

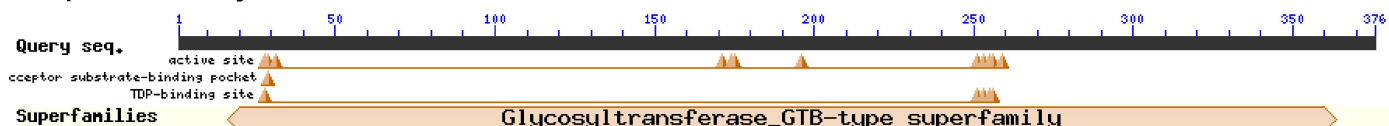
BLAST® » [blastp suite](#) » results for RID-MYJ5YKBX014

Job Title [ST0004...](#)
 RID [MYJ5YKBX014](#) Search expires on 09-03 15:24 pm
 Program BLASTP
 Database swissprot
 Query ID lc|Query_70949
 Description [None...](#)
 Molecule type amino acid
 Query Length 376

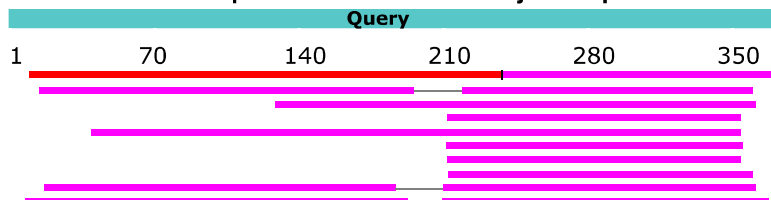
Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
RecName: Full=UDP-glycosyltransferase 90A1 [Arabidopsis thaliana]	201	370	94%	5e-59	47.01%	Q9ZVX4.1
RecName: Full=UDP-glycosyltransferase 90A2 [Arabidopsis thaliana]	181	313	84%	1e-51	47.03%	Q9SY84.1
RecName: Full=UDP-glycosyltransferase 1; Short=PIUGT1; AltName: Full=Glycosyltransferase UGT88E12; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase KGT1 [Pueraria montana var. lobata]	141	141	61%	1e-36	38.10%	A0A067YB04.1
RecName: Full=Isoflavone 7-O-glucosyltransferase 1; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase; Flags: Precursor [Glycine max]	137	137	37%	4e-35	46.10%	A6BM07.1
RecName: Full=UDP-glycosyltransferase 2; Short=PIUGT2; AltName: Full=UDP-glucose:isoflavone 4' 7-O-glucosyltransferase [Pueraria montana var. lobata]	135	135	83%	2e-34	31.84%	A0A172J2D0.1
RecName: Full=UDP-glycosyltransferase 13; Short=PIUGT13; AltName: Full=Glycosyltransferase UGT88H1; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase KGT13 [Pueraria montana var. lobata]	131	131	37%	4e-33	47.22%	A0A067YBQ3.1
RecName: Full=Anthocyanidin 5,3-O-glucosyltransferase; AltName: Full=UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase [Rosa hybrid cultivar]	129	129	37%	2e-32	44.68%	Q4R1I9.1
RecName: Full=Chalcone 4'-O-glucosyltransferase; Short=4'CGT; Short=Am4'CGT [Antirrhinum majus]	127	127	38%	1e-31	44.52%	Q33DV3.1
RecName: Full=UDP-glycosyltransferase 73C1; AltName: Full=Cytokinin-O-glucosyltransferase 1; AltName: Full=Zeatin O-glucosyltransferase 1; Short=AtZOG1 [Arabidopsis thaliana]	124	229	84%	2e-30	42.14%	Q9ZQ99.1
RecName: Full=UDP-glycosyltransferase 73C5; AltName: Full=Cytokinin-O-glucosyltransferase 3; AltName: Full=Deoxynivalenol-glucosyl-transferase 1; AltName: Full=Zeatin O-glucosyltransferase 3; Short=AtZOG3 [Arabidopsis thaliana]	124	231	90%	4e-30	42.17%	Q9ZQ94.1

Graphic Summary



Distribution of the top 14 Blast Hits on 10 subject sequences



Alignments

RecName: Full=UDP-glycosyltransferase 90A1 [Arabidopsis thaliana]
Sequence ID: **Q9ZVX4.1** Length: 478 Number of Matches: 2
Range 1: 2 to 231

