Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BPEE6D014

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Blast report description

Nucleotide Sequence (349 letters)

RID <u>B8BPEE6D014</u> (Expires on 02-06 12:10 pm)

Query ID lcl|Query_80057

Description None

Molecule type nucleic acid

Query Length 349

Database Name nr

Description All non-redundant GenBank CDS

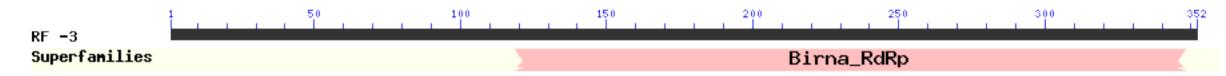
 $translations + PDB + SwissProt + PIR + PRF\ excluding$

environmental samples from WGS projects

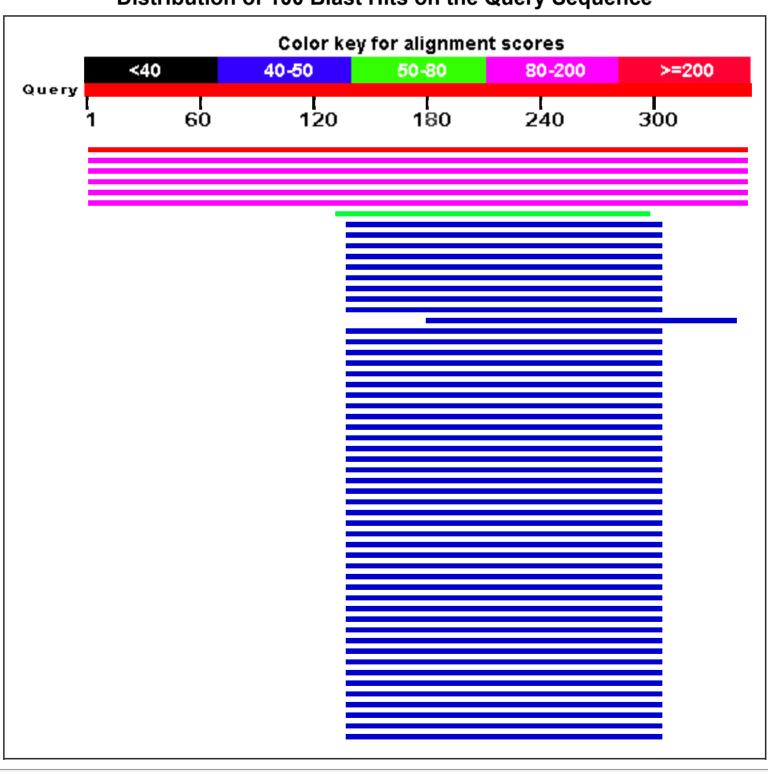
Program BLASTX 2.3.1+

□ Graphic Summary

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



Distribution of 100 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Description	Max	Total	Query	E	Ident	Accession
	score	score	cover	value		
putative RNA-dependent RNA polymerase VP1 [Drosophila x virus]	211	211	98%	5e-61	88%	NP_690806.1
VP1/RdRp [Culicine-associated Z virus]	171	171	98%	1e-46	72%	AGW51763.1
VP1/RdRp [Culicine-associated Z virus]	171	171	98%	1e-46	72%	AGW51781.1
unnamed protein product [Espirito Santo virus]	171	171	98%	2e-46	72%	YP_004956721.1
putative VP1 [Mosquitoe x virus]	170	170	98%	3e-46	71%	AFU34334.1
VP1 [Culex Y virus]	170	170	98%	3e-46	71%	AFR34027.1
RNA-dependent RNA polymerase [Blotched snakehead virus]	50.1	50.1	47%	2e-04	44%	YP_052864.1
RNA-dependant RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.002	38%	ADW65653.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.006	38%	BAH03930.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.006	38%	BAH03931.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.006	38%	BAH03929.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.006	38%	BAH03927.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.006	38%	BAT62518.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.007	38%	BAH03928.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.007	38%	BAH03932.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.007	38%	BAH03926.1
VP1 protein [Tasmanian aquabirnavirus]	45.1	45.1	46%	0.007	43%	ALF95252.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.007	38%	BAT62516.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.007	38%	BAH03935.1
VP1 protein [Infectious bursal disease virus]	45.1	45.1	47%	0.008	38%	AFX60122.1
RNA-dependant RNA polymerase [Infectious bursal disease virus]	43.5	43.5	47%	0.008	38%	ADX06843.1
viral protein 1 [Infectious bursal disease virus]	44.7	44.7	47%	0.008	38%	BAH03934.1
viral polymerase [Infectious bursal disease virus]	45.1	45.1	47%	0.008	38%	CAI54226.2
RNA-dependent RNA polymerase [Infectious bursal disease virus]	45.1	45.1	47%	0.009	38%	AKM16808.1
RNA-dependant RNA polymerase [Infectious bursal disease virus]	43.9	43.9	47%	0.009	38%	ADW65654.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.011	38%	ABB97491.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	43.9	43.9	47%	0.011	38%	AFP43762.1
RNA-dependent RNA-polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAK51523.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAT76291.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.011	38%	ABB97490.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	ACB56955.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AFI41892.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	ACB56956.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAS10170.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AKD94180.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAD49775.1
unnamed protein product [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	CAA58852.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AHW82960.1

