

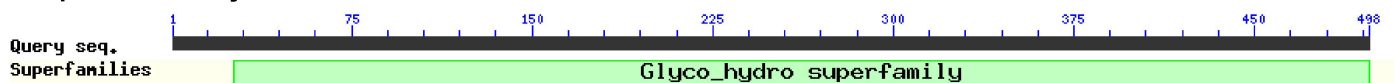
BLAST® » [blastp suite](#) » results for RID-MYJVXRND014

Job Title [ST0023 ...](#)
 RID [MYJVXRND014](#) Search expires on 09-03 15:36 pm
 Program BLASTP
 Database swissprot
 Query ID lc|Query_77003
 Description [None ...](#)
 Molecule type amino acid
 Query Length 498

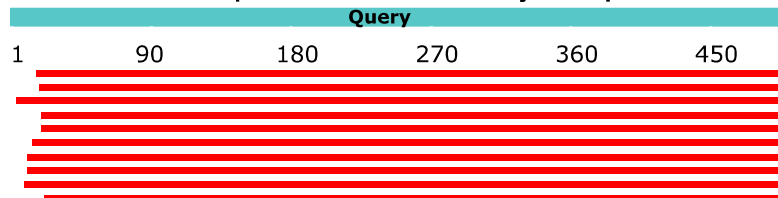
Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
RecName: Full=Beta-glucosidase 40; Short=AtBGLU40; Flags: Precursor [Arabidopsis thaliana]	702	702	96%	0.0	66.18%	Q9FZE0.1
RecName: Full=Beta-glucosidase 6; Short=Os3bglu6; Flags: Precursor [Oryza sativa Japonica Group]	700	700	96%	0.0	64.58%	Q8L7J2.1
RecName: Full=Beta-glucosidase 34; Short=Os10bglu34; Flags: Precursor [Oryza sativa Japonica Group]	687	687	99%	0.0	62.12%	Q339X2.1
RecName: Full=Beta-glucosidase 25; Short=Os6bglu25; Flags: Precursor [Oryza sativa Japonica Group]	607	607	95%	0.0	59.12%	Q0DA21.2
RecName: Full=Putative beta-glucosidase 41; Short=AtBGLU41; Flags: Precursor [Arabidopsis thaliana]	600	600	95%	0.0	58.16%	Q9FIU7.2
RecName: Full=Beta-glucosidase 11; Short=Os4bglu11; Flags: Precursor [Oryza sativa Japonica Group]	544	544	96%	0.0	54.64%	Q7XKV5.2
RecName: Full=Beta-glucosidase 12; Flags: Precursor [Oryza sativa Indica Group]	540	540	97%	0.0	55.74%	B8AVF0.1
RecName: Full=Beta-glucosidase 12; Short=Os4bglu12; Flags: Precursor [Oryza sativa Japonica Group]	538	538	97%	0.0	55.74%	Q7XKV4.2
RecName: Full=Beta-glucosidase 13; Short=Os4bglu13; Flags: Precursor [Oryza sativa Japonica Group]	536	536	97%	0.0	56.10%	Q7XKV2.2
RecName: Full=Coniferin beta-glucosidase; Flags: Precursor [Pinus contorta]	523	523	95%	0.0	53.25%	Q9ZT64.1

Graphic Summary



Distribution of the top 10 Blast Hits on 10 subject sequences



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

RecName: Full=Beta-glucosidase 40; Short=AtBGLU40; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **Q9FZE0.1** Length: 510 Number of Matches: 1
 Range 1: 27 to 508

Score	Expect	Method	Identities	Positives	Gaps	Frame
702 bits(1813)	0.0()	Compositional matrix adjust.	319/482(66%)	393/482(81%)	1/482(0%)	
Query 18	CFGQNISRASFPKGFVFGTASSAYQYEGAVSEDRGPTIWDKFSHEFGKVIDFSNADVAD					77
	C +ISR SFPKGFVFGTASSA+Q+EGAV +GRGPTIWD FSH FGK+ DFSNADVA					

