Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BM2NAN015

- ► Formatting options
- ▶ Download

Blast report description

Nucleotide Sequence (1938 letters)

RID <u>B8BM2NAN015</u> (Expires on 02-06 12:09 pm)

Query ID lcl|Query_87755

Description None **Molecule type** nucleic acid

Query Length 1938

Database Name nr

Description All non-redundant GenBank CDS

 $translations + PDB + Swiss Prot + PIR + PRF\ excluding$

environmental samples from WGS projects

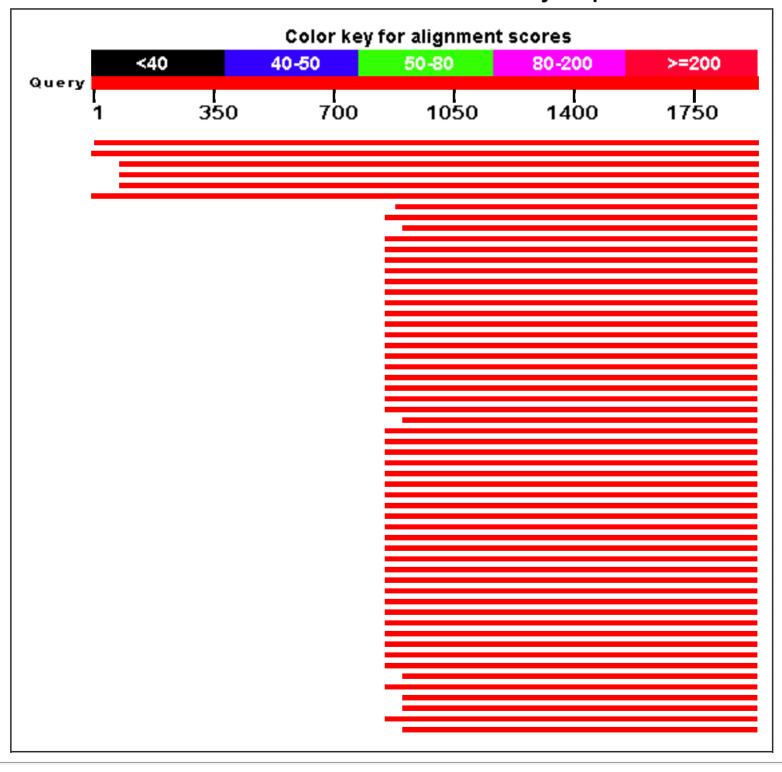
Program BLASTX 2.3.1+

□ 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 score	Total score	Query cover	E value	Ident	Accession
putative RNA-dependent RNA polymerase VP1 [Drosophila x virus]	1070	1070	99%	0.0	81%	NP_690806.1
VP1/RdRp [Culicine-associated Z virus]	887	887	100%	0.0	67%	AGW51781.1
VP1/RdRp [Culicine-associated Z virus]	884	884	95%	0.0	67%	AGW51763.1
VP1 [Culex Y virus]	871	871	95%	0.0	67%	AFR34027.1
unnamed protein product [Espirito Santo virus]	869	869	95%	0.0	67%	YP_004956721.1
putative VP1 [Mosquitoe x virus]	865	865	100%	0.0	66%	<u>AFU34334.1</u>
RNA-dependent RNA polymerase [Blotched snakehead virus]	244	244	54%	3e-66	39%	YP_052864.1
RecName: Full=RNA-directed RNA polymerase; Short=RDRP; AltName: Full=Protein VP1	236	236	55%	2e-65	38%	P31817.1
VP1 [Infectious bursal disease virus]	237	237	53%	1e-63	40%	AKU89586.1
RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	236	236	55%	2e-63	38%	AAR91595.1
RecName: Full=RNA-directed RNA polymerase; Short=RDRP; AltName: Full=Protein VP1	236	236	55%	2e-63	38%	P12918.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	236	236	55%	2e-63	38%	AEW69315.1
RNA-dependent RNA-polymerase [Infectious bursal disease virus]	236	236	55%	2e-63	38%	AAK51523.1
VP1 [Infectious bursal disease virus]	236	236	55%	2e-63	38%	ACB56956.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	236	236	55%	2e-63	38%	<u>AFN80481.1</u>
RNA-dependent RNA-polymerase [Infectious bursal disease virus]	236	236	55%	2e-63	38%	AAY16544.1
RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	236	236	55%	2e-63	38%	AAM51641.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	236	236	55%	2e-63	38%	AAS10169.1
RNA dependent RNA polymerase (RdRp) [Infectious bursal disease virus]	236	236	55%	2e-63	38%	CDP32876.1
Chain A, Crystal Structure Of A Birnavirus (Ibdv) Rna- Dependent Rna Polymerase Vp1	235	235	55%	3e-63	38%	2PGG_A
RNA-dependent RNA polymerase [Infectious bursal disease virus]	236	236	55%	3e-63	38%	AAR24134.1
VP1 [Infectious bursal disease virus]	236	236	55%	3e-63	38%	ACB56955.1
VP1 [Infectious bursal disease virus]	235	235	55%	3e-63	37%	AAD49776.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	236	236	55%	3e-63	38%	AAT76291.1
VP1 [Infectious bursal disease virus]	236	236	55%	3e-63	38%	AAG31694.1
RecName: Full=RNA-directed RNA polymerase; Short=RDRP; AltName: Full=Protein VP1 [Infectious bursal disease virus chicken/Cuba/Soroa/1998]	236	236	55%	3e-63	38%	<u>A7L9Z4.1</u>
VP1 [Infectious bursal disease virus]	236	236	53%	3e-63	40%	AIG93140.1
Chain A, Unprecedented Activation Mechanism Of A Non-Canonical Rna-Dependent Rna Polymerase	236	236	55%	3e-63	38%	2PUS_A
RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	236	236	55%	4e-63	38%	AAK69715.1
RNA-dependent RNA-polymerase [Infectious bursal disease virus]	236	236	55%	4e-63	38%	ABS86938.1
RecName: Full=RNA-directed RNA polymerase; Short=RDRP; AltName: Full=Protein VP1	236	236	55%	4e-63	38%	Q9Q6Q5.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	236	236	55%	4e-63	38%	AAK30027.1

RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	236	236	55%	4e-63	38%	AAK69714.1
VP1 [Infectious bursal disease virus]	235	235	55%	4e-63	38%	AHW82960.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	235	235	55%	5e-63	38%	ABG91146.2
unnamed protein product [Infectious bursal disease virus]	235	235	55%	5e-63	38%	CAA58852.1
VP1 [Infectious bursal disease virus]	235	235	55%	5e-63	38%	AAD49775.1
VP1 [Infectious bursal disease virus]	235	235	55%	5e-63	38%	ABG91143.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	235	235	55%	5e-63	37%	ACN69081.1
VP1 [Infectious bursal disease virus]	235	235	55%	5e-63	38%	AKD94180.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	235	235	55%	5e-63	38%	AAS10170.1
VP1 [Infectious bursal disease virus]	235	235	55%	6e-63	38%	AFP86287.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	235	235	55%	6e-63	38%	AFN80479.1
VP1 [Infectious bursal disease virus]	235	235	55%	6e-63	38%	ABG91145.1
VP1 [Infectious bursal disease virus]	235	235	55%	6e-63	38%	<u>AAM45385.1</u>
RNA-dependent RNA polymerase [Infectious bursal disease virus]	235	235	55%	7e-63	38%	<u>AEP04404.1</u>
VP1 [Infectious bursal disease virus]	235	235	55%	7e-63	37%	ABI52867.1
RNA-dependent RNA-polymerase [Infectious bursal disease virus]	235	235	55%	7e-63	38%	AAY16541.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	235	235	55%	7e-63	38%	AKM16808.1
VP1 [Infectious bursal disease virus]	235	235	55%	7e-63	37%	ABI52865.1
VP1 [Infectious bursal disease virus]	234	234	53%	8e-63	40%	ACH89972.1
VP1 [Infectious bursal disease virus]	234	234	55%	9e-63	38%	ACB56954.1
RdRp (VP1) [Infectious bursal disease virus]	234	234	53%	9e-63	40%	CDW92046.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	234	234	53%	9e-63	40%	AFN80480.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	234	234	55%	9e-63	38%	AAM97562.1
VP1 [Infectious bursal disease virus]	234	234	53%	1e-62	40%	ACV66328.1
VP1 [Infectious bursal disease virus]	234	234	53%	1e-62	40%	ACV66326.1
RNA dependent RNA polymerase (RdRp) [Infectious bursal disease virus]	234	234	55%	1e-62	38%	CDP32873.1
VP1 [Infectious bursal disease virus]	234	234	55%	1e-62	38%	AIG93143.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	234	234	55%	1e-62	38%	AAN04462.1
VP1 [Infectious bursal disease virus]	234	234	53%	1e-62	40%	ACV66327.1
viral protein 1 [Infectious bursal disease virus]	234	234	55%	1e-62	38%	<u>AAF85954.1</u>
VP1 [Infectious bursal disease virus]	234	234	55%	1e-62	38%	ABG91142.1
VP1 protein [Infectious bursal disease virus]	234	234	55%	1e-62	38%	CAC60257.1
VP1 [Infectious bursal disease virus]	234 234	234 234	55% 55%	1e-62 1e-62	38% 38%	ACB56952.1
RdRp (VP1) [Infectious bursal disease virus] VP1 [Infectious bursal disease virus]	234	234	55%	1e-62	38%	CDW92044.1 ACB56953.1
RNA-dependent RNA polymerase VP1 [Infectious bursal						
disease virus]	234	234	55%	1e-62	38%	AAK69710.1
polymerase [Infectious pancreatic necrosis virus]	234	234	58%	1e-62	37%	<u>AAV48843.1</u>
RNA-directed RNA polymerase [Infectious bursal disease virus]	234	234	55%	1e-62	38%	<u>AFN80483.1</u>
RNA-directed RNA polymerase [Infectious bursal disease virus]	234	234	53%	1e-62	39%	AFN80482.1
VP1 protein [Infectious pancreatic necrosis virus]	234	234	58%	1e-62	37%	AAC71004.1
RNA dependent RNA polymerase [Infectious bursal disease virus]	234	234	55%	1e-62	38%	<u>CAJ34340.1</u>
RNA-directed RNA polymerase [Infectious bursal disease virus]	234	234	55%	1e-62	38%	AFN80484.1

RNA-directed RNA polymerase [Infectious bursal disease virus]	234	234	55%	2e-62	38%	AAC55352.1
VP1 [Infectious pancreatic necrosis virus - Mexico]	233	233	58%	2e-62	37%	ACD14075.1
RNA dependent RNA polymerase [Infectious bursal disease virus]	234	234	55%	2e-62	38%	<u>CAJ44476.1</u>
VP1 [Infectious bursal disease virus]	234	234	55%	2e-62	38%	AEQ29951.1
VP1 [Infectious bursal disease virus]	233	233	53%	2e-62	39%	AFP86290.1
VP1 [Infectious bursal disease virus]	233	233	55%	2e-62	38%	ABP96990.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	233	233	55%	2e-62	38%	AAD23375.1
RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	233	233	55%	2e-62	38%	AAM11679.1
RNA depended RNA polymerase [Paralichthys olivaceus birnavirus]	233	233	58%	2e-62	37%	YP_001514405.1
VP1 [Infectious bursal disease virus]	233	233	55%	2e-62	37%	AAD49777.1
RNA-dependent RNA polymerase [Infectious bursal disease virus]	233	233	55%	2e-62	38%	AAN04459.1
VP1 protein [Victorian trout aquabirnavirus]	233	233	58%	2e-62	38%	ALF95259.1
VP1 [Infectious bursal disease virus]	233	233	55%	3e-62	38%	ACS44343.1
viral polymerase [Infectious bursal disease virus]	233	233	55%	3e-62	38%	CAI54226.2
RNA polymerase [Infectious bursal disease virus]	233	233	55%	3e-62	38%	AAA46237.1
RNA-directed RNA polymerase [Infectious bursal disease virus]	233	233	55%	4e-62	38%	<u>AFI41892.1</u>
RNA-dependent RNA polymerase [Infectious bursal disease virus]	233	233	55%	4e-62	38%	<u>AAT99259.1</u>
RNA-dependent RNA polymerase [Infectious bursal disease virus]	233	233	55%	4e-62	38%	AAU10476.2
VP1 [Infectious bursal disease virus]	232	232	55%	5e-62	38%	ABW38088.1
VP1 RNA polymerase [Infectious bursal disease virus]	233	233	53%	5e-62	39%	AAB68518.1
double-stranded RNA-dependent RNA polymerase VP1 [Infectious bursal disease virus]	232	232	55%	5e-62	38%	AAD32619.1
putative RNA-dependent RNA polymerase [Infectious pancreatic necrosis virus]	232	232	58%	6e-62	38%	<u>AAN04572.1</u>
Chain A, Structure Of The Rna Polymerase Vp1 From Infectious Pancreatic Necrosis Virus	231	231	58%	6e-62	37%	<u>2YI8_A</u>
VP1 [Infectious bursal disease virus]	231	231	55%	1e-61	38%	ABG91144.1
VP1 [Infectious bursal disease virus]	231	231	55%	1e-61	38%	AAZ23012.1
viral protein 1 [Infectious pancreatic necrosis virus]	231	231	58%	1e-61	37%	NP_047197.1

□<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: 352 to 992

Score		Expect Method	Identities	Positives	Gaps F	rame
1070 bit	s(2767)	0.0() Compositional matrix adjust.	520/643(81%)	590/643(91%)	2/643(0%) -	1
Features	s:					
Query	1938	HLTKTRNIWSASYVTHLIGSTISDQPA				
Sbjct	352	HLTKTRNIWSASYVTHLIGSTISDQPA HLTKTRNIWSASYVTHLIGSTISDQPA		RTPSL+KFSPT RTPSLAKFSPT		
Query	1758	LNATETVELVYADNAYIYYPNEDIWYS LNAT+ VELVYADNAYIYYPNEDIWYS				
Sbjct	412	LNATDIVELVYADNAYIYYPNEDIWYS				
Query	1578	PLYNYTWAYLSLYAIPYMTVDSISILK P+YNYTWAYL+LY IPYMTVDSIS+LK				
Sbjct	472	PIYNYTWAYLALYGIPYMTVDSISVLK				
Query	1398	IGKPOPTPEVIEKLATMTGIDFKVELVIGKPOP+P+VIEKLA+MTGIDFKVELV				
Sbjct	532	IGKPÕPSPDVIEKLASMTGIDFKVELV				
Query	1218	GWDVTHTEYGYTPVLSKERMFKSIACE	PQPPSSTFQSNI	AKQVHKYIQNV	ALLYVGAWAY	P 1039

Sbjct	592	GWDVTHTE+G+TPVLSKER+FKSIACPQPPSSTFQ+++AKQVHKYIQNVALLYVGAWAYP GWDVTHTEFGFTPVLSKERLFKSIACPQPPSSTFQTSVAKQVHKYIQNVALLYVGAWAYP	651
Query	1038	CIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDYA CIAQT+E Y NHWNTI M+RNKEY+LDKAI KAVE SPFSEV+SLLSL++PMHEQ+YA	859
Sbjct	652	CIAQTIEGYALNHWNTINIMIRNKEYDLDKAIGKAVEASPFSEVISLLSLDRPMHEQNYA	711
Query	858	QILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVSR Q+LY+QK IEK K K +NPL K D E YHEY+ RMA+ R++++MVGP+W+PII LV++	679
Sbjct	712	QVLYQQKTIEKKEAKPKVSNPLYKRDKETYHEYTTRMARMRINDDMVGPQWEPIINLVTK	771
Query	678	LYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKKI LYP+EATGEN+K+RES+TR KIR L+E++ER LES G S+ VWYNAYLTG +P+GVDKK+	499
Sbjct	772	LYPREATGENQKSRESMTRVKIRGLLENMERQLESNGRSMDVWYNAYLTGKKPSGVDKKL	831
Query	498	SDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVSK + LL +LAP R+K LP+ VY KLLGYP IDK VP+LT DEAYLYDTNSLE+NRIAYVSK	319
Sbjct	832	ATLLVLLAPKRTKKLPSGVYQKLLGYPPIDKSPVPSLTSDEAYLYDTNSLEYNRIAYVSK	891
Query	318	LNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPRF LNEDDI+VYAN+YMVYSST+LS+LLPDKVDWPELRS++V+GASDPYQVKGYKKK+LKPRF	139
Sbjct	892	LNEDDITVYANKYMVYSSTLLSNLLPDKVDWPELRSMNVEGASDPYQVKGYKKKELKPRF	951
Query	138	GEEILDEDANPSARKSSTEkrrlqrkgqkaklqkqaANSKTFV 10 GEEILD++ P+ +KSS+EKRRLQRKGQKAKLQ+QAA TFV	
Sbjct	952	GEEILDDEPTGKKSSSEKRRLORKGOKAKLOROAATGTTFV 992	

VP1/RdRp [Culicine-associated Z virus]

Sequence ID: **gb|AGW51781.1|** Length: 998 Number of Matches: 1 Range 1: 352 to 996

