BLAST ®

Basic Local Alignment Search Tool

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Blast report description

Nucleotide Sequence (1008 letters)

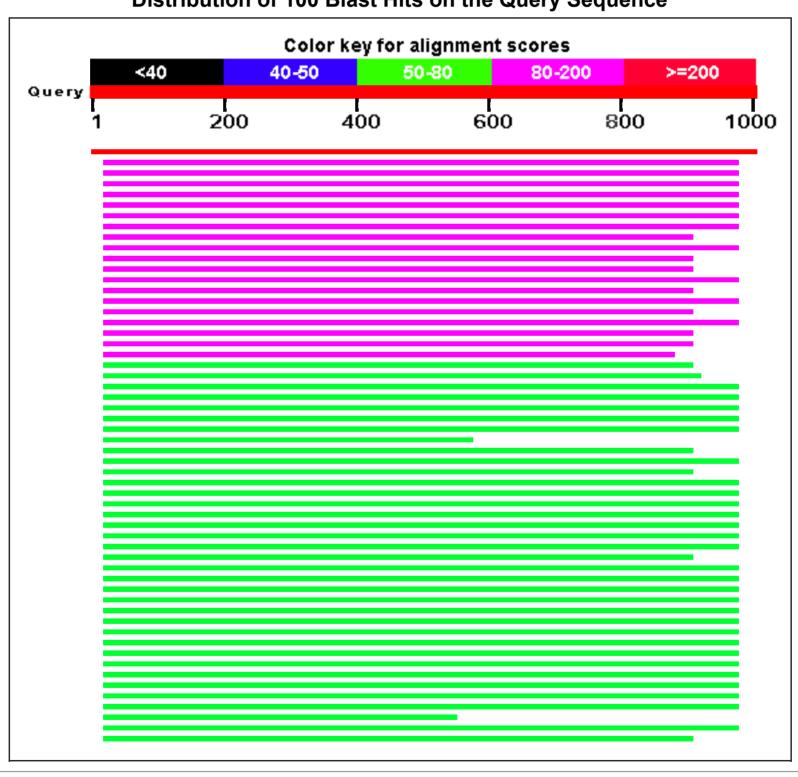|			
RID	B8BRYP9M015 (Expires on 02-06 12:11 pm)		
Query ID	lcl|Query_102347	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	nucleic acid		
Query Length	1008	**Program**	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

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
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%	Q703G9.1
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

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
polyprotein [Infectious pancreatic necrosis virus]	74.3	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	95%	5e-11	25%	CAH25439.1
108-kDa polyprotein [Infectious pancreatic necrosis virus]	74.3	74.3	95%	5e-11	25%	AAR10452.1
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%	5e-11	25%	P22495.1
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%	CAA27629.1
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; 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%	P08364.2
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%	CAA79983.1
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

⊟Alignments

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

Features:

```
Query  1007  AYIPPGPDCTVVPISAITQNEITTTATPPIPRGGSMEAALALLQHIPPGVTPFAVTGNVI   828
             AYIPPGP+CTVVPIS+ITQNEITTTATPPIPRGGSMEAALALLQ+IPPGVTPFAVTGNVI
Sbjct  592   AYIPPGPNCTVVPISSITQNEITTTATPPIPRGGSMEAALALLQYIPPGVTPFAVTGNVI   651

Query  827   EGKIVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQHPAVIGTIAT   648
             EGKIVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQHPAVIGTIA+
Sbjct  652   EGKIVPNKWADLKREGMKGTGIPLVTDQDYKTIKDLAKATEMLQRITTAQHPAVIGTIAS   711

Query  647   AMDSDSpppppP-ITDEDIMVTLEELLMAAADRDPRMAKLKEVVLWLAKIDDNNPGVLDT   471
             AMD D  PPPPP +TDE+IM TLE+LL+AAADRDPRMAKLK+VVLWLAKID+NNPGVLDT
Sbjct  712   AMDYDDFPPPPPPVTDENIMETLEDLLVAAADRDPRMAKLKDVVLWLAKIDNNNPGVLDT   771

Query  470   LHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSIEWI   291
             LHNFSRQDVEGEKMNRIVQNSLTTAVH+RGPTQ+VLQHQ+AVRIRENYL QGVDLSIEWI
Sbjct  772   LHNFSRQDVEGEKMNRIVQNSLTTAVHNRGPTQEVLQHQKAVRIRENYLNQGVDLSIEWI   831

Query  290   KNNGYRGPSAEQMKVIKTGLDPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASP   111
             KNNG+RGPSA+QMK IK GL+P P T   + P P +D STP LVM+II+NSL  HY+NASP
Sbjct  832   KNNGFRGPSADQMKTIKAGLEPPPDTTTKSPTPHNDTSTPALVMKIIKNSLGIHYDNASP   891

Query  110   ETQKEINERVTTMVINNGNRGLNQYQVKEIVQDYGK   3
             ETQKEINER+TTMVINNGNRGLNQYQ KEIVQDYGK
Sbjct  892   ETQKEINERITTMVINNGNRGLNQYQAKEIVQDYGK   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:

```
Query  980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
             T +P+  I +N     +      PI  G S +  L+LL     I   GV     TG +  E
Sbjct  606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query  818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
             I+P    D+K       G+PL+ +Q    + +++ + A  ++Q  T     A+
Sbjct  665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK   724

Query  644   MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
                 +          DE++   L   + A + +D  + KL +++ W  K D     + D +
Sbjct  725   YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM   779
```

```
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  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYEAVAAVFAENGGRGPDQDQMQDL   929
```

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	Frame
82.0 bits(201)	1e-13()	Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N     +        PI  G S + L+LL   I  GV     TG +   E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
              I+P    D+K        G+PL+ +Q     + +++ + A  ++Q  T      A+
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK   724

Query   644   MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
                   +           DE++    L    + A + +D  + KL +++ W  K D    + D +
Sbjct   725   YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM   779

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  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   929
```

polyprotein [Tasmanian aquabirnavirus]

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

Range 1: 606 to 929

Score	Expect	Method	Identities	Positives	Gaps	Frame
82.0 bits(201)	1e-13()	Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N     +        PI  G S + L+LL   I  GV     TG +   E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
              I+P    D+K        G+PL+ +Q     + +++ + A  ++Q  T      A+
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK   724

Query   644   MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
                   +           DE++    L    + A + +D  + KL +++ W  K D    + D +
Sbjct   725   YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM   779

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  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   929
```

polyprotein [Tasmanian aquabirnavirus]

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

Range 1: 606 to 929

Score	Expect	Method	Identities	Positives	Gaps	Frame
82.0 bits(201)	1e-13()	Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N     +        PI  G S + L+LL   I  GV     TG +   E
```

```
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
              I+P    D+K         G+PL+ +Q     + +++ + A  ++Q  T      A+
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK   724

Query   644   MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
                   +           DE++    L   + A + +D  + KL +++ W  K D     + D +
Sbjct   725   YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM   779

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  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   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(201)	1e-13()	Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N     +          PI  G S +  L+LL     I  GV      TG + E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
              I+P    D+K         G+PL+ +Q     + +++ + A  ++Q  T      A+
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK   724

Query   644   MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
                   +           DE++    L   + A + +D  + KL +++ W  K D     + D +
Sbjct   725   YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM   779

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   ALNNYRGPSPGQFKYYLITGRDPEPGDEYEDYIKQPITKPTDMTK--IRRLANSVYGLPH   897

Query   125   ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
              +  +PE    E  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   929
```

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: **gb|ALF95279.1|** Length: 972 Number of Matches: 1

Range 1: 606 to 929

Score	Expect	Method	Identities	Positives	Gaps	Frame
81.6 bits(200)	2e-13()	Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N     +          PI  G S +  L+LL     I  GV      TG + E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
              I+P    D+K         G+PL+ +Q     + +++ + A  ++Q  T      A+
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK   724

Query   644   MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
                   +           DE++    L   + A + +D  + KL +++ W  K D     + D +
Sbjct   725   YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM   779

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

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

Query   125   ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
              +  +PE    E  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   929
```

polyprotein [Tasmanian aquabirnavirus]

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(200)	2e-13()	Compositional matrix adjust.	84/335(25%)	147/335(43%)	26/335(7%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N    +     PI  G S+  L+LL  I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA  645
            I+P    D+K       G+PL+ +Q    + +++ + A  ++Q T    A+
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK  724

Query  644  MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL  468
             +           DE++    L   + A+ +D  + KL +++ W  K D     + D +
Sbjct  725  YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM  779

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  ALNNYRGPSPGQFKYYLITGRDPEPGDEYEDYIKQPITKPTDMTK--IRRLANSVYGLPH  897

Query  125  ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
            +  +PE    E  + V  +   NG RG +Q Q++++
Sbjct  898  QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   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  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S+  L+LL  I  GV     TG +   E  IVP    D+K       G+PLV Q
Sbjct  631  GPSCQLGLSLLVNDIDKGVPRMVFTGEIADDEETIVPICGVDIKAIAAHEHGLPLVGCQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM  567
              + + + + A+ ++Q         A +     +        DE++    L+   +
Sbjct  691  GVDEEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLQATMA  750

Query  566  AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH  390
             A + +D  + KL +++ W  K       G+ D ++ +S++D E K   +++
Sbjct  751  RAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK  805

Query  389  SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP-  219
            +GP Q   Q   +AVRI + +  G D  S +WI  NGYRGPS  Q K  + TG  P P
Sbjct  806  PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDPR  865

Query  218  ---QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG   48
               +  +R+PI R   +   + R+ +    ++  +PE    E  + V  +   NG RG
Sbjct  866  DEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGGRG  920

Query   47  LNQYQVKEI   21
            +Q Q++++
Sbjct  921  PDQDQMQDL   929
```

polyprotein [Tasmanian aquabirnavirus]

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

Range 1: 606 to 929

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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N    +     PI  G S+  L+LL  I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA  645
            I+P    D+K       G+PL+ +Q    + +++ + A  ++Q T    A+
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK  724

Query  644  MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL  468
             +           DE++    L   + A+ +D  + KL +++ W  K D     + D +
Sbjct  725  YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM  779

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

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

Query  125  ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
            +  +PE    E  + V  +   NG RG +Q Q++++
Sbjct  898  QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   929
```

polyprotein [Marine birnavirus]

Sequence ID: **gb|AAP37163.1|** Length: 972 Number of Matches: 1

Range 1: 631 to 929

Score	Expect	Method	Identities	Positives	Gaps	Frame
81.3 bits(199)	2e-13()	Compositional matrix adjust.	79/309(26%)	137/309(44%)	22/309(7%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
                G S+  L+LL  I  GV      TG +   E  I+P    D+K       G+PLV  Q
Sbjct  631  GPSCQLGLSLLVNDIDKGVPRMVFTGEIADDEESIIPICGVDIKAIAAHEHGLPLVGCQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM  567
               + + + + A+ ++Q       A  +       +          DE++   L+  +
Sbjct  691  GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLQATMA  750

Query  566  AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH  390
              A + +D  + KL +++ W  K       G+ D ++ +S++D E  K   +++
Sbjct  751  RAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK  805

Query  389  SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP-  219
              +GP Q   Q  +AVRI  + +  G D  S +WI   NGYRGPS   Q K  + TG  P P
Sbjct  806  PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDPR  865

Query  218  ---QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG  48
                 +  +R+PI R  +   + R+ +      ++ +PE   E  + V  +   NG RG
Sbjct  866  DEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGGRG  920

Query  47   LNQYQVKEI   21
              +Q  Q++++
Sbjct  921  PDQDQMQDL   929
```

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:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
                G S+  L+LL  I  GV      TG +   E  IVP      D+K        G+PLV  Q
Sbjct  631  GPSCQLGLSLLVNDIDKGVPRMVFTGEIANDEETIVPICGVDIKAIAAHEHGLPLVGCQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM  567
               + + + + A+ ++Q       A  +       +          DE++   L   +
Sbjct  691  GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLHATMA  750

Query  566  AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH  390
              A + +D  + KL +++ W  K       G+ D ++ +S++D E  K   +++
Sbjct  751  RAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK  805

Query  389  SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP-  219
              +GP Q   Q  +AVRI  + +   G D  S +WI   NGYRGPS   Q K  + TG  P P
Sbjct  806  PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDPR  865

Query  218  ---QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG  48
                 +  +R+PI R  +   + R+ +      ++ +PE   E  + V  +   NG RG
Sbjct  866  DEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGGRG  920

