Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BMU79X014

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Blast report description

Nucleotide Sequence (1396 letters)

RID <u>B8BMU79X014</u> (Expires on 02-06 12:09 pm)

Query ID lcl|Query_54659

Description None **Molecule type** nucleic acid

Molecule type nucleic acid **Query Length** 1396

Database Name nr

Description All non-redundant GenBank CDS

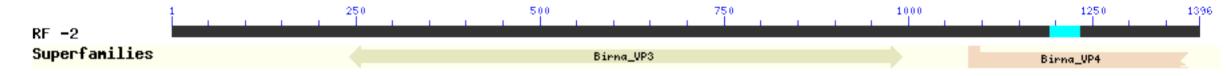
 $translations + PDB + SwissProt + PIR + PRF\ excluding$

environmental samples from WGS projects

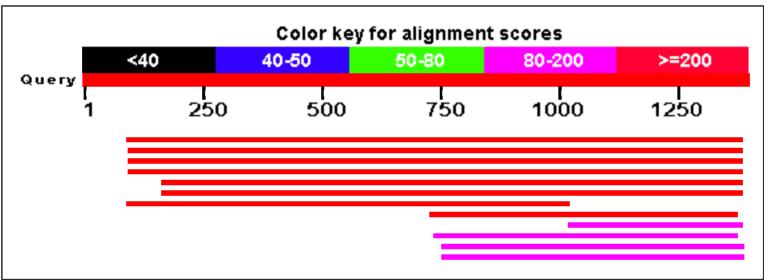
Program BLASTX 2.3.1+

□ Graphic Summary

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



Distribution of 12 Blast Hits on the Query Sequence



□ <u>Descriptions</u>

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
polyprotein [Drosophila x virus]	664	664	92%	0.0	79%	NP_690836.1
polyprotein precursor [Culex Y virus]	467	467	92%	4e-150	55%	AFR34026.1
polyprotein [Mosquitoe x virus]	462	462	92%	5e-148	55%	AFU34333.1
unnamed protein product [Espirito Santo virus]	456	456	92%	6e-146	55%	YP_004956722.1
pVP2-VP4-VP3 polyprotein [Culicine-associated Z virus]	453	453	87%	8e-145	57%	AGW51779.1
pVP2-VP4-VP3 polyprotein [Culicine-associated Z virus]	452	452	87%	2e-144	57%	AGW51761.1
unnamed protein product [Espirito Santo virus]	313	313	66%	3e-99	50%	YP_004956726.1
RecName: Full=Protein VP5 [Drosophila x virus (isolate Chung)]	206	206	46%	2e-59	54%	P0C748.1
unnamed protein product [Espirito Santo virus]	145	145	26%	1e-36	70%	YP_004956725.1
unnamed protein product [Espirito Santo virus]	132	132	45%	1e-31	38%	YP_004956723.1
pVP2-VP4N-X polyprotein [Culicine-associated Z virus]	132	132	45%	2e-29	38%	AGW51780.1
pVP2-VP4N-X polyprotein [Culicine-associated Z virus]	132	132	45%	3e-29	38%	AGW51762.1

□ <u>Alignments</u>

polyprotein [Drosophila x virus]

Sequence ID: ref|NP_690836.1| Length: 1032 Number of Matches: 1

▶ See 2 more title(s) Range 1: 602 to 1032

Score		Expect	Method			Identitie	es	Posit	ives	Gaps		Fran	ne_
664 bits	(1714)	0.0()	Compositi	onal matrix adj	just.	342/431	(79%)	389/4	31(90%) 1/431	(0%)	-2	
Features	S:												
Query	1383			LASSTSPNKVT LASSTSPNKVT									1204
Sbjct	602	ILLP(CYQLLEGR:	LASSTSPNKVT	GTSH	QLAIYA	ADDLL	KFGVI	LGKAPF	AAFTGS	VVGS	SSV	661
Query	1203			TDSLGIPLLGN TDSLGIPLLGN									1024
Sbjct	662			IDSLGIPLLGN									721
Query	1023			PFLNDEDVPLQ PFL + D P+									847
Sbjct	722			PFLEELDQPIP									781
Query	846			ISQGKGRSLVN ISQG+GRSL+N									667
Sbjct	782			ISQGRGRSLIN									841
Query	666			TQADTELAMRK ++ DTELAMR						EDDFVI DDFV			487
Sbjct	842			SKEDTELAMRI									901
Query	486			RDEDWTQPPPP + +DW+OP PP									307
Sbjct	902			KGDDWSQPIPP									961
Query	306	OGKG!	PSQEQARE:	LSHAVRRLISH LSHAVRRLISH	TLVT	OPRQAP	KVPPR	RLVS	TOVTOA	VPSSRF	RASLI RA+L		127
Sbjct	962			LSHAVRRLISH									1021
Query	126		GEDENIV GED +IV	94									
Sbjct	1022		GEDNDIV	1032									