Score		Expect	Method	Identities	Positives	Gaps	Frame
887 bits	s(2292)	0.0()	Compositional matrix adjust.	435/647(67%)	526/647(81%)	3/647(0%)	-1
Feature	es:						
Query	1938	HLTK'	TRNIWSASYVTHLIGSTISDOP	AKRMLNVLNCKT			II <u>I</u> 1759
Sbjct	352	HL K	TRNIWSASYVTHL+GS ISDÕPA TRNIWSASYVTHLLGSIISDÕPA	AKRMLNV+ AKRMLNVITSSE	TPSL+KFSPT PTPSLAKFSPT		TI 411
Query	1758		ETVELVYADNAYIYYPNEDIWY; + +ELVYADNAY+Y+P+ED+WY;				
Sbjct	412		DIMELVYADNAYMYFPDEDVWY				
Query	1578	PLYN	YTWAYLSLYAIPYMTVDSISIL YTWAYL+LY IPY TVDSISIL	KNFQIKNPGQGS	GNPWTFLNNHV	LTTILMNRW	IAE 1399
Sbjct	472	PLYN	YTWAYLALYMIPYTTVDSISILI	KNFQIKNPGQGS	GNPWTFLNNHV	LTTILMNKW	IRA 531
Query	1398		QPTPEVIEKLATMTGIDFKVEL ¹ +PT +VIEKL++ TGIDFKVEL ¹			EPRTIVEMD +PRTIV MD	
Sbjct	532		KPTAQVIEKLSSETGIDFKVEL'				
Query	1218		THTEYGYTPVLSKERMFKSIAC THT+YG+TPVL+KER+FKSIAC				
Sbjct	592		THTQYGFTPVLAKERLFKSIAC				
Query	1038		TVESYVTNHWNTIQSMLRNK-E T+E Y NHWNTI SMLRN				
Sbjct	652		TIEGYALNHWNTIDSMLRNNPN				
Query	861	AQIL A +L	YKQKPIEKIAPKAKFNNPLRKLI Y K ++ PK +NP	DIENYHEYSKRM + EN ++Y++RM			VS 682 +S
Sbjct	712		YTPKERPRVDPKRLRSNPFLIR				
Query	681		KEATGENKKNRESITRSKIRSLI +EA GEN K RE+ ++ KIR +1				KK 502
Sbjct	772		REALGENIKLRENFSKGKIREI				GN 831
Query	501	ISDL:	LTVLAPMRSKTLPNSVYNKLLG L L P RS++LP V+ KLLG			SLEHNRIAY SLEHNRI Y	
Sbjct	832		LVSLTPPRSQSLPREVFRKLLG				
Query	321		DDISVYANRYMVYSSTILSSLLI DDIS++AN+YMVYSST+LS++LI				
Sbjct	892		DDISIFANKYMVYSSTLLSTML				
Query	141		ILDEDANPSARKSSTEkrrlqri IL+E+ P A+KSSTEKRR+QRI			1	
Sbjct	952		ILEEELLP-AKKSSTEKRRMQRI			996	

VP1/RdRp [Culicine-associated Z virus]

Sequence ID: **gb|AGW51763.1|** Length: 998 Number of Matches: 1 Range 1: 352 to 970

Score		Expect	Method	Identities	Positives	Gaps	Frame
884 bits	(2283)	0.0()	Compositional matrix adjust.	414/620(67%)	501/620(80%)	2/620(0%)	-1
Features	S :						
Query	1938		TRNIWSASYVTHLIGSTISDOPA TRNIWSASYVTHL+GS ISDOPA		RTPSLSKFSPT(TPSL+KFSPT(II 1759
Sbjct	352		TRNIWSASIVIHLIGS ISDQFA				TĪ 411
Query	1758		ETVELVYADNAYIYYPNEDIWYS + +ELVYADNAY+Y+P+ED+WYS			~	
Sbjct	412		DIMELVYADNAYMYFPDEDVWYS				

Query	1578	PLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE	1399
Sbjct	472	PLYNYTWAYL+LY IPY TVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN+W PLYNYTWAYLALYMIPYTTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNKWRA	531
Query	1398	IGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRTIVEMDML	1219
Sbjct	532	+G+P+PT +VIEKL++ TGIDFKVELVV +F++KL+EA + S+P +RV+PRTIV MDML MGRPKPTAQVIEKLSSETGIDFKVELVVPDFKKKLLEAKDRSLPVEDRVKPRTIVTMDML	591
Query	1218	GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGAWAYP	1039
Sbjct	592	GWDVTHT+YG+TPVL+KER+FKSIACPQPPSSTF S+IAKQVHKYIQNVALLYVG WAYP GWDVTHTQYGFTPVLAKERLFKSIACPQPPSSTFSSSIAKQVHKYIQNVALLYVGGWAYP	651
Query	1038	CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY CIAOT+E Y NHWNTI SMLRN Y+L+KA+ KAV+TSPF+EVM+L+++ KPMHEO+Y	862
Sbjct	652	CIAQTIEGYALNHWNTIDSMLRNNPNYDLEKALVKAVDTSPFAEVMALINIRKPMHEQNY	711
Query	861	AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS A +LY K ++ PK +NP + EN +Y++RMAK R +N+MV EW PI L+S	682
Sbjct	712	AAVLYTPKERPRVDPKRLRSNPFLIREGENVSQYTRRMAKIRQENDMVSEEWAPIKGLIS	771
Query	681	RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK RL+ +EA GEN K RE+ ++ KIR +M SIE+ L+ G L VWY AY T P G+	502
Sbjct	772	RLFAREALGENIKLRENFSKGKIREIMSSIEQQLKERGLGLEVWYQAYATNTPPKGLSGN	831
Query	501	ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS	322
Sbjct	832	++ LL L P RS++LP V+ KLL Y + P LT DE Y YD SLEHNRI Y+ LAQLLVSLTPPRSQSLPREVFRKLLDYDPVGSGRTPDLTSDERYYYDLQSLEHNRIEYLR	891
Query	321	KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR KLNEDDIS++AN+YMVYSST+LS++LPDKV+WPE RS+ V+ A DP+ VKG+K +D+KPR	142
Sbjct	892	KLNEDDISIFANKYMVYSSTLLSTMLPDKVEWPEQRSMKVQDAKDPFMVKGFKARDMKPR	951
Query	141	FGEEILDEDANPSARKSSTE 82	
Sbjct	952	FG EIL+E+ P A+KSSTE FGAEILEEELLP-AKKSSTE 970	

VP1 [Culex Y virus]

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

Range 1: 352 to 970

HL KTRNIWSASYVTHL+GS ISDQPAKRMLNVL TPSLSKFSPTQGGMDAL+N I Sbjct 352 HLEKTRNIWSASYVTHLLGSIISDQPAKRMLNVLTSSEPTPSLSKFSPTQGGMDALVNRI 411 Query 1758 LNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTSTQGT L ATH ELVYADNAY+Y+P ED+WYSIDLTKGEANCTRD+AMT AMYLLTRGWTS +G Sbjct 412 LEATDITELVYADNAYMYFPREDVWYSIDLTKGEANCTRDIAMTTAMYLLTRGWTSNEGV 471 Query 1578 PLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE PLYNYTWAYL+LY IPY TVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNHW Sbjct 472 PLYNYTWAYLALYMIPYTTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNKWRA 531 Query 1398 IGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRTIVEMDML 1219 +G+P+PT +VIEKL++ TGIDFKVELVV F++KL+EA HS+P +R+ PRTIV MDML Sbjct 532 MGRPKPTAQVIEKLSSETGIDFKVELVVPEFKKKLLEAREHSLPVEDRIRPRTIVSMDML 591	Score		Expect Method	Identities	Positives	Gaps	Frame
Query 1938 HLKTRNIWSASYVTHLIGSTISDOPAKRMLNVLNCKTRTPSLSKFSPTOGGMDALINII 5Djet 352 HL KTRNIWSASYVTHLHGS ISDOPAKRMLNVL TPSLSKFSPTOGGMDALVNI 411 Query 1758 HLATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTSTQGT LATH ELVYADNAYHYPPEDHWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTSTQGT 471 Query 1578 PLYNYTWAYLSLYAIPYMTVDISILKNFQIKNPEGGSGNPWTFLINHVLTTILMNRWAE PLYNYTWAYLALYAIPYMTVDSISILKNFQIKNPEGGSGNPWTFLINHVLTTILMNRWAE 719 Query 1578 PLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPEGGSGNPWTFLINHVLTTILMNRWAE 719 Sbjct 472 PLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPEGGSGNPWTFLINHVLTTILMNRWAE 719 PLYNYTWAYLALYMIPYTTVDSISILKNFQIKNPEGGSGNPWTFLINHVLTTILMNRWAE 719 Sbjct 532 MGRPCPTPEVIEKLATMTGIDFKVELVVHNFREKLIFASHNSIPTNNRVEPRTIVEMDML 719 Sbjct 532 MGRPKPTAQVIEKLSETGIDFKVELVVHNFREKLIFASHNSIPTNNRVEPRTIVEMDML 719 Query 1218 GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHXYIQNVALLYVGAWAYP 710 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWRPIIELVS 711 Query 681 RLYPKEATGENKKNRSSITRSKIRSLMBSIERGLESGGHSLGVWNNAVLTGRNPAGYDKK 711 Query 501 ISDLLTVLAPMRSKTLENNSYNNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYN 711 Query 501 ISDLLTVLAPMRSKTLENNSYNNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYN 712 Sbjct 772 RYPKEATGENKKNRSSITRSKIRSLMBSIERGLESGGHSLGVWYNAVLTGRPPAGYDKK 712 Query 501 ISDLLTVLAPMRSKTLENSVNNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYN 712 Sbjct 772 KLAPET 711 QUERY 501 ISDLLTVLAPMRSKTLENSVNNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYN 712 Sbjct 772 KLAPET 711 P LT DE Y Y+ SLEHNRI Y+ 111 P LT D	871 bits	(2250)	0.0() Compositional matrix adjust.	415/620(67%)	499/620(80%)	2/620(0%)	-1
HL KTRNIWSASYVTHLIGS ISDOPARRMLNVL TBSLSKFSPTQGGMDALVNI 1 Query 1758 LNATETVELVYADNAYIYYPNEDLWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTSTQGT 1579 L AT+ ELVYADNAYHYPNEDLWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTSTQGT 1579 L AT+ ELVYADNAYHYPREDVWYSIDLTKGEANCTRDVAMTAMYLLTRGWTSTQGT 412 Query 1578 PLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE 1399 PLYNYTWAYLALYMIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE 551 Query 1578 PLYNYTWAYLALYMIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNKWAR 551 Query 1398 IGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRTIVEMDML 551 Query 1218 GMDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGAWAYP 651 Query 1218 GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGAWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPPSEVMSLLSLEKPMHEQDY 711 Query 861 AQILYKQKPIEKIAPKASFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS A 1LY K + PK + PP EN + Y++RMAK R + N+MVG EW PI L+S Sbjct 712 ASVLTYPKOMPRVQFKRMMSSPFLIRKDENVARYTRMAKRRONNMGERWAPPILELVS A 1LY K + PK + PP EN + Y++RMAK R + N+MVG EW PI L+S Sbjct 772 RIPAREALGENIKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 502 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTTPDEAYLVDTNSLEHNRIAYVS 322 ++LL L P +K+LP V+ +LIGY I PLT DE Y V+ SLEHNRI Y+ B) Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTTPDEAYLVDTNSLEHNRIAYVS 322 ++LL L P +K+LP V+ +LIGY I PLT DE Y V+ SLEHNRI Y+ B) Sbjct 832 KLNEDDISVYANRYMVYSSTLLSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Query 321 KLNEDDISVYANRYMVYSSTLLSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Query 421 KLNEDDISVYANRYMVYSSTLLSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Query 522 KLNEDDISIVANKYMVYSSTLLSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 RUPY FGEEILDEDANPSARKSTE 82 FGEEILDEDANPSARKSSTE 82 FGEEILDEDANPSARKSSTE 82	Features	s:					
Sbjet 352 HLEKTRNIWSASYVTHLLGSIISDÖPAKRMLNVLTSSEPTPSLSKFSPTÖGGMDALVNRI 411 Query 1758 LNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTSTQGT 1579 L AT	Query	1938					
Sbjet 412 LATH ELVYADNAYHYHP EDHWYSIDLTKGEANCTRDHAMT AMYLLTRGWTS +G LEATDITELVYADNAYMYFPREDVWYSIDLTKGEANCTRDHAMT AMYLLTRGWTS +G LEATDITELVYADNAYMYFPREDVWYSIDLTKGEANCTRDHAMT AMYLLTRGWTSNEGV 471 Query 1578 PLYNYTWAYLSLYALPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE 1399 PLYNYTWAYLALZMIPYTTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE 531 Query 1398 IGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRTIVEMDML 591 Query 1218 GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFSHIAKQVHKYIQNVALLYVGAWAYP GWDVTHTTYGHTPVL+KER+FKSIACPQPPSSTFSHIAKQVHRYIQNVALLYVGAWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY 711 Query 861 AQILYKQKPIEKIAFMSIACNHYYDYDLEKALTKAVDTSPFREVMELINIRKPMHEQNY 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS 682 A + LY K + + PK + P EN + + + + H + H + P G+ SVLYTPKDRAKGURSPFSHIAKQVHRYQDWALLVVGGWAPP 651 Query 681 RLYPKEATGENKRNESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNEGWS 771 Query 681 RLYPKEATGENKRNESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNEGWS 771 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 Sbjet 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 Sbjet 832 LAQLIVSTPPWTKSLPREVFFRILGYDPIGGSSTPELTSDERYYYNVQSLEHRRIEYLR 891 Query 321 KLNEDDISYYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Sbjet 892 KLNEDDISYYANRYMYYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Sbjet 892 KLNEDDISYYANRYMYYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 FGEEILDEDANPSARKSTE 82 FGEEILDEDANPSARKSTE 82 FGEEILDEDANPSARKSTE 82	Sbjct	352					
Sbjct 412 LEATDITELVYADNAYMYFPREDVWYSIDLTKGEANCTRDIAMTTAMYLLTRGWTSNEGV 471 Query 1578 PLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE 531 Sbjct 472 PLYNYTWAYLALYMIPYTTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE 531 Query 1398 IGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRTIVEMDML 1219 #G+P+PT +VIEKL++ TGIDFKVELVV F++KL+EA HS+P +R+ PRTIV MDML 4G+P+PT +VIEKL++ TGIDFKVELVV F++KL+EA HS+P +R+ PRTIV MDML 591 Query 1218 GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFSWIAKQVHKYIQNVALLYVGGWAYP 6WDVTHTYGYGFTPVLAKERLFKSIACPQPPSSTFSWIAKQVHKYIQNVALLYVGGWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY CIAQTTEY NHWNTI SMLRN Y+L+KA++KAV+TSPF EVM L+++ KPMHEQ+Y 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS AX +LY K +P K +P EN +Y++RMAK R +N+MVG EW PI L+S ASVLYTPKDRPRQVPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEWAPIKMRD 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLVDTNSLEHNRIAYVS 322 **PKLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLVDTNSLEHNRIAYVS 322 **PKLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 891 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 891 KLNEDDISTYANHYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 PGEEILL+E+ A+KSSTE 82 **FGEEILLDEDANPSARKSSTE 82**	Query	1758					
PLYNYTWAYL+LY IPY TVDSISILKNFQIKNPGGGSGNPWTFLNNHVLTTILMN+W Sbjct 472 PLYNYTWAYLALYMIPYTTVDSISILKNFQIKNPGGGSGNPWTFLNNHVLTTILMNKWRA 531 Query 1398 IGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRTIVEMDML 1219 Sbjct 532 MGRPKPTAQVIEKLSSETGIDFKVELVV F+KL+EA HS+P +R+ PRTIV MDML 591 Query 1218 GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGAWAYP GWDVTHT+YG+TPVL+KER+FKSIACPQPPSSTF S+IAKQVH+YIQNVALLYVGAWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEODY 651 Query 652 CIAQTEGYALNHWNTIDSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEODY 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPILELVS 682 A +LY K ++ PK +PP EN +Y++RMAK R +N+MVG EW PI L+S Sbjct 712 ASVLYTTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 502 RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+ Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKDLKPR 142 Sbjct 832 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Sbjct 892 KLNEDDISVYANRYMVYSSTILSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82	Sbjct	412					
Sbjct 472 PLYNYTWAYLALYMIPYTTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNKWRA 531 Query 1398 IGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRTIVEMDML +G+P+PT +VIEKL++ TGIDFKVELVV F++KL+EA HS+P +R+ PRTIV MDML 591 Query 1218 GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGAWAYP GWDVTHT+YG+TPVL+KER+FKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY 862 Sbjct 652 CIAQTTEGYALNHWNTIDSMLRNNPNPULEKALTKAVTTSPF EVM L+++ KPMHEQ+Y 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS 682 Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 502 RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+ 815 Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLLYDTNSLEHNRIAYVS 322 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Sbjct 892 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Sbjct 892 KLNEDDISLYYANRYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82	Query	1578					AE 1399
+G+P+PT +VIEKL++ TGIDFKVELVV F++KL+EA HS+P +R+ PRTIV MDML MGRPKPTAQVIEKLSSETGIDFKVELVVPEFKKKLLEAREHSLPVEDRIRPRTIVSMDML 591 Query 1218 GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGAWAYP GWDVTHTYGTPVLAKERLFKSIACPQPPSSTFSSNIAKQVHKYIQNVALLYVGAWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY 862 CIAQTTEY NHWNTI SMLRN Y+L+KA++KAV+TSPF EVM L+++ KPMHEQHY 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS A +LY K ++ PK ++P EN +Y++RMAK R +N+MVG EW PI L+S Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWNAYLTGNRPAGVDKK 502 Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISYYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Sbjct 892 KLNEDDISYYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEILL+E+ A+KSSTE	Sbjct	472					RA 531
Sbjct 532 MGRPKPTAQVIEKLSSETGIDFKVELVVPEFKKKLLEAREHSLPVEDRIRPRTIVSMDML 591 Query 1218 GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGAWAYP 1039 Sbjct 592 GWDVTHTYGHTPVL+KER+FKSIACPQPPSSTF S+IAKQVH+YIQNVALLYVGWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY 862 CIAQTHE Y NHWNTI SMLRN Y+1+KA++KAV+TSPF EVM L+++ KPMHEQHY 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPHIELVS 682 Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 502 RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+ Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISYYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKRP 142 Sbjct 892 KLNEDDISYYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKRP 142 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Query	1398					_
GWDVTHT+YG+TPVL+KER+FKSIACPÖPPSSTF S+IAKÖVH+YIÖNVALLYVG WAYP GWDVTHTQYGFTPVLAKERLFKSIACPÖPPSSTFSSHIAKQVHRYIÖNVALLYVGGWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY CIAQT+E Y NHWNTI SMLRN Y+L+KA++KAV+TSPF EVM L+++ KPMHEQ+Y 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS A +LY K ++ PK ++P EN +Y++RMAK R +N+MVG EW PI L+S Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGWYNAYLTGNRPAGVDKK 702 Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKENGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKNEVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 KLNEDDIS+YAN+YMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Sbjct	532					
Sbjct 592 GWDVTHTQYGFTPVLAKERLFKSIACPQPPSSTFSSHIAKQVHRYIQNVALLYVGGWAYP 651 Query 1038 CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY CIAQTHE Y NHWNTI SMLRN Y+L+KA++KAV+TSPF EVM L+++ KPMHEQ+Y 711 Query 861 CIAQTIEGYALNHWNTIDSMLRNNPNYDLEKALTKAVDTSPFREVMELINIRKPMHEQNY 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS 682 A +LY K ++ PK ++P EN +Y++RMAK R +N+MVG EW PI L+S Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 702 Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I PLT DEY Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRILGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTLLSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Sbjct 892 KLNEDDISIYANKYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Query	1218					
CIAŌT+E Y NHWNTI SMLRN Y+L+KA++KAV+TSPF EVM L+++ KPMHEŌ+Y Sbjct 652 CIAŌTIEGYALNHWNTIDSMLRNNPNYDLEKALTKAVDTSPFREVMELINIRKPMHEŌHY Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS 682 A +LY K ++ PK ++P EN +Y++RMAK R +N+MVG EW PI L+S Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 502 RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+ Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 Sbjct 892 KLNEDDISIYANKYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Sbjct	592					
Sbjct 652 CIAQTIEGYALNHWNTIDSMLRNNPNYDLEKALTKAVDTSPFREVMELINIRKPMHEQNY 711 Query 861 AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS 682 A +LY K ++ PK ++P EN +Y++RMAK R +N+MVG EW PI L+S Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 502 RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+ Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 IAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTLLSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 KLNEDDIS+YAN+YMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Query	1038					
A +LY K ++ PK ++P EN +Y++RMAK R +N+MVG EW PI L+S Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 502 RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+ RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTLLSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 KDjct 892 KLNEDDISYYANRYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Sbjct	652					
Sbjct 712 ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVGEEWAPIKGLIS 771 Query 681 RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK 502 RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+ Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 KLNEDDIS+YAN+YMVYSST+LS++LP+KV+WPE RS+ V+ A +P+ VKG+K KD+KPR Sbjct 892 KLNEDDISIYANKYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Query	861					
RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+ RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 KLNEDDIS+YAN+YMVYSST+LS++LP+KV+WPE RS+ V+ A +P+ VKG+K KD+KPR Sbjct 892 KLNEDDISIYANKYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Sbjct	712					
Sbjct 772 RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGY 831 Query 501 ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS 322 ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR KLNEDDIS+YAN+YMVYSST+LS++LP+KV+WPE RS+ V+ A +P+ VKG+K KD+KPR KLNEDDIS+YAN+YMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Query	681					KK 502
++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+ Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 KLNEDDIS+YAN+YMVYSST+LS++LP+KV+WPE RS+ V+ A +P+ VKG+K KD+KPR Sbjct 892 KLNEDDISIYANKYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Sbjct	772					GY 831
Sbjct 832 LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR 891 Query 321 KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR 142 KLNEDDIS+YAN+YMVYSST+LS++LP+KV+WPE RS+ V+ A +P+ VKG+K KD+KPR Sbjct 892 KLNEDDISIYANKYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Query	501					
KLNEDDIS+YAN+YMVYSST+LS++LP+KV+WPE RS+ V+ A +P+ VKG+K KD+KPR Sbjct 892 KLNEDDISIYANKYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Sbjct	832					
Sbjct 892 KLNEDDISIYANKYMVYSSTLLSTMLPEKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR 951 Query 141 FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	Query	321					
FGEEIL+E+ A+KSSTE	Sbjct	892					
	Query	141					
	Sbjct	952					

