Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BSTTYM014

- ► Formatting options
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Blast report description

Nucleotide Sequence (1285 letters)

RID <u>B8BSTTYM014</u> (Expires on 02-06 12:11 pm)

Query ID lcl|Query_156209

Description None Molecule type nucleic acid

Query Length 1285

Database Name nr

Description All non-redundant GenBank CDS

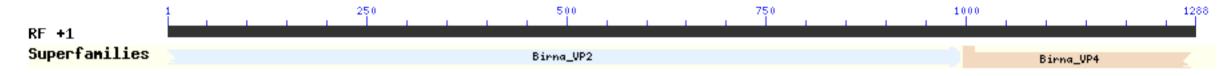
translations+PDB+SwissProt+PIR+PRF excluding

environmental samples from WGS projects

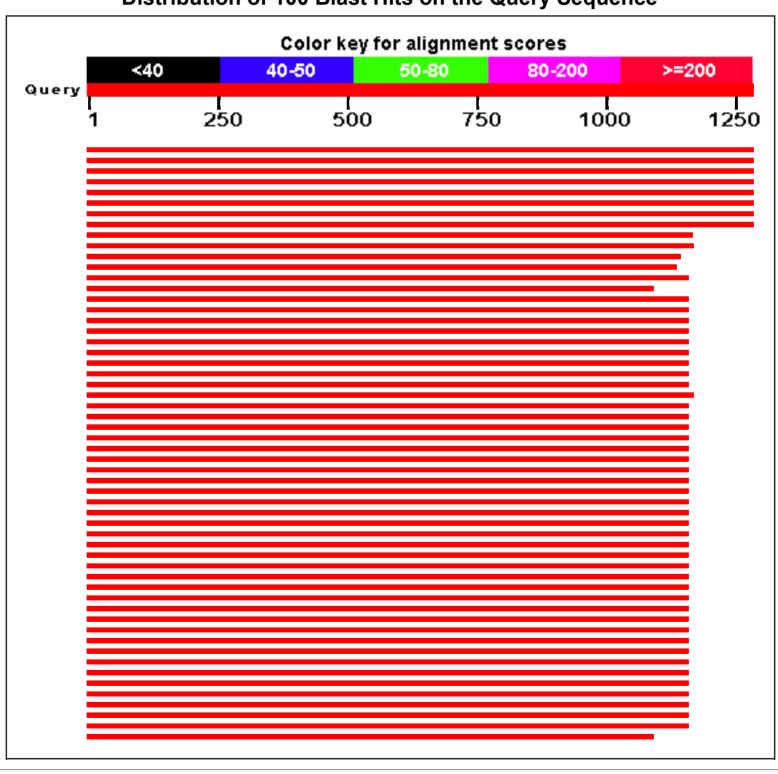
Program BLASTX 2.3.1+

□ Graphic Summary

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



Distribution of 100 Blast Hits on the Query Sequence



ullet Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
polyprotein [Drosophila x virus]	775	775	99%	0.0	89%	NP_690836.1
pVP2-VP4-VP3 polyprotein [Culicine-associated Z virus]	723	723	99%	0.0	77%	AGW51761.1
pVP2-VP4-VP3 polyprotein [Culicine-associated Z virus]	722	722	99%	0.0	77%	AGW51779.1
pVP2-VP4N-X polyprotein [Culicine-associated Z virus]	719	719	99%	0.0	77%	AGW51762.1
pVP2-VP4N-X polyprotein [Culicine-associated Z virus]	718	718	99%	0.0	77%	AGW51780.1
polyprotein [Mosquitoe x virus]	712	712	99%	0.0	76%	AFU34333.1
polyprotein precursor [Culex Y virus]	712	712	99%	0.0	76%	AFR34026.1
unnamed protein product [Espirito Santo virus]	704	704	99%	0.0	75%	YP_004956722.1
unnamed protein product [Espirito Santo virus]	642	642	90%	0.0	76%	YP_004956724.1
capsid protein [Infectious bursal disease virus]	211	211	91%	1e-58	34%	CCN97974.1
polyprotein [Blotched snakehead virus]	217	217	88%	2e-58	36%	YP_052862.1
polyprotein [Rotifer birnavirus strain Palavas]	216	216	88%	7e-58	37%	CAX33877.1
unnamed protein product [Infectious bursal disease virus]	213	213	90%	6e-57	35%	CAA79983.1
major capsid protein VP2 [Infectious bursal disease virus]	206	206	84%	7e-57	34%	AAD25073.1
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	212	212	90%	7e-57	34%	<u>P25220.1</u>
polyprotein [Infectious bursal disease virus]	211	211	90%	8e-57	34%	ABW04864.1
structural polyprotein VP2 precusor [Infectious bursal disease virus]	207	207	90%	8e-57	34%	AAC06018.1
structural polyprotein [Infectious bursal disease virus]	212	212	90%	9e-57	34%	AGM16323.1
polyprotein [Infectious bursal disease virus]	211	211	90%	2e-56	34%	ABN71594.1
polyprotein [Infectious bursal disease virus]	207	207	90%	2e-56	33%	AAA46238.1
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	211	211	90%	2e-56	34%	<u>P15480.1</u>
polyprotein [Infectious bursal disease virus]	211	211	90%	2e-56	34%	ABN71593.1
structural polyprotein [Infectious bursal disease virus]	211	211	90%	2e-56	34%	AAK69711.1
polyprotein [Infectious bursal disease virus]	211	211	91%	2e-56	33%	AAG40010.1
structural polyprotein [Infectious bursal disease virus]	211	211	90%	3e-56	34%	ABW38090.1
polyprotein [Infectious bursal disease virus]	211	211	90%	3e-56	34%	AFU10473.1
polyprotein [Infectious bursal disease virus]	211	211	90%	3e-56	34%	CAC35470.1
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	210	210	90%	4e-56	34%	Q9WI42.1
peptide 3; Short=p3; AltName: Full=pep7b; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName:	210	2.0	55 <i>7</i> 0	.00	O 170	SCOTTITAL!

Polyprotein Infectious bursal disease virus	Full=pep11; Contains: RecName: Full=Protease VP4; AltName: Full=Non-structural protein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP3						
pulyprotein [infectious bursal disease vitua]	polyprotein [Infectious bursal disease virus]	210	210	90%	5e-56	34%	ABW04865.1
Umanned protein product [Infectious bursal disease virus] 210 210 60% 6e-56 34% CAA58851.1 polyprotein [Infectious bursal disease virus] 288 298 90% 6e-56 33% ABD92250.1 Rechame: Full-Procussor of VPC, Short-Pre-VPZ, Contains: Rechame: Full-Short-Pre-VPZ, Co	VP2-4-3 polhyprotein [Infectious bursal disease virus]	210	210	90%	5e-56	34%	AFI55462.1
Polyprotein Infectious bursal disease virus 268 208 209 30% 66-56 33% ABD37260.1	polyprotein [Infectious bursal disease virus]	210	210	90%	5e-56	34%	AAG40008.1
Rechame Full-Enquired (1972 Schriffser) Rechame Full-Enquired (1972	unnamed protein product [Infectious bursal disease virus]	210	210	90%	6e-56	34%	CAA58851.1
RecVanner Full-Encoursion of VPZ, Stort=Prior VPZ, Contains RecVanner Full-Encoursing peptide 1, Stort=Prior VPZ, Contains RecVanner Full-Encoursing peptide 2, Stort=Prior VPZ, Contains RecVanner Full-Encoursing Pepti	polyprotein [Infectious bursal disease virus]	208	208	90%	6e-56	33%	ABD97260.1
Fechane Full-information (Partier Mill-inforcesse VPY, Althame: Full-inforcesse VPY, Althame: Full-inforcesse VPY, Stortien's, Contains: Rechance (Full-inforcesse VPY) Properties of the Properties VPY, Stortien's, Contains: Rechance (Full-inforcesse VPY) Properties (Full-inforce) (Properties VPY) Properties (Full-inforce) (Properties) (P	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	210	210	90%	6e-56	34%	<u>P61825.2</u>
Dolyprotein [Infectious bursal disease virus] 209 209 90% 7e-56 34% AAKS15221 Dolyprotein [Infectious bursal disease virus] 209 209 90% 7e-56 34% ALWI2285.1 Dolyprotein [Infectious bursal disease virus] 204 204 90% 8e-56 33% AGE58945.1 VP2 protein precursor [Infectious bursal disease virus] 204 204 90% 8e-56 33% AGE58945.1 VP2 protein precursor [Infectious bursal disease virus] 204 204 90% 8e-56 33% AGE58945.1 VP2 protein precursor [Infectious bursal disease virus] 204 204 90% 8e-56 33% AGE175932.1 RecName: Full-Precursor of VP2.5 Short=Pre-VP2. Contains: RecName: Full-Equation [Infectious bursal disease virus] 209 209 90% 8e-56 34% P25219.1 Pedido 3; Short=92, AllName: Full-Protease VP4, AllName: Full-Pupp P1; Contains: RecName: Full-Equation [Infectious bursal disease virus] 209 209 90% 8e-56 34% AGE3029.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 8e-56 34% AGE3029.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 9e-56 33% AGE36847.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 9e-56 33% AGE36847.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 9e-56 33% AGE36847.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 9e-56 33% AGE36847.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 33% AGE36441.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 33% AGE3444.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AGE3444.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AGE3444.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 2e-55 34% AGE3444.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 2e-55 34% AGE3444.1 Polyprotein [Infectious bursal disease virus] 209 209 90% 2e-55 34% AGE3444.1 Pol	RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep11; Contains: RecName: Full=Protease VP4; AltName: Full=Non-structural protein VP4; Short=NS; Contains:						
Dobyprotein Infectious bursal disease virus 209 209 90% 7e-56 34% ACB85949.1	polyprotein [Infectious bursal disease virus]	209	209	90%	6e-56	34%	AAP83585.2
Dobyprotein Infectious bursal disease virus 209 209 90% 7e-56 34% ACB56949.1	polyprotein [Infectious bursal disease virus]	209	209	90%	7e-56	34%	AAK51522.1
VP2 protein precursor [Infectious bursal disease virus]	polyprotein [Infectious bursal disease virus]	209	209	90%	7e-56	34%	AHW82958.1
RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pe-VP2; Contains: RecName: Full=Precursor of VP2; Short=Pe-VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; AllName: Full=pep46; Contains: RecName: Full=Structural peptide 1; Short=p1; AllName: Full=pep46; Contains: RecName: Full=Structural peptide 4; Short=p4; AllName: Full=Polyprotein; Short=P4; AllName: Full=pep476; Contains: RecName: Full=Structural peptide 4; Short=p4; AllName: Full=Polyprotein; Full	polyprotein [Infectious bursal disease virus]	209	209	90%	7e-56	34%	ACB56949.1
RecName: Full-Precursor of VP2; Short-Pre-VP2; Contains: RecName: Full-Expasid protein VP2; Contains: RecName: Full-Expasid protein VP2; Contains: RecName: Full-Expasid peptide 1; Short-p1; AllMame: Full-pep48; Contains: RecName: Full-Expasid Short-p2; AllMame: Full-pep78; Short-p2; AllMame: Full-pep78; Contains: RecName: Full-Expasid RecName: Full-E	VP2 protein precursor [Infectious bursal disease virus]	204	204	90%	8e-56	33%	AEL75032.1
110-kDa polyprotein [Infectious bursal disease virus] 209 209 90% 8e-56 34% AAK30029.1	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:	209	209	90%	8e-56	34%	<u>P25219.1</u>
Dolyprotein [Infectious bursal disease virus] 209 209 90% 8e-56 34% CDP32875.1	· ·	200	200	00%	90 F6	2.40/	A A K 20020 4
polyprotein [Infectious bursal disease virus] 209 209 90% 9e-56 33% AAY88214.1 polyprotein [Infectious bursal disease virus] 209 209 90% 9e-56 33% ACB56947.1 polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 33% ABN71592.1 polyprotein [Infectious bursal disease virus] 203 203 90% 1e-55 33% ABRA94192.1 polyprotein [Infectious bursal disease virus] 206 206 90% 1e-55 33% BAA04108.1 polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 33% BAA04108.1 polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AGS40406.1 structural polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AGS404342.1 RecName: Full=Structural polyprotein; Short=PP: Contains: RecName: Full=Structural polyprotein; Short=PP: Contains: RecName: Full=Structural polyprotein; Short=PP: Contains: RecName: Full=Structural peptide 2; Short=p2; AltName: Full=pep7a; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep7a; Contains: RecName: Full=Structural polytide 1; Short=P4; AltName: Full=Polyprotein VP4; Short=NS; Contains: RecName: Full=Structural polyprotein; Short=PP: Contains: RecName: Full=Structural polyprotein; Short=PP: Contains: RecName: Full=Structural polyprotein VP4; Short=NS; Contains: RecName: Full=Structural polyprotein VP4; Short=PP: Contains: RecName: Full=Structural polyprotein; Short=PP: Contains: RecName: Full=Structural polyprotein VP4; Short=PP: Contains: RecName: Full=Structural polyprotein VP4; Short=PP2; Contains: RecName: Full=Structural polyprotein VP4; Contains: RecName: Full=Pp7a; Contains: RecName: Full=Pp46;							
polyprotein [Infectious bursal disease virus] 209 209 90% 9e-56 33% ACB56947.1 polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 33% ABN71592.1 polyprotein [Infectious bursal disease virus] 203 203 90% 1e-55 33% ABG81111.1 polyprotein [Infectious bursal disease virus] 206 206 90% 1e-55 33% BAA04108.1 polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 33% BAA04108.1 polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 structural polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 structural polyprotein; Short=PP: Contains: RecName: Full=Structural polyprotein; Short=PP: Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Structural polyprotein VP2; 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=Portease VP4; AltName: Full=pep71; Contains: RecName: Full=Portease VP4; AltName: Full=pep7b; Contains: RecName: Full=Structural peptide 4; Short=P4; AltName: RecName: Full=Structural peptide 4; Short=P4; Contains: RecName: Full=Structural peptide 4; Short=P5; Contains: RecName: Full=Structural peptide 4; Short=P6; Contains: RecNa							
polyprotein Infectious bursal disease virus 209 209 90% 1e-55 33% ABN71592.1							
polyprotein [Infectious bursal disease virus] 203 203 90% 1e-55 33% ABG81111.1 polyprotein [Infectious bursal disease virus] 206 206 90% 1e-55 33% BAA04108.1 polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 structural polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 structural polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Percursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Percursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 2; Short=p2; AltName: Full=Structural peptide 4; Short=p4; AltName: Full=Pertractoral peptide 4; Short=p4; AltName: Full=Pertractoral protein VP4; Short=N5; Contains: RecName: Full=Structural protein VP4; Short=N5; Contains: RecName: Full=Structural protein VP4; Short=PP; Contains: RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Structural peptide 2; Short=p2; AltName: Full=Structural peptide 2; Short=p2; AltName: Full=Structural peptide 2; Short=p2; AltName: Full=Structural peptide 4; Short=p4; AltName: Full=Structural pep							
polyprotein [Infectious bursal disease virus] 206 206 90% 1e-55 33% BAA04108.1 polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 structural polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 structural polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 RecName: Full=Structural polyprotein, Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Precursor of VP2; Short=PP; Contains: RecName: Full=Structural peptide 1; Short=p1; AltName: Full=pep7a; Contains: RecName: Full=Structural peptide 2; Short=p2; AltName: Full=Structural peptide 2; Short=p2; AltName: Full=Structural peptide 4; Short=p4; AltName: Full=Structural peptide 4; Short=p4; AltName: Full=Structural peptide 4; Short=N5; Contains: RecName: Full=Structural protein VP3; Short=N5; Contains: RecName: Full=Structural protein VP3; Short=N5; Contains: RecName: Full=Capsid protein VP3; Short=PP; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=Structural peptide 1; Short=p1; AltName: Full=Structural peptide 2; Short=p2; AltName: Full=Structural peptide 2; Short=p3; AltName: Full=Structural peptide 3; Short=p3; AltName: Full=Structural peptide 4; Short=p4; AltName: Full=Structural peptide 4; Short=p5; Contains: RecName: Full=Structural peptide 4; Short=p6; AltName: Full=Structural peptide 4; Short=p6; AltName:							
polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% AAG40006.1 structural polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% ACS44342.1 RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; Contains: RecName: Full=Capsid protein VP2; Contains: RecName: Full=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 4; Short=p4; AltName: Full=pep11; Contains: RecName: Full=Protease VP4; AltName: Full=pep11; Contains: RecName: Full=Protease VP4; AltName: Full=pep11; Contains: RecName: Full=Capsid protein VP3 Polyprotein; Short=NP; Contains: RecName: Full=Capsid protein VP4; Short=NP; Contains: RecName: Full=Protease VP4; AltName: Full=Protease VP4; AltName: Full=Structural peptide 1; Short=p1; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 2; Short=p2; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 3; Short=p3; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep11; Contains: RecName: Full=pep7b; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep11; Contains: RecName: Full=Protease VP4; AltName: Full=Potein VP4; Short=NS; Contains: RecName: Full=Protease VP4; AltName: Full=Potein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP3							
structural polyprotein [Infectious bursal disease virus] 209 209 90% 1e-55 34% ACS44342.1 RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Capsid protein VP2; Short=Pre-VP2; Contains: RecName: Full=Capsid protein 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=pep7b; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep11d; Contains: RecName: Full=Protease VP4; AltName: Full=pep11d; Contains: RecName: Full=Protein VP4; Short=N5; Contains: RecName: Full=Capsid protein VP3 polyprotein [Infectious bursal disease virus] 208 208 90% 2e-55 34% AFX62899.1 RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=P6; Contains: RecName: Full=Structural peptide 1; Short=p1; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 4; Short=p2; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 4; Short=p2; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep46; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep11; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=Pon-structural peptide 4; Sh							
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=pep7b; Contains: RecName: Full=pep7a; Contains: RecName: Full=pep7b; Contains: RecName: Full=Structural peptide 4; Short=p4; AltName: Full=pep11; Contains: RecName: Full=Protease VP4; AltName: Full=Pon-structural protein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP3 polyprotein [Infectious bursal disease virus] RecName: Full=Structural polyprotein; Short=PP; Contains: RecName: Full=Precursor of VP2; Short=Pre-VP2; 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=pep11; Contains: RecName: Full=Protease VP4; AltName: Full=Pon-structural protein VP4; Short=NS; Contains: RecName: Full=Capsid protein VP4; Short=NS; Contains:		209	209		1e-55	34%	ACS44342.1
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 208 208 90% 2e-55 33% P22351.1 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	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:	209	209	90%	2e-55	34%	<u>P27276.1</u>
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 208 208 90% 2e-55 33% P22351.1 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	polyprotein [Infectious bursal disease virus]	208	208	90%	2e-55	34%	AFX62899.1
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	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;						
polyprotein [Infectious bursal disease virus] 208 208 90% 2e-55 33% BAA12175.1	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:	208	208	90%	2e-55	33%	<u>P22351.1</u>
	polyprotein [Infectious bursal disease virus]	208	208	90%	2e-55	33%	BAA12175.1

