

BLASTP

Query: Vat, PI 161376 melon variety

Subject: MEL03C004317 gene, DHL92 melon variety

> MEL03C004317

Length=1044

Score = 1933 bits (5008), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 951/1026 (93%), Positives = 978/1026 (96%), Gaps = 2/1026 (0%)

Query	1	MDILISVTAKIAEYTVPEVGRQLGYVFFIRS NFQKLKTQVEKLKITRESVQHKIHSARRN	60
		MDILISV AKIAEYTVPEVGRQLGYVFFIRS NFQKLKTQVEKLKITRESVQHKIHSARRN	
Sbjct	1	MDILISVIAKIAEYTVPEVGRQLGYVFFIRS NFQKLKTQVEKLKITRESVQHKIHSARRN	60
Query	61	AEDIKPAVEEWLKKVDDFVRESDEILANEGGHGGLCSTYLVRHKL SRKASKMVDEVLEM	120
		AEDIKPAVEEWLKKVDDFVRESDEILANEGGHGGLCSTY VRHKL SRKASKMVDEVLEM	
Sbjct	61	AEDIKPAVEEWLKKVDDFVRESDEILANEGGHGGLCSTYFVRHKL SRKASKMVDEVLEM	120
Query	121	KNEGESFDMVSYKSVIPSVDCSLPKVPDFLDFESRKSIMEQIMDALSDGNVHRIGVYGMG	180
		KNEGESFDMVSYKSVIPSVDCSLPKVPDFLDFESRKSIMEQIMDALSDGNVHRIGVYGMG	
Sbjct	121	KNEGESFDMVSYKSVIPSVDCSLPKVPDFLDFESRKSIMEQIMDALSDGNVHRIGVYGMG	180
Query	181	GVGKTMVLVKDILRKIVESKKPFDEVVTSTISQTPDFRSIQGLADKLGLKFEQETIEGRA	240
		GVGKTMVLVKDILRKIVESKKPFDEVVTSTISQTPDFRSIQGLAD LGLK EQETIEGRA	
Sbjct	181	GVGKTMVLVKDILRKIVESKKPFDEVVTSTISQTPDFRSIQGLADTLGLKLEQETIEGRA	240
Query	241	TILRKRLKMERSILVVLDDVWEYIDLETIGIPSVEDHTGCKILFTTRIKHLISNQMCANK	300
		ILRKRLKMERSILVVLDDVWE IDLETIGIPSVEDHTGCKILFTTR KHLISNQMCANK	
Sbjct	241	PILRKRLKMERSILVVLDDVWENIDLETIGIPSVEDHTGCKILFTTRNKHLISNQMCANK	300
Query	301	IFEIKVLGKDESWNLFKAMAGDIVDASDLKPIAIRIVRECAGLP IAITTVAKALRNKPSD	360
		IFEIKVLG+DESWNLFK MAG+ V+ASDLKPIAI+I RECAGLP IAITTVAKALRNKPSD	
Sbjct	301	IFEIKVLGEDESWNLFKTMAGETVEASDLKPIAIQIARECAGLP IAITTVAKALRNKPSD	360
Query	361	IWN DALDQLKTVDVGMANIGEMEKKVYLSLKLSDCLGYEEVKLLFLLCSMFPEDFSIDV	420
		IWN DAL+QLK+VDVGMANIGEME+KVYL LKLSYDCLGYEEVKLLFLLCSMFPEDF IDV	
Sbjct	361	IWN DALNQLKSVDVGMANIGEMERKVYLPKLSDCLGYEEVKLLFLLCSMFPEDFPIDV	420
Query	421	EGLHVIYAMGMGFLHGVDTVVKGRRRIKKLVDDLISSSLLQQYSEYGCNYVKMHDMVRDVA	480
		E LHVYAMGMGFLHGVDTV KGR RIKKLVDDLISSSLLQQYSEYGCNYVKMHDMVRDVA	
Sbjct	421	EELHVIYAMGMGFLHGVDTVKEGRCRIKKLVDDLISSSLLQQYSEYGCNYVKMHDMVRDVA	480
Query	481	LLIASKNEHVRTL SYVKRSNEEWEEKLLGNHTAVFIDGLHYPLPKLTLPKVQLLRLVAK	540
		LLIAS+N+H+R LSYVK NEEW+E++L GNHT V IDGLHYPLPKLT PKVQLLRLVA+	
Sbjct	481	LLIASQN DHIRILSYVKS LNEEWKEDRLSGNHTTVSIDGLHYPLPKLTFPKVQLLRLVAQ	540
Query	541	YCWEHNKRVS VVETFF EEMKELKGSIDWIGELKKLEILDFSES NITQIPTTMSQLTQLKV	600
		WEHN+ VSVVETFF EEMKELKGSIDWIGELKKLEILDF SNI+QIPTTMSQLTQLKV	
Sbjct	541	SWWEHNE SVSVVETFF EEMKELKGSIDWIGELKKLEILDFRGSNISQIPTTMSQLTQLKV	600
Query	601	LNLSSCEQLEVIPP NILSKLTKLEELDLETFDGWEGEWEYEGRKNASLSELKCLRHL YAL	660
		LNL S CEQLEVIPP NILSKLTKLEEL+LETFDGWEGEWEYEGRKNASLSELKCLRHL YAL	
Sbjct	601	LNL SFCEQLEVIPP NILSKLTKLEELNLETFDGWEGEWEYEGRKNASLSELKCLRHL YAL	660
Query	661	NLTIQDEEIMPENLFLVGK LKLQKFNICIGCESKLKYTFAY--KNRIKNFIGIKMESGRG	718
		NLTIQDEEIMPENLFLVGK LKLQKFNI IGC+SKLKYTFAY KNRIKNFIGIKMESGRG	
Sbjct	661	NLTIQDEEIMPENLFLVGK LKLQKFNIRIGCQSKLKYTFAYQNKNRIKNFIGIKMESGRG	720
Query	719	LDDWIKNLLKRSDNVLL EGSVC SKVLHSELVGANNFVIEKEKSAHNMLESKQWETSSSS	778
		LDDWIKNLLKRSDNVLL EGSVC SKVLHSELVGANNFVIEKEKSA HNMLESKQWETSSSS	

