Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BRYP9M015

- ► Formatting options
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Blast report description

Nucleotide Sequence (1008 letters)

RID <u>B8BRYP9M015</u> (Expires on 02-06 12:11 pm)

Query ID lcl|Query_102347

Description None **Molecule type** nucleic acid **Query Length** 1008 Database Name nr

Description All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding

environmental samples from WGS projects

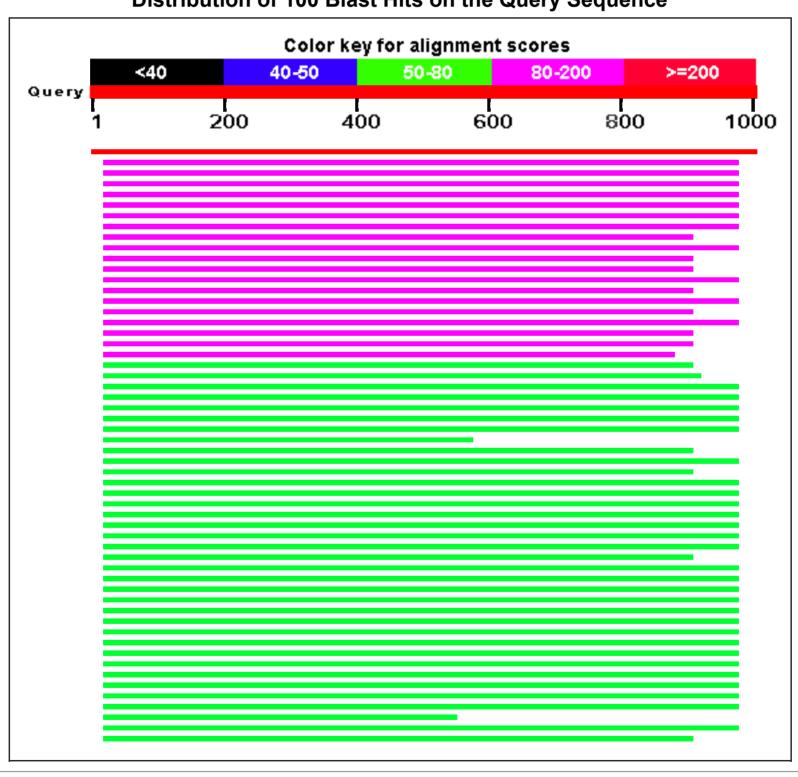
Program BLASTX 2.3.1+

□ Graphic Summary

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



Distribution of 100 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Description	Max	Total	Query	E	Ident	Accession
	score	score	cover	value		
polyprotein [Drosophila melanogaster birnavirus SW-2009a]	600	600	99%	0.0	88%	ACU32790.1
polyprotein [Tasmanian aquabirnavirus]	83.6	83.6	95%	4e-14	25%	ALF95277.1
polyprotein [Tasmanian aquabirnavirus]	82.0	82.0	95%	1e-13	25%	ALF95281.1
polyprotein [Tasmanian aquabirnavirus]	82.0	82.0	95%	1e-13	25%	ALF95271.1
polyprotein [Tasmanian aquabirnavirus]	82.0	82.0	95%	1e-13	25%	ALF95275.1
polyprotein [Tasmanian aquabirnavirus]	82.0	82.0	95%	1e-13	25%	ALF95267.1
polyprotein [Tasmanian aquabirnavirus]	81.6	81.6	95%	2e-13	25%	ALF95279.1
polyprotein [Tasmanian aquabirnavirus]	81.6	81.6	95%	2e-13	25%	ALF95273.1
polyprotein [Marine birnavirus]	81.6	81.6	88%	2e-13	26%	AAL83706.1
polyprotein [Tasmanian aquabirnavirus]	81.3	81.3	95%	2e-13	25%	ALF95269.1
polyprotein [Marine birnavirus]	81.3	81.3	88%	2e-13	26%	AAP37163.1
polyprotein [Marine birnavirus]	80.9	80.9	88%	3e-13	26%	YP_605813.1
polyprotein [Aquabirnavirus TAB98]	80.9	80.9	95%	3e-13	25%	ACD64976.1
polyprotein [Yellowtail ascites virus]	80.9	80.9	88%	3e-13	26%	NP_690805.1
polyprotein [Tasmanian aquabirnavirus]	80.9	80.9	95%	3e-13	25%	YP_009177608.1
VP2,NS,VP3 [Yellowtail ascites virus]	80.5	80.5	88%	4e-13	26%	BAA25005.1
polyprotein [Tasmanian aquabirnavirus]	80.5	80.5	95%	4e-13	25%	ALF95263.1
polyprotein [Tasmanian aquabirnavirus]	80.5	80.5	88%	4e-13	25%	ALF95265.1
polyprotein [Marine birnavirus - H1]	80.5	80.5	88%	4e-13	26%	AAP37165.1
polyprotein [Infectious pancreatic necrosis virus - He]	80.1	80.1	85%	6e-13	27%	AAK32156.1
polyprotein [Yellowtail ascites virus]	79.0	79.0	88%	1e-12	25%	BAF37013.1
polyprotein [Blotched snakehead virus]	79.0	79.0	89%	1e-12	26%	YP_052862.1
polyprotein [Tasmanian aquabirnavirus]	78.6	78.6	95%	2e-12	25%	ALF95287.1
polyprotein [Tasmanian aquabirnavirus]	78.6	78.6	95%	2e-12	25%	ALF95283.1
polyprotein [Tasmanian aquabirnavirus]	77.4	77.4	95%	5e-12	25%	ALF95285.1
polyprotein [Infectious pancreatic necrosis virus]	75.9	75.9	95%	2e-11	25%	AGW99956.1
polyprotein [Infectious pancreatic necrosis virus]	75.9	75.9	95%	2e-11	25%	AEK06233.1
VP3 protein [Blotched snakehead virus]	73.6	73.6	55%	2e-11	30%	YP_052872.1
polyprotein [Marine birnavirus]	75.5	75.5	88%	2e-11	25%	AAP37167.1
structural polyprotein [Infectious pancreatic necrosis virus]	75.5	75.5	95%	2e-11	25%	AAB39512.1
polyprotein [Victorian trout aquabirnavirus]	74.7	74.7	88%	3e-11	25%	ALF95289.1
polyprotein [Infectious pancreatic necrosis virus]	74.7	74.7	95%	4e-11	25%	AEM92169.1
107 kDa polyprotein [Infectious pancreatic necrosis virus]	74.7	74.7	95%	4e-11	25%	AAQ75363.1
polyprotein [Infectious pancreatic necrosis virus]	74.7	74.7	95%	4e-11	25%	AAK32154.1
polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	4e-11	25%	AAX24140.1
107 kDa polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	4e-11	25%	AAQ75357.1
polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	4e-11	25%	AEM92165.1
RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; Contains: RecName: Full=Structural peptide 2; Short=p2; Contains: RecName: Full=Structural peptide 3; Short=p3; Contains: RecName: Full=Protease VP4; AltName: Full=Non-structural protein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP3	74.3	74.3	95%	4e-11	25%	<u>Q703G9.1</u>
polyprotein [Paralichthys olivaceus birnavirus]	74.3	74.3	88%	4e-11	26%	YP_001514404.1
107 kDa polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	4e-11	25%	AAQ75350.1
structural polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	4e-11	25%	AAD11535.1
polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	4e-11	25%	ABF69695.1

nelyprotein [Infectious peneroetic peeroeic virus]	74.2	74.3	059/	40.11	250/	A EM02470 4
polyprotein [Infectious pancreatic necrosis virus]	74.3		95%	4e-11	25%	AEM92170.1
108-kDa polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	4e-11	25%	AAR10449.1
107 kDa polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	4e-11	25%	AAQ75352.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	74.3 74.3	74.3 74.3	95% 95%	5e-11 5e-11	25% 25%	CAH25439.1
108-kDa polyprotein [Infectious pancreatic necrosis virus] RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; Contains: RecName: Full=Structural peptide 2; Short=p2; Contains: RecName: Full=Structural peptide 3; Short=p3; Contains: RecName: Full=Protease VP4; AltName: Full=Non-structural protein VP4;	74.3	74.3	95%	5e-11	25%	<u>AAR10452.1</u> <u>P22495.1</u>
Short=NS; Contains: RecName: Full=Capsid protein VP3						
polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	5e-11	25%	AAK32160.1
108-kDa polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	5e-11	25%	AAR10446.1
polyprotein [Infectious pancreatic necrosis virus]	73.9	73.9	95%	6e-11	25%	ABP93671.1
polyprotein [Infectious pancreatic necrosis virus]	73.9	73.9	95%	6e-11	25%	AEM92168.1
polyprotein [Infectious pancreatic necrosis virus]	73.9	73.9	95%	6e-11	25%	AAK32159.1
capsid protein VP3 [Flounder aquabirnavirus DS]	70.9	70.9	52%	8e-11	28%	AAQ82706.1
polyprotein [Infectious pancreatic necrosis virus]	73.6	73.6	95%	9e-11	25%	CAD32971.1
polyprotein [Infectious pancreatic necrosis virus]	73.2	73.2	88%	1e-10	25%	CAD32964.1
107 kDa polyprotein [Infectious pancreatic necrosis virus]	73.2	73.2	95%	1e-10	25%	AAQ75364.1
polyprotein [Infectious pancreatic necrosis virus]	73.2	73.2	88%	1e-10	24%	AAK32161.1
107 kDa polyprotein [Infectious pancreatic necrosis virus]	72.8	72.8	95%	1e-10	25%	AAQ75348.1
polyprotein [Infectious pancreatic necrosis virus]	72.0	72.0	88%	3e-10	24%	AAV48858.3
polyprotein [Infectious pancreatic necrosis virus]	71.6	71.6	88%	4e-10	25%	BAA05532.1
polyprotein [Infectious pancreatic necrosis virus]	71.2	71.2	88%	5e-10	25%	NP_047196.1
polyprotein [Infectious pancreatic necrosis virus]	71.2	71.2	88%	5e-10	25%	AAK32164.1
polyprotein [Infectious pancreatic necrosis virus]	71.2	71.2	88%	6e-10	25%	AAK32162.1
polyprotein [Infectious pancreatic necrosis virus]	70.9	70.9	88%	6e-10	25%	AGC00816.1
Chain D, X-ray Structure Of The Birnavirus Vp1-vp3 Complex	68.6	68.6	58%	6e-10	26%	3ZED_D
polyprotein [Infectious pancreatic necrosis virus]	70.9	70.9	88%	6e-10	25%	AAK32165.1
VP3 protein [Infectious pancreatic necrosis virus]	68.6	68.6	58%	6e-10	26%	AGJ83948.1
polyprotein [Infectious pancreatic necrosis virus]	70.9	70.9	88%	7e-10	24%	AAK32158.1
107 kDa polyprotein [Infectious pancreatic necrosis virus]	70.9	70.9	88%	7e-10	24%	AAC71003.1
polyprotein [Infectious pancreatic necrosis virus]	70.9	70.9	88%	7e-10	24%	AAV48856.3
polyprotein [Infectious pancreatic necrosis virus]	70.9	70.9	88%	7e-10	25%	AAP37159.1
polyprotein [Infectious pancreatic necrosis virus]	70.9	70.9	88%	8e-10	25%	CAD32967.1
polyprotein [Infectious pancreatic necrosis virus]	70.5	70.5	88%	8e-10	24%	AAK32163.1
polyprotein [Tellina virus 2]	70.1	70.1	88%	1e-09	24%	AAK32157.1
polyprotein [Infectious pancreatic necrosis virus]	69.7	69.7	88%	1e-09	24%	AAV48854.3
polyprotein [Rotifer birnavirus strain Palavas]	69.7	69.7	74%	2e-09	26%	CAX33877.1
polyprotein [Infectious pancreatic necrosis virus]	69.7	69.7	88%	2e-09	24%	CAD32966.1
polyprotein [Infectious pancreatic necrosis virus]	69.3	69.3	88%	2e-09	24%	AAK32155.1
polyprotein [Infectious pancreatic necrosis virus]	69.3	69.3	88%	2e-09	24%	CAD32965.1
107 kDa polyprotein [Infectious pancreatic necrosis virus]	69.3	69.3	95%	2e-09	24%	AAQ75360.1
polyprotein [Infectious pancreatic necrosis virus]	69.3	69.3	88%	2e-09	24%	AAV48850.1
polyprotein [Infectious pancreatic necrosis virus]	69.3	69.3	88%	2e-09	24%	CAD32968.1
polyprotein [Infectious pancreatic necrosis virus]	69.3	69.3	88%	2e-09	24%	CAD32970.1
polyprotein [Infectious pancreatic necrosis virus]	69.3	69.3	88%	2e-09	24%	AAV48848.3
polyprotein [Infectious pancreatic necrosis virus]	69.3	69.3	88%	2e-09	24%	AAV48852.3
submajor capsid protein VP3 [Infectious pancreatic necrosis virus]	65.5	65.5	58%	7e-09	26%	AAM90322.1
polyprotein [Infectious bursal disease virus]	64.3	64.3	54%	9e-08	25%	AKM16810.1
structural polyprotein [Infectious bursal disease virus]	61.6	61.6	54%	6e-07	27%	ABS86936.1

VP3 protein [Infectious bursal disease virus]	60.1	60.1	55%	7e-07	27%	AFV39829.1
polyprotein [Infectious bursal disease virus]	61.2	61.2	54%	9e-07	27%	<u>CAA27629.1</u>
RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 2; Short=p2; AltName: Full=pep7a; Contains: RecName: Full=Structural peptide 3; Short=p3; AltName: Full=pep7b; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep11; Contains: RecName: Full=Protease VP4; AltName: Full=Non-structural protein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP3	61.2	61.2	54%	9e-07	27%	<u>P08364.2</u>
polyprotein [Infectious bursal disease virus]	60.8	60.8	54%	1e-06	26%	AKD94179.1
unnamed protein product [Infectious bursal disease virus]	60.8	60.8	54%	1e-06	27%	<u>CAA79983.1</u>
polyprotein [Infectious bursal disease virus]	60.5	60.5	96%	1e-06	25%	AGA84578.1
structural polyprotein [Infectious bursal disease virus]	60.5	60.5	54%	2e-06	26%	AIG93139.1
polyprotein [Infectious bursal disease virus]	60.5	60.5	54%	2e-06	26%	ACZ62645.1
polyprotein [Infectious bursal disease virus]	60.1	60.1	54%	2e-06	27%	AAC78079.1
polyprotein [Infectious bursal disease virus]	60.1	60.1	54%	2e-06	26%	BAA08555.1
polyprotein [Infectious bursal disease virus]	59.7	59.7	54%	3e-06	26%	AAD48021.1

□ <u>Alignments</u>

polyprotein [Drosophila melanogaster birnavirus SW-2009a]

Sequence ID: **gb|ACU32790.1|** Length: 979 Number of Matches: 1 Range 1: 592 to 927

Score		Expect Method	Identities	Positives	Gaps	Frame
600 bits	(1547)	0.0() Compositional matrix adjust.	294/336(88%)	316/336(94%)	1/336(0%)	-2
Feature	s:					
Query	1007	AYIPPGPDCTVVPISAITQNEITTTA				
Sbjct	592	AYIPPGP+CTVVPIS+ITQNEITTTATATATATATATATATATATATATATATATATATA				
Query	827	EGKIVPNKWADLKREGMKGTGIPLVTI				
Sbjct	652	EGKIVPNKWADLKREGMKGTGIPLVTI EGKIVPNKWADLKREGMKGTGIPLVTI				
Query	647	AMDSDSppppppP-ITDEDIMVTLEELI				
Sbjct	712	AMD D PPPPP +TDE+IM TLE+L1 AMDYDDFPPPPPPVTDENIMETLEDL1				
Query	470	LHNFSRODVEGEKMNRIVONSLTTAVI				
Sbjct	772	LHNFSRQDVEGEKMNRIVQNSLTTAVI LHNFSRQDVEGEKMNRIVQNSLTTAVI				
Query	290	KNNGYRGPSAEQMKVIKTGLDPAPQT				
Sbjct	832	KNNG+RGPSA+QMK IK GL+P P T KNNGFRGPSADQMKTIKAGLEPPPDT				
Query	110	ETQKEINERVTTMVINNGNRGLNQYQ		3		
Sbjct	892	ETQKEINER+TTMVINNGNRGLNQYQ ETQKEINERITTMVINNGNRGLNQYQA		927		

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: **gb|ALF95277.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
83.6 bits	(205)	4e-14() Compositional matrix adjust.	85/335(25%)	147/335(43%)	26/335(7%)	-2
Features	S :					
Query	980	TVVPISAITQNEITTTATPPIPRG T +P+ I +N + PI G	GSMEAALALL- S + L+LL		VTGNVIEG	K 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MG		_		T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	KTIKDLAKA + +++ + A		HPAVIGTIAT A+	A 645
Sbjct	665	TIPICGVDIKAIAAHEQĞLPLIGNÖPG				K 724
Query	644	MDSDSppppppPITDEDIMVTLEELLMA + DE++ L +		KLKEVVLWLAKI KL +++ W K		
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAR				

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Query 467 HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWI 291 + +S++D E K +++ +GP Q Q RA RI ++ G D + EW+ Sbjct 780 YEWSKEDPEAVKFGKLISTPPKHPEKPKGPDQHHAQEARAARISLDAVRAGADFATPEWV 839

Query 290 KNNGYRGPSAEQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHY 126 N YRGPS Q K + TG DP P + I++PI + T + R+ + + Sbjct 840 ALNNYRGPSPGQFKYYLITGRDPVPGDEYEDYIKQPITKPTDMTK--IRRLANSVYGLPH 897

Query 125 ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21 + +PE E E V + NG RG +Q Q++++ Sbjct 898 QEPAPE---EFYEAVAAVFAENGGRGPDQDQMQDL 929
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polyprotein [Tasmanian aquabirnavirus]

Sequence ID: gb|ALF95281.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps F	rame
82.0 bits	s(201)	1e-13() Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%) -2	2
Feature	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL SPSAQLGLSLLV		TG + E FTGEIADDEET	664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q		ATEMLQRITTAQ A ++Q T	HPAVIGTIATA A+	645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPG			:	724
Query	644	MDSDSpppppPITDEDIMVTLEELLMA + DE++ L +		KLKEVVLWLAKI KL +++ W K		
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAR				
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++	RGPTQDVLQH(+GP O O		QGVDLSI-EWI G D + EW+	
Sbjct	780	YEWSKEDPEAVKFGKLISTPPKHPEKP				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS OK + TG DP P			RIIRNSLSAHY R+ + +	126
Sbjct	840	ALNNYRGPSPGQFKYYLITGRDPVPGD				897
Query	125	ENASPETQKEINERVTTMVINNGNRGI + +PE E + V + NG RG	NQYQVKEI 2 +Q Q++++	21		
Sbjct	898	QEPAPEEFYDAVAAVFAENGGRGP		929		

