

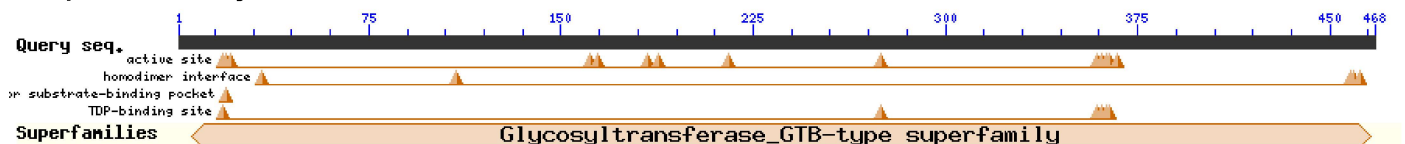
BLAST® » [blastp suite](#) » results for RID-MYHK7N21016

Job Title [ST0002 ...](#)
 RID [MYHK7N21016](#) Search expires on 09-03 15:14 pm
 Program BLASTP
 Database swissprot
 Query ID lc|Query_94544
 Description [unnamed protein product ...](#)
 Molecule type amino acid
 Query Length 468

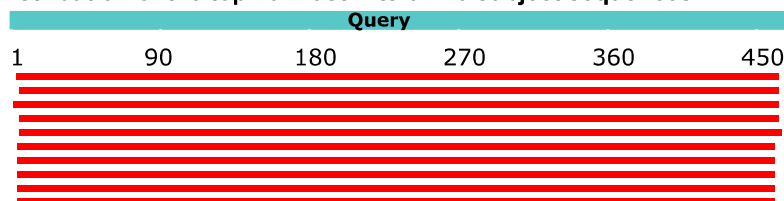
Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
RecName: Full=UDP-glucose flavonoid 3-O-glucosyltransferase 6; AltName: Full=Flavonol 3-O-glucosyltransferase 6; Short=FaGT6 [Fragaria x ananassa]	442	442	97%	2e-151	48.54%	Q2V6K0.1
RecName: Full=UDP-glycosyltransferase 71A15; AltName: Full=UDP-glucose:chalcone 2'-O-glucosyltransferase; AltName: Full=UDP-glucose:flavonol 2'-O-glucosyltransferase [Malus domestica]	436	436	97%	5e-149	47.99%	D3THI6.1
RecName: Full=Putative UDP-glucose flavonoid 3-O-glucosyltransferase 3; Short=FaGT3; AltName: Full=Flavonol 3-O-glucosyltransferase 3 [Fragaria x ananassa]	431	431	98%	7e-147	46.33%	Q66PF3.1
RecName: Full=UDP-glycosyltransferase 71A16; AltName: Full=UDP-glucose:chalcone 2'-O-glucosyltransferase; AltName: Full=UDP-glucose:flavonol 2'-O-glucosyltransferase [Pyrus communis]	426	426	97%	5e-145	47.12%	D3UAG1.1
RecName: Full=UDP-glycosyltransferase 71E1 [Stevia rebaudiana]	424	424	97%	2e-144	49.26%	Q6VAB2.1
RecName: Full=UDP-glycosyltransferase 101; Short=UGTPg101 [Panax ginseng]	402	402	97%	7e-136	46.44%	A0A0K0PVM5.1
RecName: Full=UDP-glycosyltransferase 1; Short=UGTPg1 [Panax ginseng]	402	402	97%	7e-136	46.65%	A0A068J840.1
RecName: Full=UDP-glycosyltransferase 71A27; Short=PgUGT71A27 [Panax ginseng]	390	390	97%	5e-131	45.59%	A0A0A7HB61.1
RecName: Full=UDP-glycosyltransferase 100; Short=UGTPg100 [Panax ginseng]	385	385	97%	3e-129	46.22%	A0A0K0PVW1.1
RecName: Full=UDP-glucosyltransferase 102; Short=UGTPg102 [Panax ginseng]	384	384	97%	7e-129	44.77%	A0A0K0PVL0.1

Graphic Summary



Distribution of the top 10 Blast Hits on 10 subject sequences



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

RecName: Full=UDP-glucose flavonoid 3-O-glucosyltransferase 6; AltName: Full=Flavonol 3-O-glucosyltransferase 6; Short=FaGT6 [Fragaria x ananassa]
Sequence ID: **Q2V6K0.1** Length: 479 Number of Matches: 1
Range 1: 2 to 473

