Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BNSX0W014

- ► Formatting options
- ▶ Download

Blast report description

Nucleotide Sequence (375 letters)

RID <u>B8BNSX0W014</u> (Expires on 02-06 12:10 pm)

Query ID lcl|Query_111017

Description None

Molecule type nucleic acid

Query Length 375

Database Name nr

Description All non-redundant GenBank CDS

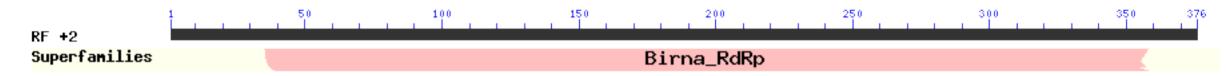
translations+PDB+SwissProt+PIR+PRF excluding

environmental samples from WGS projects

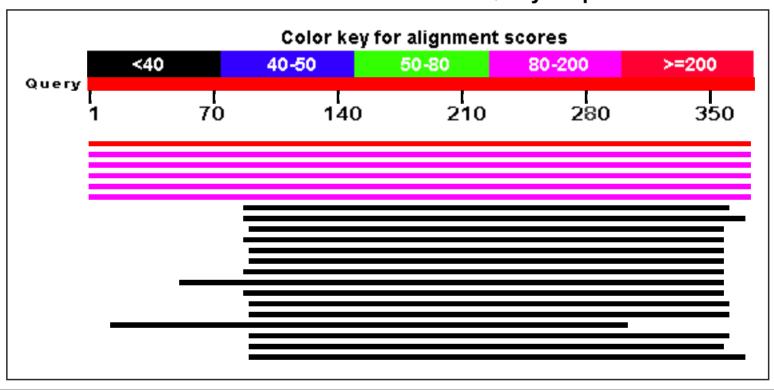
Program BLASTX 2.3.1+

□ Graphic Summary

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



Distribution of 21 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
putative RNA-dependent RNA polymerase VP1 [Drosophila x virus]	232	232	99%	2e-68	86%	NP_690806.1
putative VP1 [Mosquitoe x virus]	183	183	99%	9e-51	68%	AFU34334.1
VP1/RdRp [Culicine-associated Z virus]	182	182	99%	2e-50	66%	AGW51781.1
VP1 [Culex Y virus]	182	182	99%	2e-50	67%	AFR34027.1
VP1/RdRp [Culicine-associated Z virus]	182	182	99%	2e-50	66%	AGW51763.1
unnamed protein product [Espirito Santo virus]	181	181	99%	5e-50	67%	YP_004956721.1
viral protein 1 [Infectious bursal disease virus]	36.6	36.6	72%	3.2	28%	ALC74818.1
VP1 [Infectious bursal disease virus]	36.6	36.6	75%	3.8	27%	<u>AIF79742.1</u>
RNA-dependent RNA polymerase [Infectious bursal disease virus]	36.6	36.6	71%	4.3	30%	ABB97490.1
viral protein 1 [Infectious bursal disease virus]	36.6	36.6	72%	4.6	28%	BAT62516.1
VP1 [Infectious bursal disease virus]	36.6	36.6	71%	5.4	29%	ABG91145.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	36.6	36.6	71%	5.7	29%	ABG91146.2
VP1 [Infectious bursal disease virus]	36.6	36.6	72%	5.9	28%	AAD49777.1
RNA directed RNA polymerase [Infectious bursal disease virus]	35.8	35.8	81%	6.0	26%	AEW44032.1
VP1 [Infectious bursal disease virus]	36.2	36.2	72%	6.3	28%	ABI52865.1
viral protein 1 [Infectious bursal disease virus]	35.8	35.8	72%	7.4	28%	BAH03934.1
viral polymerase [Infectious bursal disease virus]	35.4	35.4	72%	8.2	28%	CAI47766.1
3-phosphoglycerate dehydrogenase [Vibrio sinaloensis]	35.8	35.8	77%	9.1	30%	WP_039477531.1
viral polymerase [Infectious bursal disease virus]	35.4	35.4	72%	9.6	28%	CAI47786.1
RNA directed RNA polymerase [Infectious bursal disease virus]	35.4	35.4	71%	9.8	27%	AEW44079.1
VP1 [Infectious bursal disease virus]	35.4	35.4	74%	9.9	27%	AIF79732.1