polyprotein [Infectious bursal disease virus]	208	208	90%	2e-55	33%	ABN71595.1
polyprotein [Infectious bursal disease virus]	208	208	90%	2e-55	33%	ACB56951.1
structural protein [Infectious bursal disease virus]	202	202	84%	3e-55	33%	AAB63594.1
polyprotein [Infectious bursal disease virus]	208	208	90%	3e-55	33%	ACP30638.1
structural polyprotein VP2, VP4, VP3 [Infectious bursal disease virus]	205	205	90%	3e-55	33%	AAC06017.1
structural polyprotein [Infectious bursal disease virus]	207	207	90%	3e-55	33%	BAH03940.1
structural protein [Infectious bursal disease virus]	202	202	89%	4e-55	33%	AAF86635.1
VP2 [Infectious bursal disease virus]	202	202	84%	4e-55	34%	BAA00954.1
polyprotein [Infectious bursal disease virus]	207	207	90%	4e-55	34%	AAS10174.1
polyprotein [Infectious bursal disease virus]	206	206	90%	5e-55	33%	ABB88945.1
polyprotein [Infectious bursal disease virus]	207	207	85%	6e-55	34%	AKM16810.1
polyprotein [Infectious bursal disease virus]	207	207	90%	8e-55	33%	AAC78079.1
polyprotein [Infectious bursal disease virus]	206	206	90%	8e-55	33%	ABW04866.1
VP2 [Infectious bursal disease virus]	200	200	81%	1e-54	34%	AAV88102.1
polyprotein [Infectious bursal disease virus]	206	206	90%	1e-54	33%	AEP04401.1
VP2 [Infectious bursal disease virus]	199	199	81%	1e-54	34%	AAV88104.1
VP2, VP3, and VP4 [Infectious bursal disease virus]	206	206	90%	2e-54	33%	AAA52086.1
polyprotein [Infectious bursal disease virus]	206	206	90%	2e-54	33%	ABI52866.1
polyprotein [Infectious bursal disease virus]	206	206	90%	2e-54	33%	AKU89588.1
VP2-4-3 [Infectious bursal disease virus]	206	206	90%	2e-54	33%	ABI83739.1
110 kDa polyprotein [Infectious bursal disease virus]	206	206	90%	2e-54	33%	AAR24133.1
polyprotein [Infectious bursal disease virus]	205	205	90%	2e-54	33%	AFU10443.1
polyprotein [Infectious bursal disease virus]	205	205	90%	2e-54	33%	AFU10478.1
polyprotein [Infectious bursal disease virus]	199	199	84%	3e-54	33%	AAG23824.1
polyprotein [Infectious bursal disease virus]	205	205	90%	3e-54	33%	ABG76954.1
structural polyprotein [Infectious bursal disease virus]	205	205	90%	3e-54	33%	AIG93139.1
polyprotein [Infectious bursal disease virus]	205	205	90%	3e-54	33%	ACB56941.1
polyprotein [Infectious bursal disease virus]	205	205	90%	3e-54	33%	CAJ34339.1
structural polyprotein [Infectious bursal disease virus]	205	205	90%	4e-54	33%	BAH03937.1
polyprotein [Infectious bursal disease virus]	205	205	90%	4e-54	33%	ABI52864.1
structural polyprotein [Infectious bursal disease virus]	205	205	90%	4e-54	33%	AAK69716.1
polyprotein [Infectious bursal disease virus]	204	204	90%	5e-54	33%	AAN04461.1
polyprotein [Infectious bursal disease virus]	204	204	90%	5e-54	33%	ACZ62645.1
polyprotein [Infectious bursal disease virus]	204	204	90%	5e-54	33%	CAI53892.2
polyprotein [Infectious bursal disease virus]	204	204	90%	6e-54	33%	AEQ29949.1
polyprotein [Infectious bursal disease virus]	204	204	90%	6e-54	33%	CAC60256.1
Polyprotein (VP2-VP4-VP3) [Infectious bursal disease virus]	204	204	90%	6e-54	33%	CDW92043.1
polyprotein [Infectious bursal disease virus]	204	204	90%	6e-54	33%	AEX10576.1
polyprotein [Infectious bursal disease virus]	204	204	90%	6e-54	33%	AAM28898.1
structural polyprotein [Infectious bursal disease virus]	204	204	90%	6e-54	33%	AIG93145.1
structural polyprotein [Infectious bursal disease virus]	204	204	90%	6e-54	33%	ACS44345.1
VP2-4-3 polyprotein [Infectious bursal disease virus]	204	204	90%	6e-54	33%	NP_690838.1
polyprotein [Infectious bursal disease virus]	204	204	90%	6e-54	33%	AEQ29948.1
polyprotein [Infectious bursal disease virus]	204	204	90%	7e-54	33%	BAA08555.1
polyprotein [Infectious bursal disease virus]	204	204	90%	7e-54	33%	AHW82956.1
structural polyprotein [Infectious bursal disease virus]	204	204	90%	7e-54	33%	ABW38087.1



Sequence ID: ref|NP_690836.1| Length: 1032 Number of Matches: 1

▶ See 2 more title(s) Range 1: 112 to 539

Score		Expect Method					ldent	ities	Posit	ives	Gaps	Frame		
775 bits	(2000)	0.0()	Comp	ositiona	l matrix	adjust.	380/4	28(89%)	404/4	28(94%) 0/428(0%)	+1	
Features	S :													
Query	1							SNPLDKV SNPLDKV						180
Sbjct	112							SNPLDKV						171
Query	181			TLQSPT TL SPT				IPSTTIF IP TT+F						360
Sbjct	172							IPVTTVE						231
Query	361							KTLVWSN +TL WSN						540
Sbjct	232							RTLTWSN						291
Query	541	NPPP]	EPVAA:	LKVHIT	YGNNTI	NGDSDF	SVDSS	FTINVIO FTINVIO	GATI	GVNSPTV	/VVGYO	VAE	GT	720
Sbjct	292							FTINVIC						351
Query	721							DL YIK						900
Sbjct	352							HDLTYIK						411
Query	901							KVAVPLA VAVPLA						1080
Sbjct	412							NVAVPLA						471
Query	1081							SPLGEEH SPLGEEH						1260
Sbjct	472							SPLGEER						531
Query	1261	MALF:		1284										
Sbjct	532	MALF		539										

pVP2-VP4-VP3 polyprotein [Culicine-associated Z virus]

Sequence ID: **gb|AGW51761.1|** Length: 1057 Number of Matches: 1 Range 1: 114 to 541

Score	Expect Method			Identities Positives			ves	Gaps		Frame			
723 bits(1865)	0.0()	Comp	ositional	matrix a	djust.	331/428	3(77%)	390/42	28(91%)	0/428(0)%) ·	+1
Features	:												
Query	1				LSEVSDY LSEV+D								
Sbjct	114				LSEV+D LSEVTDL								
Query	181				HITNTSR HITNTS+						NVDSVG		
Sbjct	174				HITNTSQ								
Query	361				NYQPLNI NYQPLN+								
Sbjct	234				NYQPLNL								
Query	541				YGNNTNG +GNNTNG						VVGYQA V++GYO		
Sbjct	294				FGNNTNG								
Query	721				PDLOKNL P LOKNL								
Sbjct	354				PALÕKNL								
Query	901				KEAASFD +EAASFD							ADAV	
Sbjct	414				REAASFD								
Query	1081				MPISLSR								
Sbjct	474				+PIS++R LPISMTR								
Query	1261	MALFI MALFI		1284									
Sbjct	534	MALFI		541									

pVP2-VP4-VP3 polyprotein, partial [Culicine-associated Z virus]

Sequence ID: **gb|AGW51779.1|** Length: 1049 Number of Matches: 1 Range 1: 108 to 535

Score		Expect	Method	Identities	Positives	Gaps	Frame
722 bits((1864)	0.0()	Compositional matrix adjust.	331/428(77%)	390/428(91%)	0/428(0%)	+1
Features	S :						
Query	1	YALNO	GTFNAVWFQGTLSEVSDYSYDR1	ILSITSNPLDKV	GNVLVGDGLEI	LSLPQGFNN	PY 180

		YALNGTFNAVWFQGTLSEV+D +YDRILSITSNPLDKVGNVLVGDGL ILSLPQGFNNPY	
Sbjct	108	YALNGTFNAVWFQGTLSEVTDLNYDRILSITSNPLDKVGNVLVGDGLAILSLPQGFNNPY	167
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDSVGPIDIM VRLGD+SPS+L S THITNTS+NLGYGGA+ +P T + GQ KEF+INVDSVGPID+	360
Sbjct	168	VRLGDESPSSLTSVTHITNTSQNLGYGGAFSVPQTKVAGQATFVKEFNINVDSVGPIDVT	227
Query	361	WSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNMNELNVSLFHE WSGQMTM DEWTVTANYQPLN+SGTLI GSM+T++WSN GV+NG HYMN+NE+NVS FHE	540
Sbjct	228	WSGQMTMQDEWTVTANYQPLNLSGTLITGSMRTIIWSNVGVSNGAHYMNLNEMNVSFFHE	287
Query	541	NPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSPTVVVGYQAVAEGT NPPPEPVAA+KVH+T+GNNTNG+S VD SFT +V+GGATIGVNSPTV++GYQ VAEGT	720
Sbjct	288	NPPPEPVAATKVHTITGNNINGTS VD SFI TVTGGAIIGVNSPIVTTGIQ VAEGI NPPPEPVAAIKVHLTFGNNINGESTMKVDGSFTFHVVGGATIGVNSPIVTTGIQ VAEGI	347
Query	721	AITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKLGLRSVMTLAEYNR AITISG+NNYELVPNP LQKNLPM+YG CDP DL Y+KYILS+RE+LG+RSVMTLA+Y R	900
Sbjct	348	AITISGYNNYELVPNP LQKNLPMTYGTCDPTDLTYVKYILSHRERLGIRSVMTLADYAR	407
Query	901	MKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAPIIGAASGLADAVL	1080
Sbjct	408	+KM MHV+T Y VD++EAASFDFW+LLKQIKK+AVP+A+T+ PQ+APIIGAA LA+AV+ LKMQMHVMTEYRVDDREAASFDFWNLLKQIKKLAVPVASTMLPQFAPIIGAADNLANAVM	467
Query	1081	GDSASGRPVGNSASGMPISLSRRLRNAYSADSPLGEEHWKPNESEEFNKFDIIYDVSYSS	1260
Sbjct	468	G+SASG+P+GNSASG+PIS++RR+++A+SAD+P+GE +WKPNES EFNK D+IYDVS+SS GNSASGQPIGNSASGLPISMTRRIKSAHSADTPIGESNWKPNESAEFNKLDVIYDVSHSS	527
Query	1261	MALFPVIM 1284	
Sbjct	528	MALFPVIM MALFPVIM 535	

pVP2-VP4N-X polyprotein [Culicine-associated Z virus]

Sequence ID: **gb|AGW51762.1|** Length: 868 Number of Matches: 1 Range 1: 114 to 541

Score		Expect Metl	hod	Identities	Positives	Gaps	Frame	
719 bits	(1855)	0.0() Com	positional matrix adjust.	331/428(77%)	390/428(91%)	0/428(0%)	+1	
Feature	s:							
Query	1		AVWFQGTLSEVSDYSYDR AVWFQGTLSEV+D +YDR					
Sbjct	114		AVWFQGTLSEVTD TIDK AVWFQGTLSEVTDLNYDR					
Query	181		STLQSPTHITNTSRNLGY S+L S THITNTS+NLGY			NVDSVGPID NVDSVGPID		
Sbjct	174		SSLTSVTHITNTSQNLGY					
Query	361		DEWTVTANYQPLNISGTL DEWTVTANYQPLN+SGTL					
Sbjct	234		DEWTVTANYQPLNLSGTL					
Query	541		ALKVHITYGNNTNGDSDF A+KVH+T+GNNTNG+S		GATIGVNSPTV GATIGVNSPTV			
Sbjct	294		AIKVHLTFGNNTNGESTM					
Query	721		NYELVPNPDLQKNLPMSY NYELVPNP LQKNLPM+Y					
Sbjct	354		NYELVPNPALÕKNLPMTY					
Query	901		TNYNVDEKEAASFDFWHL T Y VD++EAASFDFW+L					
Sbjct	414		TEYRVDDREAASFDFWNL					
Query	1081		VGNSASGMPISLSRRLRN +GNSASG+PIS++RR+++					
Sbjct	474		IGNSASGLPISMTRRIKS					
Query	1261	MALFPVIM MALFPVIM	_					
Sbjct	534	MALFPVIM						

pVP2-VP4N-X polyprotein, partial [Culicine-associated Z virus]

Sequence ID: gb|AGW51780.1| Length: 862 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
718 bits	(1853)	0.0() Compositional matrix adjust.	331/428(77%)	390/428(91%)	0/428(0%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDR				
Sbjct	108	YALNGTFNAVWFQGTLSEV+D +YDR YALNGTFNAVWFQGTLSEVTDLNYDR				
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGY VRLGD+SPS+L S THITNTS+NLGY			NVDSVGPID NVDSVGPID	
Sbjct	168	VRLGDESPSSLTSVTHITNTSQNLGY				
Query	361	WSGQMTMVDEWTVTANYQPLNISGTL WSGQMTM DEWTVTANYQPLN+SGTL				
Sbjct	228	WSGQMTMQDEWTVTANYQPLNLSGTL				
Query	541	NPPPEPVAALKVHITYGNNTNGDSDF NPPPEPVAA+KVH+T+GNNTNG+S		GATIGVNSPTV GATIGVNSPTV		
Sbjct	288	NPPPEPVAAIKVHLTFGNNTNGESTM				

Query	721	AITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKLGLRSVMTLAEYNR 90 AITISG+NNYELVPNP LQKNLPM+YG CDP DL Y+KYILS+RE+LG+RSVMTLA+Y R	0
Sbjct	348	AITISGVNNYELVPNPALÕKNLPMTYGTCDPTDLTYVKYILSHRERLGIRSVMTLADYAR 40	7
Query	901	MKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAPIIGAASGLADAVL 10 +KM MHV+T Y VD++EAASFDFW+LLKQIKK+AVP+A+T+ PQ+APIIGAA LA+AV+	80
Sbjct	408	LKMQMHVMTEYRVDDREAASFDFWNLLKQIKKLAVPVASTMLPQFAPIIGAADNLANAVM 46	7
Query	1081	GDSASGRPVGNSASGMPISLSRRLRNAYSADSPLGEEHWKPNESEEFNKFDIIYDVSYSS 12 G+SASG+P+GNSASG+PIS++RR+++A+SAD+P+GE +WKPNES EFNK D+IYDVS+SS	60
Sbjct	468	GNSASGQPIGNSASGLPISMTRRIKSAHSADTPIGESNWKPNESAEFNKLDVIYDVSHSS 52	7
Query	1261	MALFPVIM 1284	
Sbjct	528	MALFPVIM MALFPVIM 535	

polyprotein [Mosquitoe x virus]

Sequence ID: **gb|AFU34333.1|** Length: 1057 Number of Matches: 1 Range 1: 114 to 541

Score		Expect Method					ldenti	ties	Posi	Positives Gaps			s Frame	
712 bits	(1838)	0.0()	Comp	ositiona	l matrix	adjust.	326/42	28(76%)	388/4	128(90%) 0/428	(0%)	+1	
Feature	s:													
Query	1	YALN	GTFNA	VWFQGT	LSEVSD	YSYDR	ILSITS	SNPLDKV	GNVL	VGDGLE:	ILSLPO	GFNN	PY	180
Sbjct	114									VGDGL - VGDGLAV				173
Query	181									HTKEFS				360
Sbjct	174							-P TT+ /PQTTVA		FVKEFN:	INVDSV INVDSV			233
Query	361									NGNHYMI NG HYMI				540
Sbjct	234									NG HYMI NGPHYMI				293
Query	541			LKVHIT +KVHIT						GVNSPT' GVNSPT'				720
Sbjct	294									GVNSPT				353
Query	721									NREKLGI NREKLG-				900
Sbjct	354									NREKLG:				413
Query	901									PQYAPI PQ+API		LADA' LA+A'		1080
Sbjct	414									PQFAPI:			- —	473
Query	1081							SPLGEEH -P+GE +		ESEEFNI + EFNI				1260
Sbjct	474									RNPEFNI				533
Query	1261	MALF:		1284										
Sbjct	534	MALF: MALF:		541										

polyprotein precursor [Culex Y virus]

