Characterization of a Novel β-L-Arabinofuranosidase in *Bifidobacterium longum*: FUNCTIONAL ELUCIDATION OF A DUF1680 FAMILY MEMBER

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Running head: Characterization of a novel β-L-arabinofuranosidase.

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SUPPLEMENTARY FIGURE LEGENDS

Supplementary FIG. S1. Chemical structures of the β-L-arabinooligosaccharides used in this study. The *arrows* indicate the cleavage sites for HypBA1.

Supplementary FIG. S2. SDS-PAGE analysis of recombinant HypBA1. Purified HypBA1 was electrophoresed on a 10% polyacrylamide gel and stained with Coomassie Brilliant Blue R-250. Lane 2, purified HypBA1; lane 1 and 3, molecular size markers. The *arrow* indicates the band that corresponds to HypBA1.

Supplementary FIG. S3. TLC analysis of HypBA1 reactions in the presence of reducing agents. *Cis*-Ara_3-Hyp-DNS was incubated with the recombinant enzyme in the absence (lane 2) or presence of β-mercaptoethanol (lane 3), dithiothreitol (lane 4), or TCEP (lane 5) at 37˚C for 16 h. Lane 1, *cis*-Ara_3-Hyp-DNS.

Supplementary FIG. S4. Effects of pH and temperature on the activity of HypBA1. A, pH dependence of HypBA1 activity in various buffers at 37˚C for 10 min. Enzyme activities were expressed as the percentage of activity in sodium acetate buffer at pH 4.5. B, Temperature dependence of HypBA1 activity for 10 min. Enzyme activities were expressed as the percentage of the activity at 35˚C. Buffers: sodium acetate (closed square), MES (open circle), sodium phosphate (closed circle).

Supplementary FIG. S5. Comparison of the reactivities of HypBA1 and HypBA2 with glycoproteins. A, TLC analysis of the reaction products. Potato lectin (lane 2), extensin (lane 3), and Ara_3-Hyp (lane 4) were incubated with HypBA2-CΔ486 (lane b) or HypBA1 (lane c) at 37˚C for 16 h. Lane a, control without enzyme; lane 1, L-arabinose standard. B, HPAEC-PAD analysis of the reaction products. Potato lectin was reacted without enzyme (2a), with HypBA2-CΔ486 (2b), or with HypBA1 (2c). Extensin was reacted without enzyme (3a), with HypBA2-CΔ486 (3b) or with HypBA1 (3c).

Supplementary FIG. S6. Chemical structure and ^{1}H- and ^{13}C-NMR spectra of Ara-Me. The asterisks indicate peaks from impurity or sideband signals. The chemical shifts are listed in supplemental Table S3.

Supplementary FIG. S7. Phylogenetic relationships between HypBA1 homologs in *Bifidobacterium* strains. The black boxes indicate the DUF1680 conserved region (middle). The lengths of the sequences are shown on the right side of each schematic sequence. The organisms, locus tag, and GenBank accession numbers are as follows: BLL, *B. longum* subsp. *longum* JCM 1217, 1 (BLLJ_0211, BAJ65881), 2 (BLLJ_1826, BAJ67491), 3 (BLLJ_1848, BAJ67512), 4 (BLLJ_0089, BAJ65759); BL, *B. longum* NCC2705, 1 (BL0422, AAN24259), 2 (BL0174, AAN24029); BI, *B. longum* subsp. *infantis* 157F, 1 (BLIF_0192, BAJ70339), 2 (BLIF_1895, BAJ72029); BP, *B. pseudocatenulatum* DSM 20438, 1 (BIFPSEUDO_02879, EEG71985), 2 (BIFPSEUDO_02839, EEG71945); BC, *B. catenulatum* DSM 16992, 1 (BIFCAT_02005, EEB20621), 2 (BIFCAT_00247, EEB22303), 3 (BIFCAT_01782, EEB20699); BD, *B. dentium* ATCC 27678, 1 (BIFDEN_01462, EDT45627), 2 (BIFDEN_00978, EDT45157); BAd, *B. adolescentis* ATCC 15703 (BAD_1529, BAF40310); BAn, *B. animalis* subsp. *lactis* AD011 (BLA_1513, ACL29795); BB, *B. breve* DSM 20213 (BIFBRE_03130, EFE89858). The protein characterized in this study is enclosed in the box. The phylogenetic tree was constructed with the neighbor-joining method using MEGA5 software (left). Comparison of the gene clusters containing GH127, GH121 and GH43 members in *Bifidobacterium* strains (right).

Supplementary FIG. S8. Multiple sequence alignment of HypBA1 and its homologs. The homologous proteins are shown in supplemental Fig. S7. The alignment was created with MUSCLE and BoxShade 3.21. Identical residues and conservative substitutions are highlighted in black and dark gray, respectively. Asterisks indicate the residues selected for site-directed mutagenesis. The protein characterized in this study is enclosed in the box.

Supplementary FIG. S9. Schematic β-L-arabinooligosaccharides metabolic pathway in *B. longum.* The domain organizations of β-L-arabinooligosaccharides degradation enzymes and the predicted sugar transporters are shown in the upper panel. The gene cluster containing β-L-arabinooligosaccharides degradation enzymes is shown in the lower panel. The annotated gene products are as follows: LacI-type transcriptional regulator (BLLJ_0207) in *black*; putative ABC-type sugar transport system (BLLJ_0208–BLLJ_0210) in *yellow*; HypBA1 (BLLJ_0211) in *green*; HypBA2 (BLLJ_0212) in *red*; and putative GH43 α-L-arabinofuranosidase (BLLJ_0213) in *blue*.

Table S1. The primers used for site-directed mutagenesis.

Name	Sequence of oligonucleotide primers
E322A_Forward_Primer	5'-ACCCACGTGGGCGCGTCGTTCACCTACG-3'
E322A_Reverse_Primer	5'-CGTAGGTGAACGACGCGCCCACGTGGGT -3'
E338A_Forward_Primer	5'-CACGATGTACGGTGCGACCTGTGCTTCCG-3'
E338A_Reverse_Primer	5'-GAAGCACAGGTCGCACCGTACATCGTGTCG-3'
E366A_Forward_Primer	5'-CCGACGTGCTGGCGAAGGAACTGTTCAACG-3'
E366A_Reverse_Primer	5'-CGTTGAACAGTTCCTTCGCCAGCACGTCG-3'

The positions of the mutated sequences are underlined.

Table S2. Substrate specificity of HypBA1.

