BLAST ®

Basic Local Alignment Search Tool

Nucleotide Sequence (2139 letters)

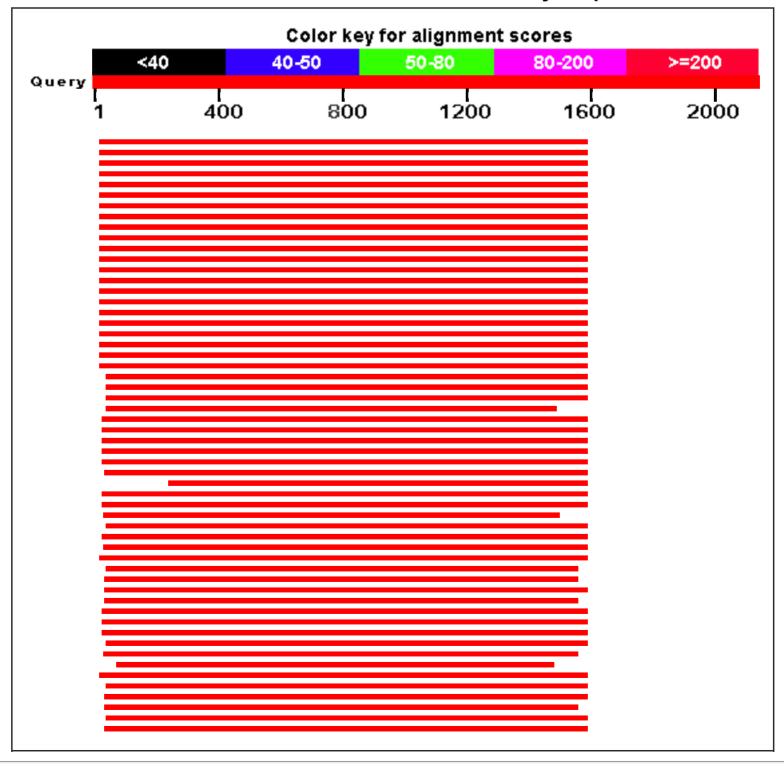|				
RID	B8BX5ZMH015 (Expires on 02-06 12:14 pm)			
Query ID	lcl|Query_247823	**Database Name**	nr	
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects	
Molecule type	nucleic acid			
Query Length	2139	**Program**	BLASTX 2.3.1+	
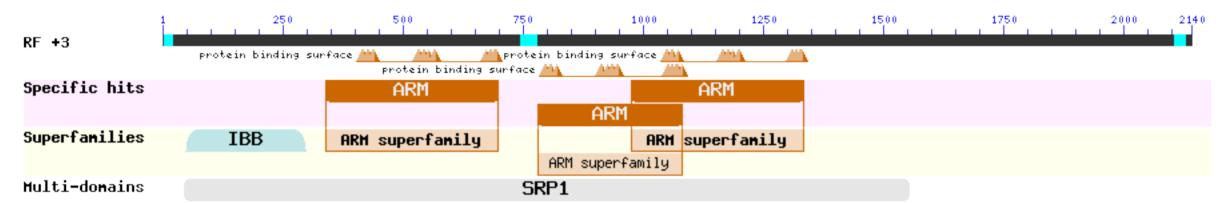
⊟ Graphic Summary

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

Distribution of 100 Blast Hits on the Query Sequence

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
pendulin [Drosophila melanogaster]	1051	1051	73%	0.0	100%	NP_477041.1
pendulin (NLS-receptor) [Drosophila melanogaster]	1047	1047	73%	0.0	99%	AAA85260.1
uncharacterized protein Dsimw501_GD23655 [Drosophila simulans]	1043	1043	73%	0.0	99%	KMY89395.1
GM17916 [Drosophila sechellia]	1041	1041	73%	0.0	99%	XP_002036427.1
uncharacterized protein Dere_GG10083 [Drosophila erecta]	1040	1040	73%	0.0	99%	XP_001969394.1
GD23655 [Drosophila simulans]	1029	1029	73%	0.0	98%	XP_002078865.1
uncharacterized protein Dyak_GE18896 [Drosophila yakuba]	992	992	73%	0.0	96%	XP_002089023.1
alpha Karyopherin-2 [Drosophila ananassae]	992	992	73%	0.0	96%	XP_001963034.1
GL18958 [Drosophila persimilis]	989	989	73%	0.0	96%	XP_002014430.1
uncharacterized protein Dpse_GA18440 [Drosophila pseudoobscura pseudoobscura]	986	986	73%	0.0	96%	XP_001356313.1
uncharacterized protein Dmoj_GI17589 [Drosophila mojavensis]	954	954	73%	0.0	89%	XP_002002818.1
alpha Karyopherin-2 [Drosophila virilis]	950	950	73%	0.0	92%	XP_002057743.2
GH11072 [Drosophila grimshawi]	939	939	73%	0.0	89%	XP_001988267.1
uncharacterized protein Dwil_GK18399 [Drosophila willistoni]	926	926	73%	0.0	90%	XP_002074226.1
Pen [Drosophila busckii]	923	923	73%	0.0	89%	ALC39141.1
Importin subunit alpha [Lucilia cuprina]	895	895	73%	0.0	84%	KNC33852.1
PREDICTED: importin subunit alpha [Bactrocera dorsalis]	878	878	73%	0.0	83%	XP_011202013.1
PREDICTED: importin subunit alpha [Musca domestica]	871	871	73%	0.0	84%	XP_005185058.1
PREDICTED: importin subunit alpha [Bactrocera oleae]	871	871	73%	0.0	83%	XP_014087960.1
PREDICTED: importin subunit alpha [Bactrocera cucurbitae]	865	865	73%	0.0	84%	XP_011188423.1
PREDICTED: importin subunit alpha [Stomoxys calcitrans]	858	858	73%	0.0	84%	XP_013105904.1
PREDICTED: importin subunit alpha [Ceratitis capitata]	855	855	73%	0.0	81%	XP_004527197.1
AAEL012960-PA [Aedes aegypti]	660	660	72%	0.0	63%	XP_001663145.1
importin alpha [Anopheles darlingi]	654	654	72%	0.0	62%	ETN61562.1
AGAP009792-PA [Anopheles gambiae str. PEST]	651	651	72%	0.0	62%	XP_318886.3
AGAP009792-PA-like protein [Anopheles sinensis]	620	620	67%	0.0	62%	KFB49217.1
PREDICTED: importin subunit alpha [Microplitis demolitor]	575	575	72%	0.0	57%	XP_008555196.1
PREDICTED: importin subunit alpha [Fopius arisanus]	566	566	72%	0.0	57%	XP_011305770.1
PREDICTED: importin subunit alpha [Diachasma alloeum]	565	565	72%	0.0	56%	XP_015123786.1
PREDICTED: importin subunit alpha [Orussus abietinus]	551	551	72%	0.0	54%	XP_012276606.1
Importin subunit alpha-2 [Zootermopsis nevadensis]	546	546	72%	0.0	54%	KDR18936.1
PREDICTED: importin subunit alpha [Nasonia vitripennis]	544	544	72%	0.0	55%	XP_008204292.1
GH20236 [Drosophila grimshawi]	540	540	62%	0.0	63%	XP_001986958.1
PREDICTED: importin subunit alpha [Athalia rosae]	538	538	72%	0.0	54%	XP_012257423.1
PREDICTED: importin subunit alpha [Apis florea]	535	535	72%	1e-179	55%	XP_003698390.1
PREDICTED: importin subunit alpha [Polistes canadensis]	535	535	68%	3e-179	57%	XP_014609001.1
PREDICTED: importin subunit alpha-1 [Ceratosolen solmsi marchali]	533	533	72%	1e-178	54%	XP_011500399.1
PREDICTED: importin subunit alpha-like [Apis dorsata]	533	533	72%	1e-178	55%	XP_006608944.1

PREDICTED: importin subunit alpha [Polistes dominula]	533	533	72%	1e-178	54%	XP_015191390.1
PREDICTED: importin subunit alpha-1 [Copidosoma floridanum]	531	531	73%	6e-178	52%	XP_014209910.1
PREDICTED: importin subunit alpha [Cerapachys biroi]	530	530	70%	9e-178	53%	XP_011339385.1
PREDICTED: importin subunit alpha [Harpegnathos saltator]	529	529	71%	3e-177	55%	XP_011146718.1
importin subunit alpha-2-like protein [Lasius niger]	529	529	72%	4e-177	53%	KMR04943.1
PREDICTED: importin subunit alpha-1 [Trichogramma pretiosum]	528	528	70%	5e-177	53%	XP_014230579.1
Importin subunit alpha-2 [Habropoda laboriosa]	527	527	72%	2e-176	54%	KOC64063.1
PREDICTED: importin subunit alpha [Bombus impatiens]	524	524	72%	2e-175	54%	XP_003484488.1
PREDICTED: importin subunit alpha [Bombus terrestris]	524	524	72%	4e-175	54%	XP_003399525.1
PREDICTED: importin subunit alpha-1 [Strongylocentrotus purpuratus]	523	523	72%	5e-175	51%	XP_011662338.1
PREDICTED: importin subunit alpha [Megachile rotundata]	523	523	71%	7e-175	56%	XP_003704950.1
uncharacterized protein Dwil_GK23224 [Drosophila willistoni]	519	519	65%	9e-174	58%	XP_002074732.1
PREDICTED: importin subunit alpha-1-like [Lingula anatina]	518	518	73%	6e-173	54%	XP_013403921.1
hypothetical protein DAPPUDRAFT_301494 [Daphnia pulex]	518	518	72%	1e-172	53%	EFX68294.1
PREDICTED: importin subunit alpha [Dinoponera quadriceps]	517	517	72%	2e-172	53%	XP_014479013.1
PREDICTED: importin subunit alpha [Solenopsis invicta]	516	516	71%	3e-172	53%	XP_011158592.1
PREDICTED: LOW QUALITY PROTEIN: importin subunit alpha-1-like [Limulus polyphemus]	516	516	72%	5e-172	52%	XP_013787969.1
Importin subunit alpha-2 [Stegodyphus mimosarum]	515	515	72%	1e-171	52%	KFM56942.1
importin alpha [Culex quinquefasciatus]	512	512	54%	2e-171	66%	XP_001847920.1
PREDICTED: importin subunit alpha-5 [Tribolium castaneum]	509	509	71%	1e-169	53%	XP_975293.1
PREDICTED: importin subunit alpha [Monomorium pharaonis]	509	509	70%	5e-169	53%	XP_012526791.1
PREDICTED: importin subunit alpha-1 [Acromyrmex echinatior]	507	507	71%	1e-168	52%	XP_011056602.1
PREDICTED: importin subunit alpha [Wasmannia auropunctata]	507	507	72%	1e-168	51%	XP_011706521.1
PREDICTED: importin subunit alpha [Vollenhovia emeryi]	507	507	71%	1e-168	52%	XP_011877264.1
hypothetical protein CAPTEDRAFT_169892 [Capitella teleta]	505	505	73%	6e-168	51%	ELU00226.1
GH11093 [Drosophila grimshawi]	502	502	57%	7e-168	67%	XP_001988308.1
PREDICTED: importin subunit alpha-1 [Atta cephalotes]	505	505	71%	9e-168	51%	XP_012061550.1
importin subunit alpha-1 [Danio rerio]	503	503	71%	4e-167	51%	NP_001002335.1
PREDICTED: importin subunit alpha-1 [Linepithema humile]	502	502	70%	1e-166	52%	XP_012217870.1
PREDICTED: importin subunit alpha-1 isoform X2 [Xenopus tropicalis]	501	501	71%	2e-166	51%	XP_012821933.1
PREDICTED: importin subunit alpha-1 [Pseudopodoces humilis]	501	501	70%	4e-166	51%	XP_014111239.1
PREDICTED: importin subunit alpha-1-like [Cyprinodon variegatus]	500	500	72%	6e-166	50%	XP_015243393.1
hypothetical protein D910_08772 [Dendroctonus ponderosae]	500	500	72%	7e-166	51%	ERL91442.1
PREDICTED: importin subunit alpha-1 [Cimex lectularius]	500	500	72%	9e-166	51%	XP_014253052.1
importin subunit alpha-1 [Xenopus tropicalis]	500	500	71%	1e-165	51%	NP_001008155.1
Importin subunit alpha-2 [Melipona quadrifasciata]	499	499	72%	1e-165	53%	KOX75105.1
PREDICTED: importin subunit alpha-1 [Halyomorpha halys]	499	499	70%	1e-165	53%	XP_014270997.1
PREDICTED: importin subunit alpha-1 [Buceros rhinoceros silvestris]	499	499	70%	1e-165	51%	XP_010138696.1
PREDICTED: importin subunit alpha-1 [Apteryx australis						

Description	Max Score	Total Score	Query Cover	E value	Ident	Accession
mantelli]	499	499	70%	2e-165	50%	XP_013808591.1
PREDICTED: importin subunit alpha-1 isoform X2 [Monodelphis domestica]	499	499	72%	2e-165	51%	XP_007482848.1
karyopherin alpha-2 subunit like [Xenopus laevis]	499	499	71%	3e-165	50%	NP_001080433.1
PREDICTED: importin subunit alpha-1 [Struthio camelus australis]	498	498	70%	4e-165	50%	XP_009677268.1
PREDICTED: importin subunit alpha-1 [Tinamus guttatus]	498	498	70%	4e-165	50%	XP_010216879.1
PREDICTED: importin subunit alpha-1 [Sturnus vulgaris]	498	498	70%	4e-165	51%	XP_014738197.1
PREDICTED: importin subunit alpha-1 [Corvus cornix cornix]	498	498	70%	4e-165	50%	XP_010405672.1
Importin subunit alpha-1 [Cathartes aura]	498	498	70%	4e-165	51%	KFP51772.1
PREDICTED: importin subunit alpha-1 [Leptosomus discolor]	498	498	70%	4e-165	50%	XP_009948935.1
PREDICTED: importin subunit alpha-1 [Pelodiscus sinensis]	498	498	70%	5e-165	51%	XP_006110655.1
PREDICTED: importin subunit alpha-1 [Chaetura pelagica]	498	498	71%	6e-165	50%	XP_010000998.1
PREDICTED: importin subunit alpha-1 [Manacus vitellinus]	498	498	70%	7e-165	50%	XP_008920062.1
PREDICTED: importin subunit alpha-1 [Picoides pubescens]	498	498	70%	8e-165	50%	XP_009900980.1
PREDICTED: importin subunit alpha-1 [Caprimulgus carolinensis]	498	498	70%	8e-165	50%	XP_010165233.1
PREDICTED: importin subunit alpha-1 [Ornithorhynchus anatinus]	498	498	72%	8e-165	50%	XP_001509792.1
Importin subunit alpha-1 [Corvus brachyrhynchos]	498	498	70%	8e-165	51%	KFO62143.1
PREDICTED: importin subunit alpha-1 [Serinus canaria]	497	497	70%	1e-164	51%	XP_009092579.1
PREDICTED: importin subunit alpha-1 [Tyto alba]	497	497	71%	1e-164	50%	XP_009970687.1
PREDICTED: importin subunit alpha-1 [Aptenodytes forsteri]	497	497	70%	1e-164	51%	XP_009285978.1
PREDICTED: importin subunit alpha-1 [Nipponia nippon]	497	497	71%	1e-164	50%	XP_009465206.1
PREDICTED: importin subunit alpha-5-like [Chelonia mydas]	497	497	72%	1e-164	50%	XP_007062787.1
PREDICTED: importin subunit alpha-1 [Chelonia mydas]	497	497	70%	1e-164	50%	XP_007055158.1
PREDICTED: importin subunit alpha-1 isoform X1 [Monodelphis domestica]	499	499	72%	2e-164	51%	XP_001379295.3
PREDICTED: LOW QUALITY PROTEIN: importin subunit alpha-1-like [Corvus brachyrhynchos]	498	498	70%	2e-164	51%	XP_008635795.1

Alignments

pendulin [Drosophila melanogaster]
Sequence ID: ref|NP_477041.1| Length: 522 Number of Matches: 1

▸ See 4 more title(s)
Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
1051 bits(2717)	0.0()	Compositional matrix adjust.	522/522(100%)	522/522(100%)	0/522(0%)	+3

Features:

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Query  24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
            MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct  1    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  60

Query  204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
            LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
            LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG
Sbjct  121  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  180

Query  564  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
            NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR
Sbjct  181  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  240

Query  744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
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Sbjct  241    LLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV
              LLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  300

Query  924    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
              PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ
Sbjct  301    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  360

Query  1104   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
              AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD
Sbjct  361    AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD  420

Query  1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA
Sbjct  421    TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  480

Query  1464   IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    1589
              IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  481    IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    522
```

pendulin (NLS-receptor) [Drosophila melanogaster]

Sequence ID: **gb|AAA85260.1|** Length: 522 Number of Matches: 1

Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
1047 bits(2707)	0.0()	Compositional matrix adjust.	521/522(99%)	521/522(99%)	0/522(0%)	+3

Features:

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Query  24     MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
              MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct  1      MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  60

Query  204    LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
              LNGQSPVQ SVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61     LNGQSPVQPSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384    LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
              LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG
Sbjct  121    LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  180

Query  564    NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
              NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR
Sbjct  181    NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  240

Query  744    llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
              LLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV
Sbjct  241    LLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  300

Query  924    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
              PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ
Sbjct  301    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  360

Query  1104   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
              AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD
Sbjct  361    AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD  420

Query  1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA
Sbjct  421    TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  480

Query  1464   IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    1589
              IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  481    IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    522
```

uncharacterized protein Dsimw501_GD23655 [Drosophila simulans]

Sequence ID: **gb|KMY89395.1|** Length: 522 Number of Matches: 1

Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
1043 bits(2698)	0.0()	Compositional matrix adjust.	518/522(99%)	520/522(99%)	0/522(0%)	+3

Features:

```
Query  24     MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
              MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct  1      MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  60

Query  204    LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
              LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61     LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384    LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
              LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKS+NLAEQAVWALG
Sbjct  121    LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSINLAEQAVWALG  180

Query  564    NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
              NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QVKR
Sbjct  181    NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQVKR  240

Query  744    llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
              LLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV
Sbjct  241    LLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  300

Query  924    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
              PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ
Sbjct  301    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  360
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```
Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
             AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD
Sbjct  361   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  420

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA
Sbjct  421   AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  480

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF       1589
             IIDTYFSN DDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  481   IIDTYFSNADDEAEQELAPQEVNGALEFNATQPKAPEGGYTF       522
```

GM17916 [Drosophila sechellia]

Sequence ID: **ref|XP_002036427.1|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
1041 bits(2693)	0.0()	Compositional matrix adjust.	517/522(99%)	520/522(99%)	0/522(0%)	+3

Features:

```
Query  24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
             MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct  1     MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  60

Query  204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
             LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61    LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
             LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKS+NLAEQAVWALG
Sbjct  121   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSINLAEQAVWALG  180

Query  564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
             NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QVKR
Sbjct  181   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQVKR  240

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
             LLPVLSQLLLSQDIQVLADACWALSYVTDDDN+KIQAVVDSDAVPRLVKLLQMDEPSIIV
Sbjct  241   LLPVLSQLLLSQDIQVLADACWALSYVTDDDNSKIQAVVDSDAVPRLVKLLQMDEPSIIV  300

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
             PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ
Sbjct  301   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  360

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
             AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD
Sbjct  361   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  420

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA
Sbjct  421   AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  480

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF       1589
             IIDTYFSN DDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  481   IIDTYFSNADDEAEQELAPQEVNGALEFNATQPKAPEGGYTF       522
```

uncharacterized protein Dere_GG10083 [Drosophila erecta]

Sequence ID: **ref|XP_001969394.1|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
1040 bits(2689)	0.0()	Compositional matrix adjust.	516/522(99%)	519/522(99%)	0/522(0%)	+3

Features:

```
Query  24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
             MSKADSNSRQGSYKAN+INTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct  1     MSKADSNSRQGSYKANTINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  60

Query  204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
             LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61    LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
             LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKS NLAEQAVWALG
Sbjct  121   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSTNLAEQAVWALG  180

Query  564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
             NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QVKR
Sbjct  181   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQVKR  240

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
             LLPVLSQLLLSQDIQVLADACWALSYVTDDDN+KIQAVVDSDAVPRLVKLLQMDEPSIIV
Sbjct  241   LLPVLSQLLLSQDIQVLADACWALSYVTDDDNSKIQAVVDSDAVPRLVKLLQMDEPSIIV  300

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
             PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ
Sbjct  301   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  360
```

```
Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
             AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD
Sbjct  361  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  420

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA
Sbjct  421  AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  480

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             IIDTYFSN DDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  481  IIDTYFSNADDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   522
```

GD23655 [Drosophila simulans]

Sequence ID: **ref|XP_002078865.1|** Length: 524 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 524

Score	Expect	Method	Identities	Positives	Gaps	Frame
1029 bits(2661)	0.0()	Compositional matrix adjust.	515/524(98%)	517/524(98%)	2/524(0%)	+3

Features:

```
Query  24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
            MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct  1   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  60

Query  204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
            LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIG GIVPICIRF
Sbjct  61  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGKGIVPICIRF  120

Query  384  LQNT--NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWA  557
            LQNT    NSMLQF AAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKS+NLAEQAVWA
Sbjct  121  LQNTFITNSMLQFLAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSINLAEQAVWA  180

Query  558  LGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQV  737
            LGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QV
Sbjct  181  LGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQV  240

Query  738  KRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSI  917
            KRLLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSI
Sbjct  241  KRLLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSI  300

Query  918  IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ  1097
            IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ
Sbjct  301  IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ  360

Query  1098  IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDL  1277
             IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDL
Sbjct  361  IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDL  420

Query  1278  LDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA  1457
             LD KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA
Sbjct  421  LDAKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA  480

Query  1458  YAIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             YAIIDTYFSN DDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  481  YAIIDTYFSNADDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   524
```

uncharacterized protein Dyak_GE18896 [Drosophila yakuba]

Sequence ID: **ref|XP_002089023.1|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
992 bits(2565)	0.0()	Compositional matrix adjust.	499/522(96%)	507/522(97%)	0/522(0%)	+3

Features:

```
Query  24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
            MSKADSNSRQGSYKAN+INTQDSRMRRHEVT+ELRK+KKEDQMFKRRNINDEDLTSPLKE
Sbjct  1   MSKADSNSRQGSYKANTINTQDSRMRRHEVTVELRKAKKEDQMFKRRNINDEDLTSPLKE  60

Query  204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
            LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
            LQN+NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKS NLAEQAVWALG
Sbjct  121  LQNSNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSTNLAEQAVWALG  180

Query  564  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
            NIAGDGAAARDIVIH+NVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QVKR
Sbjct  181  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQVKR  240

Query  744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
            LLPVLSQLL SQDIQVLADACWALSYVTDDDN+KIQAVVDS AVPRLVKLLQMDEPSIIV
Sbjct  241  LLPVLSQLLFSQDIQVLADACWALSYVTDDDNSKIQAVVDSQAVPRLVKLLQMDEPSIIV  300

Query  924  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
            PALRSVGNIVTGTDQQTDVVIASG LP LGLLLQH KSNIVKEAAWT+SNITAGNQKQIQ
Sbjct  301  PALRSVGNIVTGTDQQTDVVIASGALPLLGLLLQHKKSNIVKEAAWTISNITAGNQKQIQ  360

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
```

```
          AV  AGIF QLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKY ILKPFIDLLD
Sbjct 361 AVEDAGIFHQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYHILKPFIDLLD    420

Query 1284 TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
            KDPRTIKVVQTGLSN FALAEK  G ENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA
Sbjct 421 AKDPRTIKVVQTGLSNFFALAEKFNGIENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA    480

Query 1464 IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    1589
           IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct 481 IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    522
```

alpha Karyopherin-2 [Drosophila ananassae]

Sequence ID: ref|**XP_001963034.1**| Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
992 bits(2565)	0.0()	Compositional matrix adjust.	502/522(96%)	514/522(98%)	0/522(0%)	+3

Features:

```
Query 24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE    203
           MSKADSNSRQGSYK+N+INTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct 1    MSKADSNSRQGSYKSNTINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE    60

Query 204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF    383
           LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct 61   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF    120

Query 384  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG    563
           LQNT N+MLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKS+NLAEQAVWALG
Sbjct 121  LQNTTNTMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSINLAEQAVWALG    180

Query 564  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR    743
           NIAGDGA+ARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QV R
Sbjct 181  NIAGDGASARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQVRR    240

Query 744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV    923
           LLPVLSQLLLSQDIQVLADACWALSYVTDDDN KIQAVVDSDAVPRLVKLL+MDEPSIIV
Sbjct 241  LLPVLSQLLLSQDIQVLADACWALSYVTDDDNNKIQAVVDSDAVPRLVKLLEMDEPSIIV    300

Query 924  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ    1103
           PALRSVGNIVTGTDQQTDVVIA+GGLPRLGLLLQH+KSNIVKEAAWTVSNITAGNQKQIQ
Sbjct 301  PALRSVGNIVTGTDQQTDVVIAAGGLPRLGLLLQHSKSNIVKEAAWTVSNITAGNQKQIQ    360

Query 1104 AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
           AVIQAGIFQQLR VLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEK+KILKPFIDLLD
Sbjct 361  AVIQAGIFQQLRHVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKFKILKPFIDLLD   420

Query 1284 TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
            KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLE LQQHENEEVYKKAYA
Sbjct 421  AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLEALQQHENEEVYKKAYA   480

Query 1464 IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    1589
           IIDTYFSNGDD  EQELAPQEVNGALEF+ TQPKAPEGGYTF
Sbjct 481  IIDTYFSNGDDAVEQELAPQEVNGALEFSTTQPKAPEGGYTF    522
```