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: 352 to 970

Score Expect Method Identities Positives Gaps Frame

869 bits(2245) 0.0() Compositional matrix adjust. 413/620(67%) 498/620(80%) 2/620(0%) -1

Features:

Query	1938	HLTKTRNIWSASYVTHLIGSTISDQPAKRMLNVLNCKTRTPSLSKFSPTQGGMDALINII HL KTRNIWSASYVTHL+GS +SDQPAKRMLNVL TPSLSKFSPTQGGMDAL+N I	1759
Sbjct	352	HLEKTRNIWSASIVIHLIGS TSDQPARRMLNVLTSSEPTPSLSKFSPTQGGMDALVNRI	411
Query	1758	LNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTSTQGT L AT+ ELVYADNAY+Y+P ED+WYSIDLTKGEANCTRD+AMT AMYLLTRGWTS +G	1579
Sbjct	412	LEATDITELVYADNAYMYFPREDVWYSIDLTKGEANCTRDIAMTTAMYLLTRGWTSNEGV	471
Query	1578	PLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWAE PLYNYTWAYL+LY IPY TVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN+W	1399
Sbjct	472	PLYNYTWAYLALYMIPYTTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNKWRA	531
Query	1398	IGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRTIVEMDML +G+P+PT +VIEKL++ TGIDFKVELVV F++KL+EA HS+P +R+ PRTIV MDML	1219
Sbjct	532	MGRPKPTAQVIEKLSSETGIDFKVELVVPEFKKKLLEAREHSLPVEDRIRPRTIVSMDML	591
Query	1218	GWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAKQVHKYIQNVALLYVGAWAYP GWDVTHT+YG+TPVL+KER+FKSIACPQPPSSTF S++AKQVHKYIQ+VALLYVG WAYP	1039
Sbjct	592	GWDVTHTQYGFTPVLAKERLFKSIACPQPPSSTFSSHVAKQVHKYIQDVALLYVGGWAYP	651
Query	1038	CIAQTVESYVTNHWNTIQSMLRNK-EYNLDKAISKAVETSPFSEVMSLLSLEKPMHEQDY CIAOT+E Y NHWNTI SMLRN Y+L+KA++KAV+TSPF EVM L+++ KPMHEO+Y	862
Sbjct	652	CIAQTIEGYALNHWNTIDSMLRNNPNYDLEKALTKAVDTSPFREVMELINIRKPMHEQNY	711
Query	861	AQILYKQKPIEKIAPKAKFNNPLRKLDIENYHEYSKRMAKARMDNEMVGPEWKPIIELVS A +LY K ++ PK ++P EN +Y++RMAK R +N+MV EW PI L+S	682
Sbjct	712	ASVLYTPKDRPRVQPKRMMSSPFLIRKDENVAQYTRRMAKIRQENDMVSEEWAPIKGLIS	771
Query	681	RLYPKEATGENKKNRESITRSKIRSLMESIERGLESGGHSLGVWYNAYLTGNRPAGVDKK RL+ +EA GEN K RE+ ++ KIR LM SIE+ L+ G + VW+ AY T + P G+	502
Sbjct	772	RLFAREALGENLKLRENFSKGKIRELMTSIEQQLKERGMGMEVWHKAYQTSSPPEGLKGN	831
Query	501	ISDLLTVLAPMRSKTLPNSVYNKLLGYPAIDKKLVPTLTPDEAYLYDTNSLEHNRIAYVS ++ LL L P +K+LP V+ +LLGY I P LT DE Y Y+ SLEHNRI Y+	322
Sbjct	832	LAQLLVSLTPPWTKSLPREVFRRLLGYDPIGSGSTPELTSDEKYYYNVQSLEHNRIEYLR	891
Query	321	KLNEDDISVYANRYMVYSSTILSSLLPDKVDWPELRSISVKGASDPYQVKGYKKKDLKPR KLNEDDIS+YAN+YMVYSST+LS++LPDKV+WPE RS+ V+ A +P+ VKG+K KD+KPR	142
Sbjct	892	KLNEDDISIYANKYMVYSSTLLSTMLPDKVEWPEQRSMKVQDAMNPFMVKGFKNKDMKPR	951
Query	141	FGEEILDEDANPSARKSSTE 82 FGEEIL+E+ A+KSSTE	
Sbjct	952	FGEEILEEEQL-QAKKSSTE 970	

putative VP1 [Mosquitoe x virus]

Sequence ID: **gb|AFU34334.1|** Length: 995 Number of Matches: 1 Range 1: 352 to 993

Score		Expect	Method	Identities	Positives	Gaps	Frame
865 bits	(2235)	0.0()	Compositional matrix adjust.	429/647(66%)	516/647(79%)	6/647(0%)	-1
Features	3 :						
Query	1938		TRNIWSASYVTHLIGSTISDQP <i>I</i>				
Sbjct	352	HL K'	TRNIWSASYVTHL+GS ISDQP <i>I</i> TRNIWSASYVTHLLGSIISDQP <i>I</i>	AKRMLNV+ AKRMLNVITSSE	TPSLSKFSPT PTPSLSKFSPT		
Query	1758	LNATI	ETVELVYADNAYIYYPNEDIWYS + ELVYADNAY+Y+P ED+WYS				
Sbjct	412		DITELVYADNAYMYFPREDVWYS				G GV 471
Query	1578	PLYNY PLY	YTWAYLSLYAIPYMTVDSISILI AYL+LY IPY TVDSISILI				
Sbjct	472		AYLALYMIPYTTVDSISILE				
Query	1398		QPTPEVIEKLATMTGIDFKVEL\ +PT +VIEKL++ TGIDFKVEL\			EPRTIVEMD PRTIV MD	
Sbjct	529		RPTAQVIEKLSSETGIDFKVELV				
Query	1218		THTEYGYTPVLSKERMFKSIACI THT+YG+TPVL+KER+FKSIACI				
Sbjct	589		THTQYGFTPVLAKERLFKSIACI				
Query	1038		TVESYVTNHWNTIQSMLRNK-EY T+E Y NHWNTI SMLRN Y	NLDKAISKAVE +L+KA++KAV+	TSPFSEVMSLL	SLEKPMHEQ	DY 862
Sbjct	649		TIEGYALNHWNTIDSMLRNNPN				
Query	861	AQILY A +LY	YKQKPIEKIAPKAKFNNPLRKLI Y K ++ PK ++P		AKARMDNEMVG AK R +N+MV		VS 682 +S
Sbjct	709		YTPKDRPRVQPKRMMSSPFLIR				
Query	681		KEATGENKKNRESITRSKIRSLN +EA GEN K RE+ ++ KIR LN				KK 502
Sbjct	769		REALGENIKLRENFSKGKIRELN				GN 828
Query	501		LTVLAPMRSKTLPNSVYNKLLGY L L P +K+LP V+ +LLGY				
Sbjct	829		LVSLTPPWTKSLPREVFRRLLG				
Query	321		DDISVYANRYMVYSSTILSSLLI DDIS+YAN+YMVYSST+LS++LI				
Sbjct	889		DDISTYANKYMVYSSTLLSTMLI DDISIYANKYMVYSSTLLSTMLI				
Query	141		ILDEDANPSARKSSTEkrrlqrk			1	
Sbjct	949		I++E+ A+KSSTEKRR+QRI IVEEE-QLQAKKSSTEKRRMQRI			993	

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

See 2 more title(s)
Range 1: 319 to 675

Score	E	xpect Method	Identities	Positives	Gaps	Frame
244 bits	(624) 36	e-66() Compositional matrix adjust.	144/367(39%)	207/367(56%)	27/367(7%) -	1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTIS	~		~	
Sbjct	319	LTKTRNIWSA + THL+ STIS LTKTRNIWSAPFPTHLLLSTISWPI	+ +LNV MNSSKNNILNVI		F+P GGMDA+ FNPFSGGMDA\	
Query	1767	-NIILNATETVELVYADNAYIYYPN NI+ ET+ L+YADN YIY	EDIWYSIDLTKO + W+SIDL KO			
Sbjct	375	TNILAQPDETLFLIYADNIYIYM				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G+P +N TWA +++ P + VD	SISILKNFQIKN S + N O+K			
Sbjct	433	DDGSPAFNATWATIAMMIAPSLVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W E G+P P + L TGI+		EKLIEASNHSIE +L EA + ++		1240
Sbjct	493	KWIEAGQPNPRSKEFMDLEAATGIN				PP 552
Query	1239	IVEMDMLGWDVTHTEYGY V++D+LGW T++ + +		SIACPOP-PSST S A P+ +	FQSNIAKQV-F	
Sbjct	553	EKEGPTVDLDLLGWSATYSRHMDMW				
Query	1086	YIQNVALLYVGAWAYPCIAQTVESY ++N ALL VG W YP IA+++ +		LRNKEYNLDKAI LR K LD	SKAVETSPFSE + + FS+	
Sbjct	613	IVRNEALLMVGGWNYPLIARSLMAN				
Query	906	MSLLSLE 886 L ++				
Sbjct	669	FEDLPID 675				

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

Sequence ID: sp|P31817.1|RDRP_IBDV5 Length: 525 Number of Matches: 1

▶ See 1 more title(s) Range 1: 5 to 367

Score	E	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(601) 26	e-65() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI	-SDQPAKRMLN\ S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	5	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	60	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N ÕIK		LNNHVLTTII +NNH+L+T++	
Sbjct	117	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRE FK+E + + R			RT- 1240
Sbjct	177	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 236
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	237	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVM E S F E	ISL 898
Sbjct	297	YEALRLVGGWNYPLLNKACKN			_ ~	EG 352
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	353	FNIKLTVTSESLÄEL 367				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AKU89586.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 676

Score	E	xpect	Method	Identities	Positives	Gaps	Frame	•
237 bits	(604) 1e	e-63()	Compositional matrix adjust.	142/358(40%)	206/358(57%)	26/358(7%)	-1	
Feature	s:							
Query	1935		TRNIWSASYVTHLIGSTI	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++		71
Sbjct	331		RNIWSAPSPTHLMISMITWPVN	D				5

Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N OIK GOGSGN TF+NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P+P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGINFKIERSIDDIRGKLKQLVPLAQPGYLSGGVEPEQS	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + S + +Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFSSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077		04
Sbict	623	AL VG W YP + + + N+ + L K + LD+ +++ E S F E YEALRLVGGWNYPLLNKACKNNAGAARROLEAKGFPLDEFLAEWSELSEFGEAF 6	76

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

Sequence ID: **gb|AAR91595.1|** Length: 800 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps Fra	ıme
236 bits	(601) 26	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%) -1	
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				1771
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN- MSNSP-NNVLN		KF+P +GG++ + KFNPFRGGLNRI	385
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGWTS Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKI S ++ N OIK		LNNHVLTTILMN +NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALAVD				502
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRI FK+E + + R			1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN			·	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVMSL E S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLAEL 693				

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

Sequence ID: sp|P12918.1|RDRP_IBDVA Length: 878 Number of Matches: 1

▶ See 1 more title(s) Range 1: 330 to 692

Score	E	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(603) 26	e-63() Compositional matrix adjust.	143/375(38%)	216/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	330	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	385	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK+		LNNHVLTTIL '+NNH+L+T++	
Sbjct	442	DNGDPMFNQTWASFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			T- 1240
Sbjct	502	QWNLMKQPNPDSEEFKSIEDKLGIN				QS 561
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				~
Sbjct	562	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNK + + + L K			ISL 898
Sbjct	622	YEALRLVGGWNYPLLNKACKN				EG 677
Query	897	LSLEKPMHEQDYAQI 853 +++ + ++ A++				
Sbjct	678	FNIKLTVTRENLAEL 692				

RNA-directed RNA polymerase [Infectious bursal disease virus]

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

Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(603) 26	e-63() Compositional matrix adjust	. 143/375(38%)	213/375(56%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWP	S+ P +LN- VMSNSP-NNVLN		KF+P +GG++ KFNPFRGGLNI	
Query	1770	INIILNATETVELVYADNAYIYYPI + IL E LVYADN YI + 1			MAMYLLTRGW! Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHS				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTV	DSISILKNFQIKI DS ++ N QIK		FLNNHVLTTILI F+NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVV				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGI	DFKVELVVHNFRI +FK+E + + R			r- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGI				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTP' VE+D+LGW T++ + G Y P'			SNIA-KQVHKY S + +Q +K -	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVP				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTI AL VG W YP + + +	NHWNTIQSMLRNI N+ + L]	KEYNLDKAISKA K + LD+ +++	AVETSPFSEVMS ESFE	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACK				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLÄEL 693				

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

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

Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(603) 26	e-63() Compositional matrix adjust.	143/375(38%)) 214/375(57%)	26/375(6%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLN S+ P +LN		KFSPTQGGMDA KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTILI +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFR FK+E + + R			r- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN			• •	QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				~
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRN	KEYNLDKAISKA K + LD+ +++	VETSPFSEVMS ESFE	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLÄEL 693				

VP1 [Infectious bursal disease virus]

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

Score	Е	Expect Method	Identities	Positives	Gaps	Frame
236 bits	(603) 2	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I			KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV	D			
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	

Sbjct 386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query 1590		1411
Sbjct 443	G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++ DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD	502
Query 1410		1240
Sbjct 503	+W + +P+P E + + GI+FK+E + + R KL + + P + VEP QWNLMRQPRPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	562
Query 1239		1078
Sbjct 563	VE+D+LGW T++ + G Y PVL KER+F S A P+ + + +S + +Q +K ++ SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query 1077		898
Sbjct 623	AL VG W YP + + + N+ + L K + LD+ +++ E S F E YEALRLVGGWNYPLLNKACKNNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query 897	LSLEKPMHEQDYAQI 853	
Sbjct 679	+++ + + A++ FNIKLTVTSESLAEL 693	

RNA-directed RNA polymerase, partial [Infectious bursal disease virus] Sequence ID: **gb|AFN80481.1|** Length: 878 Number of Matches: 1 Range 1: 331 to 693

Score

Expect Method

236 bits	(603) 26	e-63() Compositional matrix adjust. 143/375(38%) 214/375(57%) 26/375(6%) -1	
Feature	s:		
Query	1935	LTKTRNIWSASYVTHLIGSTISDQPAKRMLNVLNCKTRTPSLSKFSPTQGGMDAL	1771
Sbjct	331	LTKTRNIWSA THL+ S I S+ P +LN+ C PSL KF+P +GG++ + LTKTRNIWSAPSPTHLMISMITWPVMSNSP-NNVLNIEGCPSLYKFNPFRGGLNRI	385
Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLÕIKTYGÕGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P+P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMKQPRPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + + + + Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEÕAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + + N+ + L K + LD+ +++ E S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACKNNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++	
Sbjct	679	FNIKLTVTSESLAEL 693	

