

Table 1. Predicted carbohydrate hydrolyzing enzymes of *Bifidobacterium longum* NCC2705

<u>Predicted protein</u>	<u>Predicted enzymatic activity</u>	<u>Enzyme homolog*</u>	<u>% ID[†]</u>	<u>Genomes with homologs[‡]</u>
BL1543 [§] , BL1544 [§]	Endo- β -1,4-xylanase EC 3.2.1.8	P45796 / AF005383	46 / 31	BS, CA
BL0420 [§]	Xylanase ?	AAB87371 [¶]	28	None found
BL0682	Xylan esterase?	P26223	35	CA, BF, LL
BL0544 , BL1166, BL1611	α -L-arabinofuranosidases EC 3.2.1.55	P53627	56	BF, EF, SC, BH, BS
BL0181 , BL1138	α -L-arabinosidases	AB023625	35	SC, CA
BL0187	Exo- α -1, 5-arabinosidase II	AB023626	50	CA, SC, BH, S
BL0182 , BL0183 [§]	Endo- α -arabinosidase	AB061269	31	BH, BS, CA
BL0146 [§]	Arabinosidase	PF0236 [¶]	36	None found
BL0257 [§]	Arabinogalactan endo β -galactosidases	P48841 [¶]	33	BH, EF, CA, BS, TM
BL0177	α -Galactosidase (galactomannanase?)	P14749	24	BH, BF, AT
BL1518	α -Galactosidase EC 3.1.1.22 (melibiase)	AF1245969	70	Multiple prokaryotes
BL1168 , BL0259 , BL0978	β -Galactosidase EC 3.2.1.23	AF192266 / AF192265	96 / 95	Multiple prokaryotes
BL0529	α -1-4 Glucosidase EC 3.2.1.20 (maltase)	AF411186	61	Multiple prokaryotes
BL1526	Oligo- α -1,6-glucosidase (isomaltase)	D10487	51	Multiple prokaryotes
BL1757, BL1763	β -Glucosidase EC 3.2.1.21	AF015915 / Z94045	35 / 42	Multiple prokaryotes
BL1031 [§]	β -Hexosaminidase?	BAA32403	26	LL, CA, ML, R
BL0105	β -Fructofuranosidase (inulinase?)	P40714	40	Multiple prokaryotes
BL0523 , BL1334	α -Glucosidase EC 3.2.1.20	AB061269	29	Multiple prokaryotes
BL1327 , BL1328 , BL1329	α -Mannosidase EC 3.2.1.24	P21139	31	EF, BH, BF, SC, E/A
BL0056	Hexosaminidase?	U41417 [¶]	25	None found
BL1335 [§]	Endo- β -NAC-glucosaminidase	U59168	39	BH, SP, LL
BL0527 , BL1570	4- α -Glucanotransferase EC 2.4.1.25	P15977	31	Multiple prokaryotes
BL0907	Neopullanase EC 3.2.1.135	Q08341	30	Multiple prokaryotes
BL1761	Exo- β -1,3-exo-glucanase EC 3.2.1.58	P32603	30	Only yeasts
BL0982 , BL1573	Isoamylase EC 3.2.1.68	AB031392	59	Multiple prokaryotes
BL0388	Amylase-like glucanase?	AJ001205	49	Multiple prokaryotes
BL0464	Sialidase?	Q02834 [¶]	27	SP, SC, EF
BL0536	Sucrose phosphorylase EC 2.4.1.7	P3390	55	EC, SP, EF

*Accession number of closest verified enzyme homolog.

[†]Amino acid sequence identity with verified enzyme.

[‡]Homolog = $E < 10^{-25}$. BH, *Bacillus halodurans*; EF, *Enterococcus faecium*; LL, *Lactococcus lactis*; BF, *Bacteroides fragilis*; SC, *Streptomyces coelicolor*; CA, *Clostridium acetobutylicum*; BS, *Bacillus subtilis*; EC, *Escherichia coli*; SP, *Streptococcus pneumoniae*; AT, *Arabidopsis thaliana*; E/A, multiple Eukaryotes and Archae; S, Salmonellae; R, Rickettsiae; TM, *Thermotoga maritima*; ML, *Mesorhizobium loti*.

[§]Predicted as secreted.

[¶]Partial identity (<60% of total length).

^{||}Duplications: BL0181/1138, 43% ID; BL0183/0182, 46% ID; BL0523/1334, 62% ID; BL0982/1573, 42% ID; BL1168/0259, 67% ID; BL1527/1570, 58% ID; BL1327/1328/1329, 57% ID; BL1611/0544, 80% ID; BL1611/1166, 50% ID.