Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BXX3B1015

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Blast report description

Nucleotide Sequence (248 letters)

RID <u>B8BXX3B1015</u> (Expires on 02-06 12:14 pm)

Query ID lcl|Query_196133

Description None **Molecule type** nucleic acid

Query Length 248

Database Name nr

Description All non-redundant GenBank CDS

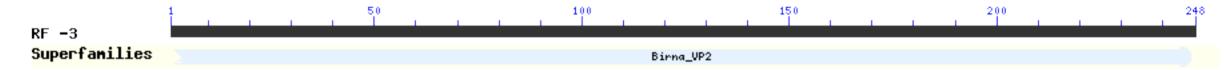
translations+PDB+SwissProt+PIR+PRF excluding

environmental samples from WGS projects

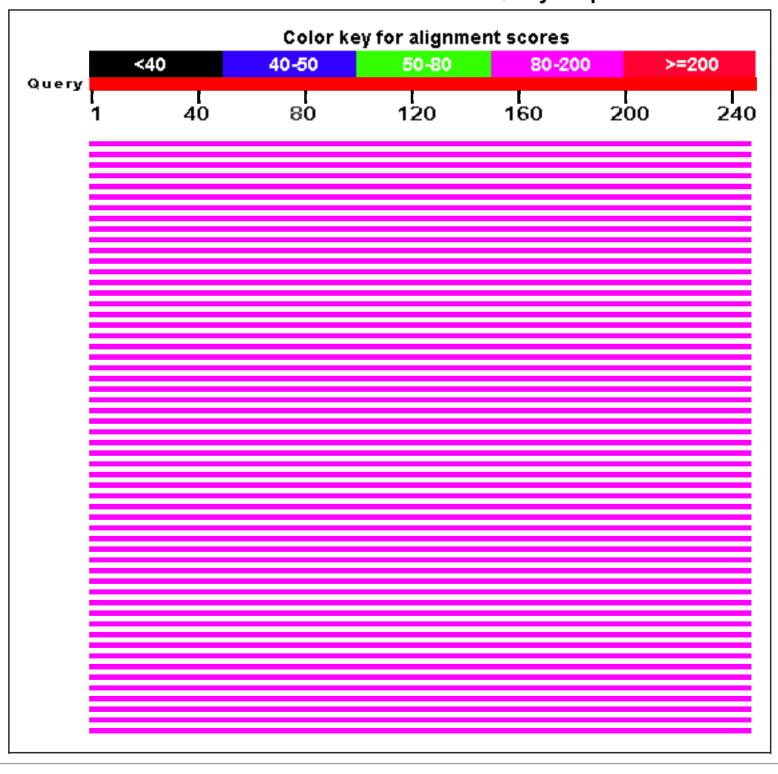
Program BLASTX 2.3.1+

□ Graphic Summary

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



Distribution of 100 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Description	Max	Total	Query	E	Ident	Accession
	score	score	cover	value		
polyprotein [Drosophila x virus]	156	156	99%	1e-41	90%	NP_690836.1
pVP2-VP4-VP3 polyprotein [Culicine-associated Z virus]	145	145	99%	7e-38	83%	AGW51761.1
pVP2-VP4-VP3 polyprotein [Culicine-associated Z virus]	145	145	99%	8e-38	83%	AGW51779.1
pVP2-VP4N-X polyprotein [Culicine-associated Z virus]	144	144	99%	1e-37	83%	AGW51762.1
pVP2-VP4N-X polyprotein [Culicine-associated Z virus]	144	144	99%	1e-37	83%	AGW51780.1
unnamed protein product [Espirito Santo virus]	135	135	99%	3e-35	74%	YP_004956724.1
polyprotein [Mosquitoe x virus]	136	136	99%	1e-34	74%	AFU34333.1
unnamed protein product [Espirito Santo virus]	136	136	99%	1e-34	74%	YP_004956722.1
polyprotein precursor [Culex Y virus]	136	136	99%	1e-34	74%	AFR34026.1
polyprotein [Infectious pancreatic necrosis virus]	97.8	97.8	99%	3e-23	54%	AAS79778.1
polyprotein [Infectious pancreatic necrosis virus]	97.1	97.1	99%	7e-23	55%	AAR99837.1
major structural protein VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	7e-23	54%	<u>AEX33173.1</u>
major structural protein VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	7e-23	54%	AEX33169.1
VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	7e-23	54%	AEV91035.1
structural protein 2 [Infectious pancreatic necrosis virus]	99.0	99.0	99%	1e-22	55%	<u>AFZ93414.1</u>
polyprotein [Infectious pancreatic necrosis virus serotype A5]	99.0	99.0	99%	1e-22	55%	<u>CAI54275.1</u>
structural protein 2 [Infectious pancreatic necrosis virus]	99.0	99.0	99%	1e-22	55%	<u>AFZ93413.1</u>
polyprotein [Infectious pancreatic necrosis virus]	96.3	96.3	99%	1e-22	54%	AAR99829.1
polyprotein [Infectious pancreatic necrosis virus]	96.3	96.3	99%	1e-22	54%	AAS79776.1
polyprotein [Infectious pancreatic necrosis virus]	96.3	96.3	99%	1e-22	54%	AAR99831.1
polyprotein [Infectious pancreatic necrosis virus]	96.3	96.3	99%	2e-22	54%	AAR99839.1
VP2 [Infectious pancreatic necrosis virus]	97.8	97.8	99%	2e-22	55%	ACY35989.1
major structural protein VP2 [Infectious pancreatic necrosis virus]	95.5	95.5	99%	2e-22	54%	AHC01907.1
major structural protein VP2 [Infectious pancreatic necrosis virus]	95.1	95.1	99%	2e-22	54%	AHC01920.1
major structural protein VP2 [Infectious pancreatic necrosis virus]	95.1	95.1	99%	3e-22	54%	AHC01914.1
VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	4e-22	54%	ACY35990.1
major structural protein [Infectious pancreatic necrosis virus]	97.4	97.4	99%	5e-22	55%	AHE78005.1
polyprotein [Infectious pancreatic necrosis virus]	97.1	97.1	99%	6e-22	54%	CAH18975.1
polyprotein [Infectious pancreatic necrosis virus]	97.1	97.1	99%	7e-22	54%	AGC81929.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	97.1	97.1	99%	7e-22	54%	CAX62746.1
polyprotein [Infectious pancreatic necrosis virus]	99.0	99.0	99%	7e-22	55%	AAA92626.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	97.1	97.1	99%	7e-22	54%	CAI54268.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	97.1	97.1	99%	7e-22	54%	CAI54262.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	7e-22	54%	<u>CAI54250.1</u>
polyprotein [Infectious pancreatic necrosis virus - Sp]	97.1	97.1	99%	7e-22	54%	CAI54260.1