Sequence ID: **gb|AFR34026.1|** Length: 1057 Number of Matches: 1 Range 1: 114 to 541

Score		Expect	Metho	d				ldent	ities		Posi	itives	3	Ga	ps		Fran	ne_
712 bits((1837)	0.0()	Comp	ositiona	ıl matri	x adjust	t. :	325/4	28(76	5%)	390/	428(91%)	0/4	28(0%	%) ·	+1	
Features	s:																	
Query	1					SDYSYD												180
Sbjct	114					SD +YD SDLNYD												173
Query	181					SRNLG									SVGP SVGP			360
Sbjct	174					STNLG												233
Query	361	WSGQI	HTMVDI	EWTVTA	NYOPI	NISGT N+SGT	LIZ	AGSM	KTLVV	WSN'	TGVA	NGN	HYMN	MNE	LNVS	LFI	HE	540
Sbjct	234					LNLSGT												293
Query	541					NGDSD												720
Sbjct	294			+KVHIT [KVHIT		NGEST			FT +\ FTFH\									353
Query	721					NLPMS												900
Sbjct	354					NLPMS NLPMS												413
Query	901					SFDFWH												1080
Sbjct	414					SFDFWH SFDFWH										A+ VAV	- —	473
Query	1081					SRRLR												1260
Sbjct	474					-+RR++ ITRRIK									IYDV IYDV			533
Query	1261	MALF]	PVIM	1284														

Sbjct 534 MALFPVIM 541

unnamed protein product [Espirito Santo virus]

Sequence ID: ref|YP_004956722.1| Length: 1054 Number of Matches: 1

▶ See 1 more title(s) Range 1: 112 to 539

Score		Expect Met	hod	Identities	Positives	Gaps	Frame
704 bits	(1818)	0.0() Con	npositional matrix adjust.	322/428(75%)	387/428(90%)	0/428(0%)	+1
Features	s:						
Query	1		NAVWFQGTLSEVSDYSYDR				
Sbjct	112		IAVWFQGTLSEVS+ +YDR IAVWFQGTLSEVSNLNYDR				
Query	181		PSTLQSPTHITNTSRNLGY PS+L S THITNTS+NLGY				
Sbjct	172	VRLGD+SE VRLGDESE	PSSLTSVTHITNTSQNLGY	GGAFAVPQTTVA	GQG KEFTI .GQGTFFKEFNI	NVDSVGPID NVDSVGPID	VT 231
Query	361		DEWTVTANYQPLNISGTL DEWTVTANYQPLN+SGTL				
Sbjct	232		DEWTVTANYQPLNLSGTL DEWTVTANYQPLNLSGTL				
Query	541		AALKVHITYGNNTNGDSDF AA+KVHIT+GNNTNG+S	SVDSSFTINVIG +VD SFT +V+G			
Sbjct	292		AAIKVHITFGNNTNGESSM				
Query	721		INYELVPNPDLQKNLPMSY INYELVPNP LQKNLPMSY				
Sbjct	352		INYELVPNPALQKNLPMSY				
Query	901		TNYNVDEKEAASFDFWHL T+Y+V ++EA+SFDFWHL				
Sbjct	412		TTDYHVGDREASSFDFWHL				
Query	1081		PVGNSASGMPISLSRRLRN P+GNSASG+PIS++RR+++			FDIIYDVSY	
Sbjct	472		PIGNSASGLPISHTRRIKS				
Query	1261	MALFPVIM MALFPVIM					
Sbjct	532	MALFPVIM					

unnamed protein product [Espirito Santo virus]

Sequence ID: **ref|YP_004956724.1|** Length: 500 Number of Matches: 1 Range 1: 112 to 500

Score	Expect Method	Identities	Positives	Gaps	Frame
642 bits(1657)	0.0() Compositional matrix adjust.	296/389(76%)	353/389(90%)	0/389(0%)	+1
Features:					
Query 1	YALNGTFNAVWFQGTLSEVSDYSYDRI				
Sbjct 112	YAL GTFNAVWFQGTLSEVS+ +YDRI YALTGTFNAVWFQGTLSEVSNLNYDRI				
Query 181	VRLGDKSPSTLQSPTHITNTSRNLGYGVRLGD+SPS+L S THITNTS+NLGYG			NVDSVGPID: NVDSVGPID	
Sbjct 172	VRLGD+SPS+L S THITNIS+NLGIG VRLGDESPSSLTSVTHITNTSQNLGYG				
Query 361	WSGQMTMVDEWTVTANYQPLNISGTLI WSG MTM DEWTVTANYOPLN+SGTLI				
Sbjct 232	WSGLMTMQDEWTVTANYQPLNLSGTLI				
Query 541	NPPPEPVAALKVHITYGNNTNGDSDFS				
Sbjct 292	NPPPEPVAA+KVHIT+GNNTNG+S + NPPPEPVAAIKVHITFGNNTNGESSMN		GATIGVNSPTV GATIGVNSPTV		
Query 721	AITISGINNYELVPNPDLQKNLPMSYO				
Sbjct 352	IT+SG+NNYELVPNP LQKNLPMSYG TITLSGVNNYELVPNPALQKNLPMSYG				
Query 901	MKMYMHVLTNYNVDEKEAASFDFWHLI				
Sbjct 412	MKM M+++T+Y+V ++EA+SFDFWHLI MKMQMNIMTDYHVGDREASSFDFWHLI				
Query 1081					
Sbjct 472	G+SASG+P+GNSASG+PIS++RR+++A GNSASGQPIGNSASGLPISMTRRIKSA				

capsid protein, partial [Infectious bursal disease virus]

Sequence ID: emb|CCN97974.1| Length: 506 Number of Matches: 1 Range 1: 118 to 506

Score	Expect	Method	Identities	Positives	Gaps	Frame
211 bits(538)	1e-58()	Compositional matrix adjust	137/404(34%)	216/404(53%)	29/404(7%)	+1

Features:		
Query 1	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y	180
Sbjct 118	YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query 181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S PG G+ FS N+D+	339
Sbjct 178	VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA	236
Query 340	$egin{array}{llllllllllllllllllllllllllllllllllll$	510
Sbjct 237	ITSLSVGGELVFRTSVHGLVLGATIYLIGFDGTTVITRAVAANNGLTTGTDNL	289
Query 511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDS-DFSVDSSFTINVIGGATIGVNS N+ + N +P+ ++K+ I G GD +S S + + GG G	678
Sbjct 290	MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGGDQMSWSARGSLAVTIHGGNYPGALR	348
Query 679	PTVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREK P +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++	858
Sbjct 349	PVTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDR	408
Query 859	LGLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYA LG+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P A	1038
Sbjct 409	LGIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAA	468
Query 1039	PIIGAASGLADAVLGDSASGRPVGNSASGMPISLSRRLRNAYSA 1170 P+ A D +LGD A +ASG + S + R A +A	
Sbjct 469	PLAHAIGEGVDYLLGDEAQAASGTARAASGKARAASAA 506	

polyprotein [Blotched snakehead virus]

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

▶ See 2 more title(s) Range 1: 116 to 476

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
217 bits	(552) 26	e-58() Compositional matrix adjust.	140/390(36%)	213/390(54%)	38/390(9%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGTFN V + G+LSE+ D Y+				
Sbjct	116	YALNGTFN V + G+LSE+ D Y+ YALNGTFNGVTYIGSLSEIKDLDYN				
Query	181	VRLGDKSPSTLQSPTHI VRLGD+ PS+ P H	TNTSRNLGYGGA ++ + G	YKIPSTTIPGÇ TT		VD 336 +D
Sbjct	176	VRLGDEVPSSAGVARCSPSDRPRHY	_			_
Query	337	SVGPIDIMWSGQMTMVDEW-TVTAN + P ++ O+ + T+T	YQPLNISGTLIA + + ++G +A		GVANGNHYMNI G H+	MN 513
Sbjct	223	ATTPTEVTVDMÕIAQIAAGKTLTVT				276
Query	514	ELNVSLFHENPPPEPVAALKVHITY ++F E +PV ++V		DSSFTINVIGO DS + V GO		VV 693
Sbjct	277	TAVFGETEITQPVVGVQVLA				
Query	694	GYQAVAEGTAITISGINNYELVPNP Y++VA G+ +T+SGI+NYEL+PNP		CDPQDLNYIKY C +P ++ Y K		
Sbjct	329	AYESVATGSVLTLSGISNYELIPNP				
Query	874	VMTLAEYNRMKMYMHVLTNYNVDEK + ++ +Y M Y +++ + K		QIKKVAVPLAA I+K P+	TLAPQYAPII	GA 1053
Sbjct	389	IWSIPQYRDMMSYFREVSDRSSPLK				DL 448
Query	1054	ASGLADAVLGDSASGRPVGNSASGM ASG ++ASGRP+ +ASG	PISLS 1143 P++ S			
Sbjct	449	ASGWIKNKYPEAASGRPLAASGR				

polyprotein [Rotifer birnavirus strain Palavas]

Sequence ID: emb|CAX33877.1| Length: 1060 Number of Matches: 1 Range 1: 118 to 525

Score	E	xpect Method	Identities	Positives	Gaps	Frame
216 bits	(549) 76	e-58() Compositional matrix adjust.	155/416(37%)	231/416(55%)	45/416(10%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYS				
Sbjct	118	YALNGTFNA+ + G +SE + YALNGTFNAITYDGCVSEANLPTTQ	Y ++LS+ S+ YGQLLSLNSDV			
Query	175	PYVRLGDKSPSTLQSPTHITN P+ R+ D +PST + + I +	ITSRNLGYGGAY - + NL Y	K-IPSTTIPGQ	GIHTKEFSINV +T SINV	
Sbjct	178	PFCRMNDPAPSTGNTGALFRSSIVE				_
Query	340	VGPIDIMWSGQMTMVDEWT V G I ++ S ++ + T			-VWSNTGVANG + + A G	
Sbjct	236	VRSISVRGNIPLINSSRLNVTSVIT				
Query	496	HYMNMNELNVSLFHENPPPEF + + + S F P +F	VAALKVHI VAA+ I	TYGNN ++ N		
Sbjct	294	NQGGCSFMVESTFSAMPAGAKHTQF				•
Query	634	FTINVIGGATIGVNSPTVV T+ + A G+NSP V	VGYQAVAEGTA VV YQ +A G+			

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Sbjct 354 STSSITLTVEAVSAAFPGMNSPVTVVAYQGLAGGSVLTLSGVSNYELIPNPSLKKNLPTS 413

Query 796 YGKCDPQDLNYIKYILSNREKLGLRSVMTLAEYNRMKMYMHVLTNYNVDEKE-AASFDFW 972
YG+ DP +LNY+K +L+NRE+LG+++V L EY ++ YN+D A +FD+
Sbjct 414 YGRHDPAELNYVKMVLANREELGVKTVFALPEYKQLLTRLEEF--YNLDTNTYAEAFDWG 471

Query 973 HLLKQIKKVAVPLAATLAPQYAPIIGAASGLADAVLGD-SASGRPVGNSASGMPIS 1137
LL+ IK +AVP +T+ PQ+ P+IGA S L D +L +ASG + +ASG PI+
Sbjct 472 KLLRTIKDIAVPTLSTIFPQFGPLIGAGSALGDELLKSFAASGTAI--AASGTPIT 525
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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: 118 to 509

Score	E	Expect Method	Identities	Positives	Gaps I	Frame
213 bits	(541) 6	Se-57() Compositional matrix adjust.	139/401(35%)	221/401(55%)	24/401(5%) +	<u>+1</u>
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI				Y 180
Sbjct	118	YALNGT NAV F G+LSE++DYSY+ YALNGTINAVTFHGSLSELTDYSYN				SY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S IP G		
Sbjct	178	VRLGD F+ F + F + T + T + T + T + T + T + T +	· · · · · · · · · · · · · · · · · · ·			
Query	340	VGPIDIMWSGQMTMVDEWTVT				
Sbjct	237	LTSFSVGGELVFSQVTIQSIEVDVT				N -N 289
Query	508	MNELNVSLFHENPPPEPVAALKVHI + N+ + N +P+ ++K+ +			NVIGGATIGVN V GG G	IS 678
Sbjct	290	LVPFNL-VVPTNEITQPITSMKLEV		· · · · · · · · · · · · · · · · · · ·		LR 348
Query	679	PTVVVGYQAVAEGTAITISGINNYE P +V Y+ VA G+ +T++G++N+E			NYIKYILSNRE NY K ILS R+	
Sbjct	349	PVTLVAYERVAAGSVVTVAGVSNFE				
Query	859	LGLRSVMTLAEYNRMKMYMHVLTNYI LG+++V EY + Y + + 1				ZA 1038
Sbjct	409	LGIKTVWPTREYTDFREYFMEVADL				
Query	1039					
Sbjct	469	P+ A D +LGD A + PLAHAIGEGVDYLLGDEAQAASGTA		R+R GRIRQ 509		

major capsid protein VP2 [Infectious bursal disease virus]

Sequence ID: gb|AAD25073.1|AF121256_1 Length: 476 Number of Matches: 1

Range 1: 99 to 466

Score	Е	xpect Method	Identities	Positives	Gaps F	rame
206 bits	(524) 76	e-57() Compositional matrix adjust.	128/377(34%)	202/377(53%)	22/377(5%) +	1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDF			~	
Sbjct	99	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYNO			+LSLP ++) VLSLPTSYDLG	
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGOG Z+ S PG G		
Sbjct	159	VRLGDPIPAIGLDPKMVATCDSSDRI	_			
Query	340	VGPIDIMWSGQMTMVDEWTVTAN + + + G++ T V + A				
Sbjct	218	ITSLSVGGELVCQTSVHGLVLGAT				
Query	511	NELNVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I	YGNNTNGDS G			P 681
Sbjct	271	N+ + N +P+ ++K+ I LPFNL-VIPTNEMTQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL+			YIKYILSNREKI Y K ILS R++	
Sbjct	330	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + + N		HLLKQIKKVAV +++ I+++AV		
Sbjct	390	G+++V EY + Y + + N GIKTVWPTREYTDFREYFMEVADLNS				
Query	1042	IIGAASGLADAVLGDSA 1092				
Sbjct	450	+ A D +LGD A LAHAIGEGVDYLLGDEA 466				

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|P25220.1|POLS_IBDVP Length: 993 Number of Matches: 1

▶ See 1 more title(s) Range 1: 99 to 489

Score		Expect Method	Identities	Positives	Gaps F	rame
212 bits	(540) 7	7e-57() Compositional matrix adjust.	135/400(34%)	215/400(53%)	23/400(5%) +	·1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	99	YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGOG Z+ S PG G		
Sbjct	159	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				
Sbjct	218	ITSLSVGGELVFRTSVHGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDSD + D			P 681
Sbjct	271	MPFNL-VIPTNEITQPITSIKLEIV	_			_
Query	682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL			YIKYILSNREK Y K ILS R++	
Sbjct	330	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		HLLKQIKKVAV +++ I++AV		
Sbjct	390	GIKTVWPTREYTDFREYFMEVADLN				_
Query	1042		SASGMPISLSRF +ASG + S F			
Sbjct	450	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ABW04864.1|** Length: 778 Number of Matches: 1 Range 1: 118 to 508

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
211 bits	(536) 86	e-57() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)) +1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FÕG+LSE++D SY+ YALNGTINAVTFÕGSLSELTDVSYN	++S T+N DE GLMSATANINDE	K+GNVLVG+G+ KIGNVLVGEGVT	*LSLP ++ !VLSLPTSYD	Y LGY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				MNM 510 N+
Sbjct	237	TSLSVGGELVFQTSVHGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDS G		VIGGATIGV + GG G	NSP 681 P
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNR IY K ILS R	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		VHLLKQIKKVAV +++ I++AV		YAP 1041 AP
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRI +ASG + S I			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR		• • • •		

structural polyprotein VP2 precusor [Infectious bursal disease virus]

Sequence ID: gb|AAC06018.1| Length: 545 Number of Matches: 1

Score	E	Expect Method	Identities	Positives	Gaps	Frame
207 bits	(527) 8	e-57() Compositional matrix adjust.	134/400(34%)	212/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FOG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRNLG VRLGD P+ P + T +	YGGAYKIP V T	_		
Sbjct	178	VRLGDPIPAIGLDPKMVA-TCDSSD			1	

Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + + G++ T V + A + GT + + V +N G+ G N+	510
Sbjct	237	+ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + N +P+ ++K+ I G +SV + + GG G P	681
Sbjct	290	MPFNL-VIPTNEITOPITSIKLEIATSKSGGQAGDQMSWSVSGCLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP	1041
Sbjct	409	G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158	
Sbjct	469	+ A D +LGD A + +ASG + S R+R LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

structural polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AGM16323.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Е	Expect Method	Identities	Positives	Gaps F	rame
212 bits	(539) 9	e-57() Compositional matrix adjust.	135/400(34%)	215/400(53%)	23/400(5%) +	1
Features	S:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				-
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG '+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				
Sbjct	237	ITSLSVGGELVFRTSVHGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDSD + D		VIGGATIGVNSI + GG G I	_
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV	_			
Query	682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL			YIKYILSNREKI Y K ILS R++I	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFW K A +F F			
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ABN71594.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Expect Method	Identities	Positives	Gaps	Frame	
211 bits(538)	2e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1	
Features:						
Query 1	YALNGTFNAVWFQGTLSEVSDYSYDI					
Sbjct 118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYNO		(+GNVLVG+G+ XIGNVLVGEGVT		_	
Query 181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG + S PG G			
Sbjct 178						
Query 340	VGPIDIMWSGQMTMVDEWTVTAI + + + G++ T V + A				NM 510 N+	
Sbjct 237						
Query 511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681	
Sbjct 290						
Query 682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL-			YIKYILSNRE Y K ILS R+		
Sbjct 349						
Query 862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ I+++AV			
Sbjct 409						
Query 104		SASGMPISLSRR +ASG + S R				
Sbjct 469						