Score	Expect	Method	Identities	Positives	Gaps	Frame
442 bits(1137) 2e-151() Compositional matrix adjust. 232/478(49%) 315/478(65%) 27/478(5%)						
Query 5	EKAS	LVFIPFPVSHLVTAVKTAELLASHDSRLSITVLVMSMP-----TDTKISSY---	55			
Sbjct 2	+KAS L+VIP P + H+V+ V+ A+LL D L IT+L+M P +D I S	KKASELIFIPGIGHIVSTVEIAKLLCRDDNLFITILIMKFPFTADGSDVYIKSLAVD	61			
Query 56	---IKNPRINFVQLEQDVSN	GAEAIMKPPKSMMHFAGRHRDSARAVVSEM---KRSCRVA	109			
Sbjct 62	+K RI FV L Q+ G A F H+ + V+ + + R+A	PSLKTQIRIRFVNLPEHFQGTGAT-----GFFTFIDSHKSHVKDAVTRLMETKSETTRIA	116			
Query 110	GIFVDIMCVDIMIDVAKELKISSYIFFASGA	AVLGLTFDLQSLRDDGGRNLAIEFGSDEVV	169			
Sbjct 117	G +D+ C MID+A E + SY+P+ SCAA IGL F LQ+LRD+ ++ EF+ SD +	GFVIDMFCGTGMIDLANEFGLPSYVFYTSGAADLGLMFHLQALRDEENKDCTEFKDSDAEL	176			
Query 170	SISSYVNPVPA-RVWPESVFDGESG---FLELSRKAREADGIVINTFLELESYAIGSTYAN		226			
Sbjct 177	+SS+VNP+PA RV P VF+ E G FL +++ RE GI++NTFLELE +AI S ++	VVSSFVNPLPAARVLPVVFEEKGNFNLNFAKRYRETKGILVNTFLELEPHATQSLSSD	236			
Query 227	ERIPRFYPIGPIIG---EGKDENDESQRERGEIMRWLDGQPDSSVVFLCFGSMGAFGEEQ		283			
Sbjct 237	+I YP+GP+I+ EG + E +++ +I+ WLD QP SSVVFLCFGSMG FGE+Q	GKLLPVYPVGPILNVKSEGNQVSSEKSKQKSDILEWLDQPPSSVVFLCFGSMGCFGEDQ	296			
Query 284	VVDIAEALERSGKRFLWSLRKPIFEGGFAYPTEYENPGEVLPVGFLERTAGVGKVI	GWAP	343			
Sbjct 297	V +IA ALE+ G RFLWSLR+P E +P++Y + VLP GFL+RT +GKVI	GWAP	355			
Query 344	QVAVLSHPVSGGFVSHCGWNSTLESVCCGVPMAAWPLGAEQQTNAFQLVKDIGIAVEIKM		403			
Sbjct 356	Q+A+L+HP+VGGFVSHCGWNSTLES+ GVP+A WP AEQQ NAF+LVK++ +AVEI M	QLAILAHPAVGGFVSHCGWNSTLESIWYGVPIATWPFYAEQQVNAFELVKELKLAVEIDM	415			
Query 404	DYRKNSGEIVPKSIIIEKAIKQLMDPTNEIRVRVKELKEKSTRALMEGGSSYNHLGLLI		461			
Sbjct 416	YRK+SG IV + IEK IK++M+ +E+R RVKE+ + S +AL E GSSY+ LG +	GYRKDSGIVISRENIEKGIKEVMEQESELKRVRKEMSQMSRKALEEDGSSYSLSGRFL	473			

RecName: Full=UDP-glycosyltransferase 71A15; AltName: Full=UDP-glucose:chalcone 2'-O-glucosyltransferase; AltName: Full=UDP-glucose:flavonol 2'-O-glucosyltransferase [Malus domestica]
Sequence ID: **D3THI6.1** Length: 471 Number of Matches: 1
Range 1: 5 to 468

