

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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[Supplemental material] Table2: Genes repressed by ammonium (N) or tryptophan (T) starvation as revealed by transcriptome analysis

Operon ¹⁾	Gene	Transcriptome ²⁾					Function/Similarity ³⁾	Regulon ⁴⁾
		N		T				
		1	2	1	2			
RelA regulon:								
cell wall/peptidoglycan biosynthesis								
murAA	<i>murAA</i>	0.26	0.47	0.26	0.30	(N)T	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	RelA
murE-mraY-murD	<i>murE</i>	0.21	0.45	0.24	0.21	(N)T	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase	RelA
	<i>murD</i>	0.3	0.4	0.25	0.21	(N)T	UDP-N-acetylmuramoylalanyl-D-glutamate ligase	
	<i>mraY</i>	0.31	0.51	0.28	0.23	(N)T	phospho-N-acetylmuramoyl-pentapeptide transferase	
dltABCDE	<i>dltC</i>	0.31	0.26	0.39	0.35	N(T)	D-alanine carrier protein	RelA
gcaD-prs	<i>gcaD</i>	0.22	0.47	0.26	0.31	(N)T	UDP-N-acetylglucosamine pyrophosphorylase	RelA
	<i>prs</i>	0.24	0.36	0.29	0.24	(N)T	phosphoribosylpyrophosphate synthetase	
membrane bioenergetics								
atpIBEFHAGDC	<i>atpI</i>	0.25	0.28	0.16	0.16	NT	ATP synthase (subunit i)	RelA
	<i>atpB</i>	0.38	0.3	0.16	0.16	(N)T	ATP synthase (subunit a)	
	<i>atpE</i>	0.36	0.24	0.14	0.14	(N)T	ATP synthase (subunit c)	
	<i>atpF</i>	0.27	0.2	0.14	0.16	NT	ATP synthase (subunit b)	
	<i>atpH</i>	0.32	0.24	0.12	0.12	NT	ATP synthase (subunit delta)	
	<i>atpA</i>	0.39	0.24	0.12	0.12	(N)T	ATP synthase (subunit alpha)	
	<i>atpG</i>	0.45	0.2	0.12	0.12	(N)T	ATP synthase (subunit gamma)	
	<i>atpD</i>	0.42	0.15	0.16	0.16	(N)T	ATP synthase (subunit beta)	
	<i>atpC</i>	0.73	0.21	0.14	0.14	(N)T	ATP synthase (subunit epsilon)	
transcription and translation (1)								
infA-rpmJ-rpsMK-rpoA-rplQ	<i>infA</i>	0.75	0.16	0.11	0.14	(N)T	initiation factor IF-1	RelA
	<i>rpmJ</i>	0.64	0.21	0.18	0.20	(N)T	ribosomal protein L36 (ribosomal protein B)	
	<i>rpsM</i>	0.8	0.19	0.27	0.20	(N)T	ribosomal protein S13	
	<i>rpsK</i>	0.51	0.14	0.25	0.27	(N)T	ribosomal protein S11 (BS11)	
	<i>rpoA</i>	0.64	0.14	0.19	0.21	(N)T	RNA polymerase (alpha subunit)	
	<i>rplQ</i>	0.98	0.16	0.27	0.21	(N)T	ribosomal protein L17 (BL15)	
infC-rpmI-rplT	<i>infC</i>	0.57	0.35	0.17	0.18	T	initiation factor IF-3	RelA
	<i>rpmI</i>	0.57	0.29	0.15	0.12	(N)T	ribosomal protein L35	
	<i>rplT</i>	0.68	0.42	0.23	0.23	T	ribosomal protein L20	
nusB	<i>nusB</i>	0.67	0.51	0.23	0.27	T	probable transcription termination	RelA
pyrH-frr	<i>pyrH</i>	0.23	0.32	0.16	0.19	NT	uridylyate kinase	RelA
	<i>frr</i>	0.3	0.24	0.18	0.20	NT	ribosome recycling factor	
rnc	<i>rnc</i>	0.35	0.62	0.29	0.30	T	ribonuclease III	RelA