Sbjct	27	CICADISRGSPFKGFVFGTASSAFQHEGAVKAEGRGPTIWDTFSHTFGKITDFSADNAV	86
Query	78	DQYHLYDDDIHTMKGIGLDAYRFSIAWSRIYPKGSGEINQAGIEHYHNVIDALLAQGIQ	137
Sbjct	87	DQYH Y++D+ MK +G+DAYRFSI+W+RI+P G G IN+AGI+HY+ +I+ALLA+GI+P	146
Query	138	DQYHRYEEDVQLMKNMGMDAYRFSISWTRIFPNGVGHINEAGIDHYNKLINALLAKGIEP	197
Sbjct	147	YVTLFHWDLPLQKLEDKYNGFLHPQIIKDFTAYAETCFKEFGDKVKHWITLNEPHTFAVQG	206
Query	198	YVTL+HWDLPQ L D+Y G+L+PQII DF AYAE CF+ FGD+VKHWIT NEPHTFA+QG	257
Sbjct	207	YVTLYHWDLPQALHDRYLGWLNQIINDFAAYAEEVCFQRFGRDVKHWITFNEPHTFAIQG	266
Query	258	YDVG LQAPGHCSILLGAFCRIGNSATEPYIVGHNMLLAHASAVDVYKKKYQPKQKSGIGI	317
Sbjct	267	YDVG LQAPG C+L+ CR GNS+TEPYIVGHN++L HA+ D+Y+KKY+ KQ GS+GI	326
Query	318	AFDVMWFEPESNKTEDIEAAQRAQDFQLGWFLDPLMFGDYPSSMRSRVGSRLPVFTGSQS	377
Sbjct	327	SLDSFWYEPASDSPEDVQATQRAIDFNLGWFLLEPLIKGDYPKSMRSRVRELRPRFSVEQS	386
Query	378	+++GS DF+GINHYTT+YA+ + TN+IG LL+D+++DSG T P + +RA+S+W	437
Sbjct	387	SLVKGSLDFVGINHYTTYARNNATNLIGTLLHDAVSDSGTVLPFKGLSTIGDRASSIW	446
Query	438	LYIVPHGIRSLMNYIRKEYGNPTVIIITENGMDGNPLTPIKEALKDVKRIKYHHDYLTN	496
Sbjct	447	LYIVP G+RSLMNYI+ YGNP V ITENGMD N+ L K+ALKD KRIKYHHDYLT++	506
Query	497	LNEAIK-DGCNVKGYFVWSMLDNWEWGAGYTSRFGLYYVDYKNKNQRYPKDSATWFKNFL	
Sbjct	507	LQASIKEDGCNVKGYFVWSLLDNWEWAAGYSSRFGLYFVDYRDNLKRYPKDSVHWFTSFL	
Query	498	KS	
Sbjct	508	NS	

RecName: Full=Beta-glucosidase 6; Short=Os3bglu6; Flags: Precursor [Oryza sativa Japonica Group]