VP1 RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	NP_690839.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	ABW38088.1
RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAM51641.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAR24134.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	ABP96990.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAM97562.1
RecName: Full=RNA-directed RNA polymerase; Short=RDRP; AltName: Full=Protein VP1	44.7	44.7	47%	0.011	38%	Q9Q6Q5.1
RNA-dependent RNA-polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	ABS86938.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAS10169.1
RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	<u>AAM11679.1</u>
RNA-dependent RNA-polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AAY16544.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	ACV66327.1
VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.011	38%	AEQ29950.1
RecName: Full=RNA-directed RNA polymerase; Short=RDRP; AltName: Full=Protein VP1 [Infectious bursal disease virus chicken/Cuba/Soroa/1998]	44.7	44.7	47%	0.011	38%	A7L9Z4.1
VP1 [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AAD49776.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.012	38%	AFN80480.1
double-stranded RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	44.7	44.7	47%	0.012	38%	AAD32619.1
RNA dependent RNA polymerase (RdRp) [Infectious bursal disease virus]	44.7	44.7	47%	0.012	38%	CDP32876.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.012	38%	AAD23375.1
RNA dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.012	38%	<u>CAJ44476.1</u>
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.012	38%	AAT99259.1
VP1 RNA polymerase [Infectious bursal disease virus]	44.7	44.7	47%	0.012	38%	AAB68518.1
VP1 [Infectious bursal disease virus]	43.9	43.9	47%	0.012	38%	AGL92190.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AFN80479.1
RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AAK69715.1
VP1 [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AAD49777.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AAU10476.2
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	ACN69081.1
VP1 [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AFP86287.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AEP04404.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AAK30027.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AFN80482.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AFN80481.1
VP1 [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AIG93143.1
VP1 [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	ABW38085.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	44.3	44.3	47%	0.012	38%	AAN04462.1

virus] 44.	.3 4	14.3	47%	0.012	38%	<u>AAY16541.1</u>
VP1 protein [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	CAC60257.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	ACV83399.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	.3 4	14.3	47%	0.012	38%	AEW69315.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	ACS44343.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	.3 4	14.3	47%	0.012	38%	ABG91146.2
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	ABG91142.1
RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	AAK69710.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	AFF19376.1
viral protein 1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	AAF85954.1
RNA dependent RNA polymerase (RdRp) [Infectious bursal disease virus]	.3 4	14.3	47%	0.012	38%	CDP32873.1
Chain A, Crystal Structure Of A Birnavirus (Ibdv) Rna- Dependent Rna Polymerase Vp1	.3 4	14.3	47%	0.012	38%	2PGG_A
VP1 [Infectious bursal disease virus] 43.	.9 4	13.9	47%	0.012	38%	AGL92135.1
VP1 [Infectious bursal disease virus] 43.	.9 4	13.9	47%	0.012	38%	AGL92132.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	AEQ29951.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	ABG91145.1
VP1 [Infectious bursal disease virus] 43.	.9 4	13.9	47%	0.012	38%	AGL92161.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	ACD75786.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	AFF19377.1
VP1 [Infectious bursal disease virus] 43.	.9 4	13.9	47%	0.012	38%	AGL92188.1
VP1 [Infectious bursal disease virus] 43.	.9 4	13.9	47%	0.012	38%	AGL92137.1
RNA polymerase [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	CAD43216.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	ACB56954.1
VP1 [Infectious bursal disease virus] 44.	.3 4	14.3	47%	0.012	38%	ABI52865.1
VP1 [Infectious bursal disease virus] 43.	.5 4	13.5	47%	0.012	38%	AGL92192.1
VP1 [Infectious bursal disease virus] 43.	.5 4	13.5	47%	0.012	38%	AGL92139.1

□ <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: 227 to 341

Score		Expect	Method	Identities	Positives	Gaps	Frame
211 bits	(538)	5e-61()	Compositional matrix adjust.	101/115(88%)	107/115(93%)	0/115(0%)	-3
Features	s:						
Query	347		YTQEEAELMGVSDSLPTITQSS				
Sbjct	227		FYT EEAELMGV DSLP ITQSSA YYTPEEAELMGVPDSLPDITQSSA				
Query	167		TGTNNPLDTKKEGVAETTNKNP	~			
Sbjct	287		FTG+NNPLD KKEGVAE T KNP- FTGSNNPLDPKKEGVAEVTTKNP				1

VP1/RdRp [Culicine-associated Z virus]

Sequence ID: **gb|AGW51763.1|** Length: 998 Number of Matches: 1 Range 1: 227 to 341

Score	Expect	Method	Identities	Positives	Gaps	Frame
171 bits(434)	1e-46()	Compositional matrix adjust.	83/115(72%)	96/115(83%)	0/115(0%)	-3
Features:						

Query 347 LDWLIYTQEEAELMGVSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLL 168
LDWL+YT +EAELMGV DSLP I+ SSAAGLPWLGKKKGEVA+SALITANMLI+D S +L
Sbjct 227 LDWLVYTPQEAELMGVPDSLPAISHSSAAGLPWLGKKKGEVAISALITANMLIQDTSRIL 286

Query 167 KENLFTGTNNPLDTKKEGVAETTNKNPKRAADQFSRLLLDRIVKEYSYTMMGLLF 3
KE LF+G+N+PL+ KKEGVA T K+ KR+A QFS +L I EYSYTMMGLLF
Sbjct 287 KETLFSGSNDPLEAKKEGVAAETAKSKKRSAGQFSAEILKMITTEYSYTMMGLLF 341

VP1/RdRp [Culicine-associated Z virus]

Sequence ID: gb|AGW51781.1| Length: 998 Number of Matches: 1

Range 1: 227 to 341

Score		Expect Method	Identities	Positives	Gaps	Frame
171 bits	(433)	1e-46() Compositional matrix adjust.	83/115(72%)	96/115(83%)	0/115(0%)	-3
Features	s:					
Query	347	LDWLIYTQEEAELMGVSDSLPTITQSSA LDWL+YT +EAELMGV DSLP I+ SSA				
Sbjct	227	LDWLVYTPQEAELMGVPDSLPAISHSSA				
Query	167	KENLFTGTNNPLDTKKEGVAETTNKNPK				
Sbjct	287	KE LF+G+N+PL+ KKEGVA T K+ K KETLFSGSNDPLEAKKEGVAAETAKSKK				41

unnamed protein product [Espirito Santo virus]

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

▶ See 1 more title(s) Range 1: 227 to 341

Score		Expect	Method	Identities	Positives	Gaps	Frame
171 bits	(432)	2e-46()	Compositional matrix adjust.	83/115(72%)	95/115(82%)	0/115(0%)	-3
Features	S :						
Query	347		TQEEAELMGVSDSLPTITQSSA TT +EAELMGV DSLP IT SSA				
Sbjct	227		TT TEAELMGV DSLP IT SSAZ TTPQEAELMGVPDSLPAITHSSAZ				
Query	167		TGTNNPLDTKKEGVAETTNKNPKI				
Sbjct	287		+G+N+PL+ K+EGVA T K+ I SGSNDPLEAKREGVAAETAKSKTI				11

putative VP1 [Mosquitoe x virus]

Sequence ID: gb|AFU34334.1| Length: 995 Number of Matches: 1

Range 1: 227 to 341

Score		Expect Method	Identities	Positives	Gaps	Frame
170 bits	(431)	3e-46() Compositional matrix adjust.	82/115(71%)	95/115(82%)	0/115(0%)	-3
Features	s:					
Query	347	LDWLIYTQEEAELMGVSDSLPTITQSSA LDWL+YT +EAELMGV DSLP IT SSA				
Sbjct	227	LDWLVYTPQEAELMGVPDSLPAITHSSA				
Query	167	KENLFTGTNNPLDTKKEGVAETTNKNPK KE LF+G+N+PL+ K+EGVA T K+		DRIVKEYSYTM		
Sbjct	287	KETLFSGSNDPLEAKREGVAAETAKSKT				41

VP1 [Culex Y virus]

Sequence ID: **gb|AFR34027.1|** Length: 998 Number of Matches: 1

Range 1: 227 to 341

Score		Expect Method	Identities	Positives	Gaps	Frame
170 bits	(431)	3e-46() Compositional matrix adjust.	82/115(71%)	95/115(82%)	0/115(0%)	-3
Features	s:					
Query	347	LDWLIYTQEEAELMGVSDSLPTITQSSA LDWL+YT +EAELMGV DSLP IT SSA				
Sbjct	227	LDWLVYTPQEAELMGVPDSLPAITHSSA				
Query	167	KENLFTGTNNPLDTKKEGVAETTNKNPK KE LF+G+N+PL+ K+EGVA T K+	KRAADQFSRLLI R+A OFS +I		MMGLLF 3	
Sbjct	287	KETLFSGSNDPLEAKREGVAAETAKSKT				41

RNA-dependent RNA polymerase [Blotched snakehead virus]
Sequence ID: **ref|YP_052864.1|** Length: 867 Number of Matches: 1

▶ See 2 more title(s) kange 1: 237 to 291

Score		Expect	Method	Identities	Positives	Gaps	Frame
50.1 bits	s(118)	2e-04()	Compositional matrix adjust.	24/55(44%)	32/55(58%)	0/55(0%)	-3
Features	s:						
Query	296	DSLPTI	TQSSAAGLPWLGKKKGEVAVSALI T S++GLP++GK KGE SAL			TNNPL 1	32
Sbjct	237		TMKSSSGLPFIGKTKGETVTSAL		·		91

