



Figure S1. Enzyme reaction of BLGLB1 (a), BPGLB1 (b) and commercial β -galactosidase E (c) at different dilution gradients and reaction times. The numbers in the legend indicate the dilution factor, The initial concentration of BLGLB1, BPGLB1 and commercial β -galactosidase E were 34.8 mg/mL, 17.8 mg/mL, and 21.92 mg/mL respectively.

(a)

Descriptions	Graphic Summary	Alignments	Taxonomy						
Sequences producing significant alignments									
Download ▼ New Select columns ▼ Show 100 ▼ ?									
<input checked="" type="checkbox"/> select all 100 sequences selected									
GenPept Graphics Distance tree of results Multiple alignment New MSA Viewer									
	Description ▼	Scientific Name ▼	Max Score	Total Score	Query Cover	E value ▼	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1492	1492	100%	0.0	100.00%	719	WP_032737298.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1491	1491	100%	0.0	99.86%	719	WP_118378847.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1491	1491	100%	0.0	99.86%	719	WP_117726849.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1491	1491	100%	0.0	99.86%	719	WP_137658343.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1491	1491	100%	0.0	99.86%	719	WP_032745970.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1490	1490	100%	0.0	99.86%	719	WP_209153332.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1490	1490	100%	0.0	99.86%	719	WP_131219566.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1490	1490	100%	0.0	99.86%	719	WP_059290615.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1490	1490	100%	0.0	99.72%	719	WP_195338401.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium longum]	Bifidobacterium longum	1489	1489	100%	0.0	99.72%	719	WP_217052804.1

(b)

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

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New

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select all

100 sequences selected

GenPept

Graphics

Distance tree of results

Multiple alignment

New

MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1444	1444	100%	0.0	99.86%	696	WP_117656455.1
<input checked="" type="checkbox"/>	MULTISPECIES: beta-galactosidase [Bifidobacterium]	Bifidobacterium	1442	1442	100%	0.0	99.71%	696	WP_065441898.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1440	1440	100%	0.0	99.57%	696	WP_055063652.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1440	1440	100%	0.0	99.57%	696	WP_195552043.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1439	1439	100%	0.0	99.57%	696	WP_117750590.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1439	1439	100%	0.0	99.43%	696	MZL55701.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1439	1439	100%	0.0	99.57%	696	RHH03385.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1439	1439	100%	0.0	99.57%	696	WP_118279679.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1439	1439	100%	0.0	99.57%	696	WP_004221064.1
<input checked="" type="checkbox"/>	beta-galactosidase [Bifidobacterium pseudocatenulatum]	Bifidobacterium pseudocatenulatum	1439	1439	100%	0.0	99.57%	696	WP_118269314.1

Figure S2. NCBI BLASTp results of the BLGLB1 (a), BPGLB1 (b).

