

from

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**Global gene expression profiling of *Bacillus subtilis*
in response to ammonium and tryptophan starvation
as revealed by transcriptome and proteome analysis**

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Table1: Genes induced by ammonium (N) or tryptophan (T) starvation as revealed by transcri

Operon ¹⁾	Gene	Transcriptome ²⁾				Proteome ³⁾							
		N		T		N				T			
		1	2	1	2	1	2	3	4	1	2	3	4
Genes specifically induced by ammonium starvation													
TnrA regulon (positive control)													
asnZ (yccC)	asnZ	13.7	36.5	0.8	0.7	4	3	3	-				
comGA-B-C-D-E-F-G	comGC	5.2	3.4	1.2	1.4								
	comGG	7.0	3.1	1.4	1.6								
gabP	gabP	8.0	11.1	1.8	1.8								
nasA	nasA	3.4	4.9	1.2	1.4								
nasBCDEF	nasB	4.5	4.5	1.4	1.5								
	nasC	13.3	10.0	1.8	1.6								
	nasD	18.0	15.2	1.0	1.1								
	nasE	11.9	17.4	1.0	1.0								
	nasF	5.3	9.7	1.1	1.4								
nrgAB	nrgA	118.0	80.3	1.1	1.2								
	nrgB	68.4	69.8	2.1	1.9								
tnrA	tnrA	328.0	11.9	1.4	1.6								
yzkB-ykoL	yzkB	150.0	8.0	1.2	0.9								
yrbD	yrbD	3.4	5.9	1.0	1.0								
ywrD	ywrD	3.1	7.5	0.9	1.3								
pucJKLM	pucL	0.8	1.0	0.8	1.0	4	5	27	18				
tasA	tasA	2.4	1.7	1.9	2.1	2	4	3	3				
ureABC-ywnA-B	ureA	24.8	32.2	3.7	3.9								
	ureB	30.4	30.0	3.9	4.8								
	ureC	16.3	43.1	2.5	3.0	19	75	25	12	2	2	3	3
	ywnA	2.8	3.4	1.2	1.3								
ykfABCD	ykfA	3.2	4.6	2.9	2.3								
	ykfD	3.3	2.9	1.5	2.0								
oppABCDEF	oppA	2.7	6.1	6.8	5.9	4	6	12	9				
cah	cah	1.0	1.2	1.5	1.7	17	24	13	25	13	18	26	32
TnrA regulon (negative control), GlnR derepression													
glnRA	glnR	8.6	3.7	0.4	0.5								
	glnA	5.6	8.9	0.4	0.3	2	2	3	3				
yurG	yurG	2.7	9.3	1.5	1.8								
σ ^L (BkdR/RocR)													
bkdR-ptb-bcd-buk-	ptb	6.7	17.7	1.8	1.5								
lpdV-bkdAA-bkdAB-	bcd	5.5	23.4	1.3	1.6	9	12	14	8				
	buk	2.7	8.3	1.2	1.3								
	lpdV	2.3	8.6	0.9	0.9	6	5	1	1				
	bkdAA	0.7	2.8	0.4	0.4	10	6	1	1				
rocABC	rocA	2.4	3.3	2.1	2.0	24	12	-	-				
rocDEF	rocD	1.3	1.7	1.4	1.2	4	4	2	-				
	rocF	0.8	1.4	0.9	1.0	5	2	-	-				
Carbon catabolite control:													
CcpA dependent repression by glucose													
acsA	acsA	1.5	1.7	0.9	1.2	5	6	9	5				
citB	citB	---	---	---	---	2	4	3	4				
dhaS	dhaS	2.0	4.2	2.1	2.2	3	1	8	8				
ysiB	ysiB	0.7	0.9	0.9	0.8	-	-	-	6				
yvmB	yvmB	53.4	7.4	0.8	1.1								
yvnA	yvnA	5.2	3.7	1.4	1.5								
ywsA	ywsA	4.3	4.8	1.7	1.5								
yojL	yojL	3.3	3.1	1.8	1.6								
folD	folD	0.7	0.6	0.3	0.3	1	1	2	13 ^{MenB}	5	4	3	5
yqxl	yqxl	3.0	4.0	2.0	3.1								