Sequence ID: gb|AAA46238.1| Length: 598 Number of Matches: 1

Range 1: 118 to 508

Score		Expect	Method	Identities	Positives	Gaps	Frame
207 bits	(528) 2	2e-56()	Compositional matrix adjust.	133/400(33%)	213/400(53%)	23/400(5%)	+1
Features	s:						
Query	1		NGTFNAVWFQGTLSEVSDYSYDI NGT NAV FQG+LSE++D SY+				PY 180
Sbjct	118		NGT NAV FOGTLSETTD SIT NGTINAVTFQGSLSELTDVSYNO				_
Query	181	VRL VRL	GDKSPSTLQSPTHITNTSRN GD P+ P + +		KIPSTTIPGQG + S G G		
Sbjct	178		GD PT P T T GDPIPAIGLDPKMVATCDSSDRI				
Query	340		IDIMWSGQMTMVDEWTVTAN + + G++ T V + A				NM 510 N+
Sbjct	237	•	LSVGGELVFKTSVQSLVLGA				
Query	511		NVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I	GNNTNGDSD + D		VIGGATIGVN + GG G	SP 681
Sbjct	290		NL-VIPTNEITQPITSIKLEIV	_			
Query	682		VGYQAVAEGTAITISGINNYELV V Y+ VA G+ +T++G++N+EL-			YIKYILSNRE Y K ILS R+	
Sbjct	349		VAYERVATGSVVTVAGVSNFEL				
Query	862	GLR G++	SVMTLAEYNRMKMYMHVLTNYNV +V EY + Y + H N		HLLKQIKKVAV +++ I+++AV		AP 1041
Sbjct	409		TVWPTREYTDFREYFMEVADLNS				
Query	1042		AASGLADAVLGDSA-SGRPVGNS A D +LGD A +	SASGMPISLSRR +ASG + S R			
Sbjct	469		A THE THE ATTENDED A THE AIGEGVOYLLGDEAQAASGTAR				

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|P15480.1|POLS_IBDVC Length: 1012 Number of Matches: 1

▶ See 3 more title(s) kange 1: 118 to 508

Score	l	Expect	Method	Identities	Positives	Gaps I	Frame
211 bits	(537) 2	2e-56()	Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%) +	<u>-1</u>
Features	s:						
Query	1		NGTFNAVWFQGTLSEVSDYSYDI				
Sbjct	118		NGT NAV FQG+LSE++D SY+ NGTINAVTFQGSLSELTDVSYN(_
Query	181	VRL VRL	GDKSPSTLQSPTHITNTSRN GD P+ P + +		KIPSTTIPGQG + S PG G		
Sbjct	178		GDPIPAIGLDPKMVATCDSSDRI	_			
Query	340	VGP +	IDIMWSGQMTMVDEWTVTAI + + G++ T V + A				IM 510 I+
Sbjct	237		LSVGGELVFQTSVHGLVLGA				•
Query	511		NVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVNS + GG G	SP 681
Sbjct	290		NL-VISTNEITQPITSIKLEIV				RP 348
Query	682		VGYQAVAEGTAITISGINNYELV V Y+ VA G+ +T++G++N+EL-			YIKYILSNREK Y K ILS R++	
Sbjct	349		VAYERVATGSVVTVAGVSNFEL:				
Query	862	GLR G++	SVMTLAEYNRMKMYMHVLTNYNV +V EY + Y + H N	VDEKEAASFDFW K A +F F		PLAATLAPQYA P+ +TL P A	
Sbjct	409	_	TVWPTREYTDFREYFMEVADLNS				
Query	1042	IIG.	AASGLADAVLGDSA-SGRPVGNS A D +LGD A +	SASGMPISLSRR +ASG + S R			
Sbjct	469		A D FLGD A F AIGEGVDYLLGDEAQAASGTARA				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ABN71593.1| Length: 1012 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps	Frame
211 bits(537)	2e-56()	Compositional matrix adjust.	134/400(34%)	214/400(53%)	23/400(5%)	+1
Features:						

Query	1	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y	180
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S PG G+ FS N+D+	339
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA	236
Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + + G++ T V+ + A + GT + + V +N G+ G N+	510
Sbjct	237	ITSLSVGGELVFQTSVNGLVLGATIYLIGFDGTTVITRAVAANNGLTTGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + N +P+ ++K+ I G +S + + GG G P	681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP	1041
Sbjct	409	G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158	
Sbjct	469	+ A D +LGD A + +ASG + S R+R LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

structural polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AAK69711.1|** Length: 992 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
211 bits	(536) 2	e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Features:						
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FOG+LSE++D SY+				IPY 180
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				LGY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S PG G		
Sbjct	178	VRLGD PT P T T T T T T T T T T T T T T T T T	_			
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				INM 510 N+
Sbjct	237	TTSLSVGGELVFQTSVHGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681
Sbjct	290	MPFNL-VISTNEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL		~	YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		VHLLKQIKKVAV +++ I+++AV		AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN	SASGMPISLSRF +ASG + S F			
Sbjct	469	+ A D +LGD A + LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AAG40010.1|AF321056_2** Length: 1012 Number of Matches: 1 Range 1: 118 to 512

Score	E	xpect Method	Identities	Positives	Gaps	Frame
211 bits((537) 26	e-56() Compositional matrix adjust.	135/404(33%)	215/404(53%)	23/404(5%)	+1
Features	S :					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNO				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDRI	_			
Query	340	VGPIDIMWSGQMTMVDEWTVTAN + + + G++ T V + A				NM 510 N+
Sbjct	237	ITSLSVGGELVFQTSVHGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVN + GG G	SP 681
Sbjct	290	LPFNL-VIPTNEITQPITSIKLEIV	•			RP 348
Query	682	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL-			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + + N				AP 1041 AP

Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP 468

Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRNAYSA 1170

+ A D +LGD A + +ASG + S R+R A

Sbjct 469 LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQLTRA 512

structural polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ABW38090.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score		Expect Method	Identities	Positives	Gaps F	rame
211 bits((536)	3e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%) +	1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				-
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				
Sbjct	237	ITSLSVGGELVFQTSVQGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDS G			P 681 P
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL				
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	$egin{array}{lll} GLRSVMTLAEYNRMKMYMHVLTNYN \ G+++V & EY & + Y & + + N \end{array}$		VHLLKQIKKVAV +++ I++AV		
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				_
Query	1042		SASGMPISLSRI +ASG + S I			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AFU10473.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score	Expec	t Method	Identities	Positives	Gaps	Frame	
211 bits(53	36) 3e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1	
Features:							
Query 1		LNGTFNAVWFQGTLSEVSDYSYDF					
Sbjct 1		LNGT NAV FQG+LSE++D SY+ LNGTINAVTFQGSLSELTDVSYNG				_	
Query 1		LGDKSPSTLQSPTHITNTSRN LGD P+ P + +		KIPSTTIPGQG: + S PG G			
Sbjct 1		LGD P+ P + + LGDPIPAIGLDPKMVATCDSSDRF				_	
Query 3		PIDIMWSGQMTMVDEWTVTAN ++ G++ T V + A				INM 510 N+	
Sbjct 2	•	SLSVGGELVFQTSVHGLVLGAT				-, .	
Query 5	11 NEI	LNVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I	GNNTNGDS G		VIGGATIGVN + GG G	ISP 681	
Sbjct 2	90 MPI	FNL-VIPTNEITQPITSIKLEIVI					
Query 6		VVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL+			YIKYILSNRE Y K ILS R+		
Sbjct 3		LVAYERVATGSVVTVAGVSNFELI					
Query 8		RSVMTLAEYNRMKMYMHVLTNYNV ++V EY + Y + + N	DEKEAASFDFW K A +F F				
Sbjct 4	_	KTVWPTREYTDFREYFMEVADLNS					
Query 1	042 IIC	GAASGLADAVLGDSA-SGRPVGNS A D +LGD A + +	SASGMPISLSRR SASG + S R				
Sbjct 4	•	HAIGEGVDYLLGDEAQAASGTARA					

polyprotein [Infectious bursal disease virus]

Sequence ID: emb|CAC35470.1| Length: 1012 Number of Matches: 1

▶ See 1 more title(s) Range 1: 118 to 508

Score Expect Method Identities Positives Gaps Frame

Feature	S:		
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y	180
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S PG G+ FS N+D+	339
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA	236
Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + + G++ T V + A + GT + + V +N G+ G N+	510
Sbjct	237	ITSLSVGGELVFRTSVHGLVLGATIYLIGFDGTTVITRAVAANNGLTTGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + N +P+ ++K+ I G +S + + GG G P	681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	

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|Q9WI42.1|POLS_IBDVB Length: 1012 Number of Matches: 1

Sbjct 469 LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508

▶ See 1 more title(s) Range 1: 118 to 508

Score	Е	expect Method	Identities	Positives	Gaps	Frame	
210 bits	(535) 4	e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	<u>+1</u>	
Features	Features:						
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI					
Sbjct	118	YALNGT NAV FÖG+LSE++D SY+ YALNGTINAVTFÖGSLSELTDVSYN	GLMSATANINDE	K+GNVLVG+G+ KIGNVLVGEGVT	+LSLP ++ VLSLPTSYDLO	_	
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGOG Z+ S PG G			
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR	_				
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + + G++ T V + A				IM 510 I+	
Sbjct	237	TSLSVGGELVFRTSVHGLVLGA					
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G		VIGGATIGVNS + GG G	SP 681 P	
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV					
Query	682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL-	VPNPDLQKNLPN	ISYGKCDPQDLN YG+ DP +N	YIKYILSNREK Y K ILS R++	KL 861	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:					
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN' G+++V EY + Y + + N	VDEKEAASFDFV K A +F F		PLAATLAPQY <i>F</i> P+ +TL P <i>F</i>		
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN					
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F				
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR					

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ABW04865.1| Length: 1012 Number of Matches: 1

Score	E	Expect Method	Identities	Positives	Gaps	Frame
210 bits	(534) 5	ie-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDASYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN		KIPSTTIPGQG C+ S PG G		
Sbjct	178	VRLGD P+ P + + + VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				
Sbjct	237	TTSLSVGGELVFQTSVHGLVLGA			-	N+ ·NL 289

Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + N +P+ ++K+ I G +S + + GG G P	681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

Sequence ID: **gb|AFI55462.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps I	Frame
210 bits	(534) 5	e-56() Compositional matrix adjust	. 134/400(34%)	213/400(53%)) 23/400(5%) +	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSY YALNGT NAV FQG+LSE++D SY	DRILSITSNPLD	KVGNVLVGDGLI	EILSLPQGFNNE	Y 180
Sbjct	118	YALNGTINAVTFQGSLSELTDVSY				
Query	181	VRLGDKSPSTLQSPTHITNTSRN- VRLGD P+ P + +				
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSD	•	Y+ S PG (YQFSSQYQPG-(
Query	340	VGPIDIMWSGQMTMVDEWTVT + + + G++ T V +				
Sbjct	237	+ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$	A + GT - ATIYLIGFDGTAV			1+ IL 289
Query	511	NELNVSLFHENPPPEPVAALKVHI N+ + N +P+ ++K+ I				SP 681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEI				
Query	682	TVVVGYQAVAEGTAITISGINNYE +V Y+ VA G+ +T++G++N+E			NYIKYILSNREK NY K ILS R++	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFE				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNY				
Sbjct	409	G+++V EY + Y + + GIKTVWPTREYTDFREYFMEVADL		A+++I +++ ADIIRAIRRIAY		
Query	1042	IIGAASGLADAVLGDSA-SGRPVG				
Sbjct	469	+ A D +LGD A + LAHAIGEGVDYLLGDEAQAASGTA	+ASG + S I RAASGKARAASGI			

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AAG40008.1|AF321055_2** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Ex	rpect Method	Identities	Positives	Gaps	Frame
210 bits(5	34) 5e	-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Features:						
Query 1	1	YALNGTFNAVWFQGTLSEVSDYSYDF YALNGT NAV FQG+LSE++D SY+				
Sbjct 1	118	YALNGTINAVTFQGSLSELTDVSYNO				_
Query 1	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG + S PG G		
Sbjct 1	178	VRLGDPIPAIGLDPKMVATCDSSDRE				
Query 3	340	VGPIDIMWSGQMTMVDEWTVTAN + + + G++ T V + A				NM 510
Sbjct 2	237	ITSLSVGGELVFQTSVHGLVLGAT				•
Query 5	511	NELNVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I	ZGNNTNGDS G	DFSVDSSFTING +S S +		SP 681
Sbjct 2	290	LPFNL-VIPTNEITQPITSIKLEIVI	_			_
Query 6	682	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL+		~	YIKYILSNREF Y K ILS R+-	
Sbjct 3	349	VTLVAYERVATGSVVTVAGVSNFELI				
Query 8	862	GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + + N	DEKEAASFDFW KA+FF			
Sbjct 4	409	GIKTVWPTREYTDFREYFMEVADLNS				
Query 1	1042	IIGAASGLADAVLGDSA-SGRPVGNS + A D +LGD A + +	SASGMPISLSRR -ASG + S R			
Sbjct 4	469	LAHAIGEGVDYLLGDEAQAASGTARA				

Sequence ID: emb|CAA58851.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
210 bits	(534) 6	e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI				
Sbjct	118	YALNGT NAV FÖG+LSE++D SY+ YALNGTINAVTFOGSLSELTDVSYN	GLMSATANINDE	K+GNVLVG+G+ KIGNVLVGEGVT	+LSLP ++ VLSLPTSYDL	_
Query	181	VRLGDKSPSTLQSPTHITNTSRN				
Sbjct	178	VRLGD P+ P + + VRLGDPIPAIGLDPKMVATCDSSDR	_			
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + + G++ T V + A				
Sbjct	237	+ + + G++ T V + A ITSLSVGGELVFRTSVHGIVLGA				N+ NL 289
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G	SDFSVDSSFTIN +S S +		SP 681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				RP 348
Query	682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		VHLLKQIKKVAV +++ T++AV		AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNS + A D +LGD A +	SASGMPISLSRI +ASG + S I			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ABD97260.1| Length: 817 Number of Matches: 1

Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
208 bits	(530) 6	e-56() Compositional matrix adjust.	132/400(33%)	213/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD	RILSITSNPLDE	KVGNVLVGDGLE	ILSLPQGFNN	
Sbjct	118	YALNGT NAV FÕG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				Y GY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN				
Sbjct	178	VRLGD P+ P + + VRLGDPIPAIGLDPKMVATCDSSDF		Z+ S PG G ZQFSSQYQPG-G		
Query	340	VGPIDIMWSGQMTMVDEWTVTA				
Sbjct	237	+ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$				N+ NL 289
Query	511	NELNVSLFHENPPPEPVAALKVHIT				
Sbjct	290	N+ + N +P+ ++K+ + MPFNL-VIPTNEITQPITSIKLEVV	G TSKSGGQAGDQM		+ GG G 'IHGGNYPGALI	P RP 348
Query	682	TVVVGYQAVAEGTAITISGINNYEI				
Sbjct	349	+V Y+ VA G+ +T++G++N+EI VTLVAYERVATGSVVTVAGVSNFEI			Y K ILS R+- YTKLILSERDI	
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN				
Sbjct	409	G+++V EY + Y + + N GIKTVWPTREYTDFREYFMEVADLN		+++ I++AV DIIRAIRRIAV		AP AP 468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN				
Sbjct	469	+ A D +LGD A + LAHAIGEGVDYLLGDEAQAASGTAF	+ASG + S F RAASGKARAASGF			

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|P61825.2|POLS_IBDV** Length: 1012 Number of Matches: 1

▶ See 2 more title(s) Range 1: 118 to 508

Score	Ехр	ect Method	Identities	Positives	Gaps	Frame
210 bits((534) 6e-5	66() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Features	s :					
Query		ALNGTFNAVWFQGTLSEVSDYSYD ALNGT NAV FQG+LSE++D SY+				

Sbjct 11	18	YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query 18	81	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S PG G+ FS N+D+	339
Sbjct 17	78	VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA	236
Query 34	40	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM	510
Sbjct 23	37	+ + + + G++ TV + A + GT + + V + NG + G N + ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTAVITRAVAANNGLTTGTDNL	289
Query 51	11	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP	681
Sbjct 29	90	N++N+P+++K+I G +S S + + GG G P LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP	348
Query 68	82	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL	861
Sbjct 34	49	+V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query 86	62	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP	1041
Sbjct 40	09	G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query 10	042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158	
Sbjct 46	69	+ A D +LGD A + +ASG + S R+R LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

Sequence ID: gb|AAP83585.2| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
209 bits	(533) 66	e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN		KIPSTTIPGQG S+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				INM 510 N+
Sbjct	237	ITSLSVGGELVFQTSVHGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681
Sbjct	290	LPFNL-VIPTNEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFW K A +F F			AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +				
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AAK51522.1| Length: 1009 Number of Matches: 1

