2	4.7 ± 2.1	3.8 ± 1.0	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	aspartate carbamoyltransferase
<i>pyrC</i>	0.9 ± 0.1	5.2 ± 1.0	3.1 ± 0.3	4.3 ± 0.8	3.4 ± 0.8	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	dihydroorotase
<i>pyrD</i>	1.2 ± 0.1	4.3 ± 1.0	3.5 ± 0.2	3.7 ± 1.0	3.7 ± 0.3	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	dihydroorotate dehydrogenase
<i>pyrE</i>	0.9 ± 0.1	6.9 ± 0.3	4.2 ± 0.1	8.9 ± 1.2	5.4 ± 0.9	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	orotate phosphoribosyltransferase
<i>pyrF</i>	1.0 ± 0.1	5.6 ± 0.7	3.9 ± 0.2	7.5 ± 2.1	4.1 ± 0.6	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	orotidine 5'-phosphate decarboxylase
<i>pyrG</i>	2.3 ± 0.3	4.3 ± 1.1	4.3 ± 0.7	8.5 ± 1.4	4.3 ± 1.7	<i>pyrG-rpoE</i>	CTP synthetase
<i>pyrH</i>	1.6 ± 0.2	6.1 ± 1.6	7.7 ± 1.8	3.8 ± 0.6	8.7 ± 1.7	<i>pyrH-frr</i>	uridylate kinase
<i>pyrK</i>	0.9 ± 0.2	11.5 ± 1.2	5.6 ± 0.9	10.9 ± 1.2	9.4 ± 0.5	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	dihydroorotate dehydrogenase
<i>pyrP</i>	1.1 ± 0.3	5.4 ± 0.7	3.6 ± 0.1	4.1 ± 1.1	3.6 ± 0.3	<i>pyrR-P-B-C-AA-AB-K-D-F-E</i>	uracil permease
<i>udk</i>	1.5 ± 0.3	3.1 ± 0.1	4.0 ± 0.4	4.0 ± 0.7	3.5 ± 0.4	<i>udk</i>	uridine kinase
<i>ymaA</i>	1.3 ± 0.4	2.6 ± 0.2	2.4 ± 0.8	3.5 ± 0.3	3.4 ± 1.0	<i>ymaA-F</i>	similar to Nrdl protein
<i>BLi02962</i>	1.7 ± 0.1	2.4 ± 0.2	3.9 ± 0.1	3.5 ± 0.7	5.6 ± 0.6		putative branched-chain amino acid aminotransferase
Metabolism of lipids							
<i>accA</i>	0.6 ± 0.1	3.1 ± 1.0	2.0 ± 0.2	3.6 ± 0.6	2.6 ± 0.6	<i>pfkA-accA-D</i>	acetyl-CoA carboxylase (alpha subunit)
<i>bkdAA</i>	2.2 ± 0.1	4.0 ± 0.4	4.1 ± 0.6	3.5 ± 0.8	3.0 ± 0.4	<i>lpdV-bkdAA-AB-B</i>	branched-chain alpha-keto acid dehydrogenase E1 subunit
<i>bkdAB</i>	2.3 ± 0.3	5.4 ± 0.6	3.2 ± 0.8	3.7 ± 0.7	2.2 ± 0.5	<i>lpdV-bkdAA-AB-B</i>	Bbranched-chain alpha-keto acid dehydrogenase E1 subunit
<i>cdsA</i>	1.6 ± 0.2	6.3 ± 1.7	6.8 ± 1.7	5.3 ± 1.7	6.1 ± 1.5	<i>uppS-cdsA-dxr</i>	phosphatidate cytidylyltransferase
<i>fabD</i>	2.8 ± 0.1	4.8 ± 0.7	6.7 ± 0.5	8.2 ± 0.3	6.3 ± 1.3	<i>plsX-fabD-G</i>	malonyl CoA-acyl carrier protein transacylase
<i>fabG</i>	2.7 ± 0.2	4.6 ± 0.2	6.3 ± 0.6	5.6 ± 1.1	6.0 ± 0.6	<i>plsX-fabD-G</i>	beta-ketoacyl-acyl carrier protein reductase

<i>fabL</i>	1.4 ± 0.1	3.1 ± 0.3	3.2 ± 0.5	4.8 ± 1.0	3.4 ± 0.8	<i>fabL</i>	enoyl-acyl carrier protein reductase
<i>lpdV</i>	2.0 ± 0.1	3.6 ± 0.7	3.0 ± 0.9	2.8 ± 0.5	2.2 ± 0.3	<i>lpdV-bkdAA-AB-B</i>	probable branched-chain alpha-keto acid dehydrogenase E3 subunit
<i>plsX</i>	2.1 ± 0.2	2.8 ± 0.6	3.2 ± 1.0	3.4 ± 0.8	2.5 ± 0.1	<i>plsX-fabD-G</i>	involved in fatty acid/phospholipid synthesis
<i>ptb</i>	2.3 ± 0.1	5.9 ± 0.7	3.6 ± 0.7	5.0 ± 0.9	3.2 ± 0.9	<i>ptb</i>	probable phosphate butyryltransferase
<i>uppS</i>	1.1 ± 0.1	3.9 ± 0.6	3.7 ± 1.6	3.9 ± 1.5	2.3 ± 0.4	<i>uppS-cdsA-dxr</i>	probable undecaprenyl pyrophosphate synthetase
Metabolism of coenzymes and prosthetic groups							
<i>bioA</i>	1.9 ± 0.4	8.5 ± 1.2	11.7 ± 3.6	11.1 ± 3.9	11.4 ± 0.9	<i>bioA-F-D-B-I</i>	adenosylmethionine-8-amino-7-oxononanoate aminotransferase
<i>bioB</i>	1.7 ± 0.4	20.0 ± 0.3	16.5 ± 3.1	21.7 ± 2.9	12.9 ± 2.8	<i>bioA-F-D-B-I</i>	biotin synthetase
<i>bioD</i>	1.8 ± 0.2	28.9 ± 7.7	25.7 ± 7.6	25.8 ± 5.5	30.8 ± 5.5	<i>bioA-F-D-B-I</i>	dethiobiotin synthetase
<i>bioF</i>	1.9 ± 0.1	12.1 ± 4.8	10.9 ± 1.2	10.1 ± 1.0	12.5 ± 1.5	<i>bioA-F-D-B-I</i>	8-amino-7-oxononanoate synthase
<i>biol</i>	2.2 ± 0.3	9.6 ± 2.4	10.0 ± 1.8	12.5 ± 1.8	10.5 ± 2.3	<i>bioA-F-D-B-I</i>	cytochrome P450 enzyme
<i>dhbC</i>	0.6 ± 0.5	1.5 ± 0.2	2.8 ± 0.7	3.2 ± 0.5	3.2 ± 0.2	<i>dhbA-B-C-D-E-F</i>	isochorismate synthase
<i>menF</i>	1.3 ± 0.2	2.2 ± 0.3	3.3 ± 0.5	4.8 ± 1.0	3.4 ± 0.6	<i>men operon</i>	menaquinone-specific isochorismate synthase
<i>moaB</i>	2.1 ± 0.1	6.3 ± 0.9	5.1 ± 0.6	3.1 ± 0.5	1.2 ± 0.4	<i>moaB-ackA</i>	molybdopterin precursor biosynthesis
<i>panB</i>	1.2 ± 0.5	2.6 ± 0.2	2.9 ± 0.6	3.3 ± 0.4	2.9 ± 0.3	<i>panB-C</i>	ketopantoate hydroxymethyltransferase
<i>panC</i>	1.4 ± 0.1	4.3 ± 0.7	3.7 ± 0.5	3.5 ± 1.1	3.6 ± 1.0	<i>panB-C</i>	pantothenate synthetase
<i>thiF</i>	0.9 ± 0.2	3.4 ± 0.4	2.1 ± 0.6	7.7 ± 0.5	4.5 ± 0.8	<i>tenA-l-goxB-thiG-F-yjbV</i>	hydroxyethylthiazole phosphate biosynthesis
<i>thiG</i>	0.9 ± 0.1	3.4 ± 1.0	2.7 ± 0.4	4.1 ± 1.0	2.8 ± 0.6	<i>tenA-l-goxB-thiG-F-yjbV</i>	hydroxyethylthiazole phosphate biosynthesis
<i>yjbV</i>	1.0 ± 0.1	3.0 ± 0.1	2.1 ± 0.2	5.3 ± 0.7	4.0 ± 0.1	<i>tenA-l-goxB-thiG-F-yjbV</i>	similar to phosphomethylpyrimidine kinase
<i>ylnD</i>	1.8 ± 0.1	3.5 ± 1.1	3.1 ± 0.8	2.8 ± 0.5	3.1 ± 0.5	<i>cysP-sat-cysC-ylnD-E-F</i>	similar to uroporphyrin-III C-methyltransferase
Metabolism of sulfur							
<i>sat</i>	2.1 ± 0.1	4.6 ± 0.9	3.8 ± 0.6	6.3 ± 0.9	3.5 ± 0.9	<i>cysH-P-sat-cysC-ylnD-E-F</i>	probable sulfate adenylyltransferase
<i>yvgQ</i>	6.4 ± 0.4	8.9 ± 2.6	10.5 ± 2.7	13.5 ± 2.7	10.3 ± 1.6	<i>yvgQ-R</i>	similar to sulfite reductase
<i>yvgR</i>	6.1 ± 0.6	8.3 ± 0.1	8.2 ± 1.4	15.3 ± 5.5	9.1 ± 2.2	<i>yvgQ-R</i>	similar to sulfite reductase
DNA restriction/modification and repair							
<i>mutS</i>	0.9 ± 0.1	2.8 ± 0.2	3.2 ± 0.6	3.7 ± 0.8	3.2 ± 0.2	<i>mutS-L</i>	DNA mismatch repair (recognition)
<i>radC</i>	0.9 ± 0.1	4.8 ± 0.6	1.8 ± 0.3	4.3 ± 0.5	2.0 ± 0.1	<i>radC</i>	probable DNA repair protein
DNA replication							
<i>dnaA</i>	1.6 ± 0.2	3.7 ± 0.4	3.1 ± 0.8	3.8 ± 0.8	4.0 ± 0.5	<i>dnaA-N</i>	initiation of chromosome replication
<i>dnaN</i>	1.6 ± 0.3	3.3 ± 0.7	2.1 ± 0.3	3.2 ± 0.6	2.5 ± 0.5	<i>dnaA-N</i>	DNA polymerase III (beta subunit)
<i>polC</i>	1.3 ± 0.1	3.8 ± 0.5	3.0 ± 0.6	3.2 ± 0.9	3.0 ± 0.2	<i>polC-proS</i>	DNA polymerase III (alpha subunit)
<i>ssb</i>	2.3 ± 0.1	12.1 ± 1.5	13.3 ± 3.2	16.9 ± 2.3	18.3 ± 1.9	<i>ssb</i>	single-strand DNA-binding protein
DNA packaging and segregation							
<i>parC</i>	0.9 ± 0.1	5.2 ± 0.1	4.0 ± 0.7	6.9 ± 0.6	2.6 ± 0.1	<i>parC</i>	subunit of DNA topoisomerase IV