Score	Expect	Method	Identities	Positives	Gaps	Frame
436 bits(1120) 5e-149() Compositional matrix adjust. 227/473(48%) 308/473(65%) 27/473(5%)						
Query 7	ASLVFIPFPVSHLVTAVKTAELLASHDSRLSITVLVMSMP-----TDTKISSYIKNP		59			
Sbjct 5	A LVF+P P + H+V+ V+ A+ LA+ D +L ITVLV+P TD+ IS	AQLVFPVAPGIGHIVSTVEMAKQLAARDQQLFITVLVVKMLPYAQPTNTDSSISH-----	59			
Query 60	RINFVQLEQDVSN	GAEAIMKPPKSMMHFAGRHRDSARAVV-----SEMKRSCR	110			
Sbjct 60	RINFV L + + + + P F H+ R V SE +R+AG	RINFVNLEAQPDKQDIVPNPGSFFRMFVENHKSHVRDAVINVLPESDQSESTSKPRLAG	119			
Query 111	IFVDIMCVDIMIDVAKELKISSYIFFASGA	AVLGLTFDLQSLRDDGGRNLAIEFGSDEVVS	170			
Sbjct 120	+D+ +IDVA E K+ SY+FF S A+ L L QSLRD+GG ++ E S ++	FVLDMFSAASLIDVANEFKVPSYLFFTSNASALALMSHFQSLRDEGGIDITELTSSAELA	179			
Query 171	ISSYVNPVPA	RVWPESVFDGESGFLELSR---KAREADGIVINTFLELESYAIGSTYANER	228			
Sbjct 180	+S++NP PA V P S+ D ES L+ K ++ GI++NTF+ELES+A+ + ++	VPSFINPYPAAVLPGSLDDMESTKSTLNVHVKYKQTKGILVNTFMELESHALHYLDSGDK	239			
Query 229	IPRFYPIGPIIIEGKDENDESQRERGEIMRWLDGQPDSSVVFLCFGSMGAFGEEQ	VVDIA	288			
Sbjct 240	IP YP+GP++ + D++ +I+RWLD QP SVVFLCFGSMG+FGE QV +IA	IPPVYPVGPGLNLNKSSDEDKA---SDILRWLDQPPFVVFLCFGSMGSPGAEQVKEIA	295			
Query 289	EALERSGKRFLWSLRKPIFEGGFAYPTEYENPGEVLPVGFLERTAGVGKVI	GWAPQVAVL	348			
Sbjct 296	ALE SG RFLWSLR+P +G A P++YE+ VLP GFL+RTA VGKVI	GWAPQ A+L	355			
Query 349	SHPSVGGFVSHCGWNSTLESVCCGVPMAAWPLGAEQQTNAFQLVKDIGIAVEIKMDYRKN		408			
Sbjct 356	HP+ GGFVSHCGWNSTLES+ GVP+AAWPL AEQ NAFQLV ++G+AVEIKMDYR++	GHPATGGFVSHCGWNSTLESLNWGVPIAAWPLYAEQNLNAFQLVVELGLAVEIKMDYRRD	415			
Query 409	SGEIVPKSIIIEKAIKQLMDPTNEIRVRVKELKEKSTRALMEGGSSYNHLGLLI		461			
Sbjct 416	S +V IE+ I+++M+ +++R RVKE+ EKS +AL++GGSSY+ LG I	SDVVVSAEDIERGIRRVMELDSDVRKVRKEMSEKSKKALVDGGSSYSLSGRFI	468			

RecName: Full=Putative UDP-glucose flavonoid 3-O-glucosyltransferase 3; Short=FaGT3; AltName: Full=Flavonol 3-O-glucosyltransferase 3 [Fragaria x ananassa]
Sequence ID: **Q66PF3.1** Length: 478 Number of Matches: 1
Range 1: 1 to 475

Score	Expect	Method	Identities	Positives	Gaps	Frame
431 bits(1107) 7e-147() Compositional matrix adjust. 221/477(46%) 315/477(66%) 20/477(4%)						
Query 3	VDEKASLVFIPFPVSHLVTAVKTAELLASHDSRLSITVLVMSMPTDTK-ISSYIKN---		58			
Sbjct 1	+++ A LV IP P + HLV+ ++ A+LL S D +L ITVL+M P +K +Y+++	MEKPAELVLIPSPGTGHLVSTLETAKLLVSRDDKLFITVLIMHFPAVSKGTDAYVQSLAD	60			
Query 59	-----PRINFVQLEQDVSN	GAEAIMKPPKSMMHFAGRHRDSARAVVSEMK---RSCR	110			