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 bits(198)	3e-13()	Compositional matrix adjust.	84/335(25%)	146/335(43%)	26/335(7%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
              T +P+  I +N     +      PI  G S+  L+LL  I  GV      TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA  645
              I+P    D+K        G+PL+ +Q    + +++ + A  ++Q  T     A
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAKGSNKRIK  724

Query  644  MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL  468
              +           DE++   L   +  A + +D  + KL +++ W  K D     + D +
Sbjct  725  YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM  779
```

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

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

Query   125   ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
              +  +PE  E  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL    929
```

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(198)	3e-13()	Compositional matrix adjust.	80/309(26%)	136/309(44%)	22/309(7%)	-2

Features:

```
Query   911   GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD   741
              G S+  L+LL   I  GV     TG +   E  IVP    D+K       G+PLV  Q
Sbjct   631   GPSCQLGLSLLVNDIDKGVPRMVFTGEIANDEETIVPICGVDIKAIAAHEHGLPLVGCQP   690

Query   740   Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM   567
                + + + A+ ++Q         A   +       +      DE++    L    +
Sbjct   691   GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLHATMA   750

Query   566   AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH   390
              A + +D  + KL +++ W  K       G+ D ++ +S++D E K   +++
Sbjct   751   RAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK   805

Query   389   SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP-   219
              +GP Q   Q +AVRI  + +  G D  S +WI  NGYRGPS  Q K  + TG  P P
Sbjct   806   PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDPR   865

Query   218   ---QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG   48
                 + +R+PI R + + + R+ +      ++ +PE  E  + V  +   NG RG
Sbjct   866   DEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGGRG   920

Query   47    LNQYQVKEI    21
              +Q Q++++
Sbjct   921   PDQDQMQDL    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(198)	3e-13()	Compositional matrix adjust.	84/335(25%)	146/335(43%)	26/335(7%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N     +        PI  G S+  L+LL   I  GV     TG +   E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
              I+P    D+K       G+PL+ +Q     + +++ + A  ++Q  T      A
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAKGSNKRIK   724

Query   644   MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
              +           DE++    L    + A + +D  + KL +++ W  K D      + D +
Sbjct   725   YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM   779

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   ALNNYRGPSPGQFKYYLITGRDPEPGDEYEDYIKQPITKPTDMTK--IRRLANSVYGLPH   897

Query   125   ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
              +  +PE  E  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL    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-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S+  L+LL   I  GV      TG +   E  IVP   D+K      G+PLV  Q
Sbjct  631  GPSCQLGLSLLVNDIDKGVPRMVFTGEIANDEETIVPICGVDIKAIAAHEHGLPLVGCQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM  567
            + + + + A+ ++Q       A   +          +      DE++    L   +
Sbjct  691  GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLHATMA  750

Query  566  AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH  390
            A + +D  + KL +++ W  K       G+ D ++ +S++D  E  K   +++
Sbjct  751  RAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK  805

Query  389  SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP-  219
            +GP Q  Q  +AVRI  + + G D  S +WI  NGYRGPS  Q K  + TG   P P
Sbjct  806  PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDPR  865

Query  218  ---QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG  48
               +  +R+PI R  +  + + R+           ++  +PE  E  + +   NG RG
Sbjct  866  DEYEDYVRKPITRPTDM--DKIRRLANGVYGLPHQEPAPE---EFYQAVVEIFAENGGRG  920

Query  47   LNQYQVKEI   21
            +Q Q++++
Sbjct  921  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(197)	4e-13()	Compositional matrix adjust.	84/335(25%)	146/335(43%)	26/335(7%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N   +        PI  G S+  L+LL   I  GV      TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA  645
            I+P    D+K      G+PL+ +Q     + +++ + A  ++Q  T    A
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAKGSNQRIK  724

Query  644  MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL  468
            +          DE++   L   + A + +D  + KL +++ W  K D      + D +
Sbjct  725  YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM  779

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  ALNNYRGPSPGQFKYYLITGRDPEPGDEYEDYIKQPITKPTDMTK--IRRLANSVYGLPH  897

Query  125  ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
            + +PE   E  + +   NG RG +Q Q++++
Sbjct  898  QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL  929
```

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(197)	4e-13()	Compositional matrix adjust.	78/309(25%)	136/309(44%)	22/309(7%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S+  L+LL   I  GV      TG +   E  IVP   D+K      G+PL+ +Q
Sbjct  631  GPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEETIIPICGVDIKAIAAHEQGLPLIGNQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM  567
            + +++ + A  ++Q  T    A                       DE++    L   +
Sbjct  691  GVDEEVRNTSLAAHLIQTGTLPVQKAKGSNQRIKYLGELMASTASGMDEELQSLLNATMA  750

Query  566  AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH  390
            A + +D  + KL +++ W  K D      + D ++ +S++D  E  K   +++
Sbjct  751  RAKEVKDVEIYKLLKLMAWTRKND-----LTDHMYEWSKEDPEAVKFGKLISTPPKHPEK  805

Query  389  SRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQMK-VIKTGLDPAP-  219
            +GP Q  Q  RA RI  + + G D +  EW+  N YRGPS  Q K  + TG DP P
Sbjct  806  PKGPDQHHAQEARAARISLDAVRAGADFATPEWVALNNYRGPSPGQFKYYLITGRDPEPG  865

Query  218  ---QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG  48
               +  I++PI +  + T   + R+  +       ++ +PE   E  + +   NG RG
Sbjct  866  DEYEDYIKQPITKPTDMTK--IRRLANSVYGLPHQEPAPE---EFYDAVAAVFAENGGRG  920

Query  47   LNQYQVKEI   21
            +Q Q++++
Sbjct  921  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(197)	4e-13()	Compositional matrix adjust.	79/309(26%)	136/309(44%)	22/309(7%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S+  L+LL   I GV      TG +  E  IVP   D+K       G+PLV  Q
Sbjct  631  GPSCQLGLSLLVNDIDKGVPRMVFTGEIANDEETIVPICGVDIKAIAAHEHGLPLVGCQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM  567
            + + + + A+ ++Q       A   +       DE++   L   +
Sbjct  691  GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLHATMA  750

Query  566  AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH  390
            A + +D + KL +++ W  K     G+ D ++ +S++D E  K  +++
Sbjct  751  RAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK  805

Query  389  SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP-  219
            +GP Q   Q  +AVRI  + +  G D  S +W+  NGYRGPS  Q K + TG  P P
Sbjct  806  PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWVAENGYRGPSPGQFKYYVITGRVPDPR  865

Query  218  ---QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG  48
               +  +R+PI R +   + + R+  +      ++  +PE   E  + V  +  NG RG
Sbjct  866  DEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGGRG  920

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(196)	6e-13()	Compositional matrix adjust.	82/304(27%)	130/304(42%)	31/304(10%)	-2

Features:

```
Query  884  LLQHIPPGVTPFAVTGNV--IEGKIVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLA  717
            L+  I GV      TG +  E  I+P   D+K       G+PLV +Q   + +    +
Sbjct  641  LVNDIQEGVPRMVFTGELGQDEESIIPICGVDIKAIAAHELGLPLVGNQPGVDEEVPTTS  700

Query  716  KATEMLQRITTAQHPAV-----IGTIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-  555
            A ++Q+ T     A       I +   MDS++       DE++   L   + A +
Sbjct  701  LAAHLIQKGTLPVQKACGVDKRIKHLGLLMDSNASGM-----DEELQRLLSATMARAKEV  755

Query  554  RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPT  375
            +D + KL ++ W  K     G+ D ++ +SR+D +  K  R++          +GP
Sbjct  756  KDAEIYKLLRLMSWTRK-----NGLTDHMYEWSREDPDAVKFGRLISTPPKHQEKPKGPD  810

Query  374  QDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMKVIK-TGLDPAP----QT  213
            Q   Q  RA RI  + +  G D  S EWI  N YRGPS  Q K  K TG  P P    +
Sbjct  811  QHTAQEARAARISLDAVKAGADFASPEWIAENNYRGPSPGQFKYYKITGNTPNPGDEYED  870

Query  212  IIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRGLNQYQ  33
            + PI R + T + R+  +      ++  +PE   E  V  +  NG RG +Q Q
Sbjct  871  YVTRPITRPTDMT--RIRRLANSVYGLPHQEPAPE---EFYNAVAAVFSENGGRGPDQDQ  925

Query  32   VKEI   21
            + ++
Sbjct  926  MLDL   929
```

polyprotein [Yellowtail ascites virus]

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

Range 1: 631 to 929

Score	Expect	Method	Identities	Positives	Gaps	Frame
79.0 bits(193)	1e-12()	Compositional matrix adjust.	78/309(25%)	136/309(44%)	22/309(7%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S+  L+LL   I GV      TG +  E  I+P   D+K       G+PLV  Q
Sbjct  631  GPSCQLGLSLLVNDIDRGVPRMVFTGEIADDEETIIPIYGVDIKAIAAHEHGLPLVGCQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM  567
            + + + + A+ ++Q       A   +       DE++   L+  +
Sbjct  691  GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLQATMA  750

Query  566  AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH  390
            A + +D + KL +++ W  K     G+ D ++ +S++D E  K  +++
Sbjct  751  RAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK  805

Query  389  SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAP-  219
            +GP Q   Q  +A RI  + +  G D  S +WI  NGYRGPS  Q K  + TG  P P
Sbjct  806  PKGPDQHTAQEAKAARISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDPR  865

Query  218  ---QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG  48
Sbjct  806  PKGPDQHTAQEAKAARISLDAVKAGADFASPDWIAENGYRGPSPGQFKYYVITGRVPDPR  865
```

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

Query    47   LNQYQVKEI   21
                  +Q Q++++
Sbjct   921   PDQDQMQDL   929
```

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(193)	1e-12()	Compositional matrix adjust.	92/355(26%)	151/355(42%)	74/355(20%)	-2

Features:

```
Query   923   PIPRGGSMEAALALLQHIPPGVTPFAVTGNVIEGKIVPNKWADLKREGMKGTGIPLV---   753
              P   G S    ALAL   +P  V   A TG +    + P ++ +LK       G+PLV
Sbjct   686   PAVAGQSSSIALALASSLP-FVPKAAYTGCLSGTNVQPVQFGNLKARAAHKIGLPLVGMT   744

Query   752   ----TDQDYKTIKDLA-KATEMLQRITTAQHPAVIGTIAT--------AMDSDSpppppP   612
                  D   T+ D A  A + ++  +T    P  +G  A         A D ++
Sbjct   745   QDGGEDTRICTLDDAADHAFDSME--STVTRPESVGHQAAFQGWFYCGAADEETIEEL--   800

Query   611   ITDEDIMVTLE---------------ELLMAAADRDPRMAKLKEVVLWLAKIDDNNPGV   480
                ED + +++E              ELLM  A +DP+M+K+  ++ W+         G+
Sbjct   801   ---EDFLDSIELHSKPTVEQPQTEEAMELLMELARKDPQMSKILVILGWV-----EGAGL   852

Query   479   LDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSR----GPT-------------QDVLQHQ   354
              +D L+N+++ D  G +M  +++N       S+     GP            +    + +
Sbjct   853   IDALYNWAQLDDGGVRMRNMLRNLPHEGSKSQRRKHGPAPESRESTRMEVLRREAAAKRK   912

Query   353   RAVRIRENYLIQGVDLS-IEWIKNNGYRGPSAEQMKVIK-TGLDPAP--QTIIREPIPRS   186
              +A RI E+ +  G + + I+W+   NG RGP+   Q  K TGLDP P       + EP
Sbjct   913   KAQRISEDAMDNGFEFATIDWVLENGSRGPNPAQAKYYKATGLDPEPGLTEFLPEPTHAP   972

Query   185   DNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
              +N   +L   I +           N +P   + E    ++ NNG RG NQ Q++E+
Sbjct   973   ENKAAKLAATIYGS------PNQAPAPPEFVEEVAAVLMENNG-RGPNQAQMREL   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(192)	2e-12()	Compositional matrix adjust.	83/335(25%)	146/335(43%)	26/335(7%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N   +          PI  G S  L+LL    I  GV     TG +   E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
              I+P    D+K       G+PL+ +Q   + +++ + A  ++Q  T     A+
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK   724

Query   644   MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
                +          DE++    L   + A + +D  + KL +++ W  K D      + D +
Sbjct   725   YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM   779

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

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

Query   125   ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
              +  +PE   E  + V  +   NG RG +Q Q++++
Sbjct   898   QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   929
```

polyprotein [Tasmanian aquabirnavirus]