iptome and proteome analysis

	Function/Similarity ⁴⁾	Regulon ⁵⁾
N	similar to asparaginase	TnrA+
N	exogenous DNA-binding	TnrA+
N	DNA transport machinery	
N	gamma-aminobutyrate permease	TnrA+,CodY,RelA,CcpA
N	nitrate transporter	TnrA+
N	assimilatory nitrate reductase (electron transfer subunit)	TnrA+
N	assimilatory nitrate reductase (catalytic subunit)	
N	assimilatory nitrite reductase (subunit)	
N	assimilatory nitrite reductase (subunit)	
N	uroporphyrin-III C-methyltransferase	
N	ammonium transporter	TnrA+
N	nitrogen-regulated PII-like protein	
N	transcriptional pleiotropic regulator invoved in global nitrogen regulation	TnrA+,GlnR
N	unknown	TnrA+
N	similar to sodium/proton-dependent alanine carrier protein	TnrA+
N	similar to gamma-glutamyltransferase	TnrA+
N	uricase	TnrA+,SigmaE,PucR
N	translocation-dependent antimicrobial spore component	TnrA+,SigmaH
NT	urease (gamma subunit)	TnrA+,GlnR,PucR,CodY,RelA,SigmaH
NT	urease (beta subunit)	
NT	urease (alpha subunit)	
N	putative transcriptional regulator	
N(T)	similar to immunity to bacteriotoxins	TnrA+,?
N(T)	similar to oligopeptide ABC transporter (permease)	
NT	oligopeptide ABC transporter (binding protein) (initiation of sporulation, competence development)	TnrA+,Hpr
NT	cephalosporin C deacetylase	TnrA+,?
N	transcriptional repressor of the glutamine synthetase gene	TnrA-,GlnR
N	glutamine synthetase	
N	similar to aspartate aminotransferase	TnrA-,GlnR?
N	probable phosphate butyryltransferase	CodY,TnrA-,SigmaL,BkdR
N	leucine dehydrogenase	
N	probable branched-chain fatty-acid kinase (butyrate kinase)	
N	probable branched-chain alpha-keto acid dehydrogenase E3 subunit (dihydrolipoamide dehydrogenase)	
N	branched-chain alpha-keto acid dehydrogenase E1 subunit (2-oxoisovalerate dehydrogenase alpha subunit)	
N	pyrroline-5 carboxylate dehydrogenase	CodY,SigmaL,RocR,AhrC,CcpA
N	ornithine aminotransferase	CodY,SigmaL,RocR,AhrC,CcpA
N	arginase	
N	acetyl-CoA synthetase	CcpA,CodY,SigmaB
N	aconitate hydratase	CcpA,CcpC,TnrA,CodY
N	aldehyde dehydrogenase	CcpA
N	similar to 3-hydroxybutyryl-CoA dehydratase	CcpA
N	similar to possible transcriptional regulator	CcpA
N	similar to possible transcriptional regulator	CcpA
N	unknown	CcpA
N	similar to cell wall-binding protein	CcpA,SigmaH
NT	methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase	CcpA
N(T)	unknown	CcpA

Operon ¹⁾	Gene	Transcriptome ²⁾				Proteome ³⁾							
		N		T		N				T			
		1	2	1	2	1	2	3	4	1	2	3	4
CcpA independent repression by glucose													
glmS	<i>glmS</i>	0.7	1.9	0.7	0.6	7	11	10	16				
iolS	<i>iolS</i>	2.1	1.8	1.4	1.7	3	3	-	3				
positive control by CcpA													
alsR	<i>alsR</i>	5.8	5.8	1.4	1.5								
alsSD	<i>alsS</i>	12.2	18.3	1.7	1.7								
	<i>alsD</i>	5.5	14.2	1.6	1.4								
σ ^F regulon													
rsfA	<i>rsfA</i>	1.0	1.6	1.0	1.3	3	4	10	11 ^{SigF}				
spolIQ	<i>spolIQ</i>	1.4	2.0	1.1	1.2	-	3	18	12				
spoVT	<i>spoVT</i>	3.1	1.1	0.7	1.0	Coom							
σ ^E regulon													
asnO	<i>asnO</i>	0.8	1.1	1.0	1.3	Coom							
kamA	<i>kamA</i>	0.8	1.3	1.1	1.1	Coom							
patB	<i>patB</i>	7.0	43.0	1.0	1.2								
prkA	<i>prkA</i>	0.8	1.4	0.9	1.2	1	2	13	71				
safA	<i>safA</i>	0.7	0.8	0.8	1.4	2	4	12	53				
spolVA	<i>spolVA</i>	0.7	0.4	0.6	0.5	-	-	19	128				
spoVR	<i>spoVR</i>	1.1	1.0	1.4	1.4	2	1	2	6				
spoVID-ysxE	<i>spoVID</i>	0.9	1.1	1.0	0.8	-	-	-	14				
yaaH	<i>yaaH</i>	0.6	0.5	0.5	0.5	1	3	26	105				
yhbH	<i>yhbH</i>	0.9	1.4	0.9	1.0	1	1	4	20				
yjbX	<i>yjbX</i>	0.8	1.3	0.6	0.7	1	1	1	11				
yuaE	<i>yuaE</i>	2.1	1.4	2.0	1.9	10	10	32	30				
sporulation and competence													
cotG	<i>cotG</i>	5.8	4.6	1.2	1.2								
cotH	<i>cotH</i>	3.5	5.1	1.2	1.2								
kapB	<i>kapB</i>	4.4	26.3	1.5	1.5								
kapD	<i>kapD</i>	3.5	18.4	1.3	1.7								
kinB	<i>kinB</i>	3.0	17.7	0.8	0.7								
pbpD	<i>pbpD</i>	3.2	6.3	1.4	2.2								
pbpE	<i>pbpE</i>	1.6	1.3	0.7	0.9	34	17	14	10				
others													
alaR-T-yugI	<i>alaR</i>	10.9	14.4	0.9	1.5								
	<i>alaT</i>	8.1	9.5	1.0	1.3								
	<i>yugI</i>	3.6	3.9	1.1	1.5								
cypX	<i>cypX</i>	12.3	9.9	0.9	1.0								
flgL	<i>flgL</i>	3.1	3.7	1.4	1.7								
unknown function (1)													
ycbU	<i>ycbU</i>	2.8	3.0	1.9	1.8								
yfhM	<i>yfhM</i>	1.4	1.4	1.9	1.0	4	5	19	16				
yfjA	<i>yfjA</i>	3.1	3.3	2.0	2.6								
yjbCD	<i>yjbC</i>	1.3	1.6	1.8	1.5	3	3	3	3				
yjbG	<i>yjbG</i>	1.2	1.3	1.1	1.7	3	5	4	4				
yqeH	<i>yqeH</i>	0.4	0.6	0.6	0.6	1	2	6	15				
ysnA	<i>ysnA</i>	0.8	0.9	1.1	0.9	-	-	-	6				
yugE	<i>yugE</i>	5.0	12.1	1.2	1.3								
yurU	<i>yurU</i>	0.8	1.1	1.1	1.2	4	8	12	8				
yuxJ	<i>yuxJ</i>	5.2	39.0	1.3	1.6								
yvaB	<i>yvaB</i>	---	---	---	---	2	2	3	4				
yvmC	<i>yvmC</i>	31.3	18.6	0.7	1.0								
yvyG	<i>yvyG</i>	4.5	3.5	1.7	1.8								
ywmF	<i>ywmF</i>	3.6	2.9	1.4	1.5								
ywoEF	<i>ywoE</i>	4.2	4.2	0.9	1.0								
ywrE	<i>ywrE</i>	4.4	4.5	1.6	1.4								
ywrK	<i>ywrK</i>	3.4	4.4	1.3	1.2								
yxiE	<i>yxiE</i>	1.6	1.6	1.6	1.7	6	6	11	7				