□ <u>Alignments</u>

putative RNA-dependent RNA polymerase VP1 [Drosophila x virus] Sequence ID: ref|NP_690806.1| Length: 997 Number of Matches: 1

▶ See 2 more title(s) Range 1: 67 to 190

Score		Expect	Method	Identities	Positives	Gaps	Frame
232 bits	(592)	2e-68()	Compositional matrix adjust.	107/124(86%)	117/124(94%)	0/124(0%)	+2
Feature	s:						
Query	2		VNIPFREAACPRMMALYGELLD' VNIPF EAA PRMMALYGELLD		~		
Sbjct	67		VNIPFIEAASPRMMALYGELLD				
Query	182		MHYISKSSNDAWDERVYETLRE: MHYI+ S+ND WD+++YETL+E:				
Sbjct	127		MHYIANSANDTWDKQIYETLKE:				
Query	362	GHHK GHHK	373				
Sbjct	187	GHHK	190				

putative VP1 [Mosquitoe x virus]

Sequence ID: **gb|AFU34334.1|** Length: 995 Number of Matches: 1 Range 1: 67 to 190

Score		Expect Meth	od	Identities	Positives	Gaps	Frame
183 bit	s(465)	9e-51() Com	positional matrix adjust.	84/124(68%)	100/124(80%)	0/124(0%)	+2
Feature	es:						
Query	2		PFREAACPRMMALYGELLD PF EAA PRM+ LY E L		LQIPTYKPGHEV +PTYKPGHE+		
Sbjct	67		PFTEAASPRMLDLYEEQLG				•
Query	182	LAYEYMHYI LA+EYM YI	SKSSNDAWDERVYETLRE SSN +D +Y T++E		TGSLLGQVKRVA TGSLLGOVKR+A		
Sbjct	127		EGSSNPEFDSAIYRTIKE				
Query	362	GHHK 373 GHHK	}				
Sbjct	187	GHHK 190					

VP1/RdRp [Culicine-associated Z virus]

Sequence ID: **gb|AGW51781.1|** Length: 998 Number of Matches: 1 Range 1: 67 to 190

Score		Expect Method	Identities	Positives	Gaps	Frame
182 bits	(463)	2e-50() Compositional matrix adjust.	82/124(66%)	101/124(81%)	0/124(0%)	+2
Features	S :					
Query	2	PYDELVNIPFREAACPRMMALYGELLD PYDEL+N+PF EAA PRM+ LY E L				
Sbjct	67	PYDELINVPFTEAASPRMLDLYEEQLG				•
Query	182	LAYEYMHYISKSSNDAWDERVYETLRE LA+EYM YI SSN +D +Y T++E		TGSLLGQVKRVA TGSL+GQV+R+A		
Sbjct	127	LAFEYMKYIEGSSNPDFDAAIYRTIKE				
Query	362	GННК 373 GННК				
Sbjct	187	GHHK 190				

VP1 [Culex Y virus]

Sequence ID: **gb|AFR34027.1|** Length: 998 Number of Matches: 1 Range 1: 67 to 190

Score		Expect Method	Identities	Positives	Gaps	Frame
182 bits	(463)	2e-50() Compositional n	natrix adjust. 83/124(67%)	100/124(80%)	0/124(0%)	+2
Features	s:					
Query	2		MMALYGELLDTKDVSLPVGSD			
Sbjct	67		M+ LY E L +KDVSLP+G+ MLDLYEEQLGSKDVSLPIGAG	+PTYKPGHE+ QILPTYKPGHEI		•
Query	182		DERVYETLRELLVAQATTRFS D +Y T++ELL Q TRFS	TGSLLGQVKRVA TGSLLGOVKR+A		
Sbjct	127		DSAIYRTIKELLEIQGATRFS			
Query	362	GННК 373 GННК				
Sbjct	187	GHHK 190				

VP1/RdRp [Culicine-associated Z virus]

Sequence ID: **gb|AGW51763.1|** Length: 998 Number of Matches: 1 Range 1: 67 to 190