DNA recombination						
<i>recF</i>	1.1 ± 0.1	4.0 ± 0.3	2.8 ± 0.4	4.4 ± 0.9	2.9 ± 0.3	<i>gyrA-B-recF</i>
<i>recO</i>	0.8 ± 0.1	3.0 ± 0.4	2.5 ± 0.3	2.8 ± 0.4	2.1 ± 0.5	<i>recO</i>
RNA modification						
<i>miaA</i>	1.5 ± 0.1	3.2 ± 0.3	2.4 ± 0.3	5.0 ± 1.5	2.7 ± 0.8	<i>miaA</i>
<i>rimM</i>	1.6 ± 0.2	3.0 ± 0.2	2.6 ± 0.2	3.0 ± 0.6	2.9 ± 0.3	<i>rimM</i>
<i>rnc</i>	2.2 ± 0.2	4.5 ± 1.0	5.7 ± 1.0	4.3 ± 1.0	5.3 ± 0.5	<i>rnc</i>
<i>rnhC</i>	1.0 ± 0.1	1.4 ± 0.1	1.6 ± 0.1	4.6 ± 1.5	2.5 ± 0.4	<i>rnhC</i>
<i>rnpA</i>	1.8 ± 0.2	8.7 ± 1.5	6.2 ± 0.5	7.0 ± 1.1	5.3 ± 0.9	<i>rnpA-spolIIJ-jag</i>
<i>trmD</i>	1.5 ± 0.4	4.4 ± 1.6	2.5 ± 0.5	1.7 ± 0.1	2.7 ± 0.4	<i>trmD</i>
<i>truA</i>	1.9 ± 0.2	4.5 ± 1.1	4.8 ± 0.3	3.3 ± 1.1	3.6 ± 0.9	<i>truA</i>
<i>truB</i>	1.8 ± 0.1	8.2 ± 3.1	3.5 ± 0.8	2.5 ± 0.3	1.0 ± 0.2	<i>truB-infB-nusA</i>
<i>ydbR</i>	1.5 ± 0.3	2.1 ± 0.2	2.2 ± 0.6	3.3 ± 0.9	2.9 ± 0.6	<i>ydbR-T</i>
<i>yloM</i>	1.1 ± 0.2	3.3 ± 0.5	1.6 ± 0.1	3.6 ± 0.6	2.6 ± 0.3	<i>yloM-N</i>
<i>yugl</i>	1.7 ± 0.1	3.0 ± 0.6	3.5 ± 0.8	4.1 ± 0.6	3.1 ± 0.5	<i>yugl</i>
Transcription elongation						
<i>rpoA</i>	2.8 ± 0.2	8.0 ± 1.0	11.6 ± 1.8	10.4 ± 0.6	11.5 ± 2.2	<i>rpoA</i>
<i>rpoB</i>	1.7 ± 0.1	6.3 ± 1.2	3.5 ± 0.6	4.3 ± 0.2	3.8 ± 0.7	<i>rpoB-C</i>
<i>rpoC</i>	1.8 ± 0.2	8.7 ± 1.8	5.0 ± 0.5	5.8 ± 0.2	4.7 ± 1.2	<i>rpoB-C</i>
<i>rpoE</i>	1.4 ± 0.2	2.6 ± 0.2	3.2 ± 0.2	4.0 ± 0.4	3.4 ± 0.5	<i>pyrG-rpoE</i>
Transcription regulation						
<i>cheB</i>	1.6 ± 0.5	4.7 ± 0.8	4.2 ± 0.8	4.7 ± 1.0	4.9 ± 1.0	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>
<i>cggR</i>	1.8 ± 0.1	26.7 ± 3.6	21.7 ± 2.9	30.6 ± 4.8	17.0 ± 5.0	<i>cggR</i>
<i>cheY</i>	1.5 ± 0.2	4.0 ± 0.3	5.6 ± 0.8	8.1 ± 0.4	11.5 ± 2.1	<i>cheD.ylxH-flhF.fliP.cheY-fliY.flgE-ylxG-fliK-ylxF-fliI.cotY</i>
<i>codY</i>	1.2 ± 0.1	2.4 ± 0.1	3.2 ± 0.2	3.3 ± 0.1	3.4 ± 0.6	<i>cotY-clpY-Q</i>
<i>BLi04205</i>	1.4 ± 0.1	5.4 ± 0.5	3.8 ± 0.8	4.8 ± 0.7	5.0 ± 0.8	putative transcriptional regulation
<i>tenl</i>	1.0 ± 0.1	3.3 ± 0.6	1.9 ± 0.2	5.7 ± 0.6	2.3 ± 0.4	<i>tenA-l-goxB</i>
<i>ykvE</i>	0.8 ± 0.1	4.6 ± 0.4	5.4 ± 1.0	6.2 ± 0.7	5.6 ± 0.5	<i>ykvE</i>
<i>ytrA</i>	0.4 ± 0.1	2.1 ± 0.2	4.5 ± 0.5	5.4 ± 1.2	5.1 ± 1.0	<i>ytrA-B-C-E-F</i>
<i>yvhJ</i>	1.9 ± 0.1	3.3 ± 0.6	3.6 ± 0.6	4.1 ± 0.9	4.1 ± 0.5	<i>yvhJ</i>
<i>yvrG</i>	1.0 ± 0.1	5.2 ± 1.1	4.6 ± 0.3	6.5 ± 0.7	3.1 ± 0.3	<i>yvrG-H</i>
<i>yvrH</i>	1.0 ± 0.6	4.9 ± 0.9	4.8 ± 1.8	6.7 ± 1.3	3.3 ± 0.7	<i>yvrG-H</i>
<i>ywtF</i>	1.0 ± 0.1	2.3 ± 0.1	2.8 ± 0.5	3.4 ± 0.9	3.0 ± 0.6	<i>ywtA-B-D-E-F</i>
						similar to transcriptional regulator

transcriptional terminator							
<i>nusA</i>	1.8 ± 0.1	10.3 ± 1.5	7.8 ± 0.8	9.1 ± 1.6	6.7 ± 1.6	<i>infB-nusA</i>	transcription termination
<i>nusB</i>	1.1 ± 0.2	4.1 ± 1.7	2.5 ± 0.5	1.8 ± 0.4	3.3 ± 0.9	<i>nusB-foldD</i>	probable transcription termination
<i>rho</i>	1.2 ± 0.2	3.8 ± 0.9	3.4 ± 0.5	4.3 ± 0.7	3.8 ± 1.0	<i>tdk-rho</i>	transcriptional terminator Rho
Translation elongation							
<i>efp</i>	1.2 ± 0.1	2.2 ± 0.1	3.7 ± 1.0	4.4 ± 0.4	4.5 ± 0.5	<i>efp</i>	elongation factor P
<i>lepA</i>	1.2 ± 0.1	3.0 ± 0.2	2.6 ± 0.5	4.6 ± 1.2	3.0 ± 0.3	<i>lepA</i>	GTP-binding protein
<i>tsf</i>	1.6 ± 0.2	10.3 ± 1.0	7.5 ± 0.8	8.3 ± 1.3	7.2 ± 0.4	<i>tsf</i>	elongation factor Ts
Translation initiation							
<i>infB</i>	2.0 ± 0.2	5.6 ± 1.0	6.2 ± 1.5	6.7 ± 0.7	7.8 ± 1.4	<i>infB-nusA</i>	initiation factor IF-2
<i>infC</i>	2.5 ± 0.2	2.6 ± 0.1	3.9 ± 0.9	3.4 ± 1.4	3.4 ± 1.0	<i>infC</i>	initiation factor IF-3
<i>ykrS</i>	4.8 ± 0.1	5.0 ± 0.4	5.4 ± 0.7	5.6 ± 1.6	5.8 ± 0.5	<i>ykr operon</i>	similar to initiation factor eIF-2B (alpha subunit)
Translation termination							
<i>frr</i>	1.6 ± 0.2	4.6 ± 0.9	5.1 ± 0.8	4.2 ± 0.4	6.5 ± 0.7	<i>pyrH-frr</i>	ribosome recycling factor
Ribosomal proteins							
<i>rplA</i>	2.0 ± 0.1	8.0 ± 0.4	9.9 ± 1.1	10.4 ± 1.2	9.6 ± 0.8	<i>rpl operon</i>	ribosomal protein L1 (BL1)
<i>rplB</i>	2.2 ± 0.2	27.1 ± 8.0	20.0 ± 0.1	25.0 ± 0.2	18.6 ± 2.9	<i>rpl operon</i>	ribosomal protein L2 (BL2)
<i>rplC</i>	1.9 ± 0.1	6.0 ± 0.6	8.3 ± 1.9	5.7 ± 0.2	6.5 ± 1.2	<i>rpl operon</i>	ribosomal protein L3 (BL3)
<i>rplD</i>	2.1 ± 0.1	20.2 ± 5.6	17.6 ± 1.5	17.3 ± 3.6	14.5 ± 1.9	<i>rpl operon</i>	ribosomal protein L4
<i>rplE</i>	2.7 ± 0.2	27.6 ± 5.8	21.0 ± 2.2	23.6 ± 6.3	25.2 ± 5.5	<i>rpl operon</i>	ribosomal protein L5 (BL6)
<i>rplF</i>	2.5 ± 0.1	21.1 ± 2.5	17.2 ± 1.4	14.9 ± 1.2	14.9 ± 2.6	<i>rpl operon</i>	ribosomal protein L6 (BL8)
<i>rplJ</i>	2.4 ± 0.1	33.3 ± 0.1	27.8 ± 4.3	41.7 ± 11.8	24.7 ± 5.5	<i>rpl operon</i>	ribosomal protein L10 (BL5)
<i>rplK</i>	2.3 ± 0.1	8.5 ± 0.7	8.5 ± 1.4	6.9 ± 0.6	7.6 ± 0.6	<i>rpl operon</i>	ribosomal protein L11 (BL11)
<i>rplL</i>	2.8 ± 0.1	10.0 ± 1.2	7.4 ± 1.8	13.0 ± 3.0	13.6 ± 2.9	<i>rpl operon</i>	ribosomal protein L12 (BL9)
<i>rplM</i>	2.1 ± 0.2	5.3 ± 0.9	5.8 ± 1.0	7.3 ± 0.7	5.5 ± 0.8	<i>rpl operon</i>	ribosomal protein L13
<i>rplN</i>	2.7 ± 0.3	25.8 ± 5.5	25.6 ± 4.3	31.3 ± 4.2	25.5 ± 3.9	<i>rpl operon</i>	ribosomal protein L14
<i>rplO</i>	2.0 ± 0.1	18.2 ± 1.9	18.3 ± 1.9	17.6 ± 6.2	15.6 ± 2.9	<i>rpl operon</i>	ribosomal protein L15
<i>rplP</i>	2.1 ± 0.2	21.1 ± 4.1	13.8 ± 1.7	17.6 ± 2.8	13.6 ± 2.5	<i>rpl operon</i>	ribosomal protein L16
<i>rplQ</i>	2.2 ± 0.1	7.1 ± 1.0	8.3 ± 0.9	9.3 ± 2.2	9.0 ± 1.8	<i>rpl operon</i>	ribosomal protein L17 (BL15)
<i>rplR</i>	2.3 ± 0.3	29.2 ± 4.8	25.0 ± 0.1	30.6 ± 4.8	33.3 ± 8.3	<i>rpl operon</i>	ribosomal protein L18
<i>rplS</i>	3.0 ± 0.5	2.6 ± 4.9	3.2 ± 0.6	3.7 ± 2.3	2.3 ± 1.2	<i>rpl operon</i>	ribosomal protein L19
<i>rplT</i>	2.7 ± 0.1	3.8 ± 0.9	8.1 ± 1.8	6.4 ± 2.7	6.7 ± 1.3	<i>rpl operon</i>	ribosomal protein L20
<i>rplV</i>	2.4 ± 0.3	18.2 ± 1.9	12.0 ± 3.3	12.6 ± 1.3	14.4 ± 0.8	<i>rpl operon</i>	ribosomal protein L22 (BL17)
<i>rpsB</i>	1.8 ± 0.1	14.3 ± 0.1	13.3 ± 2.3	12.9 ± 1.3	12.1 ± 2.2	<i>rps operon</i>	ribosomal protein S2