	Function/Similarity ⁴⁾	Regulon ⁵⁾
N	L-glutamine-D-fructose-6-phosphate amidotransferase	glu-
N	myo-inositol catabolism	glu-, lolR
N	transcriptional regulator of the alpha-acetolactate operon	CcpA+
N	alpha-acetolactate synthase	CcpA+
N	alpha-acetolactate decarboxylase	
N	probable regulator of transcription of sigma-F-dependent genes	SigmaF
N	required for completion of engulfment	SigmaF
N	transcriptional positive and negative regulator of sigma-G-dependent genes	SigmaF
N	asparagine synthetase	SigmaE
N	lysine 2,3-aminomutase	SigmaE
N	aminotransferase, cystathione beta lyase/cysteine desulphydrase	SigmaE, ?
N	serine protein kinase	SigmaE
N	morphogenetic protein associated with SpoVID	SigmaE
N	required for proper spore cortex formation and coat assembly	SigmaE
N	involved in spore cortex synthesis	SigmaE
N	required for assembly of the spore coat	SigmaE
N	similar to cortical fragment-lytic enzyme	SigmaE, SigmaB
N	putative stress response protein	SigmaE
N	glutamic acid-rich protein	SigmaE
N	unknown	SigmaE
N	spore coat protein	
N	spore coat protein (inner)	
N	activator of KinB in the initiation of sporulation	
N	inhibitor of the KinA pathway to sporulation	
	two-component sensor histidine kinase involved in the initiation of	
N	sporulation	CodY
N	penicillin-binding protein 4*	
N	penicillin-binding protein 4	
N	transcriptional regulator of the alaRT operon	AlaR
N	putative alanine transaminase	
N	similar to polyribonucleotide nucleotidyltransferase	
N	cytochrome P450-like enzyme	
N	flagellar hook-associated protein 3 (HAP3)	RelA
N	similar to putative aminotransferase	
N	similar to epoxide hydrolase	SigmaB
N	unknown	
N	similar to N-acetyltransferase	SigmaB
N	similar to oligoendopeptidase	
N	similar to GTP-binding protein	
N	similar to xanthosine triphosphate pyrophosphatase	
N	unknown	
N	similar to ABC transporter	
N	similar to multidrug-efflux transporter	
N	similar to NAD(P)H dehydrogenase (quinone)	
N	similar to unknown proteins	
N	similar to flagellar protein	RelA
N	similar to unknown proteins	RelA
N	similar to permease	
N	unknown	
N	similar to arsenical pump membrane protein	
N	similar to universal stress protein	