Substrates	Activity
β-Ara$_2$	+[a]
Ara$_4$-Hyp	ND[b]
Ara$_3$-Hyp	+
Ara$_2$-Hyp	+
Ara-Hyp	+
Ara$_2$−Me	+
Ara−Me	+
Extensin	ND
Potato lectin	ND
*p*NP-α-L-arabinofuranoside	ND
*p*NP-α-L-arabinopyranoside	ND
*p*NP-β-L-arabinopyranoside	ND
*p*NP-α-D-xylopyranoside	ND
*p*NP-β-D-xylopyranoside	ND
*p*NP-α-D-galactopyranoside	ND
*p*NP-β-D-galactopyranoside	ND
*p*NP-α-D-glucopyranoside	ND
*p*NP-β-D-glucopyranoside	ND

[a] Cleavage of substrate was detected.
[b] Cleavage of substrate was not detected.

Table S3. Assignments of signals in ^{1}H and ^{13}C NMR spectra of methyl β-L-arabinofuranoside.

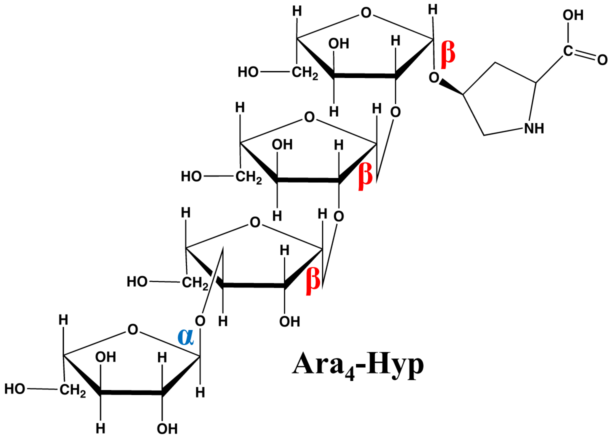
	1	2	3	4	5		Me
^{1}H (δ)	4.74	3.99	3.85	3.73	3.61	3.46	3.26
J (Hz)	4.8	8.2, 4.8	7.5	7.1, 3.1	12.2, 3.4	12.2, 7.5	-
^{13}C (δ)	102.72	76.86	75.03	82.54	63.65		55.65

Table S4. Growth capacity of *Bifidobacterium* strains on carbohydrates.

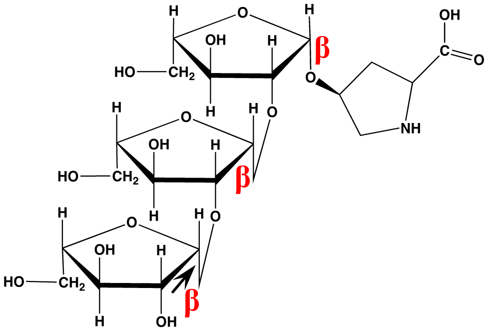
Carbon source	*B. longum* JCM 1217	*B. adolescentis* JCM 1275
Glucose	++	++
L-Arabinose	++	–
β-Ara$_2$	++	–

Judgment of bacterial growth: –,⊿pH <0.5; ±, 0.5≤⊿pH<1.0; +, 1.0≤⊿pH<1.5; ++, 1.5≤⊿pH. ⊿pH=(test pH)-(control pH)