Sequence ID: **gb|ALF95283.1|** Length: 972 Number of Matches: 1
Range 1: 606 to 929

Score	Expect	Method	Identities	Positives	Gaps	Frame
78.6 bits(192)	2e-12()	Compositional matrix adjust.	83/335(25%)	146/335(43%)	26/335(7%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N   +          PI  G S  L+LL    I  GV     TG +   E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
```

```
                 I+P     D+K        G+PL+ +Q    + +++ + A  ++Q T      A+
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK  724

Query  644  MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL  468
                 +       DE++    L   + A + +D  + KL +++ W  K D      + D +
Sbjct  725  YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM  779

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

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

Query  125  ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
            +   +PE     E   + V   +   NG RG +Q Q++++
Sbjct  898  QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   929
```

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(189)	5e-12()	Compositional matrix adjust.	83/335(25%)	145/335(43%)	26/335(7%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +        PI  G S + L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEEGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA  645
            I P     D+K        G+PL+ +Q    + +++ + A  ++Q T      A+
Sbjct  665  ITPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQKAMGSNKRIK  724

Query  644  MDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTL  468
                 +       DE++    L   + A + +D  + KL +++ W  K D      + D +
Sbjct  725  YLGELMASTASGMDEELQSLLNATMARAKEVKDVEIYKLLKLMAWTRKND-----LTDHM  779

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

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

Query  125  ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
            +   +PE     E   + V   +   NG RG +Q Q++++
Sbjct  898  QEPAPE---EFYDAVAAVFAENGGRGPDQDQMQDL   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  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +        PI  G S + L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P +  D+K        G+PL+ +Q    + +++ + A  ++Q T      A     I
Sbjct  665  IIPIRGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQAGTLPVQRAQGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++     DE++    L   + A + +D  + KL  ++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLRLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D + K  +++         RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

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:

```
Query  980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEGK--   819
             T +P+  I +N     +      PI  G S +  L+LL   I  GV    TG + E +
Sbjct  606   TALPLKEIKKNGNIIVEKIFAGPI-MGPSAQLGLSLLVNDIDEGVPRMVFTGEIAEDEET   664

Query  818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA   645
             I+P    D+K     G+PL+ +Q    + +K+ + A ++Q T    A   +
Sbjct  665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVKNTSLAAHLIQSGTLPVQKAKGASKRIK   724

Query  644   MDSDSpppppPITDEDIMVTLEELLM-AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTL   468
                 +         DE++  L  +  A A +D + KL  ++ W  K D    + D +
Sbjct  725   YLGELMQTTASGMDEELQSLLAATMARAKAVKDAEIYKLLRLMSWTRKND-----LTDHM   779

Query  467   HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWI   291
             + +SR+D + K  +++            +GP Q   Q  +A+RI + +  G + + EW+
Sbjct  780   YEWSREDPDAIKFGKLISTPPKHPEKPKGPDQHQAQEAKAIRISLDAVRAGANFATTEWV   839

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

Query  125   ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
             +  +PE    E  V  +  +NG RG +Q Q++++
Sbjct  898   QEPAPE---PFYEAVAAVFADNGGRGPDQDQMQDL   929
```

VP3 protein [Blotched snakehead virus]

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

Range 1: 34 to 229

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:

```
Query  578   ELLMAAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQN----   411
             ELLM  A +DP+M+K+  ++ W+       G++D L+N+++ D  G +M   +++N
Sbjct  34    ELLMELARKDPQMSKILVILGWV-----EGAGLIDALYNWAQLDDGGVRMRNMLRNLPHE   88

Query  410   -------SLTTAVHSRGPTQ-DVLQHQ------RAVRIRENYLIQGVDLS-IEWIKNNGY   276
                    A  SR  T+ +VL+ +       +A RI E+ +  G + + I+W+  NG
Sbjct  89    GSKSQRRKHGPAPESRESTRMEVLRREAAAKRKKAQRISEDAMDNGFEFATIDWVLENGS   148

Query  275   RGPSAEQMKVIK-TGLDPAP--QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPET   105
             RGP+  Q K  K TGLDP P    + EP    +N  +L    I  +      N +P
Sbjct  149   RGPNPAQAKYYKATGLDPEPGLTEFLPEPTHAPENKAAKLAATIYGSP------NQAP-A   201

Query  104   QKEINERVTTMVINNGNRGLNQYQVKEI   21
              E  E V  +++ N  RG NQ Q++E+
Sbjct  202   PPEFVEEVAAVLMENNGRGPNQAQMREL   229
```

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(184)	2e-11()	Compositional matrix adjust.	78/309(25%)	135/309(43%)	22/309(7%)	-2

Features:

```
Query  911   GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD   741
             G S +  L+LL   I  GV    TG +  E   IVP   ++K     G+PLV  Q
Sbjct  631   GPSCQLGLSLLVNDIDKGVPRMVFTGEIADDEETIVPICGVNIKAIAAHEHGLPLVGCQP   690

Query  740   Y--KTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLM   567
                + + + + A+ ++Q         A   +      +      DE++    L    +
Sbjct  691   GVDEVVANTSLASHLIQSGALPVQKAQGASRRIKYLGELMRTTASGMDEELQKLLHATMA   750

Query  566   AAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVH   390
             A + +D + KL  +++ W  K       G+ D ++  +S++D E  K   +++
Sbjct  751   RAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQEK   805

Query  389   SRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAPQ   216
             +GP Q   Q  +AVRI + +  G  D  S +WI  N YRGPS  Q K  + TG  P P+
Sbjct  806   PKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENRYRGPSPGQFKYYVITGSVPDPR   865

Query  215   ----TIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRG   48
                 +R+PI R +    + R+ +      ++  +PE   E  + V +   NG RG
Sbjct  866   DEYDDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGGRG   920

Query  47    LNQYQVKEI   21
             +Q Q++++
Sbjct  921   PDQEQMQDL   929
```

structural polyprotein [Infectious pancreatic necrosis virus]

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

Range 1: 606 to 929

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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +      PI  G S+ L+LL   I  GV     TG +    E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P    D+K        G+PL+ +Q     + +++ + A  ++Q T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++          DE++   L   + A ++D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D +  K  +++       +GP Q   Q  RA RI  + +   G D+
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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

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

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(182)	3e-11()	Compositional matrix adjust.	80/317(25%)	134/317(42%)	38/317(11%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S+ L+LL   I  GV     TG +    E I+P     D+K        G+PLV  Q
Sbjct  631  GPSCQLGLSLLVNDIEEGVPRMVFTGEISGDEETIIPICGVDIKAIAAHEHGLPLVGCQ-  689

Query  740  YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPI----------TDEDIM  591
                E++    + A H     G +      + +          +           DE++
Sbjct  690  -------PGVDEVVANTSLASHLIQTGALPVQKTQGASRRIRYLGELMRTTASGMDEELQ  742

Query  590  VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ  414
             L+   + A + +D  + A ++D  + KL +++ W  K D       + D L  +SR+D + K  R++
Sbjct  743  GLLQATMARAKEVKDVEIFKLLKLMSWTRKND-----LTDNLFEWSREDPDAIKFGRLIS  797

Query  413  NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK  240
             +GP Q   Q  +AVRI  + +   G D  S EW+  +NGYRGP+  Q K  +
Sbjct  798  TPPKHQEKPKGPDQHTAQEAKAVRISLDAVRAGADFASPEWVADNGYRGPNPGQFKYYMI  857

Query  239  TGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM  72
            TG  P P    +  +R+PI R  N   + + R+  +   ++  +PE  +  + V  +
Sbjct  858  TGEVPNPGDDYEDYVRKPITRPTNM--DKIRRLANSIYGLPHQEPAPE---QFYDAVVEV  912

Query  71   VINNGNRGLNQYQVKEI  21
             +   N RG +Q Q++++
Sbjct  913  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(182)	4e-11()	Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +      PI  G S+ L+LL   I  GV     TG +    E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P    D+K        G+PL+ +Q     + +++ + A  ++Q T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++          DE++   L   + A ++D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D +  K  +++       +GP Q   Q  RA RI  + +   G D+
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

107 kDa polyprotein [Infectious pancreatic necrosis virus]
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(182)	4e-11()	Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+ I +N     +      PI G S+ L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P    D+K     G+PL+ +Q     + +++ + A  ++Q  T      A      I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++        DE++   L   + A ++D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D +  K   +++          +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+ I +N     +      PI G S+ L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P    D+K     G+PL+ +Q     + +++ + A  ++Q  T      A      I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++        DE++   L   + A ++D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D +  K   +++          +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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

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

polyprotein [Infectious pancreatic necrosis virus]
Sequence ID: **gb|AAX24140.1|** 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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+ I +N     +      PI G S+ L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P    D+K     G+PL+ +Q     + +++ + A  ++Q  T      A      I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++        DE++   L   + A ++D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D +  K   +++          +GP Q   Q  RA RI  + +  G D +
```

```
Sbjct   775   LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA   834

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
```

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

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N    +       PI G S+ L+LL   I GV      TG +    E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG   660
              I+P    D+K      G+PL+ +Q   + +++ + A  ++Q  T      A     I
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK   724

Query   659   TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLEVVLWLAKIDDNNPG   483
                +    M S++         DE++    L    + A + +D  + KL +++ W  K D
Sbjct   725   YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----   774

Query   482   VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS   303
              + D ++ +S++D +  K   +++             +GP Q   Q  RA RI  + +  G D +
Sbjct   775   LTDHMYEWSKEDPDALKFGKLISTPPKRPEKPKGPDQHHAQEARATRISLDAVRAGADFA   834

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
```

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:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+  I +N    +       PI G S+ L+LL   I GV      TG +    E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG   660
              I+P    D+K      G+PL+ +Q   + +++ + A  ++Q  T      A     I
Sbjct   665   IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK   724

Query   659   TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLEVVLWLAKIDDNNPG   483
                +    M S++         DE++    L    + A + +D  + KL +++ W  K D
Sbjct   725   YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----   774

Query   482   VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS   303
              + D ++ +S++D +  K   +++             +GP Q   Q  RA RI  + +  G D +
Sbjct   775   LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA   834

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
```

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:

Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +        PI  G S+ L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P   D+K       G+PL+ +Q      + +++ + A  ++Q T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++         DE++   L   + A + +D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D + K  +++          +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

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(181)	4e-11()	Compositional matrix adjust.	80/311(26%)	133/311(42%)	26/311(8%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S+ L+LL   I  GV     TG +   E IVP   ++K       G+PLV  Q
Sbjct  631  GPSCQLGLSLLVNDIDKGVPRMVFTGEIADDEETIVPICGVNIKAIAAHEHGLPLVGCQ-  689

Query  740  YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLMAA  561
            + ++    T +   +      V T    +           L++LL A
Sbjct  690  -PGVDEVVANTSLASHLIQSGALPVQKTQGASRRIKYLGELMRTTASGMDEELQKLLHAT  748

Query  560  ADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTA  396
             R      D  + KL +++ W  K       G+ D ++ +S++D E K   +++
Sbjct  749  MARAKEVKDAEVFKLLKLMSWTRK-----NGLTDHMYEWSKEDPEAVKFGKLISTPPKHQ  803

Query  395  VHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPA  222
             +GP Q   Q  +AVRI  + +  G D  S +WI  N YRGPS  Q K  + TG  P
Sbjct  804  EKPKGPDQHTAQEAKAVRISLDAVKAGADFASPDWIAENRYRGPSPGQFKYYVITGSVPD  863

Query  221  PQ----TIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGN  54
            P+       +R+PI R  +    + + R+  +      ++  +PE  E  + V  +   NG
Sbjct  864  PRDEYDDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPE---EFYQAVVEIFAENGG  918

Query  53   RGLNQYQVKEI  21
            RG +Q Q++++
Sbjct  919  RGPDQEQMQDL  929
```

107 kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAQ75350.1|** 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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +        PI  G S+ L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P   D+K       G+PL+ +Q      + +++ + A  ++Q T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++         DE++   L   + A + +D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D + K  +++          +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

structural polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAD11535.1| 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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +      PI G S+ L+LL   I GV    TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P   D+K       G+PL+ +Q    + +++ + A  ++Q T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
            +   M S++         DE++    L   A  +D  KL +++  W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D +  K  +++      +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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

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

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

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +      PI G S+ L+LL   I GV    TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P   D+K       G+PL+ +Q    + +++ + A  ++Q T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
            +   M S++         DE++    L   A  +D  KL +++  W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D + K   +++      +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AEM92170.1| 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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +      PI G S+ L+LL   I GV    TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P   D+K       G+PL+ +Q    + +++ + A  ++Q T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
            +   M S++         DE++    L   A  +D  KL +++  W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D + K   +++      +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834
```

```
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
```