	1	10	20	30	40	50
AAR24113.1MSA	RRNFEWPEL	LLTADGRG	IAFGGDYND	PDQWSEDIW	DDDLRLMKQAGVNT
ACJ53184.1MRA	RRDFAWPKL	LLTADGRG	IAFGGDYND	PDQWPEDEV	DDDLRLMKQAGVNT
BPGLB1M	HRTFKWPEL	LLTDNGKG	IAYGGDYND	PDQWSEDEV	DDDLRLMKQAGVNT
ABE95118.1MTT	RRAFRWPSL	LLTESGRG	IAFGGDYND	PDQWPEETL	DDDLRLMGEGAGVNV
BAR71185.1MTT	RRAFRWPSL	LLTESGRG	IAFGGDYND	PDQWPEETL	DDDLRLMDEAGVNV
ALO71994.1MTT	RRAFRWPSL	LLTESGRG	IAFGGDYND	PDQWPEETL	DDDLRLMGEGAGVNV
BLGLB1MTT	RRTFRWPSL	LLTESGRG	IAFGGDYND	PDQWSEETL	DDDLRLMVQAGVNT
ACJ53083.1ME	HRAFKWQPL	LAGNKPR	IWYGGDYND	PDQWPEEVW	DDDLVALMQQAGVNL
AAL02053.1ME	HRAFKWQPL	LAGNKPR	IWYGGDYND	PDQWPEEVW	DDDLVALMQQAGVNL
AAU00556.1ME	HREFKWQPL	LAGGKPR	IWYGGDYND	PDQWPEEVW	DDDLVALMQKAGVNL
ABE95226.1ME	HREFKWQPL	LAGGKPR	IWYGGDYND	PDQWPEEVW	DDDLVALMQKAGVNL
ACD98372.1ME	RKEFKWQPL	LAGNEPR	IWYGGDYND	PDQWPEEVW	DDDLRLMQQAGVNL
BAQ98551.1MERN	MSKRRKHSWP	PLKGAESR	LWYGGDYND	PDQWPEEVW	DDDLRLMKKAGVNL
ABP87597.1MSK	RRKHSWP	PLKGAESR	LWYGGDYND	PDQWPEEVW	DDDLRLMKKAGVNL
ADO53518.1MSK	RRKHSWP	PLKGAESR	LWYGGDYND	PDQWPEEVW	DDDLRLMKKAGVNL
CAC14567.1MAQ	RRHRWPKP	LSGRPDR	IWYGGDYND	PDQWPEDEV	DDDLRLMRQAGVNL
AGH68883.1MSASTQ	HRHRWPKP	PLPGNDRK	IWFGADYND	PDQWPEDEV	QDDDLRLMKQAGVNT
ACS45863.1MSASTQ	HRHRWPKP	PLPGNDRK	IWFGADYND	PDQWPEDEV	QDDDLRLMKQAGVNT
ACJ53470.1	MTDTMAHTQ	PASPASPAPT	ITAPGGRFV	FGGDWNPE	QWDESTWADD	IAKLERAGINE
ACS45449.1MAR	AYTDPLF	LG.....	AAYYDEYIP	..RDLDR	IDTDMEMMTRAGENV

	60	70	80	90	100	110
AAR24113.1	VALAIFS	WDRIQP	TEDRW	WDFGWL	DRIID	KLGNAGIVVDLASATATAPLWLYESHPEVLP
ACJ53184.1	VALAIFS	WDRIQP	TEDRW	WDFGWL	DRIID	KLGNAGIVVDLASATATAPLWLYENHPEVLP
BPGLB1	VALAIFS	WDRIQP	ENRW	WDFGWL	DRIID	KLGNAGIVVDLASATATAPLWLYEKHPEVLP
ABE95118.1	VSLAIFS	WDKIEP	VEGAF	TFEFLD	HVID	DLGKAGIAVDLASATATAPLWLYESHPEVLP
BAR71185.1	VSLAIFS	WDKIEP	VEGAF	TFEFLD	HVID	DLGKAGIAVDLASATATAPLWLYESHPEVLP
ALO71994.1	VSLAIFS	WDKIEP	VEGAF	TFEFLD	HVID	DLGKAGIAVDLASATATAPLWLYESHPEVLP
BLGLB1	VALAIFS	WDKIEP	REGF	TFEFLD	HVID	DLGAAGIAVDLASATATAPLWLYERHPEVLP
ACJ53083.1	VSVAFIS	WAKLEP	EEGV	YDFDWL	DRVID	KLGNAGIAVDLASATASPMMWMTQAHPEILWV
AAL02053.1	VSVAFIS	WAKLEP	EEGV	YDFDWL	DRVID	KLGNAGIAVDLASATASPMMWMTQAHPEILWV
AAU00556.1	VSVAFIS	WAKLEP	EEGV	YDFDWL	DRVID	KLGNAGIAVDLASATASPMMWMTQAHPEILWV
ABE95226.1	VSVAFIS	WAKLEP	EEGV	YDFDWL	DRVID	KLGNAGIAVDLASATASPMMWMTQAHPEILWV
ACD98372.1	VSVAFIS	WAKLEP	EEGV	YDFDWL	DRVID	KLGNAGIAVDLASATASPMMWMTQAHPEILWV
BAQ98551.1	VSVGIFS	WAKIEP	EEGK	YDFDWL	DRAID	KLGNAGIAVDLASATASPMMWMTQAHPEILWK
ABP87597.1	VSVGIFS	WAKIEP	EEGK	YDFDWL	DRAID	KLGNAGIAVDLASATASPMMWMTQAHPEILWK
ADO53518.1	VSVGIFS	WAKIEP	EEGK	YDFDWL	DRAID	KLGNAGIAVDLASATASPMMWMTQAHPEILWK
CAC14567.1	VSVGIFS	WAKIEP	EEGK	YDFDWL	DRAID	KLGNAGIAVDLASATASPMMWMTQAHPEILWK
AGH68883.1	VSLAIFS	WANIEP	SDGN	FEFDWL	DRVID	KLGNAGIAVDLASATASPMMWMTSAHPEVLR
ACS45863.1	VSLAIFS	WANIEP	SDGN	FEFDWL	DRVID	KLGNAGIAVDLASATASPMMWMTSAHPEVLR
ACJ53470.1	ATTNVFS	WALIQP	DES	RDFDWL	DRVID	LLVAHDFGFVLAISGALPAWTAQRYPDATRT
ACS45449.1	IRIGESTW	STCEP	QPGH	FDWTHI	DRAID	DAATNAGINVIIVGTIYAVPTWLVAMYPDVILAT