Identities

Gaps

Frame

Positives

RNA-dependent RNA-polymerase [Infectious bursal disease virus] Sequence ID: **gb|AAY16544.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	rpect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 2e	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	3 :					
Query	1935	LTKTRNIWSASYVTHLIGSTI	-SDQPAKRMLN\ S+ P +LN-		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTIL '+NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRI FK+E + + R			RT- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV			NIA-KQVHKY + +O +K	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVM E S F E	ISL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				'EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLAEL 693				

▶ See 1 more title(s) Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 2e	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV			KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD				
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRI FK+E + + R			T- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN			• •	QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVM E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLAEL 693				

RNA-dependent RNA polymerase [Infectious bursal disease virus]
Sequence ID: **gb|AAS10169.1|** Length: 881 Number of Matches: 1
Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 26	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%) -	1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV			KF+P +GG++ KFNPFRGGLNF	
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW! Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD				
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRI FK+E + + R			1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN			• •	S 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV	LSKERMFKSIAC	CPOP-PSSTFQS	SNIA-KQVHKYI S + +O +K +	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVMS E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN			_ ~	EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				
Sbjct	679	FNIKLTVTSESLAEL 693				

RNA dependent RNA polymerase (RdRp) [Infectious bursal disease virus] Sequence ID: **emb|CDP32876.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 26	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				

Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLÕIKTYGÕGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P+P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + S + +Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + + N+ + L K + LD+ +++ E S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACKNNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853 +++ + A++	
Sbjct	679	FNIKLTVTSESLAEL 693	

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: 301 to 663

Score	E	xpect Method	Identities	Positives	Gaps	Frame
235 bits	(599) 36	e-63() Compositional matrix adju	ust. 143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	Features:					
Query	1935	LTKTRNIWSASYVTHLIGSTI-				
Sbjct	301	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMIT	S+ P +LN- WPVMSNSP-NNVLN		KF+P +GG++ KFNPFRGGLNI	
Query	1770	INIILNATETVELVYADNAYIY + IL E LVYADN YI			MAMYLLTRGW! Y+LTRGW	
Sbjct	356	VEWILAPEEPKALVYADNIYIV				
Query	1590	TQGTPLYNYTWAYLSLYAIPYM' G P++N TWA ++ P +	TVDSISILKNFQIKI VDS ++ N QIK		LNNHVLTTILN HNNH+L+T++	
Sbjct	413	DNGDPMFNQTWATFAMNIAPAL				
Query	1410	RWAEIGKPQPTPEVIEKLATMT(GIDFKVELVVHNFR GI+FK+E + + R			Γ- 1240
Sbjct	473	QWNLMRQPRPDSEEFKSIEDKL				QS 532
Query	1239	IVEMDMLGWDVTHT-EYG-Y VE+D+LGW T++ + G Y	TPVLSKERMFKSIAG		SNIA-KQVHKYI S + +O +K -	
Sbjct	533	SPTVELDLLGWSATYSKDLGIY				
Query	1077	NVALLYVGAWAYPCIAQTVESY AL VG W YP + + +		KEYNLDKAISKA K + LD+ +++	AVETSPFSEVMS	SL 898
Sbjct	593	YEALRLVGGWNYPLLNKACK				EG 648
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	649	FNIKLTVTSESLAEL 663				

RNA-dependent RNA polymerase [Infectious bursal disease virus] Sequence ID: **gb|AAR24134.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	kpect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 3e	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN+ MSNSP-NNVLN]		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK		LNNHVLTTII +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRE FK+E + + R			RT- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNE	KEYNLDKAISKA K + LD+ +++	VETSPFSEVM E S F E	ISL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				

Sbjct 679 FNIKLTVTSESLAEL 693

VP1 [Infectious bursal disease virus]

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

Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 36	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%) -	1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN-		SKFSPTQGGMD <i>I</i> KF+P +GG++	
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			TLNNHVLTTILN T+NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRI FK+E + + R			T- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV			SNIA-KQVHKYI S + +O +K +	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	AVETSPFSEVMS ESFE	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSEGLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AAD49776.1|** Length: 795 Number of Matches: 1 Range 1: 247 to 609

Score	E	xpect Method	Identities	Positives	Gaps	Frame
235 bits	(599) 36	e-63() Compositional matrix adjust.	140/374(37%)	213/374(56%)	24/374(6%)	-1
Features	Features:					
Query	1935	LTKTRNIWSASYVTHLIGSTIS LTKTRNIWSA THL+ S I+	-DQPAKRMLNVI + +LN+		FSPTQGGMDAF+P +GG++	
Sbjct	247	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1767	NIILNATETVELVYADNAYIYYPNE I+ E LVYADN YI + N	DIWYSIDLTKGI WYSIDL KGI		IAMYLLTRGWT Y+LTRGW	
Sbjct	303	EWIMAPDEPKALVYADNIYIVHSN-				
Query	1587	QGTPLYNYTWAYLSLYAIPYMTVDS G P++N TWA ++ P + VDS			NNHVLTTILM NNH+L+T+++	
Sbjct	360	NGDPMFNQTWATFAMNIAPALVVDS				
Query	1407	WAEIGKPOPTPEVIEKLATMTGIDF W + +P P E + + GI+F			NNRVEPRT + VEP	1240
Sbjct	420	WNLMKQPSPDSEEFKSIEDKLGINF			• •	PS 479
Query	1239	-IVEMDMLGWDVTHT-EYG-YTPVL VE+D+LGW T++ + G Y PVL				~
Sbjct	480	PTVELDLLGWSATYSKDLGIYVPVL				
Query	1074	VALLYVGAWAYPCIAQTVESYVTNH AL VG W YP + + + N+	WNTIQSMLRNKI + + L K		ETSPFSEVMS	LL 895
Sbjct	540	EALRLVGGWNYPLLNKACKNN			_ ~	GF 595
Query	894	SLEKPMHEQDYAQI 853				
Sbjct	596	NIKLTVTPESLAEL 609				

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAT76291.1| Length: 879 Number of Matches: 1

Score	Е	Expect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 3	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	S :					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				

Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P+P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + S + +Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFYSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + + N+ + L K + LD+ +++ E S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACKNNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853	
Sbjct	679	FNIKLTVTSEGLAEL 693	

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAG31694.1| Length: 879 Number of Matches: 1

Range 1: 331 to 693

Score	E	kpect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 3e	e-63() Compositional matrix adjust.	143/375(38%)	215/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN+ MSNSP-NNVLN]		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN: + IL E + LVYADN YI + N		GEANCTRDVAMT GEANCTR		
Sbjct	386	+ IL E + LVYADN YI + N VEWILAPEEPMALVYADNIYIVHSN			Y LTRGW AMFYFLTRGW	
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD	SISILKNFQIKN S ++ N OIK			
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID: +W + +P+P E + + GI+	FKVELVVHNFRE FK+E + + R			
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN				SL 898
Sbjct	623	AL VG W YP + + + N YEALRLVGGWNYPLLNKACKN	+ + + L I NASAARRHLEAI		E S F E SELSEFGEAF	QG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKPTVTSETLARL 693				

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: 331 to 693

Score	Ex	spect Method	Identities	Positives	Gaps I	Frame
236 bits	(602) 3e	-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%) -	1
Features	3:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I			KFSPTQGGMDA KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVI				
Query	1770	INIILNATETVELVYADNAYIYYPNI + IL E LVYADN YI + N	EDIWYSIDLTKG WYSIDL KG		MAMYLLTRGWT Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN-				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDS G P++N TWA ++ P + VDS				
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDI +W + +P+P E + + GI+1	FKVELVVHNFRE FK+E + + R			1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN			• •	S 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNI AL VG W YP + + + N-		EYNLDKAISKA (+ LD+ +++	VETSPFSEVMS ESFE	SL 898

Sbjct 623 YEALRLVGGWNYPLLNKACK----NNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG 678

Query 897 LSLEKPMHEQDYAQI 853
+++ + + A++
Sbjct 679 FNIKLTVTSESLAEL 693

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AlG93140.1| Length: 879 Number of Matches: 1

Range 1: 331 to 676

Score	E	kpect Method	Identities	Positives	Gaps	Frame
236 bits	(602) 3e	e-63() Compositional matrix adjust.	143/358(40%)	206/358(57%)	26/358(7%)	-1
Features	Features:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV			KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN I IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	IEWILGPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTIL +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			1243
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				HS 562
Query	1242	-TIVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV			NIA-KQVHKY + +Q +K	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNK + + + L K		VETSPFSEVM E S F E	904
Sbjct	623	YEALRLVGGWNYPLLNKACKN				676

Chain A, Unprecedented Activation Mechanism Of A Non-Canonical Rna-Dependent Rna Polymerase Sequence ID: **pdb|2PUS|A** Length: 852 Number of Matches: 1

▶ See 3 more title(s) Range 1: 338 to 700

Score	E	rpect Method	Identities	Positives	Gaps	Frame			
236 bits	(601) 3e	e-63() Compositional matrix adjust	. 143/375(38%)	214/375(57%)	26/375(6%)	-1			
Features	Features:								
Query	1935	LTKTRNIWSASYVTHLIGSTI							
Sbjct	338	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWP			KF+P +GG++ KFNPFRGGLNI				
Query	1770	INIILNATETVELVYADNAYIYYPI	-						
Sbjct	393	+ IL E LVYADN YI + I VEWILAPEEPKALVYADNIYIVHSI			Y+LTRGW AMYYILTRGW-				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVI							
Sbjct	450	G P++N TWA ++ P + VI DNGDPMFNQTWATFAMNIAPALVVI	DS ++ N QIK DSSCLIMNLQIKT		'+NNH+L+T++- 'INNHLLSTLVI				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGI				г- 1240			
Sbjct	510	+W + +P+P E + + GI- QWNLMRQPRPDSEEFKSIEDKLGII	+FK+E + + R NFKIERSIDDIRG			QS 569			
Query	1239	IVEMDMLGWDVTHT-EYG-YTP			~	~			
Sbjct	570	VE+D+LGW T++ + G Y PY SPTVELDLLGWSATYSKDLGIYVPY	VL KER+F S A VLDKERLFCSAA)						
Query	1077	NVALLYVGAWAYPCIAQTVESYVTI				SL 898			
Sbjct	630	AL VG W YP + + + I YEALRLVGGWNYPLLNKACKI			E S F E SELSEFGEAFI	EG 685			
Query	897	LSLEKPMHEQDYAQI 853							
Sbjct	686	+++ + + A++ FNIKLTVTSESLAEL 700							

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

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

Score	E	xpect	Method			Identities	Positiv	es	Gaps	Fram	e
236 bits	(601) 4e	e-63()	Composition	nal matrix adju	ust.	143/375(38%	6) 214/37 !	5(57%)	26/375(6%)	-1	
Features	s:										
Query	1935			THLIGSTI THL+ S I			NVLNCKTF N+ C		KFSPTQGGMI KF+P +GG++		1771

Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVMSNSP-NNVLNIEGCPSLYKFNPFRGGLNRI	385
Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + TL E LVYADN YT + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	+ IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN	1411
Sbjct	443	G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++ ${ m DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD}$	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT-	1240
Sbjct	503	+W + +P+P E + + GI+FK+E + + R KL + + P + VEP QWNLMRQPRPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVLLAQPGYLSGGVEPEQS	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ	1078
Sbjct	563	VE+D+LGW T++ + G Y PVL KER+F S A P+ + + +S + +Q +K ++ SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL	898
Sbjct	623	AL VG W YP + + + N+ + L K + LD+ +++ E S F E YEALRLVGGWNYPLLNKACKNNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853	
Sbjct	679	+++ + + A++ FNIKLTVTSESLAEL 693	

RNA-dependent RNA-polymerase [Infectious bursal disease virus]
Sequence ID: **gb|ABS86938.1|** Length: 881 Number of Matches: 1

Range 1: 331 to 693

Score	Ex	spect Method	Identities	Positives	Gaps	Frame		
236 bits(6	601) 4e	-63() Compositional matrix a	djust. 143/375(38%)	214/375(57%)	26/375(6%)	<u>-1</u>		
Features:								
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I						
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMI			KF+P +GG++ KFNPFRGGLN			
Query	1770	INIILNATETVELVYADNAY] + IL E LVYADN Y]			MAMYLLTRGW Y+LTRGW			
Sbjct	386	VEWILAPEEPKALVYADNIY						
Query	1590	TQGTPLYNYTWAYLSLYAIPY G P++N TWA ++ P	MTVDSISILKNFQIK + VDS ++ N ÕIK		FLNNHVLTTIL			
Sbjct	443	DNGDPMFNQTWATFAMNIAPA						
Query	1410	RWAEIGKPOPTPEVIEKLATM +W + +P+P E + +	TGIDFKVELVVHNFR GI+FK+E + + R			T- 1240		
Sbjct	503	QWNLMRQPRPDSEEFKSIED				QS 562		
Query	1239	IVEMDMLGWDVTHT-EYG- VE+D+LGW T++ + G	YTPVLSKERMFKSIA Y PVL KER+F S A			~		
Sbjct	563	SPTVELDLLGWSATYSKDLG1						
Query	1077	NVALLYVGAWAYPCIAQTVES AL VG W YP + + +	SYVTNHWNTIQSMLRN N+ + L	KEYNLDKAISK <i>I</i> K + LD+ +++	AVETSPFSEVM	SL 898		
Sbjct	623	YEALRLVGGWNYPLLNKACK-				EG 678		
Query	897	LSLEKPMHEQDYAQI 853						
Sbjct	679	FNIKLTVTSESLAEL 693						

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: 331 to 693

Score	E	cpect Method	Identities	Positives	Gaps	<u>Frame</u>
236 bits	(601) 4e	-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	3:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMDA KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVI				
Query	1770	INIILNATETVELVYADNAYIYYPNI + IL E LVYADN YI + N	EDIWYSIDLTKO WYSIDL KO		MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN-				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDS G P++N TWA ++ P + VDS	SISILKNFQIKN S ++ N QIK		LNNHVLTTILN +NNH+L+T++-	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDI +W + +P+P E + + GI+1	FKVELVVHNFRE FK+E + + R			r- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNI AL VG W YP + + + N-		KEYNLDKAISKA K + LD+ +++	VETSPFSEVMS E S F E	SL 898

Sbjct 623 YEALRLVGGWNYPLLNKACK----NNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG 678 LSLEKPMHEQDYAQI 853 +++ + A++ FNIKLTVTSESLAEL 693 Query 897 Sbjct 679

RNA-dependent RNA polymerase [Infectious bursal disease virus]

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

Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame		
236 bits	(601) 46	e-63() Compositional matrix adjus	st. 142/375(38%)	215/375(57%)	26/375(6%)	-1		
Features:								
Query	1935	LTKTRNIWSASYVTHLIGSTI			~			
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWI	S+ P +LN+ PVMSNSP-NNVLNI		KF+P +GG++ KFNPFRGGLN			
Query	1770	INIILNATETVELVYADNAYIYYI + IL E LVYADN YI +			MAMYLLTRGW Y+LTRGW			
Sbjct	386	VEWILAPEEPKALVYADNIYIVHS						
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTV G P++N TWA ++ P + V	JDSISILKNFQIKN JDS ++ N ÕIK		LNNHVLTTIL: '+NNH+L+T++			
Sbjct	443	DNGDPMFNQTWATFAMNIAPALV						
Query	1410	RWAEIGKPQPTPEVIEKLATMTG	IDFKVELVVHNFRI I+FK+E + + R			T- 1240		
Sbjct	503	QWNLMRQPRPDSDEFKSIEDKLG				QS 562		
Query	1239	IVEMDMLGWDVTHT-EYG-YTI VE+D+LGW T++ + G Y I	PVLSKERMFKSIAG			~		
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVI						
Query	1077	NVALLYVGAWAYPCIAQTVESYV				SL 898		
Sbjct	623	AL VG W YP + + + YEALRLVGGWNYPLLNKACK		<pre> </pre> <pre> <pre> </pre> <pre> <pre> </pre> <pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> </pre> <pre> <td></td><td>EG 678</td></pre></pre></pre></pre></pre></pre>		EG 678		
Query	897	LSLEKPMHEQDYAQI 853						
Sbjct	679	+++ + + A++ FNIKLTVTSESLAEL 693						

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

Sequence ID: gb|AAK69714.1| Length: 879 Number of Matches: 1

Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
236 bits	(601) 46	e-63() Compositional matrix adjust.	143/375(38%)	213/375(56%)	26/375(6%) -	.1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWP\			KF+P +GG++ KFNPFRGGLNF	
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVI G P++N TWA ++ P + VI			LNNHVLTTILM +NNH+L+T+++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVI				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGII +W + +P P E + + GI+	FKVELVVHNFR FK+E + + R			r- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVMS ESFE	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN			_ ~	EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				
Sbjct	679	FNIKLTVTSESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AHW82960.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	Expect	Method	Identities	Positives	Gaps	Frame
235 bits(600)	4e-63()	Compositional matrix adjust.	142/375(38%)	213/375(56%)	26/375(6%)	-1

Features:

Query	1935	LTKTRNIWSASYVTHLIGSTISDQPAKRMLNVLNCKTRTPSLSKFSPTQGGMDAL LTKTRNIWSA THL+SI S+P +LN+C PSL KF+P+GG+++	1771
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVMSNSP-NNVLNIEGCPSLYKFNPFRGGLNRI	385
Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLÕIKTYGÕGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P+P + + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMRQPRPDSDEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + + + + + Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + + N+ + L K + LD+ +++ E S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACKNNAGAARRHLEGKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853 ++ + A++	
Sbjct	679	FNIRLTVTSESLAEL 693	