108-kDa polyprotein [Infectious pancreatic necrosis virus]

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

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
             T +P+  I +N     +      PI  G S+  L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
             I+P    D+K       G+PL+ +Q    + +++ + A  ++Q  T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +    M S++          DE++    L  +  A +D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM------DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
             + D ++ +S++D + K  +++       +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

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

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
             T +P+  I +N     +      PI  G S+  L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
             I+P    D+K       G+PL+ +Q    + +++ + A  ++Q  T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +    M S++          DE++    L  +  A +D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM------DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
             + D ++ +S++D + K  +++       +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

polyprotein [Infectious pancreatic necrosis virus - Sp]

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

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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
             T +P+  I +N     +      PI  G S+  L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664
```

```
Query   818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG   660
             I+P    D+K      G+PL+ +Q     + +++ + A  ++Q  T      A     I
Sbjct   665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK   724

Query   659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLEVVLWLAKIDDNNPG   483
             +   M S++          DE++   L   + A + +D  + KL +++ W  K D
Sbjct   725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----   774

Query   482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS   303
             + D ++ +S++D + K  +++            +GP Q   Q  RA RI  + +  G D +
Sbjct   775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA   834

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
```

108-kDa polyprotein [Infectious pancreatic necrosis virus]

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(181)	5e-11()	Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2

Features:

```
Query   980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
             T +P+  I +N     +      PI  G S + L+LL   I  GV     TG +   E
Sbjct   606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET   664

Query   818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG   660
             I+P    D+K      G+PL+ +Q     + +++ + A  ++Q  T      A     I
Sbjct   665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK   724

Query   659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLEVVLWLAKIDDNNPG   483
             +   M S++          DE++   L   + A + +D  + KL +++ W  K D
Sbjct   725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----   774

Query   482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS   303
             + D ++ +S++D + K  +++            +GP Q   Q  RA RI  + +  G D +
Sbjct   775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA   834

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
```

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:

```
Query   980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
             T +P+  I +N     +      PI  G S + L+LL   I  GV     TG +   E
Sbjct   606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET   664

Query   818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG   660
             I+P    D+K      G+PL+ +Q     + +++ + A  ++Q  T      A     I
Sbjct   665  IIPICGVDIKAIAAHEPGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK   724

Query   659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLEVVLWLAKIDDNNPG   483
             +   M S++          DE++   L   + A + +D  + KL +++ W  K D
Sbjct   725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----   774

Query   482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS   303
             + D ++ +S++D + K  +++            +GP Q   Q  RA RI  + +  G D +
Sbjct   775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA   834

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
```

polyprotein, partial [Infectious pancreatic necrosis virus]

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(181)	5e-11()	Compositional matrix adjust.	83/335(25%)	146/335(43%)	26/335(7%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEGK--  819
            T +P+  I +N     +      PI  G S   L+LL    I   GV     TG + E +
Sbjct  606  TALPLKEIKKNGNIIVEKIFAGPI-MGPSAQLGLSLLVNDIDEGVPRMVFTGEIAEDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA  645
            I+P   D+K       G+PL+ +Q    + +K+ + A  ++Q  T     A    +
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVKNTSLAAHLIQSGTLPVQKAKGVSKRIK  724

Query  644  MDSDSpppppPITDEDIMVTLEELLM-AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTL  468
              +            DE++    L   + A A +D + KL +++ W  K D     + D +
Sbjct  725  YLGELMQTTASGMDEELQSLLAATMARAKAVKDAEIYKLLKLMSWTRKND-----LTDHM  779

Query  467  HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWI  291
            + +SR+D + K  +++         +GP Q   Q +A+RI + +  G + +  EW+
Sbjct  780  YEWSREDPDAIKFGKLISTPPKHPEKPKGPDQHQAQEAKAIRISLDAVRAGANFATTEWV  839

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

Query  125  ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
            +  +PE        E V  +  +NG RG +Q Q++++
Sbjct  898  QEPAPE---PFYEAVAAVFTDNGGRGPDQDQMQDL   929
```

108-kDa polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAR10446.1|** Length: 972 Number of Matches: 1

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:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +      PI  G S   L+LL    I   GV     TG +  E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIDEGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P   D+K       G+PL+ +Q    + +++ + A  ++Q  T     A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++            DE++    L   + A + +D  + KL +++ W   K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D +  K   +++         +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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

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

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(180)	6e-11()	Compositional matrix adjust.	84/340(25%)	149/340(43%)	36/340(10%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N     +      PI  G S   L+LL    I   GV     TG +  E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIDEGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P   D+K       G+PL+ +Q    + +++ + A  ++Q  T     A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAQGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
             +   M S++            DE++    L   + A + +D  + KL  ++ W   K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLRLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D +  K   +++         +GP Q   Q  RA RI  + +  G D +
Sbjct  775  LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

Query  302  I-EWIKNNGYRGPSAEQMKV-IKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNS  141
```

```
              EW+  N YRGPS  Q K  + TG +P P    +  I++PI +  +      + R+  +
Sbjct  835  TPEWVALNNYRGPSPGQFKYHLITGREPEPGDEYEDYIKQPIVKPTDMNK--IRRLANSV  892

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

polyprotein [Infectious pancreatic necrosis virus]

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(180)	6e-11()	Compositional matrix adjust.	84/340(25%)	150/340(44%)	36/340(10%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
              T +P+  I +N     +     PI  G S+  L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
              I+P   D+K      G+PL+ +Q      + +K + A  ++Q  T    A     I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
              +   M S++         DE++    L   + A + +D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
              + D ++ +S++D + K  +++            +GP Q   Q  RA RI  + +   G D +
Sbjct  775  LTDHMYEWSKEDPBALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

Query  302  I-EWIKNNGYRGPSAEQMKV-IKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNS  141
              EW+  N YRGPS  Q K  + TG +P P    +  I++PI +  +      + R+  +
Sbjct  835  TPEWVALNNYRGPSPGQFKYXLITGREPEPGDEYEDYIKQPIVKPTDMNK--IRRLANSV  892

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

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(180)	6e-11()	Compositional matrix adjust.	83/335(25%)	144/335(42%)	26/335(7%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVIEGK--  819
              T +P+  I +N     +     PI  G S+  L+LL   I  GV     TG + E +
Sbjct  606  TALPLKEIKKNGNIIVEKIFAGPI-MGPSAQLGLSLLVNDIDEGVPRMVFTGEIAEDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAVIGTIATA  645
              I+P   D+K      G+PL+ +Q      + +K + A  ++Q  T    A     I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVKTTSLAAHLIQSGTLPVQKAKGASKRIK  724

Query  644  MDSDSpppppPITDEDIMVTLEELLM-AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTL  468
              +           DE++    L   + A A +D  + KL  ++ W  K D      + D +
Sbjct  725  YLGELMQTTASGMDEELQNLLAATMARAKAVKDAEIYKLLRLMSWTRKND-----LTDHM  779

Query  467  HNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWI  291
              + +SR+D + K  +++            +GP Q   Q  +A+RI  + +   G + +  EW+
Sbjct  780  YEWSREDPDAIKFGKLISTPPKHPEKPKGPDQHQAQEAKAIRISLDAVRAGANFATTEWV  839

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

Query  125  ENASPETQKEINERVTTMVINNGNRGLNQYQVKEI   21
              +  +PE    E  V  +   NG RG  +Q Q++++
Sbjct  898  QEPAPEP---FYEAVAAVFAENGGRGPDQDQMQDL   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(172)	8e-11()	Compositional matrix adjust.	51/184(28%)	89/184(48%)	16/184(8%)	-2

Features:

```
Query  554  RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPT  375
              +D  + KL +++ W  K       G+ D ++ +S++D E  K   +++            +GP
Sbjct  8    KDAEVFKLLKLMSWTRKN-----GLTDHMYEWSKEDPEAVKFGKLISTPPKHQEKPKGPD  62

Query  374  QDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIKTGLDPAPQ----T  213
              Q   Q   +AVRI  + +   G D  S +WI  N YRGPS  Q K  + TG   P P+
Sbjct  63   QHTAQEAKAVRISLDAVKAGADFASPDWIAENRYRGPSPGQFKYYVITGSVPDPRDEYDD  122
```

```
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
```

polyprotein [Infectious pancreatic necrosis virus]

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(179)	9e-11()	Compositional matrix adjust.	84/340(25%)	149/340(43%)	36/340(10%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+ I +N   +      PI G S+ L+LL  I  GV     TG +  E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG   660
              I P    D+K       G+PL+ +Q    + +++ + A  ++Q T   A      I
Sbjct   665   ITPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK   724

Query   659   TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG   483
                +   M S++     DE++   L   + A  +D  + KL +++ W  K D
Sbjct   725   YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----   774

Query   482   VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS   303
              + D ++ +S++D +  K   +++      +GP Q   Q  RA RI    + + G D +
Sbjct   775   LTDHMYEWSKEDPDALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA   834

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
```

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-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD   741
              G S+ L+LL  I  GV     TG +  E I+P    D+K       G+PL+ +Q
Sbjct   631   GPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEETIIPICGVDIKAIAAHEQGLPLIGNQP   690

Query   740   Y--KTIKDLAKATEMLQRITTAQHPAV-----IGTIATAMDSDSpppppPITDEDIMVTL   582
                + +++ + A  ++Q T   A      I +   M S++     DE++   L
Sbjct   691   GVDEEVRNTSLAAHLIQTGTLPVQRAQGSNKRIKYLGELMASNASGM-----DEELQRLL   745

Query   581   EELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSL   405
                 + A  +D  + KL +++ W  K D       + D ++ +S++D +  K   +++
Sbjct   746   NATMARAKEVQDAEIYKLLRLMAWTRKND-----LTDHMYEWSKEDPDALKFGKLISTPP   800

Query   404   TTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQMK-VIKTGL   231
                +GP Q   Q  RA RI    + + G D +  EW+  N YRGPS  Q K  + TG
Sbjct   801   KHPEKPKGPDQYHAQEARATRISLDAVRAGADFATPEWVALNNYRGPSPGQFKYYLITGR   860

Query   230   DPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVIN   63
              +P P   +   I++PI + +      + R+  +    ++  +PE   E  + V  +
Sbjct   861   EPEPGDEYEDYIKQPIVKPTDMNK--IRRLANSVYGLPHQEPAPE---EFYDAVAAVFAQ   915

Query   62    NGNRGLNQYQVKEI   21
              NG RG +Q Q++++
Sbjct   916   NGGRGPDQDQMQDL   929
```

107 kDa polyprotein [Infectious pancreatic necrosis virus]

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

Range 1: 606 to 929

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.2 bits(178)	1e-10()	Compositional matrix adjust.	84/340(25%)	149/340(43%)	36/340(10%)	-2

Features:

```
Query   980   TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK   819
              T +P+ I +N   +      PI G S+ L+LL  I  GV     TG +  E
Sbjct   606   TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET   664

Query   818   IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG   660
```

```
                     I+P      D+K       G+PL+ +Q    +  +++ + A  ++Q  T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
                +  M S++         DE++    L    +  A + +D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D    K  +++         +GP Q   Q  RA RI  + +   G D +
Sbjct  775  LTDHMYEWSKEDPYALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAK32161.1|AF342735_1** Length: 968 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.	76/317(24%)	134/317(42%)	38/317(11%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL    I  G+     TG +     E  ++P   D+K       G+PL+  Q
Sbjct  631  GPSAQLALSLLVNDIEEGIPRMVFTGEIANDEETVIPICGVDIKAIAAHEHGLPLIGCQ-  689

Query  740  YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPI----------TDEDIM  591
                     EM+   + A H   G +     +      +      +          DE++
Sbjct  690  -------PGVDEMVANTSLASHLIQSGALPVQKAQGACRRIRHLGQLMRTTASGMDEELQ  742

Query  590  VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ  414
            L+  +  A + +D  + KL +++ W  K D    + D L+ +S++D    K  R++
Sbjct  743  RLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHLYEWSKEDPGAIKFGRLIS  797

Query  413  NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK  240
                  +GP Q   Q  +A+RI  + +   G D  S EW+  N YRGPS  Q K   +
Sbjct  798  TPPKHQEKPKGPDQHTAQEAKAIRISLDAVKAGADFASSEWVAENNYRGPSPGQFKYYMI  857

Query  239  TGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM  72
            TG  P P     + +R+PI R  +   + + R+  +      ++  +P+  +  + V   +
Sbjct  858  TGRVPTPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---DFYQAVVEV  912

Query  71   VINNGNRGLNQYQVKEI   21
             NG RG +Q Q++++
Sbjct  913  FAENGGRGPDQDQMQDL   929
```