Sequence ID: **Q8L7J2.1** Length: 521 Number of Matches: 1

Range 1: 42 to 521

Score	Expect	Method	Identities	Positives	Gaps	Frame
700 bits(1806)	0.0()	Compositional matrix adjust.	310/480(65%)	391/480(81%)	1/480(0%)	
Query	20	GQNISRASFPGKFVFGTASSAYQYEGAVSEDGRGPTIWDKFSHEFGKVIDFSNADVADDQ				79
Sbjct	42	G +R SFP+GFVFGTAS+AYQYEGAV EDGRG TIWD F+H FGK+ DFSNADVA DQ				101
Query	80	GGGLTRGSFPEGFVFGTASAAAYQYEGAVKEDGRGQTIWDTFAHTFGKITDFSADVAVDQ				
Sbjct	102	YHLYDDDIHTMKGIGLDAYRFSIAWSRIYPKGSGEINQAGIEHYHNVIDALLAQGIQPYV				139
Query	140	YH +++DI M +G+DAYRFSIAWSRIYP G G++NQAGI+HY+ +IDALLA+GIQPYV				161
Sbjct	162	YHRFEEDIQLMADMGMDAYRFSIAWSRIYPNGVGQVQAGIDHYNKLIDALLAKGIQPYV				
Query	200	TLFHWDLPLQKLEDKYNGFLHPQIIKDFTAYAETCFKEFGDKVKHWITLNEPHTFAVQGYD				199
Sbjct	222	TL+HWDLPQ LEDKY G+L QI+ DF AYAETCF+EFGD+VKHWITLNEPHT A+QGYD				221
Query	260	TLYHWDLPQALEDKYKGWLDRIQVDDFAAYAETCFREFGDRVKHWITLNEPHTVAIQGYD				
Query	260	VGLQAPGHCSILLGAFCRIGNSATEPYIVGHNMLLAHASAVDVYKKKYQPKQKSGISL				259
Sbjct	222	GLQAPG CS+LL +C+ GNS TEPY+V H+ +LAHA+A +Y+ KY+ Q G +GI+				281
Query	260	AGLQAPGRCSVLLHLYCKAGNSGTEPYVVAHHF ILAHAAAAS IYRTKYKATQNGQLGIAF				
Query	260	DSFWYEPASDSPEDVQATQRAIDFNLGWFLLEPLIKGDYPKSMRSRVRELRPRFSVEQSVM				319
Sbjct	282	D+W+EP S++ D++A +RA +F LGWF +P GDYP +MR+RV ERLPRF+ +++ +				341
Query	320	DVMWFEPMSNTTIDIEAAKRAQEFQLGWFDPPFFGDYPATMRARVGERLPRFTADEAAV				
Query	320	LRGSHDFIGINHYTTWYAQRDTTNIIGVLLNDSLADSGAFTFPIALGKPVYERANSVWLY				379
Sbjct	342	++G+ DF+GINHYTT+Y + + TNIIG LLN++LAD+G + P GKP+ +RANS+WLY				401
Query	380	VKGALDFVGINHYTTYTRHNNTNIIIGTLLNNTLADTGTVSLPFKNGKPIGDRANSIWLY				
Query	402	IVPHGIRSLMNYIRKEYGNPTVIIITENGMDGNPLTPIKEALKDVKRIKYHHDYLTNLN				439
Sbjct	402	IVP G+RSLMNY+++ Y +P V ITENGMD NNP TK+ALKD KRIKYH+DYLTNL				461
Query	440	IVPRGMRLSMNYVKERYNSPPVYITENGMDSNPFIISKALKDSKRIKYHNDYLTNLA				
Query	440	EAIK-DGCNVKGYFVWSMLDNWEWGAGYTSRFGLYYVDYKNKNQRYPKDSATWFKNFLKS				498
Sbjct	462	+IK DGC+V+GYF WS+LDNWEW AGY+SRFGLY+VDYK+ +RYPK+S WFK LK+				521
		ASIKEDGCDVRGYFAWSLLDNWEWAAGYSSRFGLYFVDYKDNLKRYPKNSVQWFKALLKT				

RecName: Full=Beta-glucosidase 34; Short=Os10bglu34; Flags: Precursor [Oryza sativa Japonica Group]