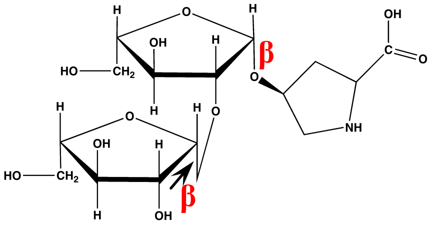
Figure S1



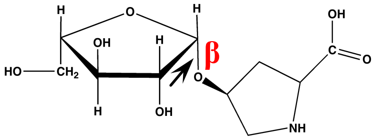
Ara$_4$-Hyp



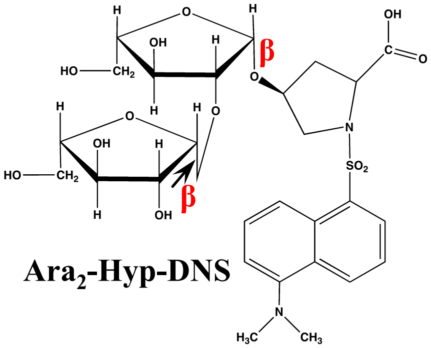
Ara$_3$-Hyp



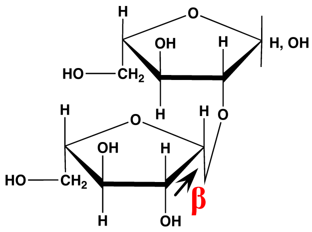
Ara$_2$-Hyp



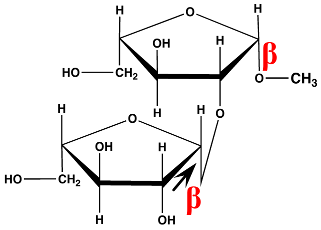
Ara-Hyp



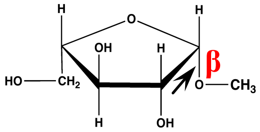
Ara$_2$-Hyp-DNS



β-Ara$_2$



Ara$_2$-Me



Ara-Me

Figure S2

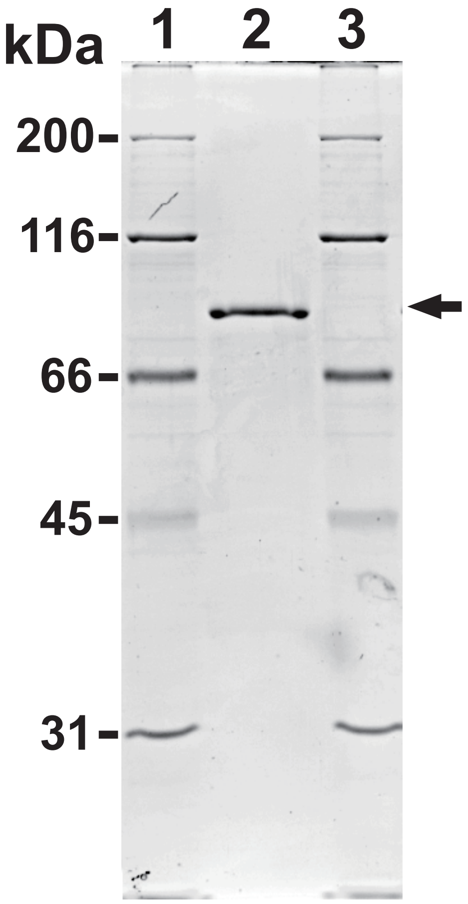


Figure S3

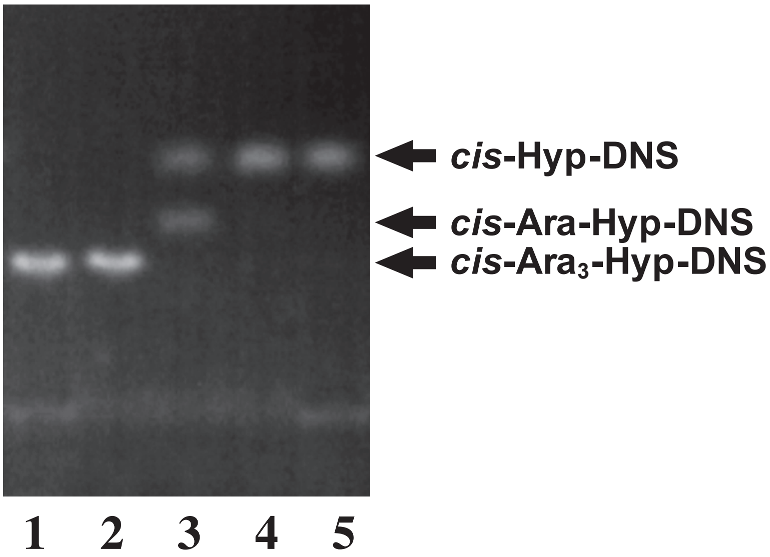
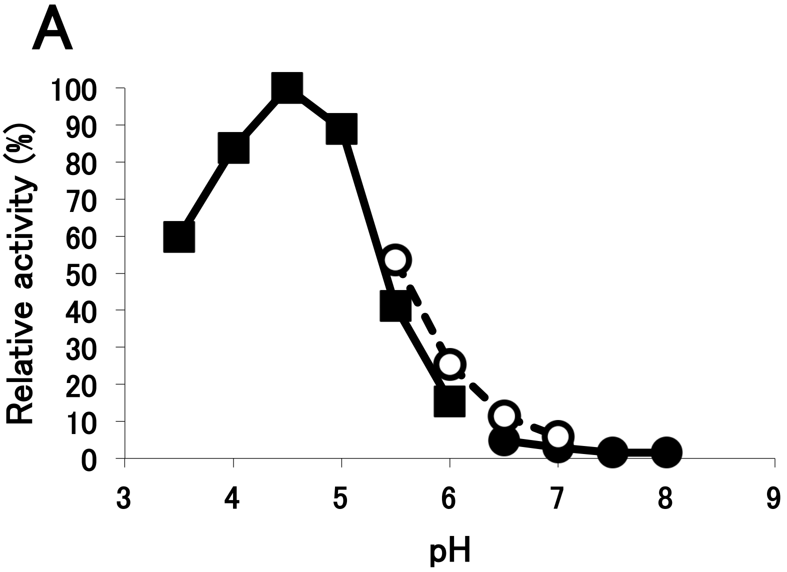


Figure S4


A
Relative activity (%)
100
90
80
70
60
50
40
30
20
10
0
3
4
5
6
7
8
9
pH

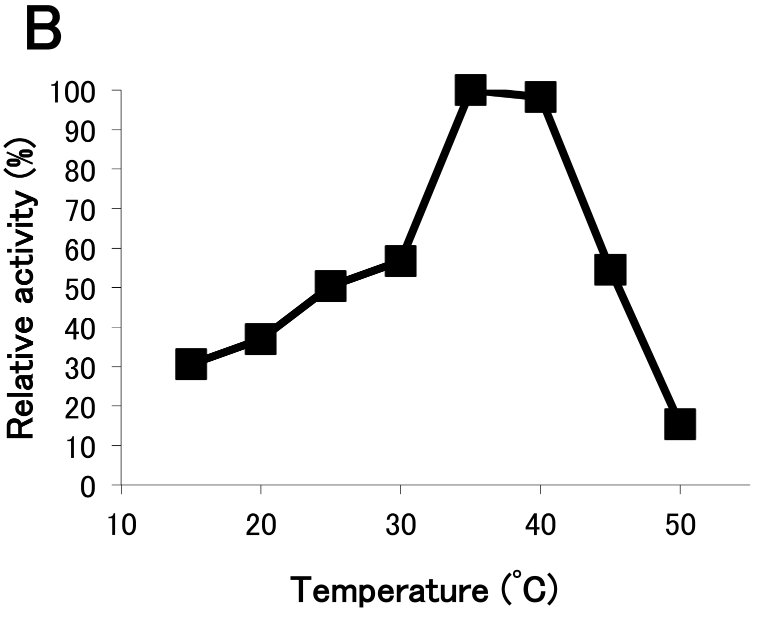

B
Relative activity (%)
100
90
80
70
60
50
40
30
20
10
0
10
20
30
40
50
Temperature (°C)