RNA-dependant RNA polymerase [Infectious bursal disease virus]
Sequence ID: **gb|ADW65653.1|** Length: 152 Number of Matches: 1

Range 1: 91 to 145

Score		Expect Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.002() Compositional matrix adjus	it. 21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEV V D LP I S++GLP++G+ KGE		OVSSLLKENLF ++S+LLK+	TGTNN 1	38
Sbjct	91	VEDYLPRINLKSSSGLPYVGRTKGET			,	45

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03930.1| Length: 332 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.006() Compositional matrix adj	ust. 21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGE V D LP I S++GLP++G+ KGE			TGTNN 1	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKGE			,	99

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03931.1| Length: 332 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.006() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS				38
Sbjct	245	V D LP I S++GLP++G+ KGE VEDYLPKINLKSSSGLPYVGRTKGETIGE	+ +N +R- MIAISNQFLRI		T +N FTKGSN 2	99

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03929.1| Length: 332 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.006()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGEN			,	99

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03927.1| Length: 332 Number of Matches: 1

Score Expect Method Identities **Positives** Gaps **Frame** 44.7 bits(104) 0.006() Compositional matrix adjust. 0/55(0%) -3 21/55(38%) 34/55(61%) Features: Query 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN S++GLP++G+ KGE + +N +R++S+LLK+ Sbjct 245 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSALLKQGAGTKGSN 299

viral protein 1, partial [Infectious bursal disease virus]

Sequence ID: dbj|BAT62518.1| Length: 332 Number of Matches: 1

Range 1: 245 to 299

Identities **Score Expect Method Positives** Gaps **Frame** 44.7 bits(104) 0.006() Compositional matrix adjust. 21/55(38%) 34/55(61%) 0/55(0%) -3 Features: 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN 138 Query V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSALLKQGAGTKGSN 299

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03928.1| Length: 332 Number of Matches: 1

Range 1: 245 to 299

Score **Positives Expect Method** Identities Gaps **Frame** 44.7 bits(104) 0.007() Compositional matrix adjust. 21/55(38%) 34/55(61%) 0/55(0%) -3 Features: VSDSLPTITOSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN Query 302 138 S++GLP++G+ KGE V D LP I + +N +R++S+LLK+ Sbjct 245 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSALLKQGAGTKGSN 299

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03932.1| Length: 332 Number of Matches: 1

▶ See 6 more title(s) Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.007()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	S :						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGEN			,	99

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03926.1| Length: 332 Number of Matches: 1

▶ See 4 more title(s) Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.007()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVSA PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE			,	99

VP1 protein [Tasmanian aquabirnavirus]

Sequence ID: gb|ALF95252.1| Length: 844 Number of Matches: 1

▶ See 1 more title(s) Range 1: 223 to 274

Score	Expect Method	Identities	Positives	Gaps	Frame

45.1 bits(105) 0.007() Compositional matrix adjust. 23/54(43%) 32/54(59%) 2/54(3%) -3

Features:

Query 341 WLIYTQEEAELMGVSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDV 180 WLI Q E + LP +T S+AGLP++GK KG+ AL+ A+ IRD+ Sbjct 223 WLI--QYTGEPLTDRSYLPHVTVKSSAGLPYIGKTKGDTTAEALVLADSFIRDL 274

viral protein 1, partial [Infectious bursal disease virus]

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

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.007() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKGETIGE			,	99

viral protein 1 [Infectious bursal disease virus]

Sequence ID: dbj|BAH03935.1| Length: 332 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.007()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP' V D LP	TITQSSAAGLPWLGKKKGEVAVS <i>I</i> I S++GLP++G+ KGE		VSSLLKENLF +S+LLK+	TGTNN 1	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGEN			,	99

VP1 protein [Infectious bursal disease virus]

Sequence ID: gb|AFX60122.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Met	thod	Identities	Positives	Gaps	Frame
45.1 bits	s(105)	0.008() Con	npositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLPTIT(QSSAAGLPWLGKKKGEVAVSA S++GLP++G+ KGE	LITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245		LKSSSGLPYVGRTKGETIGGM			,	99

RNA-dependant RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|ADX06843.1| Length: 183 Number of Matches: 1

Range 1: 67 to 121

Score		Expect Method	Identities	Positives	Gaps	Frame
43.5 bits	s(101)	0.008() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE		OVSSLLKENLF -+S+LLK+	TGTNN 1	38
Sbjct	67	VEDYLPKINLKSSSGLPYVGRTKGETIGE			,	21

viral protein 1 [Infectious bursal disease virus]

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

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.008()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	S :						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGEN			1	99

viral polymerase [Infectious bursal disease virus]

Sequence ID: emb|CAI54226.2| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
45.1 bits	s(105)	0.008() Compositional matrix adjust	t. 21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVA V D LP I S++GLP++G+ KGE		OVSSLLKENLF ++S+LLK+	TGTNN 1	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKGETI				99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AKM16808.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect N	Method	Identities	Positives	Gaps	Frame
45.1 bits	s(105)	0.009() C	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:						
Query	302	VSDSLPT: V D LP	ITQSSAAGLPWLGKKKGEVAVSA I S++GLP++G+ KGE		VSSLLKENLF +S+LLK+	TGTNN 1 T +N	38
Sbjct	245		INLKSSSGLPYVGRTKGETVGEM			,	99