Score	Expect	Method	Identities	Positives	Gaps	Frame
201 bits(511) 5e-59() Compositional matrix adjust. 110/234(47%) 147/234(62%) 11/234(4%)						
Query 11	SSSSSKPNIVVPFMSK	GHTIPLLLHLAQLLLDRGLA----	TVTIFTTPANHPFISQSLAG	66		
Sbjct 2	S S+ ++V+FPFMSKGH	IPLL +LLL TVT+FTTP N PFIS L+	SVSTHHHHVVLFPFMSKGH	IPLLQFGRLLLRHHRKEPTITVTVFTTPKNQPFISDFLSD	61	
Query 67	A-HVSIVDLPFPRNIQGV	PPGVESTDKLP	SMALFIPFVRGLELMQPAFEQELEKIH	SQVT 125		
Sbjct 62	TPEIKVISLPPENITGIP	PGVENTEKLPSMSLFV	PFTRATKLLQPFEE	TLKTL-PKVS 120		
Query 126	CIISDGFLPWTL	ESASRFGIPRLSYYGMSYYSMAVSRDAAFSGLMSSPE--	TDDEPFTVK	183		
Sbjct 121	FMVSDGFLWWTSESAAKF	NIPRFVSYGMNSYSAAVSISVFKHEL	FTEPESKSDTEPVTVP	180		
Query 184	SFPWIIQITRND	FDEPGRGELL	MGGKEERLELLSDDFQSTV	SERGIIVTDWVDQE 237		
Sbjct 181	DFPWIKVKCDFH	-GTTPEESGA--ALELSMDQIKSTTT	SHGFLVNSFYELE 231			

Range 2: 306 to 476

Score	Expect	Method	Identities	Positives	Gaps	Frame
169 bits(428) 6e-47() Compositional matrix adjust. 85/171(50%) 111/171(64%) 1/171(0%)						
Query 197	EPGRGELL	MGGKEERLELLSDDFQSTV	SERGIIVTDWVDQEEILEHPIVQGFLSHCGWNS	256		
Sbjct 306	EDSKVNFLWTRKDVEE	IIGEGFNDRIRESGMIVRDWVDQWEILSHESVKGFLSHCGWNS		365		
Query 257	VLDGICAGVPILAWP	MAEQGLNAKLVVEEIKVGLRIGTV	DGRSGFVTANLKS	AVREL 316		
Sbjct 366	AQESICVGPVLLAWP	MAEQPLNAKMVVEEIKVGVRVETEDGSVKG	FVTREELSGKIKEL 425			
Query 317	M	GS	KGKQLRERVKEIAKAAIEATSEG-GSSWNALSNLISEIQREKEINSS 366			
Sbjct 426	MEGETGKTARKNVKEYSK	MAKAALVEGTGSSWKNLDMILKELCKSRDSNGA 476				

RecName: Full=UDP-glycosyltransferase 90A2 [Arabidopsis thaliana]
Sequence ID: **Q9SY84.1** Length: 467 Number of Matches: 2
Range 1: 5 to 188

Score	Expect	Method	Identities	Positives	Gaps	Frame
181 bits(460) 1e-51() Compositional matrix adjust. 87/185(47%) 127/185(68%) 6/185(3%)						
Query 16	KPNIVVPFMSK	GHTIPLLLHLAQLLLDRGLA----	TVTIFTTPANHPFISQSLAGHVSIV	72		
Sbjct 5	K ++V+FP++SKGH	IP+L LA+LLL A +VT+FTTP N PFI SL+G +IV	KVHVLFPPYLSKGHMIPMLQLARLLLSHSFAGDISVTVFTTPLNRPFI	VDLSLGTKATIV 64		
Query 73	DLFPFPRNIQGV	PPGVESTDKLP	SM--ALFIPFVRGLELMQPAFEQELEKIH	SQVTCTIISD 130		
Sbjct 65	D+PFP N+ +PPGVE	TDKLP++ +LF+PF R + MQ FE+EL + +V+ ++SD	DVPFDPNVPEIPPGVECTDKLPALSSSLFVPFTRATKSMQADFERELMSL-PRVS	FMVSD 123		
Query 131	GFLPWTL	ESASRFGIPRLSYYGMSYYSMAVSRDAAFSGLMSSPETDDEPFTVK	SFPWIIQI 190			
Sbjct 124	GFLWWTQESARKL	GFPRLVFFGMNCATVICS	VFQNL	LSNVKSETEPVSVPEFPWIKV 183		
Query 191	TRNDF 195					
Sbjct 184	RKCDF 188					