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: gb|ALF95271.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

82.0 bits(201) 1e-13() Compositional matrix adjust. 84/335(25%) 147/335(43%) 26/335(7%) -2	
Features:	
Query 980 TVVPISAITQNEITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEGK T +P+ I +N + PI G S + L+LL I GV TG + E	819
Sbjct 606 TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET	664
Query 818 IVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQHPAVIGTIATA I+P D+K G+PL+ +Q + +++ + A ++Q T A+	645
Sbjct 665 IIPICGVDIKAIAAHEQGLPLIGNÕPGVDEEVRNTSLAAHLIÕTGTLPVQKAMGSNKRIK	724
Query 644 MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL + DE++ L + A + +D + KL +++ W K D + D +	468
Sbjct 725 YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKNDLTDHM	779
Query 467 HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWI + +S++D E K +++ +GP Q Q RA RI + + G D + EW+	291
Sbjct 780 YEWSKEDPEAVKFGKLISTPPKHPEKPKGPDQHHAQEARAARISLDAVRAGADFATPEWV	839
Query 290 KNNGYRGPSAEQMK-VIKTGLDPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHY N YRGPS Q K + TG DP P + I++PI + + T + R+ + +	126
Sbjct 840 ALNNYRGPSPGQFKYYLITGRDPVPGDEYEDYIKQPITKPTDMTKIRRLANSVYGLPH	897
Query 125 ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21 + +PE E + V + NG RG +Q Q++++	
Sbjct 898 QEPAPEEFYDAVAAVFAENGGRGPDQDQMQDL 929	

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: gb|ALF95275.1| Length: 972 Number of Matches: 1

Score	Expec	t Method		Identities	Positives	Gaps	Frame
82.0 bits(20	01) 1e-13() Compositional	matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2
Features:							
Query 9	80 TVVP T +P	ISAITQNEI + I +N +		GGSMEAALALL- G S + L+LL	-QHIPPGVTPFA I GV	VTGNVIEG TG + E	SK 819

Sbjct 606	TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET	664
Query 818	IVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQHPAVIGTIATA I+P D+K G+PL+ +Q + +++ + A ++Q T A+	645
Sbjct 665	I+P D+K G+PL+ +Q + +++ A ++Q T A+ IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK	724
Query 644	MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL + DE++ L + A + +D + KL +++ W K D + D +	468
Sbjct 725	YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKNDLTDHM	779
Query 467	$ ext{HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWI} + + S + + D = K + + + + + + + + + + + + + + + + + +$	291
Sbjct 780	YEWSKEDPEAVKFGKLISTPPKHPEKPKGPDQHHAQEARAARISLDAVRAGADFATPEWV	839
Query 290	KNNGYRGPSAEQMK-VIKTGLDPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHY N YRGPS Q K + TG DP P + I++PI + + T + R+ + + +	126
Sbjct 840	ALNNYRGPSPGQFKYYLITGRDPVPGDEYEDYIKQPITKPTDMTKIRRLANSVYGLPH	897
Query 125	ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21 + +PE E + V + NG RG +Q Q++++	
Sbjct 898	QEPAPEEFYDAVAAVFAENGGRGPDQDQMQDL 929	

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: **gb|ALF95267.1**| Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
82.0 bits	s(201)	1e-13() Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2
Feature	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO T +P+ I +N + PI O				K 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MO	G S + L+LL GPSAQLGLSLL\		TG + E FTGEIADDEE	T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Õ	YKTIKDLAKA + +++ + A		HPAVIGTIAT	'A 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPO				K 724
Query	644	MDSDSpppppPITDEDIMVTLEELLMA + DE++ L +				
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAF				
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++		QRAVRIRENYLI RA RI + +		
Sbjct	780	YEWSKEDPEAVKFGKLISTPPKHPEKE				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS O K + TG DP P				126 +
Sbjct	840	ALNNYRGPSPGQFKYYLITGRDPEPGI				•
Query	125	ENASPETQKEINERVTTMVINNGNRGI + +PE E + V + NG RG	NOYOVKEI 2 +O O++++	21		
Sbjct	898	QEPAPEEFYDAVAAVFAENGGRGE		929		

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: **gb|ALF95279.1**| Length: 972 Number of Matches: 1 Range 1: 606 to 929

Expect Method	Identities	Positives	Gaps	Frame
2e-13() Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2
				K 819
				ET 664
				A 645
				K 724
				126 Y
				рн 897
		21		
		929		
	TVVPISAITQNEITTTATPPIPROT +P+ I +N + PI OF TALPLKEIKRNGNIVVEKIFAGPI-MOST IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q IIPICGVDIKAIAAHEQGLPLIGNQPOST MDSDSpppppPITDEDIMVTLEELLMAH + DE++ L + YLGELMASTASGMDEELQSLLNATMAR HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++ YEWSKEDPEAVKFGKLISTPPKHPEKP KNNGYRGPSAEQMK-VIKTGLDPAP-N YRGPS Q K + TG DP PALNNYRGPSPGQFKYYLITGRDPEPGDENASPETQKEINERVTTMVINNGNRGIH + +PE E + V + NG RG	TVVPISAITQNEITTTATPPIPRGGSMEAALALL- T +P+ I +N + PI G S + L+LL TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLV IVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKA I+P D+K G+PL++Q + +++ + A IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLA MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAA + DE++ L + A + +D + P YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYE HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQ + +S++D E K +++ +GP Q Q YEWSKEDPEAVKFGKLISTPPKHPEKPKGPDQHHAQEA KNNGYRGPSAEQMK-VIKTGLDPAPQTIIREPIE N YRGPS Q K + TG DP P + I++PI ALNNYRGPSPGQFKYYLITGRDPEPGDEYEDYIKQPIT ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 2 + +PE E + V + NG RG +Q Q++++	2e-13() Compositional matrix adjust. 84/335(25%) 147/335(43%) TVVPISAITQNEITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAT +P+ I +N + PI G S + L+LL I GV TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMV IVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQI+P D+K G+PL+ +Q + +++ + A ++Q T IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPV MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKI+ DE++ L + A + +D + KL +++ W K YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKN HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLI+ +S++D E K +++ +GP Q Q RA RI + + YEWSKEDPEAVKFGKLISTPPKHPEKPKGPDQHHAQEARAARISLDAVR KNNGYRGPSAEQMK-VIKTGLDPAPQTIIREPIPRSDNSTPELVM N YRGPS Q K + TG DP P + I++PI + T + ALNNYRGPSPGQFKYYLITGRDPEPGDEYEDYIKQPITKPTDMTKIR ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21 + +PE E + V + NG RG +Q Q++++	2e-13() Compositional matrix adjust. 84/335(25%) 147/335(43%) 26/335(7%) TVVPISAITQNEITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEGT +P+ I +N + PI GS + L+LL I GV TG + ETALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRNVFTGEIADDEEIVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQHPAVIGTIATIHP D+K G+PL++Q + +++ + A ++Q T A+IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDT + DE++ L + A ++D + KL +++ W K D + DYLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKNDLTDEHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWHSHD E K +++ GD + EWYEWSKEDPEAVKFGKLISTPPKHPEKPKGPDQHHAQEARAARISLDAVRAGADFATTEWKNNGYRGPSAEQMK-VIKTGLDPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAEN YRGPS Q K + TG DP P + I++PI + T + R+ + ALNNYRGPSPGQFKYYLITGRDPEPGDEYEDYIKQPITKPTDMTKIRRLANSVYGLEENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21 + +PE E + V + NG RG +Q Q++++

Sequence ID: **gb|ALF95273.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
81.6 bits	s(200)	2e-13() Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%) -	2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRG T +P+ I +N + PI G	GSMEAALALL- S + L+LL		VTGNVIEGE TG + E	819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MG				664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O			HPAVIGTIATA A+	A 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPG				724
Query	644	MDSDSpppppPITDEDIMVTLEELLMA + DE++ L +		KLKEVVLWLAKI KL +++ W K		
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAR				
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++		QRAVRIRENYLI RA RI + +		
Sbjct	780	YEWSKEDPEAVKFGKLISTPPKHPEKP				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS OK + TG DP P			RIIRNSLSAHY R+ +	
Sbjct	840	ALNNYRGPSPGQFKYYLITGRDPEPGD				
Query	125	ENASPETQKEINERVTTMVINNGNRGL + +PE E + V + NG RG	NQYQVKEI 2 +Q Q++++	21		
Sbjct	898	QEPAPEEFYDAVAAVFAENGGRGP		929		

polyprotein [marine birnavirus]

Sequence ID: gb|AAL83706.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score	Expect Method	Identities	Positives	Gaps	Frame
81.6 bits(200	2e-13() Compositional matrix adjust.	80/309(26%)	137/309(44%)	22/309(7%)	-2
Features:					
Query 911					D 741
Sbjct 631	${ t G} ext{ } S ext{ } + ext{ } L + LL ext{ } I ext{ } GV ext{ } TG ext{ } GPSCQLGLSLLVNDIDKGVPRMVFTGE $		D+K ICGVDIKAIAAH	G+PLV Q IEHGLPLVGCQ	P 690
Query 740	YKTIKDLAKATEMLQRITTAQHPAV + + + + A+ ++O A			DIMVTLEELLE C++ L+ +	
Sbjct 691					
Query 566	AAAD-RDPRMAKLKEVVLWLAKIDDNN A + +D + KL +++ W K		SRQDVEGEKMNF S++D E K +		н 390
Sbjct 751					к 805
Query 389	SRGPTQDVLQHQRAVRIRENYLIQGVD +GP Q Q +AVRI + + G D		GYRGPSAEQMK- GYRGPS OK	VIKTGLDPAP + TG P P	- 219
Sbjct 806					R 865
Query 218	QTIIREPIPRSDNSTPELVMRIIF + +R+PI R + + + R+		SPETQKEINERV PPE E + V		
Sbjct 866					_
Query 47	LNQYQVKEI 21 +Q Q++++				
Sbjct 921					

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: gb|ALF95269.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
81.3 bits	(199)	2e-13() Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRG				SK 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL PSAQLGLSLLV		TG + E FTGEIADDEI	ET 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O			HPAVIGTIAT	TA 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPG				K 724
Query	644	MDSDSpppppPITDEDIMVTLEELLMA + DE++ L +		KLKEVVLWLAKI KL +++ W K		
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAR				
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++		RAVRIRENYLI RA RI + +		
Sbjct	780	YEWSKEDPEAVKFGKLISTPPKHPEKP				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS Ö K + TG DP P	QTIIREPIF + I++PI		RIIRNSLSAF R+ +	HY 126
Sbjct	840	ALNNYRGPSPGQFKYYLITGRDPEPGD				РН 897
Query	125	ENASPETQKEINERVTTMVINNGNRGL + +PE E + V + NG RG	NQYQVKEI 2 +Q Q++++	21		
Sbjct	898	QEPAPEEFYDAVAAVFAENGGRGP		29		

polyprotein [Marine birnavirus]

Sequence ID: **gb|AAP37163.1**| Length: 972 Number of Matches: 1 Range 1: 631 to 929

	Expect Method	Identities	Positives	Gaps	Frame
s(199)	2e-13() Compositional matrix adjust.	79/309(26%)	137/309(44%)	22/309(7%)	-2
S :					
911					
631					
740					
691					
566					н 390
751					к 805
389					
806					
218					
866					
47	LNQYQVKEI 21				
921	PDÕDÕMQDL 929				
	911 631 740 691 566 751 389 806 218 866 47	S(199) 2e-13() Compositional matrix adjust. S: 911 GGSMEAALALL-QHIPPGVTPFAVTGN G S + L+LL I GV TG 631 GPSCQLGLSLLVNDIDKGVPRMVFTGE 740 YKTIKDLAKATEMLQRITTAQHPAV + + + + A+ ++Q A 691 GVDEVVANTSLASHLIQSGALPVQKAQ 566 AAAD-RDPRMAKLKEVVLWLAKIDDNN A + +D + KL +++ W K 751 RAKEVKDAEVFKLLKLMSWTRK 389 SRGPTQDVLQHQRAVRIRENYLIQGVD +GP Q Q +AVRI + + G D 806 PKGPDQHTAQEAKAVRISLDAVKAGAD 218QTIIREPIPRSDNSTPELVMRIIR + +R+PI R + + + R+ 866 DEYEDYVRKPITRPTDMDKIRRLAN 47 LNQYQVKEI 21 +Q Q++++	S(199) 2e-13() Compositional matrix adjust. 79/309(26%) S: 911 GGSMEAALALL-QHIPPGVTPFAVTGNVIEGKIVPN G S + L+LL I GV TG + E I+P 631 GPSCQLGLSLLVNDIDKGVPRMVFTGEIADDEESIIP1 740 YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSI + + + + A+ ++Q A + + + 4	S(199) 2e-13() Compositional matrix adjust. 79/309(26%) 137/309(44%) S: 911 GGSMEAALALL-QHIPPGVTPFAVTGNVIEGKIVPNKWADLKREGMKGS+L+LLIGVTG+EIADDEESIIPICGVDIKAIAAH 631 GPSCQLGLSLLVNDIDKGVPRMVFTGEIADDEESIIPICGVDIKAIAAH 740 YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPPITDE	S(199) 2e-13() Compositional matrix adjust. 79/309(26%) 137/309(44%) 22/309(7%) S: 911 GGSMEAALALL-QHIPPGVTPFAVTGNVIEGKIVPNKWADLKREGMKGTGIPLVTDO G S + L+LL I GV TG + E I+P D+K G+PLV Q 631 GPSCQLGLSLLVNDIDKGVPRMVFTGEIADDEESIIPICGVDIKAIAAHEHGLPLVGCQ 740 YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPPITDEDIMVTLEELL + + + + A + ++Q A + DE++ L+ + 691 GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLQATM 566 AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAV A + +D + KL +++ W K G+ D ++ +S++D E K +++ 751 RAKEVKDAEVFKLLKLMSWTRKNGLTDHMYEWSKEDPEAVKFGKLISTPPKHQE 389 SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP +GP Q Q +AVRI ++ G D S +WI NGYRGPS Q K + TG P P 806 PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDP 218 QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNR + +R+PI R + + + R+ + + + +PE E + V + NG R 866 DEYEDYVRKPITRPTDMDKIRRLANSVYGLPHQEPAPEEFYQAVVEIFAENGGR

polyprotein [Marine birnavirus]

Sequence ID: ref|YP_605813.1| Length: 972 Number of Matches: 1

▶ See 1 more title(s) Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
80.9 bits	(198)	3e-13() Compositional matrix adjust.	80/309(26%)	136/309(44%)	22/309(7%)	-2
Features	S :					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN G S + L+LL I GV TG		NKWADLKREGMK D+K	GTGIPLVTDQ G+PLV O	D 741
Sbjct	631	GPSCQLGLSLLVNDIDKGVPRMVFTGE				P 690
Query	740	YKTIKDLAKATEMLQRITTAQHPAV + + + + A+ ++O A	'IGTIATAMDSI + +		DIMVTLEELL ++ L +	M 567
Sbjct	691	GVDEVVANTSLASHLIÕSGALPVQKAQ			-	A 750
Query	566	AAAD-RDPRMAKLKEVVLWLAKIDDNN A + +D + KL +++ W K	PGVLDTLHNFS G+ D ++ +S		IVQNSLTTAV	н 390
Sbjct	751	RAKEVKDAEVFKLLKLMSWTRK				K 805
Query	389	SRGPTQDVLQHQRAVRIRENYLIQGVD +GP Q Q +AVRI + + G D			VIKTGLDPAP + TG P P	- 219
Sbjct	806	PKGPDÕHTAÕEAKAVRISLDAVKAGAD				R 865
Query	218	QTIIREPIPRSDNSTPELVMRIIR + +R+PI R + + + R+		SPETQKEINERV PPE E + V		
Sbjct	866	DEYEDYVRKPITRPTDMDKIRRLAN				_
Query	47	LNQYQVKEI 21 +Q Q++++				
Sbjct	921	PDQDQMQDL 929				

polyprotein [Aquabirnavirus TAB98]

Sequence ID: **gb|ACD64976.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
80.9 b	its(198)	3e-13() Compositional matrix adjust.	84/335(25%)	146/335(43%)	26/335(7%)	-2
Featur	es:					
Query	980	TVVPISAITQNEITTTATPPIPRO				K 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL SPSAQLGLSLLV		TG + E FTGEIADDEE	T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	KTIKDLAKA + +++ + A		HPAVIGTIAT A	'A 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPG		~		K 724
Query	644	MDSDSpppppPITDEDIMVTLEELLMA + DE++ L +		KLKEVVLWLAKI KL +++ W K		
Sbjct	725	YLGELMASTASGMDEELOSLLNATMAF				

```
HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWI + +S++D E K +++ +GP Q Q RA RI + + G D + EW+
Query 467
                                                                      291
           839
Sbjct
      780
          126
Query
      290
Sbjct
      840
                                                                      897
          ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI
+ +PE E + V + NG RG +Q Q++++
QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL
Query
      125
Sbjct
      898
```

polyprotein [Yellowtail ascites virus]

Sequence ID: ref|NP_690805.1| Length: 972 Number of Matches: 1

▶ See 2 more title(s) Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
80.9 bits	s(198)	3e-13() Compositional matrix adjust.	80/309(26%)	136/309(44%)	22/309(7%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN				
Sbjct	631	G S $+$ $L+LL$ I GV TG $GPSCQLGLSLLVNDIDKGVPRMVFTGE$		D+K CGVDIKAIAAH	G+PLV Q EHGLPLVGCQ	
Query	740	YKTIKDLAKATEMLQRITTAQHPAV + + + + A+ ++O A	'IGTIATAMDSI + +		DIMVTLEELL ++ L +	
Sbjct	691	GVDEVVANTSLASHLIQSGALPVQKAQ			<u> </u>	
Query	566	AAAD-RDPRMAKLKEVVLWLAKIDDNN A + +D + KL +++ W K		SRQDVEGEKMNR S++D E K +		н 390
Sbjct	751	RAKEVKDAEVFKLLKLMSWTRK				К 805
Query	389	SRGPTQDVLQHQRAVRIRENYLIQGVD +GP Q Q +AVRI + + G D		GYRGPSAEQMK- GYRGPS Q K		
Sbjct	806	PKGPDOHTAQEAKAVRISLDAVKAGAD				
Query	218	QTIIREPIPRSDNSTPELVMRIIR + +R+PI R + + + R+		SPETQKEINERV -PE E + V		
Sbjct	866	DEYEDYVRKPITRPTDMDKIRRLAN				_
Query	47	LNQYQVKEI 21 +Q Q++++				
Sbjct	921	PDÕDÕMQDL 929				

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: ref|YP_009177608.1| Length: 972 Number of Matches: 1