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AAR24113.1	DKYGH	HPVNA	GSRO	SWSP	SPVFKEYALT	LCKRLAERYGTNPYVTAWHMGNEYGWNNRDDY
ACJ53184.1	DKYGH	HPVNA	GSRO	SWSP	SPVFKEYALT	LCKRLAERYGTNPYVTAWHMGNEYGWNNRDDY
BPGLB1	DKYGH	HPVNA	GSRO	SWSP	SPVFKEYALT	LCKRLAERYGTNPYVTAWHMGNEYGWNNRDDY
ABE95118.1	DRYGH	IVNAG	GSRO	SWQPT	SPVFKEYALT	LCKRLAERYGTNPYVTAWHMGNEYGWNNRDDY
BAR71185.1	DRYGH	IVNAG	GSRO	SWQPT	SPVFKEYALT	LCKRLAERYGTNPYVTAWHMGNEYGWNNRDDY
ALO71994.1	DRYGH	IVNAG	GSRO	SWQPT	SPVFKEYALT	LCKRLAERYGTNPYVTAWHMGNEYGWNNRDDY
BLGLB1	DRYGH	IVNAG	GSRO	SWQPT	SPVFKEYALT	LCKRLAERYGTNPYVTAWHMGNEYGWNNRDDY
ACJ53083.1	DYRGD	VQCQP	GARGH	WRATSP	VFVLDYALN	LCKRMAEHYKDNYPYVSWHVSNEYGCHNRFDY
AAL02053.1	DYRGD	VQCQP	GARGH	WRATSP	VFVLDYALN	LCKRMAEHYKDNYPYVSWHVSNEYGCHNRFDY
AAU00556.1	DYRGD	VQCQP	GARGH	WRATSP	VFVLDYALN	LCKRMAEHYKDNYPYVSWHVSNEYGCHNRFDY
ABE95226.1	DYRGD	VQCQP	GARGH	WRATSP	VFVLDYALN	LCKRMAEHYKDNYPYVSWHVSNEYGCHNRFDY
ACD98372.1	DYRGD	VQCQP	GARGH	WRATSP	VFVLDYALN	LCKRMAEHYKDNYPYVSWHVSNEYGCHNRFDY
BAQ98551.1	DERGD	TVWVP	GAREH	WRPTSP	VFREYALN	LCKRMAEHYKGNPYVVAWHVSNEYGCHNRFDY
ABP87597.1	DERGD	TVWVP	GAREH	WRPTSP	VFREYALN	LCKRMAEHYKGNPYVVAWHVSNEYGCHNRFDY
ADO53518.1	DERGD	TVWVP	GAREH	WRPTSP	VFREYALN	LCKRMAEHYKGNPYVVAWHVSNEYGCHNRFDY
CAC14567.1	DERGD	VQCQP	GARGH	WRPTSP	VFREYALN	LCKRMAEHYKGNPYVVAWHVSNEYGCHNRFDY
AGH68883.1	DEQGH	VIWVP	GARGH	WRPTSP	TFRTYALN	LCKRMAEHYKGNPYVVAWHVSNEYGCHNRFDY
ACS45863.1	DEQGH	VIWVP	GARGH	WRPTSP	TFRTYALN	LCKRMAEHYKGNPYVVAWHVSNEYGCHNRFDY
ACJ53470.1	DYRGD	RRHRF	GVRHNA	CNSP	SNFLRLAGA	LCKRMAEHYKGNPYVVAWHVSNEYGCHNRFDY
ACS45449.1	TPAC	G.EPHY	GARGO	IMN	IVNPEAYRLYGER	VIRSLISHVAQQPCVIGYQVDNETKYYDSVSH