Range 2: 325 to 462

Score	Expect	Method	Identities	Positives	Gaps	Frame
132 bits(331) 3e-33() Compositional matrix adjust. 73/141(52%) 93/141(65%) 5/141(3%)						
Query 219	FQSTV	SERGIIVTD-WVDQEEILEHPIVQGFLSHCGWNSVLDGICAGVPILAWPMAEQG	277			
Sbjct 325	F+ V ERG++V D WVDQ +ILEH V+GFLSHCGWNS+ + IC+ VPILA+P+ AEQ	FEERVGERGMVRDEWVDQRKILEHESVRGFLSHCGWNSLTESICSEVPILAFPLAAEQP	384			
Query 278	LN	AKLVVEEIKVGLRIGTV	DGRSGFVTANLKS	AVRELMGSGKGKQLRERVKEIAKAAI 337		
Sbjct 385	LNA LVVEE++V R+ S+G V + V+ELM KGK+LR V+ K A	LNAILVVEELVAERVVAA--SEGVRREEIAEKVKELMEGEKKGELRRNVEAYGKMAK	441			
Query 338	EATSEG-GSSWNALSNLISEI 357					
Sbjct 442	+A EG GSS L NLI+E KALEEGIGSSRK	NLDNLINEF 462				

RecName: Full=UDP-glycosyltransferase 1; Short=PIUGT1; AltName: Full=Glycosyltransferase UGT88E12; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase KGT1 [Pueraria montana var. lobata]
Sequence ID: **A0A067YB04.1** Length: 471 Number of Matches: 1
Range 1: 262 to 470

Score	Expect	Method	Identities	Positives	Gaps	Frame
141 bits(355) 1e-36() Compositional matrix adjust. 88/231(38%) 129/231(55%) 22/231(9%)						
Query	130	DGFLPWTLESASRFGIPRLSYYGMSYYSMAVSRDAAFSGLMSSPETDDEPFTVKSPFWIQ	189			
		DG L W L+S + LS+ M +S R+ A GL S + F W+				
Sbjct	262	DGCLSW-LDSQPSHSVVFLSFGSMGRFSRTQLREIAT-GLEKSEQ-----RFLWV-	309			
Query	190	ITRNDFDEPGRGELLMGKKEERLELLSDDFQSTVSEIRGIIVTDWVDQEEILEHPIVQGFL	249			
		R++F+E E ELL + F +G+++ DW Q IL H V GF+				
Sbjct	310	-VRSEFEEGDSVE-----PPSLDELLPEGFLERTKGGKGMVLRDWPQAAILSHDSVGGFV	363			
Query	250	SHCGWNSVLDGICAGVPILAWPMAEQGLNAKLVEEIKVGLRIGTVDGRSKGFVTANNL	309			
		+HCGWNSVL+ +C GVP++AWP+ AEQ LN ++VEE+KVGL V G V++ L				
Sbjct	364	THCGWNSVLEAVCEGVPMAWPLYAEQKLNKVLVEEMKVGL---AVKQNKDGLVSSTEL	420			
Query	310	KSAVRELMGSGKGKQLRERVKEIAKAAIEATSEGGSSWNALSNI LSEIQRE	360			
		VRELM S +GK++R+++ ++ +A EA ++GGSS AL+ L+ E+ RE				
Sbjct	421	GDRVRELMDSDRGKETRQKIFKMKMSANEAMAKGSSIMALNRLV-EVWRE	470			

RecName: Full=Isoflavone 7-O-glucosyltransferase 1; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase; Flags:
Precursor [Glycine max]
Sequence ID: **A6BM07.1** Length: 474 Number of Matches: 1
Range 1: 330 to 467