Figure S5

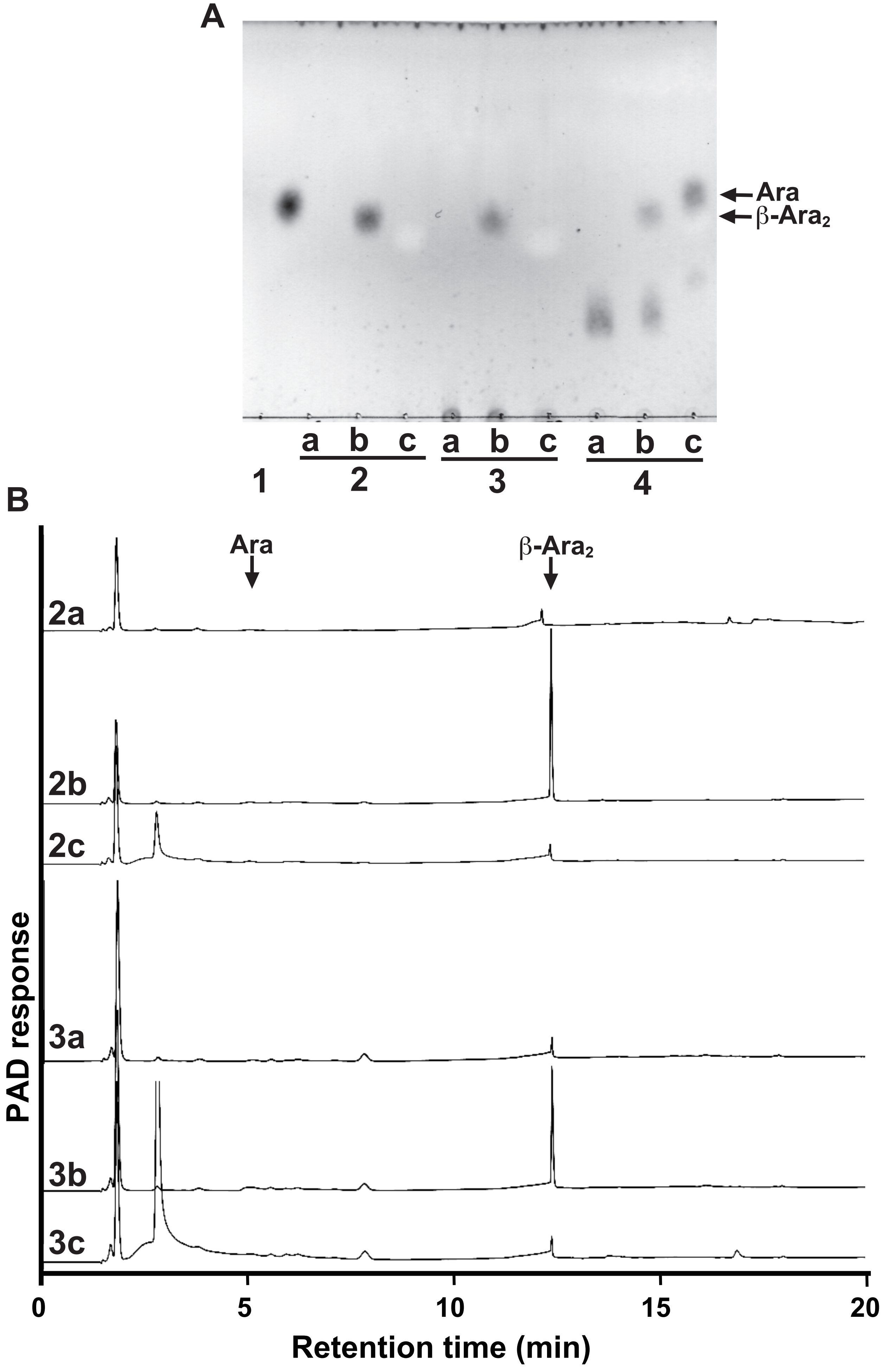
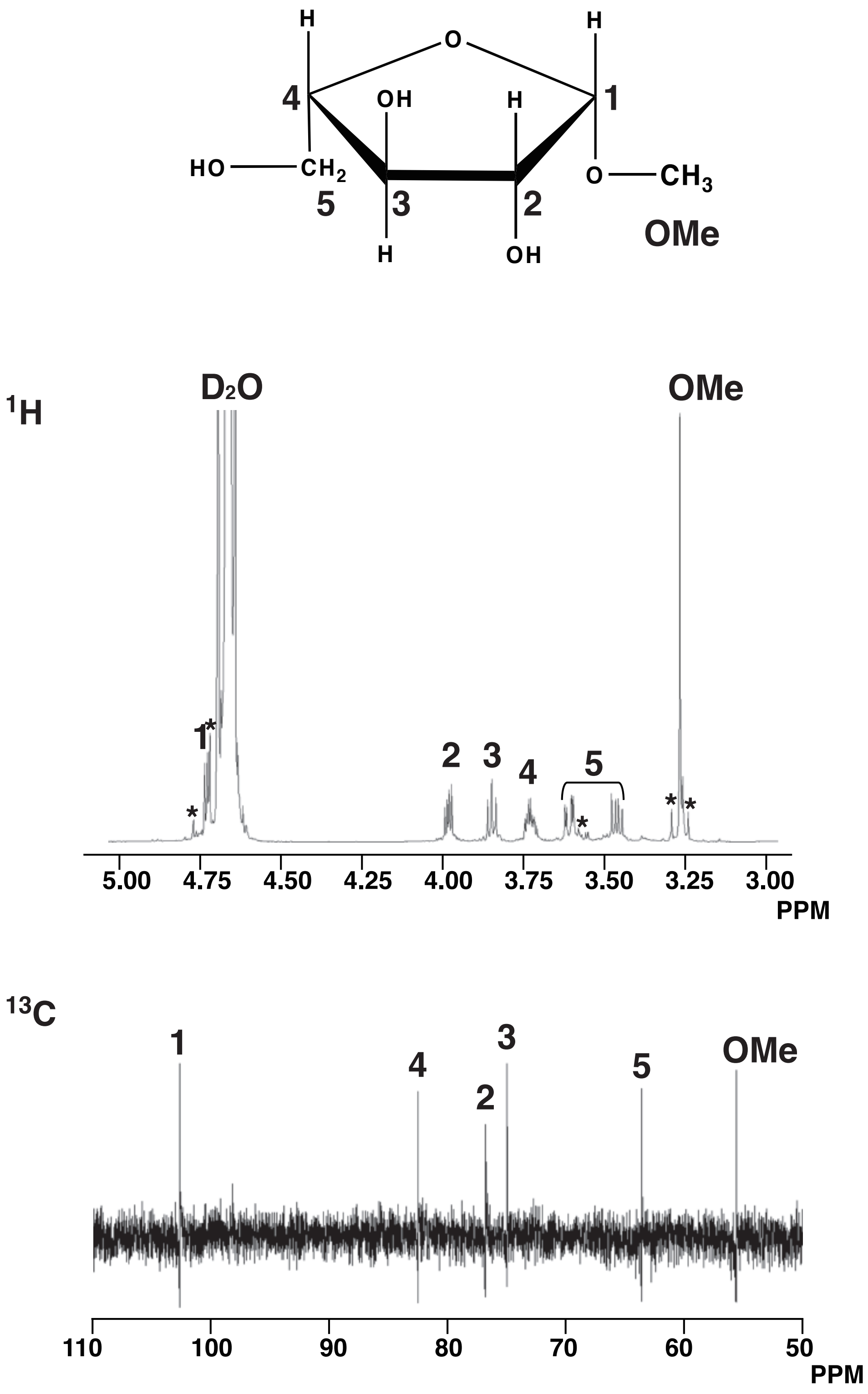

A
Ara
β-Ara2
a b c a b c a b c
1
2
3
4
B
Ara
β-Ara2
2a
2b
2c
3a
3b
3c
PAD response
0
5
10
15
20
Retention time (min)