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|ABG91146.2|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	Ex	spect Method	Identities	Positives	Gaps	Frame	
235 bits	(600) 5e	-63() Compositional matrix adjust.	142/375(38%)	215/375(57%)	26/375(6%)	-1	
Features:							
Query	1935	LTKTRNIWSASYVTHLIGSTI	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++		
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV					
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW		
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN					
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD	SISILKNFQIKN S ++ N QIK		LNNHVLTTIL +NNH+L+T++		
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD					
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID: +W + +P+P + ++ GI+	FKVELVVHNFRE FK+E + + R			T- 1240	
Sbjct	503	QWNLMKQPRPDSDELKSIEDKLGIN				QS 562	
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV					
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV					
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN		XEYNLDKAISKA X + LD+ +++	VETSPFSEVM ESFE	ISL 898	
Sbjct	623	YEALRLVGGWNYPLLNKACKN			_ ~	EG 678	
Query	897	LSLEKPMHEQDYAQI 853					
Sbjct	679	FNIKLTVTSESLAEL 693					

unnamed protein product [Infectious bursal disease virus]

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

▶ See 1 more title(s) Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame		
235 bits	(600) 5e	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1		
Features:								
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I			KFSPTQGGMD KF+P +GG++			
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV						
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW			
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN						
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD; G P++N TWA ++ P + VD;			LNNHVLTTIL +NNH+L+T++			
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD			INNHLLSTLV	LD 502		
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID: +W + +P+P E + + GI+	FKVELVVHNFRE FK+E + + R			T- 1240		
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 562		
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV						
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV						

```
Query 1077 NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL 898
AL VG W YP + + + N+ + L K + LD+ +++ E S F E
Sbjct 623 YEALRLVGGWNYPLLNKACK----NNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG 678

Query 897 LSLEKPMHEQDYAQI 853
+++ + + A++
Sbjct 679 FNIKLTVTSESLAEL 693
```

VP1 [Infectious bursal disease virus]

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

▶ See 14 more title(s) Range 1: 331 to 693

Score	E	kpect Method	Identities	Positives	Gaps F	rame
235 bits	(600) 5e	e-63() Compositional matrix adj	ust. 143/375(38%)) 214/375(57%)	26/375(6%) -1	
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI- LTKTRNIWSA THL+ S I			SKFSPTQGGMDAI	
Sbjct	331	LTKTRNIWSAPSPTHLMISMIT				
Query	1770	INIILNATETVELVYADNAYIY + IL E LVYADN YI			MAMYLLTRGWTS Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIV				-
Query	1590	TQGTPLYNYTWAYLSLYAIPYM G P++N TWA ++ P +	TVDSISILKNFQIK VDS ++ N ÕIK			
Sbjct	443	DNGDPMFNQTWATFAMNIAPAL			T+NNH+L+T++++ TINNHLLSTLVLI	
Query	1410	RWAEIGKPOPTPEVIEKLATMT	GIDFKVELVVHNFR GI+FK+E + + R			- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKL			• •	5 562
Query	1239	IVEMDMLGWDVTHT-EYG-Y				
Sbjct	563	VE+D+LGW T++ + G Y SPTVELDLLGWSATYSKDLGIY	PVL KER+F S A VPVLDKERLFCSAA			
Query	1077	NVALLYVGAWAYPCIAQTVESY				L 898
Sbjct	623	AL VG W YP + + + YEALRLVGGWNYPLLNKACK		K + LD+ +++ KGFPLDEFLAEV	E S F E SELSEFGEAFE	G 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	+++ + + A++ FNIKLTVTSESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ABG91143.1| Length: 879 Number of Matches: 1

Range 1: 331 to 693

Score	E	cpect Method	Identities	Positives	Gaps	Frame
235 bits	(600) 5e	-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I			KFSPTQGGMDA KF+P +GG++	
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPVI				
Query	1770	INIILNATETVELVYADNAYIYYPNI + I+ E LVYADN YI + N	EDIWYSIDLTKO WYSIDL KO		MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD: G P++N TWA ++ P + VD:	SISILKNFQIKN S ++ N ÕIK			
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDE +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			Γ- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN			• • • • •	QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				~
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNI AL VG W YP + + + N-	HWNTIQSMLRNK + + + L K		VETSPFSEVM: ESFE	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKNI				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|ACN69081.1| Length: 879 Number of Matches: 1

Range 1: 331 to 693

Score Expect Method Identities Positives Gaps Frame

235 bits(600) 5e-63() Compositional matrix adjust. 140/374(37%) 213/374(56%) 24/374(6%) -1

Features:

Query	1935	LTKTRNIWSASYVTHLIGSTISDQPAKRMLNVLNCKTRTPSLSKFSPTQGGMDALI LTKTRNIWSA THL+ S I+ + +LN+ C PSL KF+P +GG++ ++	1768
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVMSNSSNNVLNIEGCPSLYKFNPFRGGLNRIV	386
Query	1767	NIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTST I+ E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1588
Sbjct	387	EWIMAPDEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-SD	443
Query	1587	QGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNR G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T+++++	1408
Sbjct	444	NGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLDQ	503
Query	1407	WAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT W + +P P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	504	WNLMKQPSPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQPS	563
Query	1239	-IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQN	1075
Sbjct	564	VE+D+LGW T++ + G Y PVL KER+F S A P+ + + +S + +Q +K ++ PTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVRY	623
Query	1074	VALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSLL	895
Sbjct	624	AL VG W YP + + + N+ + + L K + LD+ +++ E S F E EALRLVGGWNYPLLNKACKNNASAARRHLEAKGFPLDEFLAEWSELSEFGEAFEGF	679
Query	894	SLEKPMHEQDYAQI 853	
Sbjct	680	+++ + + A++ NIKLTVTSESLAEL 693	

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AKD94180.1|** Length: 878 Number of Matches: 1 Range 1: 331 to 693

Score	E	kpect Method	Identities	Positives	Gaps	Frame
235 bits	(600) 5e	e-63() Compositional matrix adjust.	143/375(38%)	214/375(57%)	26/375(6%) -	1
Features	3:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLN\ S+ P +LN+		KFSPTQGGMD <i>F</i> KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK		LNNHVLTTILM +NNH+L+T+++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRE FK+E + + R			7- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVMS ESFE	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN			_ ~	EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLÄEL 693				

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|AAS10170.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
235 bits	(600) 56	e-63() Compositional matrix adjust.	143/375(38%)	213/375(56%)	26/375(6%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLN\ S+ P +LN-		KFSPTQGGMDA	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTILN +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P+P E + + GI+	FKVELVVHNFRI FK+E + + R			Γ- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				~

Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + + N+ + L K + LD+ +++ E S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACKNNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853 ++ + A++	
Sbjct	679	FNIRLTVTSESLAEL 693	

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AFP86287.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
235 bits	(600) 66	e-63() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	SDQPAKRMLNV S+ P +LN-		KFSPTQGGMD. KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTILI '+NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID	FKVELVVHNFRI FK+E + + R			T- 1240
Sbjct	503	QWNLMKQPRPDSDEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				~
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N			VETSPFSEVM E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				
Sbjct	679	FNIKLTVTSESLAEL 693				

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

Sequence ID: **gb|AFN80479.1|** Length: 878 Number of Matches: 1 Range 1: 331 to 693

235 bits(6	600) 6e-	-63() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%) -1	
Features:						
Query	1935	LTKTRNIWSASYVTHLIGSTI				1771
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPVN	S+ P +LN+ MSNSP-NNVLNI		KF+P +GG++ + KFNPFRGGLNRI	385
Query	1770	INIILNATETVELVYADNAYIYYPNI + IL E LVYADN YI + N	EDIWYSIDLTKO WYSIDL KO		MAMYLLTRGWTS Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN-	-			442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDS G P++N TWA ++ P + VDS			LNNHVLTTILMN +NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDS				502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDE +W + +P+P + + + GI+E				1240
Sbjct	503	QWNLMRQPRPDSDEFKSIEDKLGINE				562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVI VE+D+LGW T++ + G Y PVI				1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVI				622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNI AL VG W YP + + + N+				898
Sbjct	623	AL VG W YP + + + N-YEALRLVGGWNYPLLNKACKNN		(+ LD+ +++ GFPLDEFLAEW	E S F E SELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABG91145.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Expect Method Identities Score **Positives** Gaps Frame 235 bits(599) 6e-63() Compositional matrix adjust. 142/375(38%) 214/375(57%) 26/375(6%) -1

Features:

Query	1935	LTKTRNIWSASYVTHLIGSTISDQPAKRMLNVLNCKTRTPSLSKFSPTQGGMDAL LTKTRNIWSA THL+ S I S+ P +LN+ C PSL KF+P +GG++ +	1771
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVMSNSP-NNVLNIEGCPSLYKFNPFRGGLNRI	385
Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P+P + + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMKQPRPDSDEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + S + +Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + + N+ + L K + LD+ +++ E S F E	898
Sbjct	623	AL VG W YP + + + N+ + L K + LD+ +++ E S F E YEALRLVGGWNYPLLNKACKNNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853 +++ + A++	
Sbjct	679	FNIKLTVTSESLAEL 693	

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AAM45385.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
235 bits	(599) 66	e-63() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N OIK		LNNHVLTTII +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			RT- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNF + + + L F		VETSPFSEVM E S F E	ISL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				'EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLAEL 693				

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|AEP04404.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
235 bits	(599) 76	e-63() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK		LNNHVLTTII '+NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P+P + + + GI+	FKVELVVHNFRE FK+E + + R			RT- 1240
Sbjct	503	QWNLMKQPRPDSDEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				~

Sbjct 563 SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR 622

Query 1077 NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL 898
 AL VG W YP + + + N+ + L K + LD+ +++ E S F E

Sbjct 623 YEALRLVGGWNYPLLNKACK----NNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG 678

Query 897 LSLEKPMHEQDYAQI 853
 +++ + + A++

Sbjct 679 FNIKLTVTSESLAEL 693

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ABI52867.1| Length: 879 Number of Matches: 1

Range 1: 331 to 693

Identities Score Expect Method Positives Gaps Frame 235 bits(599) 7e-63() Compositional matrix adjust. 140/374(37%) 213/374(56%) 24/374(6%) -1 Features: LTKTRNIWSASYVTHLIGSTIS----DQPAKRMLNVLNCKTRTPSLSKFSPTQGGMDALI LTKTRNIWSA THL+ S I+ + +LN+ C PSL KF+P +GG++ ++ Query 1935 1768 LTKTRNIWSAPSPTHLMISMITWPVMSNSSNNVLNIEGC---PSLYKFNPFRGGLNRIV Sbjct 331 386 1767 NIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTST 1588 Query WYSIDL KGEANCTR E LVYADN YI + N Y+LTRGW S EWIMAPDEPKALVYADNIYIVHSN--TWYSIDLEKGEANCTRQHMQAAMYYILTRGW-SD Sbjct 387 443 1587 QGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNR 1408 Query G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T+++++
NGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLDQ 503 Sbjct 444Query 1407 WAEIGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPT--NNRVEPRT--1240 GI+FK+E + + R KL +W + +PPE + ++ P WNLMKQPSPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQPS Sbjct 504 563 -IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQN 1239 1075 Query VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + + S + + + Q +K ++ Sbjct 564 PTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVRY 623 VALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSLL AL VG W YP + + + N+ + + L K + LD+ +++ E S F E EALRLVGGWNYPLLNKACK----NNASAARRHLEAKGFPLDEFLAEWSELSEFGEAFEGF Query 1074 895 679 Sbjct 624 894 SLEKPMHEODYAOI 853 Query +++ + + A++ NIKLTVTPESLAEL Sbjct 680 693

RNA-dependent RNA-polymerase [Infectious bursal disease virus]
Sequence ID: **gb|AAY16541.1**| Length: 881 Number of Matches: 1

Range 1: 331 to 693

Score	E	kpect Method	Identities	Positives	Gaps	Frame
235 bits	(599) 7e	e-63() Compositional matrix adjust.	143/375(38%)	213/375(56%)	26/375(6%)	-1
Features	S :					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV			KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD				
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI	FKVELVVHNFRI FK+E + + R			RT- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIS				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRN	KEYNLDKAISKA K + LD+ +++	VETSPFSEVM ESFE	ISL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN			_ ~	'EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				
Sbjct	679	FNIKLTVTSESLAEL 693				

RNA-dependent RNA polymerase [Infectious bursal disease virus]
Sequence ID: **gb|AKM16808.1|** Length: 879 Number of Matches: 1
Range 1: 331 to 693

Score Expect Method Identities Positives Gaps Frame

235 bits(599) 7e-63() Compositional matrix adjust. 142/375(38%) 213/375(56%) 26/375(6%) -1

Features:

Query	1935	LTKTRNIWSASYVTHLIGSTISDQPAKRMLNVLNCKTRTPSLSKFSPTQGGMDAL LTKTRNIWSA THL+ S I S+ P +LN+ C PSL KF+P +GG++ +	1771
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVMSNSP-NNVLNIEGCPSLYKFNPFRGGLNRI	385
Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N OIK GOGSGN TF+NNH+L+T++++	1411
Sbjct	443	G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++ DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT-	1240
Sbjct	503	+W $+$ $+$ $+$ P $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ	1078
Sbjct	563	VE+D+LGW T++ + G Y PVL KER+F S A P+ + + +S + +Q +K ++ SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL	898
Sbjct	623	AL VG W YP + + + N+ + L K + LD+ +++ E S F E YEALRLVGGWNYPLLNKACKNNAGAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853	
Sbjct	679	+++ + + A++ FNIKLTVTSESLAEL 693	

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABI52865.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	cpect Method	Identities	Positives	Gaps	Frame
235 bits	(599) 7e	-63() Compositional matrix adjust.	140/374(37%)	213/374(56%)	24/374(6%) -	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTIS LTKTRNIWSA THL+ S I+			FSPTQGGMDAI F+P +GG++ -	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1767	NIILNATETVELVYADNAYIYYPNE I+ E LVYADN YI + N	DIWYSIDLTKGE WYSIDL KGE		AMYLLTRGWTS Y+LTRGW	
Sbjct	387	EWIMAPDEPKALVYADNIYIVHSN-				
Query	1587	QGTPLYNYTWAYLSLYAIPYMTVDS G P++N TWA ++ P + VDS				
Sbjct	444	NGDPMFNQTWATFAMNIAPALVVDS	++ N QIK SCLIMNLQIKTY		NNH+L+T+++- NNHLLSTLVLI	
Query	1407	WAEIGKPOPTPEVIEKLATMTGIDF				1240
Sbjct	504	W + +P P E + + GI+F; WNLMKQPSPDSEEFKSIEDKLGINF;			• •	PS 563
Query	1239	-IVEMDMLGWDVTHT-EYG-YTPVL				
Sbjct	564	VE+D+LGW T++ + G Y PVL PTVELDLLGWSATYSKDLGIYVPVL				
Query	1074	VALLYVGAWAYPCIAQTVESYVTNH				LL 895
Sbjct	624	AL VG W YP + + + N+ EALRLVGGWNYPLLNKACKNN	+ + L K ASAARRHLEAKO		E S F E ELSEFGEAFE(GF 679
Query	894	SLEKPMHEQDYAQI 853				
Sbjct	680	+++ + + A++ NIKLTVTPESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ACH89972.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 676

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 86	e-63() Compositional matrix adjust.	142/358(40%)	206/358(57%)	26/358(7%) -	1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLN\ S+ P +LN+		KFSPTQGGMDA	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTILM +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			1243
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				IS 562
Query	1242	-TIVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				~

VP1 [Infectious bursal disease virus]

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

Range 1: 331 to 693

Score	E	kpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 9e	e-63() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	<u>-1</u>
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV			KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK		LNNHVLTTILI +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRI FK+E + + R			T- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNI + + + L I	KEYNLDKAISKA	VETSPFSEVM E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

RdRp (VP1) [Infectious bursal disease virus]

Sequence ID: emb|CDW92046.1| Length: 879 Number of Matches: 1

Range 1: 331 to 676

Score	E	cpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 9e	e-63() Compositional matrix adjust.	142/358(40%)	206/358(57%)	26/358(7%)	-1
Features	3:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I			KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK		LNNHVLTTIL +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			1243
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN			• • • • • •	HS 562
Query	1242	-TIVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	VE+D+LGW T++ + G Y PV SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVM ESFE	904
Sbjct	623	YEALRLVGGWNYPLLNKACKN			_ ~	676

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

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

	Score	E	Expect	Method		Identities	Positives	Gaps	Frame	_
	234 bits(598) 9	e-63()	Composition	al matrix adjust.	142/358(40%)	205/358(57%)	26/358(7%)	-1	
Features:										
	Query	1935				SDQPAKRMLNV S+ P +LN+				771
	Sbjct	331			THL+ S I THLMISMITWP\	MSNSP-NNVLNI		KF+P +GG++ KFNPFRGGLN		85

Query	1770	INIILNATETVELVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTS + IL E LVYADN YI + N WYSIDL KGEANCTR Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSNTWYSIDLEKGEANCTRQHMQAAMYYILTRGW-S	442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N QIK GQGSGN TF+NNH+L+T++++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P+P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMKQPRPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S+A P+ + + + + S + + + Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSVAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	04
Sbict	623		76

RNA-dependent RNA polymerase [Infectious bursal disease virus] Sequence ID: **gb|AAM97562.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 96	e-63() Compositional matrix adju	st. 142/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI	SDQPAKRMLNV S+ P +LN-			
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITW			KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYY + IL E LVYADN YI +			MAMYLLTRGW! Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVH				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMT G P++N TWA ++ P +	VDSISILKNFQIKN VDS ++ N ÕIK		LNNHVLTTIL +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALV				
Query	1410	RWAEIGKPOPTPEVIEKLATMTG	IDFKVELVVHNFRI I+FK+E + + R			1243
Sbjct	503	QWNLMKQPRPDSDEFKSIEDKLG				HS 562
Query	1242	-TIVEMDMLGWDVTHT-EYG-YT VE+D+LGW T++ + G Y	PVLSKERMFKSIAO PVL KER+F S A		SNIA-KQVHKY S + +O +K	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYV				
Query	1077	NVALLYVGAWAYPCIAQTVESYV AL VG W YP + + +		KEYNLDKAISKA K + LD+ +++	VETSPFSEVM E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACK				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLÄEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ACV66328.1| Length: 879 Number of Matches: 1

