Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BVXPKJ014

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Blast report description

Nucleotide Sequence (467 letters)

RID <u>B8BVXPKJ014</u> (Expires on 02-06 12:13 pm)

Query ID lcl|Query_163280

Description None

Molecule type nucleic acid

Query Length 467

Database Name nr

Description All non-redundant GenBank CDS

 $translations + PDB + SwissProt + PIR + PRF\ excluding$

environmental samples from WGS projects

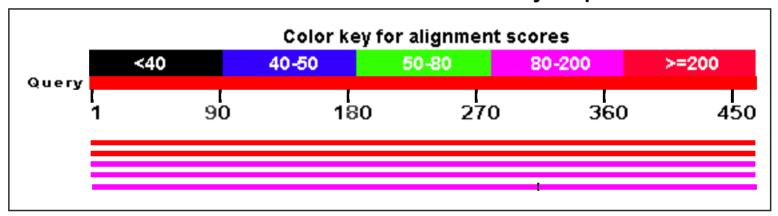
Program BLASTX 2.3.1+

□ Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 16 Blast Hits on the Query Sequence



□ <u>Descriptions</u>

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
gag protein [Drosophila melanogaster]	211	691	99%	6e-60	77%	AAT12844.1
putative single-stranded nucleic acid binding protein [Drosophila melanogaster]	207	688	99%	8e-59	75%	AAC46493.1
gag protein [Drosophila melanogaster]	192	470	99%	1e-53	70%	CAD92792.1
gag protein [Drosophila melanogaster]	192	470	99%	1e-53	70%	AAS68533.1
GH13568p [Drosophila melanogaster]	155	264	99%	4e-44	71%	ABN49245.1

□ <u>Alignments</u>

gag protein [Drosophila melanogaster]

Sequence ID: **gb|AAT12844.1|** Length: 1047 Number of Matches: 4 Range 1: 208 to 365

Score		Expect Method	Identities	Positives	Gaps	Frame
211 bits(5	536)	6e-60() Compositional matrix adjust.	121/158(77%)	130/158(82%)	3/158(1%)	-2
Features:						
Query	466	ASKTAKIISTQTHLGETKPIQPAKDPS ASKTAKIISTO HL ETKP OPAKDPS				
Sbjct	208	ASKTAKIISTQLHLRETKPTQPAKDPS				
Query	286	INSPTQYNDTNATKASKTAKI-ISTQT INSPTQYNDTNAT A KTAKI S+ +			NKAAETLTH +++A T TH	
Sbjct	268	INSPTQYNDTNATNALKTAKINFSSHS				-
Query	109	DKLIASQNLVPAKTHINSPTQYNDT DK ASONL AKTHINSPTO+NDT		2		
Sbjct	328	DK ASONL AKTHINSPIQHNDI DKHKNTASONLFSAKTHINSPIQHNDI		365		

Range 2: 140 to 288

Frame
-2
H 287
193
107
253
H 28 H 19 D 10

Range 3: 282 to 439

Score		Expect Method	Identities	Positives	Gaps	Frame
166 bits	(421)	4e-44() Compositional matrix adjust.	103/158(65%)	118/158(74%)	4/158(2%)	-2
Features	s:					
Query	466	ASKTAKI-ISTOTHLGETKPIQPAKDE			~	
Sbjct	282	A KTAKI S+ +H E KP Q AK+ ALKTAKINFSSHSHQSEIKPTQSAKNI			ASQNL NTASQNLFS	
Query	295	KTHINSPTQYNDTNATKASKTAKII-S KTHINSPTO+NDT+A ASKTAK+I S			PIANKAAET I + AA+T	
Sbjct	342	KTHINSPTQHNDTSAATASKTAKLILS				
Query	118	THTDKLIASQNLVPAKTHINSPTQYND THT+K ASON +PAKTHIN PTOYND		5		
Sbjct	402	THTNKHTASQNFIPAKTHINIPTQYND		439		