<i>rpsC</i>	2.2 ± 0.3	12.1 ± 2.4	8.3 ± 2.2	12.1 ± 2.8	9.6 ± 1.7	<i>rps operon</i>	ribosomal protein S3 (BS3)
<i>rpsD</i>	2.5 ± 0.5	4.3 ± 1.4	4.4 ± 1.2	9.2 ± 2.5	6.3 ± 1.5	<i>rps operon</i>	ribosomal protein S4 (BS4)
<i>rpsE</i>	2.3 ± 0.1	3.3 ± 0.3	3.5 ± 0.7	1.9 ± 0.3	2.8 ± 0.8	<i>rps operon</i>	ribosomal protein S5
<i>rpsG</i>	1.5 ± 0.3	10.3 ± 0.6	8.2 ± 1.4	8.2 ± 0.4	8.3 ± 1.5	<i>rps operon</i>	ribosomal protein S7 (BS7)
<i>rpsI</i>	2.2 ± 0.2	5.4 ± 1.1	4.8 ± 1.2	5.6 ± 0.5	5.5 ± 0.5	<i>rps operon</i>	ribosomal protein S9
<i>rpsK</i>	2.5 ± 0.1	18.2 ± 2.9	15.4 ± 1.4	12.9 ± 6.3	16.1 ± 1.2	<i>rps operon</i>	ribosomal protein S11 (BS11)
<i>rpsL</i>	1.7 ± 0.2	8.5 ± 1.8	7.4 ± 1.8	5.4 ± 1.0	6.7 ± 1.5	<i>rps operon</i>	ribosomal protein S12 (BS12)
<i>rpsM</i>	2.5 ± 0.3	15.4 ± 2.1	15.6 ± 1.8	16.7 ± 3.9	16.8 ± 1.8	<i>rps operon</i>	ribosomal protein S13
Aminoacyl-tRNA synthetases							
<i>alaS</i>	1.2 ± 0.1	2.9 ± 0.3	2.8 ± 0.5	3.1 ± 0.1	3.0 ± 0.5	<i>alaS</i>	alanyl-tRNA synthetase
<i>asnS</i>	1.3 ± 0.1	3.1 ± 0.4	3.6 ± 1.0	4.3 ± 0.5	4.3 ± 0.6	<i>asnS</i>	asparaginyl-tRNA synthetase
<i>aspS</i>	1.3 ± 0.2	2.6 ± 0.2	2.4 ± 1.0	3.1 ± 0.5	4.2 ± 0.3	<i>aspS-hisS</i>	aspartyl-tRNA synthetase
<i>gatA</i>	1.3 ± 0.2	4.2 ± 0.2	3.1 ± 0.7	5.1 ± 0.8	4.1 ± 0.9	<i>gatA-B</i>	glutamyl-tRNA(Gln) amidotransferase
<i>gatB</i>	1.5 ± 0.2	3.7 ± 0.3	3.7 ± 0.5	4.5 ± 0.6	3.9 ± 0.6	<i>gatA-B</i>	glutamyl-tRNA(Gln) amidotransferase
<i>gatC</i>	1.2 ± 0.1	2.7 ± 0.3	2.5 ± 0.2	4.0 ± 1.3	2.9 ± 0.5	<i>gatC</i>	glutamyl-tRNA(Gln) amidotransferase
<i>hisS</i>	1.0 ± 0.2	2.5 ± 0.2	1.9 ± 0.1	3.1 ± 0.2	3.2 ± 0.2	<i>aspS-hisS</i>	histidyl-tRNA synthetase
<i>proS</i>	1.3 ± 0.1	4.1 ± 0.3	5.0 ± 0.8	4.0 ± 0.2	4.3 ± 0.8	<i>polC-proS</i>	prolyl-tRNA synthetase
Adaptation to atypical conditions							
<i>clpQ</i>	1.2 ± 0.1	4.0 ± 0.7	3.2 ± 0.7	3.7 ± 0.6	4.0 ± 0.5	<i>cotY-clpY-Q</i>	two-component ATP-dependent protease
<i>clpY</i>	1.2 ± 0.2	6.3 ± 2.0	3.8 ± 0.6	4.3 ± 0.2	4.5 ± 0.9	<i>cotY-clpY-Q</i>	two-component ATP-dependent protease
<i>dnaJ</i>	1.5 ± 0.1	4.1 ± 0.4	3.9 ± 0.8	5.6 ± 1.1	4.3 ± 0.5	<i>dnaK-J</i>	heat-shock protein activation of DnaK
<i>grpE</i>	0.7 ± 0.1	2.4 ± 0.4	2.5 ± 0.7	4.2 ± 0.3	3.6 ± 0.5	<i>grpE</i>	heat-shock protein
<i>lonA</i>	0.8 ± 0.1	3.0 ± 0.3	2.2 ± 0.5	2.6 ± 0.1	3.5 ± 0.8	<i>lonA</i>	class III heat-shock ATP-dependent protease
<i>rpsR</i>	1.6 ± 0.1	4.3 ± 0.6	3.4 ± 1.0	5.9 ± 0.1	3.8 ± 0.7	<i>rsbR-S-T-U-V-W-sigB-rsbX</i>	positive regulator of sigma-B activity
Detoxification							
<i>mrpB</i>	1.4 ± 0.1	3.1 ± 1.2	1.9 ± 0.3	1.7 ± 0.1	3.3 ± 1.0	<i>mrpA-B-C-E-G</i>	multiple resistance and pH homeostasis
<i>mrpG</i>	1.0 ± 0.1	1.8 ± 0.1	2.4 ± 0.3	2.0 ± 0.1	2.9 ± 0.1	<i>mrpA-B-C-E-G</i>	multiple resistance and pH homeostasis
<i>yvbT</i>	1.4 ± 0.1	5.1 ± 0.7	3.7 ± 0.5	3.0 ± 0.6	3.0 ± 0.5	<i>yvbT-W</i>	putative alkanal monooxygenase
Protein folding							
<i>groEL</i>	0.4 ± 0.1	1.9 ± 0.1	3.0 ± 0.3	5.3 ± 0.3	4.1 ± 0.5	<i>groEL</i>	class I heat-shock protein
<i>tig</i>	1.8 ± 0.1	11.4 ± 2.1	13.3 ± 1.9	16.7 ± 1.2	12.5 ± 1.7	<i>tig-clpX</i>	trigger factor
Protein modification							
<i>map</i>	2.5 ± 0.1	12.5 ± 0.6	17.1 ± 2.9	17.6 ± 6.2	15.9 ± 5.0	<i>rplR-secY-adk-map</i>	methionine aminopeptidase
<i>prpC</i>	1.2 ± 0.1	1.8 ± 0.2	3.5 ± 0.5	4.1 ± 0.8	4.3 ± 0.9	<i>prpC</i>	protein phosphatase

<i>sppA</i>	1.2 ± 0.2	4.1 ± 0.5	4.6 ± 0.5	5.2 ± 0.3	3.1 ± 0.3	<i>sppA</i>	signal peptide peptidase
<i>yqhT</i>	1.0 ± 0.1	2.6 ± 0.3	3.3 ± 0.2	3.0 ± 0.5	4.1 ± 0.7	<i>yqhM-T-V</i>	similar to Xaa-Pro dipeptidase
Unknown function							
<i>BLi00800</i>	2.1 ± 0.2	2.1 ± 0.1	2.1 ± 0.1	4.0 ± 1.3	3.0 ± 0.3		hypothetical
<i>BLi00156</i>	2.5 ± 0.1	22.2 ± 2.9	22.2 ± 2.7	22.2 ± 2.9	20.0 ± 2.9		conserved hypothetical
<i>BLi00991</i>	1.8 ± 0.1	4.1 ± 1.2	2.9 ± 0.4	3.0 ± 0.8	3.6 ± 0.8		putative permease
<i>BLi00733</i>	1.6 ± 0.5	1.9 ± 0.1	2.4 ± 0.3	2.2 ± 0.1	1.5 ± 0.6		hypothetical
<i>ybaF</i>	1.8 ± 0.1	4.7 ± 0.8	3.4 ± 0.3	3.2 ± 0.6	2.8 ± 1.1	<i>ybxA-ybaE-F</i>	unknown
<i>ybxB</i>	2.1 ± 0.1	4.1 ± 0.8	4.1 ± 0.5	3.5 ± 1.2	3.5 ± 0.6	<i>ybxB</i>	unknown
<i>ydaT</i>	1.3 ± 0.3	1.4 ± 0.1	1.4 ± 0.1	1.5 ± 0.1	1.5 ± 0.7	<i>ydaT</i>	unknown
<i>yerH</i>	0.9 ± 0.1	2.5 ± 0.3	2.6 ± 0.2	4.1 ± 1.0	3.4 ± 0.7	<i>yerH</i>	unknown
<i>yitJ</i>	5.6 ± 0.2	3.7 ± 0.7	4.9 ± 0.8	5.5 ± 0.7	4.1 ± 0.8	<i>yitK-J</i>	unknown
<i>yjbL</i>	1.2 ± 0.2	3.0 ± 0.4	3.3 ± 0.3	4.3 ± 0.3	3.8 ± 0.9	<i>yjb operon</i>	unknown
<i>yjIC</i>	0.7 ± 0.1	3.0 ± 0.2	3.5 ± 0.9	5.0 ± 0.4	4.2 ± 0.6	<i>yjIC-D</i>	unknown
<i>ykoC</i>	1.9 ± 0.1	4.8 ± 1.9	5.0 ± 1.0	5.1 ± 1.1	6.4 ± 2.1	<i>ykoC-D-E</i>	unknown
<i>ykoE</i>	1.5 ± 0.1	8.2 ± 1.5	6.1 ± 0.7	8.3 ± 1.2	5.6 ± 1.5	<i>ykoC-D-E</i>	unknown
<i>ykrT</i>	5.9 ± 0.3	3.4 ± 0.4	2.9 ± 0.8	2.5 ± 0.8	2.2 ± 0.9	<i>ykr operon</i>	unknown
<i>ykrU</i>	2.0 ± 0.1	3.5 ± 1.4	3.1 ± 0.5	4.3 ± 1.1	2.4 ± 0.8	<i>ykr operon</i>	unknown
<i>ykrY</i>	5.2 ± 0.6	3.9 ± 0.3	7.9 ± 2.1	9.1 ± 2.2	9.6 ± 1.7	<i>ykr operon</i>	unknown
<i>ykrZ</i>	4.7 ± 0.1	3.3 ± 0.5	3.8 ± 0.5	3.1 ± 0.6	4.4 ± 1.0	<i>ykr operon</i>	unknown
<i>yloQ</i>	1.3 ± 0.1	3.6 ± 1.0	2.8 ± 0.2	3.2 ± 0.9	3.1 ± 1.0	<i>ylo operon</i>	unknown
<i>ylpC</i>	2.2 ± 0.3	2.8 ± 0.5	4.2 ± 0.9	3.5 ± 0.7	3.5 ± 0.9	<i>ylpC</i>	unknown
<i>ylqD</i>	2.0 ± 0.1	4.1 ± 0.3	4.1 ± 0.6	3.3 ± 0.6	3.2 ± 0.1	<i>ylqD</i>	unknown
<i>ylqG</i>	1.2 ± 0.2	4.0 ± 1.3	4.8 ± 0.8	5.0 ± 0.8	4.3 ± 0.7	<i>ylqG</i>	unknown
<i>yluC</i>	1.0 ± 0.1	4.3 ± 0.8	3.2 ± 0.6	3.3 ± 0.4	3.3 ± 0.6	<i>yluC</i>	unknown
<i>ylxF</i>	1.4 ± 0.2	5.0 ± 1.5	9.2 ± 2.4	14.3 ± 2.3	11.8 ± 0.1	<i>ylx operon</i>	unknown
<i>yoaZ</i>	1.2 ± 0.2	8.4 ± 2.2	5.0 ± 0.5	4.7 ± 0.4	4.9 ± 0.7	<i>yoaZ</i>	unknown
<i>yqeN</i>	0.9 ± 0.1	3.8 ± 1.3	2.7 ± 0.2	3.2 ± 0.2	3.4 ± 0.2	<i>yqeN</i>	unknown
<i>yqeU</i>	1.8 ± 0.1	3.4 ± 1.5	3.0 ± 1.0	3.4 ± 1.1	3.4 ± 0.7	<i>yqeT-U-V</i>	unknown
<i>ysoA</i>	2.1 ± 0.1	5.9 ± 0.5	5.3 ± 0.9	5.5 ± 0.1	5.1 ± 1.1	<i>ysoA</i>	unknown
<i>ytmQ</i>	1.6 ± 0.1	2.7 ± 0.8	3.9 ± 0.4	4.2 ± 0.4	3.5 ± 0.9	<i>ytmQ</i>	unknown
<i>ytpQ</i>	1.3 ± 0.3	2.9 ± 0.4	3.5 ± 0.8	4.0 ± 0.6	3.4 ± 0.8	<i>ytpQ-R-T</i>	unknown
<i>ytrC</i>	0.5 ± 0.6	1.8 ± 0.1	3.4 ± 0.7	3.4 ± 1.2	3.6 ± 0.6	<i>ytrA-B-C-E-F</i>	unknown
<i>ytrF</i>	0.5 ± 0.5	0.9 ± 0.1	5.0 ± 1.1	5.5 ± 1.1	5.3 ± 1.4	<i>ytrA-B-C-E-F</i>	unknown

<i>yueB</i>	1.1 ± 0.1	4.0 ± 1.7	3.3 ± 0.6	5.9 ± 0.5	3.1 ± 0.4	<i>yueA-B-C-D-E</i>	unknown
<i>yuil</i>	0.4 ± 0.1	5.4 ± 2.5	4.5 ± 0.6	6.6 ± 0.4	4.9 ± 0.9	<i>yuil-dhbA-B-C-D-E-F</i>	unknown
<i>yukA</i>	1.2 ± 0.2	3.3 ± 0.5	3.2 ± 0.4	3.5 ± 0.6	3.7 ± 0.6	<i>yukA-C-F</i>	unknown
<i>yukC</i>	0.9 ± 0.1	3.9 ± 0.5	3.8 ± 0.9	4.0 ± 0.4	3.8 ± 0.3	<i>yukA-C-F</i>	unknown
<i>yunG</i>	1.8 ± 0.3	4.5 ± 0.3	4.9 ± 1.0	5.1 ± 0.9	4.7 ± 0.4	<i>yunG</i>	unknown
<i>yusA</i>	4.7 ± 0.3	6.2 ± 1.9	6.0 ± 0.8	7.8 ± 1.0	9.3 ± 2.3	<i>yusA-B-C-D</i>	unknown
<i>yusB</i>	5.9 ± 0.1	8.0 ± 0.8	12.0 ± 1.4	13.3 ± 2.8	17.4 ± 3.2	<i>yusA-B-C-D</i>	unknown
<i>yuxK</i>	1.3 ± 0.1	3.6 ± 0.5	2.9 ± 0.4	2.7 ± 0.2	2.7 ± 0.3	<i>yuxK</i>	unknown
<i>yvbl</i>	1.6 ± 0.3	4.3 ± 1.7	3.1 ± 0.1	4.5 ± 0.5	3.3 ± 0.8	<i>yvbF-I-J</i>	unknown
<i>yvbJ</i>	1.2 ± 0.1	4.3 ± 1.7	3.8 ± 0.4	3.7 ± 0.5	3.9 ± 0.6	<i>yvbF-I-J</i>	unknown
<i>ywnB</i>	1.3 ± 0.2	1.6 ± 0.1	2.2 ± 0.5	4.6 ± 1.3	2.3 ± 0.5	<i>ywnA-B</i>	unknown
<i>yxjG</i>	4.5 ± 0.5	3.3 ± 0.8	4.0 ± 1.0	3.8 ± 0.6	4.2 ± 1.4	<i>yxjG</i>	unknown