Figure S6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O
H
4
OH
H
1
HO
CH2
O
CH3
5
3
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OMe
H
OH
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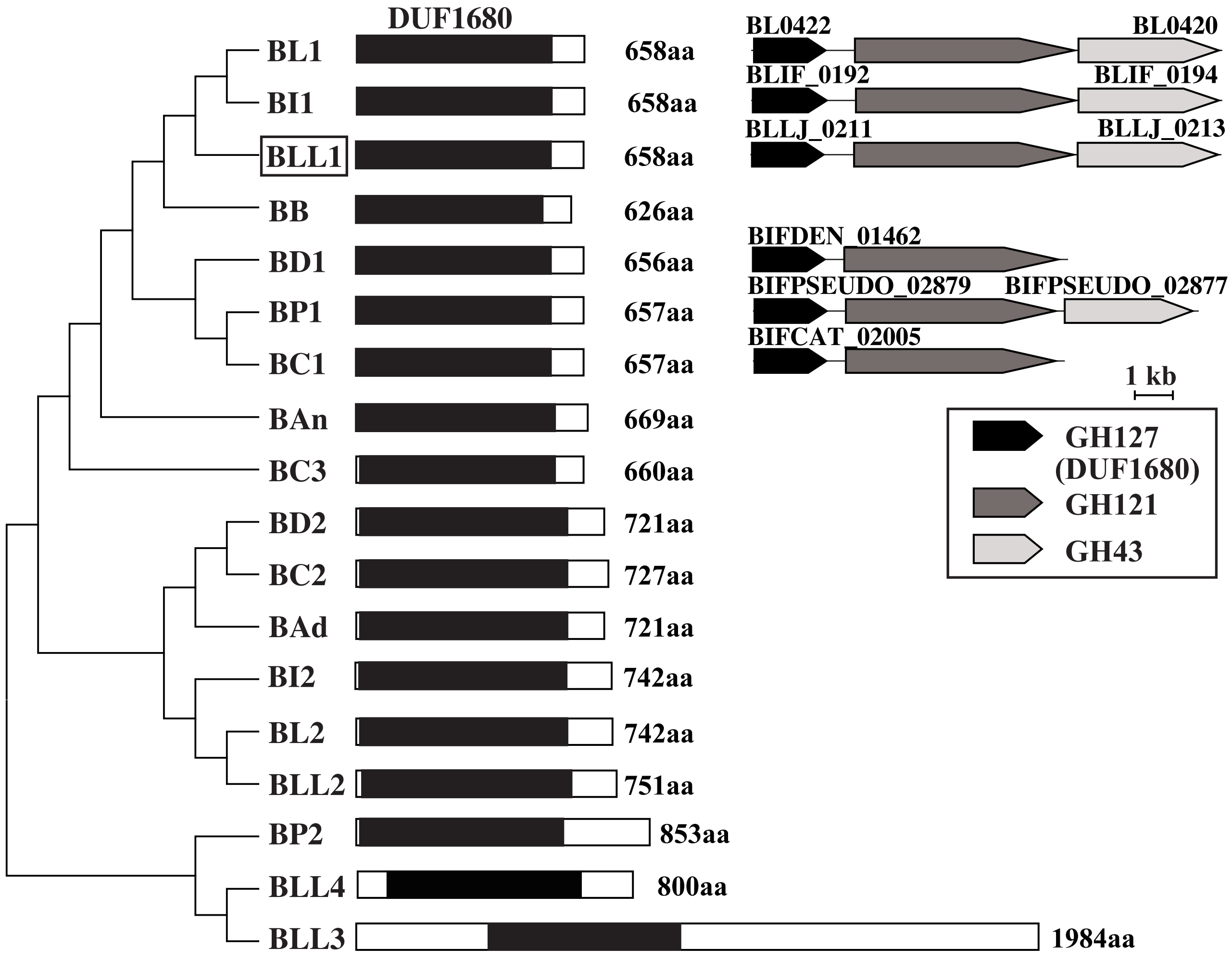
D2O
OMe
1*
*
2
3
4
5
*
*
*
5.00
4.75
4.50
4.25
4.00
3.75
3.50
3.25
3.00
PPM
13C
1
4
3
2
5
OMe
110
100
90
80
70
60
50
PPM

Figure S7


DUF1680
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BI1
658aa
BLL1
658aa
BB
626aa
BD1
656aa
BP1
657aa
BC1
657aa
BAn
669aa
BC3
660aa
BD2
721aa
BC2
727aa
BAd
721aa
BI2
742aa
BL2
742aa
BLL2
751aa
BP2
853aa
BLL4
800aa
BLL3
1984aa
BL0422
BL0420
BLIF_0192
BLIF_0194
BLLJ_0211
BLLJ_0213
BIFDEN_01462
BIFPSEUDO_02879
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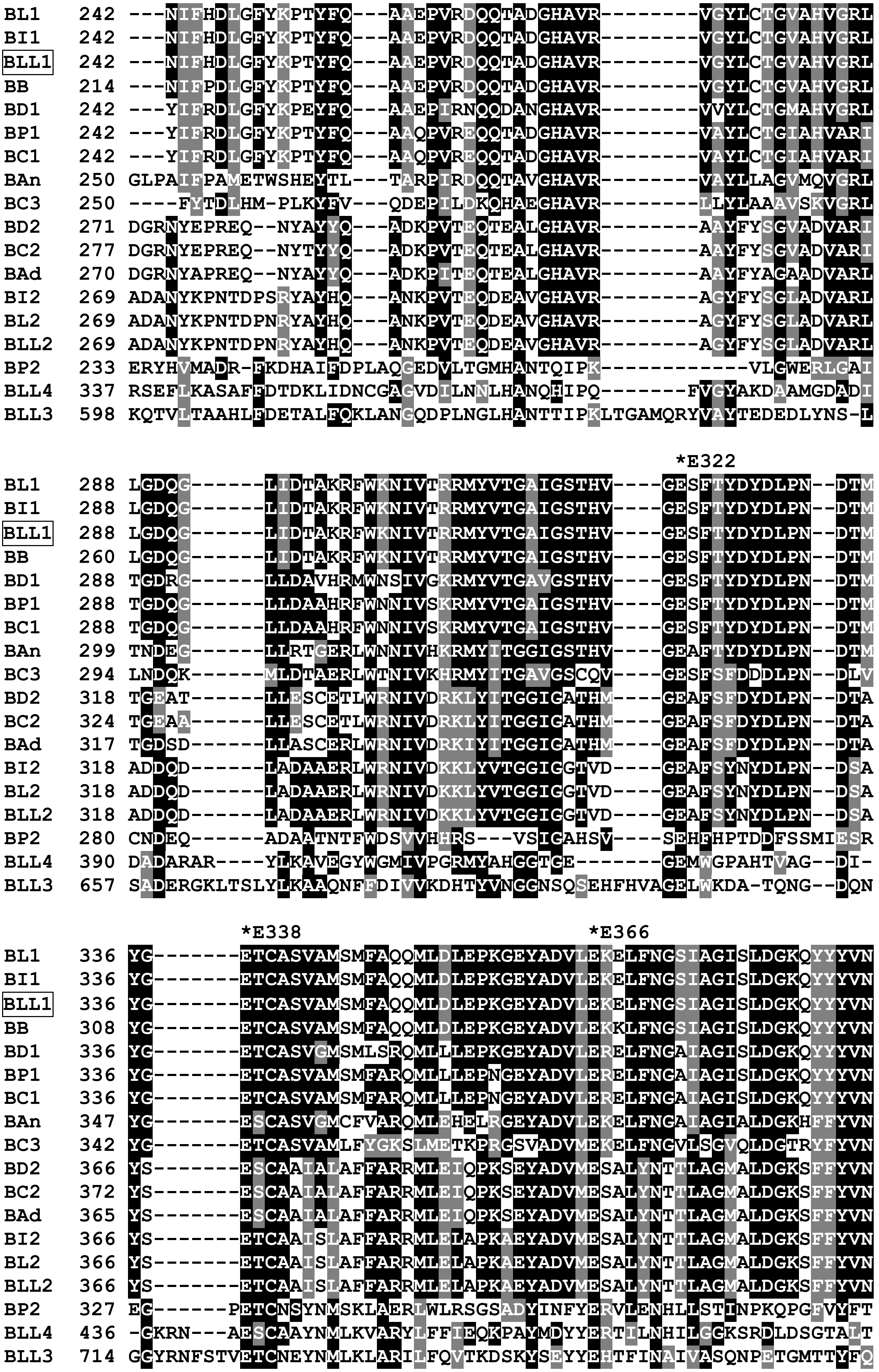
GH127
(DUF1680)
GH121
GH43