RNA-dependant RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|ADW65654.1| Length: 212 Number of Matches: 1

Range 1: 91 to 145

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits((102)	0.009()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:	:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVS <i>I</i> P I S++GLP++G+ KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	91		RINLKSSSGLPYVGRTKGETIGEN			,	45

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|ABB97491.1| Length: 405 Number of Matches: 1

Range 1: 238 to 292

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVSA PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	238		PKINLKSSSGLPYVGRTKGETIGE			,	92

RNA-dependent RNA polymerase, partial [Infectious bursal disease virus]

Sequence ID: gb|AFP43762.1| Length: 249 Number of Matches: 1

Range 1: 82 to 136

Score	E	Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits(102) 0	.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:							
Query 3		SDSLP'	TITQSSAAGLPWLGKKKGEVAVSA I S++GLP++G+ KGE	LITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct 8	•		RINLKSSSGLPYVGRTKGETIGEM				36

RNA-dependent RNA-polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAK51523.1| Length: 878 Number of Matches: 1

Score Expect Method I	Identities	Positives	Gaps	Frame
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44.7 bits(104) 0.011() Compositional matrix adjust. 21/55(38%) 34/55(61%) 0/55(0%) -3 Features:

Query 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N Sbjct 245 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSTLLKQGAGTKGSN 299

RNA-dependent RNA polymerase [Infectious bursal disease virus]
Sequence ID: **gb|AAT76291.1**| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Identities Score **Expect Method Positives** Gaps **Frame** 0/55(0%) -3 44.7 bits(104) 0.011() Compositional matrix adjust. 21/55(38%) 34/55(61%) Features: VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN Query 302 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSTLLKQGAGTKGSN 299

RNA-dependent RNA polymerase [Infectious bursal disease virus]

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

Range 1: 238 to 292

Score Identities **Expect Method Positives** Gaps **Frame** 44.3 bits(103) 0.011() Compositional matrix adjust. 21/55(38%) 34/55(61%) 0/55(0%) -3 Features: Query 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ Sbjct 238 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSTLLKQGAGTKGSN 292

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ACB56955.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVS PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245	. – ––	PKINLKSSSGLPYVGRTKGETIGE			,	99

RNA-directed RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AFI41892.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVS <i>I</i> I S++GLP++G+ KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245	. – –-	KINLKSSSGLPYVGRTKGETIGEN			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ACB56956.1| Length: 879 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	S :						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAS10170.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVS PIS++GLP++G+ KGE			TGTNN 1	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIG			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AKD94180.1| Length: 878 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits((104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:	:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVS.	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAD49775.1| Length: 878 Number of Matches: 1

▶ See 14 more title(s) Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA			TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE			,	99

unnamed protein product [Infectious bursal disease virus]

Sequence ID: emb|CAA58852.1| Length: 878 Number of Matches: 1

▶ See 1 more title(s) kange 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits(1	104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:							
Query 3	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVSA PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct 2	245	. – ––	KINLKSSSGLPYVGRTKGETIGEN			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AHW82960.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bit	ts(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	es:						
Query	302	VSDSLF V D LF	PTITQSSAAGLPWLGKKKGEVAVS P I S++GLP++G+ KGE		OVSSLLKENLF -+S+LLK+	TGTNN 1	38
Sbict	245	. – –-	PKINLKSSSGLPYVGRTKGETIGE			_ '11	99

VP1 RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: ref|NP_690839.1| Length: 879 Number of Matches: 1

▶ See 2 more title(s) Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011() Compositional matrix	(adjust. 21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGK				38
Sbjct	245	V D LP I S++GLP++G+ VEDYLPKINLKSSSGLPYVGRT			T +N TKGSN 2	99

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABW38088.1|** Length: 879 Number of Matches: 1 Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVS PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE	1 - 1		,	99

RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus] Sequence ID: gb|AAM51641.1| Length: 879 Number of Matches: 1

▶ See 1 more title(s) Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:							
Query :	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct :	245		KINLKSSSGLPYVGRTKGETIGEN			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAR24134.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	3 :						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA TIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGEN			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ABP96990.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAV V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R		TGTNN 1	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKGETIG			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAM97562.1| Length: 879 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3

Features:

Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN	138
_		V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N	
Shict	245	VEDVI.PKINI.KSSSCI.PVVCRTKCETTCEMIAISNOFI.REI.STI.KOCACTKCSN	299

RecName: Full=RNA-directed RNA polymerase; Short=RDRP; AltName: Full=Protein VP1

Sequence ID: sp|Q9Q6Q5.1|RDRP_IBDV Length: 881 Number of Matches: 1

▶ See 1 more title(s) Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVS I S++GLP++G+ KGE	SALITANMLIRD + +N +R+		TGTNN 1	.38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE			,	.99