Score	Expect	Method	Identities	Positives	Gaps	Frame
137 bits(345) 4e-35() Compositional matrix adjust. 65/141(46%) 94/141(66%) 3/141(2%)						
Query	213	ELLSDDFQSTVSEIRGIIVTDWVDQEEILEHPIVQGFLSHCGWNSVLDGICAGVPILAWPM			272	
		ELL + F E+G++V DW Q IL H V GF++HCGWNSVL+ +C GVP++AWP+				
Sbjct	330	ELLPEGLFERTKEKGMVVRDWPQAAILSHDSVGGFVTHCGWNSVLEAVCEGVPMAWPL			389	
Query	273	MAEQGLNAKLVEEIKVGLRIGTVDGRSKGFVTANNLSAVRELMGSGKGKQLRERVKEI			332	
		AEQ +N ++V+E+KV L V+ GFV++ L VRELM S KGK++R+R+ ++				
Sbjct	390	YAEQKMNRMVMVKEMKVAL---AVNENKDGFSSTELGDRVRELMESDKGKETRQIRFKM			446	
Query	333	AKAAIEATSEGGSSWNALSNI	353			
		+A EA +EGG+S +L L				
Sbjct	447	KMSAAEAMAEGGTSRASLDKL	467			

RecName: Full=UDP-glycosyltransferase 2; Short=PIUGT2; AltName: Full=UDP-glucose:isoflavone 4' 7-O-glucosyltransferase
[Pueraria montana var. lobata]
Sequence ID: **A0A172J2D0.1** Length: 472 Number of Matches: 1
Range 1: 137 to 465

Score	Expect	Method	Identities	Positives	Gaps	Frame
135 bits(341) 2e-34() Compositional matrix adjust. 114/358(32%) 171/358(47%) 74/358(20%)						
Query	41	LDRGLATVTIFTTPA-----NHPFISQSLAGAHVSIVDLFPFRNIQGVPPGVESTD--			91	
		L++ + T +T+ A ++P I ++L +V D P I G+ + + D				
Sbjct	137	LNKNHITYFYFTSGASTLALLHYPTIHETLTKNYVK--DQPLQIQIPGLRANITTDFA			194	
Query	92	---KLPSMALFIPFVRGLELMQPAF-----EQUELEKIHSQ-----VTCI---IS			129	
		K PS F++ E M+ +F E+EL + S+ + CI IS				
Sbjct	195	KDSKDPNSYSSQAFKIAETMRGSGFGIINTFEATEEELIRALSEDGTVPPLFCIGPVIS			254	
Query	130	-----DGFLPWTLESASRFGIPRLSYYGMSYYSMAVSRDAAFSGLMSSPETDDEPFTV			182	
		G L W L+S + L + M +S ++ A GL S +				
Sbjct	255	APYGEDDRGCLSW-LDSQPSQSVVLLCFGSMGSFSRTQLKEIAV-GLEKSEQ-----			304	
Query	183	KSEFPWIIQITRNDF-----EPGRGELLMGKKEERLELLSDDFQSTVSEIRGIIVTDWVD			235	
		F W+ R + D +P EL+ GG ER E+G++V DW				
Sbjct	305	-RFLWV--VRAELDCADSVDEQPSLDELMPGGFLER-----TKEKGLVVRDWP			350	
Query	236	QEEILEHPIVQGFLSHCGWNSVLDGICAGVPILAWPMAEQGLNAKLVEEIKVGLRIGT			295	
		Q +IL H V GF++HCGWNSVL+ +C GVP+ AWP+ AEQ +N ++VE++KV L				
Sbjct	351	QVQILSHDSVGGFVTHCGWNSVLEAVCEGVPMAAWPLYAEQVRNVRIMVEDMKVAL---A			407	
Query	296	VDGRSKGFVTANNLKSAVRELMGSGKGKQLRERVKEIAKAAIEATSEGGSSWNALSNI			353	
		V+ GFV+A L VRELM S KGK++R+R ++ +A EA +EGG+S AL L				
Sbjct	408	VNEDKAGFVSATELGDRVRELMESDKGKETRQRTFKMKISAAEAMAEGGTSRVALDKL			465	

RecName: Full=UDP-glycosyltransferase 13; Short=PIUGT13; AltName: Full=Glycosyltransferase UGT88H1; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase KGT13 [Pueraria montana var. lobata]
Sequence ID: **A0A067YBQ3.1** Length: 451 Number of Matches: 1
Range 1: 305 to 446