		RINF+ L + E ++ S++ F + + V+ ++ ++ R+AG	
Sbjct	61	SSSPTSQRINFINLPHNTMDHTEGSRV--NSLVGFVESQQPHVKDAVANLRDSKTTRLAG	118
Query	111	IFVDIMCVDIMIDVAKELKISSYIFFASGAAVLGLTFDLQSLRDDGGRNLAEFEQSDEVVVS	170
		VD+ C MI+VA +L + SY+FF SGAA LGL F LQ LRD ++ EF+ SD +	
Sbjct	119	FVVDMFCTTMINVANQLGVPSYVFFTSGAATLGLLFLQLERLDQYNKDCTEFKDSDAELI	178
Query	171	ISSYVNPVPARVWPESVF--DGESGFLELSRKAREADGIVINTFLELESYAIGSTYANER	228
		I S+ NP+PA+V P + D FL + ++ RE GI++NTF +LES+A+ + ++	
Sbjct	179	IPSPFNPLPAKVLPGRMLVKDSAEPFLNVIKRFRETKGILVNTFTDLESHALHALSSDAE	238
Query	229	IPRFYPIGPIIGEGKDE---NDESRRRGEIMRWLDGQPDSSVFLCFGSMGAFGEEQVV	285
		IP YP+GP++ +E + + +++ +I++WLD QP SVVFLCFGSMG+F E QV	
Sbjct	239	IPPVYPVGPLNLNLSNESRVDSDSEVKKKNDILKWLDDQPPLSVVFLCFGSMGSFDESQVR	298
Query	286	DIAEALERSGKRFLWSLRKPIFEGGFAYPTEYENPGEVLPVGFLERTAGVGKIVGWAPQV	345
		+IA ALE +G RFLWSLR+ G A+P++Y++ VLP GFL+RT +G+KIVGWAPQV	
Sbjct	299	EIANALEHAGHRFLWSLRSPPTGKVAFPSPDYDDHTGVLPEGLDRTGGIGKIVGWAPQV	358
Query	346	AVLSHPSVGGFVSHCGWNSTLESVCCGVPMAAWPLGAEQQTNAFQLVKDIGIAVEIKMDY	405
		AVL+HPSVGGFVSHCGWNSTLES+ GVP+A WPL AEQQ NAFQ VK++ +AVEI M Y	
Sbjct	359	AVLAHPSVGGFVSHCGWNSTLESLWHGVPVATWPLYAEQQNNAFPVKELELAVEIDMSY	418
Query	406	RKNSGEIYVPKSIEKAIKQLMD-PTNEIRVRVKELKEKSTRALMEGGSSYNHLGLLI	461
		R S +V IE+ I+++M+ +++IR RVKE+ EK +ALM+GGSSY LG I	
Sbjct	419	RSKSPVLVSAKEIERGIREVMELDSSDIRKRVKEMSEKSKKALMDGGSSYSLSLGHFI	475

RecName: Full=UDP-glycosyltransferase 71A16; AltName: Full=UDP-glucose:chalcone 2'-O-glucosyltransferase; AltName: Full=UDP-glucose:flavonol 2'-O-glucosyltransferase [Pyrus communis]

Sequence ID: **D3UAG1.1** Length: 471 Number of Matches: 1
Range 1: 5 to 468

Score	Expect	Method	Identities	Positives	Gaps	Frame
426 bits(1094) 5e-145() Compositional matrix adjust. 221/469(47%) 300/469(63%) 19/469(4%)						
Query	7	ASLVFIPIFPVSHLVTAVKTAELLASHDSRLSITVLVMSMPTD---TKISSYIKNPRINF				63
		A LVF+P P + H+V+ V+ A+ L + D +L ITVLVM +P D T S I + RINF				
Sbjct	5	AQLVFPVAPAGIGHIVSTVEMAKQLVARDDQLFITVLVMKLPYDQPFTNTDSSISH-RINF				63
Query	64	VQLEQDVSNGAEAIMKPPKSMHFAGRHRDSARAVV-----SEMKRSCRVAGIFVD				114
		V L + + + + P F H+ R V SE R+AG +D				
Sbjct	64	VNLPEAQLDKQDTPVNPGPSFFRMFVENHKTHVRDAVINLLPESDQSESTSKPRLAGFVL				123
Query	115	IMCVDIMIDVAKELKISSYIFFASGAAVLGLTFDLQSLRDDGGRNLAEFEQSDEVVSISSY				174
		+ +IDVA E ++ SY+FF S ++ L L QSLRD+GG ++ E S +++ S+				
Sbjct	124	MFSASLIDVANEFVPSYVFFTSNSSTLALLSHFQSLRDEGGIDITELTSSTAELAVPSF				183
Query	175	VNPVPARVWPESVFDGESGFLELSRKAR--EADGIVINTFLELESYAIGSTYANERIPRF				232
		+NP P V P S D ES L+ R + GI++NTFLELES+A+ + +IP				
Sbjct	184	INPYPAVLPGSFLDKESTKSTLNNVGRYKQTKGILVNTFLELESHALHYLDGSGVKIPPV				243
Query	233	YPGPIIGEGKDENDESRQRGEIMRWLDGQPDSSVFLCFGSMGAFGEEQVVDIAEAL				292
		YP+GP++ D+ +I+RWLD QP SVVFLCFGSMG+FG+ QV +IA LE				
Sbjct	244	YPVGPLNLNLSKSHEDKG---SDTLRWLDDQPPLSVVFLCFGSMGSFGDAQVKEIACLE				299
Query	293	RSGKRFLWSLRKPIFEGGFAYPTEYENPGEVLPVGFLERTAGVGKIVGWAPQVAVLSHPS				352
		SG RFLWSLR+P +G A P++Y + VLP GFL+RTA VG+VIGWAPQ A+L HP+				
Sbjct	300	HSGHRFLWSLRQPPSKGKRALPSDYADLKTVLPEGLDRTATVGRVIGWAPQAAILGHPA				359
Query	353	VGGFVSHCGWNSTLESVCCGVPMAAWPLGAEQQTNAFQLVKDIGIAVEIKMDYRKNSGEI				412
		+GGFVSHCGWNSTLES+ GVP+AAWP+ AEQ NAFQLV ++G+AVEIKMDYRK+S +				
Sbjct	360	IGGFVSHCGWNSTLESITWNGVPIAAWPMYAEQNMNAFQLVVELGLAVEIKMDYRKSDV				419
Query	413	VPKSIEKAIAIKQLMDPTNEIRVRVKELKEKSTRALMEGGSSYNHLGLLI				461
		V IE+ I+Q+M+ +++R RVKE+ EKS +AL++GGSSY+ LG I				
Sbjct	420	VSAEDIERGIRQVMELDSDVRKRVKEMSEKSKKALVDGGSSYSLSLGRFI				468