Sequence ID: **Q339X2.1** Length: 510 Number of Matches: 1

Range 1: 11 to 508

Score	Expect	Method	Identities	Positives	Gaps	Frame
687 bits(1773)	0.0()	Compositional matrix adjust.	310/499(62%)	390/499(78%)	6/499(1%)	
Query	5	IFMIFVAAVGVPPCFGQN-----ISRASFPGKFVFGTASSAYQYEGAVSEDGRGPTIWDKF				60
Sbjct	11	+ ++ V C QN ++R SFP GFVFGTASSAYQYEGAV EDGRGPTIWDKF				70
Query	61	VVILLVLMMSCQDCAQNTTGGLTRKSPNGFVFGTASSAYQYEGAVKEDGRGPTIWDKF				
Query	61	SHEFGKVIDFSNADVADDQYHLYDDDIHTMKGIGLDAYRFSIAWSRIYPKGSGEINQAGI				120
Sbjct	71	+H FGK+IDFSNADVA DQYH +++DI M +G+DAYRFSI+WSRI+P G+GE+NQAGI				130
Query	121	AHTFGKITDFSADVAVDQYHRYFEEDIQLMADMGMDAYRFSISWSRIFPNGTGEVQAGI				
Query	121	EHYHNVIDALLAQGIQPYVTLFHWDLPLQKLEDKYNGFLHPQIIKDFTAYAETCFKEFGDK				180
Sbjct	131	+HY+ +I+ALLA+GI+PYVTL+HWDLPQ LEDKY G+L QII D+ YAETCF+ FGD+				190
Query	181	DHYNKLINALLAKGIEPYVTLYHWDLPQALEDKYTGWLDRIINDYAVYAETCFQAFGDR				
Query	181	VKHWITLNEPHTFAVQGYDVG LQAPGHCSILLGAFCRIGNSATEPYIVGHNMLLAHASAV				240
Sbjct	191	VKHWIT NEPHT AVQ YD G+ APG CS+LL +C+ GNS TEPYIV HNM+L+HA+				250
Query	241	VKHWITFNEPHTAVQAYDSGMHAPGRCSVLLHLYCKGNSGTEPYIVAHNMILSHATVS				
Query	241	DVYKKKYQPKQKSGISLDSFWYEPASDSPEDVQATQRAIDFNLGWFLLEPLIKGDYPKS				300
Sbjct	251	D+Y+KKY+ Q G +GIS D WYEP S+S D++A +RA +F LGWF +P GDYP +				310
		DIYRKKYKASQNGELGTSFDVIWYEPMSNSTADIEAAKRAQEFQLGWFDPPFFGDYPAT				

Query	301	MRSRVRLPRFSVEQSVMLRGSHDFIGINHYTTWYAQRDTTNIIGVLLNDSLADSGAFT	360
Sbjct	311	MRSRV RLP+F+ +++ ++ GS DF+GINHYTT+Y + D + +I LLN++LAD+ + MRSRVGSRLPKFTEKEAALVNGSLDFMGINHYTTFTYTKDDQSTVIEKLLNNTLADTATIS	370
Query	361	FPIALGKPVYERANSVWLYIVPHGIRSLMNYIRKEYGNPTVITITENGMDGNNPLTPIKE	420
Sbjct	371	P G+P+ +RANS+WLYIVP +R LMNY++ Y PTV ITENGMDGNNP +K VPFRNGQPIGDRANSIWLYIVPRSMRILMNYVKDRYNKPTVYITENGMDGNSPFIISLKN	430
Query	421	ALKDKVKRIKYHHDYLTNLNEATK-DGCNVKGYFVWSMLDNWEWGAGYTSRFGLYYVDYKN	479
Sbjct	431	ALKD KR KYH+DYLTNL ++I+ DGC+V+GYF WS+LDNWEW AGYTSRFGLYYVDYKN ALKDDKRIKYHNDYLTNLADS IREDGCDVRGYFAWSLLDNWEWAAGYTSRFGLYYVDYKN	490
Query	480	KNQRYPKDSATWFKNFLKS 498	
		+ +RYPK+S WFKN L S	
Sbjct	491	R-KRYPKNSVQWFKNLLAS 508	

RecName: Full=Beta-glucosidase 25; Short=Os6bglu25; Flags: Precursor [Oryza sativa Japonica Group]

