

Table S6. Proteomic profile of *B. longum* subsp. *infantis* ATCC15697 grown on HMO

Locus Tag	Description	MW (kD)	<i>P</i> ¹	Sample 1			Sample 2			
				Unique peptides	Total spectra	Sequence coverage	<i>P</i>	Unique peptides	Total spectra	Sequence coverage
Central fermentative pathway proteins										
Blon_0565	Putative glucokinase	32.8	99%	2	3	6%	99%	2	2	9%
Blon_0417	Glucose-6-phosphate isomerase	62.8	100%	18	81	34%	100%	24	106	46%
Blon_1722	Fructose-6-phosphate phosphoketolase	92.4	100%	38	191	42%	100%	42	243	54%
Blon_1095	Transaldolase	39.6	100%	22	173	54%	100%	24	273	67%
Blon_1096	Transketolase	75.7	100%	18	81	25%	100%	27	140	38%
Blon_2191	Ribose 5-phosphate isomerase	25.2	99%	2	14	14%	100%	5	16	23%
Blon_1368	Ribulose-phosphate 3-epimerase	24.1	99%	2	3	11%				
Blon_0900	Glyceraldehyde-3-phosphate dehydrogenase	37.8	100%	16	97	38%	100%	15	46	37%
Blon_1087	Phosphoglycerate kinase	41.9	100%	12	38	41%	100%	24	94	61%
Blon_2152	Phosphoglycerate mutase	27.6	100%	10	154	44%	100%	15	66	60%
Blon_1731	Acetate kinase	44.1	100%	13	47	44%	100%	20	80	54%
Blon_1836	Enolase	46.6	100%	15	134	35%	100%	19	196	47%
Blon_1745	Pyruvate kinase	52.1	100%	20	81	44%	100%	26	105	54%
Blon_0840	L-lactate dehydrogenase	34.2	100%	8	35	26%	100%	12	71	41%
Catabolic enzymes active on HMO constituents										
Blon_2062	Galactokinase	44.2	100%	9	27	24%	100%	11	37	31%
Blon_2171	UDP-glucose 4-epimerase	37.2	100%	3	14	13%	100%	7	18	33%
Blon_2184	Phosphoglucomutase	60.2	100%	19	49	40%	100%	22	55	43%
Blon_2349	N-acetylneuraminatase lyase	34.0					99%	2	2	8%
Blon_2031	Phosphoglucosamine mutase	48.6	100%	3	3	8%	100%	10	16	24%
Blon_0882	N-acetylglucosamine-6-phosphate deacetylase	45.2	100%	4	11	14%	100%	4	8	14%
Blon_0881	Glucosamine-6-phosphate isomerase	28.7	100%	11	147	28%	100%	10	111	41%
Blon_0540	Lactaldehyde reductase	40.5	100%	4	7	10%	100%	5	28	18%
43 kbp HMO cluster proteins										
Blon_2334	Beta-galactosidase	114.5	100%	8	14	9%	100%	17	39	22%
Blon_2336	alpha-fucosidase	53.0	100%	3	12	8%	100%	6	10	14%
Blon_2338	Dihydrodipicolinate synthetase	32.0	100%	4	21	23%	100%	6	40	32%
Blon_2339	oxidoreductase	28.6	100%	3	4	13%	100%	5	10	30%
Blon_2340	Mandelate racemase/muconate lactonizing enzyme, C-terminal domain	47.2	100%	10	48	30%	100%	11	34	30%
Blon_2343	Binding-protein-dependent transport systems inner membrane component	35.3	98%	2	5	6%				
Blon_2344	Extracellular solute-binding protein, family 1	58.7	100%	9	30	21%	100%	19	64	37%
Blon_2347	Extracellular solute-binding protein, family 1	58.7	100%	4	6	11%	100%	12	33	37%
Blon_2348	Sialidase II	42.0	99%	2	3	7%				
Blon_2349	N-acetylneuraminatase lyase	34.0					99%	2	2	8%
Blon_2352	Extracellular solute-binding protein, family 1	58.6					100%	3	4	18%

¹ Probability score (see proteomics methods)