▶ See 1 more title(s) Range 1: 331 to 676

Score	Ex	kpect Method	Identities	Positives	Gaps	Frame
234 bits((598) 1e	e-62() Compositional matrix adjust.	142/358(40%)	206/358(57%)	26/358(7%)	-1
Features	S:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD: G P++N TWA ++ P + VD:	SISILKNFQIKN S ++ N QIK		LNNHVLTTII +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID: +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			1243
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				HS 562
Query	1242	-TIVEMDMLGWDVTHT-EYG-YTPV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNI AL VG W YP + + + N	HWNTIQSMLRNK + + + L K			904
Sbjct	623	YEALRLVGGWNYPLLNKACKN				676

VP1 [Infectious bursal disease virus]

Sequence ID: gb|ACV66326.1| Length: 879 Number of Matches: 1

▶ See 2 more title(s) Range 1: 331 to 676

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 16	e-62() Compositional matrix adjust	. 142/358(40%)	206/358(57%)	26/358(7%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I			SKFSPTQGGMDA KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWP				
Query	1770	INIILNATETVELVYADNAYIYYPI + IL E LVYADN YI + 1			MAMYLLTRGW! Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHS				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTV G P++N TWA ++ P + V			LNNHVLTTILI '+NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVI				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGI +W + +P P E + + GI	DFKVELVVHNFRI +FK+E + + R			1243
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGI				HS 562
Query	1242	-TIVEMDMLGWDVTHT-EYG-YTP	VLSKERMFKSIAG VL KER+F S A			
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVP				
Query	1077	NVALLYVGAWAYPCIAQTVESYVT	NHWNTIQSMLRNI N+ +		VETSPFSEVM E S F E	904
Sbjct	623	YEALRLVGGWNYPLLNKACK			_ ~	676

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

Sequence ID: **emb|CDP32873.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 1e	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTII +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			T- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVM E S F E	ISL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				
Sbjct	679	FNIKLTVTPESLÄEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AIG93143.1| Length: 879 Number of Matches: 1

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 16	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI			~	
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPVI	S+ P +LN+ MSNSP-NNVLN]		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD; G P++N TWA ++ P + VD;		-	LNNHVLTTII +NNH+L+T++	

Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD	502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQP	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + S + +Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + + N+ + L K + LD+ +++ E S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACKNNASAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853	
Sbjct	679	FNIKLTVTPESLAEL 693	

RNA-dependent RNA polymerase [Infectious bursal disease virus]

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

Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 1e	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWP\			KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVI G P++N TWA ++ P + VI	OSISILKNFQIKI OS ++ N QIK		LNNHVLTTILI +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVI				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGII +W + +P P E + + GI+	OFKVELVVHNFRI FFK+E + + R			T- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNI + + + L I			SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				
Sbjct	679	FNIKLTVTPESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ACV66327.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 676

Score	E	rpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 1e	-62() Compositional matrix adjust.	142/358(40%)	206/358(57%)	26/358(7%)	-1
Features	3:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN+ MSNSP-NNVLNI		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK		LNNHVLTTIL +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			1243
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN			• •	HS 562
Query	1242	-TIVEMDMLGWDVTHT-EYG-YTPV				
Sbjct	563	VE+D+LGW T++ + G Y PV SPTVELDLLGWSATYSKDLGIYVPV			~	
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN				904
Sbjct	623	AL VG W YP + + + N YEALRLVGGWNYPLLNKACKN	+ + + L K NASAARRHLEAK			676

▶ See 3 more title(s) Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 1e	e-62() Compositional matrix adjus	st. 142/375(38%) 214/375(57%) 26/375(6%) -	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I			SKFSPTQGGMDA KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITW				
Query	1770	INIILNATETVELVYADNAYIYYI + I+ E LVYADN YI +			MAMYLLTRGW! Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVH				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTY G P++N TWA ++ P + Y	VDSISILKNFQIK VDS ++ N ÕIK		FLNNHVLTTILN F+NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALV				
Query	1410	RWAEIGKPOPTPEVIEKLATMTG: +W + +P P E + + G:		EKLIEASNHSII		Γ- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLG:				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTI VE+D+LGW T++ + G Y I	PVLSKERMFKSIA PVL KER+F S A		SNIA-KQVHKYI S + +O +K -	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYV				
Query	1077	NVALLYVGAWAYPCIAQTVESYV	TNHWNTIQSMLRN N+ + + L		AVETSPFSEVMS ESFE	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACK	- ·			EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABG91142.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 1e	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	<u>-1</u>
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN+ MSNSP-NNVLN]		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTIL +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID	FKVELVVHNFRE FK+E + + R			T- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				RP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNI + + + L F		VETSPFSEVM E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

VP1 protein [Infectious bursal disease virus]

Sequence ID: emb|CAC60257.1| Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 16	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Features	S :					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I		/LNCKTRTPSLS - C PSL		
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTII +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				

Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQP	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + + + + + Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + + N+ + L K + LD+ +++ E S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACKNNASAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853	
Sbjct	679	FNIKLTVTPESLAEL 693	

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ACB56952.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	Expec	t Method	lo	dentities	Positives	Gaps F	rame
234 bits(59	8) 1e-62() Compositional matri	x adjust. 14	42/375(38%)	214/375(57%)	26/375(6%) -1	
Features:							
Query 19		KTRNIWSASYVTHLIGS	STIS	DQPAKRMLNV	LNCKTRTPSLS	KFSPTQGGMDA:	ւ 1771
Sbjct 33		KTRNIWSA THL+ S KTRNIWSAPSPTHLMIS		+ P +LN+ NSP-NNVLNI		KF+P +GG++ KFNPFRGGLNR	
Query 17		ILNATETVELVYADN					
Sbjct 38	+ 36 VEV	I+ E LVYADN VIMAPDEPKALVYADN		WYSIDL KG TWYSIDLEKG		Y+LTRGW ; AMYYILTRGW-	-
Query 15		GTPLYNYTWAYLSLYA					
Sbjct 44		G P++N TWA ++ GDPMFNQTWATFAMNI <i>I</i>					
Query 14		AEIGKPQPTPEVIEKLA					- 1240
Sbjct 50	YWQ EC	+ +P P E + + NLMKQPSPDSEEFKSI	GI+FK EDKLGINFK			+ VEP GYLSGGVEPEQ:	P 562
Query 12	239	VEMDMLGWDVTHT-EY	G-YTPVLS	KERMFKSIAC	POP-PSSTFQS	NIA-KQVHKYI	Q 1078
Sbjct 56	63 SPT	VE+D+LGW T++ + TVELDLLGWSATYSKDI	LGIYVPVLD	KER+F S A KERLFCSAAY	P+ + + +S PKGVENKSLKS	KVGIEQAYKVVI	+ R 622
Query 10		ALLYVGAWAYPCIAQTV					և 898
Sbjct 62		AL VG W YP + + ALRLVGGWNYPLLNKAO			+ LD+ +++ GFPLDEFLAEW	E S F E SELSEFGEAFE(G 678
Query 89		EKPMHEQDYAQI 85	53				
Sbjct 67	•	++ + + A++ [KLTVTPESLAEL 69	93				

RdRp (VP1) [Infectious bursal disease virus]

Sequence ID: emb|CDW92044.1| Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	rpect Method	Identities	Positives	Gaps	Frame
234 bits	(598) 1e	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV			KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N OIK		LNNHVLTTIL +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			T- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN				SL 898
Sbjct	623	AL VG W YP + + + N YEALRLVGGWNYPLLNKACKN		<pre> < + LD+ +++ </pre> <pre> <gfpldeflaew <="" pre=""></gfpldeflaew></pre>	E S F E SELSEFGEAF	EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	+++ + + A++ FNIKLTVTPESLAEL 693				

Sequence ID: gb|ACB56953.1| Length: 879 Number of Matches: 1

Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(597) 1e	e-62() Compositional matrix adjust.	142/375(38%) 214/375(57%)	26/375(6%) -	·1
Features	S :					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN MSNSP-NNVLN		KF+P +GG++ KFNPFRGGLNF	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD				
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+		EKLIEASNHSII		Γ- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				~
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISK K + LD+ +++	AVETSPFSEVMS E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

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

Sequence ID: **gb|AAK69710.1|AF362770_1** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(597) 1e	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%) -	1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN-		KFSPTQGGMD <i>F</i> KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD				
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRI FK+E + + R			7- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				P 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV				
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV			~	
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N			VETSPFSEVMS E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLÄEL 693				

polymerase [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAV48843.1| Length: 845 Number of Matches: 1

▶ See 1 more title(s) Range 1: 317 to 699

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(596) 16	e-62() Compositional matrix adjust.	150/401(37%)	208/401(51%)	41/401(10%)	-1
Features	s:					
Query	1929	KTRNIWSASYVTHLIGSTISDQPA- KTRNIWSA Y THL+ S +S P		TRTPSLSKFSP T+TPSL FSP	TQGGMDALINI GGMD ++ T	
Sbjct	317	KTRNIWSAPYPTHLLLSMVS-SPVM			00112	_
Query	1758	LNATETVELVYADNAYIYYPNEI L+ E + ++YADN YI N	OIWYSIDLTKGE WYSIDL KGE			
Sbjct	374	DSLDNNEDLVMIYADNIYILQDN				
Query	1584	GTPLYNYTWAYLSLYAIPYMTVDSI G+P YN TWA ++ P M VDS		GQGSGNPWTFLI GQGSGN +TFLI		RW 1405 W

Sbjct	432	GSPRYNPTWATFAMNVAPSMVVDSSCLLMNLQLKTYGQGSGNAFTFLNNHLMSTIVVAEW	491
Query	1404	AEIGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNN + GKP P + L TGI+FK+E + N RE +IE A +P N	1258
Sbjct	492	VKAGKPNPMTKEFMDLEEKTGINFKIERELKNLRETIIEAVETAPQDGYLADGSDLPPN-	550
Query	1257	RVEPRTIVEMDMLGWDVTHTEYGYTPVLSKERMFKSIACPQPPSSTFQSNIAK P VE+D+LGW ++ + P+L ER+ S A P+ + + IA	1099
Sbjct	551	RPGKAVELDLLGWSAIYSRQMEMFVPILENERLIASAAYPKGLENKTLARKPGAEIAY	608
Query	1098	QVHKYIQNVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSP	919
Sbjct	609	Q++Y A+ VG W P + + + + L K ++ + + S $QIVRYEAIRLVGGWNNPLLETAAKHMSLDKRKRLEVKGLDVTGFLDAWNDMSE$	661
Query	918	FSEVMSLLSLEKPMHEQDYAQILYKQKPIEKIAPKAKFNNP 796	
Sbict	662	F + ++L +P+ Q I P+E PKA+ P FGGDLEGITLSEPLTNOTLIDINTPLESFDPKARPOTP 699	

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

Sequence ID: gb|AFN80483.1| Length: 878 Number of Matches: 1

Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(597) 1e	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWP\	S+ P +LN+ MSNSP-NNVLN		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVI G P++N TWA ++ P + VI	OSISILKNFQIKN OS ++ N ÕIK		LNNHVLTTILI +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVI				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGII				T- 1240
Sbjct	503	+W + +P P E + + GI+ QWNLMKQPSPDSEEFKSIEDKLGIN	+FK+E + + R NFKIERSIDDIR(QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV			SNIA-KQVHKY S + +O +K	
Sbjct	563	VE+D+LGW T++ + G Y PV SPTVELDLLGWSATYSKDLGIYVPV	LDKERLFCSAA	PKGVENKSLKS		
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	NHWNTIQSMLRNI N+ + L I			SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN			E S F E ISELSEFGEAF	EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

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

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

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(597) 1e	e-62() Compositional matrix adjust.	141/358(39%)	206/358(57%)	26/358(7%)	-1
Features	S :					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I			KFSPTQGGMDA KF+P +GG++	
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTIL	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P+P E + + GI+		EKLIEASNHSIP KL + + + P		r- 1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV		CPQP-PSSTFQS P+ + + +S		
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVM E S F E	904
Sbjct	623	YEALRLVGGWNYPLLNKACKN				676

▶ See 3 more title(s) Range 1: 317 to 699

Score	Ex	rpect Method	Identities	Positives	Gaps	Frame
234 bits	(596) 1e	e-62() Compositional matrix adjust.	150/401(37%)) 208/401(51%)	41/401(10%)	-1
Features	S :					
Query	1929	KTRNIWSASYVTHLIGSTISDQPA- KTRNIWSA Y THL+ S +S P	-KRMLNVLNCF + LN+ N	(TRTPSLSKFSP' T+TPSL FSP	TQGGMDALINI GGMD ++ II	
Sbjct	317	KTRNIWSAPYPTHLLLSMVS-SPVM				
Query	1758	LNATETVELVYADNAYIYYPNED L+ E + ++YADN YI N	IWYSIDLTKGE WYSIDL KGE			TQ 1585
Sbjct	374	DSLDNNEDLVMIYADNIYILQDN				ED 431
Query	1584	GTPLYNYTWAYLSLYAIPYMTVDSI G+P YN TWA ++ P M VDS		PGQGSGNPWTFL GQGSGN +TFL		RW 1405
Sbjct	432	GSPRYNPTWATFAMNVAPSMVVDSS				• •
Query	1404	AEIGKPQPTPEVIEKLATMTGIDFK + GKP P + L TGI+FK	VELVVHNFREF HE + N RE	KLIE	ASNHSIPTI A +P 1	
Sbjct	492	VKAGKPNPMTKEFMDLEEKTGINFK				- •
Query	1257	RVEPRTIVEMDMLGWDVTHTEYG P VE+D+LGW ++	YTPVLSKERME + P+L ER+		rfQSNIZ + IZ	
Sbjct	551	RPGKAVELDLLGWSAIYSRQMEM				-
Query	1098	QVHKYIQNVALLYVGAWAYPCIAQT O+ +Y A+ VG W P +	VESYVTNHWNT			
Sbjct	609	QIVRYEAIRLVGGWNNPLLETA				•
Query	918	FSEVMSLLSLEKPMHEQDYAQILYK F + ++L +P+ O I	QKPIEKIAPKA P+E PKA			
Sbjct	662	F + ++L +P+ Q I FGGDLEGITLSEPLTNQTLIDI				

RNA dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: emb|CAJ34340.1| Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	s(597) 1e	e-62() Compositional matrix adjust.	141/375(38%)	213/375(56%)	26/375(6%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN-		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMTPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD				
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD	SSCLIMNLÕIK	TYGQGSGNAATF	INNHLLSTLV	7LD 502
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRI FK+E + + R			RT- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				EQP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW ++ + G Y PV	LSKERMFKSIAG L KER+F S A			
Sbjct	563	SPTVELDLLGWSAAYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNI + + + L I			ISL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

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

Sequence ID: gb|AFN80484.1| Length: 878 Number of Matches: 1

Score	E	kpect Method	Identities	Positives	Gaps	Frame	
234 bits(597) 1e	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1	
Features	:						
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I		LNCKTRTPSLS C PSL			
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVI					
Query	1770	INIILNATETVELVYADNAYIYYPNI + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW		
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN-				_	
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDS G P++N TWA ++ P + VDS	SISILKNFQIKN S ++ N ÕIK		LNNHVLTTIL +NNH+L+T++		
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD					

Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQP	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + S + +Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL	898
Sbjct	623	AL VG W YP + + + N+ + L K + LD+ +++ E S F E YEALRLVGGWNYPLLNKACKNNASAARRHLEAKGFPLDEFLTEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853	
Sbjct	679	FNIKLTVTPESLAEL 693	

RNA-directed RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|AAC55352.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

234 bits(596) 2e-62() Composition Features: Query 1935 LTKTRNIWSASYV LTKTRNIWSA Sbjct 331 LTKTRNIWSAPSI Query 1770 INIILNATETVED + IL E IN Sbjct 386 VEWILAPEEPKAN		Identities	Positives	Gaps Fr	ame
Query 1935 LTKTRNIWSASYY LTKTRNIWSA Sbjct 331 LTKTRNIWSAPSI Query 1770 INIILNATETVEI + IL E	nal matrix adjust.	142/375(38%)	213/375(56%)	26/375(6%) -1	
Sbjct 331 LTKTRNIWSA Sbjct 331 LTKTRNIWSAPSI Query 1770 INIILNATETVEI + IL E					
Sbjct 331 LTKTRNIWSAPSI Query 1770 INIILNATETVEI + IL E		-SDQPAKRMLN			
+ IL E]	THL+ S I PTHLMISMITWPV			KF+P +GG++ + KFNPFRGGLNRI	
				MAMYLLTRGWTS Y+LTRGW S	
Query 1590 TQGTPLYNYTWAY					
Sbjct 443 DNGDPMFNQTWA	++ P + VD FAMNIAPALVVD			'+NNH+L+T++++ 'INNHLLSTLVLD	
Query 1410 RWAEIGKPQPTPI		FKVELVVHNFR FK+E + + R			1240
Sbjct 503 QWNLMKQPSPDSI				• •	562
Query 1239 IVEMDMLGWDV	/THT-EYG-YTPV T++ + G Y PV	LSKERMFKSIA	CPQP-PSSTFQS	SNIA-KQVHKYIÇ	1078
Sbjct 563 SPTVELDLLGWS					
Query 1077 NVALLYVGAWAYI					898
AL VG W YI Sbjct 623 YEALRLVGGWNYI		J+ + + L] INASAARRHLEA		E S F E AELSEFGEAFEG	678
Query 897 LSLEKPMHEQDY	0.5				
Sbjct 679 FNIKLTVTSESLA					

VP1 [Infectious pancreatic necrosis virus - Mexico]

Sequence ID: **gb|ACD14075.1|** Length: 845 Number of Matches: 1 Range 1: 317 to 699

