

TBLASTN results of identity of CjNRSV1 L protein (RdRP) to partial fragments of Wardell virus encoded L protein.

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Percent identity

Wardell virus RNA-dependent RNA polymerase (QK845_sLgp1) gene, partial cds

Sequence ID: [NC_079018.1](#) Length: 4338 Number of Matches: 7

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Range 1: 2648 to 2947 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
207 bits(528)	0.0	Compositional matrix adjust.	99/100(99%)	99/100(99%)	0/100(0%)	+2
Query 1117	LEFMNKALSLWPRKRLSFPLKQASSLSANMKLKTSNDTYMKFKEEFEAGTGMFVRPRSNL	1176	LEFMNKALSLWPRKRLSFPLKQASSLSANMKLKTSNDTYMKFKEEFE GTGMFVRPRSNL			
Sbjct 2648	LEFMNKALSLWPRKRLSFPLKQASSLSANMKLKTSNDTYMKFKEEFETGTGMFVRPRSNL	2827				
Query 1177	IEVISGMFQGILHTTSSLYHTMIQEVMMQVMLTACKGRLG	1216	IEVISGMFQGILHTTSSLYHTMIQEVMMQVMLTACKGRLG			
Sbjct 2828	IEVISGMFQGILHTTSSLYHTMIQEVMMQVMLTACKGRLG	2947				

Range 2: 2292 to 2567 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
194 bits(492)	0.0	Compositional matrix adjust.	88/92(96%)	91/92(98%)	0/92(0%)	+3
Query 994	HISQLAPWCLKSLLEKGYFDSQFDKSQHGGEREIHVLEFKARIVQYFVELIARTICSYF	1053	HISQLAPWCLKSLL KGYFDSQFDKSQHGGEREIHVLEFKARIVQ+FVEL+ARTICSYF			
Sbjct 2292	HISQLAPWCLKSLLSKGYFDSQFDKSQHGGEREIHVLEFKARIVQFFVELVARTICSYF	2471				
Query 1054	PSETTINPDTKDNFVKDHYAKSREMFGDNFTT	1085	PSETTINPDTKDNFVKDHYAKS+EMFGDNFTT			
Sbjct 2472	PSETTINPDTKDNFVKDHYAKSKEMFGDNFTT	2567				

Range 3: 724 to 1074 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
228 bits(582)	4e-56	Compositional matrix adjust.	107/117(91%)	114/117(97%)	0/117(0%)	+1
Query 495	KRQMOTKLELSEDDKVELALSGLGGKKYKDEELIRDHKERSKLSFHPHTNTDDIEDFCKR	554	KRQMOTKLELSEDDKVELALSG+GGKKYK+E LI++H+ERSKLSFHPHTNT+DIEDFCKR			
Sbjct 724	KRQMOTKLELSEDDKVELALSGVGGKKYKNEALIQEHRERSKLSFHPHTNTDIEDFCKR	903				
Query 555	NLLVKDDALPDTVPYLLKTAVRMSKISISCEPNTNYSVDAWESLLKTDFMQYSMLMTR	611	NLLVKDD LPDTVPYLLK AVRMSKISISCEPNTNYSVDAWESLL+TDFMQYSMLMTR			
Sbjct 904	NLLVKDDVLPDTVPYLLKAAVRMSKISISCEPNTNYSVDAWESLLRTDFMQYSMLMTR	1074				

Range 4: 30 to 326 [GenBank](#) [Graphics](#)

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Score	Expect	Method	Identities	Positives	Gaps	Frame
210 bits(535)	2e-50	Composition-based stats.	90/99(91%)	96/99(96%)	0/99(0%)	+3
Query 1	MECGHSFVDGRCGLYCDDFVLNTRGICYLYAFYAEERASVFKDLKEYPEVSAFNLYYNKH					60
Sbjct 30	MECGHSF+DGRCGL+CDDFVLNTRGICYLYAFY EERASV+KDLKEYPEVSAFNLYYN+H					209
Query 61	KLTSRASVIPPSEPGGYLHIQSESIAGQKPTVAHLGECT			99		
Sbjct 210	KLTSRASVIPP+E GG+LHIQSESIAGQKPTV HLGECT			326		

Range 5: 4139 to 4336 [GenBank](#) [Graphics](#)

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Score	Expect	Method	Identities	Positives	Gaps	Frame
127 bits(319)	4e-25	Compositional matrix adjust.	59/66(89%)	65/66(98%)	0/66(0%)	+2
Query	2230	EIRINIVNIQNMESSPRGISKRLRLNIIYKDREEEIINRTDPHTDLIMLNSDILLNQ				2289
Sbjct	4139	EIRINIVNIQNMES+SP+GIS+RLLRLNIIYKDREEEIINRTDPHT+DLIMLNSD+LL Q				4318
Query	2290	MMSGFI 2295				
Sbjct	4319	MISGFI 4336				

Range 6: 3269 to 3727 [GenBank](#) [Graphics](#)

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Score	Expect	Method	Identities	Positives	Gaps	Frame
292 bits(748)	6e-76	Compositional matrix adjust.	135/153(88%)	147/153(96%)	0/153(0%)	+2
Query	1524	FTVMGDEETEDLEFGTDEGLITKKVPAKHTLLYIMSKHAKLIRESKKDWGNKEILFPYH				1583
Sbjct	3269	FTVMGDEETDDIEFGTDDGKLVKKVPAKHTLLYIMSKHAAAIAKNTKDWNNKENLFPYH				3448
Query	1584	QEYEKISSDIIVNLKNGVLDQYVVKRTSKVKITVIPKASGDVDVIDMCKRHWFDKGVPSL				1643
Sbjct	3449	QEYEKISSDI+NLK+NGV+LDQYVVKRTSKVKITVIPKASGDVDVIDMCKRHWFDKGVPSL				3628
Query	1644	SRGQFKLRWKELTSKFTFIDSSKGTGEGILATAR	1676			
Sbjct	3629	SRGQFKLRWKELT+KF+FIDSSKGTGEGILATAR	3727			