107 kDa polyprotein [Infectious pancreatic necrosis virus]

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

Range 1: 606 to 929

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.8 bits(177)	1e-10()	Compositional matrix adjust.	84/340(25%)	149/340(43%)	36/340(10%)	-2

Features:

```
Query  980  TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK  819
            T +P+  I +N    +          PI  G S +  L+LL   I  GV     TG +   E
Sbjct  606  TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET  664

Query  818  IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG  660
            I+P      D+K       G+PL+ +Q    +  +++ + A  ++Q  T    A       I
Sbjct  665  IIPICGVDIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAKGSNKRIK  724

Query  659  TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG  483
                +  M S++         DE++    L    +  A + +D  + KL +++ W  K D
Sbjct  725  YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----  774

Query  482  VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS  303
            + D ++ +S++D    K  +++         +GP Q   Q  RA RI  + +   G D +
Sbjct  775  LTDHMYEWSKEDPGALKFGKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFA  834

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
```

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-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL    I  G+      TG +   E  ++P   D+K       G+PL+  Q
Sbjct  631  GPSAQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQ-  689

Query  740  YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPI----------TDEDIM  591
                          EM+   + A H   G +      +     +          DE++
Sbjct  690  -------PGVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDEELQ  742

Query  590  VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ  414
            L+  +   A+ +D  + KL +++ W   K D     + D ++ +S++D + K   R++
Sbjct  743  GLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDANKFGRLIS  797

Query  413  NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK  240
               +GP  Q    Q  +A RI  + +   G D  S EWI   N YRGP+   Q K   +
Sbjct  798  TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAPGQFKYYMI  857

Query  239  TGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM  72
            TG  P P    + +R+PI R  +   + + R+ +      ++  +P+    +  + V  +
Sbjct  858  TGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---DFYQAVVEV  912

Query  71   VINNGNRGLNQYQVKEI    21
                NG RG +Q Q++++
Sbjct  913  FAENGGRGPDQDQMQDL    929
```


polyprotein [Infectious pancreatic necrosis virus]

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(174)	4e-10()	Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL    I  G+      TG +   E  ++P   D+K       G+PL+  Q
Sbjct  631  GPSSQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAMAAHEHGLPLIGCQP  690

Query  740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
              + + + + A+ ++Q     +  AQ         ++ T A+ MD++
Sbjct  691  GVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDAE----------  740

Query  602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                 L+ LL A    R      D  + KL +++ W   K D     + D ++ +S++D +
Sbjct  741  ------LQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query  437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
             K  R++       +GP  Q    Q  +A RI  + +   G D  S EWI   N YRGPS
Sbjct  790  IKFGRLISTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPSP  849

Query  260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE  96
             Q K  + TG  P P    + +R+PI R  +   + + R+ +      ++  +P+    +
Sbjct  850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query  95   INERVTTMVINNGNRGLNQYQVKEI    21
             + V  +   NG RG +Q Q++++
Sbjct  905  FYQAVVEVFAENGGRGPDQDQMQDL    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(173)	5e-10()	Compositional matrix adjust.	81/325(25%)	141/325(43%)	54/325(16%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL    I  G+      TG +   E  ++P   D+K       G+PL+  Q
Sbjct  631  GPSSQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQP  690

Query  740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
              + + + + A+ ++Q     +  AQ         ++ T A+ MD++
Sbjct  691  GVDEMVANTSLASHLIQGGALPVQKAQGACRRIKYLGQLMRTTASGMDAE----------  740

Query  602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                 L+ LL A    R      D  + KL +++ W   K D     + D ++ +S++D +
Sbjct  741  ------LQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query  437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
             K  R+V       +GP  Q    Q  +A RI  + +   G D  S EWI   N YRGPS
Sbjct  790  IKFGRLVSTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPSP  849

Query  260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE  96
             Q K  + TG  P P    + +R+PI R  +   + + R+ +      ++  +P+    +
Sbjct  850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query  95   INERVTTMVINNGNRGLNQYQVKEI    21
             + V  +   NG RG +Q Q++++
Sbjct  905  FYQAVVEVFAENGGRGPDQDQMQDL    929
```

polyprotein, partial [Infectious pancreatic necrosis virus]

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(173)	5e-10()	Compositional matrix adjust.	81/325(25%)	141/325(43%)	54/325(16%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL   I  G+        TG +  E   ++P    D+K       G+PL+   Q
Sbjct  631  GPSSQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQP  690

Query  740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
             + + + + A+ ++Q      + AQ         ++ T A+ MD++
Sbjct  691  GVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDAE----------  740

Query  602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                L+ LL A  R      D  + KL +++ W  K D     + D ++ +S++D +
Sbjct  741  ------LQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query  437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
             K  R+V         +GP Q  Q  +A RI + +  G D  S EWI  N YRGPS
Sbjct  790  IKFGRLVSTPPKHREKPKGPDQHTAQEAKATRISLDGVKAGADFASPEWITENNYRGPSP  849

Query  260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE  96
             Q K + TG P P   +  +R+PI R +   + + R+ +      ++  +P+     +
Sbjct  850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query  95   INERVTTMVINNGNRGLNQYQVKEI   21
             + V  +   NG RG +Q Q++++
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(173)	6e-10()	Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL   I  G+        TG +  E   ++P    D+K       G+PL+   Q
Sbjct  631  GPSSQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAMAAHEHGLPLIGCQP  690

Query  740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
             + + + + A+ ++Q      + AQ         ++ T A+ MD++
Sbjct  691  GVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDAE----------  740

Query  602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                L+ LL A  R      D  + KL +++ W  K D     + D ++ +S++D +
Sbjct  741  ------LQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query  437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
             K  R+V         +GP Q  Q  +A RI + +  G D  S EWI  N YRGP+
Sbjct  790  IKFGRLVSTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFVSPEWIAENNYRGPAP  849

Query  260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE  96
             Q K + TG P P   +  +R+PI R +   + + R+ +      ++  +P+     +
Sbjct  850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query  95   INERVTTMVINNGNRGLNQYQVKEI   21
             + V  +   NG RG +Q Q++++
Sbjct  905  FYQAVVEVFAENGGRGPDQDQMQDL   929
```


polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AGC00816.1|** Length: 972 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:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL   I  G+        TG +  E   ++P    D+K       G+PL+   Q
Sbjct  631  GPSSQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAMAAHEHGLPLIGCQP  690

Query  740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
             + + + + A+ ++Q      + AQ         ++ T A+ MD++
Sbjct  691  GVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDAE----------  740

Query  602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                L+ LL A  R      D  + KL +++ W  K D     + D ++ +S++D +
Sbjct  741  ------LQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query  437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
```

```
              K  R+V              +GP Q   Q  +A RI  + +  G D  S EWI  N YRGP+
Sbjct   790  IKFGRLVSTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAP  849

Query   260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE   96
              Q K  + TG  P P    +  +R+PI R +   + + R+ +      ++  +P+     +
Sbjct   850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query    95  INERVTTMVINNGNRGLNQYQVKEI   21
              + V  +   NG RG +Q Q++++
Sbjct   905  FYQAVVEVFAENGGRGPDQDQMQDL  929
```

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(166)	6e-10()	Compositional matrix adjust.	53/202(26%)	95/202(47%)	17/202(8%)	-2

Features:

```
Query   605  DEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKM  429
              D ++   L+  +  A + +D  + KL +++ W  K D    + D ++ +S++D +   K
Sbjct     8  DAELQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDAIKF   62

Query   428  NRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQM  252
              R+V           +GP Q   Q  +A RI  + +  G D  S EWI  N YRGPS  Q
Sbjct    63  GRLVSTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPSPGQF  122

Query   251  KVIK-TGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINE   87
              K   TG  P P    + +R+PI R +   + + R+ +      ++  +P+    +  +
Sbjct   123  KYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---DFYQ  177

Query    86  RVTTMVINNGNRGLNQYQVKEI   21
              V   +   NG RG +Q Q++++
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:

```
Query   911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
              G S + AL+LL  I  G+       TG +  E   ++P    D+K     G+PL+ Q
Sbjct   631  GPSSQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAMAAHEHGLPLIGCQP  690

Query   740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
              + + + + A+ ++Q       ++ T A+  MD++
Sbjct   691  GVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDAE----------  740

Query   602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
              L+  LL A  R      D  + KL +++ W  K D     + D ++ +S++D +
Sbjct   741  ------LQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query   437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
              K  R+V           +GP Q   Q  +A RI  + +  G D  S EWI  N YRGP+
Sbjct   790  IKFGRLVSTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFVSPEWIAENNYRGPAP  849

Query   260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE   96
              Q K  + TG  P P    +  +R+PI R +   + + R+ +      ++  +P+     +
Sbjct   850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query    95  INERVTTMVINNGNRGLNQYQVKEI   21
              + V  +   NG RG +Q Q++++
Sbjct   905  FYQAVVEVFAENGGRGPDQDQMQDL  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-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKM  429
              DE++   L   + A + +D  + KL ++ W  K D    + D ++ +S++D +   K
Sbjct     5  DEELQRLLNATMARAKEVQDAEIYKLLRLMAWTRKND-----LTDHMYEWSKEDPDALKF   59

Query   428  NRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
              +++           +GP Q   Q  RA RI  + +      EW+  N YRGPS  Q
Sbjct    60  GKLISTPPKHPEKPKGPDQHHAQEARATRISLDAVRAGADFATPEWVALNNYRGPSPGQF  119

Query   251  K-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINE   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(172)	7e-10()	Compositional matrix adjust.	76/315(24%)	136/315(43%)	34/315(10%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S +  L+LL   I  GV     TG +   E  I+P   D+K       G+PL+ +Q
Sbjct  631  GPSAQLGLSLLVNDIEEGVPRMVFTGEIASDEETIIPICGVDIKAIAAHEQGLPLIGNQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPA--------VIGTIATAMDSDSpppppPITDEDIM  591
             + +++ + A  ++Q       A       +G + T++ S            DE++
Sbjct  691  GVDEEVRNTSLAAHLIQTGALPVQKAKGANKRIKYLGELMTSIASG--------MDEELQ  742

Query  590  VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ  414
             L  +  A+ +D  + KL +++ W  K D    + D + ++S++D +  K  R++
Sbjct  743  RLLNATMARAKEVKDAEIFKLLKLMAWTRKND-----LTDHMFDWSKEDPDAIKFGRVIS  797

Query  413  NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQMK-VIK  240
                 +GP Q   Q  RA RI  + +  G D +  EW+  N YRGPS   Q K  +
Sbjct  798  TPPKHPEKPKGPDQRTAQEARATRISLDAVRAGADFATTEWVALNNYRGPSPGQFKYYLI  857

Query  239  TGLDPAPQTIIREPIPRSDNSTPEL--VMRIIRNSLSAHYENASPETQKEINERVTTMVI  66
            TG  P P     + I ++    ++  + R+ +     ++ +PE   E  E V +
Sbjct  858  TGRTPDPDDEYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFYEAVAAVFA  914

Query   65  NNGNRGLNQYQVKEI    21
             N  RG +Q Q++++
Sbjct  915  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(172)	7e-10()	Compositional matrix adjust.	75/317(24%)	134/317(42%)	38/317(11%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL   I  G+     TG +   E  ++P   D+K       G+PL+  Q
Sbjct  631  GPSAQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQ-  689

Query  740  YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPI----------TDEDIM  591
                    EM+   + A H   G +         +        DE++
Sbjct  690  -------PGVDEMVANTSLASHLIQSGALPVQKAQGACRKIKYLGQLMRTTASGMDEELQ  742

Query  590  VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ  414
             L+  +  A+ +D  + KL +++ W  K D    + D ++ +S++D +  K  R++
Sbjct  743  GLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDAIKFGRLIS  797

Query  413  NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK  240
                 +GP Q   Q   +A RI  + +  G D  S EWI  N YRGP+   Q K  +
Sbjct  798  TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAPGQFKYYMI  857