GL18958 [Drosophila persimilis]

Sequence ID: ref|**XP_002014430.1**| Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
989 bits(2556)	0.0()	Compositional matrix adjust.	501/522(96%)	514/522(98%)	0/522(0%)	+3

Features:

```
Query 24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE    203
           M+K D+N+RQGSYK+N+INTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct 1    MNKTDANTRQGSYKSNTINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE    60

Query 204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF    383
           LNGQSPVQLSVDEIVAAMNSEDQERQF+GMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct 61   LNGQSPVQLSVDEIVAAMNSEDQERQFMGMQSARKMLSRERNPPIDLMIGHGIVPICIRF    120

Query 384  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG    563
           LQNT+N+MLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQS S+NLAEQAVWALG
Sbjct 121  LQNTSNTMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSNSINLAEQAVWALG    180

Query 564  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR    743
           NIAGDGAAARDIVI HNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QV R
Sbjct 181  NIAGDGAAARDIVIQHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQVTR    240

Query 744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV    923
           LLPVLSQLLLSQDIQVLADACWALSYVTDDDNHKIQAVVDSDAVPRLVKLLQMDEPSIIV
Sbjct 241  LLPVLSQLLLSQDIQVLADACWALSYVTDDDNHKIQAVVDSDAVPRLVKLLQMDEPSIIV    300

Query 924  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ    1103
           PALRSVGNIVTGTD QTDVVIA+GGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ
Sbjct 301  PALRSVGNIVTGTDVQTDVVIAAGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ    360

Query 1104 AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
           AVI+AGIFQQLR VLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEK+KILKPFIDLLD
```

```
Sbjct   361   AVIEAGIFQQLRNVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKFKILKPFIDLLD      420

Query  1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA     1463
              KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA
Sbjct   421   AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA      480

Query  1464   IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF     1589
              IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct   481   IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF      522
```

uncharacterized protein Dpse_GA18440 [Drosophila pseudoobscura pseudoobscura]
Sequence ID: **ref|XP_001356313.1|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
986 bits(2548)	0.0()	Compositional matrix adjust.	500/522(96%)	513/522(98%)	0/522(0%)	+3

Features:

```
Query    24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE      203
              M+K D+N+RQGSYK+N+INT DSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct     1   MNKTDANTRQGSYKSNTINTLDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE       60

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF      383
              LNGQSPVQLSVDEIVAAMNSEDQERQF+GMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct    61   LNGQSPVQLSVDEIVAAMNSEDQERQFMGMQSARKMLSRERNPPIDLMIGHGIVPICIRF      120

Query   384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG      563
              LQNT+N+MLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQS S+NLAEQAVWALG
Sbjct   121   LQNTSNTMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSNSINLAEQAVWALG      180

Query   564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR      743
              NIAGDGAAARDIVI HNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QV R
Sbjct   181   NIAGDGAAARDIVIQHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQVTR      240

Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV      923
              LLPVLSQLLLSQDIQVLADACWALSYVTDDDN KIQAVVDSDAVPRLVKLLQMDEPSIIV
Sbjct   241   LLPVLSQLLLSQDIQVLADACWALSYVTDDDNHKIQAVVDSDAVPRLVKLLQMDEPSIIV      300

Query   924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ     1103
              PALRSVGNIVTGTD QTDVVIA+GGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ
Sbjct   301   PALRSVGNIVTGTDVQTDVVIAAGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ      360

Query  1104   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD     1283
              AVI+AGIFQQLR VLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEK+KILKPFIDLLD
Sbjct   361   AVIEAGIFQQLRNVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKFKILKPFIDLLD      420

Query  1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA     1463
              KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA
Sbjct   421   AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA      480

Query  1464   IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF     1589
              IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct   481   IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF      522
```

uncharacterized protein Dmoj_GI17589 [Drosophila mojavensis]
Sequence ID: **ref|XP_002002818.1|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
954 bits(2465)	0.0()	Compositional matrix adjust.	466/523(89%)	495/523(94%)	2/523(0%)	+3

Features:

```
Query    24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE      203
              M+K+D+N+RQG YKAN++N QDSRMRRHEVTIELRKSKKEDQ FKRRNINDEDLTSPLKE
Sbjct     1   MNKSDANTRQGHYKANTLNMQDSRMRRHEVTIELRKSKKEDQLFKRRNINDEDLTSPLKE       60

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF      383
              LNGQSPV LSVDEIVAAMNSED ERQF+GMQ ARKMLSRERNPPID+MI HGIVPICIRF
Sbjct    61   LNGQSPVLLSVDEIVAAMNSEDPERQFVGMQQARKMLSRERNPPIDVMISHGIVPICIRF      120

Query   384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG      563
              LQ+ NN +LQFEAAWALTNIASGTSDQTRCVIE NAVPHF+ALLQSKS+NLAEQAVWALG
Sbjct   121   LQH-NNPLLQFEAAWALTNIASGTSDQTRCVIEQNAVPHFIALLQSKSLNLAEQAVWALG      179

Query   564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR      743
              NIAGDG AARDIVI HNVIDGIL LINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR
Sbjct   180   NIAGDGPAARDIVIQHNVIDGILRLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR      239

Query   744   ll-pvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSII      920
              LL +   L+  +DIQVLADACWALSYVTDD+N KIQAVVD++AVPRLV+LLQ DEPSII
Sbjct   240   LLPVLSQLLVYQEDIQVLADACWALSYVTDDENNKIQAVVDTNAVPRLVQLLQTDEPSII      299

Query   921   VPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQI     1100
              VPALRSVGNIVTGTDQQTDVVIA+GGLP+LG+LLQH+K NIVKEAAWTVSNITAGNQKQI
Sbjct   300   VPALRSVGNIVTGTDQQTDVVIAAGGLPKLGMLLQHSKGNIVKEAAWTVSNITAGNQKQI      359

Query  1101   QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL     1280
              QAVI AGIF Q+R VLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL
Sbjct   360   QAVIDAGIFVQIRHVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL      419
```

```
Query  1281  DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY  1460
             + KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEE+GGLDKLE LQQHENEEVYKKAY
Sbjct  420  EAKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEELGGLDKLEALQQHENEEVYKKAY  479

Query  1461  AIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             A+IDTYFS GDDEAE+ELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  480  ALIDTYFSAGDDEAEKELAPQEVNGALEFNATQPKAPEGGYTF  522
```

alpha Karyopherin-2 [Drosophila virilis]

Sequence ID: **ref|XP_002057743.2|** Length: 921 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 521

Score	Expect	Method	Identities	Positives	Gaps	Frame
950 bits(2455)	0.0()	Compositional matrix adjust.	480/522(92%)	504/522(96%)	1/522(0%)	+3

Features:

```
Query  24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
            M+K+D+++RQG YKAN++NTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct  1    MNKSDASTRQGHYKANTLNTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  60

Query  204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
            LNGQSPV LSVDEIVAAMNSED ERQF+GMQ ARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61   LNGQSPVLLSVDEIVAAMNSEDSERQFVGMQQARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
            LQ++N ++LQFEAAWALTNIASGTS+QTRCVIE NAVPHF+ LLQSKS+NLAEQAVWALG
Sbjct  121  LQSSN-TILQFEAAWALTNIASGTSEQTRCVIEQNAVPHFIELLQSKSLNLAEQAVWALG  179

Query  564  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
            NIAGDGAAARDIVI HNVIDGIL LINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QVKR
Sbjct  180  NIAGDGAAARDIVIQHNVIDGILRLINNETPLSFLRNIVWLMSNLCRNKNPSPPFEQVKR  239

Query  744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
            LLPVLSQLL+SQDIQVLADACWALSYVTDDDN KIQAVVD+DAVPRLV LLQ DEPSIIV
Sbjct  240  LLPVLSQLLVSQDIQVLADACWALSYVTDDDNNKIQAVVDTDAVPRLVNLLQTDEPSIIV  299

Query  924  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
            PALRSVGNIVTGTDQQTDVVIA+GGLP+LGLLLQH+K NIVKEAAWTVSNITAGNQKQIQ
Sbjct  300  PALRSVGNIVTGTDQQTDVVIAAGGLPKLGLLLQHSKGNIVKEAAWTVSNITAGNQKQIQ  359

Query  1104 AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
            AVI AGIFQQ+R VLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD
Sbjct  360  AVIDAGIFQQIRHVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  419

Query  1284 TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
             KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEE+GGLDKLE LQQHENEEVYKKAYA
Sbjct  420  AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEELGGLDKLEALQQHENEEVYKKAYA  479

Query  1464 IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
            IIDTYF+ GDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  480  IIDTYFNTGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  521
```

GH11072 [Drosophila grimshawi]

Sequence ID: **ref|XP_001988267.1|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
939 bits(2426)	0.0()	Compositional matrix adjust.	462/522(89%)	493/522(94%)	0/522(0%)	+3

Features:

```
Query  24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
            MSK+++++RQG YKAN++NTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND+DLTSPLKE
Sbjct  1    MSKSEASARQGHYKANTLNTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDDDLTSPLKE  60

Query  204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
            LNGQSPVQLSVDEIVAAMNSED ERQF+GMQ ARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61   LNGQSPVQLSVDEIVAAMNSEDAERQFVGMQQARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
            LQNT+N MLQFEAAWALTNIASGTS+QTRCVI+ NAVPHF+ALLQSK +NLAEQAVWALG
Sbjct  121  LQNTSNDMLQFEAAWALTNIASGTSEQTRCVIDENAVPHFIALLQSKHINLAEQAVWALG  180

Query  564  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
            NIAGDGAAARDIVI +NVIDGIL LINN+TPLSFLRNIVWLMSNLCRNKNPSPPF+QVKR
Sbjct  181  NIAGDGAAARDIVIQNNVIDGILRLINNDTPLSFLRNIVWLMSNLCRNKNPSPPFEQVKR  240

Query  744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
            LLPVLSQLLL+QDIQVLADACWALSYVTDDDN KIQAVV++DAVPRLV LLQ DEPSIIV
Sbjct  241  LLPVLSQLLLTQDIQVLADACWALSYVTDDDNHKIQAVVETDAVPRLVNLLQTDEPSIIV  300

Query  924  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
            PALRSVGNIVTGTDQQTDVVIA+GGLP+LG+LL H K NIVKEAAWTVSNITAGNQ QIQ
Sbjct  301  PALRSVGNIVTGTDQQTDVVIAAGGLPKLGILLHHPKGNIVKEAAWTVSNITAGNQTQIQ  360

Query  1104 AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
            AVI AG+FQ +R VLEKGDFKAQKEAAWAVTN TTSG+ EQIVDLIEK+KILKPFIDLLD
Sbjct  361  AVIDAGLFQPIRHVLEKGDFKAQKEAAWAVTNATTSGSSEQIVDLIEKHKILKPFIDLLD  420
```

```
Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
             KDPRTIKVVQTGL NLF LAEKLGGTENLCLMVEE+GGLDKLE LQQHENEEVYKKA+
Sbjct  421  AKDPRTIKVVQTGLCNLFTLAEKLGGTENLCLMVEELGGLDKLEALQQHENEEVYKKAFT  480

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             IIDTYFS  DDEAEQ+LAPQEVNGALEFNA QPKAPEGG+ F
Sbjct  481  IIDTYFSTADDEAEQQLAPQEVNGALEFNAAQPKAPEGGFNF  522
```

uncharacterized protein Dwil_GK18399 [Drosophila willistoni]

Sequence ID: **ref|XP_002074226.1|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
926 bits(2394)	0.0()	Compositional matrix adjust.	471/522(90%)	493/522(94%)	0/522(0%)	+3

Features:

```
Query  24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
            M++ ++NSR  SYK+NSINTQDSR+RRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE
Sbjct  1   MNRPEANSRLSSYKSNSINTQDSRVRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  60

Query  204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
             NGQSPVQLSVDEIVAAMNSED ERQF+GMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61  PNGQSPVQLSVDEIVAAMNSEDSERQFVGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
            LQN  N MLQFEAAWALTNIASGTSDQTRCVIE +AVPHF++LL SKS+ LAEQAVWALG
Sbjct  121  LQNVANPMLQFEAAWALTNIASGTSDQTRCVIEQDAVPHFISLLTSKSIQLAEQAVWALG  180

Query  564  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
            NIAGDG   ARDIVI+H VIDGIL LIN+ETPLSFLRNIVWLMSNLCRNKNPSPPF+QVKR
Sbjct  181  NIAGDGPIARDIVINHGVIDGILRLINDETPLSFLRNIVWLMSNLCRNKNPSPPFEQVKR  240

Query  744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
            LLP+LS LLLS DIQVLADACWALSYVTDDDN KIQAVVD+DAVPRLV LLQMDEPSIIV
Sbjct  241  LLPILSHLLLLSTDIQVLADACWALSYVTDDDNNKIQAVVDTDAVPRLVNLLQMDEPSIIV  300

Query  924  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
            PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQH+KSNIVKEAAWTVSNITAGNQKQIQ
Sbjct  301  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHSKSNIVKEAAWTVSNITAGNQKQIQ  360

Query  1104 AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
            AVI+AGIF  ++ VLE GDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD
Sbjct  361  AVIEAGIFNYIKQVLENGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  420

Query  1284 TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
             KDPRTIKVVQTGL NLF LAEKLGGTENLCLMVEEMGGLDKLE LQQHENEEVYKKAYA
Sbjct  421  AKDPRTIKVVQTGLLNLFNLAEKLGGTENLCLMVEEMGGLDKLEALQQHENEEVYKKAYA  480

Query  1464 IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
            IIDTYF+ GD+ AEQELAPQEVNGALEFNATQPKAPEGGYTF
Sbjct  481  IIDTYFNTGDEGAEQELAPQEVNGALEFNATQPKAPEGGYTF  522
```

Pen [Drosophila busckii]

Sequence ID: **gb|ALC39141.1|** Length: 523 Number of Matches: 1
Range 1: 1 to 523

Score	Expect	Method	Identities	Positives	Gaps	Frame
923 bits(2385)	0.0()	Compositional matrix adjust.	466/523(89%)	497/523(95%)	1/523(0%)	+3

Features:

```
Query  24   MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
            MSK+++N+RQG +KA S+N Q+SRMRRHEVT+ LRKS +EDQMFKRRNINDED+TSPLKE
Sbjct  1   MSKSEANARQGQFKAKSLNLQESRMRRHEVTVTLRKSNREDQMFKRRNINDEDMTSPLKE  60

Query  204  LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
            +NGQSPVQL+VDEIVAAMNSED ERQFLGMQ ARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  61  VNGQSPVQLTVDEIVAAMNSEDAERQFLGMQQARKMLSRERNPPIDLMIGHGIVPICIRF  120

Query  384  LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
            LQNTNN MLQFEAAWALTNIASGT++QTRCVI+HNAVPHF+ALLQSK++NLAEQAVWALG
Sbjct  121  LQNTNNPMLQFEAAWALTNIASGTAEQTRCVIDHNAVPHFIALLQSKAINLAEQAVWALG  180

Query  564  NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
            NIAGDGA ARDIVI +NVIDGIL LI+NETPLSFLRNIVWLMSNLCRNKNPSPPF+ VKR
Sbjct  181  NIAGDGAIARDIVIQNNVIDGILSLISNETPLSFLRNIVWLMSNLCRNKNPSPPFEHVKR  240

Query  744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
            LLPVLSQLL SQDIQVLADACWALSYVTDDDN KIQ+VVD+DAVPRLV LLQ DEPSIIV
Sbjct  241  LLPVLSQLLTSQDIQVLADACWALSYVTDDDNNKIQSVVDTDAVPRLVALLQTDEPSIIV  300

Query  924  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
            PALRSVGNIVTGTDQQTDVVIA+GGLP+LGLLLQH+KSNIVKEAAWTVSNITAGNQKQIQ
Sbjct  301  PALRSVGNIVTGTDQQTDVVIAAGGLPKLGLLLQHSKSNIVKEAAWTVSNITAGNQKQIQ  360

Query  1104 AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
            AVI AGIF Q+R VLEKGDFKAQKEAAWAVTNTTTSGT EQIVDLIEKYKILKPFIDLLD
Sbjct  361  AVIDAGIFHQIRQVLEKGDFKAQKEAAWAVTNTTTSGTHEQIVDLIEKYKILKPFIDLLD  420

Query  1284 TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
             KDPRTIKVVQTGL+NLFALAEKLGGTENLCLMVEE+GGLDKLE LQQHENEEVYKKAYA
Sbjct  421  AKDPRTIKVVQTGLANLFALAEKLGGTENLCLMVEELGGLDKLEALQQHENEEVYKKAYA  480
```

```
Query  1464  IIDTYFSNGDDE-AEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             IIDTY+  GDD+ AEQELAPQEVNGALEFN TQPKAPEGGYTF
Sbjct  481   IIDTYWPAGDDDAAEQELAPQEVNGALEFNTTQPKAPEGGYTF  523
```


Importin subunit alpha [Lucilia cuprina]

Sequence ID: **gb|KNC33852.1|** Length: 520 Number of Matches: 1

Range 1: 1 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
895 bits(2313)	0.0()	Compositional matrix adjust.	438/522(84%)	483/522(92%)	2/522(0%)	+3

Features:

```
Query  24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
             MS+ D+ +RQG+YK+N+IN+ +SR+RRHEVT+ELRKSKKEDQMFKRRNIN+E++TSPLKE
Sbjct  1     MSRMDA-TRQGAYKSNTINSNESRLRRHEVTVELRKSKKEDQMFKRRNINEEEVTSPLKE  59

Query  204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
              NGQSPVQ++VDEIVAAM+S D ERQF GMQ+ARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  60    SNGQSPVQMTVDEIVAAMHSTDPERQFTGMQAARKMLSRERNPPIDLMIGHGIVPICIRF  119

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
             LQN  N+MLQFEAAWALTNIASGTS+QTRCVIE+NAVPHF+ALLQSK++NLAEQAVWALG
Sbjct  120   LQNFENAMLQFEAAWALTNIASGTSEQTRCVIENNAVPHFIALLQSKNINLAEQAVWALG  179

Query  564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
             NIAGDGAAARDIVI HNVIDGIL L N+ TPLSFLRNIVWLMSNLCRNKNPSPPFD++KR
Sbjct  180   NIAGDGAAARDIVIEHNVIDGILCLCNDSTPLSFLRNIVWLMSNLCRNKNPSPPFDEIKR  239

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
             LLPVLSQLL   DIQVLADACWALSYVTDD+N KIQAVVD+ AVPRLV LL  +EP+IIV
Sbjct  240   LLPVLSQLLCGTDIQVLADACWALSYVTDDENQKIQAVVDTGAVPRLVALLGTNEPAIIV  299

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
             PALRSVGNIVTGTDQQTD VIA+GGLP+LG+LLQH+K+NIVKEAAWT+SNITAGN KQIQ
Sbjct  300   PALRSVGNIVTGTDQQTDAVIAAGGLPKLGILLQHSKNNIVKEAAWTISNITAGNVKQIQ  359

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
             AVI A IF Q+R VLEKGDFK+QKEAAWAVTNTTSGTPEQI+DLIEKY+ILKPF DLLD
Sbjct  360   AVIDADIFSQIRNVLEKGDFKSQKEAAWAVTNTTSGTPEQIIDLIEKYQILKPFCDLLD  419

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              KDPRTIKVV TGLSNLFALA++LGG ENLCLMVEEMGGLDKLE LQQHENEEVYKKAYA
Sbjct  420   AKDPRTIKVVLTGLSNLFALADRLGGAENLCLMVEEMGGLDKLENLQQHENEEVYKKAYA  479

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             I+D YFS+ D  AE ELAPQEVNGALEFNA Q KAPEGG+TF
Sbjct  480   IVDAYFSSADG-AESELAPQEVNGALEFNAQQTKAPEGGFTF  520
```


PREDICTED: importin subunit alpha [Bactrocera dorsalis]

Sequence ID: **ref|XP_011202013.1|** Length: 520 Number of Matches: 1

Range 1: 1 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
878 bits(2268)	0.0()	Compositional matrix adjust.	433/522(83%)	476/522(91%)	2/522(0%)	+3

Features:

```
Query  24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
             MSK+D+ SR  SYK+NSIN+QDSRMRRHEVT+ELRKSKKEDQ+FKRRNIN+ED+ SPLKE
Sbjct  1     MSKSDT-SRLNSYKSNSINSQDSRMRRHEVTVELRKSKKEDQLFKRRNINEEDIVSPLKE  59

Query  204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
              N QSPVQ+S+DE+VAAMN +D +RQF+GMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct  60    NNCQSPVQMSIDEMVAAMNGQDVDRQFVGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  119

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
             LQN  N +LQFEAAWALTNIASGTS+QTRCVIE NAVPHFVALL+SKS+NLAEQAVWALG
Sbjct  120   LQNHENPLLQFEAAWALTNIASGTSEQTRCVIEQNAVPHFVALLKSKSINLAEQAVWALG  179

Query  564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
             NIAGDGAAARDIVI HNV+DGIL L+N ETPLSFLRNIVWLMSNLCRNKNPSPPF+++KR
Sbjct  180   NIAGDGAAARDIVIQHNVVDGILGLVNFETPLSFLRNIVWLMSNLCRNKNPSPPFEEIKR  239

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
             LLPV+SQLLL  D QVLADACWALSYVTDD+N KIQAVVD+ AV  LVKLL  DE SIIV
Sbjct  240   LLPVISQLLLGDDPQVLADACWALSYVTDDENLKIQAVVDTGAVTHLVKLLGTDEASIIV  299

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
             PALRSVGNIVTGTD QTD VIA+GGLPRLG+LLQH+K NIVKEAAWTVSNITAGN KQIQ
Sbjct  300   PALRSVGNIVTGTDLQTDAVIAAGGLPRLGVLLQHSKCNIVKEAAWTVSNITAGNPKQIQ  359

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
             AVI AG+F   +R VLEKGDFK+QKEAAWAVTNTTSGTPEQI+DLIEKY+ILKPF DLLD
Sbjct  360   AVIDAGLFTPIRNVLEKGDFKSQKEAAWAVTNTTSGTPEQIIDLIEKYQILKPFCDLLD  419

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              KDPRT+KVV  GL NLF LAEKLGGTENLCLMVEEMGGLDKLE LQ+HENEE+YKKA A
Sbjct  420   AKDPRTVKVVLMGLGNLFVLAEKLGGTENLCLMVEEMGGLDKLEKLQEHENEEIYKKAFA  479

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             ++DTYF++G+D AE ELAPQEVNGALEFNA     APEGGYTF
Sbjct  480   LVDTYFNSGED-AEAELAPQEVNGALEFNAGHSNAPEGGYTF  520
```

PREDICTED: importin subunit alpha [Musca domestica]

Sequence ID: **ref|XP_005185058.1|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
871 bits(2251)	0.0()	Compositional matrix adjust.	442/524(84%)	483/524(92%)	4/524(0%)	+3

Features:

```
Query   24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE   203
              MSKA++ SRQG+YK+NSINT +SR+RRHEVT+ELRKSKKEDQMFKRRNIN+ED+TSPLKE
Sbjct   1     MSKAEA-SRQGAYKSNSINTNESRLRRHEVTVELRKSKKEDQMFKRRNINEEDITSPLKE   59

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
               NGQSPVQ++VDEIVAAM S D ERQF GMQ+ARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct   60    SNGQSPVQMTVDEIVAAMQSTDPERQFAGMQAARKMLSRERNPPIDLMIGHGIVPICIRF   119

Query   384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
              LQN  N +LQFEAAWALTNIASGTS+QTRCVIE+NAVPHF+ALLQS+++NLAEQAVWALG
Sbjct   120   LQNFENPLLQFEAAWALTNIASGTSEQTRCVIENNAVPHFIALLQSENINLAEQAVWALG   179

Query   564   NIAGDGAAARDIVIHHNVIDGILPLIN--NETPLSFLRNIVWLMSNLCRNKNPSPPFDQV   737
              NIAGDGAAARDIVIHH  IDG+L +++    + P+SFLRN VWLMSNLCRNKNPSPPF+++
Sbjct   180   NIAGDGAAARDIVIHHKCIDGVLNMVDLRKDIPISFLRNNVWLMSNLCRNKNPSPPFEEI   239

Query   738   KRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSI   917
              KRLLPVLSQLL    DIQVLADACWALSYVTDD+N KIQAVVD+ AVPRLV LL  DEP+I
Sbjct   240   KRLLPVLSQLLCGTDIQVLADACWALSYVTDDENHKIQAVVDTGAVPRLVALLGTDEPAI   299

Query   918   IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ   1097
              IVPALRSVGNIVTGTDQQTD VIA+GGLP+LGLLLQH+K+NIVKEAAWT+SNITAGNQKQ
Sbjct   300   IVPALRSVGNIVTGTDQQTDAVIAAGGLPKLGLLLQHSKNNIVKEAAWTISNITAGNQKQ   359

Query   1098  IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDL   1277
              IQAVI A IF Q+R VLEKGDFK+QKEAAWAVTNTTSGTPEQI+DLIEKY+ILKPF DL
Sbjct   360   IQAVIDAEIFAQIRKVLEKGDFKSQKEAAWAVTNTTSGTPEQIIDLIEKYQILKPFCDL   419

Query   1278  LDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA   1457
              LD KDPRTIKVV TGLSNLFALAEKLGGTENLCLMVEEMGGLDKLE LQQHENEEVYKKA
Sbjct   420   LDAKDPRTIKVVLTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLENLQQHENEEVYKKA   479

Query   1458  YAIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              YAIID YFSNGD  AE ELAPQEVNGALEFNA Q KAPEGG+TF
Sbjct   480   YAIIDAYFSNGDG-AESELAPQEVNGALEFNAAQSKAPEGGFTF   522
```