Range 7: 1202 to 2233 [GenBank](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#) [▲ First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
626 bits(1614)	0.0	Compositional matrix adjust.	297/344(86%)	315/344(91%)	0/344(0%)	+2
Query	635	GNGIYALVYNPKSAIFVSFAFPRSGAKIWDGKLGPKCYFSRTHVFTDWASFDSSQLEHF				694
Sbjct	1202	GNGIYALVYNPKSAIFVSFAFPRSGAK+WD+GKLGPKCYFSRTHVFTDW+S+DSSQLEHF				1381
Query	695	IKFGPYMGSLVELLNASESSMEHFSRYAIECVPHLLLLYCINNKTDEELVTSQRYLFMK				754
Sbjct	1382	IKFGPYMGSLVELLNASES+MEHFS+YAIECVPHLLLLYCINNKTDEVE				1561
Query	755	LLEDVGKSPYVFDRLPKVMRSRLTVFYLLKTIEMINYYDSNSITKVPKQGEDMIIYDYM				814
Sbjct	1562	XXXXXXXXXXPLDLRLPKVMRSRLTVFYLLKTIEMINYYEQNSITKVPKQGEDMIIYDYM				1741
Query	815	NIKSLFSREFISLNCKVNEFYFGYVVSKEKNTGDKTKFKVLTCLIKQEQKFRSKVKSIF				874
Sbjct	1742	NIKSLFSREFISLNCK+NEFYFGYVVSKEKNTGDKTKFKVLTCLIKQEQKFRSKV GSIF				1921
Query	875	TGDEYEEFKTNLSLMKFFSTAFKDLLVEKFGPDFREKIFDDFTHAAARTNFSDLATLKV				934
Sbjct	1922	TGDEYEEFKTNLSLMKFFSTAF DLL+EKFGP+F+EKIFDDFT+ AARTNFSDLATLKV				2101
Query	935	SSRDHSKEVEVPIGDESTEQVFERLKKDFPEEMMKRPFCMESMT	978			
Sbjct	2102	SSRDHSKEVE+P+GDESTEQVFERLKKDFPEEMMKRPFCMESMT	2233			

TBLASTN results of identity of CjNRSV1 M protein to partial fragments of Wardel virus encoded M protein.

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Percent identity

Wardell virus hypothetical protein-like (ORF1) gene, partial sequence

Sequence ID: [NC_079019.1](#) Length: 1246 Number of Matches: 2

Range 1: 10 to 360 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
240 bits(612)	2e-68	Compositional matrix adjust.	115/117(98%)	117/117(100%)	0/117(0%)	+1
Query 250	EDKQVLKFSKSIKGDGIEPDMSRDLFSVPKPTEIETMADHLNNHKSGDIFPYVSVVGNEE					309
	ED+QVLKFSKSIKGDGIEPDMSRDLFSVPKPTEIETMADHLNNHKSGDIFPYVSVVGNEE					
Sbjct 10	EDEQVLKFSKSIKGDGIEPDMSRDLFSVPKPTEIETMADHLNNHKSGDIFPYVSVVGNEE					189
Query 310	ETKDGRLSRLRAFRSAYGKENPEMRINGVILDELEGTIMVKHIGEYVNOQDRLSKSQ					366
	ETKDGRLSRLRAFRSAYGKEN+PEMRINGVILDELEGTIMVKHIGEYVNOQDRLSKSQ					
Sbjct 190	ETKDGRLSRLRAFRSAYGKENPEMRINGVILDELEGTIMVKHIGEYVNOQDRLSKSQ					360

Range 2: 750 to 1235 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
311 bits(798)	1e-95	Compositional matrix adjust.	154/162(95%)	157/162(96%)	1/162(0%)	+3
Query 532	AGDVMDIDEAKRERTKMNSYSKSTIRGATKGEAGPSHLGNQSGWEHLKGMIPRIDEGLA					591
	AGDVMDIDEAKRERTKMNSYSKSTIRGATKGEAGPSHLGNQSGWEHLKGMIPRIDEGLA					
Sbjct 750	AGDVMDIDEAKRERTKMNSYSKSTIRGATKGEAGPSHLGNQSGWEHLKGMIPRIDEGLA					929
Query 592	SVSAASDPDEDDIDVPITTREEYE-RQQEKMLQFQSPSLOTTEEISDSDIQRSSSPAMG					650
	SVSA SDPDEDDIDVPITTREEYE QEKMLQFQSPSLOTTEEISDS+QRSSSP +G					
Sbjct 930	SVSAVSDPDEDDIDVPITTREEYEXXQEKMLQFQSPSLOTTEEISDSLQRSSSPIVG					1109
Query 651	DQMPSIEQVTPRPAIKSAMKKPRFSDEGLKKPSTEDVYRFD					692
	DQMPSIEQVTPRPAIKSAMKKPRFSDEGLKKPST+DVYRFD					
Sbjct 1110	DQMPSIEQVTPRPAIKSAMKKPRFSDEGLKKPSTDDVYRFD					1235