	Expect	Method	Identities	Positives	Gaps	Frame
163)	2e-50()	Compositional matrix adjust.	82/124(66%)	101/124(81%)	0/124(0%)	+2
2						
67						
182						
127						
362	GHHK GHHK	373				
187	GHHK	190				
	2 67 182 127 362	2 PYDEL PYDEL PYDEL 67 PYDEL 182 LAYEY LA+EY 127 LAFEY	2 PYDELVNIPFREAACPRMMALYGELLD PYDEL+N+PF EAA PRM+ LY E L - 67 PYDELINVPFTEAASPRMLDLYEEQLG 182 LAYEYMHYISKSSNDAWDERVYETLREI LA+EYM YI SSN +D +Y T++EI 127 LAFEYMKYIEGSSNPDFDAAIYRTIKEI 362 GHHK 373 GHHK	2 PYDELVNIPFREAACPRMMALYGELLDTKDVSLPVGSDIPYDEL+N+PF EAA PRM+ LY E L +KDVSLP+G++ 67 PYDELINVPFTEAASPRMLDLYEEQLGSKDVSLPIGAEG 182 LAYEYMHYISKSSNDAWDERVYETLRELLVAQATTRFST LA+EYM YI SSN +D +Y T++ELL Q TRFST 127 LAFEYMKYIEGSSNPDFDAAIYRTIKELLEIQGNTRFST 362 GHHK 373 GHHK	2 PYDELVNIPFREAACPRMMALYGELLDTKDVSLPVGSDLQIPTYKPGHEV PYDEL+N+PF EAA PRM+ LY E L +KDVSLP+G++ +PTYKPGHE+ 67 PYDELINVPFTEAASPRMLDLYEEQLGSKDVSLPIGAEQILPTYKPGHEI 182 LAYEYMHYISKSSNDAWDERVYETLRELLVAQATTRFSTGSLLGQVKRVA LA+EYM YI SSN +D +Y T++ELL Q TRFSTGSL+GQV+R+A 127 LAFEYMKYIEGSSNPDFDAAIYRTIKELLEIQGNTRFSTGSLMGQVRRIA 362 GHHK 373 GHHK	2 PYDELVNIPFREAACPRMMALYGELLDTKDVSLPVGSDLQIPTYKPGHEVSPPLLTLPN PYDEL+N+PF EAA PRM+ LY E L +KDVSLP+G++ +PTYKPGHE++PPL TL N PYDELINVPFTEAASPRMLDLYEEQLGSKDVSLPIGAEQILPTYKPGHEITPPLTTLAN 182 LAYEYMHYISKSSNDAWDERVYETLRELLVAQATTRFSTGSLLGQVKRVAAGQDVAYGF LA+EYM YI SSN +D +Y T++ELL Q TRFSTGSL+GQV+R+AAGQDVAYGF 127 LAFEYMKYIEGSSNPDFDAAIYRTIKELLEIQGNTRFSTGSLMGQVRRIAAGQDVAYGF 362 GHHK 373 GHHK

Sequence ID: ref|YP_004956721.1| Length: 998 Number of Matches: 1

▶ See 1 more title(s) Range 1: 67 to 190

Score		Expect	Method	Identities	Positives	Gaps	Frame
181 bits	(460)	5e-50()	Compositional matrix adjust.	83/124(67%)	99/124(79%)	0/124(0%)	+2
Features	s:						
Query	2		VNIPFREAACPRMMALYGELLDT				
Sbjct	67		+N+PF EAA PRM+ LY E L + INVPFTEAASPRMLDLYEEQLGS		+PTYKP HE+ ILPTYKPSHEI		•
Query	182	LAYEY!	MHYISKSSNDAWDERVYETLREL M YI SSN +D +Y T++EL		GSLLGQVKRV <i>I</i> GSLLGQVKR+ <i>I</i>		
Sbjct	127		MKYIEGSSNPEFDSAIYRTIKEL				
Query	362	GHHK GHHK	373				
Sbjct	187	GHHK	190				

viral protein 1, partial [Infectious bursal disease virus]

Sequence ID: gb|ALC74818.1| Length: 181 Number of Matches: 1

▶ See 2 more title(s) Range 1: 29 to 120

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
36.6 bits	(83)	3.2()	Compositional matrix adjust.	27/98(28%)	50/98(51%)	13/98(13%)	+2	
Features	8:							
Query	89	DVSLE	PVGSDLQIPTYKPGHEVSP+G P Y P H S		LAYEYMHYISI		VY	247
Sbjct	29		PIGDQEYFPKYYPTHRPSKEKPNA		· -	· · · ·	ΓL	87
Query	248		ELLVAQATTRFSTGSLLGQVKRVA - + A+A + +G+ +GO R+ .		361			
Sbjct	88		NIRAKAYGSGTYMGQATRLV		120			