Sequence ID: **Q0DA21.2** Length: 501 Number of Matches: 1

Range 1: 18 to 494

Score	Expect	Method	Identities	Positives	Gaps	Frame
607 bits(1564) 0.0() Compositional matrix adjust. 282/477(59%) 362/477(75%) 1/477(0%)						
Query	21	QNISRASFPPKGFVFGTASSAYQYEGAVSEDRGPTIWDKFSHEFGKVIDFSNADVADDQY			80	
Sbjct	18	+ ISRA FP GF+FGTASSAYQYEGAV+E RGPTIWD + G+VIDFSNADVA D Y EATSRADFPFGFIFGTASSAYQYEGAVNEGQRGPTIWDTLTKRPGRVIDFSNADVAVDHY			77	
Query	81	HLYYDDDIHTMKGIGLDAYRFSIAWSRIYPKGSGEINQAGIEHYHNVIDALLAQGIQPYVT			140	
Sbjct	78	H Y +D+ M IG+DAYRFSI+WSRI+P G+GE N+ G+ +Y+++IDALL +GI+PYVT HRYKEDVELMNDIGMDAYRFSISWSRIFPNGTGEPNEEGLSYNSLIDALLDKGIEPYVT			137	
Query	141	LFWHDLPPQKLEDKYNGFLHPQIIKDFTAYAETCFKEFGDKVKHWITLNEPHTFAVQGYDV			200	
Sbjct	138	LFWHDLPPQ LED+Y G+L+ +II+DF YA TCFKEFGD+VKHWIT NEP+ FA+ GYD+ LFWHDLPPQLEDKYNGFLHPQIIKDFTAYAETCFKEFGDKVKHWITLNEPHTFAVQGYDV			197	
Query	201	GLQAPGHCSILLGAFCRIGNSATEPYIVGHNMMLAHASAVDVYKKKYQPKQKSGISGLD			260	
Sbjct	198	G+QAPG CSIL FCR G S+TEPYIV HN+LLAHA A Y++ ++ +Q G IGI+L+ GIQAPGRCSILSHVFCREGKSSTEPYIVAHNILLAHAGAFRAYEQHFKEQGGGLIGIALN			257	
Query	261	SFWYEPASDSPEDVQATQRAIDFNLGWFLPLEIKGDYPKSMRSRVRLPRFSVEQSVML			320	
Sbjct	258	S WYEP S++ ED +A RA+DF LGWFL+PL+ G YP SM+ +RLP+FS S ++ SRWYEPFSSNAEDTEAARAMDFFELGWFLDPLMFGHYPPSMQKLAGDRLPQFSTHASKLV			317	
Query	321	RGSHDFIGINHYTTWYAQRDTTNIIGVLLNDSLADSGAFTFPIALGKPVYERANSVWLYI			380	
Sbjct	318	GS DF+GINHYTT YA+ D I ++++D+ DS GK + E A S WL+I SGSLDFVGINHYTTLYARNDRIRKRLVMDASTDSAVIPTAYRHGKGIGETAASSWLHI			377	
Query	381	VPHGIRSLMNYIRKEYGNPTVITITENGMDGNNPLTPIKEALKDKVKRIKYHHDYLTNLNE			440	
Sbjct	378	VP G+ LM +++++YGNP V+ITENGMD N+P + +++ L+D KRI+YH+DY++NL + VPWGMFKLMKHVKEKYGNPPVVIITENGMDDANHPSRLEDVLQDDKRIQYHNDYMSNLDD			437	
Query	441	AI-KDGCNVKGYFVWSMLDNWEWGAGYTSRFGLYYVDYKNKNQRYPKDSATWFKNFL			496	
Sbjct	438	AI K+GCNV GYFVWS+LDNWEW +GYT RFGLYY+DYKN R PK S WF L AIRKEGCNVHGYFVWSLLDNWEWNSGYTVRFGLYYIDYKNNLTRIPKASVQWFSQVL			494	

RecName: Full=Putative beta-glucosidase 41; Short=AtBGLU41; Flags: Precursor [Arabidopsis thaliana]