Score	Expect	Method	Identities	Positives	Gaps	Frame
131 bits(330) 4e-33() Compositional matrix adjust. 68/144(47%) 95/144(65%) 4/144(2%)						
Query	213	ELLSDDFQSTVSEIRGIIVTDWVDQEEILEHPIVQGFLSHCGWNSVLDGICAGVPILAWPM			272	
		ELL F ERG++V +W Q ++L H V GF++HCGWNSVL+ + GVP++AWP+				
Sbjct	305	ELLPKGFLERTKERGMVKNWAPQVKVLSHDSVGGFVTHCGWNSVLEAVSWGVPMAWPL			364	
Query	273	MAEQGLNAKLVEEIKVGLRIGTVDGRSKGFVTANNLSAVRELMGS--GKGKQLRERVK			330	
		AEQ LN ++VEE+KV L + VD GFV A+ L+ VRELM S G+GK++R+RV				
Sbjct	365	YAEQRLNRVVMVEEMKVALPLKEVD--EDGFVRASELEERVRELMDSERGRGKEVRKRVL			422	
Query	331	EIAKAAIEATSEGGSSWNALSNI	354			
		A+ A S+GGSS L++L+				

RecName: Full=Anthocyanidin 5,3-O-glucosyltransferase; AltName: Full=UDP-glucose: anthocyanidin 5,3-O-glucosyltransferase [Rosa hybrid cultivar]

Sequence ID: **Q4R1I9.1** Length: 473 Number of Matches: 1
Range 1: 329 to 466

Score	Expect	Method	Identities	Positives	Gaps	Frame
129 bits(325)	2e-32()	Compositional matrix adjust.	63/141(45%)	88/141(62%)	3/141(2%)	
Query 213	ELLSDDFQSTVSEIRGIIVTDWVDQEEILEHP	IVQGFLSHCGWNSVLDGICAGVPILAWPM	272			
Sbjct 329	E+L F +RG++V W Q E+L H V GF++HCGWNSVL+ +C GVP++AWP+ EILPKGFVERTKDRGLVVRKWAPQVEVL	SHDSVGGFVTHCGWNSVLEAVCNGVPMVAWPL	388			
Query 273	MAEQGLNAKLVEEIKVGLRIGTVDRSGKGFVTANNLKSAVRELMGSGKGKQLRERVKEI	332				
Sbjct 389	AEQ L +VEE+KV + V GFV+A+ L+ VRELM S G ++R RV E YAEQGLGRVFLVEEMKAVV---	GVKESETGFVSADELEKRVRELMDSSESGDEIRGRVSEF	445			
Query 333	AKAAIEATSEGGSSWNALS	353				
Sbjct 446	+ ++A EGGSS +L+ L SNGGVKAKEEGSSVASLAKL	466				

RecName: Full=Chalcone 4'-O-glucosyltransferase; Short=4'CGT; Short=Am4'CGT [Antirrhinum majus]

Sequence ID: **Q33DV3.1** Length: 457 Number of Matches: 1
Range 1: 316 to 457

Score	Expect	Method	Identities	Positives	Gaps	Frame
127 bits(319)	1e-31()	Compositional matrix adjust.	65/146(45%)	90/146(61%)	4/146(2%)	
Query 214	LLSDDFQSTVSEIRGIIVTDWVDQEEILEHP	IVQGFLSHCGWNSVLDGICAGVPILAWPMM	273			
Sbjct 316	LL +F S + + G + WV Q+E+L H V GF++HCGW+SVL+ + GVP++ WP+ LLPEGFLSRTKGVGFVTINTWVPQKEVL	SHDAVGGFVTHCGWSSVLEALSFGVPMIGWPLY	375			
Query 274	AEQGLNAKLVEEIKVGLRIGTVDRSGKGFVTANNLKSAVRELMGSGKGKQLRERVKEIA	333				
Sbjct 376	AEQ +N +VEEIKV L + D GFVTA L+ VRELM S KGK+++ RV E+ AEQRINRVFMVEEIKVALPLDEED---	GFVTAMELEKRVRELMESVKGKEVKRRVAELK	431			
Query 334	KAIEATSEGGSSWNALS	359				
Sbjct 432	+ A S+GGSS +L I+ + R ISTKAAVSKGGSSLASLEKFINSVTR	457				

RecName: Full=UDP-glycosyltransferase 73C1; AltName: Full=Cytokinin-O-glucosyltransferase 1; AltName: Full=Zeatin O-glucosyltransferase 1; Short=AtZOG1 [Arabidopsis thaliana]