Score		Expect	Method	Identities	Positives	Gaps	Frame
467 bits	(1202)	4e-150()	Compositional matrix adjust	. 252/455(55%) 321/455(70%	%) 28/455(6%) -	·2
Feature	s:						
Query	1383		CYOLLDGKLASSTSPNKVTGTS				
Sbjct	605		CYQL DGKLA+S +PNKVTGTS CYQLFDGKLATSKTPNKVTGTS				
Query	1203		GINLKLHLTDSLGIPLLGNSPG				
Sbjct	665		GI+LK LTDSLGIPL GNS G GISLKSQLTDSLGIPLFGNSQG			RRTP+ T HWT RRTPRETPNHWT	
Query	1023		IPFLSTNPFLNDE				
Sbjct	725		PF +TNPFLN E /PFSNTNPFLNGEVDQERNVQF	LPTNTNPFLDA	VP Q AGQDVGGVPPQ-	A+ IS+DTF QMARIISDDTF	RN 783
Query	918		OGOTIPSSQEKIATIHEYILEH				
Sbjct	784		OGQ+IPSSQEKI T+HE++L++ OGQSIPSSQEKIVTVHEFLLQN				
Query	738	~	DERRORLERKIRNLENOGIYVD				
Sbjct	844	+E+T+ KELTE	-ER RLE K++NL QGI +D EERLARLEVKVQNLARQGIVLD		O DT+ A+ +- OEDTQAAISRS		
Query	558		ASISNSYTEDDFVDFWMEQESL				M 379
Sbjct	904	F NN FLNNV	SI YTED+FVDFW+ Q + /SIGREYTEDEFVDFWIRQGFI				M QM 962
Query	378		PSEDQISAVRDLVDEVYDRNQG				
Sbjct	963	LGPSI LGPSI	P + " + VR +VD VYD N PDQGLVEQVRSMVDSVYDENGN				
Query	198		/SAQTVQTVPSSRRASLLRI-R		97		
Sbjct	1023	R++ VRKI <i>R</i>	T Q RRA+L R+ R PIATGQGSNPERRAALERLQR		1057		

polyprotein [Mosquitoe x virus]

Sequence ID: **gb|AFU34333.1|** Length: 1057 Number of Matches: 1 Range 1: 605 to 1057

Score		Expect	Method	Identities	Positives	Gaps	Frame
462 bits	(1188) 5	5e-148()	Compositional matrix adjust.	249/455(55%)	321/455(70%)	28/455(6%)	-2
Feature	s:						
Query	1383		CYOLLDGKLASSTSPNKVTGTS CYOL DGKLA+S +PNKVTGTS				
Sbjct	605		CYQLFDGKLATSKTPNKVTGTS				
Query	1203		GINLKLHLTDSLGIPLLGNSPG GI+LK LTDSLGIPL GNS G				TA 1024
Sbjct	665		GISLKSQLTDSLGIPLYGNSQG				
Query	1023		NPFLSTNPFLNDE PF +TNPFLN E		DVPLQG VP O	NIAKAISEDT +A+ IS+DT	
Sbjct	725		PFSNTNPFLNGEVDQERNVQY	LPPRTNPFLDA			
Query	918		OGQTIPSSQEKIATIHEYILEH OGQ+IPSSQEKI T+HE++L++				
Sbjct	784	AFLE	OGŐSIPSSŐEKI TINETTEN OGŐSIPSSŐEKIVTVHEFLLQN	QELLEAMFGLI	SRGHEKALVNM	VTKAAVNIKT	QA 843
Query	738		DERRQRLERKIRNLENQGIYVD ++R RLE KI+NL OGI +D		QADTELAMRKA O DT+ A+ ++		
Sbjct	844		EDRLARLEVKIQNLARÕGIVLD				
Query	558	FTNN <i>F</i> F NN	ASISNSYTEDDFVDFWMEQESL SI YTED+FVDFW+ O +				LM 379
Sbjct	904		/SIGREYTEDEFVDFWIRÕGFI				
Query	378		PSEDQISAVRDLVDEVYDRNQG P + + VR +VD VYD N				
Sbjct	963		PDQGLVEQVRSMVDSVYDENGN				· · -
Query	198	PRRLV R++	/SAQTVQTVPSSRRASLLRI-R T O RRA+L R+ R		97		
Sbjct	1023		APIATGÕESNPERRAALERLOR		1057		