▶ See 1 more title(s) Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
80.9 bits	s(198)	3e-13() Compositional matrix adjust.	84/335(25%)	146/335(43%)	26/335(7%)	-2
Feature	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				K 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	GS + L+LL GPSAQLGLSLLV	I GV /NDIEEGVPRMV	TG + E FTGEIADDEE	T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	KTIKDLAKA + +++ + A		HPAVIGTIAT A	A 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPO				K 724
Query	644	MDSDSppppppPITDEDIMVTLEELLMA + DE++ L +		KLKEVVLWLAKI KL +++ W K		
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAF			_	•
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++		QRAVRIRENYLI RA RI + +		
Sbjct	780	YEWSKEDPEAVKFGKLISTPPKHPEKE				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS Q K + TG DP P			RIIRNSLSAE R+ +	IY 126
Sbjct	840	ALNNYRGPSPGQFKYYLITGRDPEPGI				•
Query	125	ENASPETQKEINERVTTMVINNGNRGI + +PE E + V + NG RG		21		
Sbjct	898	QEPAPEEFYDAVAAVFAENGGRGE		929		

VP2,NS,VP3 [Yellowtail ascites virus]

Sequence ID: dbj|BAA25005.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score Expect Method Identities Positives Gaps Frame

80.5 bits(197)	4e-13() Compositional matrix adjust. 80/309(26%) 135/309(43%) 22/309(7%) -2	
Features:		
Query 911	GGSMEAALALL-QHIPPGVTPFAVTGNVIEGKIVPNKWADLKREGMKGTGIPLVTDQD G S + L+LL I GV TG + E IVP D+K G+PLV Q	741
Sbjct 631	GPSCQLGLSLLVNDIDKGVPRMVFTGEIANDEETIVPICGVDIKAIAAHEHGLPLVGCQP	690
Query 740	YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM	567
Sbjct 691	+ + + + A + ++Q A $+ +$ DE++ L + GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLHATMA	750
Query 566	AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH A + +D + KL +++ W K G+ D ++ +S++D E K +++	390
Sbjct 751	RAKEVKDAEVFKLLKLMSWTRKNGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK	805
Query 389	SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP- +GP Q Q +AVRI + + G D S +WI NGYRGPS Q K + TG P P	219
Sbjct 806	PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDPR	865
Query 218	QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG	48
Sbjct 866	+ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$	920
Query 47	LNQYQVKEI 21	
Sbjct 921	+Q Q++++ PDQDQMQDL 929	

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: **gb|ALF95263.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
80.5 bits	s(197)	4e-13() Compositional matrix adjust.	84/335(25%)	146/335(43%)	26/335(7%)	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				к 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL SPSAQLGLSLLV		TG + E FTGEIADDEE	т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q			HPAVIGTIAT A	A 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPG				K 724
Query	644	MDSDSpppppPITDEDIMVTLEELLMA + DE++ L +		KLKEVVLWLAKI KL +++ W K		
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAR				•
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++			QGVDLSI-EW G D + EW	
Sbjct	780	YEWSKEDPEAVKFGKLISTPPKHPEKP				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS O K + TG DP P				Y 126
Sbjct	840	ALNNYRGPSPGQFKYYLITGRDPEPGD				•
Query	125	ENASPETQKEINERVTTMVINNGNRGL + +PE E + V + NG RG	NQYQVKEI 2 +O O++++	21		
Sbjct	898	QEPAPEEFYDAVAAVFAENGGRGP		29		

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: **gb|ALF95265.1|** Length: 972 Number of Matches: 1 Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
80.5 bits	s(197)	4e-13() Compositional matrix adjust.	78/309(25%)	136/309(44%)	22/309(7%)	-2
Features	S :					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN				
Sbjct	631	G S + L+LL I GV TG GPSAQLGLSLLVNDIEEGVPRMVFTGE		D+K CGVDIKAIAAH	G+PL+ +Ç EQGLPLIGNÇ	•
Query	740	YKTIKDLAKATEMLQRITTAQHPAV + +++ + A ++O T A				
Sbjct	691	+ +++ + A ++Q T A GVDEEVRNTSLAAHLIQTGTLPVQKAK	+ GSNQRIKYLGE			
Query	566	AAAD-RDPRMAKLKEVVLWLAKIDDNN A + +D + KL +++ W K D	PGVLDTLHNFS + D ++ +S		RIVQNSLTTAV	7Н 390
Sbjct	751	RAKEVKDVEIYKLLKLMAWTRKND			• •	K 805
Query	389	SRGPTQDVLQHQRAVRIRENYLIQGVD				
Sbjct	806	+GP Q Q RA RI + + G D PKGPDQHHAQEARAARISLDAVRAGAD				
Query	218	QTIIREPIPRSDNSTPELVMRIIR				
Sbjct	866	+ I++PI + + T + R+ DEYEDYIKQPITKPTDMTKIRRLAN		-PE E + V APEEFYDAV	-,	
Query	47	LNOYOVKEI 21				
Sbjct	921	+Q Q++++ PDQDQMQDL 929				

polyprotein [Marine birnavirus - H1]

Sequence ID: **gb|AAP37165.1|** Length: 972 Number of Matches: 1 Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
80.5 bits	s(197)	4e-13() Compositional matrix adjust.	79/309(26%)	136/309(44%)	22/309(7%)	-2
Feature	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN G S + L+LL I GV TG				
Sbjct	631	G S + L+LL I GV TG GPSCQLGLSLLVNDIDKGVPRMVFTGE		D+K ICGVDIKAIAAH	G+PLV Q IEHGLPLVGCQ	
Query	740	YKTIKDLAKATEMLQRITTAQHPAV + + + + A+ ++O A				
Sbjct	691	+ + + + A+ ++Q A GVDEVVANTSLASHLIQSGALPVQKAQ				
Query	566	AAAD-RDPRMAKLKEVVLWLAKIDDNN A + +D + KL +++ W K		SRQDVEGEKMNR S++D E K +		н 390
Sbjct	751	RAKEVKDAEVFKLLKLMSWTRK				к 805
Query	389	SRGPTQDVLQHQRAVRIRENYLIQGVD +GP Q Q +AVRI + + G D		GYRGPSAEQMK- GYRGPS Q K		
Sbjct	806	PKGPDQHTAQEAKAVRISLDAVKAGAD				
Query	218	QTIIREPIPRSDNSTPELVMRIIF + +R+PI R + + + R+			TTMVINNGNR + NG R	
Sbjct	866	DEYEDYVRKPITRPTDMDKIRRLAN			-,	_
Query	47	LNQYQVKEI 21 +Q Q++++				
Sbjct	921	PDQDQMQDL 929				

polyprotein, partial [Infectious pancreatic necrosis virus - He]

Sequence ID: **gb|AAK32156.1|AF342730_1** Length: 968 Number of Matches: 1 Range 1: 641 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
80.1 bits	s(196)	6e-13() Compositional matrix adjust.	82/304(27%)	130/304(42%)	31/304(10%)	-2
Features	s:					
Query	884	LLQHIPPGVTPFAVTGNVIEGKIV L+ I GV TG + E I+		MKGTGIPLVTD G+PLV +		A 717
Sbjct	641	LVNDIQEGVPRMVFTGELGQDEESII			~	S 700
Query	716	KATEMLQRITTAQHPAVIGTI A ++O+ T A I +	ATAMDSDSppp MDS++		TLEELLMAAAD L + A +	- 555
Sbjct	701	LÄAHLIÕKGTLPVQKACGVDKRIKHL				V 755
Query	554	RDPRMAKLKEVVLWLAKIDDNNPGVL +D + KL ++ W K G+	DTLHNFSRQDV D ++ +SR+D		SLTTAVHSRGP +GP	т 375
Sbjct	756	KDAEIYKLLRLMSWTRKNGLT				D 810
Query	374	QDVLQHQRAVRIRENYLIQGVDL-SI Q Q RA RI + + G D S				т 213
Sbjct	811	ÕHTAÕEARAARISLDAVKAGADFASP				D 870
Query	212	IIREPIPRSDNSTPELVMRIIRNSLS + PI R + T + R+ +	AHYENASPETQ ++ +PE	KEINERVTTMV E V +	INNGNRGLNQY NG RG +O	
Sbjct	871	YVTRPITRPTDMTRIRRLANSVYG				
Query	32	VKEI 21 + ++				
Sbjct	926	MLDL 929				

polyprotein [Yellowtail ascites virus]

Sequence ID: dbj|BAF37013.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
79.0 bits	s(193)	1e-12() Compositional matrix adjust.	78/309(25%)	136/309(44%)	22/309(7%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN				7
Sbjct	631	G S + L+LL I GV TG GPSCQLGLSLLVNDIDRGVPRMVFTGE	+ E I+P CIADDEETIIP	D+K IYGVDIKAIAAH	G+PLV (EHGLPLVGC)	÷ .
Query	740	YKTIKDLAKATEMLQRITTAQHPAV + + + + A+ ++O A			DIMVTLEELI	
Sbjct	691	GVDEVVANTSLASHLIQSGALPVQKAQ				
Query	566	AAAD-RDPRMAKLKEVVLWLAKIDDNN A + +D + KL +++ W K				7H 390
Sbjct	751	RAKEVKDAEVFKLLKLMSWTRK				EK 805
Query	389	SRGPTQDVLQHQRAVRIRENYLIQGVD +GP Q Q +A RI + + G D				
Sbjct	806	PKGPDQHTAQEAKAARISLDAVKAGAD				
Query	218	QTIIREPIPRSDNSTPELVMRIIR	RNSLSAHYENAS	SPETQKEINERV	TTMVINNGNE	RG 48

```
+ +R+PIR + + + R+ + + + +PE E + V + NG RG
Sbjct 866 DEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGGRG 920

Query 47 LNQYQVKEI 21
+Q Q++++
Sbjct 921 PDQDQMQDL 929
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polyprotein [Blotched snakehead virus]

Sequence ID: ref|YP_052862.1| Length: 1069 Number of Matches: 1

▶ See 2 more title(s) Range 1: 686 to 1020

Score		Expect Method	Identities	Positives	Gaps	Frame
79.0 bits	s(193)	1e-12() Compositional matrix adjust.	92/355(26%)	151/355(42%)	74/355(20%) -2
Features	s:					
Query	923	PIPRGGSMEAALALLQHIPPGVTPF				
Sbjct	686	P G S ALAL +P V A PAVAGQSSSIALALASSLP-FVPKAA		P ++ +LK QPVQFGNLKAR	G+PLV AAHKIGLPLV	
Query	752	TDQDYKTIKDLA-KATEMLQRI D T+ D A A + ++		TIAT	-AMDSDSppp A D ++	ppP 612
Sbjct	745	QDGGEDTRICTLDDAADHAFDSME				L 800
Query	611	ITDEDIMVTLE ED + ++E			LWLAKIDDNN W+	PGV 480 G+
Sbjct	801	EDFLDSIELHSKPTVEQPQTEE			• • •	_
Query	479	LDTLHNFSRQDVEGEKMNRIVQNSLT +D L+N+++ D G +M +++N		GPT GP	QDVL	QHQ 354
Sbjct	853	IDALYNWAQLDDGGVRMRNMLRNLPH			MEVLRRĖAAA	
Query	353	RAVRIRENYLIQGVDLS-IEWIKNNO +A RI E+ + G + + I+W+ NO			QTIIREPI + EP	PRS 186
Sbjct	913	KAQRISEDAMDNGFEFATIDWVLENG			· ——	'HAP 972
Query	185	DNSTPELVMRIIRNSLSAHYENASPE +N +L I + N +P				21
Sbjct	973	ENKAAKLAATIYGSPNQAPA				1020

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: gb|ALF95287.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
78.6 bits	s(192)	2e-12() Compositional matrix adjust.	83/335(25%)	146/335(43%)	26/335(7%)	-2
Features	S :					
Query	980	TVVPISAITQNEITTTATPPIPRO				К 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL SPSAQLGLSLLV		TG + E FTGEIADDEE	т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q			HPAVIGTIAT A+	A 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPG				К 724
Query	644	MDSDSpppppPITDEDIMVTLEELLMA + DE++ L +	AAD-RDPRMAK A + +D + K	KLKEVVLWLAKI KL +++ W K		
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAR				
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++			QGVDLSI-EW G D + EW	
Sbjct	780	YEWSKEDPEAVKFGKLISTPPKHPEKP				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS Q K + TG P P				Y 126
Sbjct	840	ALNNYRGPSPGQFKYYLITGRAPEPGD				•
Query	125	ENASPETQKEINERVTTMVINNGNRGL + +PE E + V + NG RG	NQYQVKEI 2 +Q Q++++	21		
Sbjct	898	QEPAPEEFYDAVAAVFAENGGRGP		29		

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: gb|ALF95283.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
78.6 bits	s(192)	2e-12() Compositional matrix adjust.	83/335(25%)	146/335(43%)	26/335(7%)	-2
Feature	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				K 819
Sbjct	606	T +P+ I +N + PI O TALPLKEIKRNGNIVVEKIFAGPI-MO	S + L+LL SPSAQLGLSLL		TG + E FTGEIADDEE	T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY	/KTIKDLAK	ATEMLQRITTAQ	HPAVIGTIAT	A 645

```
I+P
             D+K
                    G+PL+ +Q
                            + +++ + A ++Q T
Sbjct 665
        IIPICGVDIKAIAAHEQGLPLIGNÕPGVDEEVRNTSLAAHLIÕTGTLPVQKAMGSNKRIK
        Query
                                                   468
        YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND----LTDHM
Sbjct
    725
                                                   779
        467
                                                   291
Query
Sbjct
    780
                                                   839
       Query
    290
                                                   126
Sbjct
    840
                                                   897
       ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21
+ +PE E + V + NG RG +Q Q++++
Query
Sbjct
    898 QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL
```

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: gb|ALF95285.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
77.4 bits	s(189)	5e-12() Compositional matrix adjust.	83/335(25%)	145/335(43%)	26/335(7%)	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRG				K 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL PSAQLGLSLLV	I GV /NDIEEGVPRMV	TG + E FTGEIADDEE	T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I P D+K G+PL+ +O			HPAVIGTIAT	'A 645
Sbjct	665	ITPICGVDIKAIAAHEQGLPLIGNQPG				K 724
Query	644	MDSDSpppppPITDEDIMVTLEELLMA + DE++ L +	AAD-RDPRMAF A + +D + F			
Sbjct	725	YLGELMASTASGMDEELQSLLNATMAR				•
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +S++D E K +++			QGVDLSI-EW G D + EW	
Sbjct	780	YEWSKEDPEAVKFGKLISTPPKHPEKP				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS Q K + TG P P			RIIRNSLSAH R+ +	126 T
Sbjct	840	ALNNYRGPSPGQFKYYLITGRAPEPGD				р́н 897
Query	125	ENASPETQKEINERVTTMVINNGNRGL + +PE E + V + NG RG		21		
Sbjct	898	QEPAPEEFYDAVAAVFAENGGRGP		929		

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AGW99956.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
75.9 bits	(185)	2e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Features	:					
Query	980	TVVPISAITQNEITTTATPPIPRO				K 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S		TG + E VFTGEIADDEE	T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P + D+K G+PL+ +Õ			QHPAVI A	
Sbjct	665	IIPIRGVDIKAIAAHEQGLPLIGNQPG				
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	EELLMAAAD-R + A + +	DPRMAKLKEVVI D + KL ++		G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++		DVLQHQRAVRII Q RA RI		
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPK				
Query	302	I-EWIKNNGYRGPSAEOMK-VIKTGLE EW+ N YRGPS Q K + TG +		IREPIPRSDNS' I++PI + +	PELVMRIIRN + R+ +	
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRE				
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	IGNRGLNQYQV IG RG +Q Q+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQN				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AEK06233.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score Expect Method Identities Positives Gaps Frame

75.9 bits(185) 2e-11() Compositional matrix adjust. 83/335(25%) 145/335(43%) 26/335(7%) -2 Features: TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEGK-T +P+ I +N + PI G S + L+LL I GV TG + E +
TALPLKEIKKNGNIIVEKIFAGPI-MGPSAQLGLSLLVNDIDEGVPRMVFTGEIAEDEET Query 980 819 Sbjct 606 664 IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA Query 818 645 I+P D+K G+PL+ +Q + +K+ + A ++Q T A + IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVKNTSLAAHLIQSGTLPVQKAKGASKRIK Sbjct 724 665 Query 644468 725 779 Sbjct HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWI 291 Query 467 +GPQQA+A+RI+G+EW++ +SR+D + K +++ Sbjct 780 YEWSREDPDAIKFGKLISTPPKHPEKPKGPDQHQAQEAKAIRISLDAVRAGANFATTEWV 839 KNNGYRGPSAEQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHY N YRGPS Q K + TG P P I+ PI + + T + R+ + + Query 290 126

AENNYRGPSPGÖFKYYMITGETPDPGEEYDDYIKRPIVKPTDMTK--IRRLANSVYGLPH

897

VP3 protein [Blotched snakehead virus]

Sequence ID: ref|YP_052872.1| Length: 278 Number of Matches: 1

ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI + +PE E V + +NG RG +Q Q++++ QEPAPE---PFYEAVAAVFADNGGRGPDQDQMQDL

Range 1: 34 to 229

840

125

898

Sbjct

Query

Sbjct

Score		Expect	Method	Identities	Positives	Gaps	Frame
73.6 bits	(179)	2e-11()	Compositional matrix adjust.	62/208(30%)	102/208(49%)	34/208(16%)	-2
Features	s :						
Query	578	ELLMA ELLM	AAADRDPRMAKLKEVVLWLAKII A +DP+M+K+ ++ W+		HNFSRQDVEGEI +N+++ D G -		- 411
Sbjct	34		LARKDPOMSKILVILGWV				E 88
Query	410		SLTTAVHSRGPTQ-DVLQHQ A SR T+ +VL+ +				
Sbjct	89	GSKSQ	RRKHGPAPESRESTRMEVLRRE				
Query	275		AEQMKVIK-TGLDPAPQTIIF OKKTGLDPP+	REPIPRSDNST EP +N	PELVMRIIRNS	LSAHYENASPE N +P	T 105
Sbjct	149		PAQAKYYKATGLDPEPGLTEFLE				A 201
Query	104		IERVTTMVINNGNRGLNQYQVKE E V +++ N RG NQ Q++E				
Sbjct	202		E V TTT N KG NO OTTI EEVAAVLMENNGRGPNQAQMRE				

polyprotein [Marine birnavirus]

Sequence ID: gb|AAP37167.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
75.5 bits	s(184)	2e-11() Compositional matrix adjust.	78/309(25%)	135/309(43%)	22/309(7%)	-2
Features	S :					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN				•
Sbjct	631	G S + L+LL I GV TG GPSCQLGLSLLVNDIDKGVPRMVFTGE		++K ICGVNIKAIAAH	G+PLV Ç EHGLPLVGCÇ	
Query	740	YKTIKDLAKATEMLQRITTAQHPAV + + + + A+ ++O A			DIMVTLEELI ++ L +	
Sbjct	691	+ + + + A+ ++Q A GVDEVVANTSLASHLIQSGALPVQKAQ	•			
Query	566	AAAD-RDPRMAKLKEVVLWLAKIDDNN A + +D + KL +++ W K	PGVLDTLHNFS G+ D ++ +S		RIVQNSLTTAV	т 390
Sbjct	751	RAKEVKDAEVFKLLKLMSWTRK	_		• •	K 805
Query	389	SRGPTQDVLQHQRAVRIRENYLIQGVD +GP O O +AVRI + + G D			VIKTGLDPAP + TG P P	
Sbjct	806	PKGPDÕHTAÕEAKAVRISLDAVKAGAD				
Query	215	TIIREPIPRSDNSTPELVMRIIR +R+PI R + + + R+			TTMVINNGNR + NG R	
Sbjct	866	DEYDDYVRKPITRPTDMDKIRRLAN			-,	
Query	47	LNQYQVKEI 21 +Q Q++++				
Sbjct	921	PDQEQMQDL 929				

Sequence ID: gb|AAB39512.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
75.5 bits	(184)	2e-11() Compositional matrix adjust.	84/340(25%)	151/340(44%)	36/340(10%)	-2
Features	S :					
Query	980	TVVPISAITQNEITTTATPPIPRG T +P+ I +N + PI G	GSMEAALALL- S + L+LL		AVTGNVIEG TG + E	K 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MG				т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O			OHPAVI A	
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPG				
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	ELLMAAAD-RI + A + +I			G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++			RENYLIQGVDL + + G D	
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPK				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLD EW+ N YRGPS OK + TG +		IREPIPRSDNS' I++PI + ++	PPELVMRIIRN + R+ +	
Sbjct	835	TPEWVALNNYRGPSPGÕFKYYLITGRE				
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	GNRGLNQYQVI G RG +Q O+-			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQN				

polyprotein [Victorian trout aquabirnavirus]

Sequence ID: **gb|ALF95289.1|** Length: 972 Number of Matches: 1 Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.7 bits	s(182)	3e-11() Compositional matrix adjust.	80/317(25%)	134/317(42%)	38/317(11%)	-2
Feature	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG				
Sbjct	631	G S + L+LL I GV TG GPSCQLGLSLLVNDIEEGVPRMVFTGI			G+PLV Q HEHGLPLVGCQ	
Query	740	YKTIKDLAKATEMLQRITTAQHPAVIO E++ + A H		pppppPI	TDEDI.	
Sbjct	690	PGVDEVVANTSLASHLIQTO	•	•		
Query	590	VTLEELLMAAAD-RDPRMAKLKEVVLV		VLDTLHNFSRQ + D L +SR+		
Sbjct	743	L+ + A + +D + KL +++ W GLLQATMARAKEVKDVEIFKLLKLMSW				
Query	413	NSLTTAVHSRGPTQDVLQHQRAVRIRI +GP O O +AVRI		SIEWIKNNGYR S EW+ +NGYR		
Sbjct	798	TPPKHQEKPKGPDQHTAQEAKAVRISI				
Query	239	TGLDPAPQTIIREPIPRSDNSTI	PELVMRIIRNS + + R+ +	LSAHYENASPE ++ +PE		
Sbjct	858	TGEVPNPGDDYEDYVRKPITRPTNM				
Query	71	VINNGNRGLNQYQVKEI 21				
Sbjct	913	N RG +Q Q++++ FATNSGRGPDQDQMQDL 929				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AEM92169.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.7 bits	s(182)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO T +P+ I +N + PI O				K 819
Sbjct	606	T +P+ I +N + PI O TALPLKEIKRNGNIVVEKIFAGPI-MO	S		TG + E VFTGEIADDEE'	г 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	YKTIKDLAK + +++ +		~	G 660
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPO				K 724
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	EELLMAAAD-R + A + +;			G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++		DVLQHQRAVRII O RA RI		
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPP				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLI EW+ N YRGPS Q K + TG +		IREPIPRSDNS' I++PI + +	rpelvmriirn: + R+ +	S 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRE				V 892
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	NGNRGLNQYQV NG RG +0 0+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQN				

Sequence ID: gb|AAQ75363.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.7 bits	s(182)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%) -	-2
Feature	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				K 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S		TG + E VFTGEIADDEET	Г 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q			QHPAVIC	G 660
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPG				X 724
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	EELLMAAAD-R + A + +	DPRMAKLKEVV D + KL +++		G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++			RENYLIQGVDLS + + G D -	
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPK				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLD EW+ N YRGPS Q K + TG +	PAPQTI	IREPIPRSDNS I++PI + +	TPELVMRIIRNS + R+ +	3 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRE				V 892
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	IGNRGLNQYQV IG RG +0 0+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQN				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAK32154.1|AF342728_1** Length: 968 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.7 bits	(182)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%) -	-2
Features	S :					
Query	980	TVVPISAITQNEITTTATPPIPRO T +P+ I +N + PI O	GGSMEAALALL G S + L+LL		AVTGNVIEGI TG + E	819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MO				664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q		ATEMLQRITTA(A ++Q T	OHPAVIC	660
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQP				724
Query	659	TIATAMDSDSpppppPITDEDIMVTLI + M S++ DE++ L				483
Sbjct	725	YLGELMASNASGMDEELQRLLI				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSL			RENYLIQGVDLS + + G D -	
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPP			_	
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLI EW+ N YRGPS Q K + TG -		IREPIPRSDNS' I++PI + +	PELVMRIIRNS + R+ +	5 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGR				7 892
Query	140	LSAHYENASPETQKEINERVTTMVINI ++ +PE E + V + 1	NGNRGLNQYQV NG RG +0 0+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQI				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAX24140.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Feature	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO	GGSMEAALALL GS+L+LL		AVTGNVIEG TG + E	K 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MO				т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O		ATEMLQRITTA A ++Q T	OHPAVI A	G 660
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPO				K 724
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	EELLMAAAD-R + A + +			G 483
Sbjct	725	YLGELMASNASGMDEELQRLL				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++	TTAVHSRGPTQ +GP Q		RENYLIQGVDL + + G D	