Score	Ex	cpect Method	Identities	Positives	Gaps I	Frame
233 bits	(595) 2e	-62() Compositional matrix adjust.	149/398(37%)	208/398(52%)	35/398(8%) -	1
Features	3 :					
Query	1929	KTRNIWSASYVTHLIGSTISDQPAKE KTRNIWSA Y THL+ S +S +			GGMDALINII- GGMD ++ II	- 1759
Sbjct	317	KTRNIWSAPYPTHLLLSMVSSPVME				RD 374
Query	1758	-LNATETVELVYADNAYIYYPNEDIV L+ E + ++YADN YI N V	VYSIDLTKGEAN VYSIDL KGEAN		YLLTRGWTSTÇ YLLTRGWT+	G 1582
Sbjct	375	SLDNDEDLVMIYADNIYILQDNTV			_	G 432
Query	1581	TPLYNYTWAYLSLYAIPYMTVDSISI +P YN TWA ++ P M VDS		QGSGNPWTFLNN OGSGN +TFLNN		IA 1402 IA
Sbjct	433	SPRYNPTWATFAMNVAPSMVVDSSCI				
Query	1401	EIGKPOPTPEVIEKLATMTGIDFKVI + GKP P + L TGI+FK+F			RV	E 1249
Sbjct	493	KAGKPNPMTKEFMDLEERTGINFKI				IR 551
Query	1248	PRTIVEMDMLGWDVTHTEYGYTPVPVVE+D+LGWVTHTEYGYTPV			QSNIAKQV + IA O+	
Sbjct	552	PGKAVELDLLGWSAIYSRQMEMFVPV			z	
Query	1089	KYIQNVALLYVGAWAYPCIAQTVESY +Y A+ VG W P + +			ISKAVETSPFS + S F	SE 910
Sbjct	612	RYEAIRMVGGWNNPLLETAAKHN				G 664
Query	909	VMSLLSLEKPMHEQDYAQILYKQKPI + ++L +P+ O I P+		IP 796		
Sbjct	665	DLEGITLSEPLTNÕTLIDINTPI		_		

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

Score	E	rpect Method	Identities	Positives	Gaps	Frame
234 bits	(596) 2e	e-62() Compositional matrix adjust.	142/375(38%)	213/375(56%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P LN+ MSNSP-NNALN		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + T+ E LVYADN YT + N				
Sbjct	386	+ I+ E LVYADN YI + N VEWIMAPDEPKALVYADNIYIVHSN			Y+LTRGW AMYYILTRGW	
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD				
Sbjct	443	G P++N TWA ++ P + VD DNGDPMFNQTWATFAMNIAPALVVD			'+NNH+L+T++ 'INNHLLSTLV	
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID				T- 1240
Sbjct	503	+W + +P P E + + GI+ QWNLMKQPSPDSEEFKSIEDKLGIN	FK+E + + R FKIERSIDDIR(QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV				~
Sbjct	563	VE+D+LGW T++ + G Y PV SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN				SL 898
Sbjct	623	AL VG W YP + + + N YEALRLVGGWNYPLLNKACKN	[+ + + L F NASAARRHLEAF			EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	+++ + + A++ FNIKLTVTPESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AEQ29951.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
234 bits	(596) 26	e-62() Compositional matrix adjust.	142/375(38%)	212/375(56%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLN\ S+ P +LN+		KFSPTQGGMD KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK		LNNHVLTTIL +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD	SSCLIMNLÕIKI	TYGQGSGNAATF		
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			T- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHTE-YG-YTPV VE+D+LGW +++ G Y PV	LSKERMFKSIAC L KER+F S A			
Sbjct	563	SPTVELDLLGWSAPYSKNLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++	VETSPFSEVM E S F E	ISL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLÄEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|AFP86290.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 676

Score	E	xpect Method	Identities	Positives	Gaps	Frame
233 bits	(595) 26	e-62() Compositional matrix adjust.	140/358(39%)	206/358(57%)	26/358(7%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV		- C PSL IEGCPSLY		
Query	1770	INIILNATETVELVYADNAYIYYPN: + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				-
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD	SISILKNFQIKN S ++ N ÕIK		LNNHVLTTII +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID	FKVELVVHNFRE	EKLIEASNHSIP	TNNRVEPR	2 1243

Sbjct	503	+W + +P P E + + GI+FK+E + + R KL + + P + VEP QWNLMKQPSPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEHS	562
Query	1242	-TIVEMDMLGWDVTHTEYGYTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T+++ + Y PVL KER+F S A P+ + + +S + +Q +K ++	1078
Sbjct	563	SPTVELDLLGWSATYSKDLWIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVM SAL VG W YP + + + N+ + + L K + LD+ +++ E S F E	904
Sbjct	623		676

VP1 [Infectious bursal disease virus]

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

Range 1: 331 to 693

Score	Ex	cpect Method	Identities	Positives	Gaps F	rame	
233 bits(595) 2e-62() Compositional matrix adjust. 141/375(38%) 214/375(57%) 26/375(6%) -1							
Features:							
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLN\ S+ P +LN+		KFSPTQGGMDA KF+P +GG++		
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVI					
Query	1770	INIILNATETVELVYADNAYIYYPNI + IL E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW		
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN-	WYSIDL KO TWYSIDLEKO				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDS G P++N TWA ++ P + VDS					
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD	S ++ N QIK SSCLIMNLQIKT		+NNH+L+T+++ INNHLLSTLVL		
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDI +W + +P P E + + GI+		EKLIEASNHSIP +L + + + P		- 1240	
Sbjct	503	QWNLMKQPSPHSEEFKSIEDKLGIN				S 562	
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV					
Sbjct	563	VE+D+LGW ++ + G Y PVI SPTVELDLLGWSAAYSKDLGIYVPVI					
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNI				L 898	
Sbjct	623	AL VG W YP + + N- YEALRLVGGWNYPLLNKACKNI	+ + + L F NASAARRHLEAF		E S F E SELSEFGEAFE	G 678	
Query	897	LSLEKPMHEQDYAQI 853					
Sbjct	679	+++ + + A++ FNIKLTVTPESLAEL 693					

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|AAD23375.1|AF092944_1** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps F	rame
233 bits	(595) 2e	e-62() Compositional matrix adjust.	142/375(38%)	213/375(56%)	26/375(6%) -	1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV			KF+P +GG++ KFNPFRGGLNR	
Query	1770	INIILNATETVELVYADNAYIYYPN	-		_	
Sbjct	386	+ I+ E LVYADN YI + N VEWIMAPDEPKALVYADNIYIVHSN			Y+LTRGW AMYYILTRGW-	
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD				
Sbjct	443	G P++N TWA ++ P + VD; DNGDPMFNQTWATFAMNIAPALVVD;	S ++ N QIK SSCLIMNLQIKT			
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID				- 1240
Sbjct	503	+W + +P P E + + GI+	FK+E + + R FKIERSIDDIRG		• • • • •	P 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV	LSKERMFKSIAC	PQP-PSSTFQS		
Sbjct	563	VE+D+LGW T++ + G Y PV SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN				L 898
Sbjct	623	AL VG W YP + + + N- YEALRLVGGWNYPLLNKACKN	+ + + L K NASAARRHLEAK		E S F E ISELSEFGEAFE	G 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	+++ + + A++ FNIKLTVTPESLAEL 693				

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

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

Score	Ex	rpect Method	Identities	Positives	Gaps Fra	ame
233 bits	(595) 2e	-62() Compositional matrix adj	ust. 142/375(38%)	213/375(56%)	26/375(6%) -1	
Features	3:					
Query	1935	LTKTRNIWSASYVTHLIGSTI- LTKTRNIWSA THL+ S I	SDQPAKRMLNV S+ P +LN-		KFSPTQGGMDAL KF+P +GG++ +	1771
Sbjct	331	LTKTRNIWSAPSPTHLMISMIT				385
Query	1770	INIILNATETVELVYADNAYIY + IL E LVYADN YI			MAMYLLTRGWTS Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIV				442
Query	1590	TQGTPLYNYTWAYLSLYAIPYM G P++N TWA ++ P +			LNNHVLTTILMN HNNH+L+T+++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPAL				502
Query	1410	RWAEIGKPOPTPEVIEKLATMT +W + +P+P E + +	GIDFKVELVVHNFRI GI+FK+E + + R			1240
Sbjct	503	QWNLMRQPRPDSEEFKSIEDKL			• •	562
Query	1239	IVEMDMLGWDVTHT-EYG-Y VE+D+LGW T++ + G Y	TPVLSKERMFKSIAG			1078
Sbjct	563	SPTVELDLLGWSATYSKDLGIY				622
Query	1077	NVALLYVGAWAYPCIAQTVESY AL VG W YP + + +		KEYNLDKAISKA K + LD+ +++	VETSPFSEVMSL S F E	898
Sbjct	623	YEALRLVGGWNYPLLNKACK			~	678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTSESLAEL 693				

RNA depended RNA polymerase [Paralichthys olivaceus birnavirus]

Sequence ID: ref[YP_001514405.1] Length: 845 Number of Matches: 1

▶ See 1 more title(s) Range 1: 317 to 699

Score **Expect Method Positives** Identities **Gaps** Frame 233 bits(595) 2e-62() Compositional matrix adjust. 148/398(37%) 209/398(52%) 35/398(8%) -1 Features: KTRNIWSASYVTHLIGSTISDQPAKR-MLNVLNCKTRTPSLSKFSPTQGGMDALINIILN KTRNIWSA Y THL+ S +S + LN+ N T+TPSL FSP GGMD ++ II N KTRNIWSAPYPTHLLLSMVSSPVMEESKLNITN--TQTPSLYGFSPFHGGMDRIMTIIRN Query 1929 1753 Sbjct 317 374 ATETVE---LVYADNAYIYYPNEDIWYSIDLTKGEANCTRDVAMTMAMYLLTRGWTSTQG Query 1752 1582 + +T E ++YADN YI +D WYSIDL KGEANCT M YLLTRGWT+ G SLDTGEDLVMIYADNIYIL--QDDTWYSIDLEKGEANCTPQHMQAMMYYLLTRGWTNEDG Sbjct 375 432 TPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMNRWA 1581 1402 Query +P YN TWA ++ P M VDS +L N Q+K GQGSGN +TFLNNH+++TI++ W SPRYNPTWATFAMNVAPSMVVDSSCLLMNLQLKTYGQGSGNAFTFLNNHLMSTIVVAEWV Sbjct 433 1401EIGKPQPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRV----E 1249 Query + GKP P + L TGI+FK+E + N RE ++EA + P + + + KAGKPNPMTKEFMDLEEKTGINFKIERELKNLREVIMEAV-ETAPQDGYLADGSDLPPHK Sbjct 493 551 PRTIVEMDMLGWDVTHTEY--GYTPVLSKERMFKSIACPQPPSSTF----QSNIAKQVH 1090 Query 1248 + PVL ER+ S A P+ + PGRAVELDLLGWSAVYSRRMEMFVPVLENERLIASAAYPKGLENKTLARKPGAEIAYQIV Sbjct 552 611 KYIQNVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSE 1089 Query 910 A+ VG W P + + L K ++ + + RY---EAIRLVGGWNNPLLETAAKHMSLDK----RKRLEVKGIDVTGFLDDWNNMSEFGG Sbjct 612 Query 909 VMSLLSLEKPMHEQDYAQILYKQKPIEKIAPKAKFNNP P+E+ ++L +P+ Q I PK + DLEGITLAEPLTNÕTLIDI---NTPLESFDPKERPETP Sbjct 665

VP1 [Infectious bursal disease virus]

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

Score	E	xpect Method	Identities	Positives	Gaps	Frame
233 bits	(595) 26	e-62() Compositional matrix adjust.	140/374(37%)	213/374(56%)	24/374(6%)	-1
Features:						
Query	1935	LTKTRNIWSASYVTHLIGSTIS LTKTRNIWSA THL+ S I+	~		FSPTQGGMDA F+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1767	NIILNATETVELVYADNAYIYYPNE I+ E LVYADN YI + N	DIWYSIDLTKGE WYSIDL KGE		AMYLLTRGWT Y+LTRGW	
Sbjct	387	EWIMAPDEPKALVYADNIYIVHSN-				
Query	1587	QGTPLYNYTWAYLSLYAIPYMTVDS G P++N TWA ++ P + VDS	ISILKNFQIKNF ++ N QIK		NNHVLTTILM NNH+L+T+++	
Sbjct	444	NGDPMFNQTWATFAMNIAPALVVDS				
Query	1407	WAEIGKPQPTPEVIEKLATMTGIDF	KVELVVHNFREK	KLIEASNHSIPT	NNRVEPRI	1240

Sbjct	504	W + PP + PP + GI+FK+E + RKL + PP + VEP WNLMKQPSPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQPS	563
Query	1239	-IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQN VE+D+LGW T++ + G Y PVL KER+F S A P+ + + +S + +Q +K ++	1075
Sbjct	564	PTVELDLLGWFATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVRY	623
Query	1074	VALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSLL AL VG W YP + + + N+ + + L K + LD+ +++ E S F E	895
Sbjct	624	EALRLVGGWNYPLLNKACKNNASAARRHLEAKGFPLDEFLAEWSELSEFGEAFEGF	679
Query	894	SLEKPMHEQDYAQI 853	
Sbjct	680	NIKLTVTPESLAEL 693	

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|AAN04459.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
233 bits	(595) 26	e-62() Compositional matrix adjust.	142/375(38%)	214/375(57%)	26/375(6%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI			~	
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN+ MSNSP-NNVLN]		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK		LNNHVLTTIL +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			TI 1237
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1236	VEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV			NIA-KQVHKY + +Q +K	
Sbjct	563	SPNVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNI + + + L F		VETSPFSEVM E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN			_ ~	EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

VP1 protein [Victorian trout aquabirnavirus]

Sequence ID: **gb|ALF95259.1**| Length: 844 Number of Matches: 1 Range 1: 317 to 699

Score	E	xpect Method	Identities	Positives	Gaps I	Frame
233 bits	(594) 26	e-62() Compositional matrix adjust.	150/399(38%)	210/399(52%)	37/399(9%) -	1
Features:						
Query	1929	KTRNIWSASYVTHLIGSTISDQPA- KTRNIWSA Y THL+ S +S P		TRTPSLSKFSPT T+TPSL FSP		
Sbjct	317	KTRNIWSAPYPTHLLLSMVS-SPVM				
Query	1755	NATETVELVYADNAYIYYPNED ++ +T E ++YADN YI N	IWYSIDLTKGEA WYSIDL KGEA		MYLLTRGWTST YLLTRGWT+	Q 1585
Sbjct	374	DSLDTGEDLVMIYADNIYILQDN				DD 431
Query	1584	GTPLYNYTWAYLSLYAIPYMTVDSI G+P YN TWA ++ P M VDS		GOGSGNPWTFLN GOGSGN +TFLN		
Sbjct	432	GSPRYNPTWATFAMNVAPSMVVDSS				
Query	1404	AEIGKPOPTPEVIEKLATMTGIDFK + GKP P + L TGI+FK				- 1252
Sbjct	492	VKAGKPNPMTKEFMNLEEKTGINFK				PR 550
Query	1251	EPRTIVEMDMLGWDVTHTEYGYT +P VE+D+LGW ++ +		IACPOPPSSTF- A P+ +	QSNIAKÇ + IA Ĉ	
Sbjct	551	QPGKAVELDLLGWSAVYSRQMEMFV				
Query	1092	HKYIQNVALLYVGAWAYPCIAQTVE +Y A+ VG W P + +		SMLRNKEYNLDK L K ++	AISKAVETSPF + S F	
Sbjct	611	VRYEAIRMVGGWNNPLLETAAK				
Query	912	EVMSLLSLEKPMHEQDYAQILYKQK + ++L +P+ O I	PIEKIAPKAKFI P+E PK +	NNP 796		
Sbjct	664	GDLDGITLAEPLTNÕTLIDINT		ETP 699		

Range 1: 331 to 693

Score	Ex	cpect Method	Identities	Positives	Gaps	Frame
233 bits	(594) 3e	e-62() Compositional matrix adjust.	142/375(38%)	213/375(56%)	26/375(6%)	-1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN+ MSNSP-NNVLNI		KF+P +GG++ KFNPFRGGLN	
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD	SISILKNFQIKN S ++ N QIK			
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			T- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV	LSKERMFKSIAC L KER+F S A			
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNK + + + L K		VETSPFSEVM E S F E	SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				
Sbjct	679	FNIKLTVTPESLAEL 693				

viral polymerase [Infectious bursal disease virus]

Sequence ID: emb|CAI54226.2| Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps I	Frame	
233 bits(594) 3e-62() Compositional matrix adjust. 141/375(38%) 213/375(56%) 26/375(6%) -1							
Features:							
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN-		KFSPTQGGMDA KF+P +GG++		
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV					
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW		
Sbjct	386	VEWILAPDEPKALVYADNIYIVHSN					
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD					
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD					
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRI FK+E + + R			1243	
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				IS 562	
Query	1242	-TIVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW ++ + G Y PV	LSKERMFKSIAG L KER+F S A				
Sbjct	563	SPTVELDLLGWSAAYSKDLGIYVPV					
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N		KEYNLDKAISKA K + LD+ +++		SL 898	
Sbjct	623	YEALRLVGGWNYPLLNKACKN				EG 678	
Query	897	LSLEKPMHEQDYAQI 853					
Sbjct	679	FNIKLTVTPESLÄEL 693					

RNA polymerase [Infectious bursal disease virus]

Sequence ID: gb|AAA46237.1| Length: 876 Number of Matches: 1

▶ See 1 more title(s) Range 1: 330 to 691

Score	E	xpect Method	Identities	Positives	Gaps	Frame
233 bits	233 bits(594) 3e-62() Compositional matrix adjust. 142/375(38%) 212/375(56%) 27/375(7%) -1					-1
Features	Features:					
Query	1935	LTKTRNIWSASYVTHLIGSTI		/LNCKTRTPSLS + C PSL		
Sbjct	330	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	385	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			LNNHVLTTII +NNH+L+T++	

Sbjct	442	DNGDPMFNQTWATFAMNIAPALVVDSTCLIMNLQIKTYGQGSGNAATFINNHLLSTLVLD	501
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P P E + + GI+FK+E + + R KL + + P + VEP	1240
Sbjct	502	QWNLMKQPSPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	561
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ VE+D+LGW T++ + G Y PVL KER+F S A P+ + + + S + + O +K ++	1078
Sbjct	562	SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQGYKVVR	621
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL AL VG W YP + + ++ + + L K + LD+ +++ E S F E	898
Sbjct	622	YEALRLVGGWNYPLLNKACKNNASAARHLEAKGFPLDEFLAEWAELSEFGEAFEG	676
Query	897	LSLEKPMHEQDYAQI 853	
Shict	677	FNIKLTVTSESLAEL 691	