	180	190	200	210	220	
AAR24113.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ACJ53184.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
BPGLB1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ABE95118.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
BAR71185.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ALO71994.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
BLGLB1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ACJ53083.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
AAL02053.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
AAU00556.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ABE95226.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ACD98372.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
BAQ98551.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
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AGH68883.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ACS45863.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ACJ53470.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP
ACS45449.1	SDNAL	EAFRA	WCR	RRKYGTIDALN	QAWGTTFWQ	QEMNGFDEVLHP

230 240 250 260 270 280
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ACJ53184.1 Q K L D F E R F G N D M L L D F Y K A E R D A I A E I C P D K P F F T N F M I S T D Q C C M D Y A A W A E
BPGLB1 Q K L D F E R F G N D M L L D F Y K A E R D A I A E I C P D K P F F T N F M V S T D Q C C M D Y A A W A E
ABE95118.1 Q Q L D Y E R F G N D M L L D F Y K A E R D A I E Q I C P G K P F F T N F M V S T D Q C V M D Y A K W A G
BAR71185.1 Q Q L D Y E R F G N D M L L D F Y K A E R D A I E Q I C P D K P F F T N F M V S T D Q C V M D Y A K W A G
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K L L D W K R F S D A L L D F Y K A E R D A L L E I A P . K P Q T N F M V S A G G A G I D Y D K W G Y
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BAQ98551.1 K L L D Y K R F S D A L K E L Y I A E R D V L E S I T P G L P L T N F M V S A G G S M L D Y D D W G A
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ADO53518.1 K L L D Y K R F S D A L K E L Y I A E R D V L E S I T P G L P L T N F M V S A G G S M L D Y D D W G A
CAC14567.1 K L L D F K R F S D A L K A F Y M A E P D T L A E I T P D L P L T N F M V S A S G T G L D Y D D W G G
AGH68883.1 R L L D F K H F C S D A L K E F F C A E R D V L S E V T P N I P L T N F M V S A S Q N T L D Y D D W A H
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ACS45449.1 L R A R F D R F R R D Q V A E Y L A W Q A S I I R E Y M R D D Q F I H N F D Y E W R G H S Y G L Q P A V D H F R A A R

290 300 310 320 330
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BLGLB1 E V D F V S N D H Y F H E G E S H L D . E L A C S D A L M D S L A L G K P W Y V M E H S T S A V Q W K P L N M R K R A G
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AAL02053.1 D V D F V S N D H Y F S P G E A H F D . E M A Y A A C L T D G I A R K N P W F L M E H S T S A V N W R P T N Y R L E E F G
AAU00556.1 D V D F V S N D H Y F T P G E A H F D . E L A Y S A S L C D G I A R K N P W F L M E H S S A V N W R P I N Y R V E F G
ABE95226.1 D V D F V S N D H Y F T P G E A H F D . E L A Y S A S L C D G I A R K N P W F L M E H S S A V N W R P I N Y R V E F G
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AGH68883.1 E V D F V S N D H Y F T P G S W H I D . E L A Y S A S L V D G I S R K K P W F L M E Q S T S A V N W R E I N P R K E F G
ACS45863.1 E V D F V S N D H Y F T P G S W H I D . E L A Y S A S L V D G I S R K K P W F L M E Q S T S A V N W R E I N P R K E F G
ACJ53470.1 E M D V I S W D D Y F P P . H T T P S . D N A F K H D L M R G V D G R P F M L M E S T P N Q T N W Q E C N V L R A P G
ACS45449.1 A L D I C G V D I Y H P S E D A L T G K E I A F G G D M A R S A G G G N Y L V L E T Q A Q G Q H G W L P Y P G