PREDICTED: importin subunit alpha [Bactrocera oleae]

Sequence ID: **ref|XP_014087960.1|** Length: 520 Number of Matches: 1

Range 1: 1 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
871 bits(2250)	0.0()	Compositional matrix adjust.	431/522(83%)	474/522(90%)	2/522(0%)	+3

Features:

```
Query   24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE   203
              MSK+D+ SR  SYK+N+IN+Q+SRMRRHEVT+ELRKSKKEDQ+FKRRNINDED+ SPLKE
Sbjct   1     MSKSDT-SRLNSYKSNAINSQESRMRRHEVTVELRKSKKEDQLFKRRNINDEDIVSPLKE   59

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
               N QSPV +S+DE+V AMNS+D ERQF GMQSARKMLSRERNPPIDLMIGHGIVPICIHF
Sbjct   60    SNSQSPVPMSIDEMVTAMNSQDVERQFSGMQSARKMLSRERNPPIDLMIGHGIVPICIHF   119

Query   384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
              LQN  N +LQFEAAWALTNIASGTS+QTRCVIE NAVPHFVALL+SKS+NLAEQAVWALG
Sbjct   120   LQNHENPLLQFEAAWALTNIASGTSEQTRCVIEQNAVPHFVALLKSKSINLAEQAVWALG   179

Query   564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
              NIAGDGAAARDIVI HNV++GIL LIN ETPLSFLRNIVWLMSNLCRNKNPSPPF+++KR
Sbjct   180   NIAGDGAAARDIVIQHNVVEGILGLINCETPLSFLRNIVWLMSNLCRNKNPSPPFEEIKR   239

Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
              LLPVLS+LLL +D QVLADACWALSYVTDD+N KIQAVVD+ AV  LVKLL  DEPSIIV
Sbjct   240   LLPVLSRLLLGEDSQVLADACWALSYVTDDENLKIQAVVDTGAVTHLVKLLGTDEPSIIV   299

Query   924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
              PALRSVGNIVTGTD QTD VIA+GGLPRLG+LLQ+ K NI+KEAAWTVSNITAGN KQIQ
Sbjct   300   PALRSVGNIVTGTDLQTDAVIAAGGLPRLGVLLQNPKCNIIKEAAWTVSNITAGNPKQIQ   359

Query   1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
              AVI AG+F  +R VLEKGDFK+QKEAAWAVTNTTSGTPEQI+DLIEKY+ILKPF DLLD
Sbjct   360   AVIDAGLFTPIRHVLEKGDFKSQKEAAWAVTNTTSGTPEQIIDLIEKYQILKPFCDLLD   419

Query   1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
               KD RTIKVV  GL NLF LAEKLGGTENLCLMVEEMGGLDKLE LQ+HENEE+YKKA+A
Sbjct   420   AKDSRTIKVVLMGLGNLFVLAEKLGGTENLCLMVEEMGGLDKLEKLQEHENEEIYKKAFA   479

Query   1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              ++DTYF++G+D AE ELAPQEVNGALEFNA Q  APEGGYTF
Sbjct   480   LVDTYFNSGED-AEAELAPQEVNGALEFNAGQSNAPEGGYTF   520
```

PREDICTED: importin subunit alpha [Bactrocera cucurbitae]

Sequence ID: **ref|XP_011188423.1|** Length: 520 Number of Matches: 1

Range 1: 1 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
865 bits(2236)	0.0()	Compositional matrix adjust.	439/522(84%)	478/522(91%)	2/522(0%)	+3

Features:

```
Query   24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE   203
              MSK+D+ SR   SYK+NSIN+Q+SRMRRHEVT+ELRKSKKEDQ+FKRRNINDED+ SPLKE
Sbjct   1     MSKSDT-SRLNSYKSNSINSQESRMRRHEVTVELRKSKKEDQLFKRRNINDEDIVSPLKE   59

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
               N QSP Q+S+DE+VA+MNS+D ERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct   60    SNNQSPAQMSIDEMVASMNSQDVERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   119

Query   384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
              LQN   N +LQFEAAWALTNIASGTS+QTRCVIE NAVPHFVALL+SKS+NLAEQAVWALG
Sbjct   120   LQNHENPLLQFEAAWALTNIASGTSEQTRCVIEQNAVPHFVALLKSKSINLAEQAVWALG   179

Query   564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
              NIAGDGAAARDIVI HNV+DGIL LIN ETPLSFLRNIVWLMSNLCRNKNPSPPF+++KR
Sbjct   180   NIAGDGAAARDIVIQHNVVDGILGLINCETPLSFLRNIVWLMSNLCRNKNPSPPFEEIKR   239

Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
              LLPVLS+LLL +D QVLADACWALSYVTDD+N KIQAVVD+ AV  LVKLL  +EPSIIV
Sbjct   240   LLPVLSRLLLGEDTQVLADACWALSYVTDDENLKIQAVVDTGAVGHLVKLLGTEEPSIIV   299

Query   924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
              PALRSVGNIVTGTDQQTD VIA+GGLPRLG LLQH K NIVKEAAWTVSNITAGN KQIQ
Sbjct   300   PALRSVGNIVTGTDQQTDAVIAAGGLPRLGGLLQHPKCNIVKEAAWTVSNITAGNPKQIQ   359

Query   1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
              AVI AGIF   +R VLEKGDFK+QKEAAWAVTNTTTSGTPEQI+DLIEKY+ILKPF DLLD
Sbjct   360   AVINAGIFTPIRLVLEKGDFKSQKEAAWAVTNTTTSGTPEQIIDLIEKYQILKPFCDLLD   419

Query   1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
               KDPRTIKVV  GL NLF LAEKLGGTENLCLMVEEMGGLDKLE LQ+HENEE+YKKA+A
Sbjct   420   AKDPRTIKVVLMGLGNLFVLAEKLGGTENLCLMVEEMGGLDKLEKLQEHENEEIYKKAFA   479

Query   1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              ++DTYF++G+D AE ELAPQEVNGALEFNA Q K PEGGYTF
Sbjct   480   LVDTYFNSGED-AEAELAPQEVNGALEFNAGQSKTPEGGYTF   520
```

PREDICTED: importin subunit alpha [Stomoxys calcitrans]

Sequence ID: **ref|XP_013105904.1|** Length: 522 Number of Matches: 1
Range 1: 1 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
858 bits(2217)	0.0()	Compositional matrix adjust.	439/524(84%)	478/524(91%)	4/524(0%)	+3

Features:

```
Query   24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE   203
              MSKAD   RQ +YK+NSINT +SR+RRHEVT+ELRKSKKEDQMFKRRNIN++D+TSPLKE
Sbjct   1     MSKADP-GRQNAYKSNSINTNESRLRRHEVTVELRKSKKEDQMFKRRNINEDDITSPLKE   59

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
               NGQSPVQ++VDEIVAAM S D ERQF GMQ+ARKMLSRERNPPIDLMIGHGIVPICIRF
Sbjct   60    SNGQSPVQMTVDEIVAAMQSADPERQFTGMQAARKMLSRERNPPIDLMIGHGIVPICIRF   119

Query   384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
              LQN  + +LQFEAAWALTNIASGTSDQTRCVIE+NAVPHF+ALLQS+++NLAEQAVWALG
Sbjct   120   LQNFEHPLLQFEAAWALTNIASGTSDQTRCVIENNAVPHFIALLQSENINLAEQAVWALG   179

Query   564   NIAGDGAAARDIVIHHNVIDGILPLIN--NETPLSFLRNIVWLMSNLCRNKNPSPPFDQV   737
              NIAGDGAAARDIVI +  IDGIL +I+    P+SFLRN VWLMSNLCRNKNPSPPF+++
Sbjct   180   NIAGDGAAARDIVIQNKCIDGILNMIDLRKDIPISFLRNNVWLMSNLCRNKNPSPPFEEI   239

Query   738   KRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSI   917
              KRLLPVLSQLL   DIQVLADACWALSYVTDD+N KIQAVVD+ AVPRLV LL  DEP+I
Sbjct   240   KRLLPVLSQLLCGTDIQVLADACWALSYVTDDENNKIQAVVDTGAVPRLVALLGTDEPAI   299

Query   918   IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ   1097
              IVPALRSVGNIVTGTDQQTD VIA+GGLP+LGLLLQH+K+NIVKEAAWT+SNITAGNQKQ
Sbjct   300   IVPALRSVGNIVTGTDQQTDAVIAAGGLPKLGLLLQHSKNNIVKEAAWTISNITAGNQKQ   359

Query   1098  IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDL   1277
              IQAVI A IF Q+R VLEKGDFK+QKEAAWAVTNTTTSGTPEQI+DLIEKY ILKPF DL
Sbjct   360   IQAVIDADIFAQIRKVLEKGDFKSQKEAAWAVTNTTTSGTPEQIIDLIEKYHILKPFCDL   419

Query   1278  LDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA   1457
              LD KDPRTIKVV TG+SNLFALAEKLGGTENLCLMVEEMGGLDKLE LQQHENEEVYKKA
Sbjct   420   LDAKDPRTIKVVLTGVSNLFALAEKLGGTENLCLMVEEMGGLDKLENLQQHENEEVYKKA   479

Query   1458  YAIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              YAIID YFSNGD  AE ELAPQEVNGALEFNATQ K PEGG+TF
Sbjct   480   YAIIDAYFSNGDG-AEAELAPQEVNGALEFNATQKTPEGGFTF   522
```

PREDICTED: importin subunit alpha [Ceratitis capitata]

Sequence ID: **ref|XP_004527197.1|** Length: 520 Number of Matches: 1
Range 1: 1 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
855 bits(2209)	0.0()	Compositional matrix adjust.	423/522(81%)	469/522(89%)	2/522(0%)	+3

Features:

```
Query   24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE    203
              MSK D  SR SYK++  +  DSRMRRHEVT+ELRKSKKEDQ+FKRRNIN+ED+ SPLKE
Sbjct   1     MSKPDP-SRINSYKSSIRSATDSRMRRHEVTVELRKSKKEDQLFKRRNINEEDIVSPLKE     59

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF    383
               N QSPV +S+DE+V AM S+D ERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICI+F
Sbjct   60    NNVQSPVPMSIDEMVAMKSDDIERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIQF    119

Query   384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG    563
              LQ T N +LQFEAAWALTNIASG SDQTRCVIE NAVP+FVALL+SKS+NLAEQAVWALG
Sbjct   120   LQKTENPLLQFEAAWALTNIASGNSDQTRCVIEQNAVPYFVALLRSKSINLAEQAVWALG    179

Query   564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR    743
              NIAGDGAAARDIVIH+NV+DG+L LIN  TPLSFLRNIVWLMSNLCRNKNPSPPFD++KR
Sbjct   180   NIAGDGAAARDIVIHNNVVDGLLGLINQATPLSFLRNIVWLMSNLCRNKNPSPPFDEIKR    239

Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV    923
              LLP++SQLLL  D QVLADACWALSYVTDD+N KIQAVVD+ AV RLV LL  DEPSIIV
Sbjct   240   LLPIISQLLLGSDDQVLADACWALSYVTDDENVKIQAVVDTGAVERLVALLGTDEPSIIV    299

Query   924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ    1103
              PALR+VGNIVTGTD QTD VIA+GGL  LG+LLQ+ K NIVKEAAWT+SNITAGNQKQIQ
Sbjct   300   PALRTVGNIVTGTDTQTDAVIAAGGLQVLGVLLQNPKGNIVKEAAWTISNITAGNQKQIQ    359

Query   1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILPFIDLLD    1283
              AVI +G+F Q+R VLEKGDFK+QKEAAWAVTNTTTSGTPEQIVDLIEKY++LPF DLLD
Sbjct   360   AVIDSGVFAQIRNVLEKGDFKSQKEAAWAVTNTTTSGTPEQIVDLIEKYQLLPFCDLLD    419

Query   1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA    1463
               KDPRTIKVV TGL+NLF LA++LGGTENLCLM+EEMGGLDKLE LQ+HENEE+YKKAYA
Sbjct   420   AKDPRTIKVVLTGLANLFVLADRLGGTENLCLMIEEMGGLDKLEKLQEHENEEIYKKAYA    479

Query   1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    1589
              ++DTYF+N DD AE ELAPQEVNGALEFNA Q K PEGG+TF
Sbjct   480   MVDTYFNNEDD-AENELAPQEVNGALEFNAGQSKTPEGGFTF    520
```


AAEL012960-PA [Aedes aegypti]

Sequence ID: **ref|XP_001663145.1|** Length: 526 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 10 to 524

Score	Expect	Method	Identities	Positives	Gaps	Frame
660 bits(1702)	0.0()	Compositional matrix adjust.	328/519(63%)	415/519(79%)	7/519(1%)	+3

Features:

```
Query   42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDED--LTSPLKELNGQ    215
              NSR  SYK    +  + R RRHEVT+ELRK+KKEDQ+FKRRNI  E+  +TSPL+E N Q
Sbjct   10    NSRLASYKHGVKSNAELRQRRHEVTVELRKNKKEDQLFKRRNITSEEPTVTSPLQESNAQ     69

Query   216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT    395
              SPV L  +EI+A +NS + +++F+ +Q+ARKMLSRE+NPPID MIG G+VPIC++FL+
Sbjct   70    SPVALKFEEILAYVNSGNAQKEFVAIQTARKMLSREKNPPIDKMIGLGLVPICVKFLECF    129

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG    575
              +   LQFEAAWALTNIASGT++QT+ VI+  AVP F+ALL S S N+AEQAVWALGNIAG
Sbjct   130   DRVDLQFEAAWALTNIASGTTEQTKAVIDAGAVPKFIALLSSPSNNVAEQAVWALGNIAG    189

Query   576   DGAAARDIVIHHNVIDGILPLI-NNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllp    752
              DG+ ARDIV++ N ++ I+ L+ N  T LSFLRNIVWLMSNLCRNKNP PPF++V+ ++P
Sbjct   190   DGSKARDIVLNFNSVESIIYLVQNTNTQLSFLRNIVWLMSNLCRNKNPPPPFNRVEPMIP    249

Query   753   vlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPAL    932
              +LS+LL  +D QVLADACWALSYVTDDD  KI++VV S AVPRLV+LL  + P+II PAL
Sbjct   250   ILSKLLDHEDSQVLADACWALSYVTDDDAVKIESVVASGAVPRLVRLLGCENPAIITPAL    309

Query   933   RSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVI    1112
              RSVGNIVTG+D QTD V+A+G LP LG LL+++K++IVKEAAWT+SNITAGNQ+QI  V
Sbjct   310   RSVGNIVTGSDTQTDAVLAAGALPFLGKLLRNSKNSIVKEAAWTISNITAGNQQQIAQVF    369

Query   1113  QAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILPFIDLLDTKD    1292
               +GIF  L  VL KGDFK+QKEAAWA+TNTTT G+ EQI+ L+EKY I+KP+ DLL+ KD
Sbjct   370   DSGIFHLLIEVLIKGDFKSQKEAAWAITNTTTGGSTEQIIHLVEKYPIMKPYCDLLEAKD    429

Query   1293  PRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIID    1472
               RT++VV +G+SN+F  AEK+GGTENLC + EE+G LDKLE LQ HENEEVYKKA+ +I+
Sbjct   430   SRTVRVVLSGISNIFQFAEKIGGTENLCTLFEEIGALDKLEALQNHENEEVYKKAFQLIE    489

Query   1473  TYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    1589
              +YF++ +D   E AP+E +GALEFN   P A + G F
Sbjct   490   SYFTDAED-VNPECAPKEKDGALEFN---PSAQQNGEKF    524
```


importin alpha [Anopheles darlingi]

Sequence ID: **gb|ETN61562.1|** Length: 522 Number of Matches: 1
Range 1: 8 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
654 bits(1688)	0.0()	Compositional matrix adjust.	320/518(62%)	411/518(79%)	5/518(0%)	+3

Features:

```
Query   42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDED-LTSPLKELNGQS    218
              N+R  +YK  S  T + R RRHEVT+ELRKS+K+DQ+ KRRNIN++D  TSPL+E N QS
```

```
Sbjct     8  NNRMAAYKHGSKTTTELRQRRHEVTVELRKSRKDDQLLKRRNINEDDGPTSPLQENNAQS   67

Query   219  PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN  398
                PV L  +EI+   + S +   ++F  +Q+ARKMLSRE+NPPID +IG G+VPIC+++L+ ++
Sbjct    68  PVTLKYEEIMQFIRSGEPTKEFAAVQAARKMLSREKNPPIDKIIGLGMVPICVKYLEASD  127

Query   399  NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD  578
                  LQFEAAWALTNIASGTSDQT+ VIE NA+P F+ LL S S+ +AEQAVWALGNIAGD
Sbjct   128  RPALQFEAAWALTNIASGTSDQTKVVIEANAIPRFINLLSSPSVTVAEQAVWALGNIAGD  187

Query   579  GAAARDIVIHHNVIDGILPLINN-ETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv  755
                G+ ARD V+ +  ++ I+ L+ N   TP+SFLRNIVWLMSNLCRNKNP+PPF++++ ++PV
Sbjct   188  GSKARDTVLEYKSVEAIISLVRNANTPISFLRNIVWLMSNLCRNKNPAPPFNRIEPMIPV  247

Query   756  lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR  935
                LS LL  +D QVL+DACWALSYVTDDD+ K+++VV + AVP+LV+LL   + P+II PALR
Sbjct   248  LSALLDHEDAQVLSDACWALSYVTDDDSVKLESVVTAGAVPKLVRLLGSNNPAIITPALR  307

Query   936  SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ  1115
                SVGN+VTG D QTD VIA+G LP L   LL H+K+ IVKEAAWTVSNITAGNQ QIQ V++
Sbjct   308  SVGNVVTGNDTQTDAVIAAGSLPLLAGLLHHSKNTIVKEAAWTVSNITAGNQAQIQHVLE  367

Query  1116  AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP  1295
                +GIF  L  VL KGDFK+QKEAAWAVTNTT G+ EQIV L+EK+ ILKP+ DLL+ KD
Sbjct   368  SGIFTDLVEVLAKGDFKSQKEAAWAVTNTTGGSTEQIVLLLEKFHILKPYCDLLEAKDS  427

Query  1296  RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT  1475
                RT++VV +G++N+F +A   +GG EN+C M EE+G LDKLE LQ HENE++Y KA  +I+T
Sbjct   428  RTVRVVLSGITNIFQIAANVGGLENMCTMFEEIGALDKLEQLQNHENEDIYGKALQLIET  487

Query  1476  YFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
                YF + +DEA  E AP+E NGALEFN T P+   GG++F
Sbjct   488  YFCD-EDEANPECAPKEANGALEFNPTTPQ--NGGFSF  522
```

AGAP009792-PA [Anopheles gambiae str. PEST]

Sequence ID: **ref|XP_318886.3|** Length: 522 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 8 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
651 bits(1680)	0.0()	Compositional matrix adjust.	321/518(62%)	407/518(78%)	5/518(0%)	+3

Features:

```
Query    42  NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKELNGQS  218
                N+R  +YK  S +   + R RRHEVT+ELRK+KKEDQ+ KRRNI   DE  TSPL+E N QS
Sbjct     8  NNRLAAYKHGSKSNTELRQRRHEVTVELRKNKKEDQLLKRRNITEDEGPTSPLQENNAQS   67

Query   219  PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN  398
                PV L  D+I+   + S   E++F  +Q+ARKMLSRE+NPPID +IG G+VP+C++FL  ++
Sbjct    68  PVTLKFDDIMQYIRSGQPEKEFAAVQAARKMLSREKNPPIDKIIGLGMVPVCVKFLSASD  127

Query   399  NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD  578
                  LQFEAAWALTNIASGTS+QT+ VI+ NA+P F+ LL S S+ +AEQAVWALGNIAGD
Sbjct   128  RPALQFEAAWALTNIASGTSEQTKAVIDSNAIPRFIDLLSSPSVTVAEQAVWALGNIAGD  187

Query   579  GAAARDIVIHHNVIDGILPLINN-ETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv  755
                G+ ARDIV+ HN +D I+ L+ N   T +SFLRNIVWLMSNLCRNKNP+PPF+++++ ++PV
Sbjct   188  GSKARDIVLEHNSVDAIIALVTNGNTQISFLRNIVWLMSNLCRNKNPAPPFNRIEPMIPV  247

Query   756  lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR  935
                LS LL  +D QVL+DACWALSYVTDDD  K+++VV S AVP+LV+LL   + P+II PALR
Sbjct   248  LSALLDHEDAQVLSDACWALSYVTDDDVEKLESVVASGAVPKLVRLLGTNNPAIITPALR  307

Query   936  SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ  1115
                SVGNIVTG D+QTD VIA+  LP L   LL+H K+ IVKEAAWTVSNITAGNQ QIQ V+
Sbjct   308  SVGNIVTGNDKQTDAVIAANALPLLTNLLRHTKNTIVKEAAWTVSNITAGNQSQIQHVLD  367

Query  1116  AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP  1295
                +GIF  L  VL  GDFK+QKEAAWAVTNTT G+ EQI+ L+EKY I+KP+ DLL+ KD
Sbjct   368  SGIFNVLIDVLANGDFKSQKEAAWAVTNTTGGSTEQIIQLVEKYPIMKPYCDLLEAKDT  427

Query  1296  RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT  1475
                RT++VV +G++N+F  A ++GG ENLC + EE+G LDKLETLQ HENE++Y KA  +I+T
Sbjct   428  RTVRVVLSGVANIFQFASQIGGVENLCTLFEEIGALDKLETLQNHENEDIYQKALLLIET  487

Query  1476  YFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
                YF + +D    E AP+EVNGALEFN T P+   GG++F
Sbjct   488  YFCDAED-VNPECAPKEVNGALEFNPTTPQ--NGGFSF  522
```

AGAP009792-PA-like protein [Anopheles sinensis]

Sequence ID: **gb|KFB49217.1|** Length: 501 Number of Matches: 1
Range 1: 8 to 492

Score	Expect	Method	Identities	Positives	Gaps	Frame
620 bits(1600)	0.0()	Compositional matrix adjust.	302/485(62%)	385/485(79%)	2/485(0%)	+3

Features:

```
Query    42  NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDED-LTSPLKELNGQS  218
                N+R  SYK  S  T  + R RRHEVT+ELRK+KKEDQ+FKRRNI ++D  TSPL+E N QS
Sbjct     8  NNRLASYKNASKTTTELRQRRHEVTVELRKNKKEDQLFKRRNITEDDGPTSPLQENNAQS   67

Query   219  PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN  398
                PV L  +EI+   + S   ++F  +Q+ARKMLSRE+NPPID +IG G+VPIC++FL+   +
```

```
Sbjct   68    PVTLKFEEIMQYVKSGVPNKEFAAVQAARKMLSREKNPPIDKIIGLGMVPICVKFLEAAD   127

Query   399   NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD   578
              LQFEAAWALTNIASGTSDQT+ VI+ +A+P F+ LL S S+ +AEQAVWALGNIAGD
Sbjct   128   RPALQFEAAWALTNIASGTSDQTKAVIDAHAIPRFIDLLSSPSVTAEQAVWALGNIAGD   187

Query   579   GAAARDIVIHHNVIDGILPLINN-ETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv   755
              G+ ARD V+ +N ++ I+ L+ N  TP+SFLRNIVWLMSNLCRNKNP+PPF++++ ++PV
Sbjct   188   GSKARDNVLDYNSVEAIISLVRNPNTPISFLRNIVWLMSNLCRNKNPAPPFNRIEPMIPV   247

Query   756   lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR   935
              LS LL  +D QVL+DACWALSYVTDDD  K+++VV +  VP+LV+LL  + P+II PALR
Sbjct   248   LSVLLDHEDAQVLSDACWALSYVTDDDAVKLESVVAAGTVPKLVRLLGTNNPAIITPALR   307

Query   936   SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ   1115
              SVGNIVTG D QTD VIA+G LP L  LL+H K+ IVKEAAWTVSNITAGNQ QIQ V+
Sbjct   308   SVGNIVTGNDTQTDAVIAAGALPLLANLLRHTKNTIVKEAAWTVSNITAGNQAQIQQVLN   367

Query   1116  AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP   1295
               G+F  L  VL +GDFK+QKEAAWAVTNTTT G+ EQI+ L+EKY I+KP+ DLL+ KD
Sbjct   368   WGVFNVLIDVLARGDFKSQKEAAWAVTNTTTGGSTEQIIQLVEKYPIMKPYCDLLEAKDS   427

Query   1296  RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT   1475
              RT++VV TG++N+F +A  +GG ENLC + EE+GGLDKLE LQ H+NE++Y+KA  +I+T
Sbjct   428   RTVRVVLTGVTNIFQIASNIGGVENLCTLFEEIGGLDKLEALQSHDNEDIYRKALELIET   487

Query   1476  YFSNG   1490
              YF +G
Sbjct   488   YFCDG   492
```

PREDICTED: importin subunit alpha [Microplitis demolitor]

Sequence ID: **ref|XP_008555196.1|** Length: 524 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 9 to 524

Score	Expect	Method	Identities	Positives	Gaps	Frame
575 bits(1481)	0.0()	Compositional matrix adjust.	298/520(57%)	381/520(73%)	5/520(0%)	+3