Operon ¹⁾	Gene	Transcriptome ²⁾				Proteome ³⁾							
		N		T		N				T			
		1	2	1	2	1	2	3	4	1	2	3	4
unknown function (2)													
yhdN	yhdN	1.2	1.1	3.5	1.8	3	2	2	4				
ywqHIJKL	ywqH	3.4	3.5	2.0	3.0								
	ywqI	2.8	3.0	1.9	1.8								
Genes specifically induced by tryptophan starvation													
TRAP regulon													
pabBAC	pabB	1.2	0.9	3.0	3.3								
	pabA/trpG	1.4	1.1	6.9	10.2					38	36	32	23
	pabC	0.6	0.7	3.6	2.6								
trpEDCFBA	trpE	0.5	0.6	12.5	21.5					25	23	32	32
	trpD	0.5	0.6	44.9	50.7					12	11	11	8
	trpC	0.5	0.7	13.4	12.7								
	trpF	0.6	0.7	22.9	35.1								
	trpB	0.4	0.5	50.0	68.8					8	8	12	11
	trpA	0.5	0.4	7.8	10.1					15	14	16	14
yczA-ycbK	yczA/rtpA	0.8	0.6	7.5	9.5								
	ycbK	0.9	0.9	14.3	13.2								
yhaG	yhaG/trpP	1.2	1.4	2.9	3.1								
hisC-tyrA-aroE	hisC/aroJ	0.4	0.4	5.6	5.3								
	tyrA	0.6	0.4	3.3	4.2								
	aroE	0.5	0.4	3.6	3.5								
trpS	trpS	1.0	1.5	10.9	16.0								
RelA regulon													
adeC	adeC	0.9	1.0	3.7	3.2					4	5	6	3
ald	ald	1.2	1.4	1.1	1.3					4	4	6	8
hpr	hpr	1.9	1.2	6.3	4.6								
yetH	yetH	1.3	1.8	4.1	4.8								
other functions													
ctaBCDEF	ctaB	1.2	1.0	2.9	4.2								
degSU	degS	1.8	1.5	1.8	1.6					8	6	6	5
	degU	1.4	1.3	1.6	1.5					5	5	6	5
gsiB	gsiB	0.8	0.7	9.1	1.9					-	3	3	2
hisJ	hisJ	1.0	1.3	3.0	3.4								
hutPHUIGM	hutP	1.3	2.5	6.6	7.1								
liaIHGFSR	liaR	2.1	1.0	7.6	8.2								
	liaS	2.0	0.9	7.9	10.4								
ndhF-ybcCDFHI	ndhF	0.2	0.3	6.1	4.7								
	ybcC	0.2	0.1	5.2	3.8								
	ybcF	0.5	0.1	6.3	5.3								
	ybcH	0.5	0.1	6.5	3.3								
	ybcI	0.6	0.1	6.9	6.4								
spo0E	spo0E	1.7	1.6	3.2	3.2								
hom	hom	5.3	1.0	3.2	2.3					3	4	4	3
msrA-yppQ	msrA	3.2	2.2	3.2	3.4								
	yppQ	2.6	2.5	3.1	3.0								
thrC	thrC	3.1	1.0	4.2	3.1								
unknown function (1)													
ybgA	ybgA	0.8	0.9	3.8	2.8								
ycgB	ycgB	1.1	1.2	3.0	3.2								
yczJ	yczJ	1.0	2.2	2.8	3.3								
yfml-J	yfml	1.3	2.2	3.3	3.0								
yhaA	yhaA	2.3	2.8	3.9	3.6								

	Function/Similarity ⁴⁾	Regulon ⁵⁾
N(T)	similar to aldo/keto reductase	SigmaB
N(T)	unknown	
N	similar to unknown proteins from <i>B. subtilis</i>	
T	para-aminobenzoate synthase (subunit A)	
T	para-aminobenzoate synthase glutamine amidotransferase (subunit B) / anthranilate synthase (subunit II)	TRAP
T	aminodeoxychorismate lyase	
T	anthranilate synthase	TRAP
T	anthranilate phosphoribosyltransferase	
T	indol-3-glycerol phosphate synthase	
T	phosphoribosyl anthranilate isomerase	
T	tryptophan synthase (beta subunit)	
T	tryptophan synthase (alpha subunit)	
T	similar to inhibitor of TRAP, regulated by T-BOX (trp) sequence RtpA	TRAP
T	similar to efflux system	
T	possible transmembrane protein involved in tryptophan transport	TRAP
T	histidinol-phosphate aminotransferase / tyrosine and phenylalanine aminotransferase	
T	prephenate dehydrogenase	
T	5-enolpyruvoylshikimate-3-phosphate synthase	
T	tryptophanyl-tRNA synthetase	
T	adenine deaminase	RelA
T	L-alanine dehydrogenase	RelA, TnrA-
T	transcriptional repressor of sporulation and extracellular proteases genes	RelA
T	similar to glyoxalase/bleomycin resistance protein/dioxygenase	RelA
T	cytochrome caa3 oxidase (assembly factor)	CcpA
T	two-component sensor histidine kinase involved in degradative enzyme and competence regulation	
T	two-component response regulator involved in degradative enzyme and competence regulation	
T	general stress protein	SigmaB, CcpA+
T	histidinol phosphate phosphatase	
T	transcriptional activator of the histidine utilization operon	CodY, CcpA
T	reponse regulator induced by cell wall active antibiotics vancomycin, bacitracin	
T	sensor histidine kinase induced by cell wall active antibiotics vancomycin, bacitracin	
T	NADH dehydrogenase (subunit 5)	
T	unknown	
T	similar to carbonic anhydrase	
T	similar to probable ATPase	
T	similar to unknown proteins	
T	negative sporulation regulatory phosphatase	
T(N)	homoserine dehydrogenase	
T(N)	peptidyl methionine sulfoxide reductase	
T(N)	similar to peptide methionine sulfoxide reductase	
T(N)	threonine synthase	
T	similar to transcriptional regulator (GntR family)	
T	unknown	
T	similar to antibiotic biosynthesis monooxygenase	
T	similar to macrolide-efflux transporter	
T	similar to aminoacylase	CodY