340 350 360 370 380 390
AAR24113.1 E T V R D S L A H V A M G A D A I N F F Q W R S A F G A E A F H S A M V P H A G E D T K L F R Q V C E I G A S
ACJ53184.1 E T V R D S L A H V A M G A D A I N F F Q W R S A F G A E A F H S A M V P H A G E N T K L F R Q V C E I G A T
BPGLB1 E T V R D S I A H V A M G A D A I N F F Q W R S A F G A E S F H S A L V P H A G E D T K L F R Q V C E I G A A
ABE95118.1 E L M R D S L A H V A M G A D A I C F F Q W R Q S V S G A E A F H S A M L P H A G A D T K V F R G V C E I G K A
BAR71185.1 E L M R D S L A H V A M G A D A I C F F Q W R Q S V S G A E A F H S A M L P H A G A D S K V F R G V C E I G K A
ALO71994.1 E L M R D S L A H V A M G A D A I C F F Q W R Q S V S G A E A F H S A M L P H A G A D S K V F R G V C E I G K A
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ADO53518.1 S V V R D S L A Q V A M G A D A I C Y F Q W R Q S K A G A E K W H S S M V P H A G E D S Q I F R D V C E I G A D
CAC14567.1 Q L V R D S L A H V A M G S D A V C Y F Q W R Q S K A G A E K F H S A M L P H A G E D S Q V F R D V C E I G S G
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400 410 420 430 440 450
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460 470 480 490 500 510
AAR24113.1 RADIVPLAYDWS...S YKTIVVLP T V L L S A A D T O R L A D F A A A G G R V V V G Y A T G L I D E H F H
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520 530 540 550 560 570
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580 590 600 610 620 630
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BLGLB1 D V T S V A P D T R V L A T Y V G T A A A D W E L D G V P A I T S H P H G Q G A A I Y V G C D L G R H D I T H L K E L
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640 650
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BPGLB1 I V E D S A N V A N P T D S D V L H T V R K S A D . . A T F D F Y L S
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BLGLB1 N T T A P S D E R A P D Q R P G G G E I N A A T T T A A T T H D P R I L H T I R Q S S D G T I R F D F Y L N
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ACS45449.1 L S N A G V H T P G M E L A G T V C V R S G T N T A G D T V T Y L L N Y S G S P I T F R A P

	660	670	680	690	700																																											
AAR24113.1	R	G	K	T	V	E	L	Q	G	I	E	G	E	P	V	I	L	F	Q	T	D	R	E	E	K	P	G	S	Y	T	V	R	R	N	G	V	L	V	V	R	R	
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BPGLB1	R	G	K	K	E	I	A	L	Q	G	I	E	G	E	P	I	Y	L	F	Q	A	E	A	E	E	Q	T	G	S	Y	T	V	H	R	N	G	V	L	V	V	K	R	A
ABE95118.1	R	S	N	Q	P	V	A	I	N	G	V	E	G	K	P	I	I	A	H	R	C	E	T	D	A	V	G	.	Y	T	L	N	R	N	A	I	L	I	A	K	T	S	C
BAR71185.1	R	S	N	Q	P	V	A	I	N	G	V	E	G	K	P	I	I	A	H	R	C	E	T	D	A	V	G	.	Y	T	L	N	R	N	A	I	L	I	A	K	T	S	C
ALO71994.1	R	S	N	Q	P	V	A	I	N	G	V	E	G	D	P	I	I	A	H	R	C	E	T	D	A	V	G	.	Y	T	L	N	R	N	A	I	L	I	A	K	T	S	C
BLGLB1	R	S	K	Q	P	V	A	V	N	G	V	E	G	D	P	I	I	A	H	R	C	E	T	D	A	V	G	.	Y	T	L	N	R	N	A	I	L	I	A	K	T	S	C
ACJ53083.1	R	.	T	H	D	V	A	V	V	D	V	E	G	E	P	L	V	A	S	L	A	Q	V	N	E	S	E	H	T	A	A	I	Q	P	N	G	V	L	V	V	K	L	
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ABE95226.1	R	.	T	H	D	V	A	I	V	D	V	D	G	E	P	L	V	A	S	L	A	Q	V	N	E	S	E	H	T	A	A	I	Q	P	N	G	V	L	V	V	K	L	
ACD98372.1	R	.	T	H	D	V	A	V	V	D	V	E	G	E	P	L	V	A	S	L	A	Q	V	N	E	S	E	H	T	A	A	I	Q	P	N	G	V	L	V	V	K	L	
BAQ98551.1	R	.	T	H	E	P	V	T	V	D	V	E	G	E	A	I	A	A	S	L	A	H	V	D	D	G	.	.	R	A	T	I	D	P	T	G	V	V	V	L	R		
ABP87597.1	R	.	T	H	E	P	V	T	V	D	V	E	G	E	A	I	A	A	S	L	A	H	V	D	D	G	.	.	R	A	T	I	D	P	T	G	V	V	V	L	R		
ADO53518.1	R	.	T	H	E	P	V	T	V	D	V	E	G	E	A	I	A	A	S	L	A	H	V	D	D	G	.	.	R	A	T	I	D	P	T	G	V	V	V	L	R		
CAC14567.1	R	.	T	H	A	V	I	E	A	M	Q	D	G	R	P	V	I	A	S	L	A	D	V	G	D	G	.	.	K	V	T	V	R	P	N	G	V	I	V	L	R	K	
AGH68883.1	R	.	T	R	N	T	V	T	A	D	R	P	A	G	.	D	M	L	I	C	S	L	A	T	D	S	T	D	K	V	T	L	E	P	N	G	V	L	A	F	R		
ACS45863.1	R	.	T	R	N	T	V	T	A	D	R	P	A	G	.	D	M	L	I	C	S	L	A	T	D	S	T	D	K	V	T	L	E	P	N	G	V	L	A	F	R		
ACJ53470.1	H	A	D	T	A	T	A	W	Q	D	T	P	F	A	G	C	E	S	V	L	D	G	.	T	V	L	G	R	D	L	V	L	E	P	Y	G	V	T	V	V	R	T	A	A	.	.	.	
ACS45449.1	A	S	G	T	F	L	L	G	H	P	T	D	D	G	E	Q	A	V	T	A	E	T	P	V	T	V	G	D	A	V	T	L	P	R	N	G	V	D	I	I	V	G	R	Q	P	T	M	N