Table 4: Kinetic of the nitrogen starvation inducible genes of *B. licheniformis*. Listed are such genes, the mRNA level of which showed a more than threefold induction during at least one sampling point throughout the growth curve. Genes the expression of which is also induced under glucose starvation conditions are labelled with “*”. Trans. ph. = transient phase, SD = standard deviation

Gene name	Trans. ph.	SD	30 min	SD	60 min	SD	90 min	SD	120 min	SD	Transcriptional organisation	Function
Cell wall												
<i>yabE</i>	0.8 ± 0.1		1.4 ± 0.1		1.7 ± 0.3		3.5 ± 0.5		3.0 ± 0.6		<i>yab operon</i>	similar to cell wall-binding protein
Transport/binding proteins and lipoproteins												
<i>dppB*</i>	2.5 ± 0.6		4.2 ± 0.6		3.3 ± 0.6		2.1 ± 0.1		2.5 ± 0.4		<i>dppA-B-C-D-E</i>	dipeptide ABC transporter
<i>dppC*</i>	2.1 ± 0.2		4.1 ± 0.7		4.6 ± 0.8		3.2 ± 0.2		3.1 ± 0.7		<i>dppA-B-C-D-E</i>	dipeptide ABC transporter
<i>dppD*</i>	1.3 ± 0.1		4.0 ± 1.5		2.9 ± 0.6		2.4 ± 0.2		1.3 ± 0.5		<i>dppA-B-C-D-E</i>	dipeptide ABC transporter
<i>dppE</i>	2.6 ± 0.3		8.1 ± 2.5		10.8 ± 1.2		5.6 ± 0.9		7.2 ± 1.2		<i>dppA-B-C-D-E</i>	dipeptide ABC transporter
<i>nrgA</i>	3.0 ± 0.3		5.7 ± 0.4		5.4 ± 1.1		6.6 ± 1.2		7.3 ± 1.3		<i>nrgA-B</i>	ammonium transporter
<i>BLi03990*</i>	4.1 ± 0.4		4.7 ± 0.4		6.1 ± 0.9		13.7 ± 2.6		11.9 ± 1.9			putative benzoate transport protein
<i>BLi04117</i>	2.1 ± 0.2		2.9 ± 0.3		6.1 ± 0.6		9.3 ± 4.0		10.8 ± 2.6			putative ABC transporter ATP-binding protein
<i>BLi01175</i>	6.2 ± 0.7		20.0 ± 3.0		19.5 ± 1.5		21.0 ± 2.1		22.8 ± 2.9			putative ammonium transporter
<i>BLi03212</i>	8.1 ± 0.4		4.4 ± 0.7		5.3 ± 0.2		4.6 ± 1.4		1.4 ± 0.3			putative ABC transporter
<i>BLi00817</i>	3.9 ± 0.5		6.4 ± 1.5		12.4 ± 1.2		12.5 ± 1.3		17.1 ± 2.4			putative Na(+)-linked D-alanine glycine permease
<i>ycdH</i>	21.1 ± 0.7		7.7 ± 0.5		2.0 ± 0.1		4.5 ± 0.6		1.0 ± 0.1		<i>ycdH</i>	similar to ABC transporter (binding protein)
<i>ycgO*</i>	1.1 ± 0.1		2.1 ± 0.5		4.4 ± 0.8		3.4 ± 0.5		1.9 ± 0.3		<i>ycg operon</i>	similar to proline permease
<i>yckl</i>	3.2 ± 0.2		3.6 ± 0.3		3.6 ± 0.1		3.1 ± 0.6		2.0 ± 0.1		<i>yckl-J-K</i>	similar to glutamine ABC transporter (ATP-binding protein)
<i>ycnJ</i>	4.0 ± 0.6		5.3 ± 0.5		4.6 ± 1.1		9.4 ± 2.4		5.5 ± 0.5		<i>ycnl-J</i>	similar to copper export protein
<i>yvdH*</i>	1.1 ± 0.1		2.0 ± 0.2		2.3 ± 0.2		3.4 ± 0.3		3.3 ± 0.6		<i>yhdF-H</i>	similar to sodium-dependent transporter
<i>ywrB</i>	1.4 ± 0.1		3.2 ± 0.4		2.2 ± 0.1		3.4 ± 0.5		2.4 ± 0.8		<i>ywrD-C-B-A</i>	similar to chromate transport protein
<i>cydC*</i>	1.2 ± 0.1		2.3 ± 0.2		1.8 ± 0.1		4.7 ± 0.3		3.6 ± 0.7		<i>cydA-B-C-D</i>	ABC transporter required for expression of cytochrome bd
<i>cydD*</i>	1.2 ± 0.1		1.9 ± 0.2		2.1 ± 0.3		3.3 ± 0.7		3.3 ± 0.7		<i>cydA-B-C-D</i>	ABC transporter required for expression of cytochrome bd
<i>BLi01465*</i>	1.8 ± 0.1		3.4 ± 0.5		3.8 ± 0.6		6.4 ± 1.5		4.7 ± 1			putative portal protein
Electron transport chain and ATP synthase												
<i>BLi01934</i>	6.6 ± 1.1		4.4 ± 0.9		1.0 ± 0.1		3.9 ± 0.4		1.0 ± 0.2			NADH-ubiquinone oxidoreductase
<i>BLi04115</i>	1.4 ± 0.2		1.9 ± 0.1		1.7 ± 0.5		3.2 ± 0.4		3.0 ± 0.6			close homolog to HemH: ferrochete
<i>cydA*</i>	0.9 ± 0.1		2.4 ± 0.4		2.2 ± 0.4		4.5 ± 0.4		3.3 ± 0.6		<i>cydA-B-C-D</i>	cytochrome bd ubiquinol oxidase (subunit I)
<i>cydB*</i>	0.9 ± 0.1		2.0 ± 0.6		1.7 ± 0.1		3.5 ± 0.2		2.4 ± 0.4		<i>cydA-B-C-D</i>	cytochrome bd ubiquinol oxidase (subunit II)

	<i>tasA</i>	<i>3.3 ± 0.9</i>	<i>1.7 ± 0.4</i>	<i>4.2 ± 1.2</i>	<i>1.4 ± 0.1</i>	<i>sipW-tasA</i>	
<i>sigH</i>	<i>1.5 ± 0.1</i>	<i>2.7 ± 0.3</i>	<i>3.8 ± 0.7</i>	<i>3.0 ± 0.3</i>	<i>4.0 ± 0.5</i>	<i>sigH</i>	known RNA polymerase vegetative and early stationary-phase sigma factor
<i>spolI_{AA}*</i>	<i>1.4 ± 0.2</i>	<i>4.6 ± 0.9</i>	<i>3.7 ± 0.9</i>	<i>3.2 ± 0.4</i>	<i>3.0 ± 0.6</i>	<i>dacF-spolI_{AA}-spolI_{AB}-sigF</i>	known RNA polymerase sigma factor
<i>spolI_{AB}*</i>	<i>2.4 ± 0.5</i>	<i>7.1 ± 0.7</i>	<i>5.6 ± 1.5</i>	<i>4.9 ± 1.5</i>	<i>1.8 ± 0.4</i>	<i>dacF-spolI_{AA}-spolI_{AB}-sigF</i>	known anti-sigma F factor
Specific pathways							
<i>alsD</i>	<i>5.8 ± 0.4</i>	<i>22.2 ± 1.8</i>	<i>7.4 ± 0.8</i>	<i>38.1 ± 2.0</i>	<i>9.8 ± 1.5</i>	<i>alsR-S-D</i>	alpha-acetolactate decarboxylase
<i>alsR</i>	<i>1.7 ± 0.1</i>	<i>8.8 ± 4.5</i>	<i>7.8 ± 1.2</i>	<i>7.4 ± 0.7</i>	<i>3.9 ± 0.8</i>	<i>alsR-S-D</i>	transcriptional regulator
<i>alsS</i>	<i>17.7 ± 1.5</i>	<i>76.8 ± 8.0</i>	<i>9.7 ± 2.5</i>	<i>143.5 ± 29.3</i>	<i>22.3 ± 6.3</i>	<i>alsR-S-D</i>	alpha-acetolactate synthase
<i>BLi00828*</i>	<i>2.0 ± 0.1</i>	<i>5.2 ± 0.8</i>	<i>5.7 ± 1.0</i>	<i>5.7 ± 0.1</i>	<i>6.5 ± 1.1</i>		putative glycerol dehydrogenase
<i>BLi04208</i>	<i>1.0 ± 0.1</i>	<i>6.0 ± 1.7</i>	<i>5.1 ± 1.0</i>	<i>17.1 ± 4.4</i>	<i>3.3 ± 1</i>		putative malate synthase
<i>yoaD</i>	<i>2.4 ± 0.6</i>	<i>1.8 ± 0.1</i>	<i>3.3 ± 0.6</i>	<i>4.4 ± 1.3</i>	<i>4.6 ± 1.2</i>	<i>yoaD</i>	similar to phosphoglycerate dehydrogenase
<i>yqiQ*</i>	<i>1.1 ± 0.1</i>	<i>2.0 ± 0.2</i>	<i>3.4 ± 0.5</i>	<i>2.8 ± 0.5</i>	<i>3.2 ± 0.6</i>	<i>mmgD-E-yqiQ</i>	similar to phosphoenolpyruvate mutase
<i>ysfD</i>	<i>0.9 ± 0.1</i>	<i>1.2 ± 0.1</i>	<i>3.5 ± 0.3</i>	<i>3.5 ± 0.3</i>	<i>3.8 ± 0.6</i>	<i>ysfC-D</i>	similar to glycolate oxidase subunit
<i>ytcA</i>	<i>1.4 ± 0.1</i>	<i>3.9 ± 0.4</i>	<i>4.3 ± 0.4</i>	<i>4.6 ± 0.8</i>	<i>3.7 ± 0.4</i>	<i>ytcA</i>	similar to NDP-sugar dehydrogenase
Main glycolytic pathways							
<i>pckA*</i>	<i>0.9 ± 0.1</i>	<i>5.9 ± 0.7</i>	<i>16.9 ± 6.3</i>	<i>28.6 ± 4.6</i>	<i>14.7 ± 1.8</i>	<i>pfkA-pyk</i>	phosphoenolpyruvate carboxykinase
TCA cycle							
<i>mmgD*</i>	<i>1.3 ± 0.1</i>	<i>5.3 ± 1.5</i>	<i>6.4 ± 0.3</i>	<i>6.9 ± 1.0</i>	<i>3.5 ± 0.9</i>	<i>mmgD-E-yqiQ</i>	citrate synthase III
<i>citA*</i>	<i>1.1 ± 0.1</i>	<i>1.8 ± 0.1</i>	<i>5.8 ± 1.7</i>	<i>7.4 ± 0.6</i>	<i>10.4 ± 1</i>	<i>citA-R</i>	citrate synthase I (minor)
Metabolism of amino acids and related molecules							
<i>aroE</i>	<i>1.1 ± 0.1</i>	<i>3.9 ± 0.1</i>	<i>4.0 ± 1.0</i>	<i>3.6 ± 0.1</i>	<i>3.9 ± 0.6</i>	<i>aroF-B-H-trpE-D-C-F-B-A-hisC-tyrA-aroE</i>	5-enolpyruvoylshikimate-3-phosphate synthase
<i>asnO</i>	<i>2.2 ± 0.1</i>	<i>5.6 ± 0.1</i>	<i>5.2 ± 1.3</i>	<i>5.5 ± 1.1</i>	<i>6.1 ± 0.8</i>	<i>asnO</i>	asparagine synthetase
<i>bpr*</i>	<i>1.4 ± 0.1</i>	<i>6.3 ± 1.2</i>	<i>6.0 ± 1.1</i>	<i>7.6 ± 1.2</i>	<i>12.4 ± 1.8</i>	<i>bpr</i>	bacillopeptidase F
<i>glnA</i>	<i>5.7 ± 0.4</i>	<i>9.5 ± 0.1</i>	<i>8.1 ± 0.5</i>	<i>9.1 ± 0.9</i>	<i>8.6 ± 1.6</i>	<i>glnR-A</i>	glutamine synthetase
<i>ggt*</i>	<i>1.8 ± 0.1</i>	<i>8.6 ± 2.0</i>	<i>5.3 ± 0.8</i>	<i>8.8 ± 3.6</i>	<i>6.8 ± 1</i>	<i>ggt</i>	gamma-glutamyltranspeptidase
<i>hisC</i>	<i>1.6 ± 0.2</i>	<i>6.3 ± 0.3</i>	<i>5.2 ± 0.9</i>	<i>5.1 ± 1.0</i>	<i>5.0 ± 1.7</i>	<i>tyrA-hisC-trpA-B-F-C-D-E</i>	histidinol-phosphate aminotransferase
<i>ispA*</i>	<i>1.1 ± 0.1</i>	<i>7.0 ± 0.7</i>	<i>10.2 ± 2.6</i>	<i>19.3 ± 4.7</i>	<i>4.6 ± 1</i>	<i>ispA</i>	major intracellular serine protease
<i>nasA</i>	<i>1.6 ± 0.1</i>	<i>2.2 ± 0.2</i>	<i>2.6 ± 0.3</i>	<i>2.3 ± 0.4</i>	<i>2.7 ± 0.2</i>	<i>nasA</i>	nitrate transporter
<i>nasB</i>	<i>18.2 ± 1.6</i>	<i>22.6 ± 2.9</i>	<i>23.8 ± 2.9</i>	<i>25.2 ± 5.9</i>	<i>20.0 ± 3.7</i>	<i>nasB-C-D-E-F</i>	assimilatory nitrate reductase
<i>nasC*</i>	<i>11.1 ± 1.4</i>	<i>22.1 ± 1.4</i>	<i>22.4 ± 2.8</i>	<i>21.0 ± 1.9</i>	<i>20.5 ± 3.3</i>	<i>nasB-C-D-E-F</i>	assimilatory nitrate reductase
<i>nasD*</i>	<i>6.6 ± 0.5</i>	<i>10.6 ± 0.6</i>	<i>14.6 ± 3.7</i>	<i>20.6 ± 1.8</i>	<i>13.0 ± 2.3</i>	<i>nasB-C-D-E-F</i>	assimilatory nitrate reductase
<i>nasE*</i>	<i>10.6 ± 1.9</i>	<i>23.5 ± 6.7</i>	<i>26.8 ± 8.8</i>	<i>43.0 ± 8.5</i>	<i>23.2 ± 3.8</i>	<i>nasB-C-D-E-F</i>	assimilatory nitrate reductase