Operon ¹⁾	Gene	Transcriptome ²⁾				Proteome ³⁾							
		N		T		N				T			
		1	2	1	2	1	2	3	4	1	2	3	4
unknown function (2)													
yhdX	yhdX	0.9	1.3	2.9	3.6								
yjzD	yjzD	2.0	1.3	2.9	3.3								
ylbA	ylbA	2.1	1.5	3.2	3.2								
ylmCDEFGH	ylmC	1.4	1.4	3.6	3.5								
	ylmE	1.2	1.4	3.1	3.3								
ynfC	ynfC	2.0	1.6	4.2	4.9								
yocS	yocS	1.3	0.9	6.1	7.6								
yodF	yodF	0.4	0.4	3.3	3.2								
yoeA	yoeA	1.7	1.9	2.8	3.5								
yoze	yoze	1.2	1.0	3.4	3.4								
ypbH	ypbH	2.2	1.6	3.7	4.5								
yrpB	yrpB	1.5	1.5	5.6	5.4								
yurY	yurY	1.2	1.3	1.6	1.6					28	29	35	30
yusM	yusM	1.2	1.4	3.4	5.0								
yusT	yusT	1.2	1.9	2.9	3.6								
yutG	yutG	4.0	0.9	3.8	3.1								
yweA	yweA	1.4	4.1	3.1	3.5								
yyaK	yyaK	0.8	1.2	3.8	3.9								
yyaO	yyaO	1.3	1.3	3.1	3.0								
yybl	yybl	2.3	1.3	1.8	1.7					9	3	8	7
yacKLMN	yacL	3.1	2.2	3.1	3.2								
yfhJ	yfhJ	3.5	1.6	3.5	3.8								
yjbA	yjbA	1.7	2.8	4.1	4.8								
yolF	yolF	6.4	1.8	3.2	3.4								
yqgY	yqgY	3.1	2.0	4.1	4.6								
yrzI	yrzI	3.2	1.1	5.1	4.6								
ysdB	ysdB	4.1	2.0	3.1	3.3								
yuxK	yuxK	2.1	4.2	3.7	4.6								
yvdT	yvdT	9.2	2.3	5.6	4.7								
Genes induced by both ammonium and tryptophan starvation													
citZ-icd-mdh	citZ	1.3	1.5	1.1	0.9	3	4	7	5	3	3	3	4
	dat	2.2	3.9	3.0	3.2	3	3	4	3	3	2	3	3
menB	menB	0.5	0.6	0.7	0.7	1	1	2	13 ^{FOLD}	5	4	3	5
katA	katA	3.2	2.5	2.5	3.2	3	5	4	3	2	2	4	5
maeN	maeN	5.0	12.4	6.8	10.4								
murB	murB	0.5	0.8	0.5	0.5	5	6	7	9	2	1	4	11
mecA	mecA	5.4	3.3	8.0	9.6								
ycgN	ycgN	1.1	1.2	1.2	1.1	3	20	16	10	5	6	4	8
yfmH	yfmH	4.3	4.1	2.4	2.4								
yhfH	yhfH	30.1	8.6	13.6	18.0								
yhzC	yhzC	5.3	5.2	11.7	11.5								
yjcLK	yjcL	1.0	1.8	3.6	3.8								
	yjcK	1.3	1.2	5.1	5.1	3	3	6	6	8	7	8	8
yncM	yncM	4.4	4.4	4.6	5.4								
yoeB	yoeB	6.6	6.0	11.0	9.2								
yrhP	yrhP	20.5	3.2	10.0	10.4								
yufLM	yufL	4.1	11.6	5.1	5.4								
	yufM	3.5	13.2	5.6	7.0								
yusJ	yusJ	2.4	2.4	3.6	3.5	3	5	2	1	-	-	5	3
yusU	yusU	5.0	6.2	7.6	8.9								
yusV	yusV	6.1	6.5	7.0	10.3								
General starvation induced genes													
CodY regulon (1)													
amhX	amhX	1.1	1.9	2.4	2.6	4	4	4	3	3	3	4	4
appBC	appB	2.9	6.9	5.5	4.7								
	appC	3.0	7.0	5.9	8.2								
appDFA	appD	5.5	8.9	7.0	10.3	4	3	5	7	4	4	5	3
	appF	5.4	7.6	8.5	8.4								
	appA	2.1	4.5	4.2	4.8								