RNA-dependent RNA-polymerase [Infectious bursal disease virus]

Sequence ID: gb|ABS86938.1| Length: 881 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVS PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGE				99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAS10169.1| Length: 881 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVSA PIS++GLP++G+KGE			TGTNN 1	38
Sbjct	245		PKINLKSSSGLPYVGRTKGETIGE			,	99

RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAM11679.1|AF493979_1 Length: 879 Number of Matches: 1

▶ See 1 more title(s) Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVSA PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245	. – ––	PKINLKSSSGLPYVGRTKGETIGE			,	99

RNA-dependent RNA-polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAY16544.1| Length: 879 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits(104	l) 0.011()	Compositional matrix adjust.	. 21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:						
Query 30	VSDSL:	PTITQSSAAGLPWLGKKKGEVAV P I S++GLP++G+ KGE		VSSLLKENLF -+S+LLK+	TGTNN 1 T +N	38

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ACV66327.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLPT V D LP	ritossaaglpwlgkkkgevavs <i>a</i> i s++glp++g+ kge			TGTNN 1 T +N	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGEM			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AEQ29950.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVSA PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		PKINLKSSSGLPYVGRTKGETIGE			,	99

RecName: Full=RNA-directed RNA polymerase; Short=RDRP; AltName: Full=Protein VP1 [Infectious bursal disease virus

chicken/Cuba/Soroa/1998]

Sequence ID: sp|A7L9Z4.1|RDRP_IBDVB Length: 879 Number of Matches: 1

▶ See 1 more title(s) Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	(104)	0.011()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGEN			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAD49776.1| Length: 795 Number of Matches: 1

Range 1: 161 to 215

Score	Ехр	ect	Method	Identities	Positives	Gaps	Frame
44.3 bits(1	03) 0.01	2()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:							
Query 3		SLPT	TITQSSAAGLPWLGKKKGEVAVSA I S++GLP++G+ KGE	LITANMLIRD + +N +R+		TGTNN 1:	38
Sbjct 1			KINLKSSSGLPYVGRTKGETIGEM			,	15

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

Sequence ID: gb|AFN80480.1| Length: 878 Number of Matches: 1

Score		Expect Method	lde	entities	Positives	Gaps	Frame
44.7 bits	s(104)	0.012() Compositional	matrix adjust. 21/	55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLPTITQSSAAGLP V D LP I S++GLP		ANMLIRDY +N +R+-		rgtnn 13 r +n	38
Sbjct	245	VEDYLPKINLKSSSGLP					99

double-stranded RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAD32619.1|AF133905_1 Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score	Expect Method	Identities	Positives	Gaps	Frame
44.7 bits(104)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:					
Query 302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS. V D LP I S++GLP++G+ KGE	ALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct 245	VEDYLPKINLKSSSGLPYVGRTKGETIGE			,	99

RNA dependent RNA polymerase (RdRp) [Infectious bursal disease virus]

Sequence ID: emb|CDP32876.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score	Expect Method	Identities	Positives	Gaps	Frame
44.7 bits(104)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:					
Query 302	VSDSLPTITQSSAAGLPWLGKKKGEVAVSZ V D LP I S++GLP++G+ KGE	ALITANMLIRI + +N +R+		TGTNN 1	38
Sbjct 245	VEDYLPKINLKSSSGLPYVGRTKGETIGE			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAD23375.1|AF092944_1 Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 b	its(104)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Featur	es:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVS <i>I</i> P I S++GLP++G+ KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245	. – –-	KINLKSSSGLPYVGRTKGETIGEN			,	99

RNA dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: emb|CAJ44476.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGE			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAT99259.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKGETIG			,	99

VP1 RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAB68518.1| Length: 891 Number of Matches: 1

Score Expect Method	Identities	Positives	Gaps	Frame
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44.7 bits(104) 0.012() Compositional matrix adjust. 21/55(38%) 34/55(61%) 0/55(0%) -3 Features:

Query 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N Sbjct 257 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSTLLKQGAGTKGSN 311

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AGL92190.1| Length: 255 Number of Matches: 1

Range 1: 30 to 84

Score		Expect Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct	30	VEDYLPKINLKSSSGLPYVGRTKGETIGE			,	4

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

Sequence ID: gb|AFN80479.1| Length: 878 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA I S++GLP++G+ KGE	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGEN				99

RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAK69715.1| Length: 878 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method		Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012() Composition	onal matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:						
Query	302		GLPWLGKKKGEVAVS GLP++G+ KGE	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245		GLPYVGRTKGETIGE:			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAD49777.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:							
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245		I S++GLP++G+ KGE KINLKSSSGLPYVGRTKGETIGEN			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAU10476.2| Length: 879 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKGETIG			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus] Sequence ID: gb|ACN69081.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score	Expect Method	Identities	Positives	Gaps	Frame
44.3 bits(103)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:					
Query 302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	ALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct 245	VEDYLPKINLKSSSGLPYVGRTKGETIGE			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AFP86287.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	S :						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVSA PIS++GLP++G+KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AEP04404.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