<i>nasF</i> *	8.1 ± 0.8	16.6 ± 0.2	22.4 ± 5.0	40.2 ± 3.5	21.0 ± 2.7	<i>nasB-C-D-E-F</i>	uroporphyrin-III C-methyltransferase
<i>nrgB</i>	3.6 ± 0.6	6.9 ± 0.7	7.0 ± 1.0	10.1 ± 1.6	6.4 ± 0.9	<i>nrgA-B</i>	nitrogen-regulated PII-like protein
<i>proG</i>	1.7 ± 0.1	2.3 ± 0.5	3.0 ± 0.5	1.5 ± 0.1	1.7 ± 0.1	<i>proG</i>	pyrroline-5-carboxylate reductase
<i>BLi01747</i> *	1.2 ± 0.1	3.6 ± 1.6	2.5 ± 0.4	3.4 ± 0.8	3.6 ± 0.2		putative bacillopeptidase F
<i>BLi00301</i> *	2.3 ± 0.1	13.4 ± 1.1	6.6 ± 0.8	16.1 ± 1.7	13.2 ± 1.4		putative serine protease
<i>trpA</i>	1.0 ± 0.1	6.0 ± 0.5	6.3 ± 1.5	5.3 ± 0.8	6.8 ± 2.8	<i>tyrA-hisC-trpA-B-F-C-D-E</i>	tryptophan synthase (alpha subunit)
<i>trpB</i> *	1.5 ± 0.2	9.2 ± 1.4	8.2 ± 2.6	11.4 ± 3.4	11.9 ± 4.2	<i>tyrA-hisC-trpA-B-F-C-D-E</i>	tryptophan synthase (beta subunit)
<i>trpC</i> *	1.5 ± 0.1	12.1 ± 0.7	10.2 ± 2.6	11.2 ± 2.5	14.3 ± 5.3	<i>tyrA-hisC-trpA-B-F-C-D-E</i>	indol-3-glycerol phosphate synthase
<i>trpD</i> *	1.5 ± 0.3	10.2 ± 2.9	11.7 ± 4.0	11.9 ± 2.5	11.8 ± 3.8	<i>tyrA-hisC-trpA-B-F-C-D-E</i>	anthranilate phosphoribosyltransferase
<i>trpE</i> *	2.0 ± 0.4	26.1 ± 5.5	22.3 ± 2.0	19.7 ± 2.3	17.8 ± 4	<i>tyrA-hisC-trpA-B-F-C-D-E</i>	anthranilate synthase
<i>trpF</i> *	1.4 ± 0.1	12.0 ± 0.4	9.6 ± 1.9	11.6 ± 3.3	18.9 ± 2.1	<i>tyrA-hisC-trpA-B-F-C-D-E</i>	phosphoribosyl anthranilate isomerase
<i>tyrA</i>	1.1 ± 0.1	4.2 ± 0.3	4.2 ± 0.7	4.0 ± 0.8	3.6 ± 0.8	<i>tyrA-hisC-trpA-B-F-C-D-E</i>	prephenate dehydrogenase
<i>ycgM</i> *	1.2 ± 0.1	10.7 ± 1.7	21.5 ± 1.3	18.0 ± 3.1	3.1 ± 0.5	<i>ycgL-M-N-O-P-Q-R</i>	similar to proline oxidase
<i>ycgN</i> *	1.2 ± 0.3	7.6 ± 1.0	16.8 ± 2.5	12.1 ± 4.0	1.9 ± 0.6	<i>ycgL-M-N-O-P-Q-R</i>	similar to 1-pyrroline-5-carboxylate dehydrogenase
<i>yqjN</i>	1.6 ± 0.1	2.7 ± 0.2	4.5 ± 0.6	8.5 ± 0.5	8.0 ± 1.4	<i>yqj operon</i>	similar to amino acid degradation
<i>yusX</i>	1.3 ± 0.1	3.0 ± 0.4	3.2 ± 0.8	3.2 ± 0.5	3.2 ± 0.6	<i>yus operon</i>	similar to oligoendopeptidase
<i>BLi01109</i>	1.7 ± 0.3	13.8 ± 3.2	6.5 ± 1.1	10.9 ± 0.6	7.7 ± 0.8		known subtilisin carlsberg precursor
Metabolism of coenzymes and prosthetic groups							
<i>BLi03994</i> *	5.3 ± 0.9	9.1 ± 1.2	9.5 ± 1.8	22.4 ± 3.5	21.1 ± 3.9		close homolog to DhaS: aldehyde dehydrogenase
<i>dhaS</i> *	1.6 ± 0.1	4.3 ± 0.8	6.4 ± 1.7	5.6 ± 0.6	5.5 ± 0.6	<i>dhaS</i>	aldehyde dehydrogenase
DNA replication							
<i>ykoU</i>	1.9 ± 0.4	5.3 ± 1.4	5.2 ± 1.3	6.3 ± 1.1	6.0 ± 0.2	<i>yko operon</i>	similar to ATP-dependent DNA ligase
DNA restriction/modification and repair							
<i>dinB</i> *	1.4 ± 0.1	5.2 ± 0.3	6.4 ± 1.7	5.8 ± 0.4	5.7 ± 0.5	<i>dinB</i>	nuclease inhibitor
Transcription initiation							
<i>sigW</i>	1.0 ± 0.1	1.6 ± 0.1	4.0 ± 1.1	3.6 ± 0.6	4.8 ± 1	<i>sigW</i>	RNA polymerase ECF-type sigma factor
<i>sigX</i> *	2.2 ± 0.2	5.7 ± 0.4	2.8 ± 0.4	5.4 ± 0.9	4.3 ± 0.4	<i>sigX</i>	RNA polymerase ECF-type sigma factor
<i>yvyD</i> *	1.6 ± 0.1	10.8 ± 0.2	9.5 ± 1.7	11.5 ± 2.5	9.3 ± 1.3	<i>yvyD</i>	similar to sigma-54 modulating factor
Transcription regulation							
<i>dctR</i>	1.2 ± 0.1	4.5 ± 1.4	4.9 ± 1.1	4.4 ± 0.8	4.0 ± 0.6	<i>dctR</i>	two-component response regulator involved in C4-dicarboxylate transport
<i>glnR</i>	4.4 ± 0.2	11.7 ± 4.4	8.3 ± 1.2	8.4 ± 3.4	10.3 ± 2.3	<i>glnR-A</i>	transcriptional repressor of the glutamine synthetase gene
<i>gltC</i>	1.2 ± 0.2	3.5 ± 1.0	3.9 ± 0.7	5.2 ± 0.4	4.8 ± 1.1	<i>gltC</i>	transcriptional activator of the glutamate synthase operon
<i>pucR</i>	1.9 ± 0.1	2.8 ± 0.6	4.3 ± 0.5	5.0 ± 0.3	4.6 ± 0.9	<i>pucR</i>	transcriptional regulator of puc genes
<i>BLi04093</i> *	1.2 ± 0.2	2.6 ± 0.3	3.0 ± 0.3	3.0 ± 0.4	3.1 ± 0.5		putative transcriptional regulation