rplJL-ybxB-rpoBC	<i>rplJ</i>	0.24	0.14	0.06	0.03	NT	ribosomal protein L10 (BL5)	RelA
	<i>ybxB</i>	0.3	0.25	0.14	0.15	NT	similar to unknown proteins	
	<i>rpoB</i>	0.38	0.56	0.28	0.21	T	RNA polymerase (beta subunit)	
	<i>rpoC</i>	0.39	0.44	0.24	0.33	T	RNA polymerase (beta' subunit)	
rplKA	<i>rplA</i>	0.26	0.29	0.23	0.16	NT	ribosomal protein L1 (BL1)	RelA

Operon ¹⁾	Gene	Transcriptome ²⁾					Function/Similarity ³⁾	Regulon ⁴⁾
		N		T				
		1	2	1	2			
transcription and translation (2)								
rpIS	<i>rpIS</i>	0.71	0.3	0.14	0.13	(N)T	ribosomal protein L19	RelA
rpIU-ysxB-rpmA	<i>rpIU</i>	0.48	0.77	0.32	0.27	T	ribosomal protein L21 (BL20)	RelA
	<i>ysxB</i>	0.63	0.83	0.30	0.32	T	unknown	
rpsB	<i>rpsB</i>	0.3	0.3	0.80	0.41	N	ribosomal protein S2	RelA
rpsF-ssb-rpsR	<i>rpsF</i>	0.37	0.23	0.24	0.24	(N)T	ribosomal protein S6 (BS9)	RelA
	<i>ssb</i>	0.44	0.23	0.24	0.29	(N)T	single-strand DNA-binding protein	
rpsJ----adk-map	<i>rpsJ</i>	0.22	0.18	0.14	0.14	NT	ribosomal protein S10 (BS13)	RelA
	<i>rpIC</i>	0.22	0.16	0.09	0.09	NT	ribosomal protein L3 (BL3)	
	<i>rpID</i>	0.28	0.2	0.10	0.12	NT	ribosomal protein L4	
	<i>rpIW</i>	0.32	0.17	0.09	0.11	NT	ribosomal protein L23	
	<i>rpIB</i>	0.35	0.18	0.07	0.05	(N)T	ribosomal protein L2 (BL2)	
	<i>rpsS</i>	0.34	0.14	0.08	0.06	(N)T	ribosomal protein S19 (BS19)	
	<i>rpIV</i>	0.4	0.17	0.08	0.05	(N)T	ribosomal protein L22 (BL17)	
	<i>rpsC</i>	0.45	0.16	0.08	0.09	(N)T	ribosomal protein S3 (BS3)	
	<i>rpIP</i>	0.47	0.11	0.11	0.08	(N)T	ribosomal protein L16	
	<i>rpmC</i>	0.39	0.09	0.10	0.09	(N)T	ribosomal protein L29	
	<i>rpsQ</i>	0.44	0.1	0.12	0.08	(N)T	ribosomal protein S17 (BS16)	
	<i>rpIN</i>	0.44	0.1	0.11	0.12	(N)T	ribosomal protein L14	
	<i>rpIX</i>	0.45	0.1	0.13	0.09	(N)T	ribosomal protein L24 (BL23) (histone-like protein HPB12)	
	<i>rpIE</i>	0.46	0.12	0.15	0.12	(N)T	ribosomal protein L5 (BL6)	
	<i>rpsN</i>	0.52	0.12	0.14	0.10	(N)T	ribosomal protein S14	
	<i>rpsH</i>	0.58	0.1	0.11	0.17	(N)T	ribosomal protein S8 (BS8)	
	<i>rpIF</i>	0.41	0.13	0.22	0.13	(N)T	ribosomal protein L6 (BL8)	
	<i>rpIR</i>	0.59	0.18	0.22	0.15	(N)T	ribosomal protein L18	
	<i>rpsE</i>	0.55	0.11	0.17	0.14	(N)T	ribosomal protein S5	
	<i>rpmD</i>	0.62	0.07	0.14	0.13	(N)T	ribosomal protein L30 (BL27)	
	<i>rpIO</i>	0.76	0.15	0.15	0.21	(N)T	ribosomal protein L15	
	<i>secY</i>	0.38	0.11	0.16	0.13	(N)T	preprotein translocase subunit	
	<i>adk</i>	0.51	0.1	0.11	0.10	(N)T	adenylate kinase	
	<i>map</i>	0.55	0.1	0.14	0.11	(N)T	methionine aminopeptidase	
tig	<i>tig</i>	0.17	0.28	0.41	0.29	N(T)	trigger factor (prolyl isomerase)	RelA
tsf	<i>tsf</i>	0.32	0.22	0.25	0.19	NT	elongation factor Ts	RelA