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AIF79742.1| Length: 192 Number of Matches: 1

Range 1: 73 to 167

Score		Expect	Method	Identities	Positives	Gaps	Frame
36.6 bits	s(83)	3.8()	Compositional matrix adjust.	27/101(27%)	51/101(50%)	13/101(12%)	+2
Features	S :						
Query	89	DVSL	PVGSDLQIPTYKPGHEVS P+G P Y P H S			KSSNDAWDERV	7Y 247
Sbjct	73		PIGDQEYFPKYYPTHRPSKEKPN			· · · · · 	L 131
Query	248		ELLVAQATTRFSTGSLLGQVKRV + + A+A				
Sbjct	132		ONIRAKAYGSGTYMGÕATRL				

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|ABB97490.1| Length: 405 Number of Matches: 1

Range 1: 90 to 179

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
36.6 bits	s(83)	4.3()	Compositional matrix adjust.	29/97(30%)	45/97(46%)	15/97(15%)	+2	
Feature	s:							
Query	92	VSLPV +SLP+	GSDLQIPTYKPGHEVS		AYEYMHYISKS Y ++ I +-		ΥE	250
Sbjct	90		GDQEYFPKYYPTHRPSKEKPNAY	· -				146
Query	251		LLVAQATTR-FSTGSLLGQVKRVA LL + + +G+ +GO R+		358			
Sbjct	147		LLTQNIRDKAYGSGTYMGQATRLV		179			

viral protein 1, partial [Infectious bursal disease virus]

Sequence ID: dbj|BAT62516.1| Length: 332 Number of Matches: 1

Range 1: 96 to 186

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.6 bits(83)	4.6()	Compositional matrix adjust.	27/97(28%)	50/97(51%)	13/97(13%)	+2

Features:

Query	89	DVSLPVGSDLQIPTYKPGHEVSPPLLTLPNALAYEYMHYISKSSNDAWDERVY	247
Sbjct	96	NLSLPIGDQEYFPKYYPTHRPSKEKPNAYPPDIALLKQMIYLFLQ-VPEATDNLKDEVTL	154
Query	248	ETLRELLVAQATTRFSTGSLLGQVKRVAAGQDVAYGR 358 L + + A+A + +G+ +GO R+ A ++VA GR	
Sbjct	155	LTQNIRAKAYGSGTYMGQATRLVAMKEVATGR 186	

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABG91145.1|** Length: 879 Number of Matches: 1 Range 1: 97 to 186

Score		Expect	Method	Identities	Positives	Gaps	Fran	ne
36.6 bits	s(83)	5.4()	Compositional matrix adjust.	28/98(29%)	47/98(47%)	17/98(17%)	+2	
Features	S :							
Query	92	VSLPV +SLP+	/GSDLQIPTYKPGHEVS -G PYPH S		AYEYMHYISK		RV	244
Sbjct	97		GDQEYFPKYYPTHRPSKEKPNAY				LĽ	155
Query	245		RELLVAQATTRFSTGSLLGQVKRV		358			
Sbjct	156	· · -	R+		186			

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|ABG91146.2|** Length: 879 Number of Matches: 1 Range 1: 97 to 186

Score		Expect	Method	Identities	Positives	Gaps	Fran	ne
36.6 bits	s(83)	5.7()	Compositional matrix adjust.	28/98(29%)	47/98(47%)	17/98(17%)	+2	
Features	s:							
Query	92	VSLPV +SLP+	GSDLQIPTYKPGHEVS		AYEYMHYISK		RV :	244
Sbjct	97		GDQEYFPKYYPTHRPSKEKPNAY				LĽ	155
Query	245	YETLF + +F	RELLVAQATTRFSTGSLLGQVKRV R+ + +G+ +GO R+		358			
Sbjct	156	· · -	RDKAYGSGTYMGQATRL		186			

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AAD49777.1|** Length: 879 Number of Matches: 1 Range 1: 96 to 186

