Supplemental Material

Table S1. Relative gene expression of BB-12 genes whose expression was down-regulated according to cDNA microarrays, represented by fold-change values corresponding to mean of two analyses carried out using a dye-swap. Positive and negative values correspond to up- and down-regulation on XOS, respectively (with glucose as the reference).

ID	Description	Fold-change
Up-regulated genes		
BIF_00501	Xylose isomerase	33
BIF_00092	β-Xylosidase/α-L-arabinofuranosidase	31
BIF_00212	Sugar-binding protein	29
BIF_00257	Transporter	25
BIF_00258	Transporter	18
BIF_00405	β-Xylosidase/α-L-arabinofuranosidase	6.1
BIF_00633	Endo-1,4-β-xylanase	6.0
BIF_01688	Hypothetical protein	5.9
BIF_00829	Xylulose kinase	4.8
BIF_01171	Sialic acid-specific 9-*O*-acetylesterase	3.7
BIF_01350	NrdI	2.2
BIF_00928	Endo-1,4-β-xylanase	2.2
BIF_01170	*para*-Nitrobenzyl esterase	2.1
BIF_00432	Transcriptional repressor	2.1
Down-regulated genes		
BIF_00155	Formate acetyltransferase	-4.2
BIF_01820	Hypothetical protein	-3.5
BIF_02081	(S,S)-butane-2,3-diol dehydrogenase	-3.0
BIF_00800	Glycerol-3-phosphate-binding protein	-3.0
BIF_01895	Inosine-uridine preferring nucleoside hydrolase	-2.8
BIF_00127	LSU ribosomal protein L31P	-2.6
BIF_00712	Pyruvate formate-lyase activating enzyme	-2.3
BIF_02090	Sucrose phosphorylase	-2.2
BIF_00289	Multidrug resistance protein B	-2.2
BIF_00469	Maltose/maltodextrin-binding protein	-2.1

Figure S1. Proteomic response of BB-12 to growth in a rich broth supplemented with glucose or XOS, represented by Cy3 (green) and Cy5 (red) coloured images, respectively, as well as an overlay of the two images. Spots of differentially-expressed proteins are designated in Fig. S2.

Figure S2. Image of a representative 2D-DIGE gel. Differentially-expressed protein spots, molecular weight and isoelectric point markers are denoted. The proteins identified from the spots are listed in Table S2.

Table S2. Proteins from BB-12 identified by MALDI-TOF MS and tandem MS from the differentially-expressed protein spots shown in Fig. S2.

Spot No.	Fold Change	Protein ID	Protein description	Mascot PMF score[b]	E value	Sequence coverage (%)	No. peptides searched (matched)	Theor. (Obs.[c]) MW (kDa)	Theor. (Obs.) *pI*	Peptides identified by tandem MS[d]	Mascot Tandem MS Ion score	E value
1	-1.8[a]	57	Aconitate hydratase	80	1.7×10^{-05}	18	94 (19)	98.3 (110)	4.8 (4.8)	K.AVIVESFER.I	23	2.9×10^{-4}
2	-1.6	155	Formate acetyltransferase	50	1.6×10^{-2}	11	23 (7)	92.0 (110)	5.1 (4.9)			
3	-3.0	332	Negative regulator of genetic competence clpC/mecB	141	1.3×10^{-11}	18	27 (15)	95.6 (100)	5.3 (5.5)			
4	1.8	1199	Acetyl-/propionyl-coenzyme A carboxylase alpha chain	109	2.0×10^{-8}	28	53 (16)	68.3 (75)	5.3 (5.6)	K.HSYLVTDAQDIPR.V	19	1.7×10^{-2}
		863	Acetolactate synthase large Subunit	63	9.1×10^{-4}	17	53 (10)	70.8 (75)	5.3 (5.3)			
5	1.8	405	β-xylosidase	117	3.2×10^{-9}	26	74 (17)	76.3 (70)	5.6 (4.4)	R.IDLDAADAAGVDPESIEAAR.T	44	5.0×10^{-5}
6	2.3	400	60 kDa chaperonin GROEL	263	8.1×10^{-24}	62	96 (32)	56.5 (70)	4.7 (4.7)	K.IIEYDEEAR.Q	33	9.3×10^{-4}
										R.FGLDLDFTEGMR.F	30	4.6×10^{-3}
										K.RTDDVAGDGTTTATVLAQSLVHEGLK.N	60	6.2×10^{-8}
										K.IAEALDKVGQDGVVTVEDNNR.F	74	2.7×10^{-8}
7	2.0	400	60 kDa chaperonin GROEL	167	3.2×10^{-14}	39	54 (17)	56.5 (70)	4.7 (4.7)			
		1321	Phosphoglucomutase	121	1.3×10^{-9}	27	54 (15)	60.6 (70)	4.9 (4.7)			
8	1.8	177	ftsZ	87	3.0×10^{-6}	41	89 (13)	43.5 (60)	4.4 (4.2)	R.LLELDDSSIGIVDAFR.T	37	3.7×10^{-4}
										K.LAQANEDAQAAASAPQR.T	18	3.4×10^{-2}
										K.LAEVNQAVGFVR.E	18	2.7×10^{-2}
		1629	ABC transporter ATP-binding protein	29	2.0×10^{0}	18	88 (7)	38.6 (60)	4.3 (4.2)	K.QFDNIIDLR.-	23	1.2×10^{-2}
										R.FGENTKADESTLADELDPVDAAR.L	25	4.2×10^{-3}
9	2.5	1979	Galactokinase	186	4.0×10^{-9}	43	66 (16)	44.9 (60)	4.5 (4.3)	R.APHQLNDGQYAQR.R	48	2.7×10^{-5}
										R.EVADLVNAQADPAAALDGVLDR.L	25	4.0×10^{-3}
										R.ILGVANLR.E	19	1.1×10^{-2}
										R.TYIALSPR.D	18	2.7×10^{-2}
										R.IAQAICDEFER.R	27	2.8×10^{-3}
10	13	501	Xylose isomerase	274	6.4×10^{-25}	53	95 (33)	52.8 (60)	4.7 (4.7)	K.AKEPTTHQYDFDAATACNFLR.A	107	2.9×10^{-11}
										K.LNLEGNHANLAGHTYQHEIR.V	117	3.0×10^{-12}