polyprotein [Infectious pancreatic necrosis virus]	97.1	97.1	99%	7e-22	54%	AGC81925.1
polyprotein [Infectious pancreatic necrosis virus -	96.7	96.7	99%	7e-22	54%	CAX62748.1
Sp] polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	7e-22	54%	<u>CAI54259.1</u>
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	7e-22	54%	<u>CAI54263.1</u>
polyprotein [Infectious pancreatic necrosis virus]	97.1	97.1	99%	7e-22	54%	AGC81934.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	97.1	97.1	99%	7e-22	54%	CAI54273.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	97.1	97.1	99%	7e-22	54%	CAI54271.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	7e-22	54%	CAX62744.1
major capsid protein VP2 [Flounder aquabirnavirus DS]	98.2	98.2	99%	7e-22	54%	AAQ82705.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	7e-22	54%	<u>CAI54256.1</u>
capsid protein [Infectious pancreatic necrosis virus]	97.1	97.1	99%	8e-22	54%	AGB51152.1
VP2 [Infectious bursal disease virus]	93.2	93.2	99%	8e-22	59%	ACO59489.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAX62752.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	<u>CAI54254.1</u>
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAX62751.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAX62754.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAI54255.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAI54246.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAI54245.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAI54267.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAI54264.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	8e-22	54%	CAI54266.1
polyprotein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	9e-22	54%	ADB27125.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	CAX62759.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	<u>CAI54261.1</u>
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	<u>CAI54247.1</u>
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	CAI54249.1
polyprotein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	9e-22	54%	CAH18976.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	<u>CAI54248.1</u>
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	CAX62758.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	<u>CAI54257.1</u>
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	CAI54253.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	9e-22	54%	<u>CAI46884.1</u>
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	9e-22	54%	<u>AHE77997.1</u>

major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	9e-22	54%	AHE77992.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	9e-22	54%	AHE78010.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	9e-22	54%	AHE77987.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE77994.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE77996.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE77991.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE77989.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE77990.1
polyprotein [Infectious pancreatic necrosis virus - Sp]	96.7	96.7	99%	1e-21	54%	CAX62755.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE78012.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE78002.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE77984.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE77993.1
major structural protein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AHE78003.1
polyprotein [Infectious pancreatic necrosis virus]	99.4	99.4	99%	1e-21	56%	CAD32967.1
VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	<u>AFN26747.1</u>
polyprotein [Infectious pancreatic necrosis virus]	96.3	96.3	99%	1e-21	54%	AGC81930.1
capsid protein VP2 [Infectious pancreatic necrosis virus]	96.3	96.3	99%	1e-21	54%	AIA66833.1
VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	<u>AFN26744.1</u>
major structural protein [Infectious pancreatic necrosis virus]	96.3	96.3	99%	1e-21	54%	AHE78007.1
VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	AFN26745.1
VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	<u>AFN26742.1</u>
VP2 [Infectious pancreatic necrosis virus]	96.7	96.7	99%	1e-21	54%	<u>AFN26746.1</u>
polyprotein [Infectious pancreatic necrosis virus]	96.3	96.3	99%	1e-21	54%	AGC81935.1
VP2 [Infectious pancreatic necrosis virus]	95.5	95.5	99%	1e-21	54%	ACY35988.1
polyprotein [Infectious pancreatic necrosis virus]	96.7	96.7	99%	2e-21	54%	<u>AJK26914.1</u>
polyprotein [Tellina virus 2]	98.6	98.6	99%	2e-21	55%	AAK32157.1
VP2 structural protein [Infectious pancreatic necrosis virus]	97.4	97.4	99%	2e-21	55%	<u>AAK16604.1</u>
polyprotein [Infectious pancreatic necrosis virus]	97.4	97.4	99%	2e-21	55%	AAA92631.1
VP2 structural protein [Infectious pancreatic necrosis virus]	97.4	97.4	99%	2e-21	55%	<u>AAK16601.1</u>
VP2 structural protein [Infectious pancreatic necrosis virus]	97.4	97.4	99%	2e-21	55%	AAK16602.1

□<u>Alignments</u>

polyprotein [Drosophila x virus]

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

▶ See 2 more title(s) Range 1: 37 to 118

Score	Expect	Method	Identities	Positives	Gaps	Frame
156 bits(394)	1e-41()	Compositional matrix adjust.	74/82(90%)	80/82(97%)	0/82(0%)	-3

Features:

Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYVWNSNSSSWVFDQYIYTAQELKDSYDYGRLI	67
Sbjct	37	TYNLKSG SG+GLIV+YPNTPSSISGFHY+W+S +S+WVFDQYIYTAQELKDSYDYGRLI TYNLKSGASGTGLIVVYPNTPSSISGFHYIWDSATSNWVFDQYIYTAQELKDSYDYGRLI	96
Query	66	SGSLSIKSSTLPAGVYALNGTF 1	
Sbict	97	SGSLSIKSSTLPAGVYALNGTF SGSLSIKSSTLPAGVYALNGTF 118	

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

Sequence ID: gb|AGW51761.1| Length: 1057 Number of Matches: 1

Range 1: 39 to 120

Score		Expect	Method		Identities	Positives	Gaps	Fra	me
145 bits	(366)	7e-38()	Compositional matrix a	djust.	68/82(83%)	76/82(92%)	0/82(0%)	-3	
Features	3:								
Query	246		SGPSGSGLIVIYPNTPSS SG SG+GLIV YPNTPSS						67
Sbjct	39		SGTSGTGLIVFYPNTPSS:						98
Query	66		IKSSTLPAGVYALNGTF +KSSTLPAGVYALNGTF	1					
Sbjct	99		VKSSTLPAGVYALNGTF	120					

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

Sequence ID: gb|AGW51779.1| Length: 1049 Number of Matches: 1

Range 1: 33 to 114

Score		Expect	Method	Identities	Positives	Gaps	Frame
145 bits	(366)	8e-38()	Compositional matrix adjus	st. 68/82(83%)	76/82(92%)	0/82(0%)	-3
Features	s:						
Query	246		SGPSGSGLIVIYPNTPSSISG SG SG+GLIV YPNTPSSI+G				
Sbjct	33		SGTSGTGLIVFYPNTPSSIAG				
Query	66		IKSSTLPAGVYALNGTF 1 KSSTLPAGVYALNGTF				
Sbjct	93		VKSSTLPAGVYALNGTF 11	14			

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

Sequence ID: **gb|AGW51762.1|** Length: 868 Number of Matches: 1 Range 1: 39 to 120

Score		Expect	Method	lde	entities	Positives	Gaps	Frame
144 bits	(363)	1e-37()	Compositional matrix adju	ust. 68/	(82(83%)	76/82(92%)	0/82(0%)	-3
Features	s:							
Query	246		SGPSGSGLIVIYPNTPSSIS			~ ~		
Sbjct	39		SG SG+GLIV YPNTPSSI+ SGTSGTGLIVFYPNTPSSI <i>F</i>					
Query	66		IKSSTLPAGVYALNGTF 1 +KSSTLPAGVYALNGTF	L				
Sbjct	99			120				