unnamed protein product [Espirito Santo virus]

Sequence ID: ref|YP_004956722.1| Length: 1054 Number of Matches: 1

▶ See 1 more title(s) Range 1: 603 to 1054

Score	E	Expect	Method	Identities	Positives	Gaps	Frame
456 bits	(1173) 6	Se-146()	Compositional matrix adjust.	250/455(55%)	320/455(70%)	29/455(6%)	-2
Features	S :						
Query	1383		YOLLDGKLASSTSPNKVTGTSI YOL DGKLA+S +PNKVTGTSI				
Sbjct	603		ZYQLFDGKLATSKTPNKVTGTSI	~	-		
Query	1203	gevfG	SINLKLHLTDSLGIPLLGNSPGI	LVPVTNLRALDF	KIKDMGDVKRF	RTPKRTLPHW	TA 1024

		GEVFGI+LK LTDSLGIPL GNS GL P+ NL L++ + GDV RRTP+ T HWTA	
Sbjct	663	GEVFGISLKSQLTDSLGIPLFGNSQGL-PIQNLHQLERLLDISGDVPRRTPRETPNHWTA	721
Query	1023	GSSTNPFLSTNPFLNDEDVPLQGNIAKAISEDTRD S++ PF +TNPFLN E VP Q +A+ IS+DTR+	919
Sbjct	722	SSASVPFSNTNPFLNGEVDQERNVQFLPTNTNPFLDAGQDVGGVPPQ-QMARIISDDTRN	780
Query	918	MFLADGQTIPSSQEKIATIHEYILEHKDLEEAMFSLISQGKGRSLVNMVVKSALNIQTQS FL DGQ+IPSSQEKI T+HE++L+++L EAMF LIS+G ++LVNMV K+A+NI+TQ+	739
Sbjct	781	AFLEDGÕSIPSSÕEKIVTVHEFLLQNQELLEAMFGLISRGHEKALVNMVTKAAVNIKTÕA	840
Query	738	QEVTDERRQRLERKIRNLENQGIYVDESRIMTSGKITQADTELAMRKARKSQKAAKLRRI +++T+ER RLE KI++L QGI +D + +G+ITQ DT+ A+ +++ Q KLRR+	559
Sbjct	841	KDLTEERLARLEVKIQHLARÕGIVLDPENVKRAGRITÕEDTQAAIIRSKDHÕMRNKLRRV	900
Query	558	FTNNASISNSYTEDDFVDFWMEQESLPTGTQIALWLRDEDWTQPPPPRSIRRHYDSYTLM F NN SI YTED+FVDFW+ Q +P G QI+ WLR+EDW+ P P S +RHYDSY M	379
Sbjct	901	FLNNVSIGREYTEDEFVDFWIRQGFIPNGLQISAWLREEDWSSPTPALS-KRHYDSYLQM	959
Query	378	LGPSPSEDQISAVRDLVDEVYDRNQGKGPSQEQARELSHAVRRLISHTLVTQPRQAPKVP LGPSP + + VR +VD VYD N KGPSQ QAR LS +VRRLIS +LVT+P+ PKVP	199
Sbjct	960	LGPSPDQGLVEQVRSMVDSVYDENGNKGPSQVQARALSSSVRRLISQSLVTRPQPVPKVP	1019
Query	198	PRRLVSAQTVQTVPSSRRASLLRI-RGVQGEDENI 97 R++ T Q RRA+L R+ R GE E I	
Sbict	1020	VRKIEPIATGÖGSNPERRAALERLORARGGESEMI 1054	

pVP2-VP4-VP3 polyprotein, partial [Culicine-associated Z virus]