Score		Expect Method	Identities	Positives	Gaps	Frame			
122 bits	(307)	1e-28() Compositional matrix adjust.	78/135(58%)	95/135(70%)	2/135(1%)	-2			
Features:									
Query	466	ASKTAKII-STQTHLGETKPIQPAKDP ASKTAK+I S +HL ETKP OPA P							
Sbjct	359	ASKTAKLILSPHSHLSETKPTQPALSP	~		~				
Query	289	HINSPTQYNDTNATKASKTAKIIS-TQ' HIN PTQYNDTNATKA KTAK S + '				ГН 113 Г+			
Sbjct	419	HINIPTQYNDTNATKALKTAKAASPSH							
Query	112	TDKLIASQNLVPAKT 68 TDK A+ON+ P KT							
Sbjct	479	TDKPTATÕNIFPVKT 493							

putative single-stranded nucleic acid binding protein [Drosophila melanogaster]

Sequence ID: **gb|AAC46493.1|** Length: 1043 Number of Matches: 4 Range 1: 208 to 365

Score		Expect Method	Identities	Positives	Gaps	Frame
207 bits	(528)	8e-59() Compositional matrix adjust.	119/158(75%)	130/158(82%)	3/158(1%)	-2
Features	s:					
Query	466	ASKTAKIISTQTHLGETKPIQPAKDPS ASKTAKIISTOTHLGETKPIQPAKDPS				
Sbjct	208	ASKTAKIISIQIILGEIKFIQFAKDFS				
Query	286	INSPTQYNDTNATKASKTAKI-ISTQT IN+PTQYNDTNAT A KTAKI S+ +			NKAAETLTH +++A T TH	
Sbjct	268	INTPTÖYNDTNATNALKTAKINFSSHS				
Query	109	DKLIASQNLVPAKTHINSPTQYNDT DK ASONL AKTHINSPTO+N T		2		
Sbjct	328	DKHKNTASQNLFSAKTHINSPTQHNYT		365		

Range 2: 140 to 288

Score		Expect Method	Identities	Positives	Gaps	Frame
196 bits	(498)	1e-54() Compositional matrix adjust.	110/156(71%)	127/156(81%)	8/156(5%)	-2
Features	s:					
Query	466	ASKTAKIIS-TQTHLGETKPIQPAKDP A+KTA+II T TH+ TKP P+K+				
Sbjct	140	AAKTARIIFPTHTHIKPTKPSPPSKEL		A +TL++TDK+ ALKTLSYTDKIT	+Q +P K GTQKNLPDK	_
Query	289	HINSPTQYNDTNATKASKTAKIISTQT H+++PTO +D NATKASKTAKIISTOT				
Sbjct	193	HVDTPTQDDDINATKASKTAKIISTQT				
Query	109	DKLIASQNLVPAKTHINSPTQYNDTNA DKL ASONLVPAKTHIN+PTOYNDTNA		2		
Sbjct	253	DKLTASQNLVPAKTHINTPTQYNDTNA		288		

Range 3: 282 to 439

Score		Expect Metho	od		Identities	Positives	Gaps	Frame
163 bits(4	413) 4	1e-43() Comp	ositional matrix ad	just. 1	102/158(65%)	117/158(74%)	4/158(2%)	-2
Features:								
Query	466						~	
Sbjct	282			•				
Query	295							
Sbjct	342							
Query	118					5		
Sbjct	402					439		

Range 4: 359 to 493

Score		Expect	Method	Identities	Positives	Gaps	Frame
120 bits	(300)	7e-28()	Compositional matrix adjust.	81/144(56%)	97/144(67%)	20/144(13%)	-2
Feature	s:						
Query	466		AKII-STQTHLGETKPIQPAKDP AK+I S +HL ETKP OPA P				
Sbjct	359		AKLILSPHSHLSETKPTQPALSP				
Query	289	HINSI	PTQYNDTNATKASKTAKIIS-TQ	THLGETKPIQ-	PAKD	PSPRTQKPI	A 140