Score	E	xpect	Method	Identities	Positives	Gaps	Frame
209 bits(533) 7	e-56()	Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Features	:						
Query	1		NGTFNAVWFQGTLSEVSDYSYDI NGT NAV FQG+LSE++D SY+				
Sbjct	115		NGT NAV FOGTESETTD SIT NGTINAVTFQGSLSELTDVSYNO				_
Query	181	VRL(GDKSPSTLQSPTHITNTSRN GD P+ P + +		KIPSTTIPGQG + S PG G		
Sbjct	175		GDPIPAIGLDPKMVATCDSSDRI				
Query	340		IDIMWSGQMTMVDEWTVTAN + I G++ T V + A				INM 510 N+
Sbjct	234		LSIGGELVFQTSVQGLVLGA				
Query	511		NVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I		DFSVDSSFTIN +S S +		ISP 681
Sbjct	287	_	NL-VIPTNEITQPITSIKLEIV	_			_
Query	682		VGYQAVAEGTAITISGINNYELV V Y+ VA G+ +T++G++N+EL-	~	~	YIKYILSNRE Y K ILS R+	
Sbjct	346		VAYERVATGSVVTVAGVSNFEL				· -
Query	862	GLR:	SVMTLAEYNRMKMYMHVLTNYNV +V EY + Y + H N	JDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ I+++AV		AP 1041
Sbjct	406	•	TVWPTREYTDFREYFMEVADLNS				

Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R Sbjct 466 LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 505

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AHW82958.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps I	Frame
209 bits(533) 7	e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%) +	<u>-1</u>
Features	:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYNO				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGOG Z+ S PG G		
Sbjct	178	VRLGD P+ P + P + P + P + P + P + P + P + P +				
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + + G++ T V + A				IM 510 I+
Sbjct	237	TTSLSVGGELVFQTSVQGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHITY	YGNNTNGDS G		VIGGATIGVNS + GG G	SP 681
Sbjct	290	MPFNI-VIPTNEITQPITSIKLEIV				P 348
Query	682	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL-			YIKYILSNREK Y K ILS R++	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNY G+++V EY + Y + + N	VDEKEAASFDFV K A +F F	HLLKQIKKVAV +++ I+K+AV		AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNS + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ACB56949.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score	Expect Method	Identities	Positives	Gaps	Frame
209 bits(533)	7e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Features:					
Query 1	YALNGTFNAVWFQGTLSEVSDYSYDI				
Sbjct 118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYNO				_
Query 181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG + S PG G		
Sbjct 178		_			
Query 340	VGPIDIMWSGQMTMVDEWTVTAI + + + G++ T V + A				INM 510 N+
Sbjct 237					
Query 511	NELNVSLFHENPPPEPVAALKVHITY	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681
Sbjct 290					
Query 682	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL-			YIKYILSNRE Y K ILS R+	
Sbjct 349					
Query 862	GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + H N	VDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ I+++AV		AP 1041
Sbjct 409	— — — — — — — — — — — — — — — — — — —				
Query 104		SASGMPISLSRR +ASG + S R			
Sbjct 469					

VP2 protein precursor, partial [Infectious bursal disease virus]

Sequence ID: gb|AEL75032.1| Length: 512 Number of Matches: 1

Score	Expect Method	Identities	Positives	Gaps	Frame
204 bits(519)	8e-56() Compositional matrix adjust.	130/400(33%)	212/400(53%)	23/400(5%)	+1
Features:					
Query 1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				

Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S G G+ FS N+D+	339
Sbjct	178	$egin{array}{llllllllllllllllllllllllllllllllllll$	236
Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM	510
Sbjct	237	+ $+$ I G++ T V + A + GT + + V ++ G+ G N+ ITSLSIGGELVFQTSVQGLILGATIYLIGFDGTAVITRAVAADNGLTAGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP	681
Sbjct	290	N+++P+++K+I G $+S$ S $++$ GG G P $MPFNI-VIPTSEITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLAVTIHGGNYPGALRP$	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL	861
Sbjct	349	+V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP ++Y K ILS R++L VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMDYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP	1041
Sbjct	409	G+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158	
Sbjct	469	+ A D +LGD A + +ASG + S R+R LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

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|P25219.1|POLS_IBDV5 Length: 1012 Number of Matches: 1

▶ See 1 more title(s) Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
209 bits	(533) 8	e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FÖG+LSE++D SY+ YALNGTINAVTFÖGSLSELTDVSYNO				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN				
Sbjct	178	VRLGD P+ P + + VRLGDPIPAIGLDPKMVATCDSSDRI		Z+ S PG G ZQFSSQYQPG-G		_
Query	340	VGPIDIMWSGQMTMVDEWTVTAN				NM 510 N+
Sbjct	237	+ + I G++ TV + A ITSLSIGGELVFQTSVQGLVLGAT			-	-, .
Query	511	NELNVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I	ZGNNTNGDS G		VIGGATIGVN + GG G	SP 681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV	_			RP 348
Query	682	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL+				
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + H N	DEKEAASFDFW K A +F F	VHLLKQIKKVAV +++ I+++AV		
Sbjct	409	G+++V EY + Y + + N GIKTVWPTREYTDFREYFMEVADLNS				AP AP 468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNS				
Sbjct	469	+ A D +LGD A + - LAHAIGEGVDYLLGDEAQAASGTARA	+ASG + S F AASGKARAASGF			

110-kDa polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AAK30029.1| Length: 1012 Number of Matches: 1

Score	E	xpect Method	Identities	Positives	Gaps	Frame
209 bits	(533) 86	e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNO				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN		KIPSTTIPGQG '+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + I G++ T V + A				INM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQGLVLGA			-	
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				_

Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

Sequence ID: emb|CDP32875.1| Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Е	xpect Method	Identities	Positives	Gaps I	Frame
209 bits	(533) 86	e-56() Compositional matrix adjust.	134/400(34%)	213/400(53%)	23/400(5%) +	- 1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FÖG+LSE++D SY+ YALNGTINAVTFÖGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGOG Z+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				IM 510 I+
Sbjct	237	ITSLSIGGELVFQTSVQGLVLGA			<u> </u>	• •
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G			SP 681 P
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL			YIKYILSNREK Y K ILS R++	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + H N	VDEKEAASFDFV K A +F F		PLAATLAPQYA P+ +TL P A	
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AAY88214.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Expect Method	Identities	Positives	Gaps	Frame
209 bits(532)	9e-56() Compositional matrix adjust.	133/400(33%)	214/400(53%)	23/400(5%)	+1
Features:					
Query 1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FOG+LSE++D SY+				
Sbjct 118					
Query 181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S PG G		
Sbjct 178					
Query 340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				NM 510 N+
Sbjct 237					
Query 511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDS G	SDFSVDSSFTIN +S S +		ISP 681
Sbjct 290					
Query 682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct 349					
Query 862		VDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ I+++AV		AP 1041
Sbjct 409					
Query 104					
Sbjct 469		+ASG + S R AASGKARAASGR	• • = •		

Score		Expect Method	Identities	Positives	Gaps	Frame
209 bits	(532) 9	9e-56() Compositional matrix adjust.	133/400(33%)	213/400(53%)	23/400(5%)	+1
Features	S :					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		YKIPSTTIPGQO Y+ S PG O		
Sbjct	178	VRLGD PT P T T T T T T T T T T T T T T T T T	· · · · · · · · · · · · · · · · · · ·			
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				NM 510 N+
Sbjct	237	ITSLSVGGELVFQTSVHGLVLGA				• •
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + + +P+ ++K+ I	YGNNTNGDS G	SDFSVDSSFTIN +S S +		SP 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				RP 348
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		VHLLKQIKKVAV +++ I++AV	~	AP 1041 AP
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042		SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

Sequence ID: **gb|ABN71592.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	expect Method	Identities	Positives	Gaps	Frame
209 bits	(532) 16	e-55() Compositional matrix adjust.	133/400(33%)) 212/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		YKIPSTTIPGQG Y+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A		IAGSMKTLVWSN + + V +N		NM 510 N+
Sbjct	237	ITSLSVGGELVFQTSVQGLVLGA	TIYLIGFDGAT	VİTRAVAAN		
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGD		VIGGATIGVN + GG G	SP 681 P
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV	-			_
Query	682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE: Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N				AP 1041 AP
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSR +ASG + S			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ABG81111.1|** Length: 514 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
203 bits	(517) 1	e-55() Compositional matrix adjust.	131/400(33%)	211/400(52%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FOG+LSE++D SY+		VGNVLVGDGLE		
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG + S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				
Sbjct	237	ITSLSIGGELVFQTSVQGLILGA	_	-		N+ NL 289
Query	511	NELNVSLFHENPPPEPVAALKVHIT			VIGGATIGVN + GG G	SP 681
Sbjct	290	N+ + + +P+ ++K+ I MPFNI-VIPTSEITQPITSIKLEIV	G TSKSGGQAGDQM			RP 348

Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+E +PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEPIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

Sequence ID: dbj|BAA04108.1| Length: 681 Number of Matches: 1 Range 1: 9 to 399

			Gaps I	Frame					
1e-55() Compositional matrix adjust.	132/400(33%)	211/400(52%)	23/400(5%) +	-1					
Features:									
				_					
VRLGDKSPSTLQSPTHITNTSRN									
				•					
				SP 681 P					
				L 861					
				L 299					
	YALNGTFNAVWFQGTLSEVSDYSYDF YALNGT NAV FQG+LSE++D SY+ YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYNG VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + + VRLGDPIPAIGLDPKMVATCDSSDRF VGPIDIMWSGQMTMVDEWTVTAN + + G++ T V + A ITSLSVGGELVFHTSVQSLVLGAT NELNVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I MPFNL-VIPTNEITQPITSIKLEIVT TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL+ VTLVAYERVATGSVVTVAGVSNFELI GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + + N GIKTVWPTREYTDFREYFMEVADLNS 2 IIGAASGLADAVLGDSA-SGRPVGNS + A D +LGD A + +	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKYALNGT NAV FQG+LSE++D SY+ ++S T+N DKYALNGTINAVTFQGSLSELTDVSYNGLMSATANINDK VRLGDKSPSTLQSPTHITNTSRNLGYGGAY VRLGD P+ P + + Y VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDY VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLI + + + G++ T V + A + G+ + ITSLSVGGELVFHTSVQSLVLGATIYLIGFDGSTV NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSI N+ N +P+ ++K+ I G MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQM TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPM +V Y+ VA G+ +T++G++N+EL+PNP+L KNL VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVT GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFW G+++V EY + Y + + N K A +F F GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFK 2 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRR 2 1IGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRR	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLE YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVT VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQG VRLGD P+ P + + + Y+ S PG G VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-G VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSN + + + G+ T V + A + G+ + + V ++ ITSLSVGGELVFHTSVQSLVLGATIYLIGFDGSTVITRAVAAD NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTIN N+ + N +P+ ++K+ I G +S S + MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLAVT TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLN +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +N VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGPMN GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAV G++V EY + Y + N K A +F F +++ I++AV GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAV 2 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANID VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMN + + + G++ T V + A + G+ + + V ++ G+ G N ITSLSVGGELVFHTSVQSLVLGATIYLIGFDGSTVITRAVAADNGLTXGTDN NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNS N+ + N +P+ ++K+ I G +S S + + GG G MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLAVTIHGGNYPGXLF TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREK +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGPMNYTKLILSERXX GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYA G++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P A GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAA 2 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R					

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AAG40006.1|AF321054_2 Length: 1012 Number of Matches: 1

▶ See 1 more title(s) Range 1: 118 to 508

Score	Ex	rpect Method	Identities	Positives	Gaps	Frame
209 bits(5	31) 1e	e-55() Compositional matrix adjust.	137/400(34%)	214/400(53%)	23/400(5%)	+1
Features:						
Query 1	L	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct 1	118	YALNGT NAV FOGTESETTD SIT YALNGTINAVTFQGSLSELTDVSYNO	GLMSATANINDE	KIGNVLVGEGVT	VLSLPTSYDL	
Query 1	181	VRLGDKSPSTLQSPTHITNTS VRLGD P+ P + +N	SRNLGYGGAY R A			
Sbjct 1	L78	VRLGDPIPAIGLDPKMVATCDSSNRI				
Query 3	340	VGPIDIMWSGQMTMVDEWTVTAI + + + G++ T V + A				NM 510 N+
Sbjct 2	237	ITSLSVGGELVFQTSVHGLVLGA				
Query 5	511	NELNVSLFHENPPPEPVAALKVHITY	YGNNTNGDS G		VIGGATIGVN + GG G	SP 681
Sbjct 2	290	LPFNL-VIPTNEITQPITSIKLEIV				
Query 6	582	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL-		~	YIKYILSNRE Y K ILS R	
Sbjct 3	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query 8	362	GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + + N	VDEKEAASFDFV K A +F F			AP 1041
Sbjct 4	109	GIKTVWPTREYTDFREYFMEVADLNS				
Query 1	1042	IIGAASGLADAVLGDSA-SGRPVGNS + A D +LGD A +	SASGMPISLSRI +ASG + S I			
Sbjct 4	169	LAHAIGEGVDYLLGDEAQAASGTARA				

Sequence ID: **gb|ACS44342.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
209 bits((531) 1	e-55() Compositional matrix adjust.	136/404(34%)	213/404(52%)	31/404(7%)	+1
Features	S:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNO				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG +IS PG G		
Sbjct	178	VRLGD P+ P + T + T + T + T + T + T + T + T +				
Query	340	VGPIDIMWSGQMTMVDEWTVTAN + + + G++ T V + A				NM 510
Sbjct	237	TTSLSVGGELVFQTSVQGLVLGA				287
Query	511	NELNVSLFHENPPPEPVAALKV N+ FH N +P+ ++K-		NGDSDFSVDSS +S		IG 669 G
Sbjct	288	NLMPFHIVIPTNEITQPITSIKI				
Query	670	VNSPTVVVGYQAVAEGTAITISGINN P +V Y+ VA G+ +T++G++N				
Sbjct	345	GPRPVTLVAYERVATGSVVTVAGVSI				
Query	850	REKLGLRSVMTLAEYNRMKMYMHVLT R++LG+++V EY + Y +	INYNVDEKEAAS + N K A +		KVAVPLAATL K+AVP+ +TL	
Sbjct	405	RDRLGIKTVWPTREYTDFREYFMEVA				
Query	1030	QYAPIIGAASGLADAVLGDSA-SGRI AP+ A D +LGD A +		LSRRLRN 11	.58	
Sbjct	465	PAAPLAHAIGEGVDYLLGDEAQAASO			8	

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|P27276.1|POLS_IBDVO Length: 1012 Number of Matches: 1

▶ See 2 more title(s) Range 1: 118 to 509

Score	E	xpect Method	Identities	Positives	Gaps	Frame
209 bits	(531) 26	e-55() Compositional matrix adjust.	139/405(34%)	222/405(54%)	32/405(7%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++DYSY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDYSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRNVRLGD P+ P + +		KIPSTTIPGQG		
Sbjct	178	VRLGDPIPAAGLDPKLMATCDSSDR	_			_
Query	340	VGPIDIMWSGQMTMVDEWTVT	ANYQPLNISGTI + + GT			MN 507
Sbjct	237	LTSLSVGGELIFSQVTIHSIEVDVT				288
Query	508	MNELNVSLFHENPPPEPVAAL		NGDS-DFSVDS GD ++V	SFTINVIGGA + + V GG	TI 666
Sbjct	289	NLVPFNLGGPTSEITQPITSM				IYP 344
Query	667	GVNSPTVVVGYQAVAEGTAITISGI G P +V Y+ VA G+ +T++G+				
Sbjct	345	GALRPVTLVAYERVAAGSVVTVAGV				
Query	847	NREKLGLRSVMTLAEYNRMKMYMHV R++LG+++V EY + Y			KKVAVPLAAT +K+AVP+ +T	
Sbjct	405	ERDRLGIKTVWPTREYTDFREYFME				
Query	1027	PQYAPIIGAASGLADAVLGDSA-SG P AP+ A D +LGD A +	RPVGNSASGMPI ASG	SLSRRLRN 1 + S R+R	.158	
Sbjct	465	PPAAPLAHANREGVDYLLGDEAQAA			09	

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AFX62899.1| Length: 1012 Number of Matches: 1

Score	E	Expect Method	Identities	Positives	Gaps	Frame
208 bits	(530) 2	e-55() Compositional matrix adjust.	134/400(34%)	212/400(53%)	23/400(5%)	+1
Features	S :					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN	LGYGGAY	KIPSTTIPGQG	IHTKEFSINV	DS 339

Sbjct	178	VRLGD P+ P + + + Y+ S PG G+ FS N+D+ VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYOFSSOYOPG-GVTITLFSANIDA	236
Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM	510
Sbjct	237	+ + + + G++ TV + A + GT + + V + NG + G N + ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTTVITRAVAANNGLTTGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + N +P+ ++K+ I G +S + + GG G P	681
Sbjct	290	N++N+P+++K+I G +S S + + GG G P MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R+ L	861
Sbjct	349	+V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R+ L VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDCL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP	1041
Sbjct	409	G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158	
Sbict	469	+ A D +LGD A + +ASG + S R+R LAHAIGEGVDYLLGDEAOAASGTARAASGKARAASGRIRO 508	

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|P22351.1|POLS_IBDVS Length: 1012 Number of Matches: 1

▶ See 1 more title(s) Range 1: 118 to 508

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
208 bits	(530) 26	e-55() Compositional matrix adjust.	132/400(33%)	213/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD	RILSITSNPLD	KVGNVLVGDGLE	ILSLPQGFN	
Sbjct	118	YALNGT NAV FÖG+LSE++D SY+ YALNGTINAVTFÖGSLSELTDVSYN				Y LGY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		YKIPSTTIPGOG Y+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				MNM 510 N+
Sbjct	237	TSLSVGGELVFQTSVQGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ +	YGNNTNGD: G		VIGGATIGVI + GG G	NSP 681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEVV	•			LRP 348
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL				
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N				YAP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +				
Sbjct	469	+ A D +LGD A + LAHAIGEGVDYLLGDEAQAASGTAR	+ASG + S 1 RAASGKARAASG			

polyprotein [Infectious bursal disease virus]