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

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

Range 1: 33 to 114

Score		Expect	Method		Identities	Positives	Gaps	Frame	
144 bits	(363)	1e-37()	Compositional matrix ad	djust.	68/82(83%)	76/82(92%)	0/82(0%)	-3	,
Features	s:								
Query	246		SGPSGSGLIVIYPNTPSSI SG SG+GLIV YPNTPSSI						
Sbjct	33		GGTSGTGLIVFYPNTPSS						
Query	66		IKSSTLPAGVYALNGTF KSSTLPAGVYALNGTF	1					
Sbjct	93		KSSTLPAGVYALNGTF	114					

unnamed protein product [Espirito Santo virus]

Sequence ID: ref|YP_004956724.1| Length: 500 Number of Matches: 1

Range 1: 37 to 118

Score		Expect	Method	I	dentities	Positives	Gaps	Frame
135 bits	(339)	3e-35()	Compositional matrix ad	djust. 6	61/82(74%)	74/82(90%)	0/82(0%)	-3
Features	s:							
Query	246		GGPSGSGLIVIYPNTPSSI					
Sbjct	37		+G SG+GLIV YPNTPSS+ rGASGTGLIVFYPNTPSSV					
Query	66		KSSTLPAGVYALNGTF	1				
Sbjct	97		+KSS++P+GVYAL GTF /KSSSIPSGVYALTGTF	118				

polyprotein [Mosquitoe x virus]

Sequence ID: gb|AFU34333.1| Length: 1057 Number of Matches: 1

Range 1: 39 to 120

Score		Expect	Method	Identities	Positives	Gaps	Frame
136 bits	(342)	1e-34()	Compositional matrix adjus	st. 61/82(74%)	74/82(90%)	0/82(0%)	-3
Features	s:						
Query	246		SGPSGSGLIVIYPNTPSSISG +G SG+GLIV YPNTPSS++G				
Sbjct	39		TGASGTGLIVFYPNTPSSVAG				
Query	66		IKSSTLPAGVYALNGTF 1 +KSS++P+GVYAL GTF				
Sbjct	99		VKSSSIPSGVYALTGTF 12	10			

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: 37 to 118

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
136 bits(342)	1e-34()	Compositional matrix a	djust. 61/82(74%)	74/82(90%)	0/82(0%)	-3	
Features	:							
Query	246		SGPSGSGLIVIYPNTPSS					67
Sbjct	37		+G SG+GLIV YPNTPSS [.] rGASGTGLIVFYPNTPSS [,]					96
Query	66		IKSSTLPAGVYALNGTF	1				
Sbjct	97		+KSS++P+GVYAL GTF VKSSSIPSGVYALTGTF	118				

polyprotein precursor [Culex Y virus]

Sequence ID: gb|AFR34026.1| Length: 1057 Number of Matches: 1

Range 1: 39 to 120

Score		Expect M	lethod	Identities	Positives	Gaps	Fra	me
136 bits	(342)	1e-34() Co	ompositional matrix ac	ljust. 61/82(74%)	74/82(90%)	0/82(0%)	-3	
Features	S :							
Query	246		PSGSGLIVIYPNTPSSI SG+GLIV YPNTPSS+		~ ~			67
Sbjct	39		ASGTGLIVFYPNTPSSV		~ ~			98
Query	66	202-2-12	SSTLPAGVYALNGTF SS++P+GVYAL GTF	1				
Sbjct	99		SSSIPSGVYALTGTF	120				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAS79778.1| Length: 166 Number of Matches: 1

Range 1: 24 to 105

Score	Expect	Method	Identities	Positives	Gaps	Frame
97.8 bits(242)	3e-23()	Compositional matrix adjust.	44/82(54%)	61/82(74%)	0/82(0%)	-3

Features:

Query		+YNL+ SGSG++V +P P S +	GFHYVWNSNSSSWVFDQYIYTAQELKDSYDYGRLI G HY WN+N + FDQ++ T+Q+LK +++YGRLI	
Sbjct	24	SYNLEVSESGSGILVCFPGAPGSRT	GAHYRWNANQTGLEFDQWLETSQDLKKAFNYGRLI	83
Query	66	SGSLSIKSSTLPAGVYALNGTF 1		
		S I+SSTLPAG+YALNGT		
Sbjct	84	SRKYDIQSSTLPAGLYALNGTL 1	.05	

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAR99837.1| Length: 166 Number of Matches: 1

Range 1: 24 to 105

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits	(240)	7e-23() Compositional matrix adju	st. 45/82(55%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISG +YNL+ SGSGL+V +P P S G		DOYIYTAQEL		
Sbjct	24	SYNLEVSESGSGLLVCFPGAPGSRVG		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	84	SRKYDIQSSTLPAGLYALNGTL 10	5			

major structural protein VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AEX33173.1|** Length: 152 Number of Matches: 1 Range 1: 23 to 104

Score	Expect Method	Identities	Positives	Gaps	Frame
96.7 bits(23) 7e-23() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:					
Query 24	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEI FDO++ T+O+I		
Sbjct 23	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query 66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct 83	SRKYDIQSSTLPAGLYALNGTL 104				

major structural protein VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AEX33169.1| Length: 152 Number of Matches: 1

▶ See 33 more title(s) Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	7e-23() Compositional matrix adjust	t. 44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGE +YNL+ SGSG++V +P P S G		DOYIYTAQEL DO++ T+O+L		
Sbjct	23	SYNLEVSESGSGILVCFPGAPGSRIG				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83	SRKYDIQSSTLPAGLYALNGTL 104	1			

VP2 [Infectious pancreatic necrosis virus]

Sequence ID: gb|AEV91035.1| Length: 152 Number of Matches: 1

▶ See 9 more title(s) Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	7e-23() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Feature	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY				
Sbjct	23	+YNL+ SGSG++V +P P S G HY SYNLEVSESGSGILVCFPGAPGSRIGAHY		FDQ++ T+Q+L FDQWLETSQDL		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1				
Sbjct	83	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 104				

structural protein 2, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AFZ93414.1| Length: 358 Number of Matches: 1

▶ See 1 more title(s) Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
99.0 bits	s(245)	1e-22() Compositional matrix adju	st. 45/82(55%)	61/82(74%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISC		DOYIYTAQEL DO++ T+O+L		
Sbjct	12	SYNLEVSESGSGVLVCFPGAPSSRV				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93	3			

polyprotein [Infectious pancreatic necrosis virus serotype A5]