RecName: Full=UDP-glycosyltransferase 71E1 [Stevia rebaudiana]

Sequence ID: **Q6VAB2.1** Length: 474 Number of Matches: 1
Range 1: 4 to 468

Score	Expect	Method	Identities	Positives	Gaps	Frame
424 bits(1090) 2e-144() Compositional matrix adjust. 232/471(49%) 307/471(65%) 20/471(4%)						
Query	7	ASLVFIPIFPVSHLVTAVKTAELLASHDSRLSITVLVMSMPTDTKISSYIKN--PRINFV				64
		+ LVFIP P HL V+ A+LL D RLS+T++VM++ K ++ + P + FV				
Sbjct	4	SELVFIIPSPGAGHLPTVELAKLLHHRDQLSVTIIVMNLWLGPKHNTAARPCVPSLRFV				63
Query	65	QLEQDVSNGAEAIMKPPKSMHFAGRHRDSARAVVSEM--KRSCRVAGIFVDIMCVDIMID				122
		+ D S A++ P + F H+ R +V + S R+AG +D+ C+ M D				
Sbjct	64	DIPCDDES--TMALISPNTFISAFVEHHKPRVRDIVRGIESDSRVLAGEVLDMFCMPMSD				121
Query	123	VAKELKISSYIFFASGAAVLGLTFDLQSLRDDGGRNLAEFEQSDEVVSISSYVNPVPARV				182
		VA E + SY +F SGAA LGL F LQ RD G + E + SD +S+ SYVNPVPA+V				
Sbjct	122	VANFEGVPSYNYFTSGAATLGLMFHLQWKRDHEGYDATELKNSDTELSVPSYVNPVPAKV				181
Query	183	WPESVFDGESG--FLELSRKAREADGIVINTFLELESYAIGSTYANER-IPRFYPIGPI				238
		PE V D E G FL+L+ + RE+ GI++N+ +E +A+ +N IP +P+GPI				
Sbjct	182	LPEVLDKEGGSKMFLDLAERIERESKGIIVNSCQAIERHALEYLSSNNNGIPPVFPVGPI				241
Query	239	IGEGKDENDESRQRGEIMRWLDGQPDSSVFLCFGSMGAFGEEQVVDIAEALERSGKRF				298
		+ EN + + EIMRWL+ QP+SSVFLCFGSMG+F E+QV +IA A+ERSG RF				
Sbjct	242	LNL---ENKKDDAKTDEIMRWLNEQPSSSVFLCFGSMGSFNEKQVKEIAVAIERSGHRF				298
Query	299	LWSLRKPIFEGGFAYPTEYENPGEVLPVGFLERTAGVGKIVGWAPQVAVLSHPSVGGFVS				358
		LWSLR+P + +P EYEN EVLP GFL+RT+ +GKIVGWAPQ+AVLSHPSVGGFVS				
Sbjct	299	LWSLRRTPKKEIEFPKEYENLEEVLPPEGFLKRTSSIGKIVGWAPQMAVLSHPSVGGFVS				358

Score	Expect	Method	Identities	Positives	Gaps	Frame
390 bits(1001)	5e-131()	Compositional matrix adjust.	217/476(46%)	298/476(62%)	30/476(6%)	