Features:

```
Query   33    ADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLK-ELN   209
              A S SR  +K ++  ++D+R RR+EV+IELRK++++DQ+ KRRNI E   P    E +
Sbjct   9     ATSASRLAKFKYHN-KSEDARRRRNEVSIELRKARRDDQLLKRRNITIEATEIPKSPESS   67

Query   210   GQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQ   389
                QSP+ +SVDEIV+ M  +D  Q   Q+ RKMLSRE++PPID MI  GIVP C+ FL
Sbjct   68    VQSPILMSVDEIVSGMTCDDPHLQLQATQACRKMLSREKHPPIDTMISKGIVPRCVEFLG   127

Query   390   NTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNI   569
              +   N  LQFEAAWALTN+ASGTS+QT  VI + A+P  VALL+S + N+AEQAVWALGNI
Sbjct   128   HNWNPALQFEAAWALTNVASGTSEQTHIVINNGAIPKLVALLKSPASNVAEQAVWALGNI   187

Query   570   AGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRll   749
              AGDG A RD+V+ H  +  ++ LI  E+ LSF+RNIVW +SNLCRNKNP PPF   V+  L
Sbjct   188   AGDGPATRDLVLQHECMPILISLIQPESGLSFIRNIVWTLSNLCRNKNPPPPFAIVQTAL   247

Query   750   pvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPA   929
              P LS LL    D  VLAD+CWALSY+TD  N KIQ V++S  VP+LV+LL    E +++ PA
Sbjct   248   PTLSSLLDFTDGDVLADSCWALSYLTDGTNEKIQTVLESGVVPKLVRLLGSPEVTVLTPA   307

Query   930   LRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAV   1109
              LR+VGNIVTG D QTD +I +GGL +L LLL+H ++NIVKEAAWT+SNITAGN KQIQ +
Sbjct   308   LRAVGNIVTGNDTQTDAIINAGGLDKLRLLLKHKRTNIVKEAAWTISNITAGNSKQIQYI   367

Query   1110  IQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTK   1289
              I AGI    L  VLE GDFK+QKEAAWAVTN T+ GT EQ+V L+++  +L PF +LLD K
Sbjct   368   IDAGIISPLIEVLEIGDFKSQKEAAWAVTNLTSGGTIEQLVLLVQE-GVLGPFCNLLDAK   426

Query   1290  DPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAII   1469
              D +T+ VV  GL+N+   A K+G  EN+ +MVEE+GGLDKLE LQ HENE+VY+KA A+I
Sbjct   427   DYKTVMVVLDGLTNILNAANKMGQIENVAIMVEELGGLDKLEALQHHENEKVYQKAIAMI   486

Query   1470  DTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              D +FS+GDDE  QELAP+ +    F A+   AP+GG+ F
Sbjct   487   DAFFSDGDDE-NQELAPEANDEQFNFQASG-NAPQGGFQF   524
```

PREDICTED: importin subunit alpha [Fopius arisanus]

Sequence ID: **ref|XP_011305770.1|** Length: 520 Number of Matches: 1

▸ **See 2 more title(s)**
Range 1: 5 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
566 bits(1459)	0.0()	Compositional matrix adjust.	296/522(57%)	382/522(73%)	8/522(1%)	+3

Features:

```
Query   30    KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRN--INDEDLTSPLKE   203
              +A+ NSR  +K N+  T+D+R RR+EV++ELRK++++DQ+ KRRN  I   E   P
Sbjct   5     EANHNSRLAKFK-NNFKTEDARRRRNEVSVELRKARRDDQLLKRRNLTIEPEPLKSPDDH   63

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
              +  QSP+ +S+DEIVA MNS D+ Q   Q+ RKMLSRE++PPID+MI  GIVP CI F
Sbjct   64    V--QSPIGMSIDEIVAGMNSPDEVLQLQATQACRKMLSREKHPPIDIMICKGIVPRCIEF   121
```

```
Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
             L   +N   LQFEA+WALTN+ASGTS+QT  V  + A+P  V LL+S + N+AEQAVWALG
Sbjct  122   LSYHHNPALQFEASWALTNVASGTSEQTMIVASNGAIPKLVELLKSPATNVAEQAVWALG   181

Query  564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
             NIAGDG +ARD V+     +  +L LI  +T +SF RNIVW +SNLCRNKNP P F+ VK
Sbjct  182   NIAGDGPSARDQVLEEQCMPLLLNLIKTDTSVSFTRNIVWTISNLCRNKNPPPSFEIVKL   241

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
             LPVL++LL   +D  +LAD CWALSY+TD +N KIQAVVDS  VP+LV LL    E S++
Sbjct  242   ALPVLNRLLTGEDPDILADTCWALSYLTDGENFKIQAVVDSGVVPKLVALLASPEASVLT   301

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
             PALR+VGNIVTG D QTD +I +GGLP L  LL+H +NIVKEAAWT+SNITAGN +QIQ
Sbjct  302   PALRAVGNIVTGNDTQTDAIINAGGLPNLKGLLEHKRVNIVKEAAWTISNITAGNHEQIQ   361

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
             VI AGI    L  VL  GDFKAQKEAAWAVTN T+ G+  Q+V LI+ + +LKPF ++L
Sbjct  362   HVINAGILPPLVHVLATGDFKAQKEAAWAVTNLTSGGSIPQLVQLIQ-HGVLKPFCNILQ   420

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
              KD + I VV  GL+N+    AEK+G  E + LM+EE+ GLDKLE LQ HENE++Y+KA +
Sbjct  421   AKDQKAIIVVLDGLTNILNAAEKMGQLEQVALMIEEVRGLDKLEDLQHHENEKIYQKAAS   480

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             +IDT+FS  + E+ Q +AP  V+G L+F++T    AP+GG+ F
Sbjct  481   MIDTFFSEPESESAQ-IAPATVDGQLDFHSTD-SAPQGGFQF   520
```

PREDICTED: importin subunit alpha [Diachasma alloeum]

Sequence ID: **ref|XP_015123786.1|** Length: 520 Number of Matches: 1

▶ **See 1 more title(s)**

Range 1: 5 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
565 bits(1457)	0.0()	Compositional matrix adjust.	291/522(56%)	382/522(73%)	8/522(1%)	+3

Features:

```
Query  30    KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRN--INDEDLTSPLKE   203
             +A+ NSR   +K N+  ++D+R RR+EV++ELRK++++DQ+ KRRN   I  E L SP +
Sbjct  5     EANHNSRLAKFK-NNFKSEDARRRRNEVSVELRKARRDDQLLKRRNLTIEPEPLKSPDEH   63

Query  204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
             +  QSP+ +S+DEIVA MN  D+  Q    Q+ RKMLSRE++PPID+MI  GIVP CI F
Sbjct  64    V--QSPIGMSIDEIVAGMNGLDEVLQLQATQACRKMLSREKHPPIDIMISKGIVPRCIEF   121

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
             L   +N   LQFEA+WALTN+ASGTS+QT  V  + A+P  V L++S + N+AEQAVWALG
Sbjct  122   LSYHHNPALQFEASWALTNVASGTSEQTMIVASNGAIPKLVELMKSPAKNVAEQAVWALG   181

Query  564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
             NIAGDG  ARD V+     +  +L LI  +T +SF RNIVW +SNLCRNKNP P F+ VK
Sbjct  182   NIAGDGPEARDQVLEEQSMPLLLNLIKTDTSVSFTRNIVWTISNLCRNKNPPPSFEIVKL   241

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
             LPVL++LL    D  +LADACWALSY+TD +N KIQAVVDS  VP+LV LL    E +++
Sbjct  242   ALPVLNRLLTGDDPDILADACWALSYLTDGENYKIQAVVDSGVVPKLVALLASPEATVLS   301

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
             PALR+VGNIVTG D QTD +I +GGLP L  LL+H +NIVKEAAWT+SNITAGN +QIQ
Sbjct  302   PALRAVGNIVTGNDTQTDAIINAGGLPNLKRLLEHKRVNIVKEAAWTISNITAGNHEQIQ   361

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
             VI AGI    L  VL  GDFKAQKEAAWAVTN T+ G+  Q+V LIE +++L+PF ++L
Sbjct  362   HVINAGILPPLIHVLATGDFKAQKEAAWAVTNLTSGGSVHQLVQLIE-HRVLEPFCNILQ   420

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
              KD + + VV  GL+N+ + AEK+G  E + +M+EE+GGLDKLE LQ HENE++Y+KA +
Sbjct  421   AKDQKAVIVVLDGLTNILSAAEKMGQLEQVAMMIEEVGGLDKLEDLQHHENEKIYQKAAS   480

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             +IDT+FS+ + E  Q +AP+ V+G   F+ T    AP+GG+ F
Sbjct  481   MIDTFFSDAESENAQ-IAPETVDGQFNFHPTD-SAPQGGFQF   520
```

PREDICTED: importin subunit alpha [Orussus abietinus]

Sequence ID: **ref|XP_012276606.1|** Length: 525 Number of Matches: 1
Range 1: 5 to 525

Score	Expect	Method	Identities	Positives	Gaps	Frame
551 bits(1419)	0.0()	Compositional matrix adjust.	285/527(54%)	374/527(70%)	13/527(2%)	+3

Features:

```
Query  30    KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELN   209
             + + +SR   +K NS    + R RR+E ++ELRK++K++QM KRRNIN   +T PL  L+
Sbjct  5     EGEHSSRLAKFKFNS-KHDEVRRRRNETSVELRKARKDEQMLKRRNINV--VTEPLSPLD   61

Query  210   GQSPVQLS-------VDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVP   368
              SP  +        V +I++ MNS    Q G Q+ RKMLS+ERNPPID MI  GIVP
Sbjct  62    PLSPPDMKSSVGLMDVTQIISNMNSSVPALQLQGTQACRKMLSKERNPPIDDMIQEGIVP   121

Query  369   ICIRFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQA   548
              C+ FL   +N   LQFEAAWALTN+ASGTSDQT+ VI+H A+P   LL+S S+N+AEQA
Sbjct  122   RCVEFLSYNDNPPLQFEAAWALTNVASGTSDQTKVVIKHGAIPKLIELLKSPSLNVAEQA   181
```

```
Query  549   VWALGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF   728
             VWALGNIAGDG   RD+V+ H+ +  +L LI  +TP+SF RN+VW +SNLCRNKNP PPF
Sbjct  182   VWALGNIAGDGPVPRDLVLGHDALPLLLELIKPDTPVSFTRNLVWTLSNLCRNKNPPPPF   241

Query  729   DQVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDE   908
             VK  LPVL++LL   D VLADACWALSY++D +N KI+AVV+S  +P+LV+LL   E
Sbjct  242   QTVKAALPVLNRLLSYADNDVLADACWALSYLSDGENEKIEAVVNSGVIPKLVELLASAE   301

Query  909   PSIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSIVKEAAWTVSNITAGN   1088
             +I+ PALR+VGNIVTG D QTD VI +GGL  LG LL H + NI+KEAAW +SNI AGN
Sbjct  302   VTILTPALRAVGNIVTGNDVQTDAVITAGGLKHLGALLHHKRVNIIKEAAWAISNIAAGN   361

Query  1089  QKQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPF   1268
             QIQ +I AG+    L  VL+KGDFK +QKEAAWA+TN T+ GT +Q+  LI+   IL+PF
Sbjct  362   HNQIQHIINAGLLPSLIHVLQKGDFKSQKEAAWAITNFTSGGTVQQLAQLIQ-LGILEPF   420

Query  1269  IDLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVY  1448
             +L+ KD + I V+  GL+N+    A+K+G  E +  +M+EE+GGLDKLE LQQH+N+EVY
Sbjct  421   CSMLEAKDWKIILVILDGLTNILNAADKIGEVERVAMMIEEVGGLDKLEALQQHDNDEVY   480

Query  1449  KKAYAIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             +K A+IDT++S+G  E +  LAP     LEF  T+  AP+GG+ F
Sbjct  481   QKVMAMIDTFYSDGYTE-DNNLAPATEEEQLEFQPTE-AAPQGGFQF   525
```

Importin subunit alpha-2 [Zootermopsis nevadensis]

Sequence ID: **gb|KDR18936.1|** Length: 524 Number of Matches: 1

Range 1: 5 to 524

Score	Expect	Method	Identities	Positives	Gaps	Frame
546 bits(1406)	0.0()	Compositional matrix adjust.	283/525(54%)	373/525(71%)	10/525(1%)	+3

Features:

```
Query  30    KADSNSRQG---SYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDED-LTSPL   197
             ++D +SRQ   S+K   N  + R RR EV++ELRK++K+DQ+ KRRN++ ED    PL
Sbjct  5     ESDMSSRQNRLTSFKNKGKNVDEMRRRKEVSVELRKARKDDQLLKRRNLSTEDDHILPL   64

Query  198   KELNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICI   377
             +E N QSP  L+ +EI+  MNS D  RQ +  Q+ARK LSRER+PPID MI  GIVP C+
Sbjct  65    QE-NSQSPASLTTEEIIEGMNSSDDHRQLVATQAARKALSRERSPPIDAMIKSGIVPRCV   123

Query  378   RFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWA   557
             FL  +N  LQFEA+W LTNIASGTS+QT  V++H AVP  V LL S  M++ EQAVWA
Sbjct  124   EFLSRFDNPSLQFEASWVLTNIASGTSEQTSSVVKHGAVPKLVQLLGSSYMHVTEQAVWA   183

Query  558   LGNIAGDGAAARDIVIHHNVIDGILPLINNET-PLSFLRNIVWLMSNLCRNKNPSPPFDQ   734
             LGNIAGDG+ ARD+V++   +  +L LI  +T   SFLRN +VW +SNLCRNKNP PPF+I
Sbjct  184   LGNIAGDGSTARDLVLNSGAMPALLELIKPDTQKASFLRNVVWTLSNLCRNKNPPPPFEI   243

Query  735   VKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPS   914
             V+  LPV ++LL   D  VLADACWALSY+TD N KIQAV+D+  VPRLV+LL     +
Sbjct  244   VQMSLPVFNRLLHYADTDVLADACWALSYLTDGTNDKIQAVIDTGIVPRLVELLAAPSVA   303

Query  915   IIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSIVKEAAWTVSNITAGNQK   1094
             ++ PALR+VGNIVTG D QT+ +I +GGL  L  LL+H + NI+KEAAWTVSNITAGN
Sbjct  304   VLTPALRAVGNIVTGNDMQTNAIIQAGGLTYLRELLRHPRLNIMKEAAWTVSNITAGNVD   363

Query  1095  QIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFID  1274
             QIQ VI +G+ + L  VL  GDF++QKEAAWAVTN  + G+ +Q+   +++    +LKPF D
Sbjct  364   QIQEVINSGLLEPLIYVLSSGDFRSQKEAAWAVTNFMSGGSVQQLATIVQ-IGVLKPFCD   422

Query  1275  LLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKK  1454
             LL++KD + + VV  GL+N+    AEK+G  + +  +M+EE GGLDKLE LQ HENE+VY+K
Sbjct  423   LLNSKDWKIVVVVMDGLNNIMQTAEKMGEVDRVAIMIEECGGLDKLEQLQSHENEQVYQK   482

Query  1455  AYAIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             A  +ID+YFS D  A+  L P + NG L+FN    + P+ G++F
Sbjct  483   ALNMIDSYFSVVDC-ADPSLIPDQTNGQLDFNTD--RVPDAGFSF   524
```

PREDICTED: importin subunit alpha [Nasonia vitripennis]

Sequence ID: **ref|XP_008204292.1|** Length: 520 Number of Matches: 1

Range 1: 8 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
544 bits(1401)	0.0()	Compositional matrix adjust.	285/520(55%)	375/520(72%)	10/520(1%)	+3

Features:

```
Query  39    SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQ-   215
             +NSR  +K   ++R RR EV++ELRK+ K++Q+ KRRNINIED--EPLSPPSDQK
Sbjct  8     ANSRISKFKFQG-KFDEARRRTEVSVELRKAHKDNQLLKKRNINIED--EPLSPPSDQK   64

Query  216   SPV-QLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN   392
             SPV  +S+DEI+A M SED +  Q+ RKMLSRERNPPI+ MI  GIVP C+ FL Y
Sbjct  65    SPVFNMSIDEIIAGMTSEDDQAMLQATQACRKMLSRERNPPINDMIEKGIVPLCVEFLGY   124

Query  393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA   572
             +N MLQFEA WALTN+ASGTS+QT+ V+++ A+P  V LL+  ++N+AEQAVWALGNIA
Sbjct  125   HHNPMLQFEACWALTNVASGTSEQTQVVVKYGAIPKLVELLKCPAINVAEQAVWALGNIA   184

Query  573   GDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllp   752
             GDG AARD+V+    + ++ LI  ET LSF+RNIVW +SNLCRNKNP PPF+ VK   LP
Sbjct  185   GDGPAARDLVLKEGSLSLLIALITPETSLSFVRNIVWTVSNLCRNKNPPPPFEIVKDALP   244

Query  753   vlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPAL   932
```

```
                +L++LL   D  VL DACWALSY+TD  N +IQ V+DS  VP+LV+LL   E +++ PAL
Sbjct   245    LLNRLLSYPDKDVLGDACWALSYLTDGTNERIQTVLDSGVVPKLVELLGSSEVTVLTPAL    304

Query   933    RSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSIVKEAAWTVSNITAGNQKQIQAVI   1112
               R+VGNIVTG D QTD +I++G L  LG LL H + N+VKEAAWT+SNITAGN +QIQ +I
Sbjct   305    RAVGNIVTGNDLQTDTIISAGALNYLGALLTHKRVNLVKEAAWTISNITAGNDQQIQRII    364

Query   1113   QAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKD   1292
                AG+   L  VL  GDFK +QKEAAWA+TN T+ GT  Q+ L++   +L PF +LL++KD
Sbjct   365    DAGLLPLLIQVLHMGDFKSQKEAAWAITNLTSGGTVPQLALLVQ-LGVLTPFCNLLESKD    423

Query   1293   PRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIID   1472
                + + VV  GL+N+   AEK+G  + + L++EE+GGLDKLE LQ HENE VY+KA  +ID
Sbjct   424    WKCVLVVLDGLNNILNAAEKMGEVDRVALVIEEIGGLDKLEALQTHENENVYQKAVHMID    483

Query   1473   TYFSNGDDEAEQELAP-QEVNGALEFNATQPKAPEGGYTF   1589
               T+FS+G  EA+  LAP  ++G LEF AT   AP+GG+ F
Sbjct   484    TFFSDG--EADPNLAPTTNMDGQLEFQATT-TAPQGGFQF    520
```

GH20236 [Drosophila grimshawi]

Sequence ID: **ref|XP_001986958.1|** Length: 464 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 23 to 464

Score	Expect	Method	Identities	Positives	Gaps	Frame
540 bits(1392)	0.0()	Compositional matrix adjust.	282/449(63%)	343/449(76%)	7/449(1%)	+3

Features:

```
Query   243    IVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTNNSMLQFEA    422
               IV A+NS+D +RQ LGM+ ARK+    E NPPIDLMIGHGIVPIC+RFL+  +N +L+FEA
Sbjct   23     IVTAINSKDPQRQLLGMELARKLACNESNPPIDLMIGHGIVPICVRFLKCNSNDLLKFEA    82

Query   423    AWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGDGAAARDIV    602
                W LTNIA+GTS QT+CVI+ NAVP  +   LQS +M  IAEQAVWAL NIAGDGA ARDIV
Sbjct   83     TWILTNIAAGTSGQTQCVIDENAVPLLIHHLQSDNMYIAEQAVWALCNIAGDGAPARDIV    142

Query   603    IHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvlsqlllsqD    782
               I HNVI GILPLIN   PLS LR IVWLM NLC  K PSP +QVKRLLP+LS+LL+S D
Sbjct   143    IQHNVIGGILPLINKGMPLSLLRKIVWLMVNLC-GKRPSPTLEQVKRLLPMLSELLVSND    201

Query   783    IQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRSVGNIVTGT    962
                +V + ACWAL  VT DD  K+QAV+D+  VPRLV LL+  E  I+ PALR VG IV GT
Sbjct   202    SKVQSCACWALCSVTHDD--KLQAVIDAKTVPRLVHLLKSVELDILYPALRCVGLIVAGT    259

Query   963    DQQTDVVIASGGLPRLGLLLQHNKSIVKEAAWTVSNITAGNQKQIQAVIQAGIFQQLRT   1142
               DQ TDVVIA+G L  LG LL+H+  NIV+ AAWTVSNITA NQ  IQAVI +GIFQQL
Sbjct   260    DQHTDVVIAAGVLQPLGQLLEHSDRNIVELAAWTVSNITACNQAHIQAVIDSGIFQQLCH    319

Query   1143   VLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPRTIKVVQTG   1322
                +L    KA+K+AA AV+NTT SGT EQ+VDL++KYKI KPF+DLLD  DP TI VVQ G
Sbjct   320    LLGVNNIKARKQAACAVSNTTISGTYEQVVDLLDKYKIFKPFVDLLDVPDPHTIMVVQIG    379

Query   1323   LSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTYFSNGDDEA   1502
               LSNLF LA+ LG  +++ LM E++GGLDKLE LQ HE+E++Y+ A  II  YFS  ++++
Sbjct   380    LSNLFDLAKNLGDPKDIFLMFEQLGGLDKLEKLQLHESEDIYENACDIISNYFSEAEEDS    439

Query   1503   EQELAPQEVNGALEFNATQPKAPEGGYTF   1589
               EQ +    +N  +EFNATQP+ P+GGY+F
Sbjct   440    EQPV----INDGVEFNATQPRKPDGGYSF   464
```

PREDICTED: importin subunit alpha [Athalia rosae]

Sequence ID: **ref|XP_012257423.1|** Length: 521 Number of Matches: 1

▸ **See 2 more title(s)**
Range 1: 5 to 521

Score	Expect	Method	Identities	Positives	Gaps	Frame
538 bits(1387)	0.0()	Compositional matrix adjust.	282/521(54%)	373/521(71%)	5/521(0%)	+3

Features:

```
Query   30     KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKEL    206
               +A++  R   +K N+   +D+R RR E  +ELRK +K+DQ+ KRRNI+ D++   SPL +
Sbjct   5      EANATGRMSKFK-NASKPEDARRRRNEGFVELRKVRKDDQLLKRRNISADDEPLSPLGDH    63

Query   207    NGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFL    386
                + +  ++++I+  M+S+D+  Q   Q+ RKMLSRE+NPPID MI  GIVP C+ FL
Sbjct   64     AMLNQIGPTIEDIIIGMSSKDETIQLQSTQACRKMLSREKNPPIDNMIQKGIVPRCVEFL    123

Query   387    QNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGN    566
                + +N  LQFEAAWALTN+ASGTS+QT  VI H A+P+   ALL+S S PSPN AEQAVWALGN
Sbjct   124    THHHNPALQFEAAWALTNVASGTSEQTNVVINHGAIPYLTALLKSPSPNVAEQAVWALGN    183

Query   567    IAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl    746
               IAGDG  ARD+V+ +   +L LI  +T +  RNIVW +SNLCRNKNP P F++VK
Sbjct   184    IAGDGHVARDLVLANKALPLLLDLIKPDTQVTIARNIVWTLSNLCRNKNPPPDFEKVKAC    243

Query   747    lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP    926
               LPVL++LL   D +LADACWALSY+TD  + KIQAVVD   VP LV LL   + +++ P
Sbjct   244    LPVLNRLLGYADKDILADACWALSYLTDGTDNKIQAVVDCGVVPNLVALLSSTKVTVLTP    303

Query   927    ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSIVKEAAWTVSNITAGNQKQIQA   1106
               ALR+VGNIVTGTD QTD +IA+GGL  L  LLQH + NIVKEAAWT+SNITAGN  QIQ
```

```
Sbjct   304   ALRAVGNIVTGTDVQTDAIIAAGGLRHLVGLLQHERLNIVKEAAWTISNITAGNVDQIQQ   363
Query   1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT  1286
              VI+AG+    L  VL+ GDFK+QKEAAWAVTN T+ G+ +Q+  L++     L P   LLD
Sbjct   364   VIEAGLLPPLLHVLQSGDFKSQKEAAWAVTNLTSGGSVQQLAQLVQ-LGALDPLCALLDA   422

Query   1287  KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI  1466
              KD +T+ VV  GL+N+    A+K+G  E + +M+EE+GGLDKLE LQ H NE+VY+KA A+
Sbjct   423   KDWKTVLVVLDGLTNILTAAQKMGEVERVAVMIEEVGGLDKLENLQHHVNEQVYQKAMAM   482

Query   1467  IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              I+TYFS+G+ E E  +AP   +G LEF  T    PEGG+ F
Sbjct   483   IETYFSDGEGE-ETTIAPTTSDGQLEFKTTDTN-PEGGFQF   521
```

PREDICTED: importin subunit alpha [Apis florea]

Sequence ID: ref|**XP_003698390.1**| Length: 520 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 5 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
535 bits(1379)	1e-179()	Compositional matrix adjust.	285/521(55%)	385/521(73%)	6/521(1%)	+3