```
Sbjct 775 LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA 834
                     I-EWIKNNGYRGPSAEQMK-VIKTGLDPAP---QTIIREPIPRSDNSTPELVMRIIRNS 141
EW+ N YRGPS Q K + TG +P P + I++PI + + R+ +
TPEWVALNNYRGPSPGQFKYYLITGREPEPGDEYEDYIKQPIVKPTDMNK--IRRLANSV 892
Query 302
Sbjct
            835
Query 140 LSAHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEI ++ +PE E + V + NG RG +Q Q++++ Sbjct 893 YGLPHQEPAPE---EFYDAVAAVFAQNGGRGPDQDQMQDL
```

107 kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAQ75357.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%) -	2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				819
Sbjct	606	T +P+ I +N + PI (TALPLKEIKRNGNIVVEKIFAGPI-M	G S + L+LL GPSAQLGLSLL		TG + E VFTGEIADDEET	664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q		ATEMLQRITTA A ++Q T	QHPAVIC A I	660
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPO				724
Query	659	TIATAMDSDSpppppPITDEDIMVTLI + M S++ DE++ L				483
Sbjct	725	YLGELMASNASGMDEELQRLLI	·			- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++				
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPI	- E			
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLI EW+ N YRGPS OK + TG -			TPELVMRIIRNS + R+ +	3 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRI				892
Query	140	LSAHYENASPETQKEINERVTTMVINI ++ +PE E + V + I	NGNRGLNQYQV NG RG +0 O+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQI				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AEM92165.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Features	3 :					
Query	980	TVVPISAITQNEITTTATPPIPRG T +P+ I +N + PI G				к 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL SPSAQLGLSLL		TG + E VFTGEIADDEE	т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O		ATEMLQRITTA(A ++Q T		
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPG				
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	ELLMAAAD-R + A + +			G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++		DVLQHQRAVRII O RA RI		
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPK				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLD EW+ N YRGPS Q K + TG +			PELVMRIIRN + R+ +	
Sbjct	835	TPEWVALNNYRGPSPGÕFKYYLITGRE				
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N				
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQN				

RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; Contains: RecName: Full=Structural peptide 2; Short=p2; Contains: RecName: Full=Structural peptide 3; Short=p3; Contains: RecName: Full=Protease VP4; AltName: Full=Non-structural protein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP3

Sequence ID: sp|Q703G9.1|POLS_IPNVS Length: 972 Number of Matches: 1

▶ See 1 more title(s) Range 1: 606 to 929

Score	Expect Method	Identities	Positives	Gaps	Frame

74.3 bits(181) 4e-11() Compositional matrix adjust. 84/340(25%) 150/340(44%) 36/340(10%) -2

Features: TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK Query 980 819 + T + P + I + NTG + PI GS + L+LL I GV Sbjct 606 TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET 664 IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV----IG 818 660 Query $G+PL++\tilde{Q}$ + +++ A $++\tilde{Q}$ T IIPICGVDIKAIAAHEQGLPLIGNÕPGVDEEVRNTSLAAHLIÕTGTLPVQRAKGSNKRIK 724 Sbjct 665 Query 659 $\verb|TIATAMDSDS|| pppp| \verb|PITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG| \\$ 483 + M S++ DE++ L + A + +D + KL +++ W K D YLGELMASNASGM----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND----725 774 Sbjct VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS 303 Query 482 +GP Q Q RA RI + + G D ++ D ++ +S++D + K +++ 775 LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA Sbjct 834 I-EWIKNNGYRGPSAEQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNS EW+ N YRGPS Q K + TG +P P + I++PI + + R+ + 141Query 302 TPEWVALNNYRGPSPGQFKYYLITGREPEPGDEYEDYIKQPIVKPTDMNK--IRRLANSV 892 Sbjct 835 LSAHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEI ++ +PE E + V + NG RG +Q Q++++ YGLPHQEPAPE---EFYDAVAAVFAQNGGRGPDQDQMQDL 140 Query Sbjct 893

polyprotein [Paralichthys olivaceus birnavirus]

Sequence ID: ref|YP_001514404.1| Length: 972 Number of Matches: 1

▶ See 1 more title(s) Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	80/311(26%)	133/311(42%)	26/311(8%) -	2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN				741
Sbjct	631	G S + L+LL I GV TG GPSCQLGLSLLVNDIDKGVPRMVFTGE		++K CGVNIKAIAAH	G+PLV Q EHGLPLVGCQ-	- 689
Query	740	YKTIKDLAKATEMLQRITTAQHPAVIO	GTIATAMDSDSp T +	PPPPPITDEDI T +		A 561
Sbjct	690	-PGVDEVVANTSLASHLIQSGALPVQF				748
Query	560	ADRDPRMAKLKEVVLWLAKIDI R D + KL +++ W K			NRIVQNSLTTA	A 396
Sbjct	749	MARAKEVKDAEVFKLLKLMSWTRK				803
Query	395	VHSRGPTQDVLQHQRAVRIRENYLIQO +GP Q Q +AVRI + + O				A 222
Sbjct	804	EKPKGPDÕHTAÕEAKAVRISLDAVKA				863
Query	221	PQTIIREPIPRSDNSTPELVMRI P+ +R+PI R + + + R+			RVTTMVINNGN V + NG	1 54
Sbjct	864	PRDEYDDYVRKPITRPTDMDKIRRI				918
Query	53	RGLNQYQVKEI 21 RG +Q Q++++				
Sbjct	919	RGPDÕEÕMQDL 929				

107 kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAQ75350.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRG T +P+ I +N + PI G	GSMEAALALL S + L+LL		AVTGNVIEG	к 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MG				т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	KTIKDLAK		OHPAVIO	
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPG				
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	ELLMAAAD-RI + A + +			G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++		DVLQHQRAVRII Q RA RI		
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPK				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLD EW+ N YRGPS Q K + TG +		IREPIPRSDNS' I++PI + +	PELVMRIIRN: + R+ +	S 141
Sbjct	835	TPEWVALNNYRGPSPGÕFKYYLITGRE	PEPGDEYEDY			V 892
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	GNRGLNQYQVI G RG +Q Q+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQN				

Sequence ID: gb|AAD11535.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps F	rame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%) -2	
Features	3 :					
Query	980	TVVPISAITQNEITTTATPPIPRO T +P+ I +N + PI O	GGSMEAALALL G S + L+LL	-QHIPPGVTPF		819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MO				664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	YKTIKDLAK + +++ +		QHPAVIG A	660
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPO				724
Query	659	TIATAMDSDSpppppPITDEDIMVTLI + M S++ DE++ L	EELLMAAAD-R + A + +			483
Sbjct	725	YLGELMASNASGMDEELQRLLI				774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++				303
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPI				834
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLI EW+ N YRGPS OK + TG -		IREPIPRSDNS	TPELVMRIIRNS + R+ +	141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRI				892
Query	140	LSAHYENASPETQKEINERVTTMVINI ++ +PE E + V + 1				
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQI				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|ABF69695.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO T +P+ I +N + PI O	GSMEAALALL SS+L+LL		AVTGNVIEG TG + E	K 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MO				т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O			OHPAVI A	
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPO				
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	EELLMAAAD-R	DPRMAKLKEVVI D + KL +++		G 483
Sbjct	725	YLGELMASNASGMDEELQRLL				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++		DVLQHQRAVRII O RA RI		
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPP				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLI EW+ N YRGPS Q K + TG -			TPELVMRIIRN + R+ +	
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRE				
Query	140	LSAHYENASPETQKEINERVTTMVIND ++ +PE E + V + D	NGNRGLNQYQV NG RG +Q Q+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQI				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AEM92170.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Features	S :					
Query	980	TVVPISAITQNEITTTATPPIPRO	GGSMEAALALL G S + L+LL		AVTGNVIEG	K 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MO				г 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O		ATEMLORITTA A ++O T	OHPAVIO	G 660
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPO				K 724
Query	659	TIATAMDSDSpppppPITDEDIMVTLI + M S++ DE++ L				G 483
Sbjct	725	YLGELMASNASGMDEELQRLLI				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSL' + D ++ +S++D + K +++			RENYLIQGVDL: + + G D	
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPI				

```
Query 302 I-EWIKNNGYRGPSAEQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNS 141
EW+ N YRGPS Q K + TG +P P + I++PI + + R+ +
Sbjct 835 TPEWVALNNYRGPSPGQFKYYLITGREPEPGDEYEDYIKQPIVKPTDMNK--IRRLANSV 892