Sequence ID: dbj|BAA12175.1| Length: 1012 Number of Matches: 1

Score	E	Expect Method	Identities	Positives	Gaps	Frame
208 bits	(529) 2	e-55() Compositional matrix adjust.	133/400(33%)	213/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNO				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG '+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + I G++ T V T+ A				NM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQGLTLGA			-	
Query	511	NELNVSLFHENPPPEPVAALKVHIT			VIGGATIGVN + GG G	SP 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				_
Query	682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	

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Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408

Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP 1041
G++V EY + Y + N K A +F F +++ +++AVP+ +TL P AP
Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP 468

Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158
+ A D +LGD A + +ASG + S R+R
Sbjct 469 LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508
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Sequence ID: gb|ABN71595.1| Length: 1012 Number of Matches: 1

▶ See 1 more title(s) Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
208 bits	(529) 26	e-55() Compositional matrix adjust.	132/400(33%)	213/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI				
Sbjct	118	YALNGT NAV FÖG+LSE++D SY+ YALNGTINAVTFÖGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG '+ S PG G	IHTKEFSINV + FS N+	
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR	· -			_
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + + G++ T V + A				INM 510 N+
Sbjct	237	TSLSVGGELVFQTSVQGLVLGA			•	
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEVV	_			RP 348
Query	682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL-		ISYGKCDPQDLN YG+ DP +N		
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ I++AV		AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNS + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ACB56951.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

YALNGT NAV FÕG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY 177 Query 181 VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S PG G+ FS N+D+ SDjct 178 VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA 236 Query 340 VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + + C+ T V + A + GT + + V +N G+ G N+ SDjct 237 ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTAVITRAVAANNGLTTGTDNL 289 Query 511 NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP 681 N+ N +P+ ++K+ I G +S ++ GG G P SDjct 290 LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP 348 Query 682 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNEKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L SDjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G++V EY + Y + + N K A +F F +++ I++ VP + TL P AP SDjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Score	E	xpect Method	Identities	Positives	Gaps	Frame
Query 1 YALNGTFNAVWFOGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FÖG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y YALNGTINAVTFÖGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY 177 Query 181 VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS 33.9 VRLGD P+ P + + Y+ S PG G+ FS N+D+ SPG T S PG T S N+D+ S PG T S N+D+ S PG T S N+D+ S PG T S PG T S N+D+ S PG T S PG T S N+D+ S PG T S PG T S PG T S N+D+ S PG T	208 bits	(529) 26	e-55() Compositional matrix adjust.	133/400(33%)	212/400(53%)	23/400(5%)	+1
YALNGT NAV FÕG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY 177 Query 181 VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S PG G+ FS N+D+ Sbjct 178 VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA 236 Query 340 VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + + G+ T V + A + GT + + V +N G+ G N+ Sbjct 237 ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTAVITRAVAANNGLTTGTDNL 289 Query 511 NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP 681 N+ N +P+ ++K+ I G +S ++ GG G P Sbjct 290 LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP 348 Query 682 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNEKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G++V EY + Y + + N K A +F F +++ I++ VP + TL P AP Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Features	s:					
Sbjct 118 YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY 177 Query 181 VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS 339 VRLGD P+ P + + Y+ S PG G+ FS N+D+ Sbjct 178 VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA 236 Query 340 VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + H + H GH T V + A H GT + V + N GH G NH Sbjct 237 ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTAVITRAVAANNGLTTGTDNL 289 Query 511 NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP 681 N+ N +P+ +K+ I G + S + + GG G P Sbjct 290 LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP 348 Query 682 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL 861 +V Y+ VA G+ +T++G+N+EL+PNP+L KNL YG+ DP +NY K ILS R++L Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAAASFDFWHLLKQIKKVAVPLAATLAPQYAP 6H+V EY + Y + N K A +F F +++ I++ VP+ +TL P AP Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Query	1					
VRLGD P+ P + + + Y+ S PG G+ FS N+D+ Sbjct 178 VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA 236 Query 340 VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM 510 + + + G+ T V + A + GT + V + N G+ G N+ Sbjct 237 ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTAVITRAVAANNGLTTGTDNL 289 Query 511 NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP 681 N+ N +P+ ++K+ I G +S S + + GG G P Sbjct 290 LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP 348 Query 682 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP 104 G++V EY + Y + N K A +F F +++ I+++ VP+ +TL P AP Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Sbjct	118					_
Sbjct 178 VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQPG-GVTITLFSANIDA 236 Query 340 VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + + + G+ T V + A + GT + + V + N G+ G N+ Sbjct 237 ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTAVITRAVAANNGLTTGTDNL 289 Query 511 NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP 681	Query	181					
+ + + G++ T V + A + GT + + V +N G+ G N+ Sbjct 237 ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTAVITRAVAANNGLTTGTDNL 289 Query 511 NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP 681 N+ + N + P+ ++K+ I G +S S + + GG G P Sbjct 290 LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP 348 Query 682 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL 861 +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP 104 G+++V EY + Y + + N K A +F F +++ I+++ VP+ +TL P AP Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Sbjct	178		_			
Sbjct 237 ITSLSVGĞELVFQTSVHGLVLGĀTIYLIGFDĞTAVITRAVAANNĞLTTĞTDNL 289 Query 511 NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP 681 N+ + N +P+ ++K+ I G +S ++ GG G P Sbjct 290 LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP 348 Query 682 TVVVGYQAVAEĞTAİTISĞINNYELVPNPDLQKNLPMSYĞKCDPQDLNYİKYİLSNREKL 861 +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L Sbjct 349 VTLVAYERVATĞSVVTVAĞVSNFELIPNPELAKNLVTEYĞRFDPĞAMNYTKLİLSERDRL 408 Query 862 ĞLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQİKKVAVPLAATLAPQYAP 6++V EY +Y + N K A +F F +++ I+++ VP+ +TL P AP Sbjct 409 ĞİKTVWPTREYTDFREYFMEVADLNSPLKIAĞAFĞFKDİİRAİRRİĞVPVVSTLFPPAAP 468 Query 1042 İIĞAASĞLADAVLĞDSA-SĞRPVĞNSASĞMPİSLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Query	340					
N+ + N +P+ ++K+ I G +S S + + GG G P Sbjct 290 LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP 348 Query 682 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL 861 +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ I+++ VP+ +TL P AP Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Sbjct	237					• •
Sbjct 290 LPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP 348 Query 682 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL 861	Query	511					
+V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + N K A +F F +++ I+++ VP+ +TL P AP Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Sbjct	290					
Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP 104 G+++V EY + Y + N K A +F F +++ I+++ VP+ +TL P AP Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Query	682					
G+++V EY + Y + + N K A +F F +++ I+++ VP+ +TL P AP Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Sbjct	349					
Sbjct 409 GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIGVPVVSTLFPPAAP 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	Query	862					
+ A D +LGD A + +ASG + S R+R	Sbjct	409					
	Query	1042					
~	Sbjct	469					

Sequence ID: gb|AAB63594.1| Length: 493 Number of Matches: 1

Score	E	Expect Method	Identities	Positives	Gaps F	Frame	
202 bits	(514) 3	e-55() Compositional matrix adjust.	125/377(33%) 202/377(53%) 22/377(5%) +	·1	
Features	Features:						
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD					
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				_	
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		YKIPSTTIPGQO Y+ S PG O			
Sbjct	178	VRLGD PT P T T VRLGDPIPAIGLDPKMVATCDSSDR					
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				IM 510	
Sbjct	237	TTSLSVGGELVFQTSVHGLVLGA					
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGD G		NVIGGATIGVNS + GG+ G	SP 681	
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				P 348	
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T+ G++N+EL			NYIKYILSNREK NY K ILS R++		
Sbjct	349	VTLVAYERVATGSVVTVPGVSNFEL					
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N					
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN					
Query	1042	IIGAASGLADAVLGDSA 1092 + A D +LG A					
Sbjct	469	LAHAIGEGVDYLLGHEA 485					

Sequence ID: **gb|ACP30638.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
208 bits	(529) 36	e-55() Compositional matrix adjust.	132/400(33%)	213/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		YKIPSTTIPGQG Y+ S PG G	IHTKEFSINV + FS N+	
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				NM 510 N+
Sbjct	237	ITSLSVGGELVFQTSVQGLVLGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGD: G	SDFSVDSSFTIN +S S +		SP 681
Sbjct	290	MPFNI-VIPTNEITQPITSIKLEIV	_			_
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N			PLAATLAPQY	AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRI +ASG + S I			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

structural polyprotein VP2, VP4, VP3 [Infectious bursal disease virus] Sequence ID: **gb|AAC06017.1|** Length: 652 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
205 bits	(521) 3	e-55() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FOG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR	_			
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				NM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + +P+ ++K+ I			VIGGATIGVN + GG G	SP 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				

Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Shict	469	LAHATGEGVDYLLGDEAOAASGTARAASGKARAASGRTRO 508	

structural polyprotein [Infectious bursal disease virus]

Sequence ID: dbj|BAH03940.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
207 bits	(528) 36	e-55() Compositional matrix adjust.	131/400(33%)	213/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +			HTKEFSINVI	
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A	NYQPLNISGTL: + GT			NM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQSLILGA				•
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ +F + +P+ ++K+ I	YGNNTNGD		VIGGATIGVN: + GG G	SP 681
Sbjct	290	MPFNI-VFPTSAITQPITSIKLEIV				RP 348
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL				
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N				AP 1041 AP
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRI +ASG + S			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

structural protein, partial [Infectious bursal disease virus]

Sequence ID: gb|AAF86635.1|AF006701_1 Length: 500 Number of Matches: 1

Range 1: 118 to 500

Score	E	xpect Method	Identities	Positives	Gaps I	Frame
202 bits((513) 4e	e-55() Compositional matrix adjust.	132/398(33%)	210/398(52%)	28/398(7%)	<u>+1</u>
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTVNAVTFQGSLSELTDVSYN				Y SY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD + P + +		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPISAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + + A				IM 510 I+
Sbjct	237	ITSLSIGGELVFQTSVQDLVLGA				•
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVNS + GG G	SP 681 P
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV	•			_
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNREK Y K ILS R++	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFW K A +F F	VHLLKQIKKVAV +++ I+++AV		
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSASGRPVGNS				
Sbjct	469	+ A D +LGD A +. LALAIGEGVDYLLGDEAQA	ASG + S + ASGTARAASGKA			

VP2 [Infectious bursal disease virus]

Sequence ID: dbj|BAA00954.1| Length: 496 Number of Matches: 1

Range 1: 118 to 485

Score Expect Method Identities Positives Gaps Frame

202 bits	(513) 46	e-55() Compositional matrix adjust. 127/378(34%) 206/378(54%) 24/378(6%) +1	
Features	S :		
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y	180
Sbjct	118	YALNGT NAV FOGTESETTD SIT TTS ITN DATGNVLVGTGT TESEP TT I YALNGTINAVTFOGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S G G+ FS N+D+	339
Sbjct	178	VRLGD PT P T T T T T S G GT TS NTDT VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADNYQFSSQYQTG-GVTITLFSANIDA	236
Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + + G++ T V + A + GT + + V +N G+ G N+	510
Sbjct	237	ITSLSVGGELVFKTSVQSLVLGATIYLIGFDGTAVITRAVAANNGLTAGIDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNS N+ + N +P+ ++K+ I + ++G + +S S + + GG G	678
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIVT-SKSDGQAGEQMSWSASGSLAVTIHGGNYPGALR	347
Query	679	PTVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREK P +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++	858
Sbjct	348	PVTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDR	407
Query	859	LGLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYA LG+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P A	1038
Sbjct	408	LGIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAA	467
Query	1039	PIIGAASGLADAVLGDSA 1092 P+ A D +LGD A	
Sbjct	468	PLAHAIGEGVDYLLGDEA 485	

Sequence ID: **gb|AAS10174.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
207 bits	(528) 46	e-55() Compositional matrix adjust.	135/400(34%)	215/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				INM 510 N+
Sbjct	237	TSLSVGGELVFKTNVQNLVLGA			-	
Query	511	NELNVSLFHENPPPEPVAALKVHI- N+ + N +P+ ++K+ I			VIGGATIGVN + GG G	ISP 681 P
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		VHLLKQIKKVAV +++ I++AV		
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR		• • • •		

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ABB88945.1|** Length: 819 Number of Matches: 1 Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
206 bits	(524) 5	e-55() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG '+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A	NYQPLNISGTLI + GT +			INM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I			VIGGATIGVN + GG G	ISP 681 P
Sbjct	290	MPFNI-VIPTNEITQPITSIKLEIV				_
Query	682	TVVVGYQAVAEGTAITISGINNYEL	VPNPDLQKNLPM	ISYGKCDPQDLN	YIKYILSNRE	KL 861

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+V Y+ VA G+ +T++G++N+EL+PNP+L KNL
                                              YG+ DP +NY K ILS R++L
Sbjct 349
           VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL
                                                                    408
           Query
      862
                                                                    1041
Sbjct
      409
           GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP 468
Query
     1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158
           + A D +LGD A + +ASG + S R+R
LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ
Sbjct 469
                                                  508
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Sequence ID: gb|AKM16810.1| Length: 1013 Number of Matches: 1

Range 1: 118 to 488

Score	Е	xpect Method	Identities	Positives	Gaps F	Frame
207 bits	(526) 6	e-55() Compositional matrix adjust.	129/380(34%)	214/380(56%)	23/380(6%) +	-1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++DYSY+ YALNGTINAVTFQGSLSELTDYSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S +P G		
Sbjct	178	VRLGDPIPAAGPDPKLMATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVT + + ++++S E VT				IN 507 N
Sbjct	237	LTSLSVGGELVFSQVTIQSIEVDVT				
Query	508	MNELNVSLFHENPPPEPVAALKVHI + N+ + + +P+ ++K+ +			NVIGGATIGVN V GG G	IS 678
Sbjct	290	LVPFNL-VVPTSEITQPITSMKLEV		· · · · ·		ıR 348
Query	679	PTVVVGYQAVAEGTAITISGINNYE P +V Y+ VA G+ +T++G++N+E			NYIKYILSNRE NY K ILS R+	
Sbjct	349	PVTLVAYERVAAGSVVTVAGVSNFE				
Query	859	LGLRSVMTLAEYNRMKMYMHVLTNY LG+++V EY + Y + + +				A 1038
Sbjct	409	LGIKTVWPTREYTDFREYFMEVADL				
Query	1039	PIIGAASGLADAVLGDSASG 109 P+ A D +LGD A	8			
Sbjct	469	PLAHAIGEGVDYLLGDEAQA 488				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AAC78079.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score	Expect Method	Identities	Positives	Gaps F	rame
207 bits(526)	8e-55() Compositional matrix adjust.	132/400(33%)	213/400(53%)	23/400(5%) +	1
Features:					
Query 1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV OG+LSE++D SY+				
Sbjct 118					_
Query 181	VRLGDKSPSTLQSPTHITNTSRN RLGD P+ P + +		_		
Sbjct 178			T++ S PG G QLSSQYQPG-G		
Query 340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				
Sbjct 237					
Query 511					
Sbjct 290	+ N+ + N +P+ ++K+ I SPFNL-VIPTNGITQPITSIKLEIV	G TSRSGGQAGDQM			P P 348
Query 682					
Sbjct 349	+V Y+ VA G+ +T++G++N+EL VTLVAYERVATGSVVTVAGVSNFEL			Y K ILS R++ YTKLILSERDR	
Query 862					
Sbjct 409	G+++V EY + Y + + N $GIKTVWPTREYTDFREYFMEVADLN$	K A +F F SPLKIAGAFGFK	+++ I+++AV DIIRAIRRIAV		_
Query 104					
Sbjct 469		+ASG + S R AASGKARAASGR			

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ABW04866.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score Expect Method Identities Positives Gaps Frame

206 bits(525) 8e-55() Compositional matrix adjust. 132/400(33%) 213/400(53%) 23/400(5%) +1

Features:

Query	1	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y	180
Sbjct	118	YALNGTINAVTFQGSLSELTDASYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S P G+ FS N+D+	339
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDRPRVCTITAADDYQFSSQYQP-DGVTITLFSANIDA	236
Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + + G++ T V + A + GT + + V ++ G+ G N+	510
Sbjct	237	ITSLSVGGELVFQTSVHGLVLGATIYLIGFDGTTVITRAVAAHNGLTTGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + N +P+ ++K+ I G +S + + GG G P	681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIVTSKSGGQAGDQMSWSARGSLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y +++ N K A +F F +++ I+++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVSDLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158	
Sbjct	469	+ A D +LGD A + +ASG + S R+R LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

VP2, partial [Infectious bursal disease virus]

Sequence ID: **gb|AAV88102.1|** Length: 469 Number of Matches: 1 Range 1: 112 to 466

Score	E	xpect M	ethod	Identities	Positives	Gaps	Frame
200 bits	(508) 1	e-54() Co	ompositional matrix adjust.	124/364(34%)	197/364(54%)	22/364(6%)	+1
Features	s:						
Query	1		TFNAVWFQGTLSEVSDYSYD T NAV FQG+LSE++D SY+				
Sbjct	112		TVNAVTFQGSLSELTDVSYN				_
Query	181	VRLGD VRLGD	KSPSTLQSPTHITNTSRN P+ P + +		KIPSTTIPGOG		
Sbjct	172		PIPAIGLDPKMVATCDSSDR	· -			_
Query	340	VGPID:	IMWSGQMTMVDEWTVTA + G++ T V + + A				INM 510 N
Sbjct	231		VGGELVFQTSVQDLVLGA				
Query	511		SLFHENPPPEPVAALKVHIT +F N +P+ ++K+ I	YGNNTNGDS G T		VIGGATIGVN + GG G	ISP 681
Sbjct	284		-VFPTNEITQPITSIKLEIV				
Query	682		YQAVAEGTAITISGINNYEL ¹ Y+ VA G+ +T++G++N+EL [.]			YIKYILSNRE Y K ILS R+	
Sbjct	343		YERVATGSVVTVAGVSNFEL:				
Query	862	GLRSVI G+++V	$egin{array}{llll} MTLAEYNRMKMYMHVLTNYN \\ EY & + & Y & + & N \end{array}$	VDEKEAASFDFW K A +F F	HLLKQIKKVAV		AP 1041
Sbjct	403	• • • •	WPTREYTDFREYFMEVADLN:				
Query	1042	IIGA + A	1053				
Sbjct	463	+ A LAHA	466				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AEP04401.1|** Length: 995 Number of Matches: 1 Range 1: 118 to 508