Sequence ID: **Q9ZQ99.1** Length: 491 Number of Matches: 2
Range 1: 327 to 485

Score	Expect	Method	Identities	Positives	Gaps	Frame
124 bits(311)	2e-30()	Compositional matrix adjust.	67/159(42%)	97/159(61%)	9/159(5%)	
Query 210	ERLELLSDD-FQSTVSEIRGIIVTDWVDQEEILEHP	IVQGFLSHCGWNSVLDGICAGVPIL	268			
Sbjct 327	E LE +F S + + + ERG+++T W Q IL HP V GFL+HCGWNS L+GI +GVP+L ELLEWISESGYKERIKERGLLITGWSPQMLILTHPAVGGFLTHCGWNSTLEGITSGVPLL		386			
Query 269	AWPMAEQGLNAKLVEEIKVGLRIGTVDRSGK-----FVTANNLKSAVRELMG-SG	320				
Sbjct 387	WP+ +Q N KL V+ +K G+R G + G V +K AV ELMG S TWPLFGDQFCNEKLAVQILKAGVRAGVEESMRWGEEKIGVLVDKEGVKKAVEELMGDSN	446				
Query 321	KGKQLRERVKEIAKAAIEATSEGGSSWNALS	359				
Sbjct 447	K+ R+RVKE+ + A +A EGGSS + ++ L+ +I + DAKERRRKRKELGELAHKAVEEGSSHSNITFLLQDIMQ	485				

Range 2: 10 to 183

Score	Expect	Method	Identities	Positives	Gaps	Frame
104 bits(260)	2e-23()	Compositional matrix adjust.	57/175(33%)	98/175(56%)	7/175(4%)	
Query 18	NIVVFPFMSKGHTIPLLHLAQLLLDRGLATVTIFTTPANHPFISQSLA-----GAHVSIV	72				
Sbjct 10	+ V+FPFM++GH IP++ +A+LL RG+ T+TI TTP N L+ G +++V HFVLFPFMAQGHMIPMVDIARLLAQRGV-TITIVTTPQAGRFKNVLSRATQSGLPINLV	68				
Query 73	DLPFPRNIQGVPPGVESTDKLPMSMALFIPFVRGLELMQPAFEQELEKIHSQVTCIISDGF	132				
Sbjct 69	+ FP G P G E+ D L S+ + F + L++ E+ L++I + CII+D QVKFPSEQSGSPEGQENLDDLDSLGLSTFFKAFSLLEEPVEKLLKEIQPRPNCIADMC	128				
Query 133	LPWTLESASRFGIPRLSYYGMSYYMAVSRDAAFSG-LMSSPETDDEPFTVKSEF	186				
Sbjct 129	LP+T A GIP++ ++GM +++ + + + E+D E F + +PP LPYTNRIAKNLGIPKTIIFHGMCCFNLLCTHIMHQNHEFLETIESDKEYFPINFP	183				

RecName: Full=UDP-glycosyltransferase 73C5; AltName: Full=Cytokinin-O-glucosyltransferase 3; AltName: Full=Deoxynivalenol-glucosyl-transferase 1; AltName: Full=Zeatin O-glucosyltransferase 3; Short=AtZOG3 [Arabidopsis thaliana]

Sequence ID: **Q9ZQ94.1** Length: 495 Number of Matches: 2
Range 1: 330 to 495

Score	Expect	Method	Identities	Positives	Gaps	Frame
124 bits(310)	4e-30()	Compositional matrix adjust.	70/166(42%)	97/166(58%)	9/166(5%)	
Query 209	EERLELLSDD-FQSTVSE	RGITVTDWVDQEEI	LEHPTVQGFLSHCGWNSVLDGICAGVPI		267	
Sbjct 330	KELVEWFSESGFEDRIQDRGLLIK	GWSPQMLILSHPSVGGFLTHCGWNSTLEGITAGLPL		389		
Query 268	LAWPMMAEQGLNAKL	VVEIKVGLRIGTV	GRSKG-----FVTANNLKS	SAVRELMG-S	319	
Sbjct 390	L WP+ A+Q N KL	VE +K G+R G	G V +K AV	ELMG S	449	
Query 320	GK GKQLRERVKEIAKAA	IEATSEGGSSWNALS	NLSEIQREKINS	365		
Sbjct 450	DDAKERRRRRAKELGDS	SAHKAEEGGSSHSNIS	FLLQDIMELAE	PNN 495		