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BI1   242 ---NIFHDLGFYKPTYFQ---AAEPVRDQQTADGHAVR--------VGYLCTGVAHVGRL
BLL1  242 ---NIFHDLGFYKPTYFQ---AAEPVRDQQTADGHAVR--------VGYLCTGVAHVGRL
BB    214 ---NIFPDLGFYKPTYFQ---AAEPVRDQQTADGHAVR--------VGYLCTGVAHVGRL
BD1   242 ---YIFRDLGFYKPEYFQ---AAEPIRNQQDANGHAVR--------VVYLCTGMAHVGRL
BP1   242 ---YIFRDLGFYKPTYFQ---AAQPVREQQTADGHAVR--------VAYLCTGIAHVARI
BC1   242 ---YIFRDLGFYKPTYFQ---AAQPVREQQTADGHAVR--------VAYLCTGIAHVARI
BAn   250 GLPAIFPAMETWSHEYTL---TARPIRDQQTAVGHAVR--------VAYLLAGVMQVGRL
BC3   250 ----FYTDLHM-PLKYFV---QDEPILDKQHAEGHAVR--------LLYLAAAVSKVGRL
BD2   271 DGRNYEPREQ--NYAYYQ---ADKPVTEQTEALGHAVR--------AAYFYSGVADVARI
BC2   277 DGRNYEPREQ--NYTYYQ---ADKPVTEQTEALGHAVR--------AAYFYSGVADVARI
BAd   270 DGRNYAPREQ--NYAYYQ---ADKPITEQTEALGHAVR--------AAYFYAGAADVARL
BI2   269 ADANYKPNTDPSRYAYHQ---ANKPVTEQDEAVGHAVR--------AGYFYSGLADVARL
BL2   269 ADANYKPNTDPNRYAYHQ---ANKPVTEQDEAVGHAVR--------AGYFYSGLADVARL
BLL2  269 ADANYKPNTDPNRYAYHQ---ANKPVTEQDEAVGHAVR--------AGYFYSGLADVARL
BP2   233 ERYHVMADR-FKDHAIFDPLAQGEDVLTGMHANTQIPK------------VLGWERLGAI
BLL4  337 RSEFLKASAFFDTDKLIDNCGAGVDILNNLHANQHIPQ-------FVGYAKDAAMGDADI
BLL3  598 KQTVLTAAHLFDETALFQKLANGQDPLNGLHANTTIPKLTGAMQRYVAYTEDEDLYNS-L

                                                 *E322
BL1   288 LGDQG------LIDTAKRFWKNIVTRRMYVTGAIGSTHV----GESFTYDYDLPN--DTM
BI1   288 LGDQG------LIDTAKRFWKNIVTRRMYVTGAIGSTHV----GESFTYDYDLPN--DTM
BLL1  288 LGDQG------LIDTAKRFWKNIVTRRMYVTGAIGSTHV----GESFTYDYDLPN--DTM
BB    260 LGDQG------LIDTAKRFWKNIVTRRMYVTGAIGSTHV----GESFTYDYDLPN--DTM
BD1   288 TGDRG------LLDAVHRMWNSIVGKRMYVTGAVGSTHV----GESFTYDYDLPN--DTM
BP1   288 TGDQG------LLDAAHRFWNNIVSKRMYVTGAIGSTHV----GESFTYDYDLPN--DTM
BC1   288 TGDQG------LLDAAHRFWNNIVSKRMYVTGAIGSTHV----GESFTYDYDLPN--DTM
BAn   299 TNDEG------LLRTGERLWNNIVHKRMYITGGIGSTHV----GEAFTYDYDLPN--DTM
BC3   294 LNDQK------MLDTAERLWTNIVKHRMYITGAVGSCQV----GESFSFDDDLPN--DLV
BD2   318 TGEAT------LLESCETLWRNIVDRKLYITGGIGATHM----GEAFSFDYDLPN--DTA
BC2   324 TGEAA------LLESCETLWRNIVDRKLYITGGIGATHM----GEAFSFDYDLPN--DTA
BAd   317 TGDSD------LLASCERLWRNIVDRKIYITGGIGATHM----GEAFSFDYDLPN--DTA
BI2   318 ADDQD------LADAAERLWRNIVDKKLYVTGGIGGTVD----GEAFSYNYDLPN--DSA
BL2   318 ADDQD------LADAAERLWRNIVDKKLYVTGGIGGTVD----GEAFSYNYDLPN--DSA
BLL2  318 ADDQD------LADAAERLWRNIVDKKLYVTGGIGGTVD----GEAFSYNYDLPN--DSA
BP2   280 CNDEQ------ADAATNTFWDSVVHHRS---VSIGAHSV----SEHFHPTDDFSSMIESR
BLL4  390 DADARAR----YLKAVEGYWGMIVPGRMYAHGGTGE-------GEMWGPAHTVAG--DI-
BLL3  657 SADERGKLTSLYLKAAQNFFDIVVKDHTYVNGGNSQSEHFHVAGELWKDA-TQNG--DQN