(ybxA-ybaEF)-truA-rpIM-rpsI	<i>ybxA</i>	0.57	0.38	0.29	0.25	(N)T	similar to ABC transporter	RelA
	<i>ybaF</i>	0.51	0.36	0.30	0.31	(N)T	similar to cobalt transport protein	
	<i>truA</i>	0.39	0.25	0.23	0.16	(N)T	pseudouridylate synthase I	
	<i>rpIM</i>	0.29	0.46	0.24	0.19	(N)T	ribosomal protein L13	
	<i>rpsI</i>	0.45	0.35	0.25	0.20	(N)T	ribosomal protein S9	
ybxF-rpsLG-fus-tufA	<i>ybxF</i>	0.27	0.22	0.10	0.12	NT	similar to ribosomal protein L7AE family	RelA
	<i>rpsL</i>	0.33	0.26	0.10	0.08	NT	ribosomal protein S12 (BS12)	
	<i>rpsG</i>	0.28	0.26	0.10	0.09	NT	ribosomal protein S7 (BS7)	

Operon ¹⁾	Gene	Transcriptome ²⁾					Function/Similarity ³⁾	Regulon ⁴⁾
		N		T				
		1	2	1	2			
transcription and translation (3)								
ylbN-rpmF	<i>ylbN</i>	0.23	0.23	0.16	0.17	NT	predicted metal-binding, possibly nucleic acid-binding protein	RelA
ylxS-nusA-ylxRQ-infB-ylxP-rbfA-polC	<i>ylxS</i>	0.23	0.32	0.25	0.23	NT	unknown	RelA
	<i>ylxR</i>	0.31	0.24	0.14	0.19	NT	similar to nucleic acid-binding protein	
	<i>ylxQ</i>	0.35	0.22	0.18	0.15	(N)T	similar to ribosomal protein L7AE family	
	<i>nusA</i>	0.3	0.3	0.15	0.23	NT	transcription termination	
	<i>rbfA</i>	0.85	0.27	0.32	0.30	(N)T	ribosome-binding factor A	
RNA modification								
rnpA	<i>rnpA</i>	0.27	0.3	0.33	0.31	NT	protein component of ribonuclease P (RNase P)	RelA
TnrA regulon:								
synthesis of branched chain amino acids								
ilvBN-ilvC-leuABCD	<i>leuA</i>	0.16	0.27	0.68	0.83	N	2-isopropylmalate synthase	TnrA-
	<i>leuB</i>	0.17	0.28	0.59	0.65	N	3-isopropylmalate dehydrogenase	
	<i>leuC</i>	0.25	0.3	0.58	0.59	N	3-isopropylmalate dehydratase (large subunit)	
	<i>leuD</i>	0.22	0.29	0.64	0.65	N	3-isopropylmalate dehydratase (small subunit)	
other regulation:								
glycolysis								
cggR-gapA-pgk-tpi-pgm-eno	<i>cggR</i>	0.1	0.16	0.52	0.47	N(T)	transcriptional repressor of gapA	CggR
	<i>pgk</i>	0.47	0.2	0.30	0.24	(N)T	phosphoglycerate kinase	
	<i>pgm</i>	0.49	0.42	0.31	0.27	(N)T	phosphoglycerate mutase	
	<i>eno</i>	0.46	0.21	0.32	0.23	(N)T	enolase	
pdhABCD	<i>pdhA</i>	0.46	0.14	0.17	0.28	(N)T	pyruvate dehydrogenase (E1 alpha subunit)	
	<i>pdhB</i>	0.5	0.08	0.08	0.06	(N)T	pyruvate dehydrogenase (E1 beta subunit)	
	<i>pdhC</i>	0.4	0.13	0.16	0.14	(N)T	pyruvate dehydrogenase (dihydrolipoamide acetyltransferase E2 subunit)	
	<i>pdhD</i>	0.78	0.57	0.17	0.17	T	pyruvate dehydrogenase / 2-oxoglutarate dehydrogenase (dihydrolipoamide dehydrogenase E3 subunit)	
amino acid biosynthesis (1)								
argCJBD-carAB-argF	<i>argC</i>	0.06	0.97	0.05	0.06	(N)T	N-acetylglutamate gamma-semialdehyde dehydrogenase	
	<i>argJ</i>	0.03	0.8	0.05	0.03	(N)T	ornithine acetyltransferase / amino-acid acetyltransferase	
