

tBLASTn | Query = NP_001089379 (protein) | Subject = LOC108705441 (mRNA)

Range 1: 112 to 624

	Score	Expect	Method	Identities	Positives	Gaps	Frame
	296 bits(759)	0.0(4)	Compositional matrix adjust.		149/176(85%)	157/176(89%)	5/176(2%) +1
Query	2			TLSKEVEYQTPQKQVSSTGLYPSTKDVEFSASLEQMNGEIFQSVEPPRRSTGRLIMHSMA			61
				TLSKEVEYQT Q QVSST LYPSTK+VEFSASLEQ NG+IF SVEPPRRS GRLIM			
Sbjct	112			TLSKEVEYQTSQNQVSSTRLYPSTKEVEFSASLEQSNKIF *SVEPPRRSMGRLIM----			279
Query	62			MFGREFCYAVEAAYVTPVLLSVGLPKSLYSLVWLISPIILGFILQPVVGASDHCERSRWGR			121
				FGREF YA+EAAYVTPVLLS+GL KSLYSLVWLISPIILGFILQPVVGASDHCERS WGR			
Sbjct	280			-FGRFYYAMEAAYVTPVLLSLGLTKSLYSLVWLISPIILGFILQPVVGASDHCERS *WGR			456
Query	122			RRPYILCLGIIMVLGMTLYLNGDTAVTAVLGTSAEKTWAIWITMLGVVAFDFAAD			177
				R PYILCLGII+VLGMT YLNGDTAV+AVLG+SAEK TWAIW+T LGVVAFDFA D			
Sbjct	457			RSPYILCLGIIVVLGMTFYLNGDTAVSAVLGSSAEKRTWAIWVTKLGVVAFDFAVD			624

Range 2: 620 to 1318

	Score	Expect	Method	Identities	Positives	Gaps	Frame
	359 bits(922)	0.0(4)	Compositional matrix adjust.		199/234(85%)	211/234(90%)	1/234(0%) +2
Query	178			FIDGPIKAYLFDVCSHHDKERGLHYHAlftgllggalgyltgaMDWGSTFLGRIMGSEFQV			237
				+IDGPIKAYLFDVCSHH KERGLHYH LFTGLGG LGYLTGAMDWGSTFLGRI GSEFQV			
Sbjct	620			WIDGPIKAYLFDVCSHHYKERGLHYHVLFTGLGGVLYLTGAMDWGSTFLGRIRGSEFQV			799
Query	238			MFFFASAVFLILLVVHLCSPEIPIADEKQESQMLLKHDHLGAYGSIDKTQNGILKTKTT			297
				MFFFAS+VFL+LLVVHLCSPEI +AD+KQE QMLLK D LGAYGSID TQNGI TKTT			
Sbjct	800			MFFFASSVFLLLLVLVHLCSPEITLADDKQERQMLLKQDQLGAYGSIDNTQNGI *-TKTT			976
Query	298			RSLSQVEENDSSDREEQVQKRMVKS LINALLTMPAHYRYLCISHLIGWTAFLSNMLFFT			357
				RSLSQ +EN+ R+ QVQKRM+VKSL ALLTMPAHYRYLC+SH I WT FLSNMLFFT			
Sbjct	977			RSLSQTKENPLSRKPQVQKRMVKS LTTALLTMPAHYRYLC LSHFIRWTVFLSNMLFFT			1156
Query	358			DFMQQIVYHGPNPYAEHNSTAHLIYERGVEVGCWGMCAINAISSALYSYLQKALLP			411
				DF+GQIVYHGPNPYAEHNSTA+ IYERGVEVGCW MCINAISSALYSYLQKALLP			
Sbjct	1157			DFIQQIVYHGPNPYAEHNSTAYHIYERGVEVGCWVMCAINAISSALYSYLQKALLP			1318

Range 3: 1393 to 1578

	Score	Expect	Method	Identities	Positives	Gaps	Frame
	100 bits(250)	0.0(4)	Compositional matrix adjust.		53/69(77%)	53/69(76%)	7/69(10%) +1
Query	437			PNVYSTLVLCSLFGVMSSTLYTVPFNLISEYHREEEQMKQPNGKTPSPDNRGKIDCAA			496
				PNV STLVLC SFGVMSSTLYTVPFNLISEYHREEE D RKGKIDCAA			
Sbjct	1393			PNV *STLVLC SFFGVMSSTLYTVPFNLISEYHREEEVSF -----AFVDYRGKIDCAA			1551
Query	497			LTCMVQLAQ 505			
				LTCMVQLAQ			
Sbjct	1552			LTCMVQLAQ 1578			

Range 4: 1658 to 1690

	Score	Expect	Method	Identities	Positives	Gaps	Frame
	25.4 bits(54)	0.0(4)	Compositional matrix adjust.		10/11(91%)	11/11(100%)	0/11(0%) +2
Query	538			CFVALFVRYVE 548			
				CFVA+FVRYVE			
Sbjct	1658			CFVAVFVRYVE 1690			