Sequence ID: emb|CAI54275.1| Length: 359 Number of Matches: 1

Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
99.0 bits	(245)	1e-22() Compositional matrix adjust.	45/82(55%)	61/82(74%)	0/82(0%)	-3
Features	3 :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P PSS G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	12	SYNLEVSESGSGVLVCFPGAPSSRVGAH				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

structural protein 2, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AFZ93413.1|** Length: 358 Number of Matches: 1 Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
99.0 bits	s(245)	1e-22() Compositional matrix adjust.	45/82(55%)	61/82(74%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P PSS G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	12	SYNLEVSESGSGVLVCFPGAPSSRVGAH		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1				
Sbjct	72	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAR99829.1| Length: 166 Number of Matches: 1

Range 1: 24 to 105

Score		Expect Method	Identities	Positives	Gaps	Frame
96.3 bits	s(238)	1e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQELDOH		
Sbjct	24	+YNL+ SGSG++V +P P S G HY SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	84	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 105				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAS79776.1| Length: 166 Number of Matches: 1

Range 1: 24 to 105

Score Expect Method Identities **Positives** Gaps Frame

96.3 bits	s(238)	1e-22() Compositional matrix adjust. 44/82(54%) 60/82(73%) 0/82(0%) -3	
Feature	s:			
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYVWNSNSSSWVFDQYIYTAQF +YNL+ SGSG++V +P P S G HY WN+N + FDQ++ T+Q+		67
Sbjct	24	SYNLEVSESGSGILVCFPGAPGSRIGAHYRWNANQTGLEFDQWLETSQI		83
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT		
Sbjct	84	SRKYDIQSSTLPAGLYALNGTL 105		

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAR99831.1| Length: 166 Number of Matches: 1

▶ See 7 more title(s) Range 1: 24 to 105

Score		Expect Method	Identities	Positives	Gaps	Frame
96.3 bits	s(238)	1e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY		~ ~		
Sbjct	24	+YNL+ SGSG++V +P P S G HY SYNLEVSESGSGILVCFPGAPGSRIGAHY		'DQ++ T+Q+L 'DQWLETSQDL		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S T+SSTLPAG+YALNGT				
Sbjct	84	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 105				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAR99839.1| Length: 166 Number of Matches: 1

Range 1: 24 to 105

Score		Expect Method	Identities	Positives	Gaps	Frame
96.3 bits	s(238)	2e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY				
Sbjct	24	SYNLEVSESGSGVLVCFPGAPGSRVGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	84	SRKYDIQSSTLPAGLYALNGTL 105				

VP2 [Infectious pancreatic necrosis virus]

Sequence ID: **gb|ACY35989.1|** Length: 260 Number of Matches: 1 Range 1: 26 to 107

Score	Expect Method	Identities	Positives	Gaps	Frame
97.8 bits(242)	2e-22() Compositional matrix adjust.	45/82(55%)	60/82(73%)	0/82(0%)	-3
Features:					
Query 246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYV +YNL+ SGSGL+V +P P S G HY		DQYIYTAQELDO		
Sbjct 26	SYNLEVSESGSGLLVCFPGAPGSRIGAHY				
Query 66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct 86	SRKYDIQSSTLPAGLYALNGTL 107				

major structural protein VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHC01907.1| Length: 152 Number of Matches: 1

▶ See 2 more title(s) Range 1: 23 to 104

Score	Expect Method	Identities	Positives	Gaps	Frame
95.5 bits(236)	2e-22() Compositional matrix adjust.	44/82(54%)	59/82(71%)	0/82(0%)	-3
Features:					
Query 246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY				
Sbjct 23	+YNL+ SGSGL+V +P P S G HY SYNLEVSDSGSGLLVCFPGAPGSRVGAHY				

Query 66 SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT Sbjct 83 SRKYDIQSSTLPAGLYALNGTL 104

major structural protein VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHC01920.1| Length: 152 Number of Matches: 1

Range 1: 23 to 104

Score	Expect Method	Identities	Positives	Gaps	Frame
95.1 bits(235	2e-22() Compositional matrix adjus	t. 44/82(54%)	59/82(71%)	0/82(0%)	-3
Features:					
Query 246	TYNLKSGPSGSGLIVIYPNTPSSISGI +YNL+ SGSG++V +P P S G		FDQYIYTAQEL FDO++ T+O+L		
Sbjct 23	SYNLEVSESGSGILVCFPGAPGSRIGA				
Query 66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct 83	SRKYDIQSSTLPAGLYALNGTL 104	4			

major structural protein VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHC01914.1| Length: 152 Number of Matches: 1

▶ See 5 more title(s) Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
95.1 bits	s(235)	3e-22() Compositional matrix adjust.	44/82(54%)	59/82(71%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY		~ ~		
Sbjct	23	+YNL+ SGSGL+V +P P S G HY SYNLEVSDSGSGLLVCFPGAPGSRVGAHY		~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1				
Sbjct	83	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 104				

VP2 [Infectious pancreatic necrosis virus]

Sequence ID: gb|ACY35990.1| Length: 260 Number of Matches: 1

Range 1: 26 to 107

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits(2	239)	4e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:						
Query 2	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct 2	26	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query (66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct 8	86	SRKYDIQSSTLPAGLYALNGTL 107				

major structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHE78005.1| Length: 377 Number of Matches: 1

Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
97.4 bits	s(241)	5e-22() Compositional matrix adjust.	45/82(55%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFF +YNL+ SGSGL+V +P P S G F				
Sbjct	23	SYNLEVSESGSGLLVCFPGAPGSRVGAR				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 104				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: emb|CAH18975.1| Length: 311 Number of Matches: 1

Range 1: 19 to 100

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits	s(240)	6e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY				
Sbjct	19	+YNL+ SGSG++V +P P S G HY SYNLEVSESGSGILVCFPGAPGSRIGAHY		FDQ++ T+Q+I FDQWLETSQDI		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	79	SRKYDIQSSTLPAGLYALNGTL 100				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AGC81929.1|** Length: 358 Number of Matches: 1 Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits	s(240)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAH				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: **emb|CAX62746.1|** Length: 341 Number of Matches: 1 Range 1: 17 to 98

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits	s(240)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY				
Sbjct	17	+YNL+ SGSG++V +P P S G HY SYNLEVSESGSGILVCFPGAPGSRIGAHY		FDQ++ T+Q+I FDQWLETSQDI		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	77	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 98				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAA92626.1|** Length: 556 Number of Matches: 1 Range 1: 57 to 138

Score		Expect Method	Identities	Positives	Gaps	Frame
99.0 bits	s(245)	7e-22() Compositional matrix adj	ust. 45/82(55%)	61/82(74%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSIS +YNL+ SGSGL+V +P P S				
Sbjct	57	SYNLEVSDSGSGLLVCFPGAPGSRV				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S T+SSTLPAG+YALNGT				
Sbjct	117	D I DDILLIO IIILIOI	.38			

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAl54268.1| Length: 359 Number of Matches: 1 Range 1: 12 to 93