	Function/Similarity ⁴⁾	Regulon ⁵⁾
T	unknown	CodY
T	similar to unknown proteins	
T	similar to unknown proteins	
T	similar to unknown proteins	
T	similar to unknown proteins	
T	unknown	
T	similar to sodium-dependent transporter	
T	similar to proline permease	TnrA-
T	similar to Na ⁺ driven multidrug efflux pump	SigmaH
T	unknown	SigmaE, ?
T	similar to negative regulation of competence MecA homolog	
T	similar to 2-nitropropane dioxygenase	
T	similar to ABC transporter (ATP-binding protein)	
T	similar to proline dehydrogenase	
T	similar to transcriptional regulator (LysR family)	
T	similar to low temperature requirement C protein	
T	similar to unknown proteins	
T	similar to unknown proteins	
T	similar to peptidase M14, carboxypeptidase A	
T	unknown	SigmaE
T(N)	similar to unknown proteins	SigmaB
T(N)	similar to catalase	
T(N)	similar to unknown proteins	SigmaF, ?
T(N)	similar to unknown proteins	
T(N)	similar to unknown proteins	
T(N)	unknown	
T(N)	similar to unknown proteins	
T(N)	similar to unknown proteins	
T(N)	similar to transcriptional regulator (TetR/AcrR family)	
NT	citrate synthase II (major)	CcpA, CcpC
NT	probable D-alanine aminotransferase	
NT	dihydroxynaphthoic acid synthetase	
NT	vegetative catalase 1	SigmaE, PerR
NT	Na ⁺ /malate symporter	
NT	UDP-N-acetylenolpyruvoylglucosamine reductase	
NT	negative regulator of competence	
NT	similar to 1-pyrroline-5-carboxylate dehydrogenase	
N(T)	unknown	
NT	unknown	
NT	unknown	
(N)T	similar to unknown proteins	
NT	similar to ribosomal-protein-alanine N-acetyltransferase	
NT	similar to unknown proteins	
NT	unknown	SigmaE
NT	similar to efflux protein	
NT	similar to two-component sensor histidine kinase [YufM]	
NT	similar to two-component response regulator [YufL]	
NT	similar to butyryl-CoA dehydrogenase	
NT	similar to unknown proteins	
NT	similar to iron(III) dicitrate transport permease	
NT	amidohydrolase	CodY
NT	oligopeptide ABC transporter (permease)	CodY, Hpr
NT	oligopeptide ABC transporter (permease)	
NT	oligopeptide ABC transporter (ATP-binding protein)	CodY, RelA, CcpA, Hpr
NT	oligopeptide ABC transporter (ATP-binding protein)	
(N)T	oligopeptide ABC transporter (oligopeptide-binding protein)	