                  *E338                        *E366
BL1   336 YG--------ETCASVAMSMFAQQMLDLEPKGEYADVLEKELFNGSIAGISLDGKQYYYVN
BI1   336 YG--------ETCASVAMSMFAQQMLDLEPKGEYADVLEKELFNGSIAGISLDGKQYYYVN
BLL1  336 YG--------ETCASVAMSMFAQQMLDLEPKGEYADVLEKELFNGSIAGISLDGKQYYYVN
BB    308 YG--------ETCASVAMSMFAQQMLDLEPKGEYADVLEKKLFNGSIAGISLDGKQYYYVN
BD1   336 YG--------ETCASVGMSMLSRQMLLLEPKGEYADVLERELFNGAIAGISLDGKQYYYVN
BP1   336 YG--------ETCASVAMSMFARQMLLLEPNGEYADVLERELFNGAIAGISLDGKQYYYVN
BC1   336 YG--------ETCASVAMSMFARQMLLLEPNGEYADVLERELFNGAIAGISLDGKQYYYVN
BAn   347 YG--------ESCASVGMCFVARQMLEHELRGEYADVLEKELFNGAIAGIALDGKHFFYVN
BC3   342 YG--------ETCASVAMLFYGKSLMETKPRGSVADVMEKELFNGVLSGVQLDGTRYFYVN
BD2   366 YS--------ESCAAIALAFFARRMLEIQPKSEYADVMESALYNTTLAGMALDGKSFFYVN
BC2   372 YS--------ESCAAIALAFFARRMLEIQPKSEYADVMESALYNTTLAGMALDGKSFFYVN
BAd   365 YS--------ESCAAIALAFFARRMLEIQPKSEYADVMESALYNTTLAGMALDGKSFFYVN
BI2   366 YS--------ETCAAISLAFFARRMLELAPKAEYADVMESALYNTTLAGMALDGKSFFYVN
BL2   366 YS--------ETCAAISLAFFARRMLELAPKAEYADVMESALYNTTLAGMALDGKSFFYVN
BLL2  366 YS--------ETCAAISLAFFARRMLELAPKAEYADVMESALYNTTLAGMALDGKSFFYVN
BP2   327 EG-------PETCNSYNMSKLAERLWLRSGSADYINFYERVLENHLLSTINPKQPGFVYFT
BLL4  436 -GKRN---AESCAAYNMLKVARYLFFIEQKPAYMDYYERTILNHILGGKSRDLDSGTALT
BLL3  714 GGYRNFSTVETCNEYNMLKLARILFQVTKDSKYSEYYEHTFINAIVASQNPETGMTTYFQ
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Fig. S8a