RNA-directed RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|AFI41892.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	kpect Method	Identities	Positives	Gaps Fra	me
233 bits	(594) 4e	e-62() Compositional matrix adjust.	141/375(38%)	213/375(56%)	26/375(6%) -1	
Features	S :					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMDAL KF+P +GG++ +	1771
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPVI				385
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGWTS Y+LTRGW S	1591
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				442
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD: G P++N TWA ++ P + VD:	SISILKNFQIKN S ++ N QIK		LNNHVLTTILMN +NNH+L+T+++	1411
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				502
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDE +W + +P P E + + GI+	FKVELVVHNFRE FK+E + + R			1243
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN			· · · · · · · · · · · · · · · · · · ·	562
Query	1242	-TIVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW ++ + G Y PV			NIA-KQVHKYIQ + +O +K ++	1078
Sbjct	563	SPTVELDLLGWSAAYSRDLGIYVPV				622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNI AL VG W YP + + + N-	HWNTIQSMLRNK + + + L K		VETSPFSEVMSL E S F E	898
Sbjct	623	AL VG W YP + + + N- YEALRLVGGWNYPLLNKACKNI				678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

RNA-dependent RNA polymerase [Infectious bursal disease virus] Sequence ID: **gb|AAT99259.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score E	xpect Method	Identities	Positives	Gaps	Frame
233 bits(593) 4	e-62() Compositional matrix adjust.	141/375(38%)	213/375(56%)	26/375(6%)	-1
Features:					
Query 1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct 331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN+ MSNSP-NNVLN]		KF+P +GG++ KFNPFRGGLN	
Query 1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct 386	VEWILAPEEPKALVYADNIYIVHSN				
Query 1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD				
Sbjct 443	G P++N TWA ++ P + VD DNGDPMFNQTWATFAMNIAPALVVD	S ++ N QIK SSCLIMNLQIKT		+NNH+L+T++ INNHLLSTLV	
Query 1410	RWAEIGKPOPTPEVIEKLATMTGID				r- 1240
Sbjct 503	+W + +P P E + + GI+ QWNLMKQPSPDSEEFKSIEDKLGIN	FK+E + + R FKIERSIDDIRG		• •	QS 562
Query 1239	IVEMDMLGWDVTHT-EYG-YTPV				
Sbjct 563	VE+D+LGW ++ + G Y PV SPTVELDLLGWSAAYSKDLGIYVPV	L KER+F S A LDKERLFCSAA)			
Query 1077	NVALLYVGAWAYPCIAQTVESYVTN				SL 898
Sbjct 623	AL VG W YP + + + N YEALRLVGGWNYPLLNKACKN		<pre> < + LD+ +++ </pre> <pre> <gfpldeflaew <="" pre=""></gfpldeflaew></pre>	E S F E SELSEFGEAF	EG 678
Query 897	LSLEKPMHEQDYAQI 853				
Sbjct 679	+++ + + A++ FNIKLTVTPESLAEL 693				

RNA-dependent RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|AAU10476.2|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
233 bits	(593) 46	e-62() Compositional matrix adjust.	141/375(38%)	213/375(56%)	26/375(6%) -	·1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	SDQPAKRMLN' S+ P +LN:		KFSPTQGGMD <i>I</i> KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGW' Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSI				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVI G P++N TWA ++ P + VI	OSISILKNFQIK OS ++ N ÕIK		LNNHVLTTILN +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVI				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGII	OFKVELVVHNFR FFK+E + + R			r- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QS 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV	/LSKERMFKSIA		NIA-KQVHKYI + +O +K +	
Sbjct	563	VE+D+LGW ++ + G Y PV SPTVELDLLGWSAAYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVT				SL 898
Sbjct	623	AL VG W YP + + + N YEALRLVGGWNYPLLNKACKN	N+ + + L I NASAARRHLEA		E S F E SELSEFGEAFE	EG 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIKLTVTPESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABW38088.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps F	rame
232 bits	(592) 5e	e-62() Compositional matrix adjust.	141/375(38%)	213/375(56%)	26/375(6%) -	1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA THL+ S I	-SDQPAKRMLNV S+ P +LN+		KFSPTQGGMDA KF+P +GG++	
Sbjct	331	LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW	
Sbjct	386	VEWIIAPDEPKALVYADNIYIVHSN				
Query	1590	TOGTPLYNYTWAYLSLYAIPYMTVD				
Sbjct	443	G P++N TWA ++ P + VD; DNGDPMFNQTWATFAMNIAPALVVD;			+NNH+L+T+++ INNHLLSTLVL	
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID				- 1240
Sbjct	503	+W + +P P E + + GI+	FK+E + + R FKIERSIDDIRG			P 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV				
Sbjct	563	VE+D+LGW T++ + G Y PV SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN				L 898
Sbjct	623	AL VG W YP + + + N· YEALRLVGGWNYPLLNKACKN	+ + + L K NASAARRHLEAK		ESF+ SELSEFGDAFE	G 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	+++ + + A++ FNIKLTVTPESLAEL 693				

VP1 RNA polymerase [Infectious bursal disease virus]

Sequence ID: **gb|AAB68518.1|** Length: 891 Number of Matches: 1 Range 1: 343 to 688

Score	E	xpect Method	Identities	Positives	Gaps	Frame
233 bits	(593) 56	e-62() Compositional matrix adjust.	141/358(39%)	204/358(56%)	26/358(7%)	-1
Features	S :					
Query	1935	LTKTRNIWSASYVTHLIGSTI	~		KFSPTQGGMD KF+P +GG++	
Sbjct	343	LTKTRNIWSAPSPTHLMISMITWPV	D,			
Query	1770	INIILNATETVELVYADNAYIYYPN + TL E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	398	VEWILAPEEPKALVYADNIYIVHSN				-

Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVDSISILKNFQIKNPGQGSGNPWTFLNNHVLTTILMN G P++N TWA ++ P + VDS ++ N OIK GOGSGN TF+NNH+L+T+ ++	1411
Sbjct	455	DNGDPMFNQTWATFAMNTAPALVVDSSCLIMNLQIKTYGQGSGNAATFINNHLLSTLALD	514
Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT-	1240
Sbjct	515	+W + +P+P E + + GI+FK+E + + R KL + + P + VEP QWNLMRQPRPDSEEFKSIEDKLGINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQS	574
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ	1078
Sbjct	575	VE+D+LGW T++ + G Y PVL KER+F S A P+ + + +S + +Q +K ++ SPTVELDLLGWSATYSKDLGIYVPVLDKERLFSSAAYPKGVENKSLKSKVGIEQAYKVVR	634
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVM 9 AL VG W YP + + + N+ + L K LD+ +++ E S F E	04
Sbict	635		88

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: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps I	rame
232 bits	(592) 5e	e-62() Compositional matrix adjust.	141/375(38%) 212/375(56%)	26/375(6%) -	1
Features	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI				
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV	S+ P +LN MSNSP-NNVLN		KF+P +GG++ KFNPFRGGLNR	
Query	1770	INIILNATETVELVYADNAYIYYPN + IL E LVYADN YI + N			MAMYLLTRGWT Y+LTRGW	
Sbjct	386	VEWILAPEEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD			FLNNHVLTTILM F+NNH+L+T+++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPOPTPEVIEKLATMTGID		REKLIEASNHSII R KL +		- 1240
Sbjct	503	QWNLMRQPRPDSDEFKSIEDKLGIN				S 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV	LSKERMFKSIA	CPQP-PSSTFQ	SNIA-KQVHKYI S + +O +K +	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN				L 898
Sbjct	623	AL VG W YP + + + N YEALRLVGGWNYPLLNKGCKN		K + LD+ +++ KGFPLDEFLAEV	E S F E VSELSEFGEAFE	G 678
Query	897	LSLEKPMHEQDYAQI 853				
Sbjct	679	FNIRLTITSESLAEL 693				

putative RNA-dependent RNA polymerase [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAN04572.1|** Length: 845 Number of Matches: 1 Range 1: 317 to 699

Score	E	cpect Method	Identities	Positives	Gaps	Frame
232 bits	(591) 6e	e-62() Compositional matrix adjust.	150/399(38%)	208/399(52%)	37/399(9%)	-1
Features	s:					
Query	1929	KTRNIWSASYVTHLIGSTISDQPA-				
Sbjct	317	KTRNIWSA Y THL+ S +S P KTRNIWSAPYPTHLLLSMVS-SPVM		!+TPSL FSP !QTPSLYGFSPF	GGMD ++ I HGGMDRIMTI	
Query	1758	LNATETVELVYADNAYIYYPNED	IWYSIDLTKGEA WYSIDL KGEA		MYLLTRGWTS YLLTRGWT+	TQ 1585
Sbjct	374	DSLDNDEDLVMIYADNIYILQDN				ED 431
Query	1584	GTPLYNYTWAYLSLYAIPYMTVDSISG+P YN TWA ++ P M VDS	SILKNFQIKNPG +L N O+K G			
Sbjct	432	GSPRYNPTWATFAMNVAPSMVVDSS				
Query	1404	AEIGKPQPTPEVIEKLATMTGIDFK' + GKP P + L TGI+FK-	VELVVHNFREKI +E + N +E +			1252
Sbjct	492	VKAGKPNPMTKGFMDLEEKTGINFK			•	РН 550
Query	1251	EPRTIVEMDMLGWDVTHTEYGYT		ACPQPPSSTF- A P+ +	QSNIAK + IA	
Sbjct	551	RPGRAVELDLLGWSAIYSRQMEMFV				
Query	1092	HKYIQNVALLYVGAWAYPCIAQTVES +Y A+ VG W P + +		MLRNKEYNLDK L K ++	AISKAVETSP + S	
Sbjct	611	VRYEAIRMVGGWNNPLLETAAK				
Query	912	EVMSLLSLEKPMHEQDYAQILYKQKI + ++L KP+ O I	PIEKIAPKAKFN P+E PKA+	INP 796		
Sbjct	664	GDLEGITLSKPLTNQTLIDINT)TP 699		

▶ See 17 more title(s) Range 1: 317 to 699

Score	E	xpect Method	Identities	Positives	Gaps	Frame
231 bits	(590) 6	e-62() Compositional matrix adjust.	148/399(37%) 208/399(52%)	37/399(9%)	-1
Feature	s:					
Query	1929	KTRNIWSASYVTHLIGSTISDQPA-				
Sbjct	317	KTRNIWSA Y THL+ S +S P KTRNIWSAPYPTHLLLSMVS-TPVM			GGMD ++ I HGGMDRIMTI	
Query	1758	LNATETVELVYADNAYIYYPNED L+ E + ++YADN YI N	IWYSIDLTKGE WYSIDL KGE		MYLLTRGWTS +YLLTRGWT	
Sbjct	374	DSLDNDEDLVMIYADNIYILQDN				
Query	1584	GTPLYNYTWAYLSLYAIPYMTVDSI G+P YN TWA ++ P M VDS		GQGSGNPWTFLN GQGSGN +TFLN		IRW 1405
Sbjct	432	GSPRYNPTWATFAMNVAPSMVVDSS	CLLMNLQLKTY	GOGSGN FIFLI GOGSGNAFTFLN	NNHTHTITT NNHLMSTIVVA	EW 491
Query	1404	AEIGKPOPTPEVIEKLATMTGIDFK + GKP P + L TGI+FK				RV 1252
Sbjct	492	VKAGKPNPMTKEFMDLEEKTGINFK				•
Query	1251	EPRTIVEMDMLGWDVTHTEYGYT P VE+D+LGW ++ +		IACPQPPSSTF- A P+ +	QSNIAK + IA	~
Sbjct	551	RPGKAVELDLLGWSAIYSRQMEMFV				
Query	1092	HKYIQNVALLYVGAWAYPCIAQTVE +Y A+ VG W P + +		SMLRNKEYNLDF L K ++	KAISKAVETSP + S	
Sbjct	611	VRYEAIRLVGGWNNPLLETAAK				_
Query	912	EVMSLLSLEKPMHEQDYAQILYKQK + ++L +P+ O I	PIEKIAPKAKF P++ PKA+	NNP 796		
Sbjct	664	GDLEGITLSEPLTNQTLVDINT		QTP 699		

VP1 [Infectious bursal disease virus]

Sequence ID: **gb|ABG91144.1|** Length: 879 Number of Matches: 1 Range 1: 331 to 693

Score	E	xpect Method	Identities	Positives	Gaps	Frame
231 bits	(590) 16	e-61() Compositional matrix adjust.	141/375(38%)	213/375(56%)	26/375(6%) -	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI LTKTRNIWSA T L+ S I			KFSPTQGGMDA	
Sbjct	331	LTKTRNIWSAPSPTRLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGWY Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD G P++N TWA ++ P + VD				
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD				
Query	1410	RWAEIGKPQPTPEVIEKLATMTGID +W + +P P E + + GI+	FKVELVVHNFRI FK+E + + R			Γ- 1240
Sbjct	503	QWNLMKQPSPDSEEFKSIEDKLGIN				QP 562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPV VE+D+LGW T++ + G Y PV			NIA-KQVHKYI + +O +K	
Sbjct	563	SPTVELDLLGWSATYSKDLGIYVPV				
Query	1077	NVALLYVGAWAYPCIAQTVESYVTN AL VG W YP + + + N	HWNTIQSMLRNI + + + L]			SL 898
Sbjct	623	YEALRLVGGWNYPLLNKACKN			E S F E SELSEFGEAFI	EG 678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++				
Sbjct	679	FNIKLTVTPESLAEL 693				

VP1 [Infectious bursal disease virus]

Sequence ID: gb|AAZ23012.1| Length: 879 Number of Matches: 1

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
231 bits	(590) 1	e-61() Compositional matrix adjust.	141/375(38%)	212/375(56%)	26/375(6%)	-1
Feature	s:					
Query	1935	LTKTRNIWSASYVTHLIGSTI		/LNCKTRTPSLS + C PSL		
Sbjct	331	LTKTRNIWSA THL+ S I LTKTRNIWSAPSPTHLMISMITWPV				
Query	1770	INIILNATETVELVYADNAYIYYPN + I+ E LVYADN YI + N			MAMYLLTRGW Y+LTRGW	
Sbjct	386	VEWIMAPDEPKALVYADNIYIVHSN				
Query	1590	TQGTPLYNYTWAYLSLYAIPYMTVD	SISILKNFQIKN S ++ N OIK		LNNHVLTTII +NNH+L+T++	
Sbjct	443	DNGDPMFNQTWATFAMNIAPALVVD			— —	

Query	1410	RWAEIGKPOPTPEVIEKLATMTGIDFKVELVVHNFREKLIEASNHSIPTNNRVEPRT- +W + +P P E + I+FK+E + + R KL + + P + VEP	1240
Sbjct	503	QWNLMKQPSPDSEEFRSIEDKLDINFKIERSIDDIRGKLRQLVPLAQPGYLSGGVEPEQP	562
Query	1239	IVEMDMLGWDVTHT-EYG-YTPVLSKERMFKSIACPQP-PSSTFQSNIA-KQVHKYIQ	1078
Sbjct	563	VE+D+LGW T++ + G Y PVL KER+F S A P+ + + +S + +Q +K ++ SPTVELDLLGWSATYSKDLGIYVPVLDKERLFCSAAYPKGVENKSLKSKVGIEQAYKVVR	622
Query	1077	NVALLYVGAWAYPCIAQTVESYVTNHWNTIQSMLRNKEYNLDKAISKAVETSPFSEVMSL	898
Sbjct	623	AL VG W YP + + + N+ + + L K + LD+ +++ E S F E YEALRLVGGWNYPLLNKACKNNASAARRHLEAKGFPLDEFLAEWSELSEFGEAFEG	678
Query	897	LSLEKPMHEQDYAQI 853 +++ + + A++	
Sbjct	679	FNIKLTVTPESLAEL 693	

viral protein 1 [Infectious pancreatic necrosis virus]

Sequence ID: ref|NP_047197.1| Length: 845 Number of Matches: 1

▶ See 2 more title(s) Range 1: 317 to 699

Score	E	xpect Method	Identities	Positives	Gaps	Frame
231 bits	(589) 1e	e-61() Compositional matrix adjust.	148/399(37%) 208/399(52%)	37/399(9%) -	·1
Features	s:					
Query	1929	KTRNIWSASYVTHLIGSTISDQPA- KTRNIWSA Y THL+ S +S P		TRTPSLSKFSPT T+TPSL FSP	QGGMDALINII GGMD ++ II	
Sbjct	317	KTRNIWSAPYPTHLLLSMVS-TPVM				
Query	1758	LNATETVELVYADNAYIYYPNED L+ E + ++YADN YI N	IWYSIDLTKGE WYSIDL KGE		MYLLTRGWTST YLLTRGWT+	rQ 1585
Sbjct	374	DSLDNDEDLVMIYADNIYILQDN				ED 431
Query	1584	GTPLYNYTWAYLSLYAIPYMTVDSI				
Sbjct	432	G+P YN TWA ++ P M VDS GSPRYNPTWATFAMNVAPSMVVDSS		GQGSGN +TFLN GQGSGNAFTFLN		W EW 491
Query	1404	AEIGKPOPTPEVIEKLATMTGIDFK + GKP P + L TGI+FK				
Sbjct	492	VKAGKPNPMTKEFMDLEEKTGINFK				+ PI 550
Query	1251	EPRTIVEMDMLGWDVTHTEYGYT P VE+D+LGW ++ +		IACPOPPSSTF- A P+ +		
Sbjct	551	RPGKAVELDLLGWSAIYSRQMEMFV) H IA ARKPGAEIAYÇ	
Query	1092	HKYIQNVALLYVGAWAYPCIAQTVE				
Sbjct	611	+Y A+ VG W P + + VRYEAIRLVGGWNNPLLETAAK		· L K ++ KRLEVKGIDVTG	+ S I FLDDWNNMSEI	
Query	912	EVMSLLSLEKPMHEQDYAQILYKQK				
Sbjct	664	+ ++L +P+ Q I GDLEGITLSEPLTNQTLVDINT	P++ PKA+ PLDSFDPKARP	P QTP 699		