Query	6	KASLVFIPFPVVSHLVTAVKTAELLASHDSRLSITVLVMSMPTDTKISSYIKN-----P	59
Sbjct	2	K+ L+F+P P + HL V + A+L S LS+TVL+ DT + +Y K+ P	61
Query	60	RINFVQL-EQDVSNGAEAIMKPPKSM-HFAGRHRDSARAVVSEMKRS--CRVAGIFVDI	115
Sbjct	62	R+ V L E D N ++KP ++ + R ++S M +S RV G+ D+ RLTIVNLPETDPQN---YMLKPRHAIFPSVIETQKTHVRDIISGMTQSESTRVVGLLADL	118
Query	116	MCVDMIDVAKELKISSYIFFASGAAVLGLTFDLQSLRDDGGRNLAEFEGSDEVVSISSYV	175
Sbjct	119	+ ++++D+A E + +Y++ +GA LGL F LQ+L +D +++ EF SD + + S+ LFINIMDIANEFNVPTYVYSPAGAGHLGLAFHLQTL-NDKKQDVFTEFRNSDTELLVPSFA	177
Query	176	NPVPARVWPESVFDGESGF---LELSRKAREADGIVINTFLELESYAIGSTYANERIPRF	232
Sbjct	178	NPVPA V P D E G+ L R+ RE+ I+INTF ELE YAI S + IP NPVPAEVLPSMYVDKEGGYDYLSLFRRCRESKAI IINTFEELEPYAINSLRMDSMIPPI	237
Query	233	YPIGPII---GEGKDENDSRQRGEIMRWLDGQPDSSVVFLCFGSMGAFGEEQVVDIAE	289
Sbjct	238	YP+GPI+ G+G++ ++ + I+ WLD QP SSVVFLCFGS G+F E QV +IA YPVGPI LNLNGDGQNSDEAAV-----ILGWLDDQPPSSVVFLCFGSYGFQENQVKEIAM	292
Query	290	ALERSGKRFLWSLRKPIFEGGFAYPTEYENPGEVLPGVFLERTAGVGKIVIGWAPQVAVLS	349
Sbjct	293	LERSG RFLWSLR I +G +Y N E+LPVGFL+RT+ VGKIVIGWAPQVAVL+ GLERSGHRFLWSLRPSIPKGETKLQLKYSNLKEILPGVFLDRTSCVGKIVIGWAPQVAVLA	352
Query	350	HPSVGGFVSHCGWNSTLESVCCGVPMAAWPLGAEQQTNAFQLVKDIGIAVEIKMDYR---	406
Sbjct	353	H +VGGFVSHCGWNS LESV + +A WP+ EQQ NAF++VK++G+AVEI++DYR HKAVGGFVSHCGWNSILESVMYDMSVATWPMYGEQQ LNAFEMVKELGLAVEIEVDYRNEY	412
Query	407	KNSGEIVPKSIIEKAIKQL---DPTNEIRVRVKELKEKSTRALMEGGSSYNHLGLL	460
Sbjct	413	+G IV IE IK+LM + +EIR +VKE+KEKS A+ E GSSY L L NKTGFI VRADEIETKIKKLMDEKNSEIRKKVKEMKEKSRVAMSENGSSYTSLAKL	468

RecName: Full=UDP-glycosyltransferase 100; Short=UGTPg100 [Panax ginseng]