Figure S3. a series of conserved amino acid residues of the BLGLB1 and BPGLB1.

1 10 20 30 40 50 60
BLGLB1 MTTRRTFRWPSLLTESGRGI AF GGD YNPDQWSE ETLD EDIRLMVQAGVN TVALAI FSWDK
BPGLB1 ..MHRTFKWPPELLTDNGKGI AYGGDYNPDQWSE VWD EDVRLMKQAGVN TVAVAI FSWDR
ABI35985.1MLGVCY YPEHWPKE RWK EDAR RMRE AGLS HVRI GEFA WAL

70 80 90 100 110 120
BLGLB1 IEPREGEFTFE WLDHVIDKLGAA GTAVDLASA TATAPLWLY ERHPEVLPIDRY GHVVNAG
BPGLB1 IQPEENRWDFGWLDRIIDKLGKAGIAYDLASA TATAPLWLY EKHP EVLPIDRY GHVVNAG
ABI35985.1 IEPPEGRLENGWLD EAIATLAAE GLKVVLGTP TATP PKWLVD RYPEILPVDR EGRRRRF G

130 140 150 160 170
BLGLB1 SRQSWQP TSPV LKEYALR LCRK LAEHY KDNPY VTAW HMG NEYG WNN.RYD YSDNALA AFR
BPGLB1 SRQSWSP TSPV FKEYALT LCRK LAERY GTNPY VTAW HMG NEYG WNN.RYD YSDNALN AFR
ABI35985.1 GRRH YCF SSPV YREEARR IVTLLAERY GGLEA VAGF QTD NEYG CHD TVRC YCPRCQE AFR

180 190 200 210 220 230
BLGLB1 TWCEAKYGTVDALNEAWGTAFWSQH VNSFDEVL LPRHMGGS MVNPNPQQ LDYERFGNDMT
BPGLB1 LDWERYKAERDAIAEIC PDKPF TTNFMVSTDQCCMDYADWAEEVDFVSNDHY.....
ABI35985.1 GWLEARYGTLEALNEAWGTAFWSQRYRSFAEVELEH LTVAE..PNP SHLLDY YRFASDQV