Score		Expect	Method	Identities	Positives	Gaps	Frar	ne
36.6 bits	s(83)	5.9()	Compositional matrix adjust.	27/97(28%)	50/97(51%)	13/97(13%)	+2	
Features	s:							
Query	89		DVSLPVGSDLQIPTYKPGHEVSPPLLTLPNALAYEYMHYISKSSNDAWDERVY 2					
Sbjct	96		PIGDQEYFPKYYPTHRPSKEKPNA		· - · · ·		ΓL	154
Query	248		ELLVAQATTRFSTGSLLGQVKRVA - + A+A + +G+ +GO R+		358			
Sbjct	155	_	NIRAKAYGSGTYMGQATRLV		186			

RNA directed RNA polymerase, partial [Infectious bursal disease virus]

Sequence ID: gb|AEW44032.1| Length: 160 Number of Matches: 1

Range 1: 10 to 111

Score		Expect	Method	Identities	Positives	Gaps	Frame
35.8 bits	s(81)	6.0()	Compositional matrix adjust.	29/111(26%)	54/111(48%)	18/111(16%)	+2
Features	s:						
Query	53		YGELLDTKDVSLPVGSDLQIPTY G +L T +SLP+G P Y		PPLLTLP PP + L	NALAYEYMHY	
Sbjct	10		EGAVLKTT-LSLPIGDQEYFPKY				•
Query	212	KSSNI ++++	DAWDERVYETLRELLVAQATT + DE + + +R+				
Sbjct	68		NLKDEVTLLTQNIRDK		R+ A ++VA ATRLVAMKEVA		

Score		Expect	Method	Identities	Positives	Gaps	Frame
36.2 bits	s(82)	6.3()	Compositional matrix adjust.	27/97(28%)	50/97(51%)	13/97(13%)	+2
Features	s:						
Query	89	DVSLF ++SLF	PVGSDLQIPTYKPGHEVSP+G P Y P H S		LAYEYMHYISI		VY 247
Sbjct	96		PIGDQEYFPKYYPTHRPSKEKPNA		· - · · · ·	· · · · · — —	rL 154
Query	248		CLLVAQATTRFSTGSLLGQVKRVA		358		
Sbjct	155		- + A+A + +G+ +GQ R+ 1 NIRAKAYGSGTYMGQATRLV		186		

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03934.1| Length: 332 Number of Matches: 1

Range 1: 97 to 187

Score		Expect	Method	Identities	Positives	Gaps	Frame	
35.8 bits	s(81)	7.4()	Compositional matrix adjust.	27/98(28%)	47/98(47%)	15/98(15%)	+2	_
Features	S :							
Query	92		VSLPVGSDLQIPTYKPGHEVSPPLLTLPNALAYEYMHYISKSSNDAWDERVYE 2 +SLP+G PYPHS PP+L+Y++++++ DE					
Sbjct	97		GDQEYFPKYYPTHRPSKEKPNAY			· · · · 	15	3
Query	251	_	LVAQATTR-FSTGSLLGQVKRVA		361			
Sbjct	154		L + + +G+ +GQ R+ LTQNIRDKAYGSGTYMGQATRLV		187			

viral polymerase [Infectious bursal disease virus]

Sequence ID: emb|CAI47766.1| Length: 181 Number of Matches: 1

▶ See 1 more title(s) Range 1: 30 to 120

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
35.4 bits((80)	8.2()	Compositional matrix adjust.	27/98(28%)	45/98(45%)	15/98(15%)	+2	
Features:								
Query	92	VSLPV +SLP+	GSDLQIPTYKPGHEVS		AYEYMHYISK		ΥE	250
Sbjct	30		GDQEYFPKYYPTHRPSKEKPNAY		-			86
Query	251	_	LVAQATTR-FSTGSLLGQVKRVA L + + +G+ +GO R+		361			
Sbjct	87		LTQNIRDKAYGSGTYMGÕATRLV		120			

3-phosphoglycerate dehydrogenase [Vibrio sinaloensis]

Sequence ID: ref|WP_039477531.1| Length: 325 Number of Matches: 1

▶ See 1 more title(s) Range 1: 233 to 314

Score		Expect	Method	Identities	Positives	Gaps	Frame	
35.8 bits	s(81)	9.1()	Compositional matrix adjust.	30/99(30%)	48/99(48%)	19/99(19%)	+2	
Features	s:							
Query	14	LVNII	LVNIPFREAACPRMMALYGELLDTKDVSLPVGSDLQIPTYKPGHEVSPPLLTLPNALA 1 LVNI E P ALY L+ TK ++ V +P +E S PLLTLPN +A					
Sbjct	233		E P ALY L+ TK SRAELIAPNALYQTLVKHPTKL					
Query	188		HYISKSSNDAWDERVYETLRELLV Y+ ++S + + + +E +	'AQATTRFSTG +FS G				
Sbjct	285		GYVERNSYELYFQWAFENV					

viral polymerase [Infectious bursal disease virus]