Score	Expect Method	Identities	Positives	Gaps	Frame
97.1 bits(240)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:					
Query 246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY				
Sbjct 12	SYNLEVSESGSGILVCFPGAPGSRIGAHY				

Query 66 SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT Sbjct 72 SRKYDIQSSTLPAGLYALNGTL 93

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54262.1| Length: 359 Number of Matches: 1

Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits	(240)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	3 :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY				
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54250.1| Length: 337 Number of Matches: 1

Range 1: 5 to 86

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	5	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	65	SRKYDIQSSTLPAGLYALNGTL 86				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54260.1| Length: 359 Number of Matches: 1

Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits((240)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:	:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AGC81925.1| Length: 358 Number of Matches: 1

▶ See 3 more title(s) Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits	(240)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQEL		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1				
Sbjct	72	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAX62748.1| Length: 324 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFI				
Sbjct	11	+YNL+ SGSG++V +P P S G I SYNLEVSESGSGILVCFPGAPGSRIGAI		FDQ++ T+Q+I FDQWLETSQDI		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	71	SRKYDIQSSTLPAGLYALNGTL 92				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54259.1| Length: 334 Number of Matches: 1 Range 1: 7 to 88

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFH +YNL+ SGSG++V +P P S G H		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	7	SYNLEVSESGSGILVCFPGAPGSRIGAH				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	67	SRKYDIQSSTLPAGLYALNGTL 88				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54263.1| Length: 339 Number of Matches: 1

Range 1: 6 to 87

Score	Ex	ect	Method		Identities	Positives	Gaps	Fra	me
96.7 bits(2	39) 7e-	22()	Compositional matrix ad	ljust.	44/82(54%)	60/82(73%)	0/82(0%)	-3	
Features:									
Query 2		ILKS IL+	GPSGSGLIVIYPNTPSSI SGSG++V +P P S			DQYIYTAQEL DO++ T+O+L			67
Sbjct 6			SESGSGILVCFPGAPGSR						65
Query 6	6 SGS		KSSTLPAGVYALNGTF +SSTLPAG+YALNGT	1					
Sbjct 6				87					

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AGC81934.1|** Length: 358 Number of Matches: 1 Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits	(240)	7e-22() Compositional matrix adjust	t. 44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGE +YNL+ SGSG++V +P P S G		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGA				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54273.1| Length: 359 Number of Matches: 1

▶ See 1 more title(s) Range 1: 12 to 93

Score		Expect	Method	Identities	Positives	Gaps	Frame
97.1 bits	(240)	7e-22()	Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:						
Query	246	TYNLKS +YNL+	GPSGSGLIVIYPNTPSSISGFHY SGSG++V +P P S G HY		DOYIYTAQELDOH+ T+O+L		

Sbjct 12 SYNLEVSESGSGILVCFPGAPGSRIGAHYRWNANQTGLEFDQWLETSQDLKKAFNYGRLI 71

Query 66 SGSLSIKSSTLPAGVYALNGTF 1
S I+SSTLPAG+YALNGT
Sbjct 72 SRKYDIQSSTLPAGLYALNGTL 93

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54271.1| Length: 359 Number of Matches: 1

Range 1: 12 to 93

Score	Expect Method	Identities	Positives	Gaps	Frame
97.1 bits(240	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:					
Query 24	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct 12	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query 66	SGSLSIKSSTLPAGVYALNGTF 1				
Sbjct 72	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAX62744.1| Length: 330 Number of Matches: 1

Range 1: 6 to 87

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFH +YNL+ SGSG++V +P P S G H		FDQYIYTAQEI FDQ++ T+Q+I		
Sbjct	6	SYNLEVSESGSGILVCFPGAPGSRIGAH				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	66	SRKYDIQSSTLPAGLYALNGTL 87				

major capsid protein VP2 [Flounder aquabirnavirus DS]

Sequence ID: gb|AAQ82705.1| Length: 490 Number of Matches: 1

Range 1: 40 to 121

Score		Expect Method	Identities	Positives	Gaps	Frame
98.2 bits	s(243)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL++ SGSGL+V +P P S G HY		DQYIYTAQELDOH+ T+O+L		
Sbjct	40	SYNLEASDSGSGLLVCFPGAPGSRVGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S ++SSTLPAG+YALNGT				
Sbjct	100	SRKYDVQSSTLPAGLYALNGTL 121				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54256.1| Length: 343 Number of Matches: 1

Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	7e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFH +YNL+ SGSG++V +P P S G H		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAH				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

capsid protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AGB51152.1| Length: 393 Number of Matches: 1

Range 1: 29 to 110

Score		Expect Method	Identities	Positives	Gaps	Frame
97.1 bits	s(240)	8e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY				
Sbjct	29	+YNL+ SGSG++V +P P S G HY SYNLEVSDSGSGILVCFPGAPGSRVGAHY		FDQ++ T+Q+L FDQWLETSQDL		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	89	SRKYDIQSSTLPAGLYALNGTL 110				

VP2, partial [Infectious bursal disease virus]

Sequence ID: gb|ACO59489.1| Length: 122 Number of Matches: 1

Range 1: 28 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
93.2 bits	s(230)	8e-22() Compositional matrix adjust.	48/82(59%)	58/82(70%)	1/82(1%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY TYNL G +GSGLIV +P P SI G HY		DOYIYTAQEL DO + TAO L		
Sbjct	28	TYNLTVGDTGSGLIVFFPGFPGSIVGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S SL+++SSTLP GVYALNGT				
Sbjct	87	SRSLTVRSSTLPGGVYALNGTI 108				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAX62752.1| Length: 358 Number of Matches: 1

▶ See 4 more title(s) Range 1: 12 to 93

Score	Expect Method	Identities	Positives	Gaps	Frame
96.7 bits(239)	8e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:					
Query 246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct 12	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query 66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct 72	SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAl54254.1| Length: 359 Number of Matches: 1 Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	8e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAX62751.1| Length: 350 Number of Matches: 1

Range 1: 17 to 98

os Frame	
2(0%) -3	
YDYGRLI 67	
FNYGRLI 76	
Y	2(0%) -3 YDYGRLI 67 ++YGRLI

Query 66 SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT Sbjct 77 SRKYDIQSSTLPAGLYALNGTL 98

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAX62754.1| Length: 363 Number of Matches: 1

Range 1: 16 to 97

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	8e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	16	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	76	SRKYDIQSSTLPAGLYALNGTL 97				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54255.1| Length: 353 Number of Matches: 1

Range 1: 6 to 87

Score	Expec	t Method		Identities	Positives	Gaps	Frame
96.7 bits(23	e) 8e-22() Compositional matrix a	adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:							
Query 24	5 TYNLK +YNL+	SGPSGSGLIVIYPNTPSS SGSG++V +P P S			DOYIYTAQEL		
Sbjct 6		VSESGSGILVCFPGAPGS					
Query 66		IKSSTLPAGVYALNGTF I+SSTLPAG+YALNGT	1				
Sbjct 66		ITSSTLPAGTIALNGT	87				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54246.1| Length: 353 Number of Matches: 1