Score	Е	expect Method	Identities	Positives	Gaps	Frame
206 bits	(524) 16	e-54() Compositional matrix adjust.	132/400(33%)	212/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNO				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + I G++ T V + A	-			NM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I			VIGGATIGVN + GG G	SP 681
Sbjct	290	MPFNI-VIPTNEITQPITSIKLEIV				_
Query	682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL-			YIKYILSNRE Y K ILS R+	

Sbjct 349 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 408 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAPG+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P APGIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP 862 1041 Query Sbjct 409 468 Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 D +LGD A + +ASG + S R+R + A Sbjct 469 LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ

VP2, partial [Infectious bursal disease virus]

Sequence ID: gb|AAV88104.1| Length: 469 Number of Matches: 1

Range 1: 112 to 466

Identities **Score Expect Method Positives** Gaps Frame 199 bits(507) 1e-54() Compositional matrix adjust. 123/364(34%) 197/364(54%) 22/364(6%) +1 Features: YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVL+G+G+ +LSLP ++ Y Query 1 Sbjct 112 YALNGTVNAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLIGEGVTVLSLPTSYDLGY 171 Query 181 VRLGDKSPSTLQSPTHITNTSRN-----LGYGGAYKIPSTTIPGQGIHTKEFSINVDS 339 P + G G+ + Y+ S VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQSG-GVTITLFSANIDA Sbjct 172 230 340 VGPIDIMWSGQM---TMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM 510 Query 231 Sbjct 283 Query 511 NELNVSLFHENPPPEPVAALKVHIT---YGNNTNGDSDFSVDSSFTINVIGGATIGVNSP 681 N+ +F N +P+ ++K+ I G T +S S + + GG G P IPFNL-VFPTNEITQPITSIKLEIVTSKRGGQTGDQMSWSASGSLAVTIHGGNYPGALRP Sbjct 284 342 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL 682 861 Query +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L Sbjct 343 VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 402 Query 862 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP 1041 G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP Sbjct 403 462 Query 1042 IIGA 1053 Α Sbjct 463 LAHA466

VP2, VP3, and VP4 [Infectious bursal disease virus]

Sequence ID: gb|AAA52086.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score		Expect	Method	Identities	Positives	Gaps	Frame
206 bits	(523)	2e-54()	Compositional matrix adjust.	131/400(33%)	214/400(53%)	23/400(5%)	+1
Features	s:						
Query	1	YAL	NGTFNAVWFQGTLSEVSDYSYDI	RILSITSNPLDK	VGNVLVGDGLE	ILSLPQGFNN	
Sbjct	118	YAL	NGT NAV FÕG+LSE++D SY+ NGTINAVTFQGSLSELTDVSYN(GLMSATANINDK	GENVLVGEGVT	+LSLP ++ VLSLPTSYDLO	_
Query	181	VRL VRL	GDKSPSTLQSPTHITNTSRN GD P+ P + +				
Sbjct	178		GD PT P T T GDPIPAIGLDPKMVATCDSSDRI				
Query	340		IDIMWSGQMTMVDEWTVTAN + + G++ T V + A				
Sbjct	237	•	LSVGGELVFKTSVHSLVLGA				N+ NL 289
Query	511		NVSLFHENPPPEPVAALKVHITY N+ + N +P+ ++K+ I	GNNTNGDSD + + D		VIGGATIGVN: + GG G	SP 681
Sbjct	290		NL-VIPTNEITQPITSIKLEIV				RP 348
Query	682		VGYQAVAEGTAITISGINNYELV V Y+ VA G+ +T++G++N+EL-			YIKYILSNREI Y K ILS R+-	
Sbjct	349		VAYERVATGSVVTVAGVSNFEL				_
Query	862	GLR G++	SVMTLAEYNRMKMYMHVLTNYNV +V EY + Y + + +	DEKEAASFDFW KA+FF	HLLKQIKKVAV +++ I+++AV		AP 1041
Sbjct	409		TVWPTREYTDFREYFMEVADLS				
Query	1042	lIG.	AASGLADAVLGDSA-SGRPVGNS				
Sbjct	469		A D +LGD A + - AIGEGVDYLLGDEAQAASGTARA	+ASG + S R AASGKARAASGR			

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ABI52866.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score Expect Method Identities Positives Gaps Frame

206 bits(523) 2e-54() Compositional matrix adjust. 132/400(33%) 212/400(53%) 23/400(5%) +1

Query	1	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y	180
Sbjct	118	YALNGTINAVTFÕGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S G G+ FS N+D+	339
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQAG-GVTITLFSANIDA	236
Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + I G++ T V + A + GT + + V +N G+ G N+	510
Sbjct	237	ITSLSIGGELVFQTSVQGLILGATIYLIGFDGTAVITRAVAANNGLTAGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + + +P+ ++K+ I G +S + + GG G P	681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AKU89588.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Features:

Score	E	xpect Method	Identities	Positives	Gaps	Frame			
206 bits	(523) 26	e-54() Compositional matrix adjust.	133/400(33%)	212/400(53%)	23/400(5%)	+1			
Features:									
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				IPY 180			
Sbjct	118	YALNGT NAV FOGTLSETTD SYT YALNGTVNAVTFQGSLSELTDVSYN				_			
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGOG Z+ S G G					
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR	· -			_			
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + + G + T V + + A				INM 510 N			
Sbjct	237	TTSLSVGGGLVFQTSVQDLVLGA							
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681			
Sbjct	290	IPFNL-VFPTSEITQPITSIKLEIV							
Query	682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL-	~	~	YIKYILSNRE Y K ILS R+				
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:							
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ I+++AV		ZAP 1041			
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN							
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNS + A D +LGD A + +	SASGMPISLSRR +ASG + S R						
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGIAR							

VP2-4-3 [Infectious bursal disease virus]

Sequence ID: **gb|ABI83739.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
206 bits	(523) 26	e-54() Compositional matrix adjust.	132/400(33%)	212/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG '+ S PG G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR:				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A	-			NM 510 N+
Sbjct	237	ITSLSVGGELVFQTSVHGLVLGA				-, .
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I			VIGGATIGVN + GG G	SP 681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				_
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+ L			YIKYILSNRE Y K ILS R+	

Sbjct	349	VTLVAYERVATGSVVTVAGVSNFVLIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ I+++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRAIRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Sbict	469	LAHAIGEGVDYLLGDEAOAASGTARAASGKARAASGRIRO 508	

Sequence ID: **gb|AAR24133.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
206 bits	(523) 26	e-54() Compositional matrix adjust.	131/400(33%)	214/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FÖG+LSE++D SY+ YALNGTINAVTFÖGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGOG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + + G++ T V + A				INM 510 N+
Sbjct	237	ITSLSVGGELVFKTSVQSLVLGA				-, .
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + N +P+ ++K+ I	YGNNTNGDSD + + D		VIGGATIGVN + GG G	ISP 681
Sbjct	290	MPFNL-VIPTNEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + +				
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLS				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AFU10443.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps F	rame
205 bits	(522) 2	e-54() Compositional matrix adjust.	. 131/400(33%)	212/400(53%)	23/400(5%) +	·1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYI YALNGT NAV FQG+LSE++D SY-	DRILSITSNPLD	KVGNVLVGDGLE	ILSLPQGFNNP	
Sbjct	118	YALNGT NAV FOGTLSETTD SYT				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +				
Sbjct	178	VRLGD PT P T T VRLGDPIPAIGLDPKMVATCGSSDI	-			
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A	ANYQPLNISGTLI A + GT -			
Sbjct	237	ITSLSIGGELVFQTSVQSLILG				
Query	511	NELNVSLFHENPPPEPVAALKVHIT	TYGNNTNGD: G		VIGGATIGVNS + GG G	P 681
Sbjct	290	MPFNI-VIPTSAITQPITSIKLEIV	•			P 348
Query	682	TVVVGYQAVAEGTAITISGINNYEI +V Y+ VA G+ +T++G++N+EI	LVPNPDLQKNLPI	MSYGKCDPQDLN YG+ DP +N	YIKYILSNREK Y K ILS R++	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEI				_
Query	862	GLRSVMTLAEYNRMKMYMHVLTNY				
Sbjct	409	G+++V EY + Y + + 1 GIKTVWPTREYTDFREYFMEVADLI		+++ +++AV KDIIRALRRIAV		_
Query	1042	IIGAASGLADAVLGDSA-SGRPVG				
Sbjct	469	+ A D +LGD A + LAQAIGEGVDYLLGDEALAASGTAI	+ASG + S I RAASGKARAASGI			

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AFU10478.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Expect Method Score Identities **Positives** Gaps Frame

205 bits	(522) 26	e-54() Compositional matrix adjust. 132/400(33%) 211/400(52%) 23/400(5%) +1	
Features	S :		
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y	180
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY	177
Query	181	VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + + Y+ S G G+ FS N+D+	339
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQAG-GVTITLFSANIDA	236
Query	340	VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + I G++ T V + A + GT + V +N G+ G N+	510
Sbjct	237	ITSLSIGGELVFQTSVQGLILGATIYLIGFDGTAVTTRAVAANNGLTAGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + + +P+ ++K+ I G +S S + + GG G P	681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408

GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAPG+++VEY+Y++NKA+FF+++++++AVP++TLPAPGIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP

+ASG + S R+R

1041

468

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AAG23824.1| Length: 484 Number of Matches: 1

Query 1042 IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158

LAQAIGEGVDYLLGDEALAASGTARAASGKARAASGRIRQ

D +LGD A +

Range 1: 118 to 483

409

Sbjct

Query 862

Sbjct 469

Score	E	expect Method	Identities	Positives	Gaps	Frame
199 bits	(506) 3	e-54() Compositional matrix adjust.	124/375(33%)	201/375(53%)	22/375(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				IPY 180
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN	GLMSATANINDE	KIGNVLVGEGVT	VLSLPTSYDI	.GY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR	•			_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				INM 510 N+
Sbjct	237	TTSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV	-			_
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + H N		VHLLKQIKKVAV +++ +++AV		AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGD 1086 + A D +LGD				
Sbjct	469	LAHAIGEGVDYLLGD 483				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ABG76954.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	expect Method	Identities	Positives	Gaps	Frame
205 bits	(522) 3	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	S :					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG + S G G		
Sbjct	178	VRLGDPIPAIELDPKMVATCDSSDRI				-
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + I G++ T V + A	~			INM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHITY N+ + +P+ ++K+ I			VIGGATIGVN + GG G	ISP 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				_
Query	682	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL-			YIKYILSNRE Y K ILS R+	

Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLITEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Sbict	469	LAHAIGEGVDYLLGDEAOAASGTARAASGKARAASGRIRO 508	

structural polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AIG93139.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps Fr	ame
205 bits	(521) 3	e-54() Compositional matrix adjust.	132/400(33%)	212/400(53%)	23/400(5%) +1	
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FOG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGD PT P T T T T T T T T T T T T T T T T T				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A	~			
Sbjct	237	TTSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + +P+ +LK+ I	YGNNTNGDS G		VIGGATIGVNSP + GG G P	681
Sbjct	290	MPFNI-VIPTSEITQPITSLKLEIV	_			348
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNREKL Y K ILS R++L	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N			PLAATLAPQYAP P+ +TL P AP	
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +				
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ACB56941.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Expect Method	Identities	Positives	Gaps F	rame				
205 bits(521)	3e-54() Compositional matrix adjust.	132/400(33%)	212/400(53%)	23/400(5%) +	1				
Features:									
Query 1	YALNGTFNAVWFQGTLSEVSDYSYD								
Sbjct 118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				_				
Query 181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGOG Z+ S G G						
Sbjct 178	VI(1100 1								
Query 340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A								
Sbjct 237									
Query 511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G			P 681				
Sbjct 290		•							
Query 682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL			YIKYILSNREK Y K ILS R++					
Sbjct 349									
Query 862									
Sbjct 409	G+++V EY + Y + + N GIKTVWPTREYTDFREYFMEVADLN	K A +F F SPLKIAGAFGF		P+ +TL P A PVVSTLFPPAA					
Query 104									
Sbjct 469		+ASG + S F AASGKARAASGF	* ' = *						

polyprotein [Infectious bursal disease virus]

Sequence ID: emb|CAJ34339.1| Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Expect Method Score **Identities Positives** Gaps Frame

```
205 bits(521) 3e-54() Compositional matrix adjust. 132/400(33%) 212/400(53%) 23/400(5%) +1
Features:
              YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY
YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y
Query 1
                                                                                   180
              YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY
Sbjct 118
                                                                                  177
       181
              VRLGDKSPSTLQSPTHITNTSRN-----LGYGGAYKIPSTTIPGQGIHTKEFSINVDS
                                                                                   339
Query
              VRLGD P+ P + + + Y+ S G G+ FS N+D+ VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQQG-GVTITLFSANIDA
Sbjct
      178
                                                                                   236
              340
                                                                                   510
Query
                                                                                   289
Sbjct
       237
              Query
       511
                                                                                   681
                                                       +S S + + GG G P
Sbjct
       290
              MPFNL-VIPTNQITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLVVTIHGGNYPGALRP
                                                                                   348
Query
       682
              TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL
                                                                                   861
                +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L
              VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL
                                                                                   408
Sbjct
      349
              GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAPG+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P APGIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP
Query
       862
                                                                                   1041
```

IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158

LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ

+ASG + S R+R

468

structural polyprotein, partial [Infectious bursal disease virus]

Sequence ID: dbj|BAH03937.1| Length: 1012 Number of Matches: 1

D +LGD A +

Range 1: 118 to 508

409

469

1042

Sbjct

Query

Sbjct

Score	E	xpect Method	Identities	Positives	Gaps	Frame
205 bits	(521) 4e	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				1PY 180
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				LGY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				INM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQSLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + + +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVN + GG G	ISP 681
Sbjct	290	MPFNI-VIPTSQITQPITSIKLEIV	_			_
Query	682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ +++AV		AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ABI52864.1| Length: 1012 Number of Matches: 1

▶ See 2 more title(s) Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps F	rame
205 bits	(521) 4	e-54() Compositional matrix adjust.	132/400(33%)	211/400(52%)	23/400(5%) +	1
Features	S :					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNO				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG + S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDRI				
Query	340	VGPIDIMWSGQMTMVDEWTVTAN + + I G++ T V + A	~			
Sbjct	237	ITSLSIGGELVFQTSVQGLILGAT				
Query	511	NELNVSLFHENPPPEPVAALKVHITY				P 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				_

Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

structural polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AAK69716.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps Fra	ıme
205 bits	(521) 46	e-54() Compositional matrix adjust.	132/400(33%)	212/400(53%)	23/400(5%) +1	
Features	S :					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				180
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNG				177
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G		339
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				236
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + I G++ T V + A				510
Sbjct	237	ITSLSIGGELVFQTSVQGLILGA				289
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G			681
Sbjct	290	MPFNI-VIPTSAITQPITSIKLEIV				348
Query	682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL-			YIKYILSNREKL Y K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:				408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN	VDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ +++VAV		1041
Sbjct	409	G+++V EY + Y + + N GIKTVWPTREYTDFREYFMEVADLN				468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN				
Sbjct	469	+ A D +LGD A +	+ASG + S F AASGKARAASGF			

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AAN04461.1|AF527039_2** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
204 bits(520) 5e	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features:	:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI				
Sbjct	118	YALNGT NAV FÖG+LSE++D SY+ YALNGTINAVTFÖGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +	LGYGGAY + Y	KIPSTTIPGQG Z+ S G G	IHTKEFSINV + FS N+	
Sbjct	178	VRLGD PT PT T T T T T T T T T T T T T T T T	_			
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + I G++ T V + A				
Sbjct	237	ITSLSIGGELVFQTSVQSLILGA				N+ -NL 289
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G			
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				P LRP 348
Query	682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL-			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN				
Sbjct	409	G+++V EY + Y + + N GIKTVWPTREYTDFREYFMEVADLN	K A +F F SPLKIAGAFGFK	+++ +++AV DIIRALRRIAV		AP AAP 468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN				
Sbjct	469	+ A D +LGD A + LAHAIGEGVDYLLGDEAQAASGTAR	+ASG + S F AASGKARAASGF			

polyprotein [Infectious bursal disease virus]

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

Score	Expect Method	Identities	Positives	Gaps	Frame
204 bits(519) 5e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features:					
Query 1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				NPY 180
Sbjct 118					LGY 177
Query 183	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		KIPSTTIPGQG Z+ S G G		
Sbjct 178					_
Query 340		NYQPLNISGTLI + GT +			4NM 510 N+
Sbjct 237					-, .
Query 513	NELNVSLFHENPPPEPVAALKVHIT N+ + + +P+ ++K+ I	YGNNTNGDS G		IVIGGATIGVI + GG G	NSP 681
Sbjct 290		_			_
Query 682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRI IY K ILS R-	
Sbjct 349					
Query 862	2 GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		HLLKQIKKVAV +++ +++AV		YAP 1041
Sbjct 409					
Query 104		SASGMPISLSRF +ASG + S F			
Sbjct 469					