Query 140 LSAHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21
++ +PE E + V + NG RG +Q Q++++
Sbjct 893 YGLPHQEPAPE---EFYDAVAAVFAQNGGRGPDQDQMQDL 929
```

Sequence ID: gb|AAR10449.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%) -	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO T +P+ I +N + PI O			AVTGNVIEGF TG + E	819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MO	G S + L+LL GPSAQLGLSLL			664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O			OHPAVIO A	660
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPO				724
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	EELLMAAAD-R + A + +			483
Sbjct	725	YLGELMASNASGMDEELQRLL				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++			RENYLIQGVDLS + + G D +	
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPP				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLI EW+ N YRGPS Q K + TG -			TPELVMRIIRNS + R+ +	3 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRI				7 892
Query	140	LSAHYENASPETQKEINERVTTMVIND ++ +PE E + V + D	NGNRGLNQYQV NG RG +0 0+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQI				

107 kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAQ75352.1| Length: 972 Number of Matches: 1

▶ See 2 more title(s) Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	4e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Feature	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				к 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL SPSAQLGLSLL		TG + E /FTGEIADDEE'	т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	KTIKDLAK		OHPAVIO	
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPG				
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L				G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++		DVLQHQRAVRII Q RA RI		
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPK				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLD EW+ N YRGPS Q K + TG +			PELVMRIIRN: + R+ +	S 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRE			· · · · · · · · · · · · · · · · · ·	V 892
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N				
Sbjct	893	++ +PE E + V + N YGLPHQEPAPEEFYDAVAAVFAQN	IG RG +Q Q+ IGGRGPDQDQM			

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAH25439.1| Length: 949 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame	
74.3 bits(181) 5	5e-11()	Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2	-
Features:								
Query	980	TVVPI	SAITQNEITTTATPPIPRG	GSMEAALALL- S + L+LL		VTGNVIEG	K 819)
Sbjct	606		KEİKRNGNIVVEKIFAGPİ-MĞ			- · -	т 664	Į

Query	818	IVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQHPAVIG I+P D+K G+PL+ +O + +++ + A ++O T A I	660
Sbjct	665		724
Query	659	TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG + M S++ DE++ L + A + +D + KL +++ W K D	483
Sbjct	725	YLGELMASNASGMDEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND	774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS + D ++ +S++D + K +++ +GP Q Q RA RI + + G D +	303
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA	834
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLDPAPQTIIREPIPRSDNSTPELVMRIIRNS EW+ N YRGPS Q K + TG +P P + I++PI + + + R+ +	141
Sbjct	835		892
Query	140	LSAHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21	
Sbjct	893	++ +PE E + V + NG RG +Q Q++++ YGLPHQEPAPEEFYDAVAAVFAQNGGRGPDQDQMQDL 929	

Sequence ID: gb|AAR10452.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	5e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%) -	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				K 819
Sbjct	606	T +P+ I +N + PI (TALPLKEIKRNGNIVVEKIFAGPI-M(S S + L+LL SPSAQLGLSLL		TG + E VFTGEIADDEE	г 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q		ATEMLQRITTA(A ++O T	QHPAVIO A	
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPO				
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	EELLMAAAD-R + A + +			G 483
Sbjct	725	YLGELMASNASGMDEELQRLL				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++	TTAVHSRGPTQ +GP Ö			
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPP				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLI EW+ N YRGPS OK + TG +		IREPIPRSDNS' I++PI + +	PELVMRIIRNS + R+ +	S 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRE			· · · · · · · · · · · · · · · · ·	V 892
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	NGNRGLNQYQV NG RG +0 0+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQI				

RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; Contains: RecName: Full=Structural peptide 2; Short=p2; Contains: RecName: Full=Structural peptide 3; Short=p3; Contains: RecName: Full=Protease VP4; AltName: Full=Non-structural protein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP3
Sequence ID: sp|P22495.1|POLS_IPNVN Length: 972 Number of Matches: 1

▶ See 1 more title(s) Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	(181)	5e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
Features	3 :					
Query	980	TVVPISAITQNEITTTATPPIPRG				K 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL SPSAQLGLSLL		TG + E VFTGEIADDEE'	г 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +Q			QHPAVIO	G 660
Sbjct	665	IIPICGVDIKAIAAHEPGLPLIGNQPG				K 724
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L		DPRMAKLKEVVI D + KL +++		G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++	TAVHSRGPTQ +GP O			
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPK				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLD EW+ N YRGPS Q K + TG +			TPELVMRIIRN: + R+ +	S 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRE				V 892
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	IGNRGLNQYQVI IG RG +O O+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQN				

Sequence ID: **gb|AAK32160.1|AF342734_1** Length: 968 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	5e-11() Compositional matrix adjust.	83/335(25%)	146/335(43%)	26/335(7%)	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRG T +P+ I +N + PI G	GSMEAALALL- S + L+LL	-QHIPPGVTPFA I GV	VTGNVIEGK- TG + E +	- 819
Sbjct	606	TALPLKEIKKNGNIIVEKIFAGPI-MG				T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O			HPAVIGTIAT A +	'A 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕPG				K 724
Query	644	MDSDSpppppPITDEDIMVTLEELLM- + DE++ L +	AAADRDPRMAK A A +D + K			
Sbjct	725	YLGELMQTTASGMDEELQSLLAATMAR				
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +SR+D + K +++		RAVRIRENYLI +A+RI + +		
Sbjct	780	YEWSREDPDAIKFGKLISTPPKHPEKP				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS Q K + TG P P				Y 126
Sbjct	840	AENHYRGPSPGQFKYYMITGETPEPGE				
Query	125	ENASPETQKEINERVTTMVINNGNRGL + +PE E V + +NG RG	NQYQVKEI 2	21		
Sbjct	898	QEPAPEPFYEAVAAVFTDNGGRGP		29		

108-kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAR10446.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

	p = 31 = 1110.	-		Identities	Positives	Gaps	Frame
31) 5e-	-11() Compo	sitional ma	trix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2
							к 819
_		- •					т 664
							G 483
							- 774
)2 I-	-EWIKNNGY	RGPSAEOMI	K-VIKTGLE	PAPQTI	IREPIPRSDNS		
35 ті							
40 L							
93 Y							
	31) 5e- 80 T 06 T 18 I 59 T 25 Y 82 V 75 L 02 I 35 T 40 L	31) 5e-11() Composition 80 TVVPISAITQ T +P+ I + 06 TALPLKEIKE 18 IVPNKWADLK I+P D+K 65 IIPICGVDIK 59 TIATAMDSDS + M S++ 25 YLGELMASNA 82 VLDTLHNFSR + D ++ +S+ 75 LTDHMYEWSK 02 I-EWIKNNGY EW+ N Y 35 TPEWVALNNY 40 LSAHYENASP ++ +P	31) 5e-11() Compositional mass and selection and selection and selection and selection and selection and selection and selection and selection are selected as a selection and selection are selected as a selection and selection are selected as a selection and selection are selected as a selection and selection are selected as a selection	TVVPISAITQNEITTTATPPIPROT T +P+ I +N + PI O TALPLKEIKRNGNIVVEKIFAGPI-MO IN D+K G+PL+ +Q IIPICGVDIKAIAAHEQGLPLIGNQPO TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L YLGELMASNASGMDEELQRLLN VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++ TTDHMYEWSKEDPDALKFGKLISTPPRO I-EWIKNNGYRGPSAEQMK-VIKTGLE EW+ N YRGPS Q K + TG + TPEWVALNNYRGPSPGQFKYYLITGRE LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	31) 5e-11() Compositional matrix adjust. 84/340(25%) 80 TVVPISAITQNEITTTATPPIPRGSMEAALALL T +P+ I +N + PI G S + L+LL 06 TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLL 18 IVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAK I+P D+K G+PL+ +Q + +++ + + 65 IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSL 59 TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-R + M S++ DE++ L + A + + 25 YLGELMASNASGMDEELQRLLNATMARAKEVQ 82 VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQ + D ++ +S++D + K +++ +GP Q 75 LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQ 102 I-EWIKNNGYRGPSAEQMK-VIKTGLDPAPQTI EW+ N YRGPS Q K + TG +P P + 35 TPEWVALNNYRGPSPGQFKYYLITGREPEPGDEYEDY 40 LSAHYENASPETQKEINERVTTMVINNGNRGLNQYQV ++ +PE E + V + NG RG +Q Q+	31) 5e-11() Compositional matrix adjust. 84/340(25%) 150/340(44%) 80 TVVPISAITQNEITTTATPPIPRGGSMEAALALL-QHIPPGVTPFA T +P+ I +N + PI G S + L+LL I GV 80 TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRM 81 IVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAG 1 +P D+K G+PL+ +Q + +++ + A ++Q T 82 IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLP 83 TIATAMDSDSpppppPPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVI 1 + M S++ DE++ L + A + +D + KL +++ 84 VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRII 1 + D ++ +S++D + K +++ +GP Q Q RA RI 1 + CTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRIS 84 VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRII 1 + LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRIS 85 TPEWVALNNYRGPSAEQMK-VIKTGLDPAPQTIIREPIPRSDNS 1 EW+ N YRGPS Q K + TG +P P + I++PI + + 85 TPEWVALNNYRGPSPGQFKYYLITGREPEPGDEYEDYIKQPIVKPTDM 86 TVVPISAITQNEITTTATPPIPRGGSMEAALALL-QHIPPGVTPF 87 TO AND AND AND AND AND AND AND AND AND AND	31) 5e-11() Compositional matrix adjust. 84/340(25%) 150/340(44%) 36/340(10%) 80 TVVPISAITQNEITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEGT+P+ I +N + PI GS + L+LL I GV TG + ETHPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRNVFTGEIADDEE 18 IVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQHPAVI HP D+K G+PL++Q + +++ A ++Q T A IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRI 59 TIATAMDSDSpppppPPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNP + M S++ DE++ L + A ++D + KL +++ W K D YLGELMASNASGMDEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND 82 VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL + D ++ +S++D + K +++ +GP Q Q RA RI ++ G D LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADF 102 I-EWIKNNGYRGPSAEQMK-VIKTGLDPAPQTIIREPIPRSDNSTPELVMRIIRN EW+ N YRGPS Q K + TG +P P + I++PI + + R+ + R+ + TPEWVALNNYRGPSPGQFKYYLITGREPEPGDEYEDYIKQPIVKPTDMYKIRRLANS 40 LSAHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEI 21 ++ +PE E + V + NG RG +Q Q++++

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|ABP93671.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
73.9 bits	s(180)	6e-11() Compositional matrix adjust.	84/340(25%)	149/340(43%)	36/340(10%)	-2
Features	S :					
Query	980	TVVPISAITQNEITTTATPPIPROT +P+ I +N + PI	GGSMEAALALL G S + L+LL		AVTGNVIEGI TG + E	K 819
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-M				т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQD	YKTIKDLAK + +++ +		OHPAVIQ A	
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNÕP				
Query	659	TIATAMDSDSpppppPITDEDIMVTL: + M S++ DE++ L				G 483
Sbjct	725	YLGELMASNASGMDEELQRLL				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSL' + D ++ +S++D + K +++				
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPP	~			
Query	302	I-EWIKNNGYRGPSAEQMKV-IKTGL	DPAPQTI	IREPIPRSDNS'	rpelvmriirn:	S 141

Sequence ID: gb|AEM92168.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
73.9 bits	s(180)	6e-11() Compositional matrix adjust.	84/340(25%)	150/340(44%) 36/340(10%)	-2
Features	S :					
Query	980	TVVPISAITQNEITTTATPPIPRG T +P+ I +N + PI G				K 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKRNGNIVVEKIFAGPI-MG	S + L+LL SPSAQLGLSLL		TG + E IVFTGEIADDEE'	т 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	KTIKDLAK + +++ +		QHPAVIQ	
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPG				
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L				G 483
Sbjct	725	YLGELMASNASGMDEELQRLLN				- 774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++			RENYLIQGVDL	
Sbjct	775	LTDHMYEWSKEDPBALKFGKLISTPPK				
Query	302	I-EWIKNNGYRGPSAEQMKV-IKTGLD EW+ N YRGPS OK + TG +		IREPIPRSDNS I++PI + +	TPELVMRIIRN: + R+ +	S 141
Sbjct	835	TPEWVALNNYRGPSPGÕFKYXLITGRE			··	V 892
Query	140	LSAHYENASPETQKEINERVTTMVINN ++ +PE E + V + N	IGNRGLNQYQV IG RG +O O+			
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQN				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAK32159.1|AF342733_1 Length: 968 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
73.9 bits	s(180)	6e-11() Compositional matrix adjust.	83/335(25%)	144/335(42%)	26/335(7%)	-2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRG				- 819
Sbjct	606	T +P+ I +N + PI G TALPLKEIKKNGNIIVEKIFAGPI-MG	; S + L+LL ;PSAQLGLSLL\		TG + E + FTGEIAEDEE	T 664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P D+K G+PL+ +O	KTIKDLAKA + +K + A		HPAVIGTIAT	'A 645
Sbjct	665	IIPICGVDIKAIAAHEQGLPLIGNQPG				K 724
Query	644	MDSDSpppppPITDEDIMVTLEELLM- + DE++ L +		KLKEVVLWLAKI KL ++ W K		
Sbjct	725	YLGELMQTTASGMDEELQNLLAATMAR				
Query	467	HNFSRQDVEGEKMNRIVQNSLTTAVHS + +SR+D + K +++		QRAVRIRENYLI +A+RI + +		
Sbjct	780	YEWSREDPDAIKFGKLISTPPKHPEKP				
Query	290	KNNGYRGPSAEQMK-VIKTGLDPAP N YRGPS O K + TG P P			RIIRNSLSAH R+ +	Y 126
Sbjct	840	AENHYRGPSPGQFKYYMITGEAPEPGE				
Query	125	ENASPETQKEINERVTTMVINNGNRGL + +PE E V + NG RG		21		
Sbjct	898	QEPAPEPFYEAVAAVFAENGGRGP		929		

capsid protein VP3 [Flounder aquabirnavirus DS]

Sequence ID: gb|AAQ82706.1| Length: 224 Number of Matches: 1

Range 1: 8 to 181

Score		Expect Method	Identities	Positives	Gaps	Frame	
70.9 bits	s(172)	8e-11() Compositional matrix adjust.	51/184(28%)	89/184(48%)	16/184(8%)	-2	
Features	s:						
Query	554	RDPRMAKLKEVVLWLAKIDDNNPGVLD +D + KL +++ W K G+ D	TLHNFSRQDVE		LTTAVHSRGE +GF		
Sbjct	8	KDAEVFKLLKLMSWTRKNGLTD			. 0-		
Query	374	QDVLQHQRAVRIRENYLIQGVDL-SIE Q Q +AVRI + + G D S +				-т 213	
Sbjct	63	QHTAQEAKAVRISLDAVKAGADFASPD				DD 122	

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Query 212 IIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRGLNQYQ 33 +R+PI R + + + R+ + + + +PE E + V + NG RG +Q Q Sbjct 123 YVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGGRGPDQEQ 177

Query 32 VKEI 21 ++++ Sbjct 178 MQDL 181
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Sequence ID: emb|CAD32971.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
73.6 bits	s(179)	9e-11() Compositional matrix adjust.	84/340(25%)	149/340(43%)	36/340(10%) -	2
Features	s:					
Query	980	TVVPISAITQNEITTTATPPIPRO				819
Sbjct	606	T +P+ I +N + PI (TALPLKEIKRNGNIVVEKIFAGPI-M	G S + L+LL GPSAQLGLSLL		TG + E VFTGEIADDEET	664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I P D+K G+PL+ +Q		ATEMLQRITTA A ++Q T	OHPAVIC A	660
Sbjct	665	ITPICGVDIKAIAAHEQGLPLIGNQPO				724
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	EELLMAAAD-R + A + +			483
Sbjct	725	YLGELMASNASGMDEELQRLL				774
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++	TTAVHSRGPTQ +GP Ö	~ ~		
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPP				
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLI EW+ N YRGPS Ö K + TG -			PELVMRIIRNS + R+ +	3 141
Sbjct	835	TPEWVALNNYRGPSPGQFKYYLITGRE				892
Query	140	LSAHYENASPETQKEINERVTTMVIND ++ +PE E + V + D				
Sbjct	893	YGLPHQEPAPEEFYDAVAAVFAQI				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: emb|CAD32964.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score	Expect Method	Identities	Positives	Gaps	Frame
73.2 bits(178)	1e-10() Compositional matrix adjust.	78/314(25%)	139/314(44%)	32/314(10%)	-2
Features:					
Query 911	GGSMEAALALL-QHIPPGVTPFAVTG G S + L+LL I GV TG			KGTGIPLVTDQ G+PL+ +O	
Sbjct 631	G S + L+LL I GV TG $GPSAQLGLSLLVNDIEDGVPRMVFTGI$				
Query 740	YKTIKDLAKATEMLQRITTAQHPAY + +++ + A ++O T A			PITDEDIMVT DE++	
Sbjct 691	GVDEEVRNTSLAAHLIQTGTLPVQRA				_
Query 581	EELLMAAAD-RDPRMAKLKEVVLWLAI + A + +D + KL ++ W 1		TLHNFSRQDVE	GEKMNRIVQNS K +++	L 405
Sbjct 746	NATMARAKEVQDAEIYKLLRLMAWTRI				P 800
Query 404	TTAVHSRGPTQDVLQHQRAVRIRENYI +GP Q Q RA RI + -				
Sbjct 801	KHPEKPKGPDQYHAQEARATRISLDA				
Query 230	DPAPQTIIREPIPRSDNSTPELY	VMRIIRNSLSA + R+ +		EINERVTTMVI E + V +	N 63
Sbjct 861	EPEPGDEYEDYIKQPIVKPTDMNK				Q 915
Query 62	NGNRGLNQYQVKEI 21 NG RG +Q Q++++				
Sbjct 916	NGGRGPDÕDÕMQDL 929				

107 kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAQ75364.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Fran	ne
73.2 bits((178) <i>-</i>	1e-10() Compositional matrix adjust.	84/340(25%)	149/340(43%)	36/340(10%)	-2	
Features:							
Query	980	~		~		K	819
Sbjct	606					Т	664
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY	KTIKDLAK	ATEMLQRITTAÇ	HPAVI	G	660
	Features: Query Sbjct	73.2 bits(178) Features: Query 980 Sbjct 606	73.2 bits(178) 1e-10() Compositional matrix adjust. Features: Query 980 TVVPISAITQNEITTTATPPIPRG T +P+ I +N + PI G Sbjct 606 TALPLKEIKRNGNIVVEKIFAGPI-MG	73.2 bits(178) 1e-10() Compositional matrix adjust. 84/340(25%) Features: Query 980 TVVPISAITQNEITTTATPPIPRGGSMEAALALL- T +P+ I +N + PI G S + L+LL Sbjct 606 TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLL	73.2 bits(178) 1e-10() Compositional matrix adjust. 84/340(25%) 149/340(43%) Features: Query 980 TVVPISAITQNEITTTATPPIPRGGSMEAALALL-QHIPPGVTPFA T +P+ I +N + PI G S + L+LL I GV Sbjct 606 TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMV	73.2 bits(178) 1e-10() Compositional matrix adjust. 84/340(25%) 149/340(43%) 36/340(10%) Features: Query 980 TVVPISAITQNEITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEG	73.2 bits(178) 1e-10() Compositional matrix adjust. 84/340(25%) 149/340(43%) 36/340(10%) -2 Features: Query 980 TVVPISAITONEITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEGK

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I+P
                           D+K
                                         G+PL+ +Q
                                                           + +++ + A ++Q T
Sbjct 665
                IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK
                                                                                                         724
                TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG + M S++ DE++ L + A + +D + KL +++ W K D
Query
                                                                                                           483
                YLGELMASNASGM----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND----
Sbjct
         725
                                                                                                           774
         VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS + D ++ +S++D K +++ +GP Q Q RA RI + + G D + TTDHMYEWSKEDPYALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA
                                                                                                           303
Query
Sbjct
                                                                                                           834
                I-EWIKNNGYRGPSAEQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNS
EW+ N YRGPS Q K + TG +P P + I++PI + + + R+ +
TPEWVALNNYRGPSPGQFKYYLITGREPEPGDEYEDYIKQPIVKPTDMNK--IRRLANSV
Query
         302
Sbjct
        835
                                                                                                           892
        140 LSAHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEI
Query
                       ++ +PE \tilde{E} + V + NG RG +\tilde{Q} \tilde{Q}++++
Sbjct 893
                YGLPHQEPAPE---EFYDAVAAVFAQNGGRGPDQDQMQDL
```

Sequence ID: gb|AAK32161.1|AF342735_1 Length: 968 Number of Matches: 1

Range 1: 631 to 929

%) -2
TDQD 741
Q GCQ- 689
EDIM 591
EELQ 742
RIVQ 414 R++
RLIS 797
-VIK 240
YYMI 857
7TTM 72
VEV 912

107 kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAQ75348.1| Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score	Exp	ect	Method		Identities	Positives	Gaps	Frame
72.8 bits(1	77) 1e-1	10() (Compositiona	ıl matrix adjust.	84/340(25%)	149/340(43%)	36/340(10%)	-2
Features:								
Query 9			_	ITTTATPPIPRO				K 819
Sbjct 6	_			+ PI (VEKIFAGPI-M	G S + L+LL GPSAQLGLSLL		TG + E VFTGEIADDEE	T 664
Query 8	18 IV I+		VADLKREGMK D+K	GTGIPLVTDQDY G+PL+ +0			OHPAVI A	
Sbjct 6		_		EQGLPLIGNQPO				
Query 6	59 TI +		MDSDSppppp M S++	PITDEDIMVTLI DE++ L				PG 483
Sbjct 7				DEELQRLLI				- 774
Query 4				EKMNRIVQNSL' K +++		DVLQHQRAVRII Q RA RI		
Sbjct 7		_		LKFGKLISTPPI				
Query 3		-EWIF EW+		EQMK-VIKTGLI ÕK + TG -		IREPIPRSDNS' I++PI + +	PELVMRIIR + R+ +	
Sbjct 8				GĞFKYYLITĞRI				
Query 1	40 LS			INERVTTMVINI + V + I	NGNRGLNQYQVI NG RG +Q Q+			
Sbjct 8	93 YG			FYDAVAAVFAQI				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAV48858.3| Length: 980 Number of Matches: 1

Range 1: 631 to 929

Score Expect Method Identities Positives Gaps Frame

72.0 bits(175) 3e-10() Compositional matrix adjust. 75/317(24%) 134/317(42%) 38/317(11%) -2						
Features:						
Query 911 GGSMEAALALL-QHIPPGVTPFAVTGNVIEGKIVPNKWADLKREGMKGTGIPLVTDQD 7-G S + AL+LL I G+ TG + E ++P D+K G+PL+ Q	41					
	89					
~ ~	91					
	42					
	14					
L+ + A + +D + KL +++ W K D + D ++ +S++D + K R++ Sbjct 743 GLLQATMARAKEVKDAEVFKLLKLMSWTRKNDLTDHMYEWSKEDPDANKFGRLIS 7	97					
	40					
+GP Q Q +A RI + + G D S EWI N YRGP+ Q K + Sbjct 798 TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAPGQFKYYMI 8	57					
Query 239 TGLDPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM 7	2					
TG P P + +R+PI R + + + R+ + + + +P+ + + V + Sbjct 858 TGRVPNPGEEYEDYVRKPITRPTDMDKIRRLANSVYGLPHQEPAPDDFYQAVVEV 9	12					
Query 71 VINNGNRGLNQYQVKEI 21						
NG RG +Q Q++++ Sbjct 913 FAENGGRGPDQDQMQDL 929						