Range 1: 6 to 87

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits((239)	8e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:	:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYV +YNL+ SGSG++V +P P S G HY		DOYIYTAQEL DO++ T+O+L		
Sbjct	6	SYNLEVSESGSGILVCFPGAPGSRIGAHYI				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	66	SRKYDIQSSTLPAGLYALNGTL 87				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54245.1| Length: 366 Number of Matches: 1

Range 1: 12 to 93

Score	Expec	t Method		Identities	Positives	Gaps	Frame
96.7 bits(23	9) 8e-22() Compositional matrix a	adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:							
Query 2	6 TYNLK +YNL+	SGPSGSGLIVIYPNTPSS SGSG++V +P P S			DOYIYTAQEL DO++ T+O+L		
Sbjct 1		VSESGSGILVCFPGAPGS					
Query 6		IKSSTLPAGVYALNGTF I+SSTLPAG+YALNGT	1				
Sbjct 7	-	IQSSTLPAGLYALNGTL	93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAl54267.1| Length: 350 Number of Matches: 1

Range 1: 4 to 85

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	8e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Feature	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQELDOH+ T+O+L		
Sbjct	4	SYNLEVSESGSGILVCFPGAPGSRIGAH		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	64	SRKYDIQSSTLPAGLYALNGTL 85				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54264.1| Length: 352 Number of Matches: 1

Range 1: 5 to 86

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	8e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:						
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	5	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	65	SRKYDIQSSTLPAGLYALNGTL 86				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54266.1| Length: 351 Number of Matches: 1

Range 1: 4 to 85

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	8e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY				
Sbjct	4	+YNL+ SGSG++V +P P S G HY SYNLEVSESGSGILVCFPGAPGSRIGAHY		FDQ++ T+Q+L FDQWLETSQDL		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	64	SRKYDIQSSTLPAGLYALNGTL 85				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: **gb|ADB27125.1|** Length: 342 Number of Matches: 1 Range 1: 4 to 85

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits(2	239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:						
Query 2	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYV +YNL+ SGSG++V +P P S G HY		DQYIYTAQEL		
Sbjct '	4	SYNLEVSESGSGILVCFPGAPGSRIGAHYI				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	64	SRKYDIQSSTLPAGLYALNGTL 85				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAX62759.1| Length: 349 Number of Matches: 1

Range 1: 5 to 86

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	9e-22() Compositional matrix ac	djust. 44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSI +YNL+ SGSG++V +P P S		~ ~		
Sbjct	5	SYNLEVSESGSGILVCFPGAPGSF		'DQ++ T+Q+L 'DQWLETSQDL		
Query	66	SGSLSIKSSTLPAGVYALNGTF S I+SSTLPAG+YALNGT	1			
Sbjct	65	SRKYDIQSSTLPAGLYALNGTL	86			

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54261.1| Length: 364 Number of Matches: 1

Range 1: 13 to 94

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	9e-22() Compositional matrix adjust	st. 44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISG		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	13	+YNL+ SGSG++V +P P S G SYNLEVSESGSGILVCFPGAPGSRIG				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	73	SRKYDIQSSTLPAGLYALNGTL 94				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54247.1| Length: 346 Number of Matches: 1

Range 1: 6 to 87

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:						
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	6	SYNLEVSESGSGILVCFPGAPGSRIGAH		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	66	SRKYDIQSSTLPAGLYALNGTL 87				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54249.1| Length: 356 Number of Matches: 1

Range 1: 6 to 87

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits((239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:	:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	6	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	66	SRKYDIQSSTLPAGLYALNGTL 87				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: emb|CAH18976.1| Length: 367 Number of Matches: 1

Range 1: 15 to 96

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQEL DO++ T+O+L		
Sbjct	15	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	75	SRKYDIQSSTLPAGLYALNGTL 96				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54248.1| Length: 339 Number of Matches: 1

Range 1: 1 to 82

Score	Expect	Method	Identities	Positives	Gaps	Frame
96.7 bits(239)	9e-22()	Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3

Features:

Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYVWNSNSSSWVFDQYIYTAQELKDSYDYGRLI +YNL+ SGSG++V +P P S G HY WN+N + FDQ++ T+Q+LK +++YGRLI	67
Sbjct	1	SYNLEVSESGSGILVCFPGAPGSRIGAHYRWNANQTGLEFDQWLETSQDLKKAFNYGRLI	60
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT	
Sbict	61	SRKYDIOSSTLPAGLYALNGTL 82	

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAX62758.1| Length: 350 Number of Matches: 1

Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEI FDO++ T+O+I		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAH		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54257.1| Length: 354 Number of Matches: 1 Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEI FDO++ T+O+I		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAI54253.1| Length: 351 Number of Matches: 1 Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	3 :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEI FDO++ T+O+I		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAl46884.1| Length: 353 Number of Matches: 1

Range 1: 15 to 96

Score	Expect	Method		Identities	Positives	Gaps	Frame
96.7 bits(23	9) 9e-22()	Compositional matrix a	ıdjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:							
Query 24	6 TYNLK +YNL+	SGPSGSGLIVIYPNTPSS SGSG++V +P P S			DQYIYTAQEL DO++ T+O+L		
Sbjct 15		VSESGSGILVCFPGAPGS					
Query 66		IKSSTLPAGVYALNGTF I+SSTLPAG+YALNGT	1				
Sbjct 75		IQSSTLPAGLYALNGTL	96				

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQEL DO++ T+O+L		
Sbjct	23	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83	SRKYDIQSSTLPAGLYALNGTL 104				

major structural protein, partial [Infectious pancreatic necrosis virus] Sequence ID: **gb|AHE77992.1|** Length: 377 Number of Matches: 1

Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits(2	(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:						
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQELDOH		
Sbjct	23	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1				
Sbjct	83	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 104				

major structural protein, partial [Infectious pancreatic necrosis virus]
Sequence ID: **gb|AHE78010.1**| Length: 377 Number of Matches: 1

Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQEL DO++ T+O+L		
Sbjct	23	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83	SRKYDIQSSTLPAGLYALNGTL 104				

major structural protein, partial [Infectious pancreatic necrosis virus] Sequence ID: **gb|AHE77987.1|** Length: 377 Number of Matches: 1

▶ See 1 more title(s) Range 1: 23 to 104

Score	Expect Method	Identities	Positives	Gaps	Frame
96.7 bits(239)	9e-22() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:					
Query 246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct 23	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query 66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct 83	SRKYDIQSSTLPAGLYALNGTL 104				

major structural protein, partial [Infectious pancreatic necrosis virus] Sequence ID: **gb|AHE77994.1|** Length: 377 Number of Matches: 1