	<i>argB</i>	0.07	1.06	0.05	0.04	(N)T	N-acetylglutamate 5-phosphotransferase	
	<i>argD</i>	0.06	0.8	0.03	0.03	(N)T	N-acetylornithine aminotransferase	
	<i>carA</i>	0.03	0.9	0.02	0.03	(N)T	carbamoyl-phosphate transferase-arginine (subunit A)	
	<i>carB</i>	0.04	0.94	0.03	0.02	(N)T	carbamoyl-phosphate transferase-arginine (subunit B)	
	<i>argF</i>	0.03	1.05	0.03	0.02	(N)T	ornithine carbamoyltransferase	
argGH-ytzD	<i>argG</i>	0.05	0.63	0.06	0.05	(N)T	argininosuccinate synthase	
	<i>argH</i>	0.02	0.66	0.04	0.04	(N)T	argininosuccinate lyase	
	<i>ytzD</i>	0.04	0.6	0.04	0.07	(N)T	unknown	

Operon ¹⁾	Gene	Transcriptome ²⁾					Function/Similarity ³⁾	Regulon ⁴⁾
		N		T				
		1	2	1	2			
amino acid biosynthesis (2)								
asnB	<i>asnB</i>	0.38	0.34	0.29	0.32	T	asparagine synthetase	
hisZGDBHAFI	<i>hisZ</i>	0.48	0.05	0.17	0.28	(N)T	histidyl-tRNA synthetase	
	<i>hisG</i>	0.44	0.13	0.22	0.29	(N)T	ATP phosphoribosyltransferase	
	<i>hisB</i>	0.76	0.05	0.08	0.06	(N)T	imidazoleglycerol-phosphate dehydratase	
	<i>hisH</i>	0.97	0.02	0.09	0.10	(N)T	amidotransferase	
	<i>hisA</i>	1.26	0.05	0.08	0.07	(N)T	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	
	<i>hisF</i>	1.51	0.08	0.06	0.06	(N)T	HisF cyclase-like protein	
	<i>hisI</i>	0.16	0.11	0.09	0.09	NT	phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphohydrolase	
	<i>hisD</i>	0.68	0.08	0.12	0.11	(N)T	histidinol dehydrogenase	
purine and pyrimidine biosynthesis								
purA	<i>purA</i>	0.79	0.48	0.29	0.23	T	adenylosuccinate synthetase	PurR
purB	<i>purB</i>	0.3	0.07	0.05	0.04	NT	adenylosuccinate lyase	PurR
purEKBCSQLFMNHD	<i>purE</i>	0.62	0.12	0.06	0.08	(N)T	phosphoribosylaminoimidazole carboxylase I	PurR
	<i>purK</i>	0.43	0.1	0.07	0.10	(N)T	phosphoribosylaminoimidazole carboxylase II	
	<i>purB</i>	0.3	0.07	0.05	0.04	NT	adenylosuccinate lyase	
	<i>purC</i>	0.5	0.18	0.20	0.17	(N)T	phosphoribosylaminoimidazole succinocarboxamide synthetase	
	<i>purS</i>	0.39	0.17	0.08	0.10	(N)T	required for phosphoribosylformylglycinamide synthetase activity	
	<i>purL</i>	0.69	0.09	0.09	0.07	(N)T	phosphoribosylformylglycinamide synthetase II	
	<i>purQ</i>	0.63	0.03	0.06	0.06	(N)T	phosphoribosylformylglycinamide synthetase I	
	<i>purF</i>	1.37	0.06	0.07	0.06	(N)T	glutamine phosphoribosylpyrophosphate amidotransferase	
	<i>purM</i>	0.73	0.14	0.07	0.05	(N)T	phosphoribosylaminoimidazole synthetase	
	<i>purN</i>	0.72	0.08	0.08	0.06	(N)T	phosphoribosylglycinamide formyltransferase	
	<i>purH</i>	0.91	0.14	0.10	0.13	(N)T	phosphoribosylaminoimidazole carboxy formyl formyltransferase / inosine-monophosphate cyclohydrolase	
	<i>purD</i>	0.88	0.05	0.09	0.06	(N)T	phosphoribosylglycinamide synthetase	