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HIN PTQYNDTNATKA KTAK S + T+ +TKPI+ PA+D PSP
Sbjct 419 HINIPTQYNDTNATKALKTAKAASPSHTYSRQTKPIKSAINALHPAQDTNPSP----- 471

Query 139 NKAAETLTHTDKLIASQNLVPAKT 68
A +T+TDK A+QN+ P KT
Sbjct 472 --AISAVTYTDKPTATQNIFPVKT 493
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gag protein [Drosophila melanogaster]

Sequence ID: emb|CAD92792.1| Length: 970 Number of Matches: 3

Range 1: 208 to 362

Score		Expect Method	Identities	Positives	Gaps	Frame
192 bits	(489)	1e-53() Compositional matrix adjust.	109/155(70%)	123/155(79%)	1/155(0%)	-2
Features	s:					
Query	466	ASKTAKIISTQTHLGETKPIQPAKDPS			~	
Sbjct	208	ASKTA+I S+ + L ETKP QPAK+PS ASKTAQIDSSHSQLHETKPTQPAKNPS			SQNL P KT SQNLFPTKT	
Query	286	INSPTQYNDTNATKASKTAKI-ISTQT				
Sbjct	268	INSPTQYNDTNASTASKDGKINLSSH				
Query	109	DKLIASQNLVPAKTHINSPTQYNDTNA +K ASQN +PAKTHIN PTQYNDTNA				
Sbjct	328	NKHTASQNFIPAKTHINIPTQYNDTNA		62		

Range 2: 140 to 288

Score		Expect Method	Identities	Positives	Gaps	Frame
153 bits	(387)	1e-39() Compositional matrix adjust.	94/155(61%)	116/155(74%)	6/155(3%)	-2
Features	s:					
Query	466	ASKTAKIISTQTHLGETKPIQPAKDPS				
Sbjct	140	A+KTA+II TH I+PAK PS AAKTARII-FPTHTQIEPAK-PS			~	
Query	286	INSPTQYNDTNATKASKTAKIISTQTH +++PTQ +DTNATKASKTA+I S+ +			IKAAETLTHI IK A+T THI	
Sbjct	194	VDTPTQDDDTNATKASKTAQIDSSHSQ				
Query	106	KLIASQNLVPAKTHINSPTQYNDTNAT K ASONL P KTHINSPTOYNDTNA+				
Sbjct	254	KPTASQNLFPTKTHINSPTQYNDTNAS		88		

Range 3: 282 to 417

Score		Expect M	lethod		Identities	Positives	Gaps	Frame
123 bits	(309)	5e-29() Co	ompositional m	atrix adjust.	78/136(57%)	96/136(70%)	2/136(1%)	-2
Features	s:							
Query	466		-ISTQTHLGET +S+ +HL ET				ASONLVPAR ASON +PAR	
Sbjct	282		NLSSHSHLRET					
Query	289		YNDTNATKASK YNDTNATKA K				ANKAAETLT + A +T	
Sbjct	342		YNDTNATKALK YNDTNATKALK					
Query	112		GONLVPAKTH -ON+ PAKT	65				
Sbjct	402		QNIFPAKTF	417				

gag protein [Drosophila melanogaster]

Sequence ID: gb|AAS68533.1| Length: 970 Number of Matches: 3

Range 1: 208 to 362

Score	Expect	Method	Identities	Positives	Gaps	Frame
192 bits(489)	1e-53()	Compositional matrix adjust.	109/155(70%)	123/155(79%)	1/155(0%)	-2
Features:						
Query 466		AKIISTQTHLGETKPIQPAKDPS				
Sbjct 208		A+I S+ + L ETKP QPAK+PS AQIDSSHSQLHETKPTQPAKNPS			SQNL P KI SQNLFPTKI	
Query 286		TQYNDTNATKASKTAKI-ISTQT TOYNDTNA+ ASK KI +S+ +				
Sbjct 268		royndtnastaskogkinlsshs				
Query 109		ASQNLVPAKTHINSPTQYNDTNA ASON +PAKTHIN PTQYNDTNA				
Sbjct 328		ASQNFIPAKTHIN FIQINDINA ASQNFIPAKTHINIPTQYNDTNA		52		