<i>BLi03995*</i>	1.8 ± 0.1	5.0 ± 0.8	6.8 ± 0.8	13.7 ± 2.9	16.9 ± 1.9		
<i>BLi00353</i>	1.3 ± 0.1	1.6 ± 0.1	3.3 ± 0.4	3.0 ± 0.6	2.7 ± 0.7		putative transcriptional regulation
<i>BLi03548*</i>	1.2 ± 0.1	3.4 ± 0.5	3.9 ± 0.4	5.5 ± 0.5	3.5 ± 0.5		putative transcriptional regulation
<i>BLi01176</i>	8.3 ± 1.1	31.2 ± 7.0	29.9 ± 2.9	33.7 ± 5.5	30.8 ± 8.3		putative nitrogen regulatory protein
<i>rsiX</i>	2.1 ± 0.1	5.0 ± 0.5	2.6 ± 0.4	5.4 ± 0.7	6.1 ± 0.7	<i>sigX-rsiX</i>	negative regulator of sigma-X activity
<i>ycnK</i>	4.6 ± 0.9	10.1 ± 1.5	9.7 ± 1.5	14.5 ± 2.1	8.9 ± 1.6	<i>ycnl-J-K</i>	similar to transcriptional regulator (DeoR family)
<i>ykoM*</i>	2.1 ± 0.1	5.8 ± 0.9	6.7 ± 1.0	7.2 ± 2.0	6.2 ± 0.9	<i>yko operon</i>	similar to transcriptional regulator (MarR family)
<i>ywaE*</i>	1.2 ± 0.1	2.2 ± 0.3	2.9 ± 0.8	3.5 ± 0.3	3.6 ± 0.8	<i>ywaE</i>	similar to transcriptional regulator (MarR family)
<i>ywrC</i>	2.2 ± 0.2	5.2 ± 1.1	3.1 ± 0.4	6.5 ± 0.8	4.4 ± 0.9	<i>ywrA-B-C</i>	similar to transcriptional regulator (Lrp/AsnC family)
<i>BLi02787</i>	1.2 ± 0.1	5.1 ± 0.7	4.4 ± 0.9	4.7 ± 0.7	3.7 ± 0.9		putative two-component response regulator
Protein modification							
<i>dppA</i>	2.4 ± 0.7	3.8 ± 1.4	3.8 ± 0.6	2.3 ± 0.2	2.6 ± 0.6	<i>dppA-B-C-D-E</i>	D-alanyl-aminopeptidase
<i>yppQ</i>	1.6 ± 0.1	4.7 ± 0.6	4.8 ± 0.8	5.4 ± 1.1	4.0 ± 0.6	<i>yppQ</i>	similar to peptide methionine sulfoxide reductase
Adaptation to atypical conditions							
<i>clpC*</i>	2.3 ± 0.2	5.6 ± 0.1	4.4 ± 0.6	2.8 ± 0.1	2.8 ± 0.7	<i>ctsR-mcsA-B-clpC-radA</i>	class III stress response
<i>clpP</i>	2.6 ± 0.6	4.4 ± 1.2	3.7 ± 0.8	2.6 ± 0.5	2.9 ± 0.5	<i>clpP</i>	ATP-dependent Clp protease
<i>htrA</i>	7.9 ± 1.4	8.1 ± 0.8	2.0 ± 0.4	1.9 ± 0.1	1.7 ± 0.2	<i>htrA</i>	serine protease Do (heat-shock protein)
<i>mcsB</i>	1.8 ± 0.1	3.2 ± 0.6	3.4 ± 0.7	2.3 ± 0.3	2.0 ± 0.3	<i>ctsR-mcsA-B-clpC-radA</i>	modulator of CtsR repression
<i>mrgA*</i>	3.0 ± 0.1	3.2 ± 0.1	3.0 ± 0.8	1.6 ± 0.1	1.6 ± 0.5	<i>mrgA</i>	metalloregulation DNA-binding stress protein
<i>pspA</i>	1.6 ± 0.1	2.3 ± 0.5	3.2 ± 0.6	2.9 ± 0.3	3.3 ± 0.6	<i>pspA</i>	phage shock protein A homolog
<i>yvtA</i>	10.0 ± 2.0	3.4 ± 0.1	1.3 ± 0.2	1.6 ± 0.1	1.0 ± 0.1	<i>yvtA</i>	similar to HtrA-like serine protease
<i>ywqC*</i>	1.4 ± 0.1	3.4 ± 0.3	3.2 ± 0.6	4.3 ± 1.0	3.0 ± 0.4	<i>ywqE-C-B-A</i>	similar to capsular polysaccharide biosynthesis
<i>ywqE</i>	1.5 ± 0.1	3.0 ± 0.4	2.8 ± 0.4	3.8 ± 0.8	3.2 ± 0.7	<i>ywqE-C-B-A</i>	similar to capsular polysaccharide biosynthesis
<i>BLi04126*</i>	1.6 ± 0.2	3.7 ± 1.3	6.7 ± 1.0	6.9 ± 0.7	6.4 ± 1.2		putative bacteriocin formation
<i>BLi04128*</i>	1.5 ± 0.1	2.7 ± 0.9	3.8 ± 0.8	4.2 ± 0.8	3.6 ± 0.7		putative bacteriocin formation
Aminoacyl-tRNA synthetases							
<i>thrZ</i>	2.3 ±	4.7 ± 1.4	4.4 ± 1.5	5.6 ± 0.1	5.5 ± 1.5	<i>thrZ</i>	threonyl-tRNA synthetase
Miscellaneous							
<i>mmgE*</i>	1.0 ± 0.1	2.3 ± 0.6	3.8 ± 0.6	3.6 ± 0.4	3.6 ± 0.4	<i>mmgD-E-yqiQ</i>	function unknown
<i>ypIQ</i>	1.1 ± 0.1	2.4 ± 0.3	2.9 ± 0.3	3.3 ± 0.7	3.1 ± 0.5	<i>ypIP-Q</i>	similar to hemolysin III homolog
Detoxification							
<i>msrA</i>	1.8 ± 0.2	4.5 ± 1.0	4.3 ± 1.1	3.7 ± 0.5	3.2 ± 0.2	<i>msrA</i>	peptidyl methionine sulfoxide reductase
<i>yceC</i>	2.2 ± 0.1	3.1 ± 0.2	5.0 ± 0.9	4.7 ± 1.7	4.6 ± 0.8	<i>yceC-D-E-F</i>	similar to tellurium resistance protein
<i>yceD</i>	2.4 ± 0.4	3.9 ± 0.9	5.3 ± 0.4	4.1 ± 1.3	5.0 ± 0.7	<i>yceC-D-E-F</i>	similar to tellurium resistance protein

<i>yceE</i>	2.1 ± 0.1	3.6 ± 0.8	5.9 ± 1.3	5.4 ± 1.0	7.4 ± 0.7	<i>yceC-D-E-F</i>	similar to tellurium resistance protein
<i>yceF</i>	1.6 ± 0.2	2.0 ± 0.1	3.0 ± 0.4	2.8 ± 0.5	3.6 ± 0.6	<i>yceC-D-E-F</i>	similar to tellurium resistance protein
<i>ykfA</i>	1.9 ± 0.3	3.5 ± 0.4	4.4 ± 1.1	3.2 ± 0.4	3.6 ± 0.5	<i>ykfA-C-D</i>	similar to immunity to bacteriotoxins
<i>ahpC</i>	3.2 ± 0.1	3.2 ± 0.1	2.4 ± 0.2	0.3 ± 0.1	0.5 ± 0.1	<i>ahpC-F</i>	alkyl hydroperoxide reductase (small subunit)
<i>ahpF</i>	2.3 ± 0.2	3.1 ± 0.1	3.1 ± 1.3	0.9 ± 0.2	0.9 ± 0.1	<i>ahpC-F</i>	alkyl hydroperoxide reductase (large subunit)
<i>BLi00328</i>	1.1 ± 0.1	2.3 ± 0.8	4.1 ± 1.0	5.6 ± 0.8	4.7 ± 1		putative beta-lactamase protein
Unknown							
<i>BLi00491</i>	2.6 ± 0.7	3.8 ± 0.6	4.1 ± 0.5	3.7 ± 0.5	2.7 ± 0.7		conserved hypothetical
<i>BLi03989*</i>	2.2 ± 0.3	2.8 ± 0.1	3.9 ± 1.0	6.4 ± 0.6	7.2 ± 0.8		putative hydroxybenzoate hydroxylase
<i>BLi03991*</i>	3.3 ± 0.6	4.3 ± 0.9	6.0 ± 2.1	17.6 ± 2.1	14.7 ± 3.2		putative aromatic compounds specific dioxygenase
<i>BLi03993*</i>	3.8 ± 0.2	5.2 ± 0.2	10.5 ± 2.3	22.9 ± 1.0	23.1 ± 4.4		putative decarboxylase
<i>BLi03996*</i>	1.5 ± 0.1	2.3 ± 0.3	4.2 ± 1.0	8.8 ± 1.5	9.3 ± 0.5		conserved hypothetical
<i>BLi01482</i>	1.1 ± 0.1	2.7 ± 0.8	2.5 ± 0.5	3.3 ± 1.1	3.2 ± 0.6		putative phage protein
<i>BLi01480</i>	1.3 ± 0.1	2.6 ± 0.2	2.9 ± 1.0	3.6 ± 0.3	3.1 ± 0.7		putative phage protein
<i>BLi01470</i>	3.2 ± 0.6	14.0 ± 1.5	9.4 ± 0.9	9.1 ± 0.5	5.6 ± 0.9		putative phage capsid protein
<i>BLi01466*</i>	2.0 ± 0.2	2.6 ± 0.6	2.5 ± 0.4	6.1 ± 0.5	4.5 ± 0.6		putative phage protein
<i>BLi02233</i>	1.3 ± 0.1	3.4 ± 0.6	9.7 ± 1.3	10.2 ± 2.7	9.3 ± 1.3		putative hydrolase
<i>BLi01933</i>	6.4 ± 3.9	5.5 ± 0.8	4.1 ± 0.2	4.3 ± 1.2	1.0 ± 0.1		conserved hypothetical
<i>BLi04120*</i>	1.7 ± 0.1	2.3 ± 0.6	2.9 ± 1.0	7.6 ± 2.3	6.2 ± 0.9		conserved hypothetical
<i>BLi04124*</i>	1.2 ± 0.1	2.5 ± 0.7	4.2 ± 0.9	4.6 ± 1	6.2 ± 1.9		conserved hypothetical
<i>BLi04317</i>	1.7 ± 0.1	3.1 ± 0.8	5.0 ± 0.2	2.9 ± 0.2	2.5 ± 0.3		putative DNA-binding protein
<i>BLi01486</i>	2.2 ± 0.6	8.6 ± 1.1	15.0 ± 3.5	16.5 ± 3.2	13.5 ± 1.9		putative glycosyl hydrolase
<i>BLi03571</i>	1.9 ± 0.2	2.4 ± 0.4	2.1 ± 0.2	3.4 ± 0.7	3.5 ± 0.2		putative amidase
<i>BLi00654*</i>	1.1 ± 0.1	6.0 ± 0.4	4.2 ± 0.9	4.4 ± 0.8	4.6 ± 0.9		conserved hypothetical
<i>BLi01476</i>	1.0 ± 0.1	4.4 ± 0.5	3.6 ± 0.1	3.3 ± 0.7	2.4 ± 0.6		putative phage tail protein
<i>BLi02843</i>	1.0 ± 0.2	1.7 ± 0.1	2.7 ± 0.6	3.4 ± 0.5	3.0 ± 0.6		hypothetical
<i>BLi00431</i>	1.2 ± 0.1	4.7 ± 0.5	4.3 ± 0.4	5.0 ± 1.1	4.6 ± 0.6		hypothetical
<i>BLi01389</i>	4.3 ± 0.3	4.0 ± 0.9	1.9 ± 0.1	1.9 ± 0.1	1.7 ± 0.2		hypothetical
<i>BLi00303*</i>	1.2 ± 0.2	4.9 ± 0.6	2.6 ± 0.5	5.1 ± 0.3	4.3 ± 0.6		hypothetical
<i>BLi02331</i>	1.0 ± 0.1	1.5 ± 0.2	1.9 ± 0.2	4.1 ± 1.0	3.2 ± 0.2		hypothetical
<i>BLi00236*</i>	3.0 ± 0.8	5.2 ± 0.6	7.4 ± 2.2	7.7 ± 2.8	7.7 ± 2.8		hypothetical
<i>BLi04184</i>	2.0 ± 0.5	5.2 ± 0.1	5.1 ± 0.9	4.7 ± 0.2	4.4 ± 0.5		hypothetical
<i>BLi04185*</i>	1.2 ± 0.1	2.9 ± 0.4	2.3 ± 0.4	6.8 ± 0.7	4.9 ± 0.9		hypothetical
<i>BLi02232</i>	1.1 ± 0.1	1.7 ± 0.2	4.2 ± 1.1	4.2 ± 0.7	4.1 ± 0.6		hypothetical