pyrRPBC-AA-AB-KDFE	<i>pyrR</i>	0.14	0.19	0.25	0.25	NT	transcriptional attenuation of the pyrimidine operon / uracil phosphoribosyltransferase activity	PyrR
	<i>pyrP</i>	0.27	0.4	0.12	0.17	(N)T	uracil permease	
	<i>pyrB</i>	0.19	0.14	0.07	0.08	NT	aspartate carbamoyltransferase	
	<i>pyrC</i>	0.28	0.24	0.12	0.24	NT	dihydroorotase	
	<i>pyrAA</i>	0.27	0.18	0.06	0.05	NT	carbamoyl-phosphate synthetase (glutaminase subunit)	
	<i>pyrAB</i>	0.41	0.14	0.10	0.14	(N)T	carbamoyl-phosphate synthetase (catalytic subunit)	
	<i>pyrK</i>	0.38	0.13	0.13	0.11	(N)T	dihydroorotate dehydrogenase (electron transfer subunit)	
	<i>pyrD</i>	0.53	0.14	0.13	0.14	(N)T	dihydroorotate dehydrogenase (catalytic subunit)	
	<i>pyrF</i>	0.52	0.14	0.17	0.21	(N)T	orotidine 5'-phosphate decarboxylase	
	<i>pyrE</i>	0.7	0.12	0.21	0.14	(N)T	orotate phosphoribosyltransferase	

Operon ¹⁾	Gene	Transcriptome ²⁾					Function/Similarity ³⁾	Regulon ⁴⁾
		N		T				
		1	2	1	2			
metabolism of coenzymes and prosthetic groups								
biol	<i>biol</i>	0.46	0.83	0.23	0.22	T	cytochrome P450 enzyme	
folD-yqiBCD	<i>folD</i>	0.72	0.65	0.27	0.28	T	methylenetetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase	
	<i>yqiC</i>	0.54	0.67	0.29	0.26			
	<i>yqiD</i>	0.39	0.44	0.27	0.29	T	similar to geranyltranstransferase	
panBCD	<i>panB</i>	0.31	0.38	0.31	0.23	(N)T	ketopantoate hydroxymethyltransferase	
	<i>panC</i>	0.27	0.27	0.22	0.21	NT	pantothenate synthetase	
Protein modification								
dnaJ-yqeTUV	<i>yqeT</i>	0.34	0.52	0.28	0.26	T	similar to ribosomal protein L11 methyltransferase	
pcp	<i>pcp</i>	0.8	0.63	0.32	0.32	T	pyrrolidone-carboxylate peptidase	
transport								
pbuG	<i>pbuG</i>	0.62	0.31	0.27	0.17	(N)T	hypoxanthine/guanine permease	
xpt-pbuX	<i>pbuX</i>	0.83	0.32	0.32	0.31	(N)T	xanthine permease	
ptsGHI	<i>ptsG</i>	0.4	0.23	0.12	0.11	(N)T	PTS glucose-specific enzyme IICBA component	
yfiY	<i>yfiY</i>	0.26	0.78	0.16	0.10	(N)T	similar to iron(III) dicitrate transport permease	
yhfQ	<i>yhfQ</i>	0.44	0.7	0.22	0.19	T	similar to iron(III) dicitrate-binding protein	
ykaA-pit	<i>ykaA</i>	0.32	0.36	0.24	0.21	(N)T	putative gamma glutamyl tranferase	
	<i>pit</i>	0.29	0.43	0.28	0.31	(N)T	probable low-affinity inorganic phosphate transporter	
ykoFEDC	<i>ykoD</i>	0.48	0.59	0.23	0.23	T	similar to cation ABC transporter	
	<i>ykoC</i>	0.72	0.53	0.27	0.32	T	cobalt transport protein	
yoaDCB	<i>yoaD</i>	0.19	0.31	0.74	0.70	N	similar to phosphoglycerate dehydrogenase	S-box
	<i>yoaC</i>	0.2	0.19	0.52	0.44	N	similar to xylulokinase	
	<i>yoaB</i>	0.26	0.16	0.25	0.34	NT	similar to alpha-ketoglutarate permease	