Features:

```
Query   30    KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKEL   206
              +AD +SR+ ++K N+    +++R RR E+++ELRK++K++Q+ KRRN+N   ++  +P+ E
Sbjct   5     EADCHSRKANFKFNN-KHEEARRRRSEISVELRKARKDEQLLKRRNLNVGKESQNPVSES   63

Query   207   NGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFL   386
              N  SP+ +S++EIV  M S DQ  Q+ RKMLSRE+NPPID+MI  GIVP C+ FL
Sbjct   64    N-LSPISVSIEEIVNGMKSSDQTIQLQATQACRKMLSREKNPPIDIMIQRGIVPRCVEFL   122

Query   387   QNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGN   566
                +N+ LQFEAAWALTN+ASGTS+QT  V++H A+P  VALL+S S N+AEQAVWALGN
Sbjct   123   DYHHNAALQFEAAWALTNVASGTSEQTHVVVKHGAIPKLVALLKSASPNVAEQAVWALGN   182

Query   567   IAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl   746
              IAGDG AARD+V+ ++ +  +L LI   +T ++F RNIVW +SNLCRNKNP PPF+ V+
Sbjct   183   IAGDGPAARDLVLGYDAMPLLLELIKPDTSVTFTRNIVWTLSNLCRNKNPPPPFEIVRTA   242

Query   747   lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP   926
              LPVL++LL + D  +LADACWALSY+TD  N KIQAVV+S  +P+LV+LL    E +++ P
Sbjct   243   LPVLNRLLSNNDKDILADACWALSYLTDGSNDKIQAVVESGVIPKLVQLLTSTEVTVLTP   302

Query   927   ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA  1106
              ALR+VGNIVTG D QTD +I++GGL  LGLLLQH++ NIVKEAAWT+SNITAGN +QIQ
Sbjct   303   ALRAVGNIVTGNDMQTDAIISAGGLQHLGLLLQHHRINIVKEAAWTISNITAGNIEQIQH   362

Query   1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT  1286
              VI AG+    L  VLE GDFK+QKEAAWAVTN T+ G+ +Q+  L++     +L PF +LL+
Sbjct   363   VINAGLLPLLIHVLESGDFKSQKEAAWAVTNLTSGGSVQQLAQLVQ-LGVLAPFCNLLEA   421

Query   1287  KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI  1466
              KD +TI VV  GL+N+F  AEK+G  E + +M+EE+GGLDKLE LQ H+ E+VY+KA A+
Sbjct   422   KDWKTIIVVLDGLTNIFNAAEKMGEIERVAIMIEEVGGLDKLEALQHHDVEQVYQKATAM   481

Query   1467  IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              ID +FS + E       P  +G LEF  +    + G+ F
Sbjct   482   IDNFFSEPEAEESTLTTPTAADGQLEFKPAE--TAQKGFNF   520
```

PREDICTED: importin subunit alpha [Polistes canadensis]

Sequence ID: ref|**XP_014609001.1**| Length: 531 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 14 to 500

Score	Expect	Method	Identities	Positives	Gaps	Frame
535 bits(1377)	3e-179()	Compositional matrix adjust.	278/490(57%)	363/490(74%)	5/490(1%)	+3

Features:

```
Query   36    DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN--DEDLTSPLKELN   209
              D NSR ++K NS    +++R RR E++IELRK+KKE+Q+FKRRN+N   +++ TS   E N
Sbjct   14    DRNSRIANFKFNS-KHEEARRRRSEISIELRKAKKENQLFKRRNLNIVEDEETSIFTE-N   71

Query   210   GQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQ   389
               P   S+++IVA M S D+  Q   +Q+ RKMLSRE+NPPID MI  GIVP CIRFL
Sbjct   72    NIKPTSSSIEDIVANMLSSDETIQLQAVQACRKMLSREKNPPIDSMINLGIVPQCIRFLD   131

Query   390   NTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNI   569
              +N  LQFEA+WALTN+ASGTS+QT  V+++ A+P  + LL+S S N+AEQAVWALGNI
Sbjct   132   YHHNPALQFEASWALTNVASGTSEQTYVVVKNGAIPKLINLLKSNSSNVAEQAVWALGNI   191

Query   570   AGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRll   749
              AGDG   RD+V+ + ++   L LI  +T ++F RNIVW +SNLCRNKNP PPF+ VK  L
Sbjct   192   AGDGPVTRDLVLANGLLPVLLSLIKPDTNITFARNIVWTLSNLCRNKNPPPPFEVVKTAL   251

Query   750   pvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPA   929
              PVL++LL + D  +LADACWALSY+TD  N KIQAVV+S  +P+LV+LL    E +++ PA
Sbjct   252   PVLNRLLSNTDKDILADACWALSYLTDGPNEKIQAVVDSGITPKLVELLSSTEVTVLTPA   311

Query   930   LRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAV  1109
              LR+VGNIVTG D QTD +I++GGL  L LLL+HN+ NIVKEAAWT+SNITAG  +QIQ V
Sbjct   312   LRAVGNIVTGNDVQTDAIISAGGLNHLALLLEHNRINIVKEAAWTISNITAGTVQQIQHV   371
```

```
Query  1110  IQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTK  1289
             I A + + L  VL  GD+K+QKEAAWA+TN T+  + + I  LI+    IL PF +LLD+K
Sbjct  372   INANVLRPLCQVLRVGDYKSQKEAAWAITNLTSGCSVKHIAYLIQT-GILSPFCNLLDSK  430

Query  1290  DPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAII  1469
             D +T+ VV  GLSN+   + K+G  E + LM+EE GGLDK+E LQQ+ENE+VY++A AII
Sbjct  431   DWKTVLVVLDGLSNILEASAKMGEIERVTLMIEENGGLDKIECLQQNENEQVYQRAIAII  490

Query  1470  DTYFSNGDDE   1499
             DTYFS+ D E
Sbjct  491   DTYFSDCDQE   500
```

PREDICTED: importin subunit alpha-1 [Ceratosolen solmsi marchali]

Sequence ID: ref|XP_011500399.1| Length: 520 Number of Matches: 1

Range 1: 9 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
533 bits(1372)	1e-178()	Compositional matrix adjust.	282/519(54%)	372/519(71%)	10/519(1%)	+3

Features:

```
Query  42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMF-KRRNIN-DEDLTSPLKELNGQ  215
             NSR   +K      + ++R +R EVTIE+RK+ K+ Q+F KRRNIN D++L SP KE   +
Sbjct  9     NSRISKFKFQG-KSDEARRKRTEVTIEMRKANKDRQLFEKRRNINFDDELDSPTKE---K  64

Query  216   SPVQ-LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN  392
             S +Q +S+DEI+  M S D+  Q    Q+ RKMLS+E+NPPI+ MI  GI+P+CI+FL
Sbjct  65    SQIQTMSIDEIIIGMQSTDELVQLEATQACRKMLSQEKNPPINDMIEKGIIPLCIKFLGY  124

Query  393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA  572
             + SMLQFEA WALTN+ASGTS+QT  VI+H A+  V LL+S  MN+AEQAVWALGNIA
Sbjct  125   HHRSMLQFEACWALTNVASGTSEQTLVVIKHGAIVKLVELLKSPKMNVAEQAVWALGNIA  184

Query  573   GDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllp  752
             GDG   RD+V+  + +  I+ L+N ETP+SF+RNIVW +SNLCRNKNP+PPFD VK+ LP
Sbjct  185   GDGPLPRDMVLKEDALPHIILLLNPETPISFVRNIVWTLSNLCRNKNPAPPFDIVKQALP  244

Query  753   vlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPAL  932
             +L++LL    D  +LADACWALSY+TD  N KIQ V++S  VP+LV+LL   E +++ PA+
Sbjct  245   LLNRLLSYTDKDILADACWALSYLTDGPNDKIQTVLESGIVPKLVELLGSSEVTVLTPAV  304

Query  933   RSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVI  1112
             R VGNIVTG D QTD +IA+GGL   L  LL H K NIVKEAAW +SNITAGN +QIQAVI
Sbjct  305   RVVGNIVTGNDAQTDSIIAAGGLNYLSALLLHKKFNIVKEAAWMISNITAGNHEQIQAVI  364

Query  1113  QAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKD  1292
              AG+    L  +L  GDFK+QKEAAWA+TN T+  + + I  LI+   IL PF +LL  KD
Sbjct  365   DAGLIPPLIQILSTGDFKSQKEAAWAITNLTSGGTVPQLVYLV-KSGLLAPFCNLLESKD  423

Query  1293  PRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIID  1472
             + + VV  GL ++   +AEK+    + + LM+EE+GGLDKLE LQ H+NEE+Y+K  AIID
Sbjct  424   WKCVNVVLDGLVHILNVAEKMEEVDKVALMIEEVGGLDKLEALQTHKNEEIYEKTLAIID  483

Query  1473  TYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             +F  G+ +     +   E  G LEF A+   P+GG+ F
Sbjct  484   KFFCEGESDPNVLPSTNE-EGQLEFQASI-ATPQGGFQF   520
```

PREDICTED: importin subunit alpha-like [Apis dorsata]

Sequence ID: ref|XP_006608944.1| Length: 519 Number of Matches: 1

Range 1: 5 to 519

Score	Expect	Method	Identities	Positives	Gaps	Frame
533 bits(1372)	1e-178()	Compositional matrix adjust.	286/521(55%)	386/521(74%)	7/521(1%)	+3

Features:

```
Query  30    KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKEL  206
             +AD +SR+ ++K N+    +++R RR E+++ELRK++K++Q+ KRRN+N  ++  +P+ E
Sbjct  5     EADCHSRKANFKFNN-KHEEARRRRSEISVELRKARKDEQLLKRRNLNVGKESQNPVSES  63

Query  207   NGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFL  386
             N  SP+ +S++EIV  M S DQ  Q    Q+ RKMLSRE+NPPID+MI  GIVP C+ FL
Sbjct  64    N-LSPISVSIEEIVNGMKSSDQTIQLQATQACRKMLSREKNPPIDIMIQRGIVPRCVEFL  122

Query  387   QNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGN  566
              +N+ LQFEAAWALTN+ASGTS+QT  V++H A P  VALL+S S N+AEQAVWALGN
Sbjct  123   DYHHNAALQFEAAWALTNVASGTSEQTHVVVKHGAIPKLVALLKSASPNVAEQAVWALGN  182

Query  567   IAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl  746
             IAGDG AARD+V+ ++ +   +L LI  +T ++F RNIVW +SNLCRNKNP PPF+ V+
Sbjct  183   IAGDGPAARDLVLGYDAMPLLLLELIKPDTSVTFTRNIVWTLSNLCRNKNPPPFEIVRTA  242

Query  747   lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP  926
             LPVL++LL  + D  +LADACWALSY+TD  N KIQAVV+S  VP+LV LL   E +++ P
Sbjct  243   LPVLNRLLSNNDKDILADACWALSYLTDGSNDKIQAVVESGVIPKLVQLLTSTEVTVLTP  302

Query  927   ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA  1106
             ALR+VGNIVTG D QTD +I++GGL  LGLLLQH++ NIVKEAAWT+SNITAGN +QIQ
Sbjct  303   ALRAVGNIVTGNDMQTDAIISAGGLQHLGLLLQHHRINIVKEAAWTISNITAGNIEQIQH  362

Query  1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT  1286
             VI AG+    L  VLE GDFK+QKEAAWAVTN T+ G+ +Q+  L++   +L PF +LL+
Sbjct  363   VINAGLLPLLIHVLESGDFKSQKEAAWAVTNLTSGGSVQQLAQLVQ-LGVLAPFCNLLEA  421

Query  1287  KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI  1466
```

```
Sbjct  422   KD +TI VV  GL+N+F   AEK+G   E + +M+EE+GGLDKLE  LQ H+ E+VY+KA A+
             KDWKTIIVVLDGLTNIFNAAEKMGEIERVAIMIEEVGGLDKLEALQHHDVEQVYQKATAM   481

Query  1467  IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             ID +FS + E  E   L    +G LEF  +    + G+ F
Sbjct  482   IDNFFSEPEAE-ESTLTTPTADGQLEFKPAE--TAQKGFNF   519
```

PREDICTED: importin subunit alpha [Polistes dominula]

Sequence ID: **ref|XP_015191390.1|** Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 14 to 529

Score	Expect	Method	Identities	Positives	Gaps	Frame
533 bits(1373)	1e-178()	Compositional matrix adjust.	281/520(54%)	372/520(71%)	6/520(1%)	+3

Features:

```
Query  36    DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN--DEDLTSPLKELN   209
             + NSR  ++K NS     +++R RR E+++ELRK+KKE+Q+FKRRN+N   +E+   S L E N
Sbjct  14    ERNSRIANFKFNS-KHEEARRRRSEISVELRKAKKENQLFKRRNLNIAEEEEASVLTENN   72

Query  210   GQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQ   389
              Q P   S+++I+A M S D   Q   +Q+ RKMLSRE+NPPID MI  GIVP+CI FL
Sbjct  73    IQ-PTSSSIEDIIANMLSFDVTIQLQAVQACRKMLSREKNPPIDTMINLGIVPLCIGFLD   131

Query  390   NTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNI   569
              +N   LQFEA+WALTN+ASGTS+QT  V++H A+P   + LL+S S N+AEQAVWALGNI
Sbjct  132   YHHNPALQFEASWALTNVASGTSEQTYVVVVKHGAIPKLINLLKSNSANVAEQAVWALGNI   191

Query  570   AGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRll   749
             AGDG   RD+V+ + ++  +L LI  +T ++F RNIVW +SNLCRNKNP PPFD VK  L
Sbjct  192   AGDGPVTRDLVLANGLLPVLLSLIKPDTNITFTRNIVWTLSNLCRNKNPPPPFDVVKTAL   251

Query  750   pvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPA   929
             PVL++LL    D +LADACWALSY+TD  N  IQAVVDS   P+LV+LL   E +++ PA
Sbjct  252   PVLNRLLSHTDKDILADACWALSYLTDGPNEKIQAVVDSGITPKLVELLSYPEVTVLTPA   311

Query  930   LRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAV   1109
             LR+VGNIVTG D QTD +I++GGL  L LLLQHN+ NIVKEAAWT+SNITAG  +QIQ V
Sbjct  312   LRAVGNIVTGNDVQTDAIISAGGLNHLALLLQHNRLNIVKEAAWTISNITAGTVQQIQHV   371

Query  1110  IQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTK   1289
             I A + + L  VL  GD+K+QKEAAWA+TN T+ + + I  L++    +L PF +LLD+K
Sbjct  372   INANVLRPLCQVLGGGDYKSQKEAAWAITNLTSGCSAKHIGHLLQA-GVLPPFCNLLDSK   430

Query  1290  DPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAII   1469
             D + + VV  GLSN+   + K+G  E++ LM+EE+GGLDK+E LQ +ENE+VY++A A+I
Sbjct  431   DWKIVLVVLDGLSNILEASAKMGEIEHVTLMIEEIGGLDKIEALQHNENEQVYQRAVALI   490

Query  1470  DTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             DTYFS  D E   A      L+F A + P+ G+ F
Sbjct  491   DTYFSENDQEFNAIDAKVSEGTELQFIAPDMQ-PQQGFNF   529
```

PREDICTED: importin subunit alpha-1 [Copidosoma floridanum]

Sequence ID: **ref|XP_014209910.1|** Length: 518 Number of Matches: 1

Range 1: 1 to 518

Score	Expect	Method	Identities	Positives	Gaps	Frame
531 bits(1367)	6e-178()	Compositional matrix adjust.	274/524(52%)	371/524(70%)	8/524(1%)	+3

Features:

```
Query  24    MSKADSN-SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLK   200
             M   D N SR   +K      + ++R RR EV++ELRK+ K+DQ+ K+RNI D D   PL
Sbjct  1     MPAPDMNASRISKFKFQG-KSDEARRRRAEVSVELRKAHKDDQLLKKRNI-DIDENEPLS   58

Query  201   ELNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIR   380
             + +SPV +++DE++  M S+++    Q+ RKMLS  KNPPIDEMI  GIVPICI
Sbjct  59    PPSAKSPVNMTIDEVLCGMQSDNEMVRLQATQACRKMLSCQKNPPIDEMISKGIVPICIE   118

Query  381   FLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWAL   560
             FL+  N++MLQFE+ WALTN+ASGTS+QT+ VI+  A+P   + LLQS + N+AEQA+WAL
Sbjct  119   FLKPNNSTMLQFESCWALTNVASGTSEQTQTVIKQGAIPLLIELLQSPASNVAEQAIWAL   178

Query  561   GNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVK   740
             GNIAGDG  ARD+V+   +I+ ++ L+  ET LSF+RNIVW +SNLCRNKNPSP F+ VK
Sbjct  179   GNIAGDGPGARDLVLKEGIINLLVSLVTPETSLSFVRNIVWALSNLCRNKNPSPNFECVK   238

Query  741   RllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSII   920
             LP+L++LL    D ++L+D CWALSY+TD  N KIQAV++++ VP+LV+LL   E +I+
Sbjct  239   EALPLLNRLLNYNDKEILSDTCWALSYLTDGPNEKIQAVIEANVVPKLVELLASPEVTIL   298

Query  921   VPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQI   1100
              PALR+VGNIVTG+D QTD VIA G L   G LL H K+NIVKEAAW VSN+TAGN +QI
Sbjct  299   TPALRAVGNIVTGSDIQTDTVIAHGALRYFGNLLSHKKTNIVKEAAWAVSNVTAGNVEQI   358

Query  1101  QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL   1280
             Q VI A I   L   V+ +GDFK++KEA WA+TN T+ +  +QI  I + LKP  DLL
Sbjct  359   QQVIDANIIPPLINVMHQGDFKSKKEATWAITNLTSGGNVNQIA-FIVQCGALKPLCDLL   417

Query  1281  DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY   1460
             ++ D R I +V  GL+ +   AEK+G T+ + LM+EE+GGLDKLE LQ+HENEE+Y+KA
Sbjct  418   ESNDGRCISIVLDGLNYILTAAEKMGETDRVALMIEEVGGLDKLEALQRHENEEIYEKAA   477

Query  1461  AIIDTYFSNGDDEAEQELAPQ-EVNGALEFNATQPKAPEGGYTF   1589
```

```
                   +ID +FS  + E +Q +AP   ++G +EF   T P  P+   + F
Sbjct   478    TMIDRFFS--EVEGDQNIAPSTNIHGQVEFQVT-PVTPQDAFQF   518
```

PREDICTED: importin subunit alpha [Cerapachys biroi]

Sequence ID: **ref|XP_011339385.1|** Length: 521 Number of Matches: 1

▸ **See 2 more title(s)**
Range 1: 10 to 512

Score	Expect	Method	Identities	Positives	Gaps	Frame
530 bits(1366)	9e-178()	Compositional matrix adjust.	269/506(53%)	367/506(72%)	4/506(0%)	+3

Features:

```
Query   45     SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDED-LTSPLKELNGQSP   221
               +R  ++K +    +++R RR+ +++ELRK+KKEDQ+ MFKRRN N ED L +     SP
Sbjct   10     ARMANFKFHG-KHEEARRRRNAMSVELRKAKKEDQLSKRRNFNTEDQLFNAADPATTSSP   68

Query   222    VQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTNN   401
               S++EIV  +N+ D+  QFL  Q+ RK+LSRE+NPPI  MI  G+V  CI+ L   +N
Sbjct   69     FS-SIEEIVDGINASDESMQFLATQTCRKLLSREKNPPISAMIEGGVVERCIQLLDCDHN   127

Query   402    SMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGDG   581
               LQFEAAW LTNIASGTS+QT+ VI+  A+P  V LL+S++ ++AEQAVWALGNIAGDG
Sbjct   128    ISLQFEAAWVLTNIASGTSEQTQNVIKCGAIPKLVRLLKSQTSSVAEQAVWALGNIAGDG   187

Query   582    AAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvls   761
               RD+V+ H + +  +L LI  + P++FLRNIVW +SNLCRNKNP PPF+ +K  LPV +
Sbjct   188    PQPRDLVLGHDAMLLLLDLIKPDIPVTFLRNIVWTLSNLCRNKNPAPPFEMIKPALPVFN   247

Query   762    qlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRSV   941
               +LL    D  VLAD CWALSY+TD  N KIQAV+D+  +P+LV+LL  ++  +I+ PALR+V
Sbjct   248    RLLNYDDDDVLADTCWALSYLTDGSNDKIQAVLDTGIIPKLVQLLMSEDGTILTPALRTV   307

Query   942    GNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQAG   1121
               GNIVTG D QTD +IA+GGLP LG LL+HN+ NIVKEAAW +SNITAGN +QIQ+VI A
Sbjct   308    GNIVTGDDAQTDTIIAAGGLPHLGALLRHNRPNIVKEAAWAISNITAGNTRQIQSVISAN   367

Query   1122   IFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPRT   1301
               +   L  VL+ GD+KAQKEAAWAVTN T+ GT +Q+++L+     +L+PF +LLD KD  T
Sbjct   368    LLPSLVEVLQFGDYKAQKEAAWAVTNLTSGGTIQQLIELVNA-GVLQPFCNLLDAKDWNT   426

Query   1302   IKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTYF   1481
               I VV  G++N+   A+K+G  + + +M+EE GGLDKLE LQQHENE++Y+K+ A+IDT+F
Sbjct   427    ITVVLDGITNILHAADKMGQMDQVAIMIEEAGGLDKLEALQQHENEQIYQKSVAMIDTFF   486

Query   1482   SNGDDEAEQELAPQEVNGALEFNATQ   1559
               S + E     +  +G +EFN  +
Sbjct   487    SGEEAETLTSEVKENADGQVEFNVKE   512
```

PREDICTED: importin subunit alpha [Harpegnathos saltator]

Sequence ID: **ref|XP_011146718.1|** Length: 517 Number of Matches: 1

▸ **See 2 more title(s)**
Range 1: 8 to 509

Score	Expect	Method	Identities	Positives	Gaps	Frame
529 bits(1363)	3e-177()	Compositional matrix adjust.	281/507(55%)	364/507(71%)	5/507(0%)	+3

Features:

```
Query   39     SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQS   218
               SN R  ++K +      ++R RR+ V+IELRK+KK++Q+ KRRN+N E+    L     S
Sbjct   8      SNGRMANFKFTN-RLDEARRRRNIVSIELRKAKKDEQLSKRRNLNTEEEVLNLS-CESIS   65

Query   219    PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN   398
               P   S+D+IVA MNS D+  Q   Q+ RK+LSRE++PPI+ MI  GIVP C+  L   +
Sbjct   66     PNFSSIDDIVAGMNSPDETVQLQATQTCRKLLSREKHPPIETMINCGIVPRCVELLDCNH   125

Query   399    NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD   578
               N  LQFEAAWALTN+ASGT++QT+ VI++ AVP   V LL+S S ++AEQAVWALGNIAGD
Sbjct   126    NVALQFEAAWALTNVASGTTEQTQVVIKYGAVPRLVMLLKSPSPSVAEQAVWALGNIAGD   185

Query   579    GAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvl   758
               G + RD+++ H+ +  +L LI  +T +SF+RNIVW +SNLCRNKNP PPF+ V+  LP L
Sbjct   186    GPSTRDLILGHDAMPLLLDLIKPDTSVSFMRNIVWTLSNLCRNKNPPPPFEIVQTALPAL   245

Query   759    sqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRS   938
               ++LL S D  +LADACWALSY+TD  N KIQ V+DS  V +LV+LL   E +++ PALR+
Sbjct   246    NRLLTSTDKDILADACWALSYLTDGSNDKIQVVLDSGIVSKLVELLSSQEGTVLTPALRT   305

Query   939    VGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQA   1118
               VGNIVTG D QTD +I +GGL  LG LL H + NIVKEAAW +SNITAGN +QIQ VI A
Sbjct   306    VGNIVTGDDAQTDSIIIAGGLTHLGNLLCHPRKNIVKEAAWAISNITAGNTEQIQHVISA   365

Query   1119   GIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPR   1298
               GI    L  VL+ GDFKAQKEAAWAVTN T+ G+ +Q+ DL+ +      +L P  DLL TKD
Sbjct   366    GILTPLVQVLKSGDFKAQKEAAWAVTNLTSGGSIQQLADLVQA-GVLPLCDLLVTKDWD   424

Query   1299   TIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTY   1478
               TI V+  GL+N+    AEKLG  E + ++VEE GGLDKLE LQ HENE +Y+K+  +IDT+
Sbjct   425    TIIVILDGLNNILHAAEKLGQVEQIAIIVEEAGGLDKLEALQHHENERIYQKSMTMIDTF   484

Query   1479   FSNGDDEAEQELAPQEVNGALEFNATQ   1559
               FS GD E E ELAP   +G LEF A++
```

importin subunit alpha-2-like protein [Lasius niger]

Sequence ID: **gb|KMR04943.1|** Length: 528 Number of Matches: 1

Range 1: 14 to 528

Score	Expect	Method	Identities	Positives	Gaps	Frame
529 bits(1363)	4e-177()	Compositional matrix adjust.	273/518(53%)	369/518(71%)	4/518(0%)	+3

Features:

```
Query   39    SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQS   218
              ++ R    +K N+    +++R RR+ +++ELRK+KK+DQ+ KRRN++ E    L   N   S
Sbjct   14    NHGRMAEFKFNN-RHEEARRRRNALSVELRKAKKDDQLLKRRNLDTEQDLLNLWNQNFVS    72

Query   219   PV-QLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
              P+ QLS+DEIV  +NS ++  Q +  QS RK+LSRE++PPI+ +I  GIVP CI   L
Sbjct   73    PIPQLSIDEIVDGINSSNETTQLIATQSCRKLLSREKDPPINDIIQGGIVPRCIELLDCD   132

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
              +N  LQFEAAW LTNIASGTS+QT+ VI+H AVP  V LL+S S  + EQAVWALGNIAG
Sbjct   133   HNIRLQFEAAWVLTNIASGTSEQTQSVIKHGAVPKLVKLLKSTSPYVREQAVWALGNIAG   192

Query   576   DGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv   755
              DG  ARD ++ H+ +  +L LI +  ++F+RNIVW +SNLCRNKNP PPF+ +K   LPV
Sbjct   193   DGPHARDFILRHDALSLLLDLIKPDVSVTFMRNIVWTLSNLCRNKNPPPPFELIKPALPV   252

Query   756   lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR   935
              ++LL S DI VLAD CWALSY+TD  N KIQAV+++  +P+LV LL    E +++ PALR
Sbjct   253   FNRLLNSTDIDVLADTCWALSYLTDGSNDKIQAVLETGIIPKLVDLLTSKEGTVLTPALR   312

Query   936   SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ   1115
              +VGNIVTG D QTD VI++GGLP LG LL+H++ NIVKEAAW +SNITAGN  QIQ VI
Sbjct   313   AVGNIVTGDDLQTDAVISAGGLPHLGALLRHHRVNIVKEAAWAISNITAGNMDQIQHVIN   372

Query   1116  AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP   1295
              A +    L VL+ GD+KAQKEAAWA+TN T+ GT + + L++    +L PF +LL+TKD
Sbjct   373   ADLVPPLINVLQFGDYKAQKEAAWAITNLTSGGTIQNLAQLVQA-GVLPPFCNLLETKDW   431

Query   1296  RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT   1475
                 I VV  GL+N+   A+K+G  + L +M+EE+GGLDKLE LQ H+NE+VY+K+ A+IDT
Sbjct   432   NIIIVVLDGLTNILHAAQKMGEVDRLAIMIEEIGGLDKLEALQHHQNEQVYQKSMAMIDT   491

Query   1476  YFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              +FS  D E    ++ + ++G LEFN T+    P   + F
Sbjct   492   FFSEKDVEEAILISKEHIDGHLEFNVTE-NTPTDQFKF   528
```