▶ See 1 more title(s) Range 1: 23 to 104

Score Expect Method Identities Positives Gaps Frame

96.7 DITS(239)	1e-21() Compositional matrix adjust. 44/82(54%) 60/82(73%) 0/82(0%) -3	
Features:		
Query 246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYVWNSNSSSWVFDQYIYTAQELKDSYDYGRLI 6 +YNL+ SGSG++V +P P S G HY WN+N + FDO++ T+O+LK +++YGRLI	57
Sbjct 23		32
Query 66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT	
Sbjct 83	SRKYDIQSSTLPAGLYALNGTL 104	

major structural protein, partial [Infectious pancreatic necrosis virus] Sequence ID: **gb|AHE77996.1|** Length: 377 Number of Matches: 1 Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQELDOH		
Sbjct	23	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83	SRKYDIQSSTLPAGLYALNGTL 104				

major structural protein, partial [Infectious pancreatic necrosis virus] Sequence ID: **gb|AHE77991.1|** Length: 377 Number of Matches: 1 Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQEL DO++ T+O+L		
Sbjct	23	SYNLEVSESGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1				
Sbjct	83	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 104				

major structural protein, partial [Infectious pancreatic necrosis virus] Sequence ID: **gb|AHE77989.1|** Length: 377 Number of Matches: 1 Range 1: 23 to 104

Score	Expect Method	Identities	Positives	Gaps	Frame
96.7 bits(23) 1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:					
Query 24	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQEL		
Sbjct 23	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query 66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct 83	SRKYDIQSSTLPAGLYALNGT 104				

major structural protein, partial [Infectious pancreatic necrosis virus] Sequence ID: **gb|AHE77990.1|** Length: 377 Number of Matches: 1 Range 1: 23 to 104

Sco	ore	Expect Method	Identities	Positives	Gaps	Frar	ne
96.	7 bits(239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3	
Fea	itures:						
Que	ery 246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DQYIYTAQEL DQ++ T+Q+L			67
Sbj	jct 23	SYNLEVSESGSGILVCFPGAPGSRIGAHY					82
Que	ery 66	SGSLSIKSSTLPAGVYALNGTF 1					
Sbj	jct 83	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 104					

polyprotein [Infectious pancreatic necrosis virus - Sp]

Sequence ID: emb|CAX62755.1| Length: 368 Number of Matches: 1

Range 1: 17 to 98

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	17	SYNLEVSESGSGILVCFPGAPGSRIGAH				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	77	SRKYDIQSSTLPAGLYALNGTL 98				

major structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHE78012.1| Length: 377 Number of Matches: 1

Range 1: 23 to 104

Score	Expec	t Method	Identities	Positives	Gaps	Frame
96.7 bits(23	9) 1e-21() Compositional matrix a	djust. 44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:						
Query 2	6 TYNLF	SGPSGSGLIVIYPNTPSS - SGSG++V +P P S		DOYIYTAQEL		
Sbjct 2		CVSESGSGILVCFPGAPGS		~ ~		
Query 6		SIKSSTLPAGVYALNGTF	1			
Sbjct 8	S SRKYI	I+SSTLPAG+YALNGT DIQSSTLPAGLYALNGTL	104			

major structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHE78002.1| Length: 377 Number of Matches: 1

▶ See 1 more title(s) Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Feature	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY		~ ~		
Sbjct	23	+YNL+ SGSG++V +P P S G HY SYNLEVSESGSGILVCFPGAPGSRIGAHY		TDQ++ T+Q+L TDQWLETSQDL		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83	SRKYDIQSSTLPAGLYALNGTL 104				

major structural protein, partial [Infectious pancreatic necrosis virus] Sequence ID: **gb|AHE77984.1|** Length: 377 Number of Matches: 1

▶ See 1 more title(s) Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	1e-21() Compositional matrix adj	ust. 44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSIS				
Sbjct	23	+YNL+ SGSG++V +P P S SYNLEVSESGSGILVCFPGAPGSRI		TDQ++ T+Q+L TDQWLETSQDL		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83		.04			

major structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHE77993.1| Length: 377 Number of Matches: 1

Range 1: 23 to 104

Score Expect Method Identities Positives Gaps Frame

96.7 bits(239) 1e-21() Compositional matrix adjust. 44/82(54%) 60/82(73%) 0/82(0%) -3

Features:

Query 246 TYNLKSGPSGSGLIVIYPNTPSSISGFHYVWNSNSSSWVFDQYIYTAQELKDSYDYGRLI 67
+YNL+ SGSG++V +P P S G HY WN+N + FDQ++ T+Q+LK +++YGRLI
Sbjct 23 SYNLEVSESGSGILVCFPGAPGSRIGAHYRWNANQTGLEFDQWLETSQDLKKAFNYGRLI 82

Query 66 SGSLSIKSSTLPAGVYALNGTF 1
S I+SSTLPAG+YALNGT
Sbjct 83 SRKYDIQSSTLPAGLYALNGTL 104

major structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHE78003.1| Length: 377 Number of Matches: 1

Range 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	s(239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	23	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83	SRKYDIQSSTLPAGLYALNGTL 104				

polyprotein [Infectious pancreatic necrosis virus]

Sequence ID: emb|CAD32967.1| Length: 972 Number of Matches: 1

Range 1: 40 to 121

Score		Expect Method	Identities	Positives	Gaps	Frame
99.4 bits	(246)	1e-21() Composition-based stats.	46/82(56%)	60/82(73%)	0/82(0%)	-3
Features	:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSGL+V +P P S G HY				
Sbjct	40	SYNLEVSESGSGLLVCFPGAPGSRVGAH		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	100	SRKYDIQSSTLPAGLYALNGTL 121				

VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AFN26747.1| Length: 393 Number of Matches: 1

Range 1: 29 to 110

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	3 :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQEL DO++ T+O+L		
Sbjct	29	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	89	SRKYDIQSSTLPAGLYALNGTL 110				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AGC81930.1| Length: 358 Number of Matches: 1

Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
96.3 bits	s(238)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct	12	SYNLEVSXSGSGILVCFPGAPGSRIGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

Range 1: 20 to 101

Score		Expect Method	Identities	Positives	Gaps	Frame
96.3 bits	s(238)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DQYIYTAQELDOH+ T+O+L		
Sbjct	20	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	80	SRKYDIQSSTLPAGLYALNGTL 101				

VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AFN26744.1| Length: 393 Number of Matches: 1

Range 1: 29 to 110

Score	Expect Method	Identities	Positives	Gaps	Frame
96.7 bits(239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:					
Query 246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEL FDO++ T+O+L		
Sbjct 29	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query 66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct 89	SRKYDIQSSTLPAGLYALNGTL 110				

major structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AHE78007.1| Length: 377 Number of Matches: 1