Sbjct	721	LDDWIKNLLKRSNDNVLLGSGVCSKVLHSELVGANNFVIEKEKSADHNMLESKQWETSSSS	780
Query	779	KDGVLRRLGDGSKLFPNLKSLKLYGFVDYNSTHLPMEMLQILFQLVVFELEGAFLEEIFPS	838
Sbjct	781	KDGVLRRLGDGSKLFPNLKSLKLYGFVDYNSTHLPMEMLQILFQL VFELEGAF+EEIFPS	840
Query	839	NILIPSYMVLRRRLALSCLPKLKLHLWSEECNQNNITSVLQHLISLRISCGRLSSLSSIV	898
Sbjct	841	NILISSMDLQSLILSKLPKLKLHLWSEECNQNNITSVLQHL SL IS+CGRLSSL+SS+V	900
Query	899	CFTNLKHLRVYKCDGLTHLLNPSVATTLVQLESLTIEECKRMSSVIEGGSTEEDGNDEM	958
Sbjct	901	CFTNL+HL V KC LTHLLNPSVATTLVQLE LT+EECKRMSSVIE GSTEEDGNDEM	960
Query	959	VFSLGIVSTPRLKYENFSLKNDYDDERCHPKYPKDMLVEDMNVITREYWEDNVDTGIPNL	1018
Sbjct	961	VFSLGIVSTPRLKYENF LK DYDDERCHPKYPK+MLVEDMNV+TREYWEDNVDTGIPNL	1020
Query	1019	FAEQSLEENRSENSSSSKNNVEKE	1042
Sbjct	1021	FAEQSLEENRSENSSSSKNNVEKE	1044