PREDICTED: importin subunit alpha-1 [Trichogramma pretiosum]

Sequence ID: **ref|XP_014230579.1|** Length: 517 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 7 to 508

Score	Expect	Method	Identities	Positives	Gaps	Frame
528 bits(1361)	5e-177()	Compositional matrix adjust.	269/508(53%)	361/508(71%)	8/508(1%)	+3

Features:

```
Query   39    SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN--DEDLTSPLKELNG   212
              +NSR    +K       + ++R RR E+++ELRK+ K+DQ+ KRRNIN  DE L+ P  E
Sbjct   7     NNSRLSKFKFQG-KSDEARRRRTEISVELRKANKDDQLSKRRNINIDDEPLSPPPGE--K   63

Query   213   QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN   392
              P +S+DEI+A M S D+  +    Q+ RKMLSRERNPPI+ +I  G+VP+CI FL +
Sbjct   64    SPPFDMSIDEIIAGMTSGDEVTKLQATQACRKMLSRERNPPINDLIEKGVVPLCIEFLGH   123

Query   393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA   572
              ++ +LQFEA WALTN+ASGTS+QT+ V++H A+P  VALL+S ++N+AEQAVWALGNIA
Sbjct   124   HDSPLLQFEACWALTNVASGTSEQTQVVVKHGAIPKLVALLKSSAINVAEQAVWALGNIA   183

Query   573   GDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllp   752
              GDG   RD+V++     + L+ +  ++ L+ ETPLSF+RNIVW MSN CRNKNP PPF+ V R LP
Sbjct   184   GDGPIPRDLVLNEGALTMLIQLLTPETPLSFIRNIVWTMSNCCRNKNPPPPFEIVSRALP   243

Query   753   vlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPAL   932
              +L+++L    D  VL DACW LSY+TD  N KIQ V+DS   +P+LV LL+ HGE ++ PAL
Sbjct   244   ILNRILTYNDKDVLGDACWTLSYLTDGSNDKIQTVLDSGIVPKLVALLGHGEVTVLTPAL   303

Query   933   RSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVI   1112
              R+VGNIVTG D QTD +I++G L   LL+H + NIVKEAAWT+SNITAGN  QIQ VI
Sbjct   304   RAVGNIVTGNDSQTDAIISAGALRYFIPLLRHKRLNIVKEAAWTISNITAGNAAQIQQVI   363

Query   1113  QAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKD   1292
              AG+    L VL+ GDFK+QKEAAWA+TN T+ G  +Q+ L++    +L PF +LLD KD
Sbjct   364   DAGLLPPLIEVLQTGDFKSQKEAAWAITNLTSGGNVQQLATLVQN-GVLIPFCNLLDAKD   422

Query   1293  PRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIID   1472
              + + V+ GL+N+   A K+G  EN+ +++EE+GGLDK+ETLQ H NE+VY KA A+ID
Sbjct   423   FKCVLVILDGLTNILNTAMKMGELENISIIIEEVGGLDKIETLQSHANEQVYLKASAMID   482

Query   1473  TYFSNGDDDEAEQELAPQEVNGALEFNAT   1556
              ++FS  + E    +P  NG L+F AT
Sbjct   483   SFFS--EKEEPDMPSPSTENGQLQFQAT   508
```

Importin subunit alpha-2 [Habropoda laboriosa]
Sequence ID: **gb|KOC64063.1|** Length: 519 Number of Matches: 1
Range 1: 5 to 519

Score	Expect	Method	Identities	Positives	Gaps	Frame
527 bits(1358)	2e-176()	Compositional matrix adjust.	282/521(54%)	381/521(73%)	7/521(1%)	+3

Features:

```
Query   30    KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKEL   206
              +AD ++R+ ++K N     +++R +R+E++IELRK++K++Q+ KRRN+N  ++L SP++E
Sbjct   5     EADCHNRKANFKYN-YKQEEARRKRNEISIELRKARKDEQLLKRRNLNVGKELPSPIEES   63

Query   207   NGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFL   386
              N  SP+  S++EIV  M S D+  Q   Q+ RKMLSRE+NPPID MI  GIVP+C++FL
Sbjct   64    N-ISPISTSIEEIVNGMQSSDETIQLQATQACRKMLSREKNPPIDTMIKRGIVPLCVKFL   122

Query   387   QNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGN   566
              +N +N LQFEAAWALTN+ASGTS+QT  V++H A+P  VALL+S S N+AEQ+VWALGN
Sbjct   123   DYHHNDLLQFEAAWALTNVASGTSEQTHVVVQHGAIPKLVALLKSASANVAEQSVWALGN   182

Query   567   IAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl   746
              IAGDG  ARD+V+ H +  +L LI  +T ++F RNIVW +SNLCRNKNP P F  V+
Sbjct   183   IAGDGPVARDLVLGHAAMPILLELIKPDTSVTFTRNIVWTLSNLCRNKNPPPSFQIVRTA   242

Query   747   lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP   926
              LPVL++LL + D  +LADACWALSY+TD  N KIQAVV+S  + +LV+LL   E S++ P
Sbjct   243   LPVLNRLLSNSDKDILADACWALSYLTDGSNDKIQAVVESGVIAKLVELLASPEASVLTP   302

Query   927   ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA   1106
              ALR+VGNIVTG D QTD +I++GGL  LGLLLQH++ NIVKEAAW +SNITAGN +QIQ
Sbjct   303   ALRAVGNIVTGNDTQTDAIISAGGLQHLGLLLQHHRVNIVKEAAWAISNITAGNMEQIQH   362

Query   1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT   1286
              VI AG+   L +LE GDFK+QKEAAWA+TN T+ G+ + + LI+   +L PF +LL+
Sbjct   363   VINAGLIPPLIHILESGDFKSQKEAAWAITNLTSGGSVQHLALLIQS-GVLPPFCNLLEA   421

Query   1287  KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI   1466
              KD +T+ VV  GL+N+  AEK+G   + +M+EE+GGLDKLE LQ HE E+VY+KA A+
Sbjct   422   KDWKTVVVVLDGLTNILNAAEKMGEVVRVAIMIEEVGGLDKLEVLQNHEVEQVYQKAIAM   481

Query   1467  IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF        1589
              ID +FS  D E  L P  +  LEF T+  A + G+ F
Sbjct   482   IDNFFSEADAE-ESTLTPTAGDAQLEFKPTE--ATQKGFNF        519
```

PREDICTED: importin subunit alpha [Bombus impatiens]
Sequence ID: **ref|XP_003484488.1|** Length: 519 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 5 to 519

Score	Expect	Method	Identities	Positives	Gaps	Frame
524 bits(1350)	2e-175()	Compositional matrix adjust.	282/521(54%)	378/521(72%)	7/521(1%)	+3

Features:

```
Query   30    KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKEL   206
              +AD +SR+ ++K N     +++R RR+E+++ELRK++K++Q+ KRRN+N  ++  S + E
Sbjct   5     EADCHSRKANFKFN-YKHEEARRRRNEISVELRKARKDEQLLKRRNLNIGKESQSSVSE-   62

Query   207   NGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFL   386
                +  S+DEIV  M S D+  +    Q+ RKMLSRE++PPID MI  GIVP+C+ FL
Sbjct   63    -SDHSLLSSIDEIVTGMKSLDETIRLQATQTCRKMLSREKSPPIDNMIQRGIVPLCVEFL   121

Query   387   QNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGN   566
              +N+ LQFEAAWALTN+ASGTS+QT  V++H A+P  VALL+S S N+AEQAVWALGN
Sbjct   122   DYHHNTALQFEAAWALTNVASGTSEQTLVVVKHGAIPKLVALLKSGSPNVAEQAVWALGN   181

Query   567   IAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl   746
              IAGDGA ARD+V+  +  +L LI  +T ++F RNIVW +SNLCRNKNP PPFD V+
Sbjct   182   IAGDGAMARDLVLGTDAMPLLLELIKPDTSITFTRNIVWTLSNLCRNKNPPPPFDVVRTA   241

Query   747   lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP   926
              LPVL++LL + D  +LADACWALSY+TD  N KIQAVVD   +P+LV+LL   E +++ P
Sbjct   242   LPVLNRLLSNSDKDILADACWALSYLTDGPNDKIQAVVDCGVIPKLVQLLGSTEVTVLTP   301

Query   927   ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA   1106
              ALRSVGNIVTG D QTD +I +GGL  LGLLLQH++ NIVKEAAWT+SNITAGN +QIQ
Sbjct   302   ALRSVGNIVTGNDAQTDAIIQAGGLQYLGLLLQHHRLNIVKEAAWTISNITAGNMEQIQE   361

Query   1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT   1286
              VI A +   L  VLE GDFK+QKEAAWAVTN T+ G+ +Q+ L++   +L PF +LL+
Sbjct   362   VINAALLPPLIHVLECGDFKSQKEAAWAVTNLTSGGSVQQLAQLVQ-LGVLGPFCNLLEA   420

Query   1287  KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI   1466
              KD +TI VV  GLSN+ + AEK+G   + +M+EE+GGLDKLE LQ HE E+VY+KA A+
Sbjct   421   KDWKTIIVVLDGLSNICSAAEKMGEVDRVAIMIEEVGGLDKLEALQHHEVEQVYQKATAM   480

Query   1467  IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF        1589
              IDT+FS + +     P  +G LEF T+   + G+ F
Sbjct   481   IDTFFSEPEAQESTLATPTIADGQLEFKTTE--TAQSGFNF        519
```

PREDICTED: importin subunit alpha [Bombus terrestris]
Sequence ID: **ref|XP_003399525.1|** Length: 519 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps	Frame
524 bits(1349)	4e-175()	Compositional matrix adjust.	282/521(54%)	380/521(72%)	7/521(1%)	+3

Features:

```
Query  30    KADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKEL  206
             +AD +SR+ ++K N     +++R RR+E+++ELRK++K++Q+ KRRN+N  ++  + + E
Sbjct  5     EADCHSRKANFKFN-YKHEEARRRRNEISVELRKARKDEQLLKRRNLNIGKESQNSVSE-   62

Query  207   NGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFL  386
                + S+DEIV  M S D+  +    Q+ RKMLSRE++PPID MI  GIVP+C+ FL
Sbjct  63    -SDHLLLSSIDEIVNGMKSLDETIRLQATQTCRKMLSREKSPPIDNMIQRGIVPLCVEFL  121

Query  387   QNTNNSMLQFEAAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGN  566
              +N+ LQFEAAAWALTN+ASGT++QT  VI+H A+P  VALL+S S N+AEQAVWALGN
Sbjct  122   DYHHNNALQFEAAAWALTNVASGTTEQTLAVIKHGAIPKLVALLKSASPNVAEQAVWALGN  181

Query  567   IAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl  746
             IAGDGA  ARD+V+  + +  +L LI  +T ++F RNIVW +SNLCRNKNP PPFD V+
Sbjct  182   IAGDGAMARDLVLGTDAMPLLLELIKPDTSITFTRNIVWTLSNLCRNKNPPPPFDVVRTA  241

Query  747   lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP  926
             LPVL++LL + D  +LADACWALSY+TD  N KIQAV+D    +P+LV+LL   E +++ P
Sbjct  242   LPVLNRLLSNSDKDILADACWALSYLTDGPNDKIQAVIDCGVIPKLVQLLGSTEVTVLTP  301

Query  927   ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA  1106
             ALRSVGNIVTG D QTDV+I +GGL  LGLLLQH++ NIVKEAAWT+SNITAGN +QIQ
Sbjct  302   ALRSVGNIVTGNDAQTDVIIQAGGLQYLGLLLQHHRLNIVKEAAWTISNITAGNMEQIQE  361

Query  1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT  1286
             VI A +   L  VLE GDFK +QKEAAWAVTN T+SG+ +Q+ L++   +L PF +LL+
Sbjct  362   VINAALLPPLIHVLECGDFKSQKEAAWAVTNLTSSGSVQQLAQLVQ-LGVLGPFCNLLEA  420

Query  1287  KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI  1466
             KD +TI VV  GLSN+ + AEK+G  + + +M+EE+GGLDKLE LQ HE E+VY+KA A+
Sbjct  421   KDWKTIIVVLDGLSNICSAAEKMGEVDRVAIMIEEVGGLDKLEALQHHEVEQVYQKATAM  480

Query  1467  IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             IDT+FS  + +     P  +G LEF T+    + G+ F
Sbjct  481   IDTFFSEPEAQESTLATPAVADGQLEFKTTE--TAQSGFNF  519
```

PREDICTED: importin subunit alpha-1 [Strongylocentrotus purpuratus]

Sequence ID: **ref|XP_011662338.1|** Length: 520 Number of Matches: 1
Range 1: 6 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
523 bits(1348)	5e-175()	Compositional matrix adjust.	265/517(51%)	359/517(69%)	3/517(0%)	+3

Features:

```
Query  42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKELNGQS  218
             N+R  ++K  S ++ + R RR+EV++ELRK+KK+DQM KRRN+N DE+  SPL+E   Q
Sbjct  6     NNRMQAFKNKSKDSSELRRRRNEVSVELRKAKKDDQMLKRRNVNTDEEPVSPLQE-KKQP  64

Query  219   PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN  398
             VQ+S+ +I  A++S D   QF  +Q+AR+MLSRER PPI+ +I  G+VP + FL +++
Sbjct  65    TVQMSIPDICKAISSSDSSTQFNAVQTARRMLSRERQPPINPIIRAGLVPKFVAFLGHSD  124

Query  399   NSMLQFEAAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD  578
             N  +QFEAAAWALTNIASGT +QT+ V+  A+P F+ LL S   N+ EQAVWALGNIAGD
Sbjct  125   NPTMQFEAAAWALTNIASGTPEQTKAVVSEGAIPAFIKLLSSSHQNVCEQAVWALGNIAGD  184

Query  579   GAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvl  758
             G  RD+V  H ++  +L L   TP+ FLRN+ W +SNLCRNK+P P  + V  +LPVL
Sbjct  185   GPEMRDVVTRHGILQPLLELYQPTTPVPFLRNVTWTLSNLCRNKSPPPCDEVVSGVLPVL  244

Query  759   sqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRS  938
             L+   D +++ADACWALSY+TD  N +I+ V+ +  V R+V+LL+  E S+I PALRS
Sbjct  245   QSLIHHCDKEIVADACWALSYLTDGSNDRIELVIKAGVVTRVVELLRSQEISVITPALRS  304

Query  939   VGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQA  1118
             +GNIVTGTD+QT  VI S  LP   LLQH K NI KEA WT+SNITAGN +QIQ+V+ A
Sbjct  305   IGNIVTGTDEQTQSVIDSQSLPLFVALLQHPKQNIQKEACWTISNITAGNVQQIQSVVSA  364

Query  1119  GIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPR  1298
             G+    L  VLEKGD+K+QKEA WAVTN T+ G+ EQIV +++    LKP  DLL+ K+ +
Sbjct  365   GLLPPLVGVLEKGDYKSQKEACWAVTNLTSGGSVEQIVQIVQS-GCLKPLCDLLNVKEAK  423

Query  1299  TIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTY  1478
             I+V+    N+ + AEKL   E +CLM+EE GGLDK+E LQQHENE VY+ +  II+ Y
Sbjct  424   IIQVILDAFKNILSAAEKLEQLETVCLMIEEAGGLDKIEALQQHENENVYEMSLEIIEKY  483

Query  1479  FSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             +S  ++E +      +G  EF+ Q AP+GG+ F
Sbjct  484   YSPQEEEDVKVAPSTNESGTYEFSGQQCAAPQGGFAF  520
```

PREDICTED: importin subunit alpha [Megachile rotundata]

Sequence ID: **ref|XP_003704950.1|** Length: 518 Number of Matches: 1
Range 1: 6 to 510

Score	Expect	Method	Identities	Positives	Gaps	Frame

523 bits(1347) 7e-175() Compositional matrix adjust. 284/510(56%) 374/510(73%) 7/510(1%) +3

Features:

```
Query  36    DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRN--INDEDLTSPLKELN  209
             D  +R+ S+K N    ++R RR+E ++ELRK++K++Q+FKRRN  I  E  TS   + N
Sbjct  6     DDCARKSSFKFN-YKHDEARRRRNEASVELRKARKDEQLFKRRNLSIGKEQQTS--TDEN  62

Query  210   GQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQ  389
               S + S+++IV  M S D+ Q    Q+ RKMLSRE+NPPID MI  GIVP C+ FL
Sbjct  63    SHSRLSTSINDIVNDMKSSDETIQLQATQACRKMLSREKNPPIDNMIKQGIVPRCVEFLD  122

Query  390   NTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNI  569
              +N   LQFEAAWALTN+ASGT++QT+ V++H A+P  VALL+S S N+AEQAVWALGNI
Sbjct  123   YNHNPALQFEAAWALTNVASGTTEQTQFVVKHGAIPKLVALLKSASPNVAEQAVWALGNI  182

Query  570   AGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRll  749
             AGDG  ARD+V+ H+ +   +L LI  +T ++F RNIVW +SNLCRNKNP PPF+ V+   L
Sbjct  183   AGDGPMARDLVLGHDTMPLLLELIKPDTSVTFTRNIVWTLSNLCRNKNPPPPFEIVRTAL  242

Query  750   pvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPA  929
             PVL++LL + D  +LADACWALSY+TD  N KIQAVVDS  +P+LV+LL + E +++ PA
Sbjct  243   PVLNRLLSNTDKDILADACWALSYLTDGSNDKIQAVVDSGIIPKLVELLALPEVTVLTPA  302

Query  930   LRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAV  1109
             LR+VGNIVTG D QTD +IA+GGL  LGLLLQH++ NIVKEAAWT+SNITAGN +QIQ V
Sbjct  303   LRAVGNIVTGNDSQTDAIIAAGGLQHLGLLLQHHRINIVKEAAWTISNITAGNMEQIQHV  362

Query  1110  IQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTK  1289
             I AG+   L VL+ GDFK+QKEAAWAVTN T+ G+ +Q+  L++   +L PF  LL+ K
Sbjct  363   INAGLLPPLIHVLQCGDFKSQKEAAWAVTNLTSGGSVQQLAQLVQ-LGVLAPFCKLLEAK  421

Query  1290  DPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAII  1469
             + +T+ VV  GL+N+   AEK+G  E + LM+EE+GG+DKLE LQ HE E+VY+KA A+I
Sbjct  422   EWKTVLVVLDGLTNILNAAEKMGEVERVALMIEEVGGIDKLEDLQHHEVEQVYQKAIAMI  481

Query  1470  DTYFSNGDDEAEQELAPQEVNGALEFNATQ  1559
             DT+FS+GD E E  L P   +G LEF   +
Sbjct  482   DTFFSDGDVE-EAVLPPTATDGQLEFKTAE  510
```

uncharacterized protein Dwil_GK23224 [Drosophila willistoni]

Sequence ID: **ref|XP_002074732.1|** Length: 491 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 6 to 470

Score	Expect	Method	Identities	Positives	Gaps	Frame
519 bits(1337)	9e-174()	Compositional matrix adjust.	271/471(58%)	349/471(74%)	9/471(1%)	+3

Features:

```
Query  78    NTQDSRMRRHE--VTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQSPVQLSVDEIVA  251
             ++  D R  R    +T++LR+S+        +++   D   E     P Q SV+E++
Sbjct  6     DSNDGRETRQHFVITVQLRRSRTNSDVYQYFDYEDPD------EPESIWPFQFSVNEMLM  59

Query  252   AMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTNNSMLQFEAAWA  431
             A+ SED + QFL Q   ARKMLSRE NPP+DLMI H IVP+C+RFLQ    + M+Q+EAAWA
Sbjct  60    ALGSEDVKVQFLAVIVARKMLSRETNPPVDLMIAHDIVPVCLRFLQWVRDPMVQYEAAWA  119

Query  432   LTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGDGAAARDIVIHH  611
             L NIASG S QTR VI++ AVP  VA L+S S++  E AVWAL NIAGDGA ARD+VI
Sbjct  120   LANIASGNSAQTRAVIDNGAVPILVATLKSSSVHPVEMAVWALANIAGDGALARDVVISE  179

Query  612   NVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvlsqlllsqDIQV  791
              VIDGILPLIN++T  +FLRNIVWL++NLCR K+P   FD++KRLLP LS LLL++D ++
Sbjct  180   GVIDGILPLINDKTSQAFLRNIVWLIANLCRYKDPPASFDELKRLLPTLSDLLLNRDPKI  239

Query  792   LADACWALSYVTDDDN-TKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRSVGNIVTGTDQ  968
             L DACWAL YV+DDD+ +KIQAVVD+ AVPRLV LL  D+ +I+VPALR +GNIV+GTD+
Sbjct  240   LCDACWALFYVSDDDDVSKIQAVVDTGAVPRLVTLLDRDDTNIVVPALRCLGNIVSGTDE  299

Query  969   QTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQAGIFQQLRTVL  1148
             QTDV I SGGLP+L  LL+H KS+IVKEAAWTVSNITAGN   QI AV++  IF Q+ +L
Sbjct  300   QTDVFINSGGLPKLRNLLEHPKSSIVKEAAWTVSNITAGNPAQIHAVMRTEIFYQIYNIL  359

Query  1149  EKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPRTIKVVQTGLS  1328
             E+G  KAQKEAAWAVTNTT++GT  QI +LI KY+IL PF+ LL+ KD   + +V+TGL
Sbjct  360   ERGCVKAQKEAAWAVTNTTSTGTQIQISELIGKYRILVPFLKLLEAKDSNIVFIVETGLH  419

Query  1329  NLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTYF  1481
             +LF+LAE L   E L +++++GGL KL QQHEN +V KAY II  +
Sbjct  420   HLFSLAEDLDRVEALGILIDDLGGLKKLRALQQHENRDVRIKAYTIIYNFI  470
```

PREDICTED: importin subunit alpha-1-like [Lingula anatina]

Sequence ID: **ref|XP_013403921.1|** Length: 521 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 521

Score	Expect	Method	Identities	Positives	Gaps	Frame
518 bits(1335)	6e-173()	Compositional matrix adjust.	282/527(54%)	369/527(70%)	11/527(2%)	+3

Features:

```
Query  24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRN--INDEDLTSPL  197
```

```
           M   ++ +R  +YK    +   D R RR+EV++ELRK+KK+DQ+ KRRN  I DE  TSPL
Sbjct    1  MPSQENTARLKAYKNKGRDVDDLRRRRNEVSVELRKNKKDDQLLKRRNVAITDEP-TSPL     59

Query  198  KELNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICI    377
           +E  +  V LS+ EIV +++  D ++Q +  Q+ARKMLSRERNPPID +I  G++P  +
Sbjct   60  QE--QKQNVGLSLQEIVDSIHGTDPQKQMIATQAARKMLSRERNPPIDSIIQSGVIPRLV    117

Query  378  RFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWA    557
            FL+ +   LQFEAAWALTN+ASGTS QT+ V+  NAV  F+ALL S   N++EQAVWA
Sbjct  118  EFLRYNDRPELQFEAAWALTNVASGTSTQTKAVVNANAVVPFIALLTSPHHNVSEQAVWA    177

Query  558  LGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQV    737
           +GNIAGDG   RD VI   ++ +L L+  +   SFLRN+ W +SN+CRNKNP PPF  V
Sbjct  178  VGNIAGDGPEMRDYVIKCGAVEPLLSLVKPQIETSFLRNVTWTISNMCRNKNPPPPFATV    237

Query  738  KRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSI    917
           K+ LP LSQLLL  D +VL+DACWALSY+TD  N KIQ V++S  VPRLV+LL   EPSI
Sbjct  238  KQCLPTLSQLLLHTDKEVLSDACWALSYLTDGTNDKIQEVLNSGVVPRLVELLASPEPSI    297

Query  918  IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ   1097
           + PALR+VGNIVTG D QT  VI +G +P  LLL H+KS+I KEAAWTVSNITAGN +Q
Sbjct  298  VTPALRAVGNIVTGDDGQTQAVIDAGAVPVFNLLLTHSKSSIQKEAAWTVSNITAGNTQQ    357

Query 1098  IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDL   1277
           IQAV+ AG+  +  +L KGDFK QKEA WAVTN T+ GT EQIV L++   +L+P  +L
Sbjct  358  IQAVLDAGVIPNVVNLLVKGDFKTQKEAVWAVTNLTSGGTVEQIVHLVQ-CGVLRPLCNL    416

Query 1278  LDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA   1457
           L  K+ + I V+   L N+   A+KLG +E +C+M+EE+ G++K+E LQQHENE+VYK A
Sbjct  417  LTAKEAKVILVILDALQNILNAADKLGQSEAVCIMIEEVEGMEKIENLQQHENEQVYKAA    476

Query 1458  YAIIDTYFSNGDDEAEQELAP--QEVNGALEFN-ATQPKAPEGGYTF   1589
           Y II+ YF   D+ ++ LAP  E +   EF  ATQ   P GG++F
Sbjct  477  YGIIEKYFGGDGDDEDESLAPTCSENSNNFEFQPATQ--VPAGGFSF   521
```

hypothetical protein DAPPUDRAFT_301494 [Daphnia pulex]