Query  239  TGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM  72
            TG  P P    +  +R+PI R   +   + + R+ +     ++  +P+   +  + V  +
Sbjct  858  TGRVPNPGVEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---DFYQAVVEV  912

Query   71  VINNGNRGLNQYQVKEI    21
              NG RG +Q Q++++
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(172)	7e-10()	Compositional matrix adjust.	75/317(24%)	134/317(42%)	38/317(11%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL   I  G+     TG +   E  ++P   D+K       G+PL+  Q
Sbjct  631  GPSAQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQ-  689

Query  740  YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPI----------TDEDIM  591
```

```
                        EM+   + A H     G+         +         +               DE++
Sbjct    690  -------PGVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDEELQ  742

Query    590  VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ  414
                L+  +  A + +D  + KL +++ W  K D    + D ++ +S++D +  K  R++
Sbjct    743  GLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDAIKFGRLIS  797

Query    413  NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK  240
                +GP Q   Q  +A RI  + +  G D  S EWI  N YRGP+  Q K  +
Sbjct    798  TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAPGQFKYYMI  857

Query    239  TGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM   72
              TG  P P    +  +R+PI R  +  + + R+  +    ++ +P+   +  V   +
Sbjct    858  TGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---DFYQAVVEV  912

Query     71  VINNGNRGLNQYQVKEI    21
                NG RG +Q Q++++
Sbjct    913  FAENGGRGPDQDQMQDL    929
```

polyprotein [Infectious pancreatic necrosis virus]

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(172)	7e-10()	Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2

Features:

```
Query    911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
              G S + AL+LL    I  G+       TG +   E  ++P    D+K       G+PL+  Q
Sbjct    631  GPSSQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAMAAHEHGLPLIGCQP  690

Query    740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
                + + + + A+ ++Q      AQ         ++ T A+ MD++
Sbjct    691  GVDEMVANTSLASYLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDAE----------  740

Query    602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                 L+ LL A  R      D  + KL +++ W  K D     + D ++ +S++D +
Sbjct    741  ------LQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query    437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
               K  R+V     +GP Q   Q  +A RI  + +  G D  S EWI  N YRGP+
Sbjct    790  IKFGRLVSTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAP  849

Query    260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE   96
               Q K  + TG  P P    +  +R+PI R  +  + + R+  +    ++ +P+   +
Sbjct    850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query     95  INERVTTMVINNGNRGLNQYQVKEI    21
               + V  +    NG RG +Q Q++++
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(172)	8e-10()	Compositional matrix adjust.	80/325(25%)	141/325(43%)	54/325(16%)	-2

Features:

```
Query    911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
              G S + AL+LL    I  G+       TG +   E  ++P    D+K       G+PL+  Q
Sbjct    631  GPSSQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAMAAHEHGLPLIGCQP  690

Query    740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
                + + + + A+ ++Q      AQ         ++ T A+ MD++
Sbjct    691  GVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDAE----------  740

Query    602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                 L+ LL A  R      D  + KL +++ W  K D     + D ++ +S++D +
Sbjct    741  ------LQGLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query    437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
               K  R+V     +GP Q   Q  +A RI  + +  G D  S EWI  N YRGP+
Sbjct    790  IKFGRLVSTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAP  849

Query    260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE   96
               Q K  + TG  P P    +  +R+PI R  +  + + R+  +    ++ +P+   +
Sbjct    850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query     95  INERVTTMVINNGNRGLNQYQVKEI    21
               + V  +    NG RG +Q Q++++
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(171) 8e-10() Compositional matrix adjust. 75/317(24%) 134/317(42%) 38/317(11%) -2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL    I  G+       TG +    E     D+K        G+PL+ +Q
Sbjct  631  GPSAQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQ-  689

Query  740  YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPI----------TDEDIM  591
                            EM+   + A H   G +      +      +          DE++
Sbjct  690  -------PGVDEMVANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDEELQ  742

Query  590  VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ  414
            L+ +  A+ +D  + KL +++ W  K D    + D ++ +S++D +  K  R++
Sbjct  743  GLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDAIKFGRLIS  797

Query  413  NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK  240
                +GP Q   Q  +A RI  + +   G D  S EWI  N YRGP+   Q K   +
Sbjct  798  TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFGSPEWIAENNYRGPAPGQFKYYMI  857

Query  239  TGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM  72
            TG   P P    +   +R+PI R  +  + + R+ +      ++  +P+  +   + V  +
Sbjct  858  TGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---DFYQAVVEV  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(170)	1e-09()	Compositional matrix adjust.	77/318(24%)	137/318(43%)	40/318(12%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S +  L+LL    I  GV       TG +    E  I+P    D+K        G+PL+ +Q
Sbjct  631  GPSAQLGLSLLVNDIDEGVPRMVFTGEIASDEETIIPICGVDIKAIAAHEQGLPLIGNQP  690

Query  740  YKTIKDLAKATEMLQRITTAQHPA-----------VIGTIATAMDSDSpppppPITDEDI  594
                +++A  +      + T   P            +G + T++ S           DE++
Sbjct  691  -GVDEEVANTSLAAHLVQTGALPVQKAKGVNKRIKYLGELMTSIASG--------MDEEL  741

Query  593  MVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIV  417
            L  +  A+ +D  + KL +++ W  K D    + D + ++S++D +  K  R++
Sbjct  742  QRLLNATMARAKEVKDAEIFKLLKLMAWTRKND-----LTDHMFDWSKEDPDAIKFGRLI  796

Query  416  QNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQMK-VI  243
                +GP Q   Q  RA RI  + +   G D +   EW+  N YRGPS   Q K   +
Sbjct  797  STPPKHPEKPKGPDQRTAQEARATRISLDAVRAGADFATPEWVALNNYRGPSPGQFKYYL  856

Query  242  KTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTT  75
             TG   P P    + I++ I +  + T + + R+ +      ++  +PE   E   + V
Sbjct  857  ITGRTPDPDDEYEDYIKQTITKPTDMTK--IRRLANSVYGLPHQEPAPE---EFYDAVAA  911

Query  74   MVINNGNRGLNQYQVKEI    21
            +   +N  RG +Q Q++++
Sbjct  912  VFADNDGRGPDQDQMQDL    929
```


polyprotein [Infectious pancreatic necrosis virus]

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

Range 1: 631 to 929

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:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
            G S + AL+LL    I  G+       TG +    E     D+K        G+PL+ +Q
Sbjct  631  GPSAQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQP  690

Query  740  Y--KTIKDLAKATEMLQR----ITTAQHPA--------VIGTIATAMDSDSpppppPITD  603
              + + + + A+ ++Q       + AQ        ++ T A+ MD +
Sbjct  691  GVDEMVANTSLASHLIQSGALPVQKAQGACREIKYLGQLMRTTASGMDGE----------  740

Query  602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                L+ LL A   R      D + KL +++ W  K D        + D ++ +S++D +
Sbjct  741  ------LQGLLQATMPRAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDA  789

Query  437  EKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSA  261
             K  R++          +GP Q   Q  +A RI  + +   G D  S EWI  N YRGP+
Sbjct  790  IKFGRLISTPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAP  849

Query  260  EQMK-VIKTGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKE  96
             Q K  + TG   P P    + +R+PI R  +  + + R+ +      ++  +P+     +
Sbjct  850  GQFKYYMITGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---D  904

Query  95   INERVTTMVINNGNRGLNQYQVKEI    21
             + V  +   NG RG +Q Q++++
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	Frame
69.7 bits(169)	2e-09()	Compositional matrix adjust.	70/272(26%)	118/272(43%)	45/272(16%)	-2

Features:

```
Query  986   DCTVVPISAITQNEITTTATPPIPRGGSMEAALAL-----LQHIPPGVTPFAVTGN--VI  828
             D T++PI +I           PI  G S +A+       Q IPP +    VTGN +I
Sbjct  646   DITLLPILSIQGGFAIIPDEAPILEGTSCVSAILCAYRGDFQGIPPAL----VTGNAKLI  701

Query  827   EGK--IVPNKWADLKRE-----GMKGTGI----PLVTDQDYKTIKDLAKATEMLQRITTA  681
             EG+  ++PN   +K++      +K G      PL+T   + I +L+     +    T
Sbjct  702   EGRYVVMPNPAQQMKKQIAAQKELKFIGADLSGPLLTI--FHVINELSGLETKNKTFDTV  759

Query  680   QHPAVIGTIATAMDSDSpppppPITDEDIMVTLEELLMAAADRDPRMAKLKEVVLWLAKI  501
             +H          D D        D+D M  ++L    + +D   KL  ++ W
Sbjct  760   KH-----------DQDHSRSVNLCADDDTMQQWQDLSAQISTQDDGFRKLIHILNW----  804

Query  500   DDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDV---LQHQRAVRIREN  330
                N  G+ D L+NF+  D +G ++ + +   LT    +R P    Q  +A RI  N
Sbjct  805   -TNRNGLADMLYNFAETDPDGNRLYKTIA-PLTAEYKARNPESKTPYEAQRAKAERISAN  862

Query  329   YLIQ-GVDLSIEWIKNNGYRGPSAEQMKVIKT   237
              Q G   + EW++ +GYRGP++E+++ + +
Sbjct  863   LRKQYGEAFTPEWVEQHGYRGPTSEEIRALTS   894
```


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:

```
Query  911   GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
             G S +  L+LL   I GV       TG +   E  I+P     D+K      G+PL+  Q
Sbjct  631   GPSAQLGLSLLVNSIEEGVPRMVFTGEIAADEETIIPICGVDIKAIAAHEQGLPLIGCQP  690

Query  740   Y--KTIKDLAKATEMLQRITTAQHPA------------VIGTIATAMDSDSpppppPITD  603
             + + + + A ++Q  T      A            ++ +IA+ MD +
Sbjct  691   GVDEEVSNTSLAAHLIQTGTLPVQKAKGANKRIKYLGELMSSIASGMDEE----------  740

Query  602   EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                L+ LL A   R      D  + KL +++ W  K D       + D +  +S++D +
Sbjct  741   ------LQRLLSATMARAKEVKDAEIFKLLKLMSWTRKND-----LTDHMFEWSKEDPDA  789

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 ++       ++  + R+ +      ++  +PE   E
Sbjct  850   GQFKYYLITGRTPDPNDGYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFY  906

Query  89    ERVTTMVINNGNRGLNQYQVKEI   21
             + V  +  +N  RG +Q Q++++
Sbjct  907   DAVAAVFADNDGRGPDQDQMQDL   929
```


polyprotein, partial [Infectious pancreatic necrosis virus]
Sequence ID: gb|AAK32155.1|AF342729_1 Length: 968 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-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
             G S +  L+LL   I GV       TG +   E  I+P     D+K      G+PL+  Q
Sbjct  631   GPSAQLGLSLLVNSIEEGVPRMVFTGEIAADEETIIPICGVDIKAIAAHEQGLPLIGCQP  690

Query  740   Y--KTIKDLAKATEMLQRITTAQHPA------------VIGTIATAMDSDSpppppPITD  603
             + + + + A ++Q  T      A            ++ +IA+ MD +
Sbjct  691   GVDEEVSNTSLAAHLIQTGTLPVQKAKGANKRIKYLGELMSSIASGMDEE----------  740

Query  602   EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                L+ LL A   R      D  + KL +++ W  K D       + D +  +S++D +
Sbjct  741   ------LQRLLSATMARAKEVKDAEIFKLLKLMSWTRKND-----LTDHMFEWSKEDPDA  789

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 ++       ++  + R+ +      ++  +PE   E
Sbjct  850   GQFKYYLITGRTPDPNDGYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFY  906

Query  89    ERVTTMVINNGNRGLNQYQVKEI   21
```

polyprotein [Infectious pancreatic necrosis virus]

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:

```
Query  911    GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD    741
              G S +  L+LL   I  GV      TG +   E  I+P    D+K       G+PL+  Q
Sbjct  631    GPSAQLGLSLLVNSIEEGVPRMVFTGEIAADEETIIPICGVDIKAIAAHEQGLPLIGCQP    690

Query  740    Y--KTIKDLAKATEMLQRITTAQHPA------------VIGTIATAMDSDSpppppPITD    603
              + + + + A  ++Q  T     A          ++ +IA+ MD +
Sbjct  691    GVDEEVSNTSLAAHLIQTGTLPVQKAKGANKRIKYLGELMSSIASGMDEE---------    740