Operon ¹⁾	Gene	Transcriptome ²⁾				Proteome ³⁾							
		N		T		N				T			
		1	2	1	2	1	2	3	4	1	2	3	4
CodY regulon (2)													
dppABCDE	dppA	6.5	7.4	6.7	6.5	6	8	7	6 ^{MinD}	3	4	6	6
	dppB	3.5	4.5	4.0	2.8								
	dppC	3.5	5.7	3.3	3.8								
	dppE	3.7	7.3	4.4	3.5								
ilvD	ilvD	0.8	3.2	3.7	4.7					3	3	4	3
rapA-phrA	rapA	10.2	15.1	5.9	6.0	8	7	9	14	5	5	11	18
	phrA	10.9	12.4	5.7	5.7								
rapC-phrC	rapC	3.4	4.5	3.7	3.9								
	phrC	4.1	3.6	2.8	4.2								
spo0A	spo0A	2.1	1.8	2.0	1.8	7	6	7	6	4	2	4	3
ybgE	ybgE	2.7	4.5	3.3	3.9								
ycgA	ycgA	1.2	3.1	8.6	8.4								
yhdG	yhdG	3.9	4.2	5.5	5.8								
yufN	yufN	4.9	17.4	7.3	10.3								
yufOPQ	yufO	5.6	8.1	7.3	9.2								
	yufP	5.3	7.8	7.6	7.1								
	yufQ	3.6	5.1	4.4	4.4								
yurJ	yurJ	1.1	1.3	0.9	0.8	3	3	-	-	19	19	13	9
yurPONML	yurP	1.4	1.4	1.4	1.5	4	4	3	1	2	2	2	1
	yurO	---	---	---	---	4	7	7	2	10	10	11	6
	yurL	2.3	4.7	2.3	2.8					8	7	9	4
ywfBCDEFG	ywfB	2.1	6.8	4.2	4.4								
	ywfC	1.5	4.4	3.4	3.5	5	3	3	3	2	2	2	3
	ywfD	1.5	4.9	3.0	3.5								
yxB-A-yxN-B-asnH-yxaI	yxB	8.8	12.7	13.0	13.9	10	11	11	12	6	7	9	10
	yxB	7.0	10.2	6.2	7.2								
	yxN	7.7	5.0	5.8	7.9								
	asnH	4.5	7.7	2.9	4.7								
	yxaM	5.9	8.2	2.6	3.1								
yxB	yxB	13.9	24.8	6.9	8.6	6	9	10	11				
	yxB	4.9	6.4	3.0	2.8								
RelA regulon (positive stringent response)													
epr	epr	3.2	1.9	3.9	3.3								
spo0F	spo0F	2.7	5.3	3.4	2.8								
spoVG	spoVG	5.2	9.8	2.8	7.5	10	8	3	3	6	12	13	3
vpr	vpr	3.7	10.4	6.6	6.6	9	22	13	8				
ydaF	ydaF	1.4	3.7	5.1	5.4								
ypiB	ypiB	4.9	3.5	3.5	6.6	3	3	6	5	6	-	-	-
ytxGHJ	ytxG	2.5	2.4	5.5	3.2								
	ytxH	1.6	3.0	4.9	3.7	6	5	4	5	6	7	6	6
ytzE	ytzE	6.8	3.4	9.0	10.1								
yvyD	yvyD	6.0	4.4	8.5	9.1	47	13	3	2	76	63	50	36
ywpF	ywpF	4.0	2.1	3.7	3.3								
σ ^H regulon (1)													
bsaA-ypgQ-ypgR	bsaA	2.6	2.5	4.5	3.9								
	ypgQ	2.2	2.3	4.7	4.8								
	ypgR	1.5	2.2	2.9	4.3								
ftsAZ	ftsA	2.5	1.9	2.0	2.1					5	4	4	4
minCD	minD	---	---	---	---	6	8	7	6 ^{UppA}	3	4	6	6
rapE-phrE	phrE	3.2	4.0	2.1	2.8								
rapG-phrG	rapG	2.4	3.0	2.5	2.9	6	5	5	7	4	4	9	11
	phrG	3.5	4.2	3.6	4.7								
spoIIAA-AB-sigF	spoIIAB	3.6	6.4	4.1	3.9								
	sigF	3.9	7.0	3.5	4.4	3	4	10	11 ^{RsfA}				
	spoVS	3.1	2.0	4.4	4.6								

	Function/Similarity ⁴⁾	Regulon ⁵⁾
NT	D-alanyl-aminopeptidase	CodY, TnrA+, glu-
NT	dipeptide ABC transporter (permease) (sporulation)	
NT	dipeptide ABC transporter (permease) (sporulation)	
NT	dipeptide ABC transporter (dipeptide-binding protein) (sporulation)	
(N)T	dihydroxy-acid dehydratase	CodY
NT	response regulator aspartate phosphatase	CodY, RelA, CcpA
NT	phosphatase (RapA) inhibitor	CodY, RelA
NT	response regulator aspartate phosphatase	CodY, RelA
NT	phosphatase (RapC) regulator / competence and sporulation stimulating factor (CSF)	CodY, RelA, SigmaH, CcpA
NT	two-component response regulator central for the initiation of sporulation	CodY, RelA, SigmaH
NT	similar to branched-chain amino acid aminotransferase	CodY
(N)T	unknown; similar to putative transporter	CodY
NT	similar to amino acid transporter	CodY, TnrA+
NT	similar to lipoprotein	CodY, TnrA+
NT	similar to ABC transporter (ATP-binding protein)	CodY, TnrA+
NT	similar to sugar ABC transporter (permease)	
NT	similar to sugar ABC transporter (permease)	
NT	similar to multiple sugar ABC transporter (ATP-binding protein)	CodY, TnrA-
NT	similar to glutamine-fructose-6-phosphate transaminase	CodY, RelA, TnrA-
NT	similar to multiple sugar-binding protein	
(N)T	similar to ribokinase	
(N)T	similar to bacilysin biosynthesis protein bacA	CodY, RelA, SigmaH
NT	similar to bacilysin biosynthesis protein bacA	
(N)T	similar to glucose 1-dehydrogenase	
NT	similar to methyltransferase	CodY, TnrA+, glu-
NT	unknown	
NT	unknown	
NT	asparagine synthetase	
NT	similar to antibiotic resistance protein	
NT	similar to unknown proteins	CodY, RelA
NT	similar to N-acetyltransferase	
(N)T	minor extracellular serine protease	RelA
NT	two-component response regulator involved in the initiation of sporulation	RelA, SigmaH
NT	required for spore cortex synthesis	RelA, SigmaH, CcpA
NT	minor extracellular serine protease	RelA, SigmaH, TnrA+
(N)T	similar to acetyltransferase	RelA
NT	similar to unknown proteins	RelA, SigmaH
(N)T	similar to general stress protein	RelA, SigmaH
NT	similar to general stress protein	
NT	similar to transcriptional regulator (DeoR family)	RelA
NT	similar to sigma-54 modulating factor of gram-negative bacteria	RelA, SigmaH, SigmaB
(N)T	similar to unknown proteins	RelA
(N)T	putative glutathione peroxidase	SigmaH
(N)T	similar to phosphohydrolase	
(N)T	similar to unknown proteins	
(N)T	required for septum formatio during sporulation	SigmaH, CcpA
NT	cell-division inhibitor (septum placement)	SigmaH
N(T)	phosphatase (RapE) regulator	SigmaH, CcpA
NT	response regulator aspartate phosphatase	SigmaH
NT	phosphatase (RapG) regulator	SigmaH, CcpA
NT	anti-sigma factor / serine kinase	SigmaH, glu-
NT	RNA polymerase sporulation forespore-specific (early) sigma factor	SigmaH
(N)T	required for dehydration of the spore core and assembly of the coat	SigmaH, CcpA