Sequence ID: **gb|EFX68294.1|** Length: 522 Number of Matches: 1

Range 1: 8 to 522

Score	Expect	Method	Identities	Positives	Gaps	Frame
518 bits(1333)	1e-172()	Compositional matrix adjust.	274/518(53%)	356/518(68%)	6/518(1%)	+3

Features:

```
Query   45  SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRN--INDEDLTSPLKELNGQS    218
           SR  +K     + ++ R RR EV +ELRK+KKED + KRRN   I+DE L SPL+E N  +
Sbjct    8  SRLKDFKNKGRDVEEMRRRRTEVNVELRKAKKEDHLLKRRNLEIDDEPL-SPLQEQNRMA     66

Query  219  PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN    398
            +S+++IV  +NS D+ ++        +ARK+LSRERNPPID++I   +VP  + FL  +
Sbjct   67  AANMSIEDIVNGINSGDENKEITATHAARKILSRERNPPIDILINANVVPKLVEFLSRVS    126

Query  399  NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD    578
           N   LQFE+AWALTNIASGTSDQT+ V+   AV  F++LL S    +AEQAVWALGNIAGD
Sbjct  127  NPDLQFESAWALTNIASGTSDQTKAVVSAGAVAGFISLLGSPHPVVAEQAVWALGNIAGD    186

Query  579  GAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvl    758
           G   RD VI    +I  +L LI   +T  +FLRN+ W  +SNLCRNKNP P  +  LLP L
Sbjct  187  GPELRDHVIEQGIIKPLLTLIKPDTSATFLRNVTWTLSNLCRNKNPPSVPAVRQLLPAL    246

Query  759  sqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRS    938
           + L+ + D ++LADACWALSY+TD  N +IQ VVD+  VPRLV LL   E ++I P LR+
Sbjct  247  AHLIHNNDKEILADACWALSYLTDGPNERIQEVVDAGVVPRLVALLDHVEVAVITPTLRT    306

Query  939  VGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQA   1118
           +GNIVTG+D QTD V+A+G  P L  LL H K NIVKEAAWTVSNI AGN  QIQA+I
Sbjct  307  IGNIVTGSDIQTDSVLAAGACPLLAKLLVHAKMNIVKEAAWTVSNIAAGNAIQIQALITN    366

Query 1119  GIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPR   1298
            + +  L  VL KGDFK QKEAAWA+TN T  G  EQI  L+ ++  + P   LL+ K+P+
Sbjct  367  NVIRPLVDVLGKGDFKCQKEAAWAITNITLGGNVEQIA-LLCQFGAIAPLCTLLEAKEPK    425

Query 1299  TIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTY   1478
           TI VV  GL+N+ A AEK+G  E + L VEE GGLD++E LQ H+N E+Y K+ AI++  Y
Sbjct  426  TILVVLDGLANILAAAEKMGELEKVSLHVEECGGLDRIEALQSHDNVEIYHKSLAILEQY    485

Query 1479  FSNGDDEAEQELAPQEV-NGALEFNATQPKAPEGGYTF   1589
           FS   DE + ELAP   +G EFN +  +APEGG++F
Sbjct  486  FSTDGDE-DSELAPSTSQSGNYEFNNSPSQAPEGGFSF   522
```

PREDICTED: importin subunit alpha [Dinoponera quadriceps]

Sequence ID: **ref|XP_014479013.1|** Length: 526 Number of Matches: 1

Range 1: 16 to 526

Score	Expect	Method	Identities	Positives	Gaps	Frame
517 bits(1332)	2e-172()	Compositional matrix adjust.	275/518(53%)	361/518(69%)	8/518(1%)	+3

Features:

```
Query   39  SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQS    218
           SN R  ++K     + ++R RR+ V  ELRK+KK++Q+ KRRN+N E+   L    S
Sbjct   16  SNGRMANFKYTN-RLDEARRRRNIVYTELRKAKKDEQLSKRRNLNTEEEVLNLS-CEAIS     73

Query  219  PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN    398
           P    ++++IVAAM S D+  Q    Q+ RK+LSRE++PPI+ +I  GIVP C+  L   +
Sbjct   74  PGFSTIEDIVAAMKSPDETLQLQATQTCRKLLSREKHPPIETIINRGIVPRCVELLNCHH    133
```

```
Query   399   NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD   578
              N  LQFEAAWALTN+ASGTS+QT+ VI++ AVP  V LL+S S N+AEQAVWALGNIAGD
Sbjct   134   NVALQFEAAWALTNVASGTSEQTQVVIKYGAVPRLVVLLKSPSANVAEQAVWALGNIAGD   193

Query   579   GAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvl   758
              G  ARD+++ H+ +  +L LI  +T ++F+RNIVW +SNLCRNKNP PPFD VK   LP L
Sbjct   194   GPPARDLILAHDAVPLLLDLIKPDTSVTFMRNIVWTLSNLCRNKNPPPPFDIVKTALPAL   253

Query   759   sqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRS   938
              ++LL S D  +LAD CWALSY+TD  N KIQAV+DS  VP+LV LL   E +++ PALR+
Sbjct   254   NRLLTSPDRDILADTCWALSYLTDGSNDKIQAVLDSGVVPQLVSLLTSQEATVLTPALRT   313

Query   939   VGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQA  1118
              VGNIVTG D QTD +I +GGL  L  LL H++ NI+KEAAW +SNITAGN +QIQ VI A
Sbjct   314   VGNIVTGDDAQTDSIILAGGLKHLCNLLSHSRKNIMKEAAWAISNITAGNTEQIQHVINA   373

Query  1119   GIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPR  1298
              GI   L  VL+ GD KAQKEAAWAVTN T+ G+ +Q+ DL++    +L P +LL  KD
Sbjct   374   GILPPLIQVLDSGDLKAQKEAAWAVTNLTSGGSYQQLADLVQA-GVLPPLCNLLAAKDWS   432

Query  1299   TIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTY  1478
              T  VV  GL+N+    AEK    + + LM+EE+GGLDKLE LQ H+NE++Y+K+ A+IDT+
Sbjct   433   TTVVVLDGLTNILNTAEKCNQVDQIALMIEEIGGLDKLEALQHHKNEQIYQKSMAMIDTF   492

Query  1479   FSNGDDEAEQELAPQEVN-GALEFNATQPKAPEGGYTF   1589
              FS   DE    LAP  + G LEF A  P++    +TF
Sbjct   493   FSG--DEEHASLAPAANDEGQLEFKA--PESTSTDFTF   526
```

PREDICTED: importin subunit alpha [Solenopsis invicta]

Sequence ID: **ref|XP_011158592.1|** Length: 524 Number of Matches: 1

Range 1: 8 to 515

Score	Expect	Method	Identities	Positives	Gaps	Frame
516 bits(1330)	3e-172()	Compositional matrix adjust.	271/510(53%)	365/510(71%)	5/510(0%)	+3

Features:

```
Query   39    SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELN-GQ   215
              S+ R  ++K N+    +++R+RR+ +++ELRK +KK+DQ+ KRRN+N E   +S L +
Sbjct   8     SHGRIANFKFNN-RHEEARVRRNALSVELRKAKKDDQLSKRRNLNSEQESSSLSDKAIVS   66

Query   216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
              S    S++EIV  +NS ++   +Q+ RK+LSRER+PPI+ MI  GIVP+CI+FL N
Sbjct   67    STCIFSIEEIVNHLNSSNETLQLTAIQTCRKLLSRERDPPINDMIEGGIVPLCIKFLDND   126

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
              +N  LQFE  W LTNIASGTS QT+ V++H AVP   +LL+S   +AEQAVWALGNIAG
Sbjct   127   DNISLQFEVTWVLTNIASGTSVQTQNVVKHGAVPKLVKLLQSASPMVAEQAVWALGNIAG   186

Query   576   DGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv   755
              DG  ARD+V+ H+ +  ++ LI  +TP++F RNIVW +SNLCRNKNPSP F+ ++ LLPV
Sbjct   187   DGPYARDLVLGHDALPRLVDLIKPDTPMTFTRNIVWTLSNLCRNKNPSPSFELIRPLLPV   246

Query   756   lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR   935
              ++LL    D  VLAD CWALSY+TD  N KIQAV+++   +P+LV LL    E +I+ PALR
Sbjct   247   FNRLLSYTDRDVLADTCWALSYLTDGTNDKIQAVLETGIIPKLVELLASREGAILTPALR   306

Query   936   SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ  1115
              +VGNIVTG D QTD VI++GGL   G LL++ ++NIVKEAAW VSNITAGN  QIQ+VI
Sbjct   307   AVGNIVTGNDAQTDAVISAGGLSHFGALLRYPRANIVKEAAWAVSNITAGNPDQIQSVIN   366

Query  1116   AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP  1295
              A + Q L  +L+ GD+KAQKEAAWAVTN TT GT + + L+     +L PF +LL++KD
Sbjct   367   ADLLQPLIQILQFGDYKAQKEAAWAVTNLTTGGTVQHLTRLV-GAGVLPPFCNLLESKDW   425

Query  1296   RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT  1475
              I VV  GL+N+    AEK+G   + L +M+E+++GGLDK+E LQ HENEEVY+++ AIID
Sbjct   426   NIILVVLDGLTNILHAAEKVGQVDKLAIMIEQVGGLDKIEALQNHENEEVYQRSMAIIDA   485

Query  1476   YFSNGDDEAEQELAPQEVNG--ALEFNATQ   1559
              +FS   D E E +  + N      EFN T+
Sbjct   486   FFSQKDVEEEALVCQVKKNDDEQFEFNTTE   515
```

PREDICTED: LOW QUALITY PROTEIN: importin subunit alpha-1-like [Limulus polyphemus]

Sequence ID: **ref|XP_013787969.1|** Length: 520 Number of Matches: 1

Range 1: 5 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
516 bits(1328)	5e-172()	Compositional matrix adjust.	267/518(52%)	357/518(68%)	4/518(0%)	+3

Features:

```
Query   42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKELNGQS   218
              ++R   +K   + ++ R RR E  +ELRK KK++Q+ K+RN++   ED TSPL E N
Sbjct   5     DNRLKHFKNRGKDVEEMRRRRTEANVELRKQKKDEQLLKKRNVSFSEDPTSPLGEQNKLD   64

Query   219   PVQ-LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
              V  +S++EIV  ++S+D+    F   QSARK+LSRERNPPID +I  G+VPI +RFL
Sbjct   65    AVAVMSMEEIVQGISSQDETLNFQAAQSARKILSRERNPPIDSLIQAGVVPIFVRFLSCD   124

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
              +N  LQFEAAWALTNIASG SDQTRCV++  AVP F+ LL S+  ++ EQAVWALGNIAG
Sbjct   125   SNPPLQFEAAWALTNIASGNSDQTRCVVDAGAVPLFIKLLCSQHSHVCEQAVWALGNIAG   184

Query   576   DGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv   755
```

```
Sbjct  185   DG   RD++I H ++  +L LI +++P SFLRN+ W +SNLCRNKNP PPF+ VK+ LP
             DGPDCRDLIIRHGIMKPLLDLIKSDSPASFLRNVTWTLSNLCRNKNPPPPFEVVKQSLPT   244

Query  756   lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR   935
             L QL+    D +V+ADACW LSY+TD  N KIQ V+D+  VPRL +LL +DE SI+ P+LR
Sbjct  245   LRQLIYHNDKEVVADACWXLSYLTDGTNEKIQEVIDAGVVPRLCELLDVDEVSILTPSLR   304

Query  936   SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ   1115
             +VGNIVTG D QT  VI   LP     LL + K NI KEAAW +SN+TAGN  QIQ+VI
Sbjct  305   AVGNIVTGNDAQTQHVIDCQALPPFRKLLCNKKINIQKEAAWMISNVTAGNDSQIQSVID   364

Query  1116  AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP   1295
             +G+ + L  VL +GD+K+QKEA WAV N T+ GT EQIV L++   ++ P  D+L  DP
Sbjct  365   SGLVEPLIEVLAQGDYKSQKEATWAVANFTSGGTLEQIVYLVQA-GVVPPLCDMLKISDP   423

Query  1296  RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT   1475
             + + V+    L+N+   A+KLG  E + L++EE+GG+DK+E LQQHEN +VY   A   I+
Sbjct  424   KIVMVLIDALNNIIQAADKLGEMEKVLLLIEEVGGVDKIEALQQHENNDVYTAALEFIEK   483

Query  1476  YFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             YFS G+D +  L P+   G     +T  APEGG++F
Sbjct  484   YFS-GEDTDDAHLVPEMSAGGDYQFSTTAAAPEGGFSF  520
```

Importin subunit alpha-2, partial [Stegodyphus mimosarum]

Sequence ID: **gb|KFM56942.1|** Length: 513 Number of Matches: 1

Range 1: 3 to 513

Score	Expect	Method	Identities	Positives	Gaps	Frame
515 bits(1326)	1e-171()	Compositional matrix adjust.	269/519(52%)	353/519(68%)	10/519(1%)	+3

Features:

```
Query  39    SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKELNGQ   215
             S +R   +K    + +  R RR EV +ELRK KK++ + KRRN++ ++D  SP ++
Sbjct  3     SQARIKCFKNKGRDQEAMRRRTEVNVELRKQKKDEGLSKRRNVDINDDPLSPERD----   58

Query  216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
             V ++V+EI+   + S D + QF G Q+ARK LS+E++PPID +I  G VPI + FL  +
Sbjct  59    QKVLITVEEIMRGIKSNDPQLQFAGAQNARKYLSKEKSPPIDNLIASGAVPILVSFL-TS   117

Query  396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
             NN  LQFEA WALTNIASG S QTR V+   A+P F++LL S   N+AEQAVWALGNIAG
Sbjct  118   NNVPLQFEACWALTNIASGNSSQTRAVVNAGAIPIFISLLFSPHSNVAEQAVWALGNIAG   177

Query  576   DGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv   755
             DG   RD VI   VI  ++ L+    P  F RNI W +SN+CRNKNPSPPF+ +K+ LP
Sbjct  178   DGPELRDEVIRSGVIKPLINLLKPNIPTGFRRNITWTLSNICRNKNPSPPFEAIKQCLPA   237

Query  756   lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR   935
             + LL   D++V+ DACWALSY+TD  N KIQ V++S  VPRLV LL++ + +++ PALR
Sbjct  238   FACLLSDSDLEVVTDACWALSYLTDGSNDKIQEVINSGVVPRLVSLLEVKDVAVVTPALR   297

Query  936   SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ   1115
             +VGNIVTG D QT  VI +G L  L LL++HNKSNIVKE  W +SNITAGN +QIQAVI
Sbjct  298   AVGNIVTGDDVQTQAVIDAGALEPLRLLIRHNKSNIVKETCWAISNITAGNSRQIQAVID   357

Query  1116  AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP   1295
             AG+   QI+ VL +GD+K QKEA WAV NN T+ GT +QI+ FLL -RLGVLDPLCKLLSLKDP
Sbjct  358   AGLMSQIVDVLNEGDYKCQKEAIWAVNNFTSGGNFDQIIFLL-RLGVLDPLCKLLSLKDP   416

Query  1296  RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT   1475
             + + VV    LSN+   + K+   E +C  +EE GGLDK+E LQ HEN EVY+ A+ IID
Sbjct  417   KVLTVVLDALSNILHASAKMNAVETVCSYIEECGGLDKIENLQHHENSEVYRCAFGIIDA   476

Query  1476  YFSNGDDEAEQELAPQ-EVNGALEFNATQPKAPEGGYTF   1589
             YFSN D+E  Q+LAPQ E +G  EFNA  P AP GG++F
Sbjct  477   YFSN-DEEELQDLAPQVEGSGTYEFNAVNP-APNGGFSF   513
```

importin alpha [Culex quinquefasciatus]

Sequence ID: **ref|XP_001847920.1|** Length: 459 Number of Matches: 1

▶ **See 1 more title(s)**

Range 1: 67 to 454

Score	Expect	Method	Identities	Positives	Gaps	Frame
512 bits(1319)	2e-171()	Compositional matrix adjust.	255/389(66%)	314/389(80%)	2/389(0%)	+3

Features:

```
Query  414   FEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGDGAAAR   593
             FEAAWALTNIASGTS+QT+ VI+  AVP F+ LL S S N+AEQAVWALGNIAGDG+ AR
Sbjct  67    FEAAWALTNIASGTSEQTKAVIDAGAVPKFINLLSSPSGNVAEQAVWALGNIAGDGSKAR   126

Query  594   DIVIHHNVIDGILPLINN-ETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvlsqll   770
             DIV+ +N ++ I  L+ N +T LSFLR IVWLMSNLCRNKNP PPF +V+ ++P+LSQLL
Sbjct  127   DIVLEYNSVESINYLVQNADTQLSFLRTIVWLMSNLCRNKNPPPPFSRVEPMIPILSQLL   186

Query  771   lsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRSVGNI   950
             +D QVLADACWALSYVTDDD  KI++VV S AVPRLV+LL  D P+II PALRSVGNI
Sbjct  187   DHEDAQVLADACWALSYVTDDDAVKIESVVASGAVPRLVRLLSCDNPAIITPALRSVGNI   246

Query  951   VTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQAGIFQ   1130
             VTG D QTD VIA+G  LP LG LL+++K++IVKEAAWT+SNITAGNQ+QI V ++GI
Sbjct  247   VTGNDTQTDAVIAAGSLPALGKLLRNSKNSIVKEAAWTISNITAGNQQQIGQVFESGILH   306

Query  1131  QLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPRTIKV   1310
```

```
Sbjct  307   L  VL KGDFK+QKEAAWA+TNTTT G+ EQI+ L+EKY ++KP+ DLLD KD RT++V   366
             VLVEVLIKGDFKSQKEAAWAITNTTTGGSTEQIIHLVEKYPVMKPYCDLLDAKDSRTVRV

Query  1311  VQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTYFSNG   1490
             V +G++N+F +AEK+GG ENLC + EE+G LDKLE LQ HENEEVYKKA+ +I+TYF++
Sbjct  367   VLSGIANIFQIAEKIGGAENLCTLFEEIGALDKLEALQHENEEVYKKAFQLIETYFTDA   426

Query  1491  DDEAEQELAPQEVNGALEFNATQPKAPEG   1577
             +D    E AP+EVNGALEFN +  G
Sbjct  427   ED-VNPECAPKEVNGALEFNPSAAQQQSG   454
```

PREDICTED: importin subunit alpha-5 [Tribolium castaneum]

Sequence ID: **ref|XP_975293.1|** Length: 516 Number of Matches: 1

▶ **See 2 more title(s)**
Range 1: 5 to 513

Score	Expect	Method	Identities	Positives	Gaps	Frame
509 bits(1312)	1e-169()	Compositional matrix adjust.	268/510(53%)	356/510(69%)	2/510(0%)	+3

Features:

```
Query  45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKELNGQSP   221
             +R  S+K    + ++ R RR   TIELRK+KKEDQ+ KRRNI+  E+ ++PL+E N  S
Sbjct  5     NRIRSFKNKGKDCEEMRRRRAGQTIELRKAKKEDQLLKRRNISLQEEASTPLQENNSVSL   64

Query  222   VQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTNN   401
             + +S +EI+  M S D+  QF   Q+ RKMLSRERNPPID MI  G+VP C+ FL   T+N
Sbjct  65    ITMSAEEILMGMMSPDENLQFKATQACRKMLSRERNPPIDHMIRLGVVPRCVEFLGKTHN   124

Query  402   SMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGDG   581
               L FEA WALTNIASGTS+QT V++  A+P   LL S  +++ EQA+WA+GNIAGDG
Sbjct  125   PSLVFEACWALTNIASGTSEQTAAVVQEGALPKLQQLLSSNRIDVVEQAIWAIGNIAGDG   184

Query  582   AAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvls   761
             +RD+V+++ V+  ++ LI   T LS LRN VW++SNLCRNKNP P F+ VK   LPVL+
Sbjct  185   PESRDLVLNYGVLPSLINLIKPNTTLSLLRNTVWVISNLCRNKNPYPDFELVKPALPVLA   244

Query  762   qlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRSV   941
             +LL   D  VLAD CWALSY+TD  N KIQAV+D+  + RLV LL +E +++ PALR+V
Sbjct  245   RLLSHDDKDVLADTCWALSYLTDGSNEKIQAVLDTGLIDRLVMLLYSEESTVLTPALRAV   304

Query  942   GNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQAG   1121
             GNIVTG D QTD+VI +G L  +  LLQH++ NIVKEAAWTVSNITAGN +QIQ V+ AG
Sbjct  305   GNIVTGNDHQTDMVINAGALDCMIRLLQHSRLNIVKEAAWTVSNITAGNSEQIQKVLDAG   364

Query  1122  IFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPRT   1301
             I   L  VL+ GDFK+QKEAAWAVTN T+ G   Q+ L+E   LKP  +LL++KD +T
Sbjct  365   ILPYLLHVLQTGDFKSQKEAAWAVTNFTSGGNSAQLAQLVE-MGALKPMCNLLNSKDSKT   423

Query  1302  IKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTYF   1481
             I VV  GL+N+ + A KL   E + +M+EE GGLD +E LQ H+NE+VY++A  II+ YF
Sbjct  424   IIVVLEGLNNILSAAAKLNQAEKVAIMIEECGGLDGIEALQSHDNEKVYERALHIIENYF   483

Query  1482  SNGDDEAEQELAPQEVNGALEFNATQPKAP   1571
             ++G++      +A E+ A   A Q ++P
Sbjct  484   ADGEEGVTVTVANGEIQFATPNMADQQQSP   513
```

PREDICTED: importin subunit alpha [Monomorium pharaonis]

Sequence ID: **ref|XP_012526791.1|** Length: 544 Number of Matches: 1
Range 1: 30 to 535

Score	Expect	Method	Identities	Positives	Gaps	Frame
509 bits(1310)	5e-169()	Compositional matrix adjust.	267/508(53%)	363/508(71%)	4/508(0%)	+3

Features:

```
Query  42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQSP   221
             + R  ++K N++   +++RMRR+ +++ELRK+KK+DQ+ KRRN+     L E   S
Sbjct  30    HGRISNFKFNN-KPEEARMRRNALSVELRKAKKDDQLSKRRNLSTKQELPNLSEEAIVSS   88

Query  222   VQ-LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN   398
             +  LS+DEIV  +NS D+  Q   +Q+ RK+LSRE++PPI+ MI  GIVP+C++ L + +
Sbjct  89    ISVLSIDEIVNHINSSDETLQLAAIQTCRKLLSREKDPPINDMIEGGIVPLCVKLLDSDH   148

Query  399   NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD   578
             N  LQFE AW LTNIASGTS QT+ V++H A+P  V LL+S S   AEQAVWALGNIAGD
Sbjct  149   NVSLQFEVAWVLTNIASGTSVQTQNVVKHGAIPKLVKLLKSASPIAAEQAVWALGNIAGD   208

Query  579   GAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvl   758
             G  ARD+V+ H+ +  ++ LI  +TP++F RNIVW +SNLCRNKNP P F+ ++ LLPV
Sbjct  209   GPYARDLVLGHDALPLLIDLIKPDTPITFTRNIVWTLSNLCRNKNPPPVFESIRPLLPVF   268

Query  759   sqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRS   938
             + LL   D  VLAD CWALSY+TD  N KIQAV+++   +P+LV+LL  E +I+ PALR+
Sbjct  269   NCLLSYTDRDVLADTCWALSYLTDGANEKIQAVLETGIIPKLVELLASQEGAILTPALRA   328

Query  939   VGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQA   1118
             VGNIVTG D QTD VI +GGL  LG LL++ ++N+VKEAAW +SNITAG+  QIQ+VI A
Sbjct  329   VGNIVTGDDAQTDAVIFAGGLSHLGALLRYPRANVVKEAAWAISNITAGSPDQIQSVINA   388

Query  1119  GIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPR   1298
             +   L  VL+ GD+KAQKEAAWAVTN TT GT + + L+    +L PF +LL++KD
Sbjct  389   DLLPPLIHVLQFGDYKAQKEAAWAVTNLTTGGTVQHLTQLV-GAGVLPPFCNLLESKDWN   447

Query  1299  TIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTY   1478
```

```
Sbjct  448   I VV   GL+N+    AEK+G  E L +M+EE+GGLDK+E LQ HENE+VY+++ AIIDT+
             VILVVLDGLTNILHAAEKVGQVERLAIMIEEVGGLDKIEALQHHENEQVYQRSMAIIDTF   507

Query 1479   FSNGDDEAEQELAPQEVN-GALEFNATQ   1559
             FS D+E      +E N G +EFN T+
Sbjct  508   FSQRDEEEALACEVKENNDGQIEFNMTE   535
```

PREDICTED: importin subunit alpha-1 [Acromyrmex echinatior]

Sequence ID: **ref|XP_011056602.1|** Length: 524 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 7 to 514