_	Score		Expect	Method	Identities	Positives	Gaps	Frame
4	4.3 bits((103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
F	eatures:							
Q	uery	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	LITANMLIRD + +N +R+		TGTNN 1 T +N	38
S	bjct	245		KINLKSSSGLPYVGRTKGETIGEM			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAK30027.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame	
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3	
Features:								
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVSA PIS++GLP++G+KGE			TGTNN 1	38	
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE			,	99	

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

Sequence ID: gb|AFN80482.1| Length: 878 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:						
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVSA V D LP I S++GLP++G+ KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKGETIGEN				99

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

Sequence ID: **gb|AFN80481.1|** Length: 878 Number of Matches: 1 Range 1: 245 to 299

Score Expect Method	Identities	Positives	Gaps	Frame
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44.3 bits(103) 0.012() Compositional matrix adjust. 21/55(38%) 34/55(61%) 0/55(0%) -3 Features:

Query 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N Sbjct 245 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSTLLKQGAGTKGSN 299

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AlG93143.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Expect Method Identities Score **Positives** Gaps **Frame** 0/55(0%) -3 44.3 bits(103) 0.012() Compositional matrix adjust. 21/55(38%) 34/55(61%) Features: VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN Query 302 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSALLKQGAGTKGSN 299

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ABW38085.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Expect Method Score Identities **Positives** Gaps **Frame** 44.3 bits(103) 0.012() Compositional matrix adjust. 21/55(38%) 34/55(61%) 0/55(0%) -3 Features: VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN Query 302 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ Sbjct 245 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSALLKQGAGTKGSN 299

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAN04462.1|AF527040_1 Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGE			,	99

RNA-dependent RNA-polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAY16541.1| Length: 881 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP7 V D LP	ritgssaaglpwlgkkkgevavsa i s++glp++g+ kge			TGTNN 1 T +N	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGEM			,	99

VP1 protein [Infectious bursal disease virus]

Sequence ID: emb|CAC60257.1| Length: 879 Number of Matches: 1

Score	Expect Method	Identities	Positives	Gaps	Frame
44.3 bits(103) 0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:					
Query 30	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	ALITANMLIRI + +N +R-		TGTNN 1	.38
Sbjct 24				,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ACV83399.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012() Compositional matrix ad	ust. 21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKG V D LP I S++GLP++G+ KG			TGTNN 1 T +N	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKG				99

RNA-directed RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AEW69315.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	PTITQSSAAGLPWLGKKKGEVAVS PI S++GLP++G+ KGE		VSSLLKENLF -+S+LLK+	TGTNN 1	38
Sbjct	245		PKINLKSSSGLPYVGRTKGETIGE			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ACS44343.1|** Length: 879 Number of Matches: 1 Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	S :						
Query	302	VSDSLF V D LF	PTITQSSAAGLPWLGKKKGEVAVSA P I S++GLP++G+ KGE		VSSLLKENLF +S+LLK+	TGTNN 1 T +N	38
Sbjct	245		PKINLKSSSGLPYVGRTKGETIGE			,	99

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|ABG91146.2| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	S :						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA				38
Sbjct	245		I S++GLP++G+ KGE KINLKSSSGLPYVGRTKGETIGEN			T +N TKGSN 2	99

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABG91142.1|** Length: 879 Number of Matches: 1 Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAV V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct	245	VEDYLPKINLKSSSGLPYVGRTKGETIG			,	99

RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAK69710.1|AF362770_1 Length: 879 Number of Matches: 1

Score Expect Method	Identities	Positives	Gaps	Frame
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44.3 bits(103) 0.012() Compositional matrix adjust. 21/55(38%) 34/55(61%) 0/55(0%) -3 Features:

Query 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N Sbjct 245 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSALLKQGAGTKGSN 299

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AFF19376.1| Length: 553 Number of Matches: 1

▶ See 1 more title(s) kange 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012() Compositional matrix adju	st. 21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEV V D LP I S++GLP++G+ KGE			TGTNN 1	38
Sbjct	245	VEDYLPRINLKSSSGLPYVGRTKGET			,	99

viral protein 1 [Infectious bursal disease virus]

Sequence ID: gb|AAF85954.1|AF240687_1 Length: 879 Number of Matches: 1

▶ See 3 more title(s) kange 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	LITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGEM			,	99

RNA dependent RNA polymerase (RdRp) [Infectious bursal disease virus] Sequence ID: **emb|CDP32873.1|** Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGEN			,	99

Chain A, Crystal Structure Of A Birnavirus (Ibdv) Rna-Dependent Rna Polymerase Vp1

Sequence ID: pdb|2PGG|A Length: 774 Number of Matches: 1

Range 1: 215 to 269

Score		Expect I	Method	Identities	Positives	Gaps	Frame
44.3 bits(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:							
Query	302	VSDSLPT V D LP	TITQSSAAGLPWLGKKKGEVAVSA I S++GLP++G+ KGE		VSSLLKENLF +S+LLK+	TGTNN 1 T +N	38
Sbjct	215	. – –-	INLKSSSGLPYVGRTKGETIGEM			,	69