Operon ¹⁾	Gene	Transcriptome ²⁾				Proteome ³⁾							
		N		T		N				T			
		1	2	1	2	1	2	3	4	1	2	3	4
σ ^H regulon (2)													
yisK	yisK	1.9	2.3	3.0	3.6	4	3	-	-	5	5	4	3
ymaH	ymaH	6.5	3.4	3.4	4.6								
yoxA-dacC	yoxA	2.4	2.6	3.5	4.3								
yuxI	yuxI	0.9	0.8	1.0	0.9	28	25	21	28	2	2	3	3
σ ^B regulon													
dps	dps	1.8	1.1	6.1	2.7	2	2	2	4				
rsbV-W-sigB-rsbX	sigB	1.2	0.8	2.5	1.4	1	1	5	7				
ydaE	ydaE	1.0	1.1	2.0	1.1	9	9	8	9	10	5	9	6
yjbCD	yjbD	6.0	3.5	3.8	3.9								

1) Induced genes/proteins were assigned to known or potential operon structures.

2) The transcription level ratios (normalized intensity¹⁰/normalized intensity^{control}) of two different experiments are indicated. Only genes were considered as significant. Missed genes on microarray are indicated by "----".

3) The protein synthesis ratios correspond to one representative proteome experiment after different times of starvation (1,2,3,4) that are ratios are calculated by [%] quantity^{1,2,3,4} / [%] quantity^{control} using the Decodon Delta 2D software. In case of identification of two mixed sp second protein. Proteins only detected in coomassie-stained 2D gels but not in the autoradiograms were marked with ^{Coo}. An induction ratio

4) The function or similarity is derived from the SubtiList database (<http://genolist.fr/SubtiList/>).

5) All listed genes were classified according to the previously described regulons: TnrA (Débarbouillé and Fisher, 2002; Yoshida et al., 2001; glucose; CcpA] (Renna et al., 1993; Yoshida et al., 2001; Moreno et al., 2001; Blenke et al., 2003;), CodY (Lazazzera et al., 1999; Molle 1999; McQuade et al., 2001; Britton et al., 2002), σ^F (Steil et al., 2005), σ^E (Feucht et al., 2003; Eichenberger et al., 2003; Steil et al., 2005 (version 7.1). The genes/proteins were assigned to main regulons, that are given in bold.

	Function/Similarity ⁴⁾	Regulon ⁵⁾
NT	similar to 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase	SigmaH
NT	similar to host factor-1 protein	SigmaH
(N)T	similar to galactose mutarotase related enzyme	SigmaH
NT	unknown	SigmaH
NT	stress- and starvation-induced gene	SigmaB
N(T)	RNA polymerase general stress sigma factor	SigmaB
NT	similar to probable spore coat polysaccharide biosynthesis protein	SigmaB
NT	similar to glutaredoxin family protein Spx	SigmaB

only genes with induction factors of at least threefold during the transition phase as revealed by transcriptome analyses

,4) that are related to the transient phase (1) and 10, 30 and 60 minutes after transition to stationary phase (2,3,4). The ratio of mixed spots, only one ratio could be calculated. The ratios of mixed spots are flagged then by the protein name of the function ratio of <1 is indicated by "-".

a et al., 2003), TRAP (Babitzke and Gollnick, 2001; Sarsero et al., 2000a,b), carbon catabolite control [glu-: repressed by (1999; Molle et al., 2003), RelA (Eymann et al., 2002), σ^B (Petersohn et al., 2001), σ^H (Lee & Price, 1993; Stover & Driks, et al., 2005), σ^L (Débarbouillé et al., 1999, Gardan et al., 1995) using the Genespring software from Agilent Technologies