Sequence ID: emb|CAI47786.1| Length: 181 Number of Matches: 1

Range 1: 30 to 120

Score Expect Method Identities Positives Gaps Frame

35.4 b	its(80)	9.6() Compositional matrix adjust. 27/98(28%) 46/98(46%) 15/98(15%) +2	
Featur	es:		
Query	7 92	VSLPVGSDLQIPTYKPGHEVSPPLLTLPNALAYEYMHYISKSSNDAWDERVYE 2 +SLP+G P Y P H S PP + L + Y ++ I +++++ DE	50
Sbjct	30	LSLPIGDQEYFPKYYPTHRPSKEKPNAYPPDIALLKQMIYLFLQ-IPEATDNLKDEVT 8	6
Query	251	TLRELLVAQATTR-FSTGSLLGQVKRVAAGQDVAYGRK 361 LL + + +G+ +GQ R+ A ++VA GR	
Shict	87		

RNA directed RNA polymerase, partial [Infectious bursal disease virus] Sequence ID: **gb|AEW44079.1|** Length: 160 Number of Matches: 1 Range 1: 22 to 111

	Expect	Method	Identities	Positives	Gaps	Fra	me
80) 9	9.8()	Compositional matrix adjust.	26/98(27%)	47/98(47%)	17/98(17%)	+2	
92		~					244
22						•	80
245				358			
81		~		111			
	80) § 92 22 245	92 VSLPV +SLP+ 22 LSLPI 245 YETLR + +R	92 VSLPVGSDLQIPTYKPGHEVS	92 VSLPVGSDLQIPTYKPGHEVSPPLLTLPNALZ +SLP+G PYPHS PP+L+ 22 LSLPIGDQEYFPKYYPTHRPSKEKPNAYPPDIALLKQM 245 YETLRELLVAQATTRFSTGSLLGQVKRVAAGQDVAYGR + +R+ + +G+ +GQ R+ A ++VA GR	92 VSLPVGSDLQIPTYKPGHEVSPPLLTLPNALAYEYMHYISKS +SLP+G PYPHS PP+L + Y++ + + + + + + + + + + + + + + + +	92 VSLPVGSDLQIPTYKPGHEVSPPLLTLPNALAYEYMHYISKSSNDAWDEI +SLP+G PYPHS PP+L + Y++ + +++ D DE 22 LSLPIGDQEYFPKYYPTHRPSKEKPNAYPPDIALLKQMIYLFLQ-VPEANEDLKDEVT 245 YETLRELLVAQATTRFSTGSLLGQVKRVAAGQDVAYGR 358 + +R+ + +G+ +GQ R+ A ++VA GR	92 VSLPVGSDLQIPTYKPGHEVSPPLLTLPNALAYEYMHYISKSSNDAWDERV +SLP+G PYPHS PP+L +Y++++D DE + LSLPIGDQEYFPKYYPTHRPSKEKPNAYPPDIALLKQMIYLFLQ-VPEANEDLKDEVTLL 245 YETLRELLVAQATTRFSTGSLLGQVKRVAAGQDVAYGR 358 + +R+ + +G+ +GQ R+ A ++VA GR

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AIF79732.1| Length: 192 Number of Matches: 1

▶ See 3 more title(s) kange 1: 74 to 167

Score		Expect	Method	Identities	Positives	Gaps	Fram	е
35.4 bits	s(80)	9.9()	Compositional matrix adjust.	27/101(27%)	46/101(45%)	15/101(14%)	+2	
Features	s:							
Query	92	VSLP	VGSDLQIPTYKPGHEVS +G PYPHS		LAYEYMHYISK + Y ++ + +		E 2	50
Sbjct	74		IGDQEYFPKYYPTHRPSKEKPNA				- 1	30
Query	251		LLVAQATTR-FSTGSLLGQVKRV					
Sbjct	131		LL					