Sequence ID: **Q9FIU7.2** Length: 535 Number of Matches: 1

Range 1: 28 to 505

Score	Expect	Method	Identities	Positives	Gaps	Frame
600 bits(1547) 0.0() Compositional matrix adjust. 278/478(58%) 362/478(75%) 2/478(0%)						
Query	21	QNISRASFPPKGFVFGTASSAYQYEGAVSEDRGPTIWDKFSHEF-GKVIDFSNADVADDQ			79	
Sbjct	28	++ISRA+FP GFVFGTASSAYQ+EGAV E +G +IWD F+ E GK++DFSNAD DQ ESISRANFPDGFVFGTASSAYQFEGAVKEGNGKGESIWDFTFTKEKPGKILDFSNAIDTTVDQ			87	
Query	80	YHLYDDDIHTMKGIGLDAYRFSIAWSRIYPKGSGEINQAGIEHYHNVIDALLAQGIQPYV			139	
Sbjct	88	YH + +DI MK + +DAYRFSI+WSRI+P G+GE+N G+++++IDALLA+GI+PYV YHRFHNDIDLMDKLRMDAYRFSISWSRIFPNGTGEVNPDKVYYNSLIDALLAKGIKPYV			147	
Query	140	TLFWHDLPPQKLEDKYNGFLHPQIIKDFTAYAETCFKEFGDKVKHWITLNEPHTFAVQGYD			199	
Sbjct	148	TL+HWDLPQ LED+Y G+L. +++ DF YA TCFK FGD+VK+WIT NEPH ++QGYD TLYHWDLPQALEDRYEGWLSREVVDDEHYAFTCFKAFGDRVKYWITFNEPHGVSIQGYD			207	
Query	200	VGLQAPGHCSILLGAFCRIGNSATEPYIVGHNMMLAHASAVDVYKKKYQPKQKSGISGL			259	
Sbjct	208	G+QAPG CS+L FC+ G S+ EPYIV HN+LL+HA+A Y++ ++ KQ+G IGISL TGTQAPGRCSLLGHWFCKGKSSVEPYIVAHNILLSHAAAYHTYQRNFKQKRGQIGISL			267	
Query	260	DSFWYEPASDSPEDVQATQRAIDFNLGWFLPLEIKGDYPKSMRSRVRLPRFSVEQSVML			319	
Sbjct	268	D+ WYEP SD ED A +RA+DF LGWF++PLI GDYP SM+S V ERLP+ + E DAKWYEPMSDCDEDKDAARRAMDFFLGWFMDPLINGDYPSMKSLVEERLPKITPEMYKT			327	
Query	320	LRGSHDFIGINHYTTWYAQRDTTNIIGVLLNDSLADSGAFTFPIALGKPVYERANSVWLY			379	
Sbjct	328	++G+ D++GINHYTT YA+ D T I ++L D+ +DS T G + ERA S WL+ IKGAFDYVGINHYTTLYARNDRIRKRLILQDASSDSAVITSSFRGGVAIGERAGSSWLH			387	
Query	380	IVPHGIRSLMNYIRKEYGNPTVITITENGMDGNNPLTPIKEALKDKVKRIKYHHDYLTNLN			439	
Sbjct	388	IVP GIR L Y++ YGNP V ITENGMD+ N+P +++ALKD KRI +H DY+NL+ IVPWGIRKLAVYVKDIYGNPPVVIITENGMDKNSPFIIDMEKALKDDKRIIGHIRDYLSNLS			447	
Query	440	EATK-DGCNVKGYFVWSMLDNWEWGAGYTSRFGLYYVDYKNKNQRYPKDSATWFKNFL			496	
Sbjct	448	AI+ D C+V+GYFVWS+LDNWEW +GYT RFG+YYVDYKN R PK SA WF+ L AAIRNDECDVRGYFVWSLLDNWEWNSGYTVRFGLYYVDYKNNLTRIPKASARWFTIL			505	