Sequence ID: dbj|BAA05532.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
71.6 bits	s(174)	4e-10() Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG G S + AL+LL I G+ TG			KGTGIPLVTDQ G+PL+ Õ	D 741
Sbjct	631	G S + AL+LL I G+ TG GPSSQLALSLLVNDIDEGIPRMVFTG				P 690
Query	740	YKTIKDLAKATEMLQRITTA(+ + + + A+ ++Q	OHPA	-VIGTIATAMD: ++ T A+ MD-	SDSpppppPIT	D 603
Sbjct	691	GVDEMVANTSLASHLIÕSGALPVQKA				- 740
Query	602	EDIMVTLEELLMAAADRDPRM L+ LL A R D +	AKLKEVVLWLA KL +++ W		TLHNFSRQDVE ++ +S++D +	
Sbjct	741	LQGLLQATMARAKEVKDAEV				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQI K R++ +GP O O	HQRAVRIRENY +A RI +			A 261
Sbjct	790	IKFGRLISTPPKHQEKPKGPDÕHTAÕ				P 849
Query	260	EQMK-VIKTGLDPAPQTIIREP		VMRIIRNSLSAI + R+ +	HYENASPETQK ++ +P+	E 96
Sbjct	850	GÕFKYYMITGRVPNPGEEYEDYVRKP			· · · · · · · · · · · · · · · · · · ·	D 904
Query	95	INERVTTMVINNGNRGLNQYQVKEI + V + NG RG +Q Q++++	21			
Sbjct	905	FYQAVVEVFAENGGRĞPDÖDÖMQDL	929			

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: ref|NP_047196.1| Length: 972 Number of Matches: 1

▶ See 2 more title(s) Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
71.2 bits	s(173)	5e-10() Compositional matrix adjust.	81/325(25%)	141/325(43%)	54/325(16%)	-2
Feature	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG				
Sbjct	631	G S + AL+LL I G+ TG GPSSQLALSLLVNDIDEGIPRMVFTGI			G+PL+ Q HEHGLPLIGCQ	
Query	740	YKTIKDLAKATEMLQRITTA(D 603
Sbjct	691	+ + + + A+ ++Q + A(GVDEMVANTSLASHLIQGGALPVQKA(Q GACRRIKYLG	++ T A+ MD QLMRTTASGMD		- 740
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +	AKLKEVVLWLA KL +++ W		TLHNFSRQDVE ++ +S++D +	
Sbjct	741	LQGLLQATMARAKEVKDAEVI				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQI K R+V +GP O O		LIQGVDL-SIE' + G D S E'		
Sbjct	790	IKFGRLVSTPPKHQEKPKGPDÕHTAÕI				
Query	260	EQMK-VIKTGLDPAPQTIIREPT Q K + TG P P + +R+PT		VMRIIRNSLSA + R+ +		E 96
Sbjct	850	GÕFKYYMITGRVPNPGEEYEDYVRKP				
Query	95	<pre>INERVTTMVINNGNRGLNQYQVKEI + V + NG RG +Q Q++++</pre>	21			
Sbjct	905	FYQAVVEVFAENGGRGPDQDQMQDL	929			

Sequence ID: **gb|AAK32164.1|AF343572_1** Length: 968 Number of Matches: 1 Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
71.2 bits	s(173)	5e-10() Compositional matrix adjust.	81/325(25%)	141/325(43%)	54/325(16%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGI G S + AL+LL I G+ TG			KGTGIPLVTDO G+PL+ O	D 741
Sbjct	631	G S + AL+LL I G+ TG GPSSQLALSLLVNDIDEGIPRMVFTGI				P 690
Query	740	YKTIKDLAKATEMLQRITTA(+ + + + A+ ++O + A(QHPA	-VIGTIATAMD: ++ T A+ MD-	SDSpppppPIT	D 603
Sbjct	691	GVDEMVANTSLASHLIQSGALPVQKA				- 740
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +	AKLKEVVLWLA KL +++ W		TLHNFSRQDVE ++ +S++D +	
Sbjct	741	LQGLLQATMARAKEVKDAEVI				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQI K R+V +GP O O		LIQGVDL-SIEV + G D S EV		
Sbjct	790	IKFGRLVSTPPKHREKPKGPDÕHTAÕI				
Query	260	EQMK-VIKTGLDPAPQTIIREPT O K + TG P P + +R+PT		VMRIIRNSLSAI + R+ +	HYENASPETQK ++ +P+	E 96
Sbjct	850	GÕFKYYMITGRVPNPGEEYEDYVRKP			· · · · · <u>-</u> ·	D 904
Query	95	<pre>INERVTTMVINNGNRGLNQYQVKEI + V + NG RG +O O++++</pre>	21			
Sbjct	905	FYQAVVEVFAENGGRGPDQDQMQDL	929			

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAK32162.1|AF343570_1 Length: 968 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
71.2 bits	s(173)	6e-10() Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2
Feature	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN G S + AL+LL I G+ TG		NKWADLKREGMI D+K		
Sbjct	631	G S + AL+LL I G+ TG GPSSQLALSLLVNDIDEGIPRMVFTGE			O E	
Query	740	YKTIKDLAKATEMLQRITTAQ + + + + + A+ ++Q + AQ		-VIGTIATAMD: ++ T A+ MD-		D 603
Sbjct	691	GVDEMVANTSLASHLIQSGALPVQKAQ				- 740
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +				
Sbjct	741	LQGLLQATMARAKEVKDAEVE				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQF K R+V +GP O O		LIQGVDL-SIEV + G D S EV		
Sbjct	790	IKFGRLVSTPPKHQEKPKGPDÕHTAÕE				
Query	260	EQMK-VIKTGLDPAPQTIIREPI Q K + TG P P + +R+PI		VMRIIRNSLSAI + R+ +	HYENASPETQK	E 96
Sbjct	850	GÕFKYYMITGRVPNPGEEYEDYVRKPI			· · · · · - · · - · ·	D 904
Query	95	INERVTTMVINNGNRGLNQYQVKEI + V + NG RG +Q Q++++	21			
Sbjct	905	FYQAVVEVFAENGGRGPDQDQMQDL	929			

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AGC00816.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
70.9 bits	s(172)	6e-10() Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2
Feature	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGI G S + AL+LL I G+ TG	NVIEGKIVP + E ++P		KGTGIPLVTDO G+PL+ O	
Sbjct	631	GPSSQLALSLLVNDIDEGIPRMVFTGI			×	
Query	740	YKTIKDLAKATEMLQRITTA(+ + + + + A+ ++Q + A(-VIGTIATAMD: ++ T A+ MD-		D 603
Sbjct	691	GVDEMVANTSLASHLIQSGALPVQKA				- 740
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +			TLHNFSRQDVE ++ +S++D +	
Sbjct	741	LQGLLQATMARAKEVKDAEVI				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQI	HQRAVRIRENY	LIQGVDL-SIE	WIKNNGYRGPS	A 261

Chain D, X-ray Structure Of The Birnavirus Vp1-vp3 Complex Sequence ID: **pdb|3ZED|D** Length: 242 Number of Matches: 1

▶ See 2 more title(s) Range 1: 8 to 199

Score		Expect Method	Identities	Positives	Gaps	Frame
68.6 bits	s(166)	6e-10() Compositional matrix adjust.	53/202(26%)	95/202(47%)	17/202(8%)	-2
Features	s:					
Query	605	DEDIMVTLEELLMAAAD-RDPRMAKLKI D ++				
Sbjct	8	D ++ L+ + A + +D + KL + DAELQGLLQATMARAKEVKDAEVFKLL				
Query	428	NRIVQNSLTTAVHSRGPTQDVLQHQRAY R+V +GP Q Q +A	VRIRENYLIQG RI + + G		NGYRGPSAEQ N YRGPS Q	
Sbjct	63	GRLVSTPPKHQEKPKGPDÕHTAÕEAKA				
Query	251	KVIK-TGLDPAPQTIIREPIPRS K TG P P + +R+PI R	DNSTPELVMRI + + + R+		ASPETQKEIN	
Sbjct	123	KYYMITGRVPNPGEEYEDYVRKPITRP			· - ·	•
Query	86	RVTTMVINNGNRGLNQYQVKEI 21 V + NG RG +O O++++				
Sbjct	178	AVVEVFAENGGRGPDQDQMQDL 199				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAK32165.1|AF343573_1 Length: 968 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
70.9 bits	(172)	6e-10() Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2
Features	3 :					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG G S + AL+LL I G+ TG	NVIEGKIVP + E ++P		KGTGIPLVTDÇ G+PL+ Ĉ	D 741
Sbjct	631	GPSSQLALSLLVNDIDEGIPRMVFTG				P 690
Query	740	YKTIKDLAKATEMLQRITTA(+ + + + A+ ++Q + A(D 603
Sbjct	691	GVDEMVANTSLASHLIÕSGALPVQKA				- 740
Query	602	EDIMVTLEELLMAAADRDPRMAL+ LL A R D +	AKLKEVVLWLA KL +++ W		TLHNFSRQDVE ++ +S++D +	
Sbjct	741	LQGLLQATMARAKEVKDAEV				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQI K R+V +GP O O		LIQGVDL-SIE + G D S E		
Sbjct	790	IKFGRLVSTPPKHQEKPKGPDÕHTAÕ				
Query	260	EQMK-VIKTGLDPAPQTIIREP		VMRIIRNSLSA + R+ +	HYENASPETQK ++ +P+	Œ 96 +
Sbjct	850	GÖFKYYMITGRVPNPGEEYEDYVRKP			· · · · · · · · · · · · · · · · · · ·	•
Query	95	INERVTTMVINNGNRGLNQYQVKEI + V + NG RG +Q Q++++	21			
Sbjct	905	FYQAVVEVFAENGGRGPDÕDÕMQDL	929			

VP3 protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AGJ83948.1| Length: 239 Number of Matches: 1

Range 1: 5 to 196

Score		Expect Method	Identities	Positives	Gaps	Frame
68.6 bits	(166)	6e-10() Compositional matrix adjust.	52/202(26%)	95/202(47%)	17/202(8%)	-2
Features	:					
Query	605	DEDIMVTLEELLMAAAD-RDPRMAKLKE			~	
Sbjct	5	DE++ L + A + +D + KL DEELQRLLNATMARAKEVQDAEIYKLLF		+ D ++ LTDHMYE		-
Query	428	NRIVQNSLTTAVHSRGPTQDVLQHQRAV	RIRENYLIQG' RI + + G		NGYRGPSAEÇ N YRGPS Ĉ	M 252
Sbjct	60	GKLISTPPKHPEKPKGPDÕHHAÕEARAT			-·	F 119
Query	251	K-VIKTGLDPAPQTIIREPIPRSD	NSTPELVMRI	IRNSLSAHYEN	ASPETQKEIN	IE 87

K + TG +P P + I++PI + + R+ + + + + + PE E +
Sbjct 120 KYYLITGREPEPGDEYEDYIKQPIVKPTDMN--KIRRLANSVYGLPHQEPAPE---EFYD 174

Query 86 RVTTMVINNGNRGLNQYQVKEI 21
V + NG RG +Q Q++++
Sbjct 175 AVAAVFAQNGGRGPDQDQMQDL 196

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAK32158.1|AF342732_1 Length: 968 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
70.9 bits	s(172)	7e-10() Compositional matrix adjust.	76/315(24%)	136/315(43%)	34/315(10%) -	2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG G S + L+LL I GV TG			KGTGIPLVTDQD G+PL+ +O	741
Sbjct	631	GPSAQLGLSLLVNDIEEGVPRMVFTG				690
Query	740	YKTIKDLAKATEMLQRITTAQHPA- + +++ + A ++O A	VIG +G		ppppPITDEDIM DE++	1 591
Sbjct	691	GVDEEVRNTSLAAHLIQTGALPVQKA				742
Query	590	VTLEELLMAAAD-RDPRMAKLKEVVLV L + A + +D + KL +++ V		VLDTLHNFSRQI + D + ++S++		414
Sbjct	743	RLLNATMARAKEVKDAEIFKLLKLMA				797
Query	413	NSLTTAVHSRGPTQDVLQHQRAVRIR +GP Q Q RA RI				240
Sbjct	798	TPPKHPEKPKGPDQRTAQEARATRIS				857
Query	239	TGLDPAPQTIIREPIPRSDNSTPEL	-VMRIIRNSLS + R+ +	AHYENASPETQ	KEINERVTTMVI E E V +	66
Sbjct	858	TGRTPDPDDEYEDYIKQTITKPTDMN		· · · · · · · ·		914
Query	65	NNGNRGLNQYQVKEI 21				
Sbjct	915	N RG +Q Q++++ ENDGRGPDQDQMQDL 929				

107 kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAC71003.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
70.9 bits	s(172)	7e-10() Compositional matrix adjust.	75/317(24%)	134/317(42%)	38/317(11%)	-2
Feature	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN				
Sbjct	631	${ t G}$ ${ t S}$ ${ t +}$ ${ t AL+LL}$ ${ t I}$ ${ t G+}$ ${ t TG}$ ${ t GPSAQLALSLLVNDIDEGIPRMVFTGE}$			G+PL+ Q HEHGLPLIGCQ	
Query	740	YKTIKDLAKATEMLQRITTAQHPAVIO EM+ + A H		pppppPI		
Sbjct	690	EM+ + A H G PGVDEMVANTSLASHLIQSG		•	DE++ RTTASGMDEEL	
Query	590	VTLEELLMAAAD-RDPRMAKLKEVVLW L+ + A + +D + KL +++ W		VLDTLHNFSRQ + D ++ +S++		
Sbjct	743	GLLQATMARAKEVKDAEVFKLLKLMSW				
Query	413	NSLTTAVHSRGPTQDVLQHQRAVRIRE +GP O O +A RI	ENYLIQGVDL- + + G D			
Sbjct	798	TPPKHQEKPKGPDÕHTAÕEAKATRISI				
Query	239	TGLDPAPQTIIREPIPRSDNSTF	PELVMRIIRNS + + R+ +	LSAHYENASPE ++ +P+		
Sbjct	858	TGRVPNPGVEYEDYVRKPITRPTDM				
Query	71	VINNGNRGLNQYQVKEI 21 NG RG +O O++++				
Sbjct	913	FAENGGRGPDQDQMQDL 929				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAV48856.3| Length: 980 Number of Matches: 1

▶ See 1 more title(s) Range 1: 631 to 929

Score		Expect Method		Identities	Positives	Gaps	Frame
70.9 bits	s(172)	7e-10() Composition	onal matrix adjust.	75/317(24%)	134/317(42%)	38/317(11%)	-2
Features	s:						
Query	911	GGSMEAALALL-Q				_	D 741
Sbjct	631	G S + AL+LL GPSAQLALSLLVN				G+PL+ Ç HEHGLPLIGCÇ	689
Query	740	YKTIKDLAKATEM	LQRITTAQHPAVIO	GTIATAMDSDS	pppppPI	TDEDI	M 591

Sbjct	690	${ m EM+}$ + A H G + + + + DE++ ${ mPGVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDEELQ}$	742
Query	590	VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRODVEGEKMNRIVQ	414
Sbjct	743	L+ + A + +D + KL +++ W K D + D ++ +S++D + K R++ GLLQATMARAKEVKDAEVFKLLKLMSWTRKNDLTDHMYEWSKEDPDAIKFGRLIS	797
Query	413	NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK	240
Sbjct	798	+GP Q Q +A RI + + G D S EWI N YRGP+ Q K + TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAPGQFKYYMI	857
Query	239	TGLDPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM TG P P + +R+PI R + + + + + + + + + + + + + + + + + +	72
Sbjct	858	TGRVPNPGEEYEDYVRKPITRPTDMDKIRRLANSVYGLPHQEPAPDDFYQAVVEV	912
Query	71	VINNGNRGLNQYQVKEI 21 NG RG +O O++++	
Sbjct	913	FAENGGRGPDQDQMQDL 929	

Sequence ID: **gb|AAP37159.1|** Length: 972 Number of Matches: 1 Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
70.9 bits	s(172)	7e-10() Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN				D 741
Sbjct	631	G S + AL+LL I G+ TG GPSSQLALSLLVNDIDEGIPRMVFTGE		D+K ICGVDIKAMAA	G+PL+ Q HEHGLPLIGCQ	P 690
Query	740	YKTIKDLAKATEMLQRITTAQ + + + + A+ ++Q + AQ)HPA	-VIGTIATAMD ++ T A+ MD	SDSpppppPIT	D 603
Sbjct	691	GVDEMVANTSLASYLIQSGALPVQKAQ				- 740
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +			TLHNFSRQDVE ++ +S++D +	
Sbjct	741	LQGLLQATMARAKEVKDAEVF				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQH K R+V +GP Q Q		LIQGVDL-SIE' + G D S E'		
Sbjct	790	IKFGRLVSTPPKHQEKPKGPDÕHTAÕE				
Query	260	EQMK-VIKTGLDPAPQTIIREPI O K + TG P P + +R+PI		VMRIIRNSLSA + R+ +	HYENASPETQK ++ +P+	E 96
Sbjct	850	GÕFKYYMITGRVPNPGEEYEDYVRKPI			· · · · · · · · · · · · · · · · · · ·	D 904
Query	95	INERVTTMVINNGNRGLNQYQVKEI + V + NG RG +Q Q++++	21			
Sbjct	905	FYQAVVEVFAENGGRGPDQDQMQDL	929			

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: emb|CAD32967.1| Length: 972 Number of Matches: 1 Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
70.9 bits	s(172)	8e-10() Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2
Features	S :					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN				-
Sbjct	631	G S $+$ $AL+LL$ I $G+$ TG $GPSSQLALSLLVNDIDEGIPRMVFTGE$			G+PL+ Q HEHGLPLIGCQ	
Query	740	YKTIKDLAKATEMLQRITTAC				D 603
Sbjct	691	GVDEMVANTSLASHLIQSGALPVQKAQ				- 740
Query	602	EDIMVTLEELLMAAADRDPRMAL+ LL A R D +	AKLKEVVLWLA		rlhnfsrodve ++ +s++b +	
Sbjct	741	LQGLLQATMARAKEVKDAEVE				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQF K R+V +GP O O		LIQGVDL-SIET + G D S ET		
Sbjct	790	IKFGRLVSTPPKHQEKPKGPDÕHTAÕE				
Query	260	EQMK-VIKTGLDPAPQTIIREPI Q K + TG P P + +R+PI		VMRIIRNSLSAI + R+ +		E 96
Sbjct	850	GÕFKYYMITGRVPNPGEEYEDYVRKPI			· · · · · · · · · · · · · · · · · · ·	
Query	95	INERVTTMVINNGNRGLNQYQVKEI + V + NG RG +Q Q++++	21			
Sbjct	905	FYQAVGEVFAENGGRGPDQDQMQDL	929			

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAK32163.1|AF343571_1 Length: 968 Number of Matches: 1