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AGL92135.1| Length: 255 Number of Matches: 1

Range 1: 30 to 84

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits(102)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3

Features:

Query 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N Sbjct 30 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSTLLKQGAGTKGSN 84

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AGL92132.1| Length: 255 Number of Matches: 1

Range 1: 30 to 84

Score	Expect Method	Identities	Positives	Gaps	Frame
43.9 bits(102) 0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:					
Query 30	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct 30	VEDYLPKINLKSSSGLPYVGRTKGETIGE			,	4

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AEQ29951.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	S :						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA			TGTNN 1	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGE			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ABG91145.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012() Compositional m	natrix adjust. 21/55(38%	%) 34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	~	LGKKKGEVAVSALITANMLI +G+ KGE + +N +	RDVSSLLKENLI R++S+LLK+	FTGTNN 1 T +N	38
Sbjct	245		GRTKGETIGEMIAISNQFI			99

VP1, partial [Infectious bursal disease virus]

Sequence ID: **gb|AGL92161.1|** Length: 255 Number of Matches: 1 Range 1: 30 to 84

Score		Expect Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAV V D LP I S++GLP++G+ KGE		OVSSLLKENLF ++S+LLK+	TGTNN 1	38
Sbjct	30	VEDYLPKINLKSSSGLPYVGRTKGETIG			,	4

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ACD75786.1| Length: 871 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	S :						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA			TGTNN 1 T +N	38
Sbjct	245		KINLKSSSGLPYVGRTKGETIGEN				99

Sequence ID: gb|AFF19377.1| Length: 553 Number of Matches: 1

▶ See 2 more title(s) Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP'	TITQSSAAGLPWLGKKKGEVAVS <i>I</i> I S++GLP++G+ KGE	ALITANMLIRD + +N +R+		TGTNN 1	38
Sbjct	245		RINLKSSSGLPYVGRTKGETIGEN				99

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AGL92188.1| Length: 255 Number of Matches: 1

Range 1: 30 to 84

Score		Expect Method	Identities	Positives	Gaps	Frame
43.9 bits((102)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features:						
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAV V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct	30	VEDYLPKINLKSSSGLPYVGRTKGETIC			,	4

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AGL92137.1| Length: 255 Number of Matches: 1

Range 1: 30 to 84

Score		Expect Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R		TGTNN 1	38
Sbjct	30	VEDYLPKINLKSSSGLPYVGRTKGETIGI			,	4

RNA polymerase [Infectious bursal disease virus]

Sequence ID: emb|CAD43216.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012()	Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEVAVSA	ALITANMLIRD + +N +R+		TGTNN 1 T +N	38
Sbjct	245	. – ––	KINLKSSSGLPYVGRTKGETIGE			,	99

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ACB56954.1| Length: 879 Number of Matches: 1

Range 1: 245 to 299

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAV				38
Sbjct	245	V D LP I S++GLP++G+ KGE VEDYLPKINLKSSSGLPYVGRTKGETIG			T +N STKGSN 2	99

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABI52865.1|** Length: 879 Number of Matches: 1 Range 1: 245 to 299

Score Expect Method	Identities	Positives	Gaps	Frame
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21/55(38%) 34/55(61%) 0/55(0%) -3 Features: Query 302 VSDSLPTITQSSAAGLPWLGKKKGEVAVSALITANMLIRDVSSLLKENLFTGTNN 138 V D LP I S++GLP++G+ KGE + +N +R++S+LLK+ T +N Sbjct 245 VEDYLPKINLKSSSGLPYVGRTKGETIGEMIAISNQFLRELSALLKQGAGTKGSN 299 Query 302

VP1, partial [Infectious bursal disease virus]

44.3 bits(103) 0.012() Compositional matrix adjust.

Sequence ID: **gb|AGL92192.1|** Length: 255 Number of Matches: 1 Range 1: 30 to 84

Score		Expect Method	Identities	Positives	Gaps	Frame
43.5 bits	s(101)	0.012() Compositional matrix adjust.	21/55(38%)	34/55(61%)	0/55(0%)	-3
Feature	s:					
Query	302	VSDSLPTITQSSAAGLPWLGKKKGEVAVS V D LP I S++GLP++G+ KGE	SALITANMLIRI + +N +R-		TGTNN 1	38
Sbjct	30	VEDYLPKINLKSSSGLPYVGRTKGETIG			,	4

VP1, partial [Infectious bursal disease virus]

Sequence ID: gb|AGL92139.1| Length: 255 Number of Matches: 1

▶ See 10 more title(s) Range 1: 30 to 84

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)		0.012()	Compositional matrix adju	ıst. 21/55(38%)	34/55(61%)	0/55(0%)	-3
Features	s:						
Query	302	VSDSLP V D LP	TITQSSAAGLPWLGKKKGEV		OVSSLLKENLF -+S+LLK+	TGTNN 1	38
Sbjct	30		KINLKSSSGLPYVGRTKGE			,	4