									K.LGAEYFCFHDRDIAPEGDTLR.E	29	1.2×10^{-3}
									K.EPTTHQYDFDAATACNFLR.A	104	4.4×10^{-11}
									R.TSFSAEDLFR.A	73	1.0×10^{-7}
11	13	501	Xylose isomerase	309	2.0×10^{-28}	51	100 (32)	52.8 (60)	4.7 (4.7)	K.LNLEGNHANLAGHTYQHEIR.V	123	8.6×10^{-13}
										R.LGAENYVFWGGR.E	46	3.3×10^{-5}
										K.LGAEYFCFHDR.D	28	2.7×10^{-2}
										K.AKEPTTHQYDFDAATACNFLR.A	129	1.8×10^{-13}
										R.RTSFSAEDLFR.A	55	6.2×10^{-6}
12	7.0	501	Xylose isomerase	261	1.3×10^{-23}	56	99 (34)	52.8 (60)	4.7 (4.7)	K.LNLEGNHANLAGHTYQHEIR.V	109	2.0×10^{-11}
										K.AKEPTTHQYDFDAATACNFLR.A	48	2.2×10^{-5}
										K.EPTTHQYDFDAATACNFLR.A	23	5.2×10^{-3}
13	2.2	137	Bacterial peptide chain release factor 2 (RF-2)	190	1.6×10^{-16}	50	77 (20)	42.0 (60)	4.7 (4.8)	R.ISPFDNQGR.R	37	3.1×10^{-4}
										M.AEFDYSQAISDAR.A	69	2.3×10^{-7}
										R.TGCETSQTQAVFDGDIDEFIQAGIR.W	71	1.1×10^{-7}
14	2.2	530	Phosphoglucosamine mutase	156	4.0×10^{-13}	50	94 (20)	48.2 (60)	4.9 (4.9)	R.VLLRPSGTEPLVR.V	19	8.7×10^{-3}
										R.DLTAQLALDLGDAAVR.V	73	7.1×10^{-8}
										R.YVLEEMLR.G[e]	22	1.6×10^{-2}
										R.ASGADLGVAFDGDADR.C	26	4.9×10^{-3}
		681	Argininosuccinate synthase	83	8.5×10^{-6}	38	94 (15)	45.9 (60)	4.8 (4.9)			
15	-8.8	1197	Enolase	60	1.6×10^{-3}	27	67 (8)	46.5 (50)	4.7 (4.2)			
16	-3.7	277	Phosphoglycerate kinase	47	3.0×10^{-2}	32	81 (9)	42.1 (50)	4.8 (4.3)	K.VVPELSLAPVAAR.L	19	1.2×10^{-2}
										K.DGDVVLLENVR.F	32	1.4×10^{-3}
		1197	Enolase	47	3.3×10^{-2}	25	81 (10)	46.5 (50)	4.7 (4.3)	R.LQFVGDDLFVTNPVR.L	40	1.8×10^{-4}
										R.GNPTVEVVLDTDDGAR.G	46	5.0×10^{-5}
										M.AAIESVYAR.Q	18	3.8×10^{-2}
		1636	Choline binding protein A	46	4.0×10^{-2}	39	81 (7)	19.7 (50)	9.3 (4.3)			
17	4.1	287	Transaldolase	115	5.1×10^{-9}	28	68 (13)	39.9 (40)	4.7 (4.5)			
		212	Sugar-binding protein	73	8.9×10^{-5}	24	68 (12)	48.4 (40)	4.8 (4.5)			
18	5.1	212	Sugar-binding protein	75	5.6×10^{-5}	29	52 (10)	48.4 (40)	4.8 (4.6)	K.AFSTIPASEPAR.A	38	2.8×10^{-4}
19	4.1	287	Transaldolase	169	2.0×10^{-8}	51	99 (21)	39.9 (40)	4.7 (4.6)	K.SWDSVLTDVQSGIDR.V	31	1.6×10^{-3}
		212	Sugar-binding protein	116	4.0×10^{-5}	42	99 (18)	48.4 (40)	4.8 (4.6)	K.AFSTIPASEPAR.A	50	2.1×10^{-5}
20	2.0	665	Hypothetical protein	67	3.2×10^{-4}	18	35 (9)	48.0 (40)	4.8 (4.8)	K.TSADFVQIAHALDR.A	33	7.9×10^{-4}
										K.SMTPAEELLIR.S[e]	27	4.4×10^{-3}
										R.DFGIPIVNKR.I	38	3.0×10^{-4}
21	-1.6	207	Choloylglycine hydrolase	140	1.6×10^{-11}	61	59 (14)	37.2 (35)	4.7 (4.7)	R.AAYNNTHYPTQSGENANVNR.L	88	1.5×10^{-9}
										R.FDDGQNNMYFGR.N	45	2.7×10^{-5}