yqiXYZ	<i>yqiX</i>	0.04	0.81	0.06	0.04	(N)T	similar to amino acid ABC transporter (binding protein)	
	<i>yqiY</i>	0.11	1.24	0.13	0.13	(N)T	similar to amino acid ABC transporter (permease)	
	<i>yqiZ</i>	0.04	1.28	0.10	0.07	(N)T	similar to amino acid ABC transporter (ATP-binding protein)	
others (1)								
ackA	<i>ackA</i>	0.16	0.26	0.18	0.18	NT	acetate kinase	
cca	<i>cca</i>	0.35	0.45	0.32	0.30	T	tRNA nucleotidyltransferase	
comQ	<i>comQ</i>	0.39	0.2	0.25	0.27		transcriptional regulator of late competence operon (comG) and surfactin expression (srfA)	
dacA-yaaDE	<i>dacA</i>	0.22	0.3	0.26	0.28	NT	penicillin-binding protein 5 (D-alanyl-D-alanine carboxypeptidase)	
	<i>yaaD</i>	0.92	0.62	0.27	0.24	T	similar to pyridoxine biosynthesis protein	
	<i>yaaE</i>	1.05	0.7	0.27	0.28	T	similar to amidotransferase	
degQ	<i>degQ</i>	0.3	0.17	0.27	0.28	NT	degradative enzyme production	
metK	<i>metK</i>	0.38	0.26	0.17	0.18	(N)T	S-adenosylmethionine synthetase	
mpr-ybfJ	<i>ybfJ</i>	0.54	0.45	0.30	0.31	T	unknown	

Operon ¹⁾	Gene	Transcriptome ²⁾					Function/Similarity ³⁾	Regulon ⁴⁾
		N		T				
		1	2	1	2			
others (2)								
ndhF-ybcCDFHI	ndhF	0.19	0.3	6.10	4.70	N	NADH dehydrogenase (subunit 5)	
	ybcC	0.17	0.14	5.20	3.80	N	unknown	
pucH	pucH	0.24	0.38	0.15	0.19	(N)T	allantoinase	
sat-cysC-ylnD	sat	0.44	0.2	0.23	0.32	(N)T	probable sulfate adenylyltransferase	S-box
	cysC	0.46	0.17	0.20	0.25	(N)T	probable adenylylsulfate kinase	
	ylnD	0.44	0.25	0.28	0.28	(N)T	similar to uroporphyrin-III C-methyltransferase	
thrS	thrS	0.28	0.25	0.24	0.30	NT	threonyl-tRNA synthetase (major)	
ybaC	ybaC	0.46	0.26	0.22	0.30	(N)T	similar to proline iminopeptidase	
ybfFE	ybfE	0.52	0.24	0.22	0.20	(N)T	unknown	
yjlCD	yjlC	0.4	0.34	0.24	0.25	T	unknown	RelA
	yjlD	0.52	0.44	0.23	0.24	T	similar to NADH dehydrogenase	RelA
yrrMNO-udk	yrrM	0.26	0.32	0.18	0.22	NT	similar to caffeoyl-CoA O-methyltransferase	
	yrrN	0.29	0.33	0.22	0.21	NT	similar to protease	
	udk	0.39	0.23	0.28	0.23	(N)T	uridine kinase	
yscAB	yscA	0.51	0.3	0.23	0.24	(N)T	unknown	
yuzC	yuzC	0.31	0.31	0.36	0.32	NT	unknown	
yvgRQ	yvgQ	0.37	0.14	0.11	0.12	(N)T	similar to sulfite reductase	

1) Repressed 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 with induction factors of ≤ 0.33 during the transition phase as revealed by transcriptome analyses were considered as significant. Missed genes on microarray are indicated by "---".

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

4) All listed genes were classified according to previously described regulons: RelA (Eymann et al., 2002), TnrA- (Tojo et al., 2004) and others using the Genespring software from Silicon Genetics (version 7.1) and to their functional group.