Sequence ID: **gb|AGW51779.1|** Length: 1049 Number of Matches: 1 Range 1: 599 to 1027

Score		Expect	Method		Identities	Positives	Gaps	Frame
453 bits	(1165)	8e-145()	Composit	ional matrix adjust.	244/431(57%) 308/431(71%) 27/431(6%)	-2
Features	S :							
Query	1383			LASSTSPNKVTGTS LA+S +PN+VTGTS				
Sbjct	599			LATSLTPNRVTGTS				
Query	1203	gevf0 GEVF0		TDSLGIPLLGNSPG TDSLGIPL GNS G				VTA 1024 VTA
Sbjct	659			rdslgiplygnskg				
Query	1023	GSSTI	NPFLSTNPI NPF+STNPI	FLN FT.N		-DEDVPLQC D+DV P O	NIAKAISEDT +AK ISEDT	TRD 919
Sbjct	719			FLNGNADQEDAQPL	RTPKANPFLDD			
Query	918			QEKIATIHEYILEH OEKI T+H+++L +				
Sbjct	778			ŽEKIVTVHDFLLRN				
Query	738		DERRORLE	RKIRNLENQGIYVD K++NL ÖGI +D		QADTELAMRKA O DT+ A+ ++		
Sbjct	838			VKLQNLARÕGIVLD				
Query	558	FTNN <i>I</i> F NN		EDDFVDFWMEQESL ED+FV+FW+ O +			RSIRRHYDSYT S +RHYDSY	TLM 379 M
Sbjct	898			EDEFVEFWVRÕGFI				
Query	378	LGPSI LGPSI	SEDQISA	VRDLVDEVYDRNQG VR +VD VYD N	KGPSQEQAREI	SHAVRRLISHT	LVTQPRQAPI	KVP 199 KVP
Sbjct	957			VRIMVDNVYDENGN				
Query	198	PRRL\ R++	/SAQTVQ S T O	166				
Sbjct	1017		AŠIATGÕ	1027				

pVP2-VP4-VP3 polyprotein [Culicine-associated Z virus]

Sequence ID: **gb|AGW51761.1|** Length: 1057 Number of Matches: 1 Range 1: 605 to 1033

Score	E	Expect Method	Identities	Positives	Gaps	Frame
452 bits	(1163) 2	e-144() Compositional ma	trix adjust. 244/431(57%) 308/431(71%	5) 27/431(6%)	-2
Feature	s:					
Query	1383		PNKVTGTSHQLAIYAADDL PN+VTGTSHQLA+YAA+ L			
Sbjct	605		PNTVIGISHQLATIAAT L PNRVTGTSHQLALYAAEGL			
Query	1203		PLLGNSPGLVPVTNLRALD PL GNS GL PV +L L+			TA 1024
Sbjct	665	GEVFGINLK EIDSLGINGEVFGINLKSRLTDSLGIN				
Query	1023	GSSTNPFLSTNPFLN S++NPF+STNPFLN		DEDVPLQOD+DV P Q		
Sbjct	725		OQEDAQPLRTPKANPFLDD			
Query	918	MFLADGOTIPSSOEKIAT	IHEYILEHKDLEEAMFSLI +H+++L +++L EAMF LI			
Sbjct	784	AFLEDGŐSIPSSŐEKIVT				
Query	738		ENQGIYVDESRIMTSGKIT QGI +D + G+IT			
Sbjct	844		ARQGIVLDLENVKRVGRIT			

Query	558		379
Sbjct	904	F NN SI YTED+FV+FW+ Q +P G QI+ WL+DEDWT P P S +RHYDSY M FLNNVSIGREYTEDEFVEFWVRQGFIPNGLQISAWLKDEDWTSPTPVLS-KRHYDSYLQM 9	962
Query	378	LGPSPSEDQISAVRDLVDEVYDRNQGKGPSQEQARELSHAVRRLISHTLVTQPRQAPKVP 1 LGPSP + VR +VD VYD N KGP+Q+QAR LS +VRRLIS +LVT+P+ PKVP	199
Sbjct	963		1022
Query	198	PRRLVSAQTVQ 166 R++ S T Q	
Sbjct	1023	VRKIASIATGQ 1033	

unnamed protein product [Espirito Santo virus]