▶ See 1 more title(s) Kange 1: 23 to 104

Score		Expect Method	Identities	Positives	Gaps	Frame
96.3 bits	s(238)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYV		~ ~		
Sbjct	23	+YNL+ SGSG++V +P P S G HY SYNLEVSESGSGILVCFPGAPGSRIGAHYF		'DQ++ T+Q+L 'DQWLETSQDL		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	83	SRKYDIQSSTLPAGLYALNGTL 104				

VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AFN26745.1| Length: 393 Number of Matches: 1

Range 1: 29 to 110

Score		Expect Method	Identities	Positives	Gaps	Fram	1e
96.7 bits	(239)	1e-21() Compositional matrix adj	just. 44/82(54%)	60/82(73%)	0/82(0%)	-3	
Features							
Query	246	TYNLKSGPSGSGLIVIYPNTPSSIS +YNL+ SGSG++V +P P S		DQYIYTAQELI			67
Sbjct	29	SYNLEVSESGSGILVCFPGAPGSRI					88
Query	66	SGSLSIKSSTLPAGVYALNGTF	L				
Sbjct	89	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL	110				

VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AFN26742.1|** Length: 393 Number of Matches: 1 Range 1: 29 to 110

Score	Expect	Method	Identities	Positives	Gaps	Frame
96.7 bits(239)	1e-21()	Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3

Features:

Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYVWNSNSSSWVFDQYIYTAQELKDSYDYGRLI +YNL+ SGSG++V +P P S G HY WN+N + FDQ++ T+Q+LK +++YGRLI	67
Sbjct	29	SYNLEVSESGSGILVCFPGAPGSRIGAHYRWNANQTGLEFDQWLETSQDLKKAFNYGRLI	88
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT	
Sbjct	89	SRKYDIQSSTLPAGLYALNGTL 110	

VP2, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AFN26746.1|** Length: 393 Number of Matches: 1 Range 1: 29 to 110

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits((239)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features:						
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		DOYIYTAQELDO		
Sbjct	29	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	89	SRKYDIQSSTLPAGLYALNGTL 110				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AGC81935.1|** Length: 358 Number of Matches: 1 Range 1: 12 to 93

Score		Expect Method	Identities	Positives	Gaps	Frame
96.3 bits	s(238)	1e-21() Compositional matrix adjust.	44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSG++V +P P S G HY		FDQYIYTAQEI FDO++ T+O+I		
Sbjct	12	SYNLEVSESGSGILVCFPGAPGSRIGAHY		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	72	SRKYDIQSSTLPAGLYALNGTL 93				

VP2 [Infectious pancreatic necrosis virus]

Sequence ID: **gb|ACY35988.1|** Length: 260 Number of Matches: 1 Range 1: 26 to 107

Score		Expect Method	Identities	Positives	Gaps	Frame
95.5 bits	(236)	1e-21() Compositional matrix adjust.	44/82(54%)	59/82(71%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSGL+V +P P S G HY		FDQYIYTAQEL FD+++ T+O+L		
Sbjct	26	SYNLEVSDSGSGLLVCFPGAPGSRVGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	86	SRKYDIQSSTLPAGLYALNGTL 107				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AJK26914.1| Length: 442 Number of Matches: 1

▶ See 1 more title(s) Range 1: 40 to 121

Score		Expect Method	Identities	Positives	Gaps	Frame
96.7 bits	(239)	2e-21() Compositional matrix adju	ust. 44/82(54%)	60/82(73%)	0/82(0%)	-3
Features	3 :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSIS +YNL+ SGSG++V +P P S		DOYIYTAQEL		
Sbjct	40	SYNLEVSESGSGILVCFPGAPGSRI				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	100		21			

polyprotein, partial [Tellina virus 2]

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

Range 1: 40 to 121

Score		Expect Method	Identities	Positives	Gaps	Frame
98.6 bits	s(244)	2e-21() Composition-based stats.	45/82(55%)	61/82(74%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFH +YNL+ SGSG++V +P PSS G H		FDQYIYTAQEI FDO++ T+O+1		
Sbjct	40	+YNL+ SGSG++V +P PSS G H SYNLEVSESGSGVLVCFPGAPSSRVGAH		~ ~		
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	100	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 121				

VP2 structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAK16604.1| Length: 538 Number of Matches: 1

Range 1: 40 to 121

Score		Expect Method	Identities	Positives	Gaps	Frame
97.4 bits	s(241)	2e-21() Compositional matrix adjust.	45/82(55%)	60/82(73%)	0/82(0%)	-3
Features	S :					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY +YNL+ SGSGL+V +P P S G HY				
Sbjct	40	SYNLEVSESGSGLLVCFPGAPGSRVGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	100	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 121				

polyprotein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAA92631.1| Length: 539 Number of Matches: 1

Range 1: 40 to 121

Score		Expect Method	Identities	Positives	Gaps	Frame
97.4 bits	s(241)	2e-21() Compositional matrix adjust.	45/82(55%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHY		~ ~		
Sbjct	40	+YNL+ SGSGL+V +P P S G HY SYNLEVSESGSGLLVCFPGAPGSRVGAHY				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT				
Sbjct	100	SRKYDIQSSTLPAGLYALNGTL 121				

VP2 structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: gb|AAK16601.1| Length: 538 Number of Matches: 1

Range 1: 40 to 121

Score		Expect Method	Identities	Positives	Gaps	Frame
97.4 bits	s(241)	2e-21() Compositional matrix adj	ust. 45/82(55%)	60/82(73%)	0/82(0%)	-3
Features	s:					
Query	246	TYNLKSGPSGSGLIVIYPNTPSSIS +YNL+ SGSGL+V +P P S				
Sbjct	40	SYNLEVSESGSGLLVCFPGAPGSRV				
Query	66	SGSLSIKSSTLPAGVYALNGTF 1 S I+SSTLPAG+YALNGT	L			
Sbjct	100		121			

VP2 structural protein, partial [Infectious pancreatic necrosis virus]

Sequence ID: **gb|AAK16602.1|** Length: 538 Number of Matches: 1

Range 1: 40 to 121

Score	Expect	Method	Identities	Positives	Gaps	Frame
97.4 bits(241)	2e-21()	Compositional matrix adjust.	45/82(55%)	60/82(73%)	0/82(0%)	-3
Features:						

Query	246	TYNLKSGPSGSGLIVIYPNTPSSISGFHYVWNSNSSSWVFDQYIYTAQELKDSYDYGRLI	67
Sbjct	40	+YNL+ SGSGL+V +P P S G HY WN N ++ FDQ++ T+Q+LK +++YGRLI SYNLEVSESGSGLLVCFPGAPGSRVGAHYRWNLNQTALEFDQWLETSQDLKKAFNYGRLI	99
Query	66	SGSLSIKSSTLPAGVYALNGTF 1	
Sbjct	100	S I+SSTLPAG+YALNGT SRKYDIQSSTLPAGLYALNGTL 121	