Sequence ID: **A0A0K0PVW1.1** Length: 472 Number of Matches: 1

Range 1: 2 to 467

Score	Expect	Method	Identities	Positives	Gaps	Frame
385 bits(989) 3e-129() Compositional matrix adjust. 220/476(46%) 295/476(61%) 31/476(6%)						
Query	6	KASLVFIPFPVVSHLVTAVKTAELLASHDSRLSITVLVMSMPTDTKISSYIKN-----P			59	
Sbjct	2	K+ L+F+P P HL V+ A+L S LS+TVL+ DT I +Y K+ P			61	
Query	60	RINFVQLEQDVSNGAEAIMKPPKSM-HFAGRHRDSARAVVSEMKRS--CRVAGIFVDIM			116	
Sbjct	62	R+ + L + + + ++KP ++ + R V+S M +S RV G+ DI+ RLTIIINLPE---IDPQKYLKPRCAIFPSLIENQKTHVRDVMRMTQSESTRVVGLLADIL			119	
Query	117	CVDMIDVAKELKISSYIFFASGAAVLGLTFDLQSLRDDGGRNLAEFEGSDEVVSISSYVN			176	
Sbjct	120	VD+ D+A E + +Y++ +GA LGL F LQ+L DD +++ EF SD + + S+ N FVDIFDIADFNVPITYVYSPAGAGFLGLAFHLQTLNDDKKQDVFTEFRNSDTELLVPSFAN			179	
Query	177	PVPARVWPESVFDGESG---FLELSRKAREADGIVINTFLELESYAIGSTYANERIPRF			232	
Sbjct	180	PVPAEFLP-SIFLEKDGHRHDVLLSLYWRCREAGKITVNTFEELEPYAINSLRMDSMIPPI			238	
Query	233	YPIGPII---GEGKDENDSRQRGEIMRWLDGQPDSSVVFLCFGSMGAFGEEQVVDIAE			289	
Sbjct	239	YP+GPI+ GEG++ ++ + I+ WLD QP SSVVFLCFGS G+F E QV +IA YPVGPI LNLNGEGQNSDEAAV-----ILGWLDDQPPSSVVFLCFGSGFSPFENQVKEIAM			293	
Query	290	ALERSGKRFLWSLRKPIFEGGFAYPTEYENPGEVLPGVFLERTAGVGKIVIGWAPQVAVLS			349	
Sbjct	294	LERSG RFLWSLR I EG +Y N LP GFL+RT+ VGKIVIGWAPQ+A+L+ GLERSGHRFLWSLRPCISEGETTLQLKYSNLE--LPAGFLDRTSCVGKIVIGWAPQMAILA			351	
Query	350	HPSVGGFVSHCGWNSTLESVCCGVPMAAWPLGAEQQTNAFQLVKDIGIAVEIKMDYR---			406	
Sbjct	352	H +VGGFVSHCGWNS LESV G+P+A WP+ EQQ NAF++VK++G+AVEI++DYR HEAVGGFVSHCGWNSVLESVMYGPVATWPMYGEQQ LNAFEMVKELGLAVEIEVDYRNEY			411	
Query	407	KNSGEIVPKSIIEKAIKQL-MDPTN-EIRVRVKELKEKSTRALMEGGSSYNHLGLL			460	
Sbjct	412	S IV IE IK+L MD N +IR +VKE+KEKS A+ E GSSY L L NKSDFI VKADEIETKIKKLMMDGKNSKIRKKVKEMKEKSRVAMSENGSSYTSLAKL			467	

RecName: Full=UDP-glucosyltransferase 102; Short=UGTPg102 [Panax ginseng]

Sequence ID: **A0A0K0PVL0.1** Length: 475 Number of Matches: 1

Range 1: 2 to 470

Score	Expect	Method	Identities	Positives	Gaps	Frame
384 bits(987) 7e-129() Compositional matrix adjust. 214/478(45%) 294/478(61%) 32/478(6%)						
Query	6	KASLVFIPFPVVSHLVTAVKTAELLASHDSRLSITVLVMSMPTDTKISSYIKN-----P			59	
Sbjct	2	K+ L+F+P P + HL V + A+L S LS+TV + DT + +Y K+ P			61	
Query	60	RINFVQL-EQDVSNGAEAIMKPPKSM-HFAGRHRDSARAVVSEMKRS--CRVAGIFVDI			115	
Sbjct	62	R+ V L E D N ++KP +++ + R ++S M +S RV G+ D+ RLTIVNLPETDPQN---YMLKPRHAITLPSVIETQKTHVRDIISGMTQSESTRVVGLLADL			118	
Query	116	MCVDMIDVAKELKISSYIFFASGAAVLGLTFDLQSLRDDGGRNLAEFEGSDEVVSISSYV			175	
Sbjct	119	+ ++++D+A E + Y++ +GA LGL F LQ+L D +++ EF SD + + + LFINIMDIANEFNVPYIYVYSPAGAGYLGLAFHLQTYDKK-QDVFTEFRNSDTELLVPGFA			177	
Query	176	NPVPARVWPESVFDGESGF---LELSRKAREADGIVINTFLELESYAIGSTYANERIPRF			232	
Sbjct	178	NPVPA V P D E G+ L R+ RE+ I+INTF ELE YAI S + IP NPVPAEVLPSMYVDKEGGYDYLSLFRRCRESKAI IINTFEELEPYAINSLRMDSMIPPI			237	
Query	233	YPIGPII---GEGKDENDSRQRGEIMRWLDGQPDSSVVFLCFGSMGAFGEEQVVDIAE			289	
Sbjct	238	YP+GPI+ G+G++ ++ + I+ WLD QP SSVVFLCFGS G F E QV +IA YPVGPI LNLNGDGQNSDEAAV-----ILGWLDDQPPSSVVFLCFGSYGTGFQENQVKEIAM			292	
Query	290	ALERSGKRFLWSLRKPIFEGGFAYPTEYENPGEVLPGVFLERTAGVGKIVIGWAPQVAVLS			349	