<i>BLi01622</i>	0.9 ± 0.1	1.2 ± 0.1	2.5 ± 0.4	3.8 ± 0.4	3.1 ± 0.7		hypothetical
<i>BLi04116*</i>	1.7 ± 0.2	2.3 ± 0.5	1.8 ± 0.2	7.4 ± 3.3	7.9 ± 1.7		hypothetical
<i>BLi04119*</i>	1.5 ± 0.2	1.7 ± 0.3	1.4 ± 0.1	4.1 ± 0.8	9.6 ± 1.4		hypothetical
<i>BLi00669</i>	1.2 ± 0.1	2.4 ± 0.1	4.1 ± 0.6	6.3 ± 0.3	4.3 ± 0.7		hypothetical
<i>BLi00668</i>	1.2 ± 0.1	3.7 ± 0.4	4.3 ± 0.8	7.2 ± 1.0	4.5 ± 0.3		hypothetical
<i>BLi01488</i>	7.9 ± 1.1	73.9 ± 15.7	93.2 ± 18.1	147.4 ± 12.0	51.7 ± 11.3		hypothetical
<i>BLi03570</i>	2.6 ± 0.3	3.8 ± 0.2	3.4 ± 1.0	5.4 ± 0.2	4.5 ± 0.7		hypothetical
<i>BLi00719</i>	6.5 ± 0.3	17.7 ± 9.9	15.0 ± 3.4	18.2 ± 2.2	15.9 ± 4.8		hypothetical
<i>BLi00235*</i>	5.0 ± 0.8	10.8 ± 1.3	8.0 ± 1.2	11.4 ± 2.3	9.3 ± 1.9		hypothetical
<i>yozO</i>	1.1 ± 0.1	2.7 ± 0.5	2.4 ± 0.3	3.2 ± 0.3	3.0 ± 0.2	<i>yozO</i>	unknown
<i>ypiB*</i>	1.7 ± 0.1	5.0 ± 1.3	5.6 ± 0.7	6.2 ± 0.3	6.4 ± 0.9	<i>ypiA-B-F</i>	unknown
<i>ypjP</i>	1.3 ± 0.1	3.1 ± 0.9	3.2 ± 0.5	3.4 ± 0.4	3.7 ± 0.7	<i>ypjP-Q</i>	unknown
<i>yqeF</i>	1.1 ± 0.1	2.9 ± 0.2	3.4 ± 0.4	3.6 ± 0.3	3.0 ± 0.3	<i>yqe operon</i>	unknown
<i>yqeH</i>	1.0 ± 0.2	2.8 ± 0.3	3.0 ± 0.2	3.6 ± 0.3	2.9 ± 0.7	<i>yqe operon</i>	unknown
<i>yqfA</i>	1.3 ± 0.2	1.8 ± 0.1	4.4 ± 0.7	4.9 ± 0.2	5.8 ± 0.6	<i>yqfA</i>	unknown
<i>yqxM</i>	2.6 ± 0.1	3.5 ± 1.3	1.7 ± 0.4	4.9 ± 0.7	1.4 ± 0.1	<i>sipW-yqxM</i>	unknown
<i>yrkC</i>	3.0 ± 1.5	38.7 ± 6.9	32.3 ± 4.8	23.5 ± 1.5	15.7 ± 1.2	<i>yrkC</i>	unknown
<i>ysdB</i>	1.4 ± 0.3	2.9 ± 0.3	2.6 ± 0.1	4.0 ± 1.0	4.7 ± 1	<i>ysdB-C</i>	unknown
<i>yueE</i>	1.3 ± 0.1	4.4 ± 0.9	3.5 ± 0.8	4.2 ± 0.1	5.1 ± 0.9	<i>yue operon</i>	unknown
<i>yvcK</i>	1.5 ± 0.2	2.8 ± 0.5	3.1 ± 0.7	2.8 ± 0.2	3.1 ± 0.5	<i>yvc operon</i>	unknown
<i>yvIA</i>	1.3 ± 0.1	4.6 ± 0.2	10.3 ± 2.5	10.5 ± 2.3	11.6 ± 0.9	<i>yvIA</i>	unknown
<i>yvIB*</i>	1.5 ± 0.1	3.9 ± 0.5	8.0 ± 1.2	10.2 ± 0.4	10.3 ± 1	<i>yvIB-D</i>	unknown
<i>yvID</i>	0.9 ± 0.1	1.3 ± 0.1	3.2 ± 0.6	4.0 ± 0.2	4.5 ± 0.4	<i>yvIB-D</i>	unknown
<i>yvqH*</i>	1.0 ± 0.1	2.8 ± 0.9	6.2 ± 1.2	13.1 ± 1.0	22.1 ± 3.3	<i>yvq operon</i>	unknown
<i>yvql*</i>	1.0 ± 0.1	2.8 ± 0.6	5.2 ± 1.0	10.4 ± 1.9	21.6 ± 3.1	<i>yvq operon</i>	unknown
<i>ywbD</i>	2.5 ± 0.1	2.2 ± 0.2	4.5 ± 1.2	6.1 ± 1.1	4.2 ± 0.4	<i>ywbD</i>	unknown
<i>ywfL*</i>	2.2 ± 0.3	2.3 ± 0.1	2.8 ± 0.3	5.8 ± 1.7	4.7 ± 0.3	<i>ywfL</i>	unknown
<i>ywpF</i>	1.5 ± 0.1	3.9 ± 0.3	4.1 ± 0.8	5.1 ± 0.8	3.7 ± 0.1	<i>ywpF-H</i>	unknown
<i>ywrD</i>	2.3 ± 0.1	7.9 ± 1.8	3.2 ± 0.9	5.4 ± 1.0	3.2 ± 0.3	<i>ywrD-C-B-A</i>	unknown
<i>yxkH</i>	0.8 ± 0.1	1.7 ± 0.1	7.1 ± 0.3	6.0 ± 0.8	5.8 ± 0.3	<i>yxkH</i>	unknown

Table 5: Synthesis rates of proteins from *B. licheniformis* cells during glucose starvation conditions. Quantification of the proteins and calculation of the synthesis rates were done with the Delta 2D software (Decodon GmbH, Greifswald, Germany). Only proteins, the expression of which was induced in two independent experiments at least threefold are included in the table.

MecA	negative regulator of competence	4.35	25.1	BLi01240	5.6	6.1		
2 Intermediary metabolism								
2.1 Metabolism of carbohydrates and related molecules								
2.1.1 Specific pathways								
AcoA	acetoin dehydrogenase E1 component (TPP-dependent alpha subunit)	5.06	35.1	BLi00849			43.1	51.7
AcoB	acetoin dehydrogenase E1 component (TPP-dependent beta subunit)	4.64	36.9	BLi00850			7.7	10.3
AcoL	acetoin dehydrogenase E3 component (dihydrolipoamide dehydrogenase)	5.50	49.0	BLi00852	23.2	13.7	22.5	20.6
AcsA	acetyl-CoA synthetase (EC 6.2.1.1)	5.26	64.4	BLi03119	21.7	22.0	3.3	2.3
AcuA	acetoin dehydrogenase (EC1.1.1.5)	5.56	24.6	BLi03120	85.3	39.3	0.9	1.2
BglH	beta-glucosidase (EC 3.2.1.21)	4.92	53.4	BLi04214	2.3	2.6	4.7	4.8
GlpK	glycerol kinase (EC 2.7.1.30)	5.12	55.2	BLi00995			5.2	6.6
Kdul	5-keto-4-deoxyuronate isomerase (EC 5.3.1.17)	5.27	31.2	BLi03829	32.8	38.5	10.8	12.7
LicH	6-phospho-beta-glucosidase (EC 3.2.1.86)	5.04	48.7	BLi04086	148.4	160.4	9.4	11.3
MalL	maltose-inducible alpha-glucosidase	4.89	67.0	BLi00664	14.4	14.7		
YdaF	similar to acetyltransferase	5.96	21.4	BLi00525	235.0	147.4	2.9	3.5
YqiQ	similar to phosphoenolpyruvate mutase	5.32	33.2	BLi04096	983.2	834.9	32.3	46.4
YxiA	similar to arabinan endo-1,5-alpha-L-arabinosidase	6.63	53.1	BLi04220			197.6	142.2
BLi00749	close homolog to BglH beta-glucosidase (EC 3.2.1.21)	5.59	56.2	BLi00749	2.6	1.8	3.0	3.0
BLi02102	putative enoyl(3-hydroxyisobutyryl)-coenzyme A hydratase protein (EC 4.2.1.17)	5.15	39.4	BLi02102	17.9	19.1	12.4	13.5
BLi02103	putative enoyl-CoA hydratase (EC 4.2.1.17)	6.01	28.0	BLi02103	84.2	36.7	18.2	17.3
BLi02103 2.spot	putative enoyl-CoA hydratase (EC 4.2.1.17)	6.01	28.0	BLi02103	2.8	2.9	9.6	13.6
BLi04207	putative isocitrate lyase (EC 4.1.3.1)	5.55	46.8	BLi04207	15.8	10.4	3.2	3.0
BLi04207 2.spot	putative isocitrate lyase (EC 4.1.3.1)	5.55	46.8	BLi04207	6.3	4.0		
2.1.2 Main glycolytic pathways								
PckA	phosphoenolpyruvate carboxykinase (EC 4.1.1.49)	5.12	58.2	BLi03197	12.0	10.6	13.5	15.6
2.1.3 TCA cycle								
CitG	fumarate hydratase (EC 4.2.1.2)	5.62	50.5	BLi03486	2.1	1.9	4.9	3.6
CitZ	citrate synthase II (EC 4.1.3.7)	5.66	41.6	BLi03062	10.9	8.6	2.3	2.3
OdhA	2-oxoglutarate dehydrogenase (E1 subunit) (EC 1.2.4.2)	5.94	106.7	BLi02260	3.2	2.2	6.3	2.2

SdhA	succinate dehydrogenase (flavoprotein subunit) (EC 1.3.99.1)	5.50	65.3	BLi02993	0.4	0.4	4.0	3.0
2.2 Metabolism of amino acids and related molecules								
GltA	glutamate synthase (large subunit) (EC 1.4.1.13)	5.50	167.8	BLi02162	0.8	0.9	7.7	3.5
TrpA	tryptophan synthase (alpha subunit) (EC 4.2.1.10)	5.25	29.3	BLi02398	3.9	5.1	2.8	3.3
Ald	alanine dehydrogenase (EC 1.4.1.1)	4.94	39.6	BLi03382	11.0	10.8		
GlmS	L-glutamine-D-fructose-6-phosphate amidotransferase (EC 2.6.1.16)	5.05	65.6	BLi00204	6.4	7.6	3.3	2.8
GlmS 2.spot	L-glutamine-D-fructose-6-phosphate amidotransferase (EC 2.6.1.16)	5.05	65.6	BLi00204	5.9	5.5		
IspA	major intracellular serine protease (EC 3.4.21.-)	4.34	33.8	BLi01423	141.6	140.0	102.3	77.0
MmsA	methylmalonate-semialdehyde dehydrogenase	5.44	52.6	BLi02104	110.5	72.1	59.0	57.8
RocD	ornithine aminotransferase (EC 2.6.1.13)	5.35	43.9	BLi00422	5.4	5.9		
RocF	arginase (EC 3.5.3.1)	4.94	32.4	BLi00424	5.4	5.5		
RocG	glutamate dehydrogenase (major)	5.48	50.4	BLi02964	728.0	582.4		
Tdh	threonine 3-dehydrogenase (EC 1.1.1.103)	6.42	37.2	BLi01923	171.0	96.0		
Vpr	extracellular serine protease (EC 3.4.21.-)	8.87	85.6	BLi04019	6.9	5.1	14.4	6.5
YaaE	similar to amidotransferase	5.79	21.2	BLi00017	3.2	2.0		
YcgN	similar to 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12)	5.21	56.6	BLi00374	41.5	48.3	11.8	13.3
YhaA	similar to aminoacylase (EC 3.5.1.14)	5.76	44.8	BLi01088	11.9	5.8	2.5	2.4
YjbG	similar to oligoendopeptidase (EC 3.4.24.-)	5.03	76.9	BLi01247	3.3	4.0	3.1	2.2
YusX	similar to oligoendopeptidase	4.90	67.0	BLi03477	8.1	8.8	10.2	12.6
YuxL	similar to acylaminoacyl-peptidase	5.22	73.3	BLi03411			6.3	6.3
BLi00977	putative acylamino-acid-releasing enzyme	4.98	67.8	BLi00977	11.4	9.7	2.2	1.9
BLi04251	putative methylmalonate-semialdehyde dehydrogenase [acylating] (EC 1.2.1.27)	5.26	53.5	BLi04251	9.3	5.7		
2.3 Metabolism of nucleotides and nucleic acids								
Ndk	nucleoside diphosphate kinase (EC 2.7.4.6)	5.01	16.7	BLi02408	0.8	1.0	3.5	5.0
2.4 Metabolism of lipids								
MmgE	putative 2-methylcitrate dehydratase	5.50	53.0	BLi04095	55.9	26.1	10.0	9.6
YoxD	similar to 3-oxoacyl- acyl-carrier protein reductase (EC 1.1.1.100)	5.97	25.3	BLi02171	16.3	9.8		
YqiD	similar to geranyltranstransferase (EC 2.5.1.10)	4.98	32.6	BLi02599	3.4	4.0	2.3	3.0

YsiB	similar to 3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.17)	5.06	27.8	BLi03001	21.5	24.5	3.5	5.0
YusJ	similar to butyryl-CoA dehydrogenase (EC 1.3.99.2)	5.24	65.9	BLi03464	82.1	90.0	12.5	10.2
YusK	similar to acetyl-CoA C-acyltransferase	5.53	41.0	BLi03465	10.8	7.1	3.3	3.7
BLi00828	putative glycerol dehydrogenase (EC 1.1.1.6)	4.63	39.5	BLi00828	6.2	6.5	5.5	4.6
BLi02106	putative butyryl-CoA dehydrogenase	6.04	63.4	BLi02106	93.7	61.4	17.3	8.9
2.5 Metabolism of coenzymes and prosthetic groups								
DhaS	aldehyde dehydrogenase	5.17	54.4	BLi02249	25.4	18.2	15.2	17.9
HemZ	coproporphyrinogen III oxidase	5.68	57.5	BLi01061	16.6	18.2		
NifS	required for NAD biosynthesis	6.57	43.0	BLi02915	231.9	122.3		
YtdI	probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)	5.89	30.1	BLi03093	18.3	16.7	6.8	6.9
BLi03994	close homolog to DhaS aldehyde dehydrogenase	5.23	53.8	BLi03994	32.2	37.2	22.5	22.3
3 Information pathways								
3.5 RNA synthesis								
3.5.1 Initiation								
YvyD	similar to sigma-54 modulating factor of gram-negative bacteria	6.00	21.7	BLi03774	38.3	41.1	1.5	2.0
3.5.2 Regulation								
Hpr	transcriptional repressor of sporulation and extracellular proteases genes	6.01	24.1	BLi01078	95.4	103.3	1.8	2.2
Hpr 2.spot	transcriptional repressor of sporulation and extracellular proteases genes	6.01	24.1	BLi01078	3.0	2.0	1.1	1.4
PurR	transcriptional repressor of the purine operons	6.15	30.5	BLi00060	79.7	69.6		
Spo0A	two-component response regulator central for the initiation of sporulation	6.20	29.5	BLi02593	60.5	28.3	8.1	7.7
YmfC	similar to transcriptional regulator (GntR family)	5.13	27.8	BLi01907	7.6	8.7	1.4	1.3
YrxA	similar to transcriptional regulator	5.56	19.8	BLi02916	29.6	13.4	3.1	4.0
3.5.4 Termination								
NusA	transcription termination	4.65	41.8	BLi01885	6.8	7.1	17.7	3.4
3.6 RNA modification								
YloM	unknown; similar to RNA-binding Sun protein	5.64	49.9	BLi01795	123.9	72.1		
3.7 Protein synthesis								
3.7.2 Aminoacyl-tRNA synthetases								
LysS	lysyl-tRNA synthetase (EC 6.1.1.6)	5.25	57.7	BLi00097	26.3	37.0		