Query  602    EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG    438
              L+ LL A  R    D  + KL +++ W  K D    + D +  +S++D +
Sbjct  741    ------LQRLLSATMARAKEVKDAEIFKLLKLMSWTRKND-----LTDHMFEWSKEDPDA    789

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 ++     ++  + R+ +      ++  +PE    E
Sbjct  850    GQFKYYLITGRTPDPNDGYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFY    906

Query  89     ERVTTMVINNGNRGLNQYQVKEI    21
              + V  +    +N   RG  +Q  Q++++
Sbjct  907    DAVAAVFADNDGRGPDQDQMQDL    929
```

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	Frame
69.3 bits(168)	2e-09()	Compositional matrix adjust.	82/338(24%)	147/338(43%)	32/338(9%)	-2

Features:

```
Query  980    TVVPISAITQNE---ITTTATPPIPRGGSMEAALALL-QHIPPGVTPFAVTGNVI--EGK    819
              T +P+  I +N    +       PI  G S +  L+LL   I  GV      TG +   E
Sbjct  606    TALPLKEIKRNGNIVVEKIFAGPI-MGPSAQLGLSLLVNDIEDGVPRMVFTGEIADDEET    664

Query  818    IVPNKWADLKREGMKGTGIPLVTDQDY--KTIKDLAKATEMLQRITTAQHPAV-----IG    660
              I+P    +K       G+PL+ +Q    + +++ + A  ++Q  T     A          I
Sbjct  665    IIPICGVAIKAIAAHEQGLPLIGNQPGVDEEVRNTSLAAHLIQTGTLPVQRAQGSNKRIK    724

Query  659    TIATAMDSDSpppppPITDEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPG    483
              +  M S++    DE++    L  + A + +D  + KL +++ W  K D
Sbjct  725    YLGELMASNASGM-----DEELQRLLNATMARAKEVQDAEIYKLLKLMAWTRKND-----    774

Query  482    VLDTLHNFSRQDVEGEKMNRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLS    303
              + D ++ +S++D +  K   +++            +GP Q   Q  RA RI  + +  G D +
Sbjct  775    LTDHMYEWSKEDPDALKFGKLISTPPKRPEKPKGPDQHHAQEARATRISLDAVRAGADFA    834

Query  302    I-EWIKNNGYRGPSAEQMK-VIKTGLDPAPQTIIREPIPRSDNSTPEL--VMRIIRNSLS    135
              EW+   N YRGPS  Q K + TG +P P     + I +S     ++  + R+ +
Sbjct  835    TPEWVAMNNYRGPSPGQFKYYLITGREPEPGDEYEDYIKQSIVKPTDMNKIRRLANSVYG    894

Query  134    AHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEI    21
              ++  +PE    E  + V  +    NG RG  +Q  Q++++
Sbjct  895    LPHQEPAPE---EFYDAVAAVFAQNGGRGPDQDQMQDL    929
```

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAV48850.1|** 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-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD    741
              G S +  L+LL   I  GV      TG +   E  I+P    D+K       G+PL+  Q
Sbjct  631    GPSAQLGLSLLVNSIEEGVPRMVFTGEIAADEETIIPICGVDIKAIAAHEQGLPLIGCQP    690

Query  740    Y--KTIKDLAKATEMLQRITTAQHPA------------VIGTIATAMDSDSpppppPITD    603
              + + + + A  ++Q  T     A          ++ +IA+ MD +
Sbjct  691    GVDEEVSNTSLAAHLIQTGTLPVQKAKGANKRIKYLGELMSSIASGMDEE---------    740

Query  602    EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG    438
              L+ LL A  R    D  + KL +++ W  K D    + D +  +S++D +
Sbjct  741    ------LQRLLSATMARAKEVKDAEIFKLLKLMSWTRKND-----LTDHMFEWSKEDPDA    789
```

```
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 ++      ++  + R+ +      ++  +PE   E
Sbjct  850  GQFKYYLITGRTPDPNDGYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFY  906

Query  89   ERVTTMVINNGNRGLNQYQVKEI   21
             + V  +  +N  RG +Q Q++++
Sbjct  907  DAVAAVFADNDGRGPDQDQMQDL   929
```

polyprotein [Infectious pancreatic necrosis virus]

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(168)	2e-09()	Compositional matrix adjust.	78/323(24%)	135/323(41%)	50/323(15%)	-2

Features:

```
Query  911  GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
             G S +  L+LL   I  GV       TG +   E  I+P   D+K       G+PL+  Q
Sbjct  631  GPSAQLGLSLLVNSIEEGVPRMVFTGEIAADEETIIPICGVDIKAIAAHEQGLPLIGCQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPA------------VIGTIATAMDSDSpppppPITD  603
             +  + + + A  ++Q  T      A            ++ +IA+ MD +
Sbjct  691  GVDEEVSNTSLAAHLIQTGTLPVQKAKGANKRIKYLGELMSSIASGMDEE----------  740

Query  602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                L+ LL A  R      D  + KL +++ W  K D    + D +   +S++D +
Sbjct  741  ------LQRLLSATMARAKEVKDAEIFKLLKLMSWTRKND-----LTDHMFEWSKEDPDA  789

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 ++      ++  + R+ +      ++  +PE   E
Sbjct  850  GQFKYYLITGRTPDPNDGYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFY  906

Query  89   ERVTTMVINNGNRGLNQYQVKEI   21
             + V  +  +N  RG +Q Q++++
Sbjct  907  DAVAAVFADNDGRGPDQDQMQDL   929
```

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-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD  741
             G S +  L+LL   I  GV       TG +   E  I+P   D+K       G+PL+  Q
Sbjct  631  GPSAQLGLSLLVNSIEEGVPRMVFTGEIAADEETIIPICGVDIKAIAAHEQGLPLIGCQP  690

Query  740  Y--KTIKDLAKATEMLQRITTAQHPA------------VIGTIATAMDSDSpppppPITD  603
             +  + + + A  ++Q  T      A            ++ +IA+ MD +
Sbjct  691  GVDEEVSNTSLAAHLIQTGTLPVQKAKGANKRIKYLGELMSSIASGMDEE----------  740

Query  602  EDIMVTLEELLMAAADR-----DPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEG  438
                L+ LL A  R      D  + KL +++ W  K D    + D +   +S++D +
Sbjct  741  ------LQRLLSATMARAKEVKDAEIFKLLKLMSWTRKND-----LTDHMFEWSKEDPDA  789

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 ++      ++  + R+ +      ++  +PE   E
Sbjct  850  GQFKYYLITGRTPDPNDGYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFY  906

Query  89   ERVTTMVINNGNRGLNQYQVKEI   21
             + V  +  +N  RG +Q Q++++
Sbjct  907  DAVAAVFADNDGRGPDQDQMQDL   929
```

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAV48848.3|** Length: 980 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.	75/317(24%)	133/317(41%)	38/317(11%)	-2

Features:

```
Query   911   GGSMEAALALL-QHIPPGVTPFAVTGNVI--EGKIVPNKWADLKREGMKGTGIPLVTDQD   741
              G S + AL+LL   I  G+       TG +   E  ++P    D+K       G+PL+  Q
Sbjct   631   GPSAQLALSLLVNDIDEGIPRMVFTGEIADDEETVIPICGVDIKAIAAHEHGLPLIGCQ-   689

Query   740   YKTIKDLAKATEMLQRITTAQHPAVIGTIATAMDSDSpppppPI----------TDEDIM   591
                          EM   + A H    G +       +      +          DE++
Sbjct   690   -------PGVDEMEANTSLASHLIQSGALPVQKAQGACRRIKYLGQLMRTTASGMDEELQ   742

Query   590   VTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQ   414
                  L+ +  A + +D  + KL +++ W  K D    + D ++ +S++D +  K  R++
Sbjct   743   GLLQATMARAKEVKDAEVFKLLKLMSWTRKND-----LTDHMYEWSKEDPDAIKFGRLIS   797

Query   413   NSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDL-SIEWIKNNGYRGPSAEQMK-VIK   240
                          +GP Q   Q  +A RI  + +   G D   S EWI   N YRGP+   Q K    +
Sbjct   798   TPPKHQEKPKGPDQHTAQEAKATRISLDAVKAGADFASPEWIAENNYRGPAPGQFKYYMI   857

Query   239   TGLDPAP----QTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERVTTM   72
              TG  P P     +  +R+PI R  +   + + R+ +    ++   +P+   +   + V  +
Sbjct   858   TGRVPNPGEEYEDYVRKPITRPTDM--DKIRRLANSVYGLPHQEPAPD---DFYQAVVEV   912

Query   71    VINNGNRGLNQYQVKEI    21
                        NG  RG +Q  Q++++
Sbjct   913   FAENGGRGPDQDQMQDL    929
```

polyprotein [Infectious pancreatic necrosis virus]

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(168)	2e-09()	Compositional matrix adjust.	75/317(24%)	133/317(41%)	38/317(11%)	-2

Features:

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:

```
Query   605   DEDIMVTLEELLMAAAD-RDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKM   429
              DE++    L   + A + +D  + KL +++ W  K D    + +SR+D +  K
Sbjct   2     DEELQRLLSATMARAKEVKDAEIFKLLKLMSWTRKND-----LTDHMFEWSREDPDAIKF   56

Query   428   NRIVQNSLTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM   252
              R++              +GP Q    Q  RAVRI  + +   G + +  EWI   N YRGPS   Q
Sbjct   57    GRLISTPPKHPEKPKGPNQHAAQEARAVRISLDAVRAGAEFATPEWIATNDYRGPSPGQF   116

Query   251   K-VIKTGLDPAPQTIIREPIPRSDNSTPEL--VMRIIRNSLSAHYENASPETQKEINERV   81
              K  + TG  P P    + I ++    ++  + R+ +    ++   +PE     E   + V
Sbjct   117   KYYLITGRTPDPNDGYEDYIKQTITKPTDMNKIRRLANSVYGLPHQEPAPE---EFYDAV   173

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:

```
Query   566  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------  408
             AAA+ DP        +V +WL    ++N  G+++ + NF+  D    +M   + N+
Sbjct   775  AAANADPLFRSALQVFMWL---EEN--GIVNDMANFALSDPNAHRMKNFLANAPQAGSKS  829

Query   407  -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                    V +RGPT + Q ++ RI +     G+ + EW+ NG+RGPS  Q+
Sbjct   830  QRAKYGTAGYGVEARGPTPEEAQREKDARISKKMETMGIYFATPEWVALNGHRGPSPGQL  889

Query   251  KVIKTGLDPAPQTIIREPIPRSDNSTPELVM----------RIIRNSLSAHYENASPETQ  102
             K   +         RE IP +   P+ V           +I+R + S +        E
Sbjct   890  KYWQN--------TRE-IPEPNEDYPDYVHAEKSRLASEEQILRAATSIYGAPGQAEPP   939

Query   101  KEINERVTTMVINNGNRGLNQYQVKEIV    18
             +   + V  +  NN  RG NQ Q+K+++
Sbjct   940  QAFIDEVARVYENNHGRGPNQEQMKDLL   967
```

structural polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ABS86936.1|** Length: 1012 Number of Matches: 1
Range 1: 774 to 966

Score	Expect	Method	Identities	Positives	Gaps	Frame
61.6 bits(148)	6e-07()	Compositional matrix adjust.	55/201(27%)	91/201(45%)	26/201(12%)	-2

Features:

```
Query   566  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNSLTTA---  396
             AAA+ DP        V +WL   ++N  G++  + NF+  D    +M   + N+  T
Sbjct   774  AAANVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQTGSKS  828

Query   395  -----------VHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                        V +RGPT + Q ++ RI +     G+ L+  EW+  NG+RGPS  Q+
Sbjct   829  QRAKYGTAGYGVEARGPTPEEAQREKDTRISKRMETMGIYLATPEWVALNGHRGPSPGQL  888

Query   251  KVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERV  81
             K   +      DP   +     +S ++ E ++R   + A  +   P   Q  I+E
Sbjct   889  KYWQNTREIPDPNEDYLDYVHAEKSRLASDEQILRAATSIYGAPGQAEPP--QAFIDEVA  946

Query   80   TTMVINNGNRGLNQYQVKEIV    18
             IN+G  RG NQ Q+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  LMAAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-----  408
             + AAAD DP        V +WL   ++N  G++  + NF+  D    +M   + N+
Sbjct   17   MEAAADVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGS  71

Query   407  ---------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAE  258
                      V +RGPT + Q ++ RI +      G+  + EW+  NG+RGPS
Sbjct   72   KSQRAKYGTAGYGVEARGPTPEEAQREKDTRISKKMETMGIYFATPEWVALNGHRGPSPG  131

Query   257  QMKVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINE  87
             Q+K   +      DP   +     +S ++ E ++R   + A  +   P   Q  I+E
Sbjct   132  QLKYWQNTREIPDPNEDYLDYVHAEKSRLASEEQILRAATSIYGAPGQAEPP--QAFIDE  189

Query   86   RVTTMVINNGNRGLNQYQVKEIV    18
                  IN+G  RG NQ Q+K+++
Sbjct   190  VAKVYEINHG-RGPNQEQMKDLL   211
```