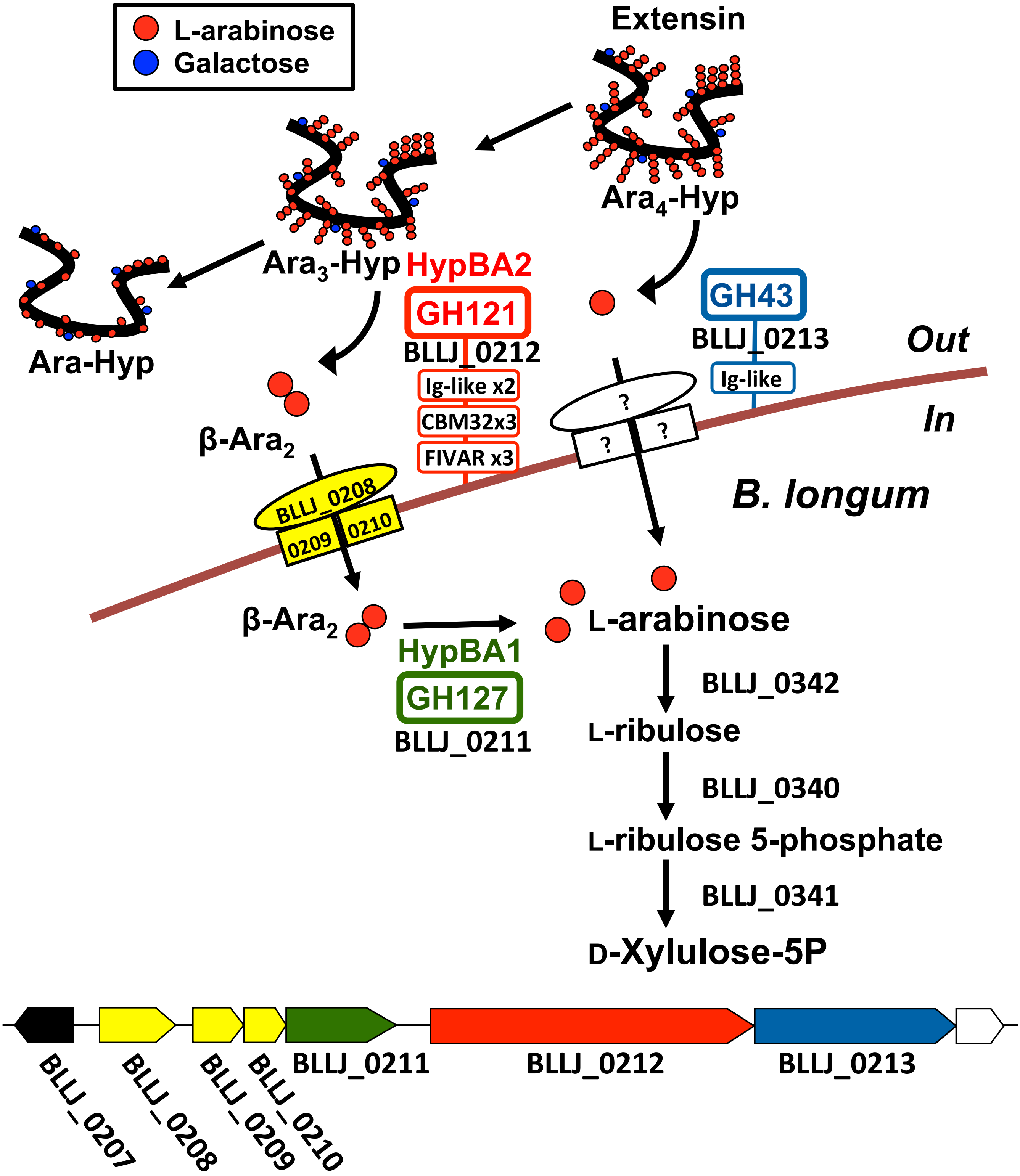
```
BL1   389 ALETTPDGLD-NPDRHHVLSHRVDWFGCA-----CCPANIARLIASVDRYIYTER-----
BI1   389 ALETTPDGLD-NPDRHHVLSHRVDWFGCA-----CCPANIARLIASVDRYIYTER-----
BLL1  389 ALETTPDGLD-NPDRHHVLSHRVDWFGCA-----CCPANIARLIASVDRYIYTER-----
BB    361 ALETTPDGLA-NPDRHHVLSHRVDWFGCA-----CCPTNIAQLIASVDRYIYTER-----
BD1   389 ALESTPDGLD-NPDRHHVLSHRVDWFGCA-----CCPANIARLIASVDRYMYTER-----
BP1   389 ALETSPDGLD-NPDRHHVLSHRVDWFGCA-----CCPANVARLIASVDRYVYTER-----
BC1   389 ALETSPDGSD-NPDRHHVLSHRVDWFGCA-----CCPANVARLIASVDRYVYTER-----
BAn   400 PLEADVQATENNPDRRHVLLERAQWFGCA-----CCPSNIARLIASVDRYLYTVR-----
BC3   395 PLEADPAASKGNPTKAHILTRRAGWFDCA-----CCPANLGRLITSLDQYLYTVS-----
BD2   419 PLEVVPEACHRDERKFHVKPVRQKWFGCA-----CCPPNIARMVESVQQYAYTVA-----
BC2   425 PLEVVPEACHRDERKFHVKPVRQKWFGCA-----CCPPNIARMVESVQQYAYTVA-----
BAd   418 PLEVVPEACHRDERKAHVKPVRQKWFGCA-----CCPPNIARIVEDVQQYAYTIG-----
BI2   419 PLEVNPYACHKDSRLRHVKPVRQKWFGCA-----CCPPNIARIVESVQEYAYTVA-----
BL2   419 PLEVNPYACHKDSRLRHVKPVRQKWFGCA-----CCPPNIARIVESVQEYAYTVA-----
BLL2  419 PLEVNPYACHKDSRLRHVKPVRQKWFGCA-----CCPPNIARIVESVQEYAYTVA-----
BP2   381 PMRSQHYRAYSTPQECF-------W---------CCVGSGLENHARYGRLIYALQRPAAQ
BLL4  492 PGNCYMYPVNPATQKEY----GDGNIGT------CCGGTALESHSKYQDSIYFHS-----
BLL3  774 PMKAGYPKVFGITGTDY----DADWFGGAIGEYWCCQGTGIENFAKLNDSFYF-------

BL1   438 --------------------------DGGKTVLSHQFIAN--KADF-ASGLTVEQR---S
BI1   438 --------------------------DGGKIVLSHQFIAN--KADF-ASGLTVEQR---S
BLL1  438 --------------------------DGGKTVLSHQFIAN--TAEF-ASGLTVEQR---S
BB    410 --------------------------DGGKTVLSHQFITN--KAEF-ASGLTVEQR---S
BD1   438 --------------------------DGGKTVLSHQFIAN--EATF-DSGLYVVQR---S
BP1   438 --------------------------DGGRTVLAHQFIAN--QASF-DSGLHVEQR---S
BC1   438 --------------------------DGGRTVLAHQFIAN--QASF-DSGLHVEQR---S
BAn   450 --------------------------EDERMIAAHQFIAN--DARF-FDDVRVKQE---S
BC3   445 --------------------------NDGKTVYAHQFVAN--KTEF-EDGFTIEQTQAGD
BD2   469 --------------------------DDASTLYVHLYMGGVVSAKLGGSDVSLEVR---A
BC2   475 --------------------------DDASTLYVHLYMGGVVSAKLGGSDVSLEVR---A
BAd   468 --------------------------DDSSTLYVHLYMGGGVHARLSGTDVRLDVM---S
BI2   469 --------------------------EDGGTLFTHLYMGGVAKAELNGTAVELDVT---A
BL2   469 --------------------------EDGGTLFTHLYMGGVAKAELNGTAVELDVT---A
BLL2  469 --------------------------EDGGTLFTHLYMGGVAKAELNGTAVELDVT---A
BP2   425 DSADSAAAGFASSAAETGNTVSNNAEAEATRLLVNLYIDS--TFDCPEQGLRITQRAARI
BLL4  537 --------------------------TDNKELYVNLFTAS--TLDWTDTGLKLAQE---T
BLL3  823 --------------------------TDENNVYVNMFWSS--TYTDTRHNLTITQT---A

BL1   466 DFPWDSHVEYTVSLPASA------ADSSVRFGLRIPGW--SLGS----YTLTVNGKPAVG
BI1   466 DFPWDSHVEYTVSLPASA------ADSSVRFGLRIPGW--SLGS----YTLTVNGKPAVG
BLL1  466 NFPWDGHVEYTVSLPASA------TDSSVRFGLRIPGW--SRGS----YTLTVNGKPAVG
BB    438 DFPWNGHVEYTVSLPASA------TDSSVRFGLRIPGW--SLGS----YALTVNGKSAVA
BD1   466 DMPWSGHVEFEVNLAEGA--------QPVRFGVRIPSW--SANA----YALAVDGEPCEK
BP1   466 DFPWNGHIEYMVELPAEA------AD-SVRFGVRIPTW--SADS----YALTCDGVAVKT
BC1   466 DFPWNGHIEYMVELPAEA------AD-SVRFGVRIPTW--SADS----YALTCDGVAVKT
BAn   478 DFPREGVVRFTVDVPEGA--------DPVIFKVRIPSW--SPE-----YRLTVDGVDVTG
BC3   476 EYPWSGDITFHVSNPNGL---------DKKVAVRIPQW--SKD-----YTLEVNGEAVEL
BD2   500 GMPWNGAGAITVTLPSSD---EGQVPEPFALALRLPAW--AGGESAA-DSIHAAGEKDSR
BC2   506 GMPWNGAGAITVTLPSSD---EGQVPESFALALRLPAW--AGGESAA-DSIHATGEKDSR
BAd   499 DMPWSGKGSVAVGFDAGDSASDASKDAVFTIALRLPAW--AGGETAS-DAVTVRGRDDIS
BI2   500 NLPWYGDGKAVVRLGNDAAGASAQAPARFTLAFRLPGW--VGEESAAAAAITATGEPESG
BL2   500 NLPWQGDGKAVVRLGGDAAGTSAQAPARFTLAFRLPGW--VGDESAAAAAITATGESESG
BLL2  500 NLPWQGDGKAVVRLGGDAAGTSAQAPARFTLAFRLPGW--VGDESAAAAAITATGESESG
BP2   483 EDGVDYTVTFTLESTAEHVPDTPGGLRETTLFLRRPWWAEHYGVMEATCAVCTLDPARTN
BLL4  566 NYPEEETSTISITAAPKS---------AVTFRIRIPAW--SKG-----AKIEVNGKAIDG
BLL3  852 NVPKTEDVTFEVSGTGSA-----------NLKLRVPDWAITNG-----VKLVVDGTEQAL
```

Fig. S8b

Figure S9



● L-arabinose
● Galactose
Extensin
Ara$_4$-Hyp
Ara$_3$-Hyp
Ara-Hyp
HypBA2
GH121
BLLJ_0212
Ig-like x2
CBM32x3
FIVAR x3
GH43
BLLJ_0213
Ig-like
Out
In
B. longum
β-Ara$_2$
BLLJ_0208
0209
0210
?
?
?
β-Ara$_2$
HypBA1
GH127
BLLJ_0211
L-arabinose
BLLJ_0342
L-ribulose
BLLJ_0340
L-ribulose 5-phosphate
BLLJ_0341
D-Xylulose-5P
BLLJ_0207
BLLJ_0208
BLLJ_0209
BLLJ_0210
BLLJ_0211
BLLJ_0212
BLLJ_0213