3.8 Protein modification

Map	methionine aminopeptidase (EC 3.4.11.18)	6.41	27.4	BLi00155	325.2	150.6		
YoaA	similar to ribosomal-protein-alanine N-acetyltransferase	4.84	20.4	BLi00277	38.0	42.6	0.4	0.5

4 Other functions

4.1 Adaptation to atypical conditions

ClpC	class III stress response-related ATPase	5.73	90.2	BLi00104	6.7	4.2	4.8	2.1
ClpP	ATP-dependent Clp protease proteolytic subunit (class III heat-shock protein) (EC 3.4.21.92)	4.92	21.8	BLi03710	6.8	7.4	1.0	1.3
BLi04126	putative bacteriocin formation protein	5.51	117.1	BLi04126	10.3	7.2	17.0	6.6
BLi04126	putative bacteriocin formation protein	5.51	117.1	BLi04126	5.3	6.7	15.1	7.4

4.2 Detoxification

YceD	similar to tellurium resistance protein	4.35	20.8	BLi00355	3.3	3.7	0.7	1.6
YvaK	similar to carboxylesterase	5.22	28.4	BLi03642	2.8	3.5	15.3	20.6

4.6 Miscellaneous

BLi01188	putative siderophore biosynthesis protein lucc	5.39	69.8	BLi01188			31.3	42.7
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5 unknown

YflIK		5.92	24.5	BLi00789	24.3	6.5		
YhfK		5.25	23.2	BLi00677	35.6	25.6	1.6	2.0
YitV		5.66	29.8	BLi01204	6.6	6.2		
YkrK		5.76	27.4	BLi01502	93.9	56.2	12.5	14.0
YlbP		5.20	18.6	BLi01727	18.8	20.7	6.2	9.2
YneT		4.66	15.2	BLi02058	43.9	55.0		
YoxA		5.33	36.9	BLi01042			9.3	13.4
YpiB		5.99	21.5	BLi02393	368.1	355.2	2.5	3.6
YqiW		5.11	16.2	BLi02578	3.2	3.8	1.0	1.4
YtxH		4.92	14.8	BLi03129	3.3	3.4	2.7	2.8
YxjG		4.97	43.0	BLi04187	5.9	7.0	0.1	0.1
BLi02008		5.62	23.1	BLi02008	6.2	6.0	1.6	2.4
BLi02801		5.57	31.5	BLi02801	16.3	19.2		
BLi03989	P-hydroxybenzoate hydroxylase	5.73	45.1	BLi03989			11.3	9.1

Table 6: Synthesis rates of proteins from *B. licheniformis* cells during nitrogen starvation conditions. Quantification of the proteins and calculation of the synthesis rates were done with the Delta 2D software (Decodon GmbH, Greifswald, Germany). Only proteins, the expression of which was induced in two independent experiments at least threefold are included in the table.

name	function	pl	MW	number	OD1 (gel 1)	OD1 (gel 2)	Od1+1h (gel 1)	Od1+1h (gel 2)
1 Cell envelope and cellular processes								
1.1 Cell wall								
PpbX	putative beta-lactamase protein	5.77	64.7	BLi00328	15.2	8.0	16.1	15.8
PpbX 2.spot	putative beta-lactamase protein	5.77	64.7	BLi00328	2.4	3.2	8.6	7.9
1.2 Transport/binding proteins and lipoproteins								
MsmX	multiple sugar-binding transport ATP-binding protein	5.87	41.5	BLi01052	3.7	3.2	1.6	1.8
1.8 Sporulation								
RapG	response regulator aspartate phosphatase	5.58	42.4	BLi01137	1.8	2.9	1.4	2.4
SpoVG	required for spore cortex synthesis	4.96	11.0	BLi00062	2.2	3.8	0.4	1.8
2 Intermediary metabolism								
2.1 Metabolism of carbohydrates and related molecules								
2.1.1 Specific pathways								
AlsD	alpha-acetolactate decarboxylase (EC 4.1.1.5)	4.64	28.9	BLi03847	16.9	21.6	14.7	27.7
AlsD 2.spot	alpha-acetolactate decarboxylase (EC 4.1.1.5)	4.64	28.9	BLi03847	1.8	18.2	1.1	2.3
AlsS	alpha-acetolactate synthase	5.04	61.9	BLi03848	25.1	30.3	20.8	22.6
AlsS 2.spot	alpha-acetolactate synthase	5.04	61.9	BLi03848	8.1	24.8	9.1	10.0
BLi00828	putative glycerol dehydrogenase (EC 1.1.1.6)	4.63	39.5	BLi00828	27.4	16.1	3.1	2.5
BLi00828 2.spot	putative glycerol dehydrogenase (EC 1.1.1.6)	4.63	39.5	BLi00828	3.2	6.6	2.2	1.9
2.1.2 Main glycolytic pathways								
YbbT	similar to phosphoglucomutase (glycolysis)	4.83	49.1	BLi00203	8.9	1.8	7.9	12.7
2.2 Metabolism of amino acids and related molecules								
AlaT	putative alanine transaminase	5.70	42.8	BLi03320			2.1	6.0
Alr	D-alanine racemase	5.64	43.7	BLi00551	2.4	2.5	1.0	2.0
AroA	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase and chorismate mutase-isozyme 3 (EC 4.1.2.15 and EC 5.4.99.5)	5.37	39.7	BLi03126	21.1	4.9	5.7	5.5
CarA	carbamoyl-phosphate transferase-arginine (subunit A) (EC 6.3.5.5)	5.52	38.9	BLi01210	0.4	0.8	2.2	4.9

GlmS	L-glutamine-D-fructose-6-phosphate amidotransferase (EC 2.6.1.16)	5.05	65.6	BLi00204	17.2	19.7	41.4	4.1
GlmS 2.spot	L-glutamine-D-fructose-6-phosphate amidotransferase (EC 2.6.1.16)	5.05	65.6	BLi00204	11.9	12.0	5.8	2.2
GlnA	glutamine synthetase (EC 6.3.1.2)	4.82	50.3	BLi01993	4.7	5.1	6.6	4.6
GlnA 2. spot	glutamine synthetase (EC 6.3.1.2)	4.82	50.3	BLi01993	2.8	4.9	1.2	1.7
GlnA 3. spot	glutamine synthetase (EC 6.3.1.2)	4.82	50.3	BLi01993	2.4	2.3	0.9	1.2
GltA	glutamate synthase (large subunit) (EC 1.4.1.13)	5.50	167.8	BLi02162	1.4	2.5	1.9	6.5
GltA 2. spot	glutamate synthase (large subunit) (EC 1.4.1.13)	5.50	167.8	BLi02162	1.3	1.8	1.4	4.9
GltA 3. spot	glutamate synthase (large subunit) (EC 1.4.1.13)	5.50	167.8	BLi02162	0.7	1.8	1.1	4.8
HisB	imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	5.72	21.8	BLi03735	34.7	5.2	1.9	1.5
HisC	histidinol-phosphate aminotransferase and tyrosine/phenylalanine aminotransferase (EC 2.6.1.9 and EC 2.6.1.5)	4.98	40.3	BLi02397	2.3	2.6	0.1	0.3
HisD	histidinol dehydrogenase (EC 1.1.1.23)	5.00	46.0	BLi03736	2.8	2.6	0.1	0.3
HisH	amidotransferase (EC 2.4.2.-)	5.88	23.3	BLi03734	4.2	3.3	0.2	0.2
PepT	peptidase T (tripeptidase) (EC 3.4.11.14)	4.85	45.3	BLi04177	1.9	4.4	1.5	2.9
TrpA	tryptophan synthase (alpha subunit) (EC 4.2.1.10)	5.25	29.3	BLi02398	5.2	7.2	1.5	1.6
TrpB	tryptophan synthase (beta subunit) (EC 4.2.1.20)	5.36	44.5	BLi02399	6.3	7.4	1.1	1.7
TrpE	anthranilate synthase (EC 4.1.3.27)	5.77	58.3	BLi02403	8.9	11.6	1.0	7.3
TrpE 2. spot	anthranilate synthase (EC 4.1.3.27)	5.77	58.3	BLi02403	6.6	7.6	1.0	7.0
TrpD	anthranilate phosphoribosyltransferase	5.40	36.1	BLi02402	5.4	6.7	5.9	3.4
YaaE	similar to amidotransferase	5.79	21.2	BLi00017	6.0	5.2	0.5	1.4
YjbG	similar to oligoendopeptidase (EC 3.4.24.-)	5.03	76.9	BLi01247	1.0	3.5	1.8	1.6
YkuQ	similar to tetrahydronicotinate succinylase	4.88	24.8	BLi01632	3.4	6.0	0.6	2.3
BLi01909	putative zinc protease (EC 3.4.99.-)	5.09	48.6	BLi01909	1.8	5.5	11.9	7.8
2.4 Metabolism of lipids								
FabHB	beta-ketoacyl-acyl carrier protein synthase III (EC 2.3.1.41)	5.79	36.2	BLi01097	9.6	6.7	2.7	3.2
2.5 Metabolism of coenzymes and prosthetic groups								
Ytdl	probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)	5.89	30.1	BLi03093	3.8	4.2		

3.3 DNA recombination

RecA	multifunctional protein involved in homologous recombination and DNA repair (LexA-autocleavage)	4.84	37.7	BLi01918	53.4	16.6	25.8	16.7
3.5.1 Initiation								
YvyD	similar to sigma-54 modulating factor of gram-negative bacteria	6.00	21.7	BLi03774	12.9	6.1	3.9	1.8
3.5.2 Regulation								
AbrB	transcriptional pleiotropic regulator of transition state genes	5.32	10.4	BLi00050	2.1	2.9	10.7	8.7
3.6 RNA modification								
YloM	similar to RNA-binding Sun protein	5.64	49.9	BLi01795	5.2	2.5	2.0	5.3
YsgA	similar to rRNA methylase	5.35	26.7	BLi03017	2.3	2.5	0.6	1.4
4 Other functions								
4.1 Adaptation to atypical conditions								
ClpC	class III stress response-related ATPase	5.73	90.2	BLi00104	8.8	8.3	1.4	3.3
ClpC	class III stress response-related ATPase	5.73	90.2	BLi00104	2.1	3.1	1.2	3.9
ClpP	ATP-dependent Clp protease proteolytic subunit (class III heat-shock protein) (EC 3.4.21.92)	4.92	21.8	BLi03710	1.6	3.4	0.9	1.4
4.2 Detoxification								
YojK	similar to macrolide glycosyltransferase	5.10	44.2	BLi00529	5.8	2.2	2.4	3.6
5 unknown								
YjbN		5.93	29.7	BLi01255	3.2	2.5	8.3	5.1
YjcG		5.78	19.5	BLi01284	5.9	9.0	2.1	1.9
YkgA		5.11	33.4	BLi01401	9.6	13.6	0.3	0.4
YurX		5.29	48.4	BLi03450	3.2	28.9	3.4	2.9
YurX		5.29	48.4	BLi03450	2.6	9.9	2.3	1.0
YutE		4.74	17.3	BLi03419	10.3	52.8	1.9	0.7
YxeH	unknown	4.49	31.4	BLi04258	18.3	5.4	2.5	5.4
BLi00258	putative oxidoreductase	5.08	37.7	BLi00258	3.6	4.3	0.6	1.2
BLi02801	unknown	5.57	31.5	BLi02801			4.9	6.5