Range 1: 631 to 929

Score **Expect Method Identities Positives** Gaps **Frame**

70.5 bits	70.5 bits(171) 8e-10() Compositional matrix adjust. 75/317(24%) 134/317(42%) 38/317(11%) -2						
Features	s:						
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGNVIEGKIVPNKWADLKREGMKGTGIPLVTDQD G S + AL+LL I G+ TG + E ++P D+K G+PL+ O	741				
Sbjct	631	${\sf G}$ ${\sf S}$ + ${\sf AL+LL}$ ${\sf I}$ ${\sf G+}$ ${\sf TG}$ + ${\sf E}$ ++P D+K G+PL+ Q GPSAQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQ-	689				
Query	740	YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIM EM+ + A H G + + + DE++	591				
Sbjct	690	PGVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDEELQ	742				
Query	590	VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ L+ + A + +D + KL +++ W K D + D ++ +S++D + K R++	414				
Sbjct	743	GLLQATMARAKEVKDAEVFKLLKLMSWTRKNDLTDHMYEWSKEDPDAIKFGRLIS	797				
Query	413	NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK +GP Q Q +A RI + + G D S EWI N YRGP+ Q K +	240				
Sbjct	798	TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFGSPEWIAENNYRGPAPGQFKYYMI	857				
Query	239	TGLDPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM TG PP + +R+PIR + + + R+ + + + +P+ + + V +	72				
Sbjct	858	TGRVPNPGEEYEDYVRKPITRPTDMDKIRRLANSVYGLPHQEPAPDDFYQAVVEV	912				
Query	71	VINNGNRGLNQYQVKEI 21 NG RG +Q Q++++					
Sbjct	913	FAENGGRGPDQDQMQDL 929					

polyprotein, partial [Tellina virus 2]

Sequence ID: gb|AAK32157.1|AF342731_1 Length: 968 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
70.1 bits	s(170)	1e-09() Compositional matrix adjust.	77/318(24%)	137/318(43%)	40/318(12%) -	2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG				741
Sbjct	631	G S $+$ $L+LL$ I GV TG $GPSAQLGLSLLVNDIDEGVPRMVFTGE$	+ E I+P EIASDEETIIP		G+PL+ +Q HEQGLPLIGNQE	690
Query	740	YKTIKDLAKATEMLQRITTAQHPA +++A + + T P	VI	GTIATAMDSDS	pppppPITDED]	594
Sbjct	691	-GVDEEVANTSLAAHLVQTGALPVQKA				
Query	593	MVTLEELLMAAAD-RDPRMAKLKEVVI L + A + +D + KL +++	WLAKIDDNNP	GVLDTLHNFSR	QDVEGEKMNRIV	417
Sbjct	742	QRLLNATMARAKEVKDAEIFKLLKLMA				
Query	416	QNSLTTAVHSRGPTQDVLQHQRAVRIF +GP O O RA RI	RENYLIQGVDL + + G D		RGPSAEQMK-VI RGPS ÕK H	
Sbjct	797	STPPKHPEKPKGPDÖRTAÖEARATRIS				
Query	242	KTGLDPAPQTIIREPIPRSDNST				75
Sbjct	857	ITGRTPDPDDEYEDYIKQTITKPTDM				911
Query	74	MVINNGNRGLNQYQVKEI 21 + +N RG +Q Q++++				
Sbjct	912	VFADNDGRGPDÕDÕMQDL 929				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAV48854.3| Length: 980 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
69.7 bits	(169)	1e-09() Compositional matrix adjust.	79/325(24%)	140/325(43%)	54/325(16%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN	IVIEGKIVP			
Sbjct	631	G S $+$ $AL+LL$ I $G+$ TG $GPSAQLALSLLVNDIDEGIPRMVFTGE$		D+K ICGVDIKAIAA	G+PL+ Q HEHGLPLIGCQ	
Query	740	YKTIKDLAKATEMLQRITTAC + + + + A+ ++Q + AC				D 603
Sbjct	691	GVDEMVANTSLASHLIQSGALPVQKAQ				- 740
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +			TLHNFSRQDVE ++ +S++D +	
Sbjct	741	LQGLLQATMPRAKEVKDAEVF				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQH K R++ +GP O O		LIQGVDL-SIEV + G D S EV		
Sbjct	790	IKFGRLISTPPKHQEKPKGPDQHTAQE				
Query	260	EQMK-VIKTGLDPAPQTIIREPI O K + TG P P + +R+PI		VMRIIRNSLSAI + R+ +		E 96
Sbjct	850	GÕFKYYMITGRVPNPGEEYEDYVRKPI			· · · · · · · · · · · · · · · · · · ·	•
Query	95	INERVTTMVINNGNRGLNQYQVKEI + V + NG RG +Q Q++++	21			
Sbjct	905	FYQAVVEVFAENGGRGPDQDQMQDL	929			

polyprotein [Rotifer birnavirus strain Palavas]

Sequence ID: emb|CAX33877.1| Length: 1060 Number of Matches: 1

Range 1: 646 to 894

Score		Expect	Method	Identities	Positives	Gaps Fi	rame
69.7 bits	s(169)	2e-09()	Compositional matrix adjust.	70/272(26%)	118/272(43%)	45/272(16%) -2	
Features	S :						
Query	986		/PISAITQNEITTTATPPIPRGG -PI +I PI G		LQHIPPGV' Q IPP +	IPFAVTGNVI VTGN +I	828
Sbjct	646		PI G PILSIQGGFAIIPDEAPILEGT				701
Query	827	EGK	-IVPNKWADLKREGMKGT ++PN +K++ +K			KATEMLQRITTA + T	681
Sbjct	702		VVMPNPAQQMKKQIAAQKELKFI			· -	759
Query	680	QHPAV +H	/IGTIATAMDSDSpppppPITDE D D D+	DIMVTLEELLI D M ++L		KLKEVVLWLAKI KL ++ W	501
Sbjct	760		DQDHSRSVNLCADD				804
Query	500		PGVLDTLHNFSRQDVEGEKMNRI G+ D L+NF+ D +G ++ +		SRGPTQDV: +R P		330
Sbjct	805		IGLADMLYNFAETDPDGNRLYKT			~	862
Query	329		-GVDLSIEWIKNNGYRGPSAEQM				
Sbjct	863	~	G + EW++ +GYRGP++E++ GEAFTPEWVEQHGYRGPTSEEI				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: emb|CAD32966.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
69.7 bits	(169)	2e-09() Compositional matrix adjust.	78/323(24%)	135/323(41%)	50/323(15%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGI			_	
Sbjct	631	G S + L+LL I GV TG GPSAQLGLSLLVNSIEEGVPRMVFTGI			G+PL+ Q HEQGLPLIGCQ	
Query	740	YKTIKDLAKATEMLQRITTAQHPA- + + + + A ++O T A		-VIGTIATAMDS ++ +IA+ MD		D 603
Sbjct	691	GVDEEVSNTSLAAHLIQTGTLPVQKA				- 740
Query	602	EDIMVTLEELLMAAADRDPRMAL+ LL A R D +	AKLKEVVLWLA KL +++ W			
Sbjct	741	LQRLLSATMARAKEVKDAEI				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQI K R++ +GP O O		LIQGVDLSI-EV + G + + EV		A 261
Sbjct	790	IKFGRLISTPPKHPEKPKGPNÕHAAÕI				P 849
Query	260	EQMK-VIKTGLDPAPQTIIREPIPRSI O K + TG P P + I ++				N 90
Sbjct	850	GÖFKYYLITGRTPDPNDGYEDYIKQT				Y 906
Query	89	ERVTTMVINNGNRGLNQYQVKEI 2: + V + +N RG +Q Q++++	1			
Sbjct	907		29			

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAK32155.1|AF342729_1 Length: 968 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
69.3 bits	s(168)	2e-09() Compositional matrix adjust.	78/323(24%)	135/323(41%)	50/323(15%)	-2
Feature	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG				
Sbjct	631	G S + L+LL I GV TG GPSAQLGLSLLVNSIEEGVPRMVFTGI	+ E I+P EIAADEETIIP		G+PL+ Q HEQGLPLIGCQ	
Query	740	YKTIKDLAKATEMLQRITTAQHPA- + + + + A ++O T A		-VIGTIATAMD: ++ +IA+ MD	SDSpppppPIT	D 603
Sbjct	691	GVDEEVSNTSLAAHLIQTGTLPVQKAI				- 740
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +	AKLKEVVLWLA KL +++ W			
Sbjct	741	L+ LL A R D + LQRLLSATMARAKEVKDAEII				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQI		LIQGVDLSI-E + G + + E		
Sbjct	790	K R++ +GP Q Q IKFGRLISTPPKHPEKPKGPNQHAAQI				
Query	260	EQMK-VIKTGLDPAPQTIIREPIPRSI				N 90
Sbjct	850	Q K + TG P P + I ++ GQFKYYLITGRTPDPNDGYEDYIKQT				Y 906
Query	89	ERVTTMVINNGNRGLNQYQVKEI 2	1			

Sequence ID: emb|CAD32965.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame	
69.3 bits	(168)	2e-09() Compositional matrix adjust.	78/323(24%)	135/323(41%)	50/323(15%)	-2	
Features	Features:						
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG G S + L+LL I GV TG					
Sbjct	631	GPSAQLGLSLLVNSIEEGVPRMVFTGE	+ E I+P EIAADEETIIP				
Query	740	YKTIKDLAKATEMLQRITTAQHPA- + + + + A ++Q T A		-VIGTIATAMD	SDSpppppPIT	D 603	
Sbjct	691	GVDEEVSNTSLAAHLIQTGTLPVQKA	KGANKRIKYLG	ELMSSIASGMDI	EE	- 740	
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +	AKLKEVVLWLA				
Sbjct	741	LQRLLSATMARAKEVKDAEI					
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQF K R++ +GP O O		LIQGVDLSI-EV + G + + EV			
Sbjct	790	IKFGRLISTPPKHPEKPKGPNQHAAQI					
Query	260	EQMK-VIKTGLDPAPQTIIREPIPRSI O K + TG P P + I ++		RIIRNSLSAHYI R+ + +-		N 90	
Sbjct	850	GOFKYYLITGRTPDPNDGYEDYIKQTI				Y 906	
Query	89	ERVTTMVINNGNRGLNQYQVKEI 21 + V + +N RG +Q Q++++	l				
Sbjct	907		29				

107 kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAQ75360.1|** Length: 972 Number of Matches: 1 Range 1: 606 to 929

Score		Expect Method	Identities	Positives	Gaps F	rame			
69.3 bits	s(168)	2e-09() Compositional matrix adjust.	82/338(24%)	147/338(43%)	32/338(9%) -2				
Features	Features:								
Query	980	TVVPISAITQNEITTTATPPIPRO T +P+ I +N + PI O	GSMEAALALL- SS+ L+LL			819			
Sbjct	606	TALPLKEIKRNGNIVVEKIFAGPI-MG			TG + E FTGEIADDEET	664			
Query	818	IVPNKWADLKREGMKGTGIPLVTDQDY I+P +K G+PL+ +Q			HPAVIG	660			
Sbjct	665	IIPICGVAIKAIAAHEQGLPLIGNÕPO				724			
Query	659	TIATAMDSDSpppppPITDEDIMVTLE + M S++ DE++ L	ELLMAAAD-RI + A + +I			483			
Sbjct	725	YLGELMASNASGMDEELQRLLN				774			
Query	482	VLDTLHNFSRQDVEGEKMNRIVQNSLT + D ++ +S++D + K +++			ENYLIQGVDLS + + G D +	303			
Sbjct	775	LTDHMYEWSKEDPDALKFGKLISTPPK		~	_	834			
Query	302	I-EWIKNNGYRGPSAEQMK-VIKTGLD EW+ N YRGPS OK + TG +		[PRSDNSTPEL- [+S ++		135			
Sbjct	835	TPEWVAMNNYRGPSPGÕFKYYLITGRE				894			
Query	134	AHYENASPETQKEINERVTTMVINNGN ++ +PE E + V + NG							
Sbjct	895	LPHQEPAPEEFYDAVAAVFAQNGO							

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAV48850.1| Length: 972 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
69.3 bits	s(168)	2e-09() Compositional matrix adjust.	78/323(24%)	135/323(41%)	50/323(15%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG				
Sbjct	631	G S + L+LL I GV TG GPSAQLGLSLLVNSIEEGVPRMVFTG			G+PL+ Ç HEQGLPLIGCÇ	
Query	740	YKTIKDLAKATEMLQRITTAQHPA + + + + A ++Q T A		-VIGTIATAMD	SDSpppppPIT	D 603
Sbjct	691	GVDEEVSNTSLAAHLIÕTGTLPVQKA				- 740
Query	602	EDIMVTLEELLMAAADRDPRM L+ LL A R D +		KIDDNNPGVLD' K D + D	~	
Sbjct	741	LQRLLSATMARAKEVKDAEI				

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Query 437 EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSA 261 K R++ +GP Q Q RAVRI ++ G ++ EW+ N YRGPS Sbjct 790 IKFGRLISTPPKHPEKPKGPNQHAAQEARAVRISLDAVRAGAEFATPEWVATNDYRGPSP 849

Query 260 EQMK-VIKTGLDPAPQTIIREPIPRSDNSTPEL--VMRIIRNSLSAHYENASPETQKEIN 90 Q K + TG P P + I ++ + + + + + + + + + + E E Sbjct 850 GQFKYYLITGRTPDPNDGYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFY 906

Query 89 ERVTTMVINNGNRGLNQYQVKEI 21 + V + +N RG +Q Q++++ Sbjct 907 DAVAAVFADNDGRGPDQDQMQDL 929
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Sequence ID: emb|CAD32968.1| Length: 972 Number of Matches: 1

▶ See 1 more title(s) Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
69.3 bits	s(168)	2e-09() Compositional matrix adjust.	78/323(24%)	135/323(41%)	50/323(15%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTGN G S + L+LL I GV TG				
Sbjct	631	G S + L+LL I GV TG GPSAQLGLSLLVNSIEEGVPRMVFTGE	+ E I+P EIAADEETIIP		G+PL+ Q HEQGLPLIGCQ	
Query	740	YKTIKDLAKATEMLQRITTAQHPA- + + + + A ++Q T A		-VIGTIATAMD	SDSpppppPIT	D 603
Sbjct	691	GVDEEVSNTSLAAHLIQTGTLPVQKA				
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +			_	
Sbjct	741	LQRLLSATMARAKEVKDAEI				
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQF K R++ +GP Q Q		LIQGVDLSI-EV + G + + EV		
Sbjct	790	IKFGRLISTPPKHPEKPKGPNÕHAAÕE				
Query	260	EQMK-VIKTGLDPAPQTIIREPIPRSI O K + TG P P + I ++		RIIRNSLSAHYI R+ + +-		N 90
Sbjct	850	GÖFKYYLITGRTPDPNDGYEDYIKQTI				Y 906
Query	89	ERVTTMVINNGNRGLNQYQVKEI 21 + V + +N RG +Q Q++++	L			
Sbjct	907	DAVAAVFADNDGRGPDÕDÕMQDL 92	29			

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: emb|CAD32970.1| Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame	
69.3 bits	(168)	2e-09() Compositional matrix adjust.	78/323(24%)	135/323(41%)	50/323(15%)	-2	
Features:							
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG					
Sbjct	631	G S + L+LL I GV TG GPSAQLGLSLLVNSIEEGVPRMVFTGE	+ E I+P EIAADEETIIP		G+PL+ Q HEQGLPLIGCQ		
Query	740	YKTIKDLAKATEMLQRITTAQHPA- + + + + A ++O T A		-VIGTIATAMD: ++ +IA+ MD		D 603	
Sbjct	691	GVDEEVSNTSLAAHLIÕTGTLPVQKA				- 740	
Query	602	EDIMVTLEELLMAAADRDPRMA L+ LL A R D +					
Sbjct	741	LQRLLSATMARAKEVKDAEI					
Query	437	EKMNRIVQNSLTTAVHSRGPTQDVLQF K R++ +GP O O		LIQGVDLSI-EV + G + + EV			
Sbjct	790	IKFGRLISTPPKHPEKPKGPNÕHAAÕI					
Query	260	EQMK-VIKTGLDPAPQTIIREPIPRSI O K + TG P P + I ++		RIIRNSLSAHYI R+ + +		N 90	
Sbjct	850	GŎFKYYLITGRTPDPNDGYEDYIKQT				Y 906	
Query	89	ERVTTMVINNGNRGLNQYQVKEI 21 + V + +N RG +Q Q++++	L				
Sbjct	907	DAVAAVFADNDGRGPDQDQMQDL 92	29				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAV48848.3|** Length: 980 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps	Frame
69.3 bits(168)	2e-09()	Compositional matrix adjust.	75/317(24%)	133/317(41%)	38/317(11%)	-2
Features:						

Query	911	GGSMEAALALL-QHIPPGVTPFAVTGNVIEGKIVPNKWADLKREGMKGTGIPLVTDQD G S + AL+LL I G+ TG + E ++P D+K G+PL+ O	741
Sbjct	631	GPSAQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQ-	689
Query	740	YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIM EM + A H G + + + DE++	591
Sbjct	690	EM + A H G + + + + DE++PGVDEMEANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDEELQ	742
Query	590	VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ L+ + A + +D + KL +++ W K D + D ++ +S++D + K R++	414
Sbjct	743	GLLQATMARAKEVKDAEVFKLLKLMSWTRKNDLTDHMYEWSKEDPDAIKFGRLIS	797
Query	413	NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK +GP Q Q +A RI + + G D S EWI N YRGP+ Q K +	240
Sbjct	798	TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAPGQFKYYMI	857
Query	239	TGLDPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM TG PP + +R+PIR + + + R+ + + + +P+ + + V +	72
Sbjct	858	\mathtt{TG} P P + +R+PI R + + + R+ + + + +P+ + + V + $\mathtt{TGRVPNPGEEYEDYVRKPITRPTDMDKIRRLANSVYGLPHQEPAPDDFYQAVVEV}$	912
Query	71	VINNGNRGLNQYQVKEI 21	
Sbjct	913	NG RG +Q Q++++ FAENGGRGPDQDQMQDL 929	

Sequence ID: **gb|AAV48852.3|** Length: 980 Number of Matches: 1 Range 1: 631 to 929