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(147)	9e-07()	Compositional matrix adjust.	54/201(27%)	89/201(44%)	26/201(12%)	-2

Features:

```
Query   566  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------  408
             AAAD DP        V +WL    ++N  G++ + NF+  D    +M   + N+
Sbjct   783  AAADVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGSKS  837

Query   407  -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                    V +RGPT + Q ++ RI +      G+ +  EW+  NG+RGPS  Q+
Sbjct   838  QRAKYGTAGYGVEARGPTPEEAQREKDTRISKKMEAMGIYFATPEWVALNGHRGPSPGQL  897

Query   251  KVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERV  81
```

```
                K  +        DP    +       +S  ++ E ++R   +   A  +  P   Q  I+E
Sbjct  898  KYWQNTREIPDPNEDYLDYVHAEKSRLASEEQILRAATSIYGAPGQAEPP--QAFIDEVA  955

Query  80   TTMVINNGNRGLNQYQVKEIV    18
                IN+G  RG  NQ  Q+K+++
Sbjct  956  KVYEINHG-RGPNQEQMKDLL    975
```

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(147)	9e-07()	Compositional matrix adjust.	54/201(27%)	89/201(44%)	26/201(12%)	-2

Features:

```
Query  566  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------  408
            AAAD DP        V +WL    ++N  G++    +M    + N+
Sbjct  774  AAADVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGSKS  828

Query  407  -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                   V +RGPT +  Q ++  RI +      G+  +  EW+  NG+RGPS  Q+
Sbjct  829  QRAKYGTAGYGVEARGPTPEEAQREKDTRISKKMEAMGIYFATPEWVALNGHRGPSPGQL  888

Query  251  KVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERV  81
            K  +        DP    +       +S  ++ E ++R   +   A  +  P   Q  I+E
Sbjct  889  KYWQNTREIPDPNEDYLDYVHAEKSRLASEEQILRAATSIYGAPGQAEPP--QAFIDEVA  946

Query  80   TTMVINNGNRGLNQYQVKEIV    18
                IN+G  RG  NQ  Q+K+++
Sbjct  947  KVYEINHG-RGPNQEQMKDLL    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(146)	1e-06()	Compositional matrix adjust.	53/201(26%)	89/201(44%)	26/201(12%)	-2

Features:

```
Query  566  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------  408
            AAA+ DP        V +WL    ++N  G++   + NF+  D    +M    + N+
Sbjct  774  AAANADPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGSKS  828

Query  407  -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                   V +RGPT +  Q ++  RI +      G+  +  EW+  NG+RGPS  Q+
Sbjct  829  QRAKYGTAGYGVEARGPTPEEAQREKDTRISKKMETMGIYFATPEWVALNGHRGPSPGQL  888

Query  251  KVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERV  81
            K  +        DP    +       +S  ++ E ++R   +   A  +  P   Q  I+E
Sbjct  889  KYWQNTREIPDPNEDYLDYVHAEKSRLASEEQILRAATSIFGAPGQAEPP--QAFIDEVA  946

Query  80   TTMVINNGNRGLNQYQVKEIV    18
                IN+G  RG  NQ  Q+K+++
Sbjct  947  KVYEINHG-RGPNQEQMKDLL    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(146)	1e-06()	Compositional matrix adjust.	56/209(27%)	91/209(43%)	42/209(20%)	-2

Features:

```
Query  566  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------  408
            AAA+ DP       +V +WL    ++N  G++   + NF+  D    +M    + N+
Sbjct  775  AAANADPLFRSALQVFMWL---EEN--GIVTDMANFALSDPNAHRMKNFLANAPQAGSKS  829

Query  407  -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                   V +RGPT +  Q ++  RI +        G+  +  EW+  NG+RGPS   Q+
Sbjct  830  QRAKYGTAGYGVEARGPTPEEAQREKDTRISKKMETMGIYFATPEWVALNGHRGPSPGQL  889

Query  251  KVIKTGLDPAPQTIIREPIPRSDNSTPELVM----------RIIRNSLSAHYENASPE-T  105
            K  +          RE IP  +   P+ V             +I+R + S +      E
Sbjct  890  KYWQN---------TRE-IPEPNEDYPDYVHAEKSRLASEEQILRAATSIYGAPGQAEPP  939

Query  104  QKEINERVTTMVINNGNRGLNQYQVKEIV    18
            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(145)	1e-06()	Compositional matrix adjust.	88/355(25%)	140/355(39%)	40/355(11%)	-2

Features:

```
Query    992   GPDCTVVPISAITQNEITTTATPPIP-RGGSMEAALALLQHIPPGV-TPFAVTGNVIEGK   819
               G D TVVPI  + +I + P PP G S  A+A +    P V   A+TG +
Sbjct    622   GRDYTVVPIDDVWDDSIMLSKDPIPPIVGNSGNLAIAYIDVFRPKVPIHVAMTGALNSYG   681

Query    818   IVPN------KWADLKREGMKGTG---IPLVTDQDYKT-IKDLAKATEMLQRITTAQHPA   669
               + N       K A  R G+K TG     + T ++ T IK          R+       P
Sbjct    682   EIENVSFRSTKLATAHRLGLKLTGPGAFDVNTGSNWATFIKRFPHNPRDWDRLPYLNLPY   741

Query    668   VIGTIATAMDSDSpppppPITDEDIMVTLEELLMAAADRDPRMAKLKEVVLWLAKIDDNN   489
               +      D        T E + +   + AAA+ DP     V +WL +
Sbjct    742   LPPNAGRQYDLAMAASEFKETPE--LESAVRAMEAAANVDPLFQSALSVFMWLEEY----   795

Query    488   PGVLDTLHNFSRQDVEGEKMNRIVQNS--------------LTTAVHSRGPTQDVLQHQR   351
               G++  + NF+  D    +M   + N+               V +RGPT +  Q ++
Sbjct    796   -GIVTDMANFALSDPNAHRMRNFLANAPQAGSKSQRAKYGTAGYGVEARGPTEEAQREK   854

Query    350   AVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQMKVIKTGL---DPAPQTIIREPIPRSD   183
                RI +      G+ +  + EW+  NG+RGPS  Q+K  +      DP    +     +S
Sbjct    855   DTRISKKMETMGIYFATPEWVALNGHRGPSPGQLKYWQNTREIPDPNEDYLDYVHAEKSR   914

Query    182   NSTPELVMRIIRNSLSAHYENASPETQKEINERVTTMVINNGNRGLNQYQVKEIV   18
               ++ E ++R   +   A  +   P Q  I+E     IN+G RG NQ Q+K+++
Sbjct    915   LASEEQILRAATSIYGAPGQAEPP--QAFIDEVAKVYEINHG-RGPNQEQMKDLL   966
```

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(145)	2e-06()	Compositional matrix adjust.	53/201(26%)	89/201(44%)	26/201(12%)	-2

Features:

```
Query    566   AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------   408
               AAA+ DP     V +WL   ++N G++  + NF+  D    +M   + N+
Sbjct    774   AAANVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGSKS   828

Query    407   -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM   252
                      V +RGPT +  Q ++ RI +      G+ +  + EW+  NG+RGPS  Q+
Sbjct    829   QRAKYGTAGYGVEARGPTEEAQREKDTRISKKMETMGIYFATPEWVALNGHRGPSPGQL   888

Query    251   KVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERV   81
               K +      DP    +     +S ++ E ++R   +   A  +   P Q  I+E
Sbjct    889   KYWQNTREIPDPNEDYLDYVHAEKSRLASEEQILRAATSIFGAPGQAEPP--QAFIDEVA   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:

```
Query    566   AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------   408
               AAA+ DP     V +WL   ++N G++  + NF+  D    +M   + N+
Sbjct    774   AAANVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGSKS   828

Query    407   -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM   252
                      V +RGPT +  Q ++ RI +      G+ +  + EW+  NG+RGPS  Q+
Sbjct    829   QRAKYGTAGYGVEARGPTEEAQREKDTRISKKMETMGIYFATPEWVALNGHRGPSPGQL   888

Query    251   KVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERV   81
               K +      DP    +     +S ++ E ++R   +   A  +   P Q  I+E
Sbjct    889   KYWQNTREIPDPNEDYLDYVHAEKSRLASEEQILRAATSIFGAPGQAEPP--QAFIDEVA   946

Query    80    TTMVINNGNRGLNQYQVKEIV   18
                IN+G RG NQ Q+K+++
Sbjct    947   KVYEINHG-RGPNQEQMKDLL   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(144)	2e-06()	Compositional matrix adjust.	54/200(27%)	91/200(45%)	24/200(12%)	-2

Features:

```
Query  566  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------  408
            AAA+ DP        V +WL    ++N  G++   + NF+  D    +M    + N+
Sbjct  774  AAANVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGSKS  828

Query  407  -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                   V +RGPT + Q ++ RI +      G+ +  EW+  NG+RGPS  Q+
Sbjct  829  QRAKYGTAGYGVEARGPTPEEAQREKDTRISKKMETMGIYFATPEWVALNGHRGPSPGQL  888

Query  251  KVIKTGLD-PAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPE-TQKEINERVT  78
            K  +   + P P    + +  ++S  L  +I+R + S +      E  Q  I+E
Sbjct  889  KYWQNTREIPDPNEDYLDYV-HAEKSRLALEEQILRAATSIYGAPGQAEPPQAFIDEVAK  947

Query  77   TMVINNGNRGLNQYQVKEIV   18
            IN+G RG NQ Q+K+++
Sbjct  948  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(144)	2e-06()	Compositional matrix adjust.	53/201(26%)	90/201(44%)	26/201(12%)	-2

Features:

```
Query  566  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------  408
            AAA+ DP        V +WL    ++N  G++   + NF+  D    +M    + N+
Sbjct  774  AAANVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGSKS  828

Query  407  -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                   V +RGPT + +Q ++ RI +      G+ +  EW+  NG+RGPS  Q+
Sbjct  829  QRAKYGTAGYGVEARGPTPEEVQREKDTRISKKMEAMGIYFATPEWVALNGHRGPSPGQL  888

Query  251  KVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERV  81
            K  +      DP   +      +S ++ E ++R  +  A  +   P  Q  I+E
Sbjct  889  KYWQNTREIPDPNEDYLDYVHAEKSRLASEEQILRAATSIYGAPGQAEPP--QAFIDEVA  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  AAADRDPRMAKLKEVVLWLAKIDDNNPGVLDTLHNFSRQDVEGEKMNRIVQNS-------  408
            AAA+ DP        V +WL    ++N  G++   + NF+  D    +M    + N+
Sbjct  774  AAANVDPLFQSALSVFMWL---EEN--GIVTDMANFALSDPNAHRMRNFLANAPQAGSKS  828

Query  407  -------LTTAVHSRGPTQDVLQHQRAVRIRENYLIQGVDLSI-EWIKNNGYRGPSAEQM  252
                   V +RGPT + Q ++ RI +      G+ +  EW+  NG+RGPS  Q+
Sbjct  829  QRAKYGTAGYGVEARGPTPEEAQREKDTRISKKMETMGIYFATPEWVALNGHRGPSPGQL  888

Query  251  KVIKTGL---DPAPQTIIREPIPRSDNSTPELVMRIIRNSLSAHYENASPETQKEINERV  81
            K  +      DP   +      +S ++ E ++R  +  A  +   P  Q  I+E
Sbjct  889  KYWQNTRVIPDPNEDYLDYVHAEKSRLASEEQILRAATSIYGAPGQAEPP--QAFIDEVA  946

Query  80   TTMVINNGNRGLNQYQVKEIV   18
            IN+G RG NQ Q+K+++
Sbjct  947  KVYEINHG-RGPNQEQMKDLL   966
```