Sequence ID: ref|YP_004956726.1| Length: 331 Number of Matches: 1 Range 1: 6 to 331

Score	E	xpect Method	Identities	Positives	Gaps	Frame
313 bits	(802) 36	e-99() Compositional matrix adjust.	164/328(50%)	226/328(68%)	21/328(6%)	-2
Features	s:					
Query	1020	SSTNPFLSTN				
Sbjct	6	S+TNPFL+ TN SNTNPFLNGEVDQERNVQFLPTNTN	IPFL+ +DV IPFLDAGQDVGGV			
Query	897	TIPSSQEKIATIHEYILEHKDLEEA +IPSSQEKI T+HE++L+++L EA				
Sbjct	65	SIPSSQEKIVTVHEFLLQNQELLEA				
Query	717	RQRLERKIRNLENQGIYVDESRIMT RLE KI++L OGI +D +	SGKITQADTELA +G+ITQ DT+ A		KLRRIFTNNA KLRR+F NN	
Sbjct	125	LARLEVKIQHLARQGIVLDPENVKR				
Query	537	SNSYTEDDFVDFWMEQESLPTGTQI YTED+FVDFW+ Q +P G QI				
Sbjct	185	GREYTEDEFVDFWIRQGFIPNGLQI				
Query	357	DQISAVRDLVDEVYDRNQGKGPSQE + VR +VD VYD N KGPSQ				'SA 178
Sbjct	244	GLVEQVRSMVDSVYDENGNKGPSQV				PI 303
Query	177	QTVQTVPSSRRASLLRIRGVQGEDE T O RRA+L R++ +G +				
Sbjct	304	ATGQGSNPERRAALERLQRARGGES				

RecName: Full=Protein VP5 [Drosophila x virus (isolate Chung)]

Sequence ID: **sp|P0C748.1|VP5_DXV96** Length: 237 Number of Matches: 1 Range 1: 1 to 216

Score	E	xpect Method	Identities	Positives	Gaps	Frame
206 bits	(525) 20	e-59() Compositional matrix adjust.	116/216(54%)	153/216(70%)	1/216(0%)	-1
Features	s:					
Query	1372	MLSVIRRKTSIVNFSKQSNGNIPPAC MLS+IRRKT IV+ +KQ NGN+PPAC				RSF 1193
Sbjct	1	MLSIIRRKTRIVDITKQGNGNVPPAC				
Query	1192	WNQPETPPDGLPWDTSTWELTRIGPS W+QPETP DGL WD++TWELTRI S		RYGRRKKKDTKK RYGRRK+K+ K		
Sbjct	61	WHOPETPIDGLSWDSTTWELTRISSS				
Query	1015	NEPVLVNEPILERRRRPPAGEHSEGN +EP+ +EPI R + + N				QR 836 O
Sbjct	121	HEPIHEHEPIPGRVGPADTKQRCKAN				~
Query	835	SGGSYVQLNQPRKRSLTREHGSEKRT G VOL++PR+R ++ +HGS+KR+		728		
Sbjct	181	VRGGNVÕLDKPRERPVSYQHGSKKRS		216		

unnamed protein product [Espirito Santo virus]

Sequence ID: **ref|YP_004956725.1|** Length: 223 Number of Matches: 1 Range 1: 103 to 223

Score		Expect	Method	Identities	Positives	Gaps	Frame
145 bits	(366)	1e-36()	Compositional matrix adjust.	85/122(70%)	99/122(81%)	1/122(0%)	-2
Features	S:						
Query	1383		CYOLLDGKLASSTSPNKVTGTSH CYOL DGKLA+S +PNKVTGTSH				
Sbjct	103		CYQLFDGKLATSKTPNKVTGTSH				
Query	1203		GINLKLHLTDSLGIPLLGNSPGI GI+LK LTDSLGIPL GNS GI				WTA 1024
Sbjct	163		GISLKSQLTDSLGIPLFGNSQGL				
Query	1023	GS	1018				

unnamed protein product [Espirito Santo virus]