Range 2: 2 to 192

Score	Expect	Method	Identities	Positives	Gaps	Frame
107 bits(268)	2e-24()	Compositional matrix adjust.	63/194(32%)	112/194(57%)	13/194(6%)	
Query 9	ISSSSSSKP-NIVVFP	MSKGHTIPLLHLAQL	LLDRGLATVTIFTTPANHPFISQSL---	64		
Sbjct 2	VSETTKSSPLH	IFVLPFPMAGGHMIP	MDIARLLAQRGV-IITIVTTPHNAARFKNVLNRA	60		
Query 65	---AGAHVSTVDLP	FPFRTIQQVPPGV	ESTDKLP	SMALFIPFVRG	LELMQPAFEQELEKIHS	122
Sbjct 61	+G +++V + FP	G+ G E+ D L +M	IPF + + ++ ++ +E+++		120	
Query 123	QVTCIISDGLP	WTLASRFGIPRL	SYGMSYY---SMAVSRDAAF	SGLMSSPETDDEP	179	
Sbjct 121	+ +C+ISD LP+T + A +F	IP++ ++GM + M V R	++ + ++D E	178		
Query 180	FTVKSFP-WIQITR	192				
Sbjct 179	FTVPDFPDRVEFTR	192				

Taxonomy

Reports

• Lineage

Organism	Blast Name	Score	Number of Hits	Description
Pentapetalae	eudicots		<u>10</u>	
.rosids	eudicots		<u>9</u>	
..Arabidopsis thaliana	eudicots	201	<u>4</u>	Arabidopsis thaliana hits
..Pueraria montana var. lobata	eudicots	141	<u>3</u>	Pueraria montana var. lobata hits
..Glycine max	eudicots	137	<u>1</u>	Glycine max hits
..Rosa hybrid cultivar	eudicots	129	<u>1</u>	Rosa hybrid cultivar hits
.Antirrhinum majus	eudicots	127	<u>1</u>	Antirrhinum majus hits

• Organism

Description	Score	E value	Accession
Arabidopsis thaliana (thale cress) [eudicots]			
RecName: Full=UDP-glycosyltransferase 90A1 [Arabidopsis thaliana]	201	5e-59	Q9ZVX4
RecName: Full=UDP-glycosyltransferase 90A2 [Arabidopsis thaliana]	181	1e-51	Q9SY84
RecName: Full=UDP-glycosyltransferase 73C1; AltName: Full=Cytokinin-O-glucosyltransferase 1; AltName: Full=Zeatin O-glucosyltransferase 1; Short=AtZOG1 [Arabidopsis thaliana]	124	2e-30	Q9ZQ99
RecName: Full=UDP-glycosyltransferase 73C5; AltName: Full=Cytokinin-O-glucosyltransferase 3; AltName: Full=Deoxynivalenol-glucosyl-transferase 1; AltName: Full=Zeatin O-glucosyltransferase 3; Short=AtZOG3 [Arabidopsis thaliana]	124	4e-30	Q9ZQ94
Pueraria montana var. lobata (kudzu vine) [eudicots]			
RecName: Full=UDP-glycosyltransferase 1; Short=PIUGT1; AltName: Full=Glycosyltransferase UGT88E12; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase KGT1 [Pueraria montana var. lobata]	141	1e-36	A0A067YB04
RecName: Full=UDP-glycosyltransferase 2; Short=PIUGT2; AltName: Full=UDP-glucose:isoflavone 4' 7-O-glucosyltransferase [Pueraria montana var. lobata]	135	2e-34	A0A172J2D0
RecName: Full=UDP-glycosyltransferase 13; Short=PIUGT13; AltName: Full=Glycosyltransferase UGT88H1; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase KGT13 [Pueraria montana var. lobata]	131	4e-33	A0A067YBQ3
Glycine max (soybean) [eudicots]			
RecName: Full=Isoflavone 7-O-glucosyltransferase 1; AltName: Full=UDP-glucose:isoflavone 7-O-glucosyltransferase; Flags: Precursor [Glycine max]	137	4e-35	A6BM07