Score		Expect Method	Identities	Positives	Gaps	Frame
153 bits	(387)	1e-39() Compositional matrix adjust.	94/155(61%)	116/155(74%)	6/155(3%)	-2
Features	S :					
Query	466	ASKTAKIISTQTHLGETKPIQPAKDPS A+KTA+II TH I+PAK PS				
Sbjct	140	AAKTARII-FPTHTQIEPAK-PS				
Query	286	INSPTQYNDTNATKASKTAKIISTQTH +++PTO +DTNATKASKTA+I S+ +				
Sbjct	194	VDTPTQDDDTNATKASKTAQIDSSHSQ				
Query	106	KLIASQNLVPAKTHINSPTQYNDTNAT K ASQNL P KTHINSPTQYNDTNA+				
Sbjct	254	KPTASQNLFPTKTHINSPTQYNDTNAS		88		

Range 3: 282 to 417

Score		Expect	Method		Identities	Positives	Gaps	Frame
123 bits(3	809)	5e-29()	Compositional m	natrix adjust.	78/136(57%)	96/136(70%)	2/136(1%)	-2
Features:								
Query	466		KI-ISTOTHLGE				~	
Sbjct 2	282		KI +S+ +HL ET KINLSSHSHLRET				ASQN +PAF ASQNFIPAF	
Query 2	289		TQYNDTNATKASI TQYNDTNATKA I				ANKAAETLT + A +T	
Sbjct :	342		TÕYNDTNATKALI					•
Query	112		ASQNLVPAKTH A+ON+ PAKT	65				
Sbjct 4	402		'ATON' FAKI 'ATONIFPAKTF	417				

GH13568p [Drosophila melanogaster]

Sequence ID: **gb|ABN49245.1|** Length: 204 Number of Matches: 2 Range 1: 20 to 174

Score		Expect Method	Identities	Positives	Gaps	Frame
155 bits(393) 4	4e-44() Compositional matrix adjust.	110/155(71%)	121/155(78%)	1/155(0%)	+3
Features	:					
Query	6	LAVFDALVALVSLYCVGEFICVLAGTR			VRGEGSLAG	
Sbjct	20	FAVFNALVALVSLYCVGMFICVLAGIK				
Query	186	IGLVSPRCVCVE-IILAVFDALVALVS		GTRFCDamsls		
Sbjct	80	VGLVSRKCECEERFILPSFDAVLALVS				
Query	363	algfwvrgegslagciglvsprcvcve: + fwvrgeg lagc+glvs c c e	IILAVFDA 46 I AVFDA	57		
Sbjct	140	VVSFWVRGEGFLAGCVGLVSCSCECDE		4		

Range 2: 94 to 197

Score		Expect Method	Identities	Positives	Gaps	Frame
108 bits	(269)	1e-25() Compositional matrix adjust.	73/104(70%)	78/104(75%)	0/104(0%)	+3
Features	S :					
Query	3	ILAVFDALVALVSLYCVGEFICVLAGTR IL FDA++ALVSLYCVGEFICVL G R				_
Sbjct	94	ILPSFDAVLALVSLYCVGEFICVLVGKR				
Query	183	CIGLVSPRCVCVEIILAVFDALVALVSI C+GLVS C C E I AVFDALVALVS	YCVGEFICVLA CVG CVL			
Sbjct	154	CVGLVSCSCECDESIWAVFDALVALVS				