Sequence ID: ref|YP_004956723.1| Length: 259 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 236

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
132 bits	(332) 16	e-31() Compositional matrix adjust.	89/237(38%)	128/237(54%)	25/237(10%)	-1
Features:						
Query	1372	MLSVIRRKTSIVNFSKQSNGNIPPA				
Sbjct	1	MLS IRRK + ++Q + ++ PA MLSTIRRKAGNLQNTEQGDRHVTPA				SF SF 60
Query	1192	WNQPETPPDGLPWDTSTWELTRIGP W+QPE P DGLPWD+S WELTRI			KKDIATLDSGI +D LD +	
Sbjct	61	WHQPEIPIDGLPWDSSVWELTRIA-				
Query	1012	EPVLVNEPILERRRRPPAG L ++ ILE R P P			GNIGRYPRHVF ++ R+P+	RR 905 R
Sbjct	120	RAFLKHKSILEWRSGPRKECTVPTN		_		
Query	904	RTDDPELPGEDSHNSRVYTGAQRSG P+L GEDSH SR+ T +		RSLTREHGSEK R + EHG +		734
Sbjct	180	WPIHPKLSGEDSHGSRIPTTEPGAS				236

pVP2-VP4N-X polyprotein, partial [Culicine-associated Z virus]

Sequence ID: gb|AGW51780.1| Length: 862 Number of Matches: 1

Range 1: 599 to 833

Score	Е	xpect Method	Identities	Positives	Gaps	Frame	
132 bits	(332) 26	e-29() Compositional matrix adjust.	89/235(38%)	130/235(55%)	24/235(10%)	-1	
Features:							
Query	1384	HPPTMLSVIRRKTSIVNFSKQSNGN HPPT+LS+IRRKT ++ +KO + N				NG 1205	
Sbjct	599	HPPTVLSIIRRKTGHLSNTKQGDRN				IS 658	
Query	1204	GRSFWNQPETPPDGLPWDTSTWELT GRSFW+OPE P DGLPWD+S WEL				DS 1025	
Sbjct	659	GRSFWHQPEIPIDGLPWDSSLWELE					
Query	1024	GIFNEPVLVNEPILERRRRPP + +P+ ++PI ER RRR	AG		EHSEGNIGRYP E+ E ++ R+		
Sbjct	719	KLNKQPLCKHQPIPERQRGSRRRSA	TADAQGQPIPG			•	
Query	916	VPRRRTDDPELPGEDSHNSRVYTGA VP P+L G+DS+ SR			GSEKRTQH 7 G + R +H	52	
Sbjct	779	VPGGWPIYPKLTGKDSYGSRFSPPK				33	

pVP2-VP4N-X polyprotein [Culicine-associated Z virus]

Sequence ID: gb|AGW51762.1| Length: 868 Number of Matches: 1

Range 1: 605 to 839

Score	E	xpect Method	Identities	Positives	Gaps	Frame	
132 bits(332) 3e-29() Compositional matrix adjust. 89/235(38%) 130/235(55%) 24/235(10%) -1							
Features:							
Query	1384	HPPTMLSVIRRKTSIVNFSKQSNGN HPPT+LS+IRRKT ++ +KQ + N				ING 1205	
Sbjct	605	HPPTVLSIIRRKTGHLSNTKQGDRN				TIS 664	
Query	1204	GRSFWNQPETPPDGLPWDTSTWELT GRSFW+OPE P DGLPWD+S WEL				LDS 1025	
Sbjct	665	GRSFWHQPEIPIDGLPWDSSLWELE					
Query	1024	GIFNEPVLVNEPILERRRRPP. + +P+ ++PI ER RRR	AG		EHSEGNIGRY		
Sbjct	725	KLNKQPLCKHQPIPERQRGSRRRSA	TADAQGQPIPG				
Query	916	VPRRRTDDPELPGEDSHNSRVYTGA VP P+L G+DS+ SR		IQPRKRSLTREH -OPR R + +H		752	
Sbjct	785	VPGGWPIYPKLTGKDSYGSRFSPPK				839	