240 250 260 270 280
BLGLB1 LD EYKAERDAI EEIC PGKPF TT NFMVSTDQCTMDY AQWANEVDFVSNDHY.....
BPGLB1 LD EYKAERDAI AEIC PDKPF TT NFMVSTDQCCMDYADWAEEVDFVSNDHY.....
ABI35985.1 RAENRLQV EILRAHAPGK FVTHNFMG..FFTD LDAFAL AQDLDFASWDSYPLGFTDLMPL

290 300 310 320 330 340
BLGLB1FH EGES HDELACSDALMDS LALGKP WYVMEHSTSA VQWKPLNMRKRA GELMRD
BPGLB1FH EGES HDELFCSDALMDS LALGKP WYVMEHSTSA VQWKPLNARKRK GETVRD
ABI35985.1 PPEEKLRYARTGHPDVA AFHHDLYR VGRGR.FWVMEQPGPVN WAPHN P SPAPGMVRLW

350 360 370 380 390 400
BLGLB1 SLAHVAMGADAINFFQWRQSASGA EAFHSAMVPHAGSDTKLFRGVCELGAA LKTLSDAGV
BPGLB1 SLIAHVAMGADAINFFQWRASAFGAESBHSALVPHAGSDTKLFRQVCELGAA LKTLSDAGV
ABI35985.1 TWEA LAHGA EVVS YFRWRQAPFAQE QMHAGLH RPD SAPDQGFEFAKRVAEE LAALALP..

410 420 430 440 450 460
BLGLB1 QDTE LKRADT AILFSAESBWA TRSETLP SMKLNHWHDVRD WYRGYLDAGARADVVP LAYD
BPGLB1 QGTE LEQSDT AILFSAESBWA TRSETLP SMKLNHWHDVRD WYRAFLNAGTRADIVPLKYD
ABI35985.1 ...PV AQAPVALVFDY EAAWILEYVQPQ.GAEW SYLGLVYL EYSALRR LGLD VDVVP GAS

470 480 490 500 510 520
BLGLB1 WSGYQTIVLPFVI ALSDDEDTRRIADFAENG GTIVVGYATGLIDEH FHHIGLGGYPGAGNGL
BPGLB1 WSA YKTIVLPFVI IMLSAEDTQRLADFAAAGGRVVI GYATGLIDEH FHTWLGGYPGAGDGL
ABI35985.1 LRCYAF AVVPSLP IVR...EEAL EAREAE GPVLEF GPRSGSKT ET FQIPKELP PGPLQAL

530 540 550 560 570 580
BLGLB1 L RDM LGIRSEEFNI LGEEAEDEPAEIG LSNGLTTRLW QNDVTSVAPDTRVLATYVGTA AA
BPGLB1 L R EMLGIRSEEFNI LGAEAE GEPSEIRLSSGAVTRLW QNDVNVDGERAQVLATYEGEEAD
ABI35985.1 LPLKVVRVESLP PG LLEVAE GALGRFP LG.....LWR.....

590 600 610 620 630 640
BLGLB1 DWELDGVPAIT TSHPHGQGAAIYV GCDLGRHDITHLLKELNTTAPSDERAPDQRP GGGEIN
BPGLB1 EWE LGAAAITRNPHY GSGETYFV GCDLNVADLTEFVREN.....I
ABI35985.1 EWVEA PLKPLTFQD GK G ALYREGRYTYLAAWPSPELAG.....

	650	660	670	680	690	700	
BLGLB1	AATTAATTHDPRILHTIRQSSDGTIR	FD	FYL	NRSKQP	VAV	NGV	EGDPIIAHRCETDAV
BPGLB1	VEDSANVANPTDSDVLHTVRKSAD	..	AT	FD	FYL	SRGKKE	IALQGI
ABI35985.1	RLLSALA	AAEAGLKVL	SLPEGLRLRRRGT	WVF	AFN	YGPEA	VEAPAS
							EGARFL
							LGSRRVGPY

	710
BLGLB1	G..YTLNRRNAILIAKTSC
BPGLB1	TGSYTVHRNGVLVVKRA.
ABI35985.1	DLAVWEEA.....

Figure S4. The key amino acid residue positions of sequence alignment of BLGLB1 and BPGLB1 with the β -galactosidase from *Thermus thermophiles*.