Sequence ID: emb|CAI53892.2| Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
204 bits	(519) 5	e-54() Compositional matrix adjust.	131/400(33%) 212/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		YKIPSTTIPGOG Y+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A	NYQPLNISGTL + GT			NM 510 N+
Sbjct	237	TTSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + +P+ ++K+ I	YGNNTNGD G		VIGGATIGVN + GG G	SP 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV	•			
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N				AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSR +ASG + S			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AEQ29949.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
204 bits	(519) 6	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGD FT F T T T T T T T T T T T T T T T T T				_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A	~			NM 510 N+
Sbjct	237	ITSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS	SDFSVDSSFTIN	VIGGATIGVN	SP 681

Sbjct 29	90	N+++P+++K+I G $+S$ S $+$ $+$ G G P $MPFNI-VIPTSEITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLAVTIHGGNYPGALRP$	348
Query 68	82	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL	861
Sbjct 34	49	+V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query 86		GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP	1041
Sbjct 40		G+++V EY + Y + + N K A +F F +++ +++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query 10	042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158	
Sbjct 46	69	+ A D +LGD A + +ASG + S R+R LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

Sequence ID: emb|CAC60256.1| Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	expect Method	Identities	Positives	Gaps	Frame
204 bits	(519) 6	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN				
Sbjct	178	VRLGD P+ P + + VRLGDPIPAIGLDPKMVATCDSSDR		Z+ S G C ZQFSSQYQAG-C		
Query	340	VGPIDIMWSGQMTMVDEWTVTA				
Sbjct	237	$+ + I G++ TV + A \\ ITSLSIGGELVFQTSVQGLILGA$			•	N+ NL 289
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + + +P+ ++K+ I	YGNNTNGDS G			
Sbjct	290	N+ + + +P+ ++K+ I MPFNI-VIPTSEITQPITSIKLEIV		+S S + ISWSASGSLAVI		P RP 348
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		HLLKQIKKVAV +++ +++AV		
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN				
Sbjct	469	+ A D +LGD A + LAHAIGEGVDYLLGDEAQAASGTAR	+ASG + S F AASGKARAASGF			

Polyprotein (VP2-VP4-VP3) [Infectious bursal disease virus]

Sequence ID: emb|CDW92043.1| Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Ex	pect	Method	Identities	Positives	Gaps	Frame
204 bits(5	19) 6e-	-54()	Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features:							
Query 1	L		NGTFNAVWFQGTLSEVSDYSYDF NGT NAV FQG+LSE++D SY+				
Sbjct 1	118		NGT NAV FOG+LSE++D SY+ NGTINAVTFQGSLSELTDVSYNO				
Query 1	181	VRLO VRLO	GDKSPSTLQSPTHITNTSRN GD P+ P + +		KIPSTTIPGQG + S G G		
Sbjct 1	L78		GDPIPAIGLDPKMVATCDSSDRE				
Query 3	340		IDIMWSGQMTMVDEWTVTAN + I G++ T V + A	NYQPLNISGTLI + GT +			INM 510 N+
Sbjct 2	237		LSIGGELVFQTSVQGLILGAT				
Query 5	511		NVSLFHENPPPEPVAALKVHITY N+ + + +P+ ++K+ I	ZGNNTNGDS G		VIGGATIGVN + GG G	ISP 681
Sbjct 2	290	_	NI-VIPTSEITQPITSIKLEIVI				
Query 6	582		JGYQAVAEGTAITISGINNYELV JY+ VA G+ +T++G++N+EL+			YIKYILSNRE Y K ILS R+	
Sbjct 3	349		JAYERVATGSVVTVAGVSNFEL				
Query 8	362	GLRS	SVMTLAEYNRMKMYMHVLTNYN\ +V EY + Y + + N	DEKEAASFDFW KA+FF	HLLKQIKKVAV +++ +++AV		AP 104
Sbjct 4	109	•	TVWPTREYTDFREYFMEVADLNS				
Query 1	1042	IIGA + A	AASGLADAVLGDSA-SGRPVGNS A D +LGD A +	SASGMPISLSRR HASG + S R			
Sbjct 4	169	_	AIGEGVDYLLGDEAQAASGTAR				

Range 1: 118 to 508

Score	E	xpect Method	Identities	Positives	Gaps	Frame
204 bits	(519) 66	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	S :					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				PY 180 Y
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR	_			_
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				NM 510 N+
Sbjct	237	TSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G		VIGGATIGVN + GG G	SP 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYELT +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE Y K ILS R+	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFW K A +F F	HLLKQIKKVAV +++ +++AV		AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AAM28898.1| Length: 1012 Number of Matches: 1

▶ See 1 more title(s) Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps F	rame
204 bits(519) 6	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%) +	1
Features	:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FOG+LSE++D SY+				
Sbjct	118	YALNGT NAV FOG+LSE++D SY+ YALNGTINAVTFOGSLSELTDVSYN				
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				
Sbjct	237	TSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + +P+ ++K+ I	YGNNTNGDS G			P 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV	•			_
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNREK Y K ILS R++	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		VAVXXILKQIKKVAV +++ +++AV		
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				_
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRI +ASG + S I			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

structural polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|AIG93145.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
204 bits	(519) 6	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYNO				
Query	181	VRLGDKSPSTLQSPTHITNTSRN		KIPSTTIPGQG Z+ S G G		
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR	_			
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				NM 510 N+

Sbjct	237	ITSLSIGGELVFQTSVQGLILGATIYLIGFDGTAVITRAVAADNGLTAGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + + +P+ ++K+ I G +S S + + GG G P	681
Sbjct	290	N++++P+++K+I G $+S$ S $+$ $+$ G G P $MPFNI-VIPTSEITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLAVTIHGGNYPGALRP$	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL	861
Sbjct	349	+V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP	1041
Sbjct	409	G+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158	
Sbjct	469	+ A D +LGD A + +ASG + S R+R LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

structural polyprotein [Infectious bursal disease virus]

Sequence ID: gb|ACS44345.1| Length: 1012 Number of Matches: 1

Range 1: 118 to 508

Score	Е	xpect Method	Identities	Positives	Gaps	Frame			
204 bits	(519) 6	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1			
Features:									
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD							
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN							
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG Z+ S G G					
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR							
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				NM 510 N+			
Sbjct	237	ITSLSIGGELVFQTSVQGLILGA			•				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + +P+ ++K+ I	YGNNTNGDS G		VIGGATIGVN: + GG G	SP 681			
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV	_			_			
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			YIKYILSNRE				
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL							
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		HLLKQIKKVAV +++ +++AV		AP 1041 AP			
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN							
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F						
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR							

VP2-4-3 polyprotein [Infectious bursal disease virus]

Sequence ID: ref|NP_690838.1| Length: 1012 Number of Matches: 1

▶ See 2 more title(s) Range 1: 118 to 508

Score		Expect	Method	Identities	Positives	Gaps	Frame
204 bits	(519)	6e-54()	Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	s:						
Query	1		IGTFNAVWFQGTLSEVSDYSYDF				
Sbjct	118		IGT NAV FQG+LSE++D SY+ IGTINAVTFQGSLSELTDVSYNO				
Query	181	VRLG VRLG	DKSPSTLQSPTHITNTSRN DP+P+++				
Sbjct	178		GD PT P T T GDPIPAIGLDPKMVATCDSSDRI	-			
Query	340		DIMWSGQMTMVDEWTVTAN				
Sbjct	237		- I G++ T V + A SIGGELVFQTSVQGLILGAT				N+ NL 289
Query	511		IVSLFHENPPPEPVAALKVHITY				ISP 681
Sbjct	290	_,	+ + + +P+ ++K+ I I-VIPTSEITQPITSIKLEIV	G TSKSGGQAGDQM		+ GG G IHGGNYPGAL	RP 348
Query	682		GYQAVAEGTAITISGINNYELV				
Sbjct	349		7 Y+ VA G+ +T++G++N+EL+ 7AYERVATGSVVTVAGVSNFEL]			Y K ILS R+ YTKLILSERD	
Query	862		VMTLAEYNRMKMYMHVLTNYN				
Sbjct	409	G+++ GIKT	-V EY + Y + + N 'VWPTREYTDFREYFMEVADLNS	K A +F F SPLKIAGAFGFK	+++ +++AV DIIRALRRIAV		AP AP 468
Query	1042		ASGLADAVLGDSA-SGRPVGNS				
Sbjct	469	+ A LAHA	A D +LGD A + A AIGEGVDYLLGDEAQAASGTAR	-ASG + S R AASGKARAASGR			

Sequence ID: **gb|AEQ29948.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	Е	xpect Method	Identities	Positives	Gaps F	rame
204 bits	(519) 6	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%) +	·1
Features	S :					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD YALNGT NAV FQG+LSE++D SY+				
Sbjct	118	YALNGTINAVTFQGSLSELTDVSYN				-
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQO Z+ S G (
Sbjct	178	VRLGDPIPAIGLDPKMVATCDSSDR				
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				M 510
Sbjct	237	TSLSIGGELVFQTSVQGLILGA				
Query	511	NELNVSLFHENPPPEPVAALKVHIT N+ + + +P+ ++K+ I	YGNNTNGDS G			P 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYEL +V Y+ VA G+ +T++G++N+EL			NYIKYILSNREK NY K ILS R++	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N	VDEKEAASFDFV K A +F F	/AVXXIQXLLHV /A+++ +++	/PLAATLAPQYA /P+ +TL P A	
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: dbj|BAA08555.1| Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
204 bits	(519) 7	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD	RILSITSNPLDK	VGNVLVGDGLE	ILSLPQGFNN	PY 180
Sbjct	118	YALNGT NAV FÕG+LSE++D SY+ YALNGTINAVTFÕGSLSELTDVSYN				GY 177
Query	181	VRLGDKSPSTLQSPTHITNTSRN				
Sbjct	178	VRLGD P+ P + + + VRLGDPIPAIGLDPKMVATCDSSDR	_	(+ S G G (QFSSQYQAG-G		
Query	340	VGPIDIMWSGQMTMVDEWTVTA + + I G++ T V + A				
Sbjct	237	+ + I G++ TV + A ITSLSIGGELVFQTSVQGLILGA				N+ NL 289
Query	511	NELNVSLFHENPPPEPVAALKVHIT	YGNNTNGDS G		VIGGATIGVN + GG G	SP 681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV	•			_
Query	682	TVVVGYQAVAEGTAITISGINNYEL' +V Y+ VA G+ +T++G++N+EL		~	YIKYILSNRE	
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYN G+++V EY + Y + + N		HLLKQIKKVAV +++ +++AV		AP 1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGN + A D +LGD A +	SASGMPISLSRF +ASG + S F			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR		• • • •		

polyprotein [Infectious bursal disease virus]

Sequence ID: gb|AHW82956.1| Length: 1012 Number of Matches: 1

Score	Е	expect Method	Identities	Positives	Gaps	Frame
204 bits	(519) 76	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Feature	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYD				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYN				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN				
Sbjct	178	VRLGD P+ P + + VRLGDPIPAIGLDPKMVATCDSSDR	-	/+ S G G /QFSSQYQAG-G		
Query	340	VGPIDIMWSGQMTMVDEWTVTA	NYQPLNISGTLI	AGSMKTLVWSN	TGVANGNHYM	INM 510

Sbjct	237	+ $+$ I G++ T V $+$ A $+$ GT $+$ $+$ V $++$ G+ G N+ ITSLSIGGELVFQTSVQGLILGATIYLIGFDGTAVITRAVAADNGLTAGTDNL	289
Query	511	NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + + +P+ ++K+ I G +S S + + GG G P	681
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIVTSKSGGQAGDQMSWSASGSLAVTIHGGNYPGALRP	348
Query	682	TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L	861
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLITEYGRFDPGAMNYTKLILSERDRL	408
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G+++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP	1041
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP	468
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNSASGMPISLSRRLRN 1158 + A D +LGD A + +ASG + S R+R	
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTARAASGKARAASGRIRQ 508	

structural polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ABW38087.1|** Length: 1012 Number of Matches: 1 Range 1: 118 to 508

Score	E	Expect Method	Identities	Positives	Gaps	Frame
204 bits	(519) 7	e-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%)	+1
Features	s:					
Query	1	YALNGTFNAVWFQGTLSEVSDYSYDI				
Sbjct	118	YALNGT NAV FQG+LSE++D SY+ YALNGTINAVTFQGSLSELTDVSYNO				_
Query	181	VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + +		KIPSTTIPGQG + S G G		
Sbjct	178	VRLGD P+ P + P + P + P + P + P + P + P + P +	•			
Query	340	VGPIDIMWSGQMTMVDEWTVTAI + + I G++ T V + A				NM 510 N+
Sbjct	237	TTSLSIGGELVFQTSVQGLILGA			•	
Query	511	NELNVSLFHENPPPEPVAALKVHITY	YGNNTNGDS G		VIGGATIGVN: + GG G	SP 681 P
Sbjct	290	MPFNI-VIPTSEITQPITSIKLEIV				
Query	682	TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL-		ISYGKCDPQDLN YG+ DP +N		
Sbjct	349	VTLVAYERVATGSVVTVAGVSNFEL:				
Query	862	GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + + N	DEKEAASFDFW KA+FF			
Sbjct	409	GIKTVWPTREYTDFREYFMEVADLN				
Query	1042	IIGAASGLADAVLGDSA-SGRPVGNS + A D +LGD A +	SASGMPISLSRR FASG + S R			
Sbjct	469	LAHAIGEGVDYLLGDEAQAASGTAR				

polyprotein [Infectious bursal disease virus]

Sequence ID: **gb|ADX87411.1|** Length: 1002 Number of Matches: 1 Range 1: 110 to 500

Ex	pect Method	Identities	Positives	Gaps Fr	ame
18) 7e	-54() Compositional matrix adjust.	131/400(33%)	212/400(53%)	23/400(5%) +1	
1					180
110					169
181					339
170		_			228
340					510
229					281
511					681
282					340
682					861
341					400
862					1041
401	<u> </u>				460
1042					
461					
	18) 7e 1 110 181 170 340 229 511 282 582 341 362 401 1042	YALNGTFNAVWFQGTLSEVSDYSYDE YALNGT NAV FQG+LSE++D SY+ 110 YALNGTINAVTFQGSLSELTDVSYNG 181 VRLGDKSPSTLQSPTHITNTSRN VRLGD P+ P + + 170 VRLGDPIPAIGLDPKMVATCDSSDRE 1840 VGPIDIMWSGQMTMVDEWTVTAN + H G++ T V + A 1829 ITSLSIGGELVFQTSVQGLILGAT 1851 NELNVSLFHENPPPEPVAALKVHITY N+ + + +P+ ++K+ I 1862 MPFNI-VIPTSEITQPITSIKLEIVT 1862 TVVVGYQAVAEGTAITISGINNYELV +V Y+ VA G+ +T++G++N+EL- 1864 VTLVAYERVATGSVVTVAGVSNFELT 1862 GLRSVMTLAEYNRMKMYMHVLTNYNV G+++V EY + Y + N 1861 GIKTVWPTREYTDFREYFMEVADLNS 1862 IIGAASGLADAVLGDSA-SGRPVGNS 1863 + A D +LGD A +	18) 7e-54() Compositional matrix adjust. 131/400(33%) 1	Te-54() Compositional matrix adjust. 131/400(33%) 212/400(53%) YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLE YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+- YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVT VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQG VRLGD P+ P + + Y+ S G G VRLGDPHPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQAG-G VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSN' + + I G++ T V + A + GT + + V ++ 229 ITSLSIGGELVFQTSVQGLILGATIYLIGFDGTAVITRAVAAD 511 NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTIN N+ + + P+ + + + + + + + + + + + + + + +	Te-54() Compositional matrix adjust. 131/400(33%) 212/400(53%) 23/400(5%) +1 YALNGTFNAVWFQGTLSEVSDYSYDRILSITSNPLDKVGNVLVGDGLEILSLPQGFNNPY YALNGT NAV FQG+LSE++D SY+ ++S T+N DK+GNVLVG+G+ +LSLP ++ Y YALNGTINAVTFQGSLSELTDVSYNGLMSATANINDKIGNVLVGEGVTVLSLPTSYDLGY VRLGDKSPSTLQSPTHITNTSRNLGYGGAYKIPSTTIPGQGIHTKEFSINVDS VRLGD P+ P + + Y+ S G G+ FS N+D+ VRLGDPIPAIGLDPKMVATCDSSDRPRVYTITAADDYQFSSQYQAG-GVTITLFSANIDA VGPIDIMWSGQMTMVDEWTVTANYQPLNISGTLIAGSMKTLVWSNTGVANGNHYMNM + + I G++ T V + A + GT + + V + G+ G N+ ITSLSIGGELVFQTSVQGLILGATIYLIGFDGTAVITRAVAADNGLTAGTDNL NELNVSLFHENPPPEPVAALKVHITYGNNTNGDSDFSVDSSFTINVIGGATIGVNSP N+ + + PP + +K+ I G +S S + + GG G P MPFNI-VIPTSEITQPITSIKLEIVTSKSGQQAGDQMSWSASGSLAVTIHGGNYPGALRP 1822 TVVVGYQAVAEGTAITISGINNYELVPNPDLQKNLPMSYGKCDPQDLNYIKYILSNREKL +V Y+ VA G+ +T++G++N+EL+PNP+L KNL YG+ DP +NY K ILS R++L VTLVAYERVATGSVVTVAGVSNFELIPNPELAKNLVTEYGRFDPGAMNYTKLILSERDRL 1842 GLRSVMTLAEYNRMKMYMHVLTNYNVDEKEAASFDFWHLLKQIKKVAVPLAATLAPQYAP G++V EY + Y + + N K A +F F +++ ++++AVP+ +TL P AP GIKTVWPTREYTDFREYFMEVADLNSPLKIAGAFGFKDIIRALRRIAVPVVSTLFPPAAP 1854 1854 1865 1866 1874 1874 1875 1876 1877 1886 1887 1