										K.NVTIVGKPINDR.F	15	7.6×10^{-4}
22	-1.8	207	Choloylglycine hydrolase	100	1.6×10^{-7}	49	60 (12)	37.2 (35)	4.7 (4.7)	R.FDDGQNNMYFGR.N	45	5.1×10^{-5}
										K.NVTIVGKPINDR.F	15	3.8×10^{-2}
										R.NLDWSEDYGEK.I	49	2.2×10^{-5}
23	-2.3	207	Choloylglycine hydrolase	99	2.1×10^{-7}	41	96 (12)	37.2 (35)	4.7 (4.8)	R.FDDGQNNMYFGR.N	56	4.3×10^{-6}
										K.NVTIVGKPINDR.F	42	9.2×10^{-5}
24	-2.3	1306	Oxidoreductase	117	3.2×10^{-9}	30	37 (12)	37.5 (30)	5.4 (5.7)	R.YNIFDR.T	15	4.3×10^{-2}
25	-1.8	1306	Oxidoreductase	196	4.0×10^{-17}	46	45 (16)	37.5 (30)	5.4 (5.9)	R.IGHDDRFLNK.S	25	6.3×10^{-3}
										K.YLLSSLDQSLER.L	26	5.0×10^{-3}
26	-1.6	2081	(S,S)-Butane-2,3-diol dehydrogenase	112	1.0×10^{-5}	35	66 (12)	29.3 (20)	5.0 (5.3)	R.CETPDDVAGVVSFLVSDNAR.Y	71	8.3×10^{-8}
										K.DGFDVAVADLEGQR.Q	81	2.1×10^{-8}
										R.VAIVTGAAR.G	30	1.6×10^{-3}
										R.IEQEGRR.A	20	4.2×10^{-2}
										K.DGFDVAVADLEGQRQEAEETIHR.I	53	6.5×10^{-6}
										R.YVTGQTVIVDGGMQYR.-[e]	23	1.0×10^{-2}
27	1.6	1681	Sugar transport ATP-binding protein	77	3.3×10^{-5}	22	51 (9)	41.4 (45)	5.7 (5.8)	M.AEVIFDHVTR.I	20	2.7×10^{-2}
										K.TTDTLMSDQNQLTTIR.V	16	3.9×10^{-2}
										K.AAEILDLTEFLDRKPK.A	15	1.6×10^{-2}
28	2.6	287	Transaldolase	162	1.0×10^{-13}	57	92 (20)	39.9 (40)	4.7 (4.6)	K.SWDSVLTDVQSGIDRVNG.-	61	1.3×10-6
										K.FAEDPRWAALEAK.G	17	4.6×10-2
		212	Sugar-binding protein	130	1.6×10^{-10}	45	92 (12)	48.4 (40)	4.8 (4.5)	K.AFSTIPASEPAR.A	61	1.5×10-6
										R.QYWENLAK.S	27	4.4×10-3

[a] Positive and negative values represent over- and under-expression in the XOS samples, respectively (with glucose as a reference).[b] Peptide mass fingerprinting (PMF) score obtained using the protein sequence database program Mascot with the genome sequence of BB-12 as taxonomy entry. Scores > 45 are significant.[c] Approximate values. [d] R. and K. denote cleavage at the C-terminal of an arginine and lysine residues, respectively.[e] Peptides oxidised at a methionine residue.