Sbjct 293 LERSG RFLW+LR I +G +Y N E+LPVGFL+RT+ VGKVGWAPQVAVL 352
GLERSGHRFLWALRPSIPKGETKLQKYSNLEEILPVGFLDRTSCVGVKVTGWAPQVAVLG
Query 350 HPSVGGFVSHCGWNSTLESVCCGVPMAAWPLGAEQQTNAFQLVKDIGIAVEIKMDYRK-- 407
H +V GF+SHCGWNSTLESV GVP+A WP+ EQ NAF++VK++G+AVEI++DY+
Sbjct 353 HEAVAGFMHSHCGWNSTLESVWFGVPVATWPMYGEQHLNAFEMVKELGLAVEIEVDYKNEY 412
Query 408 ---NSGEIVPKSIIIEKAIKQLM---DPTNEIRVRVKELKEKSTRALMEGGSSYNHLGLL 460
+ IV IE IK+LM + +EIR +VKE+KEKS A+ E GSSYN L L
Sbjct 413 FNTKNDFIVRAEEIETKIKKLMDEKNSEIRKKVKEMKEKSRVAMSENGSSYNLAKL 470

Taxonomy

Reports

◦ Lineage

Organism	Blast Name	Score	Number of Hits	Description
Pentapetalae	eudicots		<u>10</u>	
.Rosaceae	eudicots		<u>4</u>	
..Fragaria x ananassa	eudicots	442	<u>2</u>	Fragaria x ananassa hits
..Malus domestica	eudicots	436	<u>1</u>	Malus domestica hits
..Pyrus communis	eudicots	426	<u>1</u>	Pyrus communis hits
.Stevia rebaudiana	eudicots	424	<u>1</u>	Stevia rebaudiana hits
.Panax ginseng	eudicots	402	<u>5</u>	Panax ginseng hits

◦ Organism

Description	Score	E value	Accession
Fragaria x ananassa (strawberry) [eudicots]			
RecName: Full=UDP-glucose flavonoid 3-O-glucosyltransferase 6; AltName: Full=Flavonol 3-O-glucosyltransferase 6; Short=FaGT6 [Fragaria x ananassa]	442	2e-151	Q2V6K0
RecName: Full=Putative UDP-glucose flavonoid 3-O-glucosyltransferase 3; Short=FaGT3; AltName: Full=Flavonol 3-O-glucosyltransferase 3 [Fragaria x ananassa]	431	7e-147	Q66PF3
Malus domestica (apple) [eudicots]			
RecName: Full=UDP-glycosyltransferase 71A15; AltName: Full=UDP-glucose:chalcone 2'-O-glucosyltransferase; AltName: Full=UDP-glucose:flavonol 2'-O-glucosyltransferase [Malus domestica]	436	5e-149	D3THI6
Pyrus communis (pear) [eudicots]			
RecName: Full=UDP-glycosyltransferase 71A16; AltName: Full=UDP-glucose:chalcone 2'-O-glucosyltransferase; AltName: Full=UDP-glucose:flavonol 2'-O-glucosyltransferase [Pyrus communis]	426	5e-145	D3UAG1
Stevia rebaudiana [eudicots]			
RecName: Full=UDP-glycosyltransferase 71E1 [Stevia rebaudiana]	424	2e-144	Q6VAB2
Panax ginseng [eudicots]			
RecName: Full=UDP-glycosyltransferase 101; Short=UGTPg101 [Panax ginseng]	402	7e-136	A0A0K0PVM5
RecName: Full=UDP-glycosyltransferase 1; Short=UGTPg1 [Panax ginseng]	402	7e-136	A0A068J840
RecName: Full=UDP-glycosyltransferase 71A27; Short=PgUGT71A27 [Panax ginseng]	390	5e-131	A0A0A7HB61
RecName: Full=UDP-glycosyltransferase 100; Short=UGTPg100 [Panax ginseng]	385	3e-129	A0A0K0PVW1
RecName: Full=UDP-glucosyltransferase 102; Short=UGTPg102 [Panax ginseng]	384	7e-129	A0A0K0PVL0

◦ Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
Pentapetalae	<u>10</u>	5	
.Rosaceae	<u>4</u>	3	
..Fragaria x ananassa	<u>2</u>	1	Fragaria x ananassa hits
..Maleae	<u>2</u>	2	
...Malus domestica	<u>1</u>	1	Malus domestica hits
...Pyrus communis	<u>1</u>	1	Pyrus communis hits
.campanulids	<u>6</u>	2	
..Stevia rebaudiana	<u>1</u>	1	Stevia rebaudiana hits
..Panax ginseng	<u>5</u>	1	Panax ginseng hits