Score		Expect Method	Identities	Positives	Gaps	Frame
69.3 bits	s(168)	2e-09() Compositional matrix adjust	. 75/317(24%)	133/317(41%)	38/317(11%)	-2
Features	s:					
Query	911	GGSMEAALALL-QHIPPGVTPFAVTG G S + AL+LL I G+ TG			KGTGIPLVTDÇ G+PL+ Ĉ	D 741
Sbjct	631	GPSAQLALSLLVNDIDEGIPRMVFTG) - 689
Query	740	YKTIKDLAKATEMLQRITTAQHPAVI EM + A H	GTIATAMDSDS G + +		TDEDI ++DEDI	
Sbjct	690	PGVDEMEANTSLASHLIQS		•		
Query	590	VTLEELLMAAAD-RDPRMAKLKEVVL L+ + A + +D + KL +++		VLDTLHNFSRQ + D ++ +S++		
Sbjct	743	GLLQATMARAKEVKDAEVFKLLKLMS				
Query	413	NSLTTAVHSRGPTQDVLQHQRAVRIR +GP O O +A RI		SIEWIKNNGYR S EWI N YR		
Sbjct	798	TPPKHQEKPKGPDÕHTAÕEAKATRIS				
Query	239	TGLDPAPQTIIREPIPRSDNST TG P P + +R+PI R +	PELVMRIIRNS + + R+ +	LSAHYENASPE	TQKEINERVTT + + V	
Sbjct	858	TGRVPNPGEEYEDYVRKPITRPTDM-				
Query	71	VINNGNRGLNQYQVKEI 21 NG RG +Q Q++++				
Sbjct	913	FAENGGRGPDQDQMQDL 929				

submajor capsid protein VP3 [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAM90322.1|AF291752_1** Length: 237 Number of Matches: 1 Range 1: 2 to 195

Score		Expect Method	Identities	Positives	Gaps	Frame	
65.5 bits	(158)	7e-09() Compositional matrix adjust.	52/202(26%)	93/202(46%)	13/202(6%)	-2	
Features	Features:						
Query	605	DEDIMVTLEELLMAAAD-RDPRMAKLKI DE++ L + A + +D + KL -		NNPGVLDTLHN + D +	FSRQDVEGEK +SR+D + K		
Sbjct	2	DEELQRLLSATMARAKEVKDAEIFKLL				-	
Query	428	NRIVQNSLTTAVHSRGPTQDVLQHQRAY R++ + GP Q Q RAY	VRIRENYLIQG VRI + + G		INGYRGPSAEÇ N YRGPS Ö	7	
Sbjct	57	GRLISTPPKHPEKPKGPNQHAAQEARAY					
Query	251	K-VIKTGLDPAPQTIIREPIPRSDNSTI K + TG P P + I ++	PELVMRIIR		PETQKEINER PE E +		
Sbjct	117	KYYLITGRTPDPNDGYEDYIKQTITKP				•	
Query	80	TTMVINNGNRGLNQYQVKEIVQ 15 + N RG +Q Q++++ +					
Sbjct	174	AAVFAENDGRGPDQDQMQDLRE 195					

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AKM16810.1|** Length: 1013 Number of Matches: 1 Range 1: 775 to 967

Score	Expect	Method	Identities	Positives	Gaps	Frame
64.3 bits(155)	9e-08()	Compositional matrix adjust.	53/208(25%)	90/208(43%)	40/208(19%)	-2

Features: AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-----408 Query 566 AAA+ DP +V +WL ++N G+++ + NF+ D +M + N+ AAANADPLFRSALQVFMWL--EEN-GIVNDMANFALSDPNAHRMKNFLANAPQAGSKS Sbjct 775 829 Query ----LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM 252 407 Sbjct 830 889 KVIKTGLDPAPQTIIREPIPRSDNSTPELVM-----RIIRNSLSAHYENASPETO Query 251 102 Sbjct 890 939 KEINERVTTMVINNGNRGLNQYQVKEIV 18 Query 101

structural polyprotein [Infectious bursal disease virus]

Sbjct 940 QAFIDEVARVYENNHGRGPNQEQMKDLL

Sequence ID: gb|ABS86936.1| Length: 1012 Number of Matches: 1

+ V + NN RG NQ Q+K+++

Range 1: 774 to 966

Score		Expect Method	Identities	Positives	Gaps	Frame	
61.6 bits	s(148)	6e-07() Compositional matrix adjust.	55/201(27%)	91/201(45%)	26/201(12%)	-2	
Features:							
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNF AAA+ DP V +WL ++N	GVLDTLHNFSF G++ + NF+		IVQNSLTTA + N+ T	- 396	
Sbjct	774	AAANVDPLFQSALSVFMWLEEN				S 828	
Query	395	VHSRGPTQDVLQHQRA V +RGPT + Q ++			NNGYRGPSAEQ NG+RGPS Q		
Sbjct	829	QRAKYGTAGYGVEARGPTPEEAQREKD					
Query	251	KVIKTGLDPAPQTIIREPIPRSDN K + DP + +S	ISTPELVMRIIF ++ E ++R	RNSLSAHYENA + A +	SPETQKEINER P O I+E	V 81	
Sbjct	889	KYWQNTREIPDPNEDYLDYVHAEKSRI				A 946	
Query	80	TTMVINNGNRGLNQYQVKEIV 18 IN+G RG NO O+K+++					
Sbjct	947	KVYEINHG-RGPNQEQMKDLL 966					

VP3 protein, partial [Infectious bursal disease virus]

Sequence ID: gb|AFV39829.1| Length: 257 Number of Matches: 1

▶ See 1 more title(s) Range 1: 17 to 211

Score		Expect Method	Identities	Positives	Gaps	Frame	
60.1 bits	(144)	7e-07() Compositional matrix adjust.	54/203(27%)	90/203(44%)	26/203(12%)	-2	
Features:							
Query	572	LMAAADRDPRMAKLKEVVLWLAKIDDN + AAAD DP V +WL ++N		SRQDVEGEKM	_	- 408	
Sbjct	17	MEAAADVDPLFQSALSVFMWLEEN				S 71	
Query	407	LTTAVHSRGPTQDVLQHQ V +RGPT + O +				E 258	
Sbjct	72	KSQRAKYGTAGYGVEARGPTPEEAQRE				G 131	
Query	257	QMKVIKTGLDPAPQTIIREPIPRS O+K + DP + +S	SDNSTPELVMRI S ++ E ++R				
Sbjct	132	QLKYWQNTREIPDPNEDYLDYVHAEKS				_	
Query	86	RVTTMVINNGNRGLNQYQVKEIV 18 IN+G RG NO Q+K+++	3				
Sbjct	190	VAKVYEINHG-RGPNQEQMKDLL 21	11				

polyprotein [Infectious bursal disease virus]

Sequence ID: emb|CAA27629.1| Length: 1021 Number of Matches: 1

Range 1: 783 to 975

Score		Expect Method	Identities	Positives	Gaps	Frame
61.2 bits	s(147)	9e-07() Compositional matrix adjust.	54/201(27%)	89/201(44%)	26/201(12%)	-2
Feature	s:					
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNP AAAD DP V +WL ++N		RQDVEGEKMNR D +M	IVQNS + N+	- 408
Sbjct	783	AAADVDPLFQSALSVFMWLEEN				s 837
Query	407	LTTAVHSRGPTQDVLQHQRA V +RGPT + Q ++			NNGYRGPSAEQ NG+RGPS O	•
Sbjct	838	QRAKYGTAGYGVEARGPTPEEAÕREKD				•
Query	251	KVIKTGLDPAPQTIIREPIPRSDN	STPELVMRIII	RNSLSAHYENA	SPETQKEINER	V 81

RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; Contains: RecName:

Full=Capsid protein VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; AltName: Full=pep46; Contains: RecName:

Full=Structural peptide 2; Short=p2; AltName: Full=pep7a; Contains: RecName: Full=Structural peptide 3; Short=p3; AltName: Full=pep7b;

Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep11; Contains: RecName: Full=Protease VP4; AltName:

Full=Non-structural protein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP3

Sequence ID: sp|P08364.2|POLS_IBDVA Length: 1012 Number of Matches: 1

Range 1: 774 to 966

Score		Expect Method	Identities	Positives	Gaps	Frame
61.2 bits	s(147)	9e-07() Compositional matrix adjust.	54/201(27%)	89/201(44%)	26/201(12%)	-2
Features	s:					
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNI AAAD DP V +WL ++N		RQDVEGEKMNR D +M	IVQNS	408
Sbjct	774	AAADVDPLFQSALSVFMWLEEN		_		S 828
Query	407	LTTAVHSRGPTQDVLQHQRA V +RGPT + Q ++			NNGYRGPSAEÇ NG+RGPS Ĉ	•
Sbjct	829	QRAKYGTAGYGVEARGPTPEEAQREKI				
Query	251	KVIKTGLDPAPQTIIREPIPRSDN K + DP + +S	NSTPELVMRIIF ++ E ++R			RV 81
Sbjct	889	KYWONTREIPDPNEDYLDYVHAEKSRI				7A 946
Query	80	TTMVINNGNRGLNQYQVKEIV 18 IN+G RG NO O+K+++				
Sbjct	947	KVYEINHG-RGPNÕEÕMKDLL 966				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AKD94179.1| Length: 1012 Number of Matches: 1

Range 1: 774 to 966

Score	Expect Method	Identities	Positives	Gaps	Frame
60.8 bits(14	6) 1e-06() Compositional matrix ad	just. 53/201(26%)	89/201(44%)	26/201(12%)	-2
Features:					
Query 5	66 AAADRDPRMAKLKEVVLWLAKID AAA+ DP V +WL +	DNNPGVLDTLHNFSF +N G++ + NF+	~	IVQNS + N+	- 408
Sbjct 7					S 828
Query 40		HQRAVRIRENYLIQG ++ RI + G		NNGYRGPSAEQ NG+RGPS O	
Sbjct 82					
Query 25			NSLSAHYENA: + A +	SPETOKEINER P O I+E	V 81
Sbjct 88				- 2	A 946
Query 80	TTMVINNGNRGLNQYQVKEIV IN+G RG NO O+K+++	18			
Sbjct 94		966			

unnamed protein product [Infectious bursal disease virus]

Sequence ID: emb|CAA79983.1| Length: 1013 Number of Matches: 1

• See 1 more title(s) Range 1: 775 to 967

Score		Expect Method	Identities	Positives	Gaps	Frame
60.8 bits	s(146)	1e-06() Compositional matrix adjust.	56/209(27%)	91/209(43%)	42/209(20%)	-2
Features	s:					
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNE AAA+ DP +V +WL ++N	GVLDTLHNFSI G++ + NF+		IVQNS	- 408
Sbjct	775	AAANADPLFRSALQVFMWLEEN				S 829
Query	407	LTTAVHSRGPTQDVLQHQRA V +RGPT + Q ++			NNGYRGPSAEÇ NG+RGPS C	-
Sbjct	830	QRAKYGTAGYGVEARGPTPEEAQREKI				•
Query	251	KVIKTGLDPAPQTIIREPIPRSDNSTE K + RE IP + F	PELVM P+ V			т 105
Sbjct	890	KYWQNTRE-IPEPNEDYE			_	P 939
Query	104	QKEINERVTTMVINNGNRGLNQYQVKE Q I+E IN+G RG NQ Q+K+				

Sbjct 940 QAFIDEVARVYEINHG-RGPNQEQMKDLL 967

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AGA84578.1| Length: 1012 Number of Matches: 1

Range 1: 622 to 966

Score		Expect	Method		Identities	Positives	Gaps	Frame
60.5 bits	s(145)	1e-06()	Compositiona	l matrix adjust.	88/355(25%)	140/355(39%)	40/355(11%)	-2
Features	s:							
Query	992	GPDCT G D T	VVPISAITQNI	EITTTATPPIP I + P P	-RGGSMEAALA G S A+A	LLQHIPPGV-TI + P V	PFAVTGNVIEC A+TG +	SK 819
Sbjct	622					YIDVFRPKVPI		G 681
Query	818	IVPN- + N	KWADLI K A		-IPLVTDQDYK + T ++	T-IKDLAKATEN	MLQRITTAQHI R+	
Sbjct	682					TFIKRFPHNPRI		
Query	668	VIGTI	ATAMDSDSpp1	PPPITDEDIM T E +	VTLEELLMAAA + + AAA	DRDPRMAKLKE	VVLWLAKIDDI V +WL +	IN 489
Sbjct	742	LPPNA	_			NVDPLFQSALS		795
Query	488	PGVLD G++	TLHNFSRQDVI + NF+ D	EGEKMNRIVQN +M + N	S	LTTAVHSI V +1	RGPTQDVLQHQ RGPT + O +	R 351
Sbjct	796	_				KYGTAGYGVEAI	z	
Query	350	AVRIF RI			RGPSAEQMKVI RGPS Q+K	KTGLDPAP(+ DP		
Sbjct	855					QNTREIPDPNEI		•
Query	182		LVMRIIRNSLS : ++R +	SAHYENASPET	OKEINERVTTM	VINNGNRGLNQ IN+G RG NO	YOVKEIV 18	3
Sbjct	915					EINHG-RGPNQI		56

structural polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AIG93139.1| Length: 1012 Number of Matches: 1

Range 1: 774 to 966

Score		Expect Method	Identities	Positives	Gaps	Frame
60.5 bits	s(145)	2e-06() Compositional matrix adjust.	53/201(26%)	89/201(44%)	26/201(12%)	-2
Features	s:					
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNE AAA+ DP V +WL ++N	GVLDTLHNFSF G++ + NF+	~	IVQNS + N+	- 408
Sbjct	774	AAANVDPLFQSALSVFMWLEEN				S 828
Query	407	LTTAVHSRGPTQDVLQHQRA V +RGPT + 0 ++		GVDLSI-EWIK G+ + EW+	NNGYRGPSAEQ NG+RGPS O	' .
Sbjct	829	QRAKYGTAGYGVEARGPTPEEAQREKI				
Query	251	KVIKTGLDPAPQTIIREPIPRSDN K + DP + +S	ISTPELVMRIIF ++ E ++R	RNSLSAHYENA + A +	SPETQKEINER P O I+E	.V 81
Sbjct	889	KYWQNTREIPDPNEDYLDYVHAEKSRI			- 2	A 946
Query	80	TTMVINNGNRGLNQYQVKEIV 18 IN+G RG NQ Q+K+++				
Sbjct	947	KVYEINHG-RGPNQEQMKDLL 966				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ACZ62645.1| Length: 1012 Number of Matches: 1

▶ See 1 more title(s) Range 1: 774 to 966

Score		Expect Method	Identities	Positives	Gaps	Frame
60.5 bits	(145)	2e-06() Compositional matrix adjust.	53/201(26%)	89/201(44%)	26/201(12%)	-2
Features	S :					
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNI AAA+ DP V +WL ++N		RQDVEGEKMNR D +M	IVQNS + N+	- 408
Sbjct	774	AAANVDPLFQSALSVFMWLEEN-				S 828
Query	407	LTTAVHSRGPTQDVLQHQRA V +RGPT + Q ++			NNGYRGPSAEÇ NG+RGPS C	•
Sbjct	829	QRAKYGTAGYGVEARGPTPEEAQREKI				,
Query	251	KVIKTGLDPAPQTIIREPIPRSDI K + DP + +S	NSTPELVMRIIF ++ E ++R		SPETQKEINER P O I+E	2V 81
Sbjct	889	KYWQNTREIPDPNEDYLDYVHAEKSRI			~	'A 946
Query	80	TTMVINNGNRGLNQYQVKEIV 18 IN+G RG NO O+K+++				
Sbjct	947	KVYEINHG-RGPNÕEÕMKDLL 966				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AAC78079.1|** Length: 1012 Number of Matches: 1 Range 1: 774 to 966

Score		Expect Method	Identities	Positives	Gaps	Frame
60.1 bits	s(144)	2e-06() Compositional matrix adjust.	54/200(27%)	91/200(45%)	24/200(12%)	-2
Features	s:					
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNF AAA+ DP V +WL ++N	GVLDTLHNFSF G++ + NF+		IVQNS + N+	- 408
Sbjct	774	AAANVDPLFQSALSVFMWLEEN			· - ·	S 828
Query	407	LTTAVHSRGPTQDVLQHQRA V +RGPT + Q ++			NNGYRGPSAEQ NG+RGPS O	
Sbjct	829	QRAKYGTAGYGVEARGPTPEEAQREKD				
Query	251	KVIKTGLD-PAPQTIIREPIPRSDNSTK + + P P + + + + S	PELVMRIIRNS L +I+R +			т 78
Sbjct	889	KYWQNTREIPDPNEDYLDYV-HAEKSF			E Q I+E EPPQAFIDEVA	K 947
Query	77	TMVINNGNRGLNQYQVKEIV 18				
Sbjct	948	IN+G RG NQ Q+K+++ VYEINHG-RGPNQEQMKDLL 966				

polyprotein [Infectious bursal disease virus]

Sequence ID: dbj|BAA08555.1| Length: 1012 Number of Matches: 1 Range 1: 774 to 966

Score		Expect Method	Identities	Positives	Gaps	Frame
60.1 bits	s(144)	2e-06() Compositional matrix adjust.	53/201(26%)	90/201(44%)	26/201(12%)	-2
Feature	s:					
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNE AAA+ DP V +WL ++N	GVLDTLHNFSF G++ + NF+		IVQNS	- 408
Sbjct	774	AAANVDPLFQSALSVFMWLEEN				S 828
Query	407	LTTAVHSRGPTQDVLQHQRA V +RGPT + +O ++		GVDLSI-EWIK G+ + EW+		M 252
Sbjct	829	QRAKYGTAGYGVEARGPTPEEVQREKI				•
Query	251	KVIKTGLDPAPQTIIREPIPRSDN K + DP + +S	ISTPELVMRIIF ++ E ++R		SPETQKEINER P O I+E	8V 81
Sbjct	889	KYWQNTREIPDPNEDYLDYVHAEKSRI			~	'A 946
Query	80	TTMVINNGNRGLNQYQVKEIV 18 IN+G RG NQ Q+K+++				
Sbjct	947	KVYEINHG-RGPNQEQMKDLL 966				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AAD48021.1|AF165149_2** Length: 1012 Number of Matches: 1 Range 1: 774 to 966

Score		Expect Method	Identities	Positives	Gaps	Frame
59.7 bits((143)	3e-06() Compositional matrix adjust.	53/201(26%)	89/201(44%)	26/201(12%)	-2
Features						
Query	566	AAADRDPRMAKLKEVVLWLAKIDDNNF AAA+ DP V +WL ++N	GVLDTLHNFSF G++ + NF+	~	IVQNS + N+	- 408
Sbjct	774	AAANVDPLFQSALSVFMWLEEN	_		- · · · · - · · · · · · · · · · · · · ·	S 828
Query	407	LTTAVHSRGPTQDVLQHQRA V +RGPT + Q ++		GVDLSI-EWIK G+ + EW+	NNGYRGPSAEQ NG+RGPS O	٠.
Sbjct	829	QRAKYGTAGYGVEARGPTPEEAQREKD				•
Query	251	KVIKTGLDPAPQTIIREPIPRSDN K + DP + +S	STPELVMRIIF ++ E ++R	RNSLSAHYENA + A +		V 81
Sbjct	889	KYWQNTRVIPDPNEDYLDYVHAEKSRI	ASEEQILRAAT	SIYGAPGQAE:		A 946
Query	80	TTMVINNGNRGLNQYQVKEIV 18 IN+G RG NQ Q+K+++				
Sbjct	947	KVYEINHG-RGPNQEQMKDLL 966				