Score	Expect	Method	Identities	Positives	Gaps	Frame
507 bits(1306)	1e-168()	Compositional matrix adjust.	265/512(52%)	363/512(70%)	9/512(1%)	+3

Features:

```
Query   36   DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQ   215
             +S+ R+ ++K N+    +++R+RR+ +++ELRK+KK+DQ+ KRRN++  +    L +L+ +
Sbjct    7   NSHGRKANFKFNN-KHEEARIRRNALSVELRKAKKDDQLSKRRNLDTSN--QELSDLSNK    63

Query  216   SPVQ----LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
             + V    LS+DEIV  +NS D+ Q  +Q+ RK+LSRE+NPPI+ +I GIVP CI
Sbjct   64   ATVSPTPTLSIDEIVNHINSSDETLQLSAIQTCRKLLSREKNPPINDIIEGGIVPRCIAL   123

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
             L N  N  LQFE AW LTNIASGTS QT+ VI++ A+P  V LL+S S  +AEQAVWALG
Sbjct  124   LDNDYNVALQFEVAWVLTNIASGTSLQTQNVIKYGAIPKLVNLLKSTSPVVAEQAVWALG   183

Query  564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
             NIAGDG   ARD+V+ H+ +  +L LI  +T ++FLRN+VW +SNLCRNKNP PPF+ ++
Sbjct  184   NIAGDGPYARDLVLGHDALPLLLDLIKPDTSITFLRNVVWTLSNLCRNKNPPPPFELIRP   243

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
             +LP+ ++LL    D  VLAD CWALSY+TD  N KIQAV+++    +PRLV++ + E  I+
Sbjct  244   VLPIFNRLLSYTDRDVLADTCWALSYLTDGSNDKIQAVLETGIIPRLVQMLTLQEGMILT   303

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
             PALR+VGNIVTG D QTD VI +GGL  LG LL++++ NIVKEAAW +SNI AGN  QIQ
Sbjct  304   PALRTVGNIVTGDDAQTDAVILAGGLSHLGALLRYHRVNIVKEAAWAISNIMAGNTNQIQ   363

Query 1104   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
              VI AG+   L  VL+ GD+K+QKEAAWA+TN TT GT + + L+     +L PF +LL+
Sbjct  364   NVIDAGLLSPLIEVLQFGDYKSQKEAAWAITNLTTGGTIQHLSQLV-GVGVLPPFCNLLE   422

Query 1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
             +KD  + VV GL+N+    AEK+G  E L +++EE GGLDK+E LQ H+NE+VY+K+ A
Sbjct  423   SKDWNIVIVVLDGLTNILHAAEKIGQVEKLAILIEEAGGLDKIEALQHHQNEQVYQKSMA   482

Query 1464   IIDTYFSNGDDEAEQELAPQE-VNGALEFNAT   1556
             IID +FS D E     QE   G +EFN T
Sbjct  483   IIDAFFSQKDVEETLTSEVQENCEGQIEFNMT   514
```

PREDICTED: importin subunit alpha [Wasmannia auropunctata]

Sequence ID: **ref|XP_011706521.1|** Length: 523 Number of Matches: 1

Range 1: 8 to 523

Score	Expect	Method	Identities	Positives	Gaps	Frame
507 bits(1306)	1e-168()	Compositional matrix adjust.	268/522(51%)	365/522(69%)	11/522(2%)	+3

Features:

```
Query   39   SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQS   218
             S+ R  ++K N+    +++R+RR+ +++ELRK+KK+DQ+ KRRN++  +       L    S
Sbjct    8   SHGRIANFKFNN-KHEEARIRRNTLSVELRKAKKDDQLSKRRNLDTKQELPDLSNEAEHS    66

Query  219   PVQ-LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
             P   LS+DEIV  +NS D+   Q L +Q+ RK+LSRE+NPPI+ MI  G+VP CI+  L +
Sbjct   67   PTTALSIDEIVNYINSSDETLQLLAIQTCRKLLSREKNPPINDMIEGGVVPRCIKLLDSD   126

Query  396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
             +N  LQFE AW LTNIASGTS+QT+ V+ + AVP  V LL+S S  +AEQAVWALGNIAG
Sbjct  127   HNIPLQFEVAWVLTNIASGTSEQTQNVVNYGAVPKLVKLLKSASPIVAEQAVWALGNIAG   186

Query  576   DGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv   755
             DG   ARD+V+ H+ +  +L LI  ET ++F RNIVW +SNLCRNKNP P F+ ++ +LPV
Sbjct  187   DGPYARDLVLEHDALPLLLNLIKPETSMTFMRNIVWTLSNLCRNKNPPPSFELIRPVLPV   246

Query  756   lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR   935
             ++LL    D  VLAD CWALSY+TD  N KIQAV+++   +P+LV+LL   + +I+ PALR
Sbjct  247   FNRLLNCTDQDVLADTCWALSYLTDGSNDKIQAVLETGIIPKLVELLTSQKGTILTPALR   306

Query  936   SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ   1115
             +VGNIVTG D QTD VI +GGL  LG LL+H+++NIVKEAAW +SNI AGN  QI++VI
Sbjct  307   TVGNIVTGDDAQTDAVILAGGLSYLGALLRHHRANIVKEAAWAISNIMAGNTDQIESVIN   366

Query 1116   AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP   1295
             AG+   L  VL+ GD+KAQKE AWA++N TT GT + + L+  +  +L PF +LL+ K+
Sbjct  367   AGLLSPLIEVLQVGDYKAQKEVAWAISNLTTGGTIQHLTQLV-GAGVLPPFCNLLEAKDW   425

Query 1296   RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT   1475
              I VV  GL+N+    AEK+G  E L +M+EE GGLDK+E LQ H+NE+VY+K+ AIID
Sbjct  426   NIIIVVLDGLTNILHAAEKIGQVERLAIMIEEAGGLDKIEALQHHQNEQVYQKSMAIIDA   485

Query 1476   YFSNGDDEAEQELAPQEV----NGALEFNATQPKAPEGGYTF   1589
```

```
+FS  D E   E    EV    +G +EFN +   +P    + F
Sbjct  486    FFSQRDTE---ETLTSEVKENSDGQIEFNMME-DSPINKFNF  523
```


PREDICTED: importin subunit alpha [Vollenhovia emeryi]

Sequence ID: **ref|XP_011877264.1|** Length: 523 Number of Matches: 1

Range 1: 8 to 514

Score	Expect	Method	Identities	Positives	Gaps	Frame
507 bits(1305)	1e-168()	Compositional matrix adjust.	266/516(52%)	360/516(69%)	18/516(3%)	+3

Features:

```
Query  39     SNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELN---  209
              S R  ++K N+    +++R RR  +++ELRK+KK+DQ+ KRRN++        P +EL+
Sbjct  8      SQGRMANFKFNN-KHEEARRRRTTLSVELRKAKKDDQLSKRRNLD------PQQELDLSD  60

Query  210    --GQSPVQ-LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIR  380
                SP   LS +EIV +NS D+  Q L +Q+ RK+LSRE+NPPI+ MI  GIVP CI+
Sbjct  61     QAASSPTSVLSTNEIVKHINSSDESSQLLAIQTCRKLLSREKNPPINDMIEGGIVPRCIQ  120

Query  381    FLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWAL  560
              L + +N  LQFE AW LTNIASGTS+QT+ V++H AVP  + LL+S S  +AEQAVW L
Sbjct  121    LLDSEHNIQLQFEVAWVLTNIASGTSEQTQIVVKHGAVPKLINLLKSVSPIVAEQAVWTL  180

Query  561    GNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVK  740
              GNIAGDG  ARDIV+ H+ +  +L LI  +TP+SF+RNIVW +SNLCRNKNP P F+ +K
Sbjct  181    GNIAGDGPYARDIVLAHDALPILLDLIKPDTPISFVRNIVWTLSNLCRNKNPPAFEYIK  240

Query  741    RllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSII  920
                LP+ ++LL    D VLAD CWALSY+TD  N KIQAV+D+  +P+LV+LL   E +I+
Sbjct  241    PALPIFNRLLSYTDHDVLADTCWALSYITDGSNDKIQAVLDTGIIPQLVQLLACQEGTIL  300

Query  921    VPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQI  1100
               PALR+VGNIVTG D QTD VI +GGL  L  LL++++ NIVKEAAW +SN+ AGN  QI
Sbjct  301    TPALRTVGNIVTGDDAQTDAVILAGGLTHLVTLLRYHRVNIVKEAAWAISNVMAGNTSQI  360

Query  1101   QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL  1280
              Q+ I AG+    L   VL+ GD+KAQKEAAWA+TN TT GT + + L+        +L PF +LL
Sbjct  361    QSAISAGLLPPLIEVLQFGDYKAQKEAAWAITNMTTGGTIQHLTQLV-GAGVLPPFCNLL  419

Query  1281   DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY  1460
              +TKD    I +V  GL+N+   AE++    E + +M+EE GGLDK+E LQ H+NE+VY+K+
Sbjct  420    ETKDWNVIIVLDGLTNILNAAERIDQVEKVAIMIEEAGGLDKIEALQHHQNEQVYQKSM  479

Query  1461   AIIDTYFSNGDDEAEQELAP---QEVNGALEFNATQ  1559
              AI+D +FS  +DE E L     +  +G +EFN T+
Sbjct  480    AILDAFFSQ-EDEEEASLTSKVNENADGQIEFNVTE  514
```


hypothetical protein CAPTEDRAFT_169892 [Capitella teleta]

Sequence ID: **gb|ELU00226.1|** Length: 520 Number of Matches: 1

Range 1: 1 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
505 bits(1301)	6e-168()	Compositional matrix adjust.	269/524(51%)	354/524(67%)	6/524(1%)	+3

Features:

```
Query  24     MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE  203
              M+  +  ++R  +YK     +  D R RR+E ++ELRK+KK+DQ+ KRRN+    D+ SPLKE
Sbjct  1      MASQERDTRLKNYKNKGKDCDDLRRRRNETSVELRKAKKDDQLSKRRNLTLTDV-SPLKE  59

Query  204    LNGQSPVQL-SVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIR  380
               N Q   L  + +I+ ++ S+DQE+ FL   QSARK+LSRERNPPI  +I  GI+       +
Sbjct  60     QNNQPAAPLMPMSDIIKSIKSQDQEKWFLATQSARKLLSRERNPPIGDIIDAGILSNLVA  119

Query  381    FLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWAL  560
              FL + +N  LQFEAAWALTNIASGTS QT  V+   AV F+ LL S   N+AEQAVWAL
Sbjct  120    FLDHADNPDLQFEAAWALTNIASGTSMQTHTVVSIGAVRPFIKLLSSTIPNVAEQAVWAL  179

Query  561    GNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVK  740
              GNIAGDG  RD++I  +  +L LI+ +TP++FLRN W +SNLCRNKNP PPF +VK
Sbjct  180    GNIAGDGPELRDLLIKEGCLPPLLSLISPKTPVAFLRNVTWTLSNLCRNKNPPPPFEAVK  239

Query  741    RllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSII  920
              + LP L+QL+ + +D ++L+DACWALSY+TD G   +IQAV+D MG VP+VV LL  HDE SI+
Sbjct  240    QCLPALAQLIHTADKEILSDACWALSYLTDGANDKIQAVIDMGVIPRVVHLLSHDEVSVI  299

Query  921    VPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQI  1100
               PALR++GNIVTG D QT V +     L      LL HNK+++ KEA WT+SNITAGN  QI
Sbjct  300    TPALRTIGNIVTGDDSQTQVALDHNMLMAFPTLLTHNKASVQKEACWTISNITAGNSSQI  359

Query  1101   QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL  1280
              Q V+  +    L KGDFK QKEAAWA+TN T+ GTP+QI L+E   +  P   LL
Sbjct  360    QMVVDCQLLPLIVDCLAKGDFKTQKEAAWAITNLTSGGTPQQISHLVE-LGVTVPLSQLL  418

Query  1281   DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY  1460
              +K+P+  I VV   + N+   A+      E  CL +EE+GGL K+ETLQ H+NEEVY+KA
Sbjct  419    TAKEPKIILVVLDAIRNILITAKAFEKLEQACLHLEEIGGLTKIETLQNHDNEEVYRKAL  478

Query  1461   AIIDTYFSNGDDEAEQELAPQEV-NGALEFNATQPKAPEGGYTF  1589
              II+ +FS  +DE  QELAP+    G  EF+A     AP GG++F
Sbjct  479    FIIEKFFSEEEDEV-QELAPESTEQGNYEFSAAG-DAPNGGFSF  520
```

GH11093 [Drosophila grimshawi]

Sequence ID: **ref|XP_001988308.1|** Length: 432 Number of Matches: 1

▶ **See 1 more title(s)**

Range 1: 5 to 415

Score	Expect	Method	Identities	Positives	Gaps	Frame
502 bits(1292)	7e-168()	Compositional matrix adjust.	274/412(67%)	326/412(79%)	2/412(0%)	+3

Features:

```
Query  207   NGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFL   386
             N ++ VQLS+D+IV A+NSED E+QFLGMQ ARKM+S    + PIDLMIG GIVP  I+FL
Sbjct  5     NEETAVQLSIDQIVVAVNSEDPEQQFLGMQEARKMVSG-GDIPIDLMIGRGIVPTFIQFL   63

Query  387   QNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGN   566
             Q+ +N+ LQFEAAWALTNI SGT++QT  VI+ NAVPHF LLQS  M+L EQAVWAL N
Sbjct  64    QHNDNNRLQFEAAWALTNITSGTTEQTHYVIQMNAVPHFITLLQSPYMDLVEQAVWALSN   123

Query  567   IAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl   746
             IAGDGAAARDIVI HNVIDGILPLI+NETPLS LR IVWLMSNLCRN  PSPPF QV+RL
Sbjct  124   IAGDGAAARDIVIQHNVIDGILPLISNETPLSLLRKIVWLMSNLCRNNIPSPPFGQVRRL   183

Query  747   lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP   926
             LPV SQ+LLSQDI +L DAC +L  V D +N  IQAV+D++AVPRLV LLQ   +  II
Sbjct  184   LPVFSQMLLSQDIPILIDACSSLVNVADAENNGIQAVIDAEAVPRLVHLLQSSDFRIIAL   243

Query  927   ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA   1106
             AL  +GNI  GTDQQTD +I++GGL +LGLLLQH+   +IV+E AW +SNITAG+Q QIQA
Sbjct  244   ALHIIGNIAFGTDQQTDSLISAGGLTKLGLLLQHSNGHIVQETAWIISNITAGSQTQIQA   303

Query  1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT   1286
             VI AGIFQQ+R +LEKG+ KAQK AAW VTNT  SGT EQ+++LIE  KI+KP+IDLL+
Sbjct  304   VIDAGIFQQIRHLLEKGNVKAQKNAAWTVTNTILSGTSEQVLNLIENQKIIKPYIDLLEI   363

Query  1287  KD-PRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENE   1439
               P  I VV  GL  LF  +E++ GTENLCLMVE++ GLDKL+ L  HE E
Sbjct  364   NTYPAIINVVLLGLEKLFRFSEQICGTENLCLMVEDLSGLDKLKALLFHEKE   415
```


PREDICTED: importin subunit alpha-1 [Atta cephalotes]

Sequence ID: **ref|XP_012061550.1|** Length: 524 Number of Matches: 1

Range 1: 7 to 514

Score	Expect	Method	Identities	Positives	Gaps	Frame
505 bits(1300)	9e-168()	Compositional matrix adjust.	263/512(51%)	363/512(70%)	9/512(1%)	+3

Features:

```
Query  36    DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQ   215
             +S+ R+ ++K N+    +++R+RR+ +++ELR++KK+DQ+ KRRN++   +   L +L+ +
Sbjct  7     NSHGRKANFKFNN-KHEEARIRRNALSVELRRAKKDDQLSKRRNLDTSN--QELSDLSNK   63

Query  216   SPVQ----LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
             + V    LS++EIV  +NS D+ Q   +Q+ RK+LSRE+NPPI+ +I  GIVP CI
Sbjct  64    ATVSPTPTLSINEIVNHINSSDETLQLSAIQTCRKLLSREKNPPINDIIEGGIVPRCIEL   123

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
             L N  N  LQFE AW LTNIASGTS  QT+ V+++ A+P  V LL+S S  +AEQAVWALG
Sbjct  124   LDNDYNIALQFEVAWVLTNIASGTSLQTQNVVKYGAIPKLVKLLKSTSPVVAEQAVWALG   183

Query  564   NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
             NIAGDG  ARD+V+ H+ +   +L LI  +T ++FLRN+VW +SNLCRNKNP PPF+ ++
Sbjct  184   NIAGDGPYARDLVLGHDALPLLLDLIKPDTSITFLRNVVWTLSNLCRNKNPPPPFELIRP   243

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
             +LP+ ++LL   D  VLAD CWALSY+TD  N KIQAV+++   +PRLV++L + E  I+
Sbjct  244   VLPIFNRLLSYTDRDVLADTCWALSYLTDGSNDKIQAVLETGIIPRLVQMLTLQEGMILT   303

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
             PALR+VGNIVTG D QTDV+ +GGL  LG LL++++ NIVKEAAW +SNI AGNTNQIQ
Sbjct  304   PALRTVGNIVTGDDAQTDAVILAGGLSHLGALLRYHRVNIVKEAAWAISNIMAGNTNQIQ   363

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
               VI AG+   L  VL+ GD+K+QKEAAWA+TN TT GT QHL QL+ A  +L PF N+L+
Sbjct  364   NVIDAGLLSPLIEVLQFGDYKSQKEAAWAITNLTTGGTIQHLSQLVGA-GVLPPFCNLLE   422

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
             +KD  I VV  GL+N+   AEK+G  E L +++EE GGLDK+E LQ H+NE+VY+K+ A
Sbjct  423   SKDWNVIIVVLDGLTNILHAAEKIGQVEKLAILIEEAGGLDKIEALQHHQNEQVYQKSMA   482

Query  1464  IIDTYFSNGDDEAEQELAPQE-VNGALEFNAT   1556
             IID +FS  D E    QE    G +EFN T
Sbjct  483   IIDAFFSQKDIEETLTSEVQENYEGQIEFNMT   514
```


importin subunit alpha-1 [Danio rerio]

Sequence ID: **ref|NP_001002335.1|** Length: 525 Number of Matches: 1

▶ **See 1 more title(s)**

Range 1: 1 to 514

Score	Expect	Method	Identities	Positives	Gaps	Frame

503 bits(1296) 4e-167() Compositional matrix adjust. 262/516(51%) 356/516(68%) 10/516(1%) +3

Features:

```
Query  24    MSKADSNS-RQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSP  194
             MS A+ N+ R   +K   + + R RR EV +ELRK+KK++Q+ KRRN++    ++ TSP
Sbjct  1     MSAANENTARLTQFKNKGKDATELRRRRIEVNVELRKAKKDEQILKRRNVSSFPDEATSP  60

Query  195   LKELNGQSPVQ-LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPI  371
             L+E +    Q   +V+EIV  +NS + E Q   Q+ARK+LSRER+PPID +I  G++P
Sbjct  61    LQEKSQNCQAQHWTVEEIVNGVNSNNLETQVQATQAARKLLSRERHPPIDRIISAGLIPK  120

Query  372   CIRFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAV  551
              + FL  ++  +QFEAAWALTNIASGTSDQT  V++  A+P F++L+ S   +++EQAV
Sbjct  121   FVGFLSLVDSPPIQFEAAWALTNIASGTSDQTSAVVQGGAIPAFISLISSPHAHISEQAV  180

Query  552   WALGNIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPS  719
             WALGNIAGDG+  RD VI H  I  +L L+     + P +LRN+ W +SNLCRNKNP+
Sbjct  181   WALGNIAGDGSGYRDRVIKHGAIPPLLALLAVPDLSVFPAGYLRNVTWTLSNLCRNKNPA  240

Query  720   PPFDQVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQ  899
             PP + VK++LP L  LL    D +VLAD CWA+SY+TD  N +I+ VV++  VPRLV+LL
Sbjct  241   PPLEAVKQILPTLICLLQHSDKEVLADTCWAISYLTDGPNDRIEVVVNAGVVPRLVQLLA  300

Query  900   MDEPSIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNIT  1079
              E SI+ P+LRS GNIVTGTD+QT  V+  +G LP    LL+H KSNI KEA+WT+SNIT
Sbjct  301   SGELSIVTPSLRSIGNIVTGTDEQTQAVLEAGALPMFPALLRHQKSNIQKEASWTLSNIT  360

Query  1080  AGNQKQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKIL  1259
             AG   QIQ VI AGI   L  VL +GD+K QKEA WAVTN T+ GT EQ+V L++   +L
Sbjct  361   AGRDYQIQEVINAGIVPYLVEVLRRGDYKTQKEAVWAVTNYTSGGTVEQVVYLVQA-NVL  419

Query  1260  KPFIDLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENE  1439
             +P ++LL TKD  TI V+   ++N+F   EK+G  E LCLM+EE GGLDK+E LQ HENE
Sbjct  420   EPLLNLLSTKDSTTILVILDAITNIFLAGEKIGEVEKLCLMIEECGGLDKIEALQSHENE  479

Query  1440  EVYKKAYAIIDTYFSNGDDEAEQELAPQEVNGALEF  1547
             VYK +  +I+ YFS G++E ++ +AP+  +    F
Sbjct  480   MVYKASLNLIEKYFS-GEEEGDECVAPEATDDGYAF  514
```


PREDICTED: importin subunit alpha-1 [Linepithema humile]

Sequence ID: ref|**XP_012217870.1**| Length: 520 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 9 to 508

Score	Expect	Method	Identities	Positives	Gaps	Frame
502 bits(1292)	1e-166()	Compositional matrix adjust.	264/507(52%)	353/507(69%)	12/507(2%)	+3

Features:

```
Query  45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQ---  215
             +R+   +K N+ + +++R RR+   ++ELRK+KK+DQ+ KRRN+N E+     KE N Q
Sbjct  9     TRKAYFKFNNKH-EEARRRRNAASVELRKAKKDDQLSKRRNLNCEE-----KESNPQIEE  62

Query  216   -SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN  392
              +    S+DE++ ++ S D+  L   Q+ RK+LSRE+NPPI+ MI  GIVP  CI  L
Sbjct  63    STTFTFSLDELIQSIKSSDETTRLLATQTCRKLLSREKNPPINDMIEAGIVPCCIELLDY  122

Query  393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA  572
              +N  LQFEAAW LTNIASGTS QT+ VI+  AV   V LL+S+S N+AEQAVWALGNIA
Sbjct  123   DHNIPLQFEAAWVLTNIASGTSVQTQTVIKCGAVQKLVRLLKSESSNVAEQAVWALGNIA  182

Query  573   GDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllp  752
             GDG  ARD V+ +  +  +L LI +  ++FLRNIVW +SNLCRNKNP P F+ ++  L
Sbjct  183   GDGPTARDFVLTNEAMPQLLELIRPDISVTFLRNIVWTLSNLCRNKNPPPSFEMIQPALA  242

Query  753   vlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPAL  932
             +   +LL + D  VLAD CWALSY++D  N KIQA++D+  +P LV+LL+  + S++ PAL
Sbjct  243   IFIRLLTNTDQDVLADTCWALSYLSDGSNDKIQAILDTGIIPLLVELLKSQQTSVLTPAL  302

Query  933   RSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVI  1112
             R+VGNIVTG D QTD V+++G LP LG LL+H+++NIVKEAAW +SNITAGN  QIQ VI
Sbjct  303   RTVGNIVTGDDAQTDAVISAGALPHLGALLRHSRSNIVKEAAWAISNITAGNAGQIQHVI  362

Query  1113  QAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKD  1292
             +AG +  L  VL+ GD+KAQKEAAWAVTN T+ GT  ++  L++  +L    +L F +LLD+KD
Sbjct  363   NANLLTPLVEVLQFGDYKAQKEAAWAVTNLTSGGTVQHLSQLVAA-GVLPYFCNLLDSKD  421

Query  1293  PRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIID  1472
               T+ VV  GLSNL   A K+G   NL +++EE+G LDKLE LQ HENE+VY K+ A+ID
Sbjct  422   WNTVIVVLDGLSNLLHTAAKMGEETNLAILIEEIGALDKLEALQHHENEQVYMKSMALID  481

Query  1473  TYFSNGDDEAEQELAPQ-EVNGALEFN  1550
              YF+  D E   L P+ E N L+F+
Sbjct  482   AYFTEKDTEEVGTLTPKVEDNNQLQFD  508
```


PREDICTED: importin subunit alpha-1 isoform X2 [Xenopus tropicalis]

Sequence ID: ref|**XP_012821933.1**| Length: 526 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 514

Score	Expect	Method	Identities	Positives	Gaps	Frame
501 bits(1291)	2e-166()	Compositional matrix adjust.	264/516(51%)	355/516(68%)	10/516(1%)	+3

Features:

```
Query    24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPL    197
               MS  ++ +R   +K    +T + R RR EV +ELRK+KK+DQM KRRN++   ++ TSPL
Sbjct    1     MSNNENAARLTRFKNKGKDTTEMRRRIEVNVELRKAKKDDQMLKRRNVSTFPDEPTSPL    60

Query    198   KELN--GQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPI    371
               +E N  GQ+  Q SV+EIV + S  E Q   Q+ARK+LSRER PPID +I  G++P
Sbjct    61    QEKNQNGQTSTQWSVEEIVRGVASSSLEIQLQATQAARKLLSREREPPIDRIIQAGLIPK    120

Query    372   CIRFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAV    551
               + FL  T+ S +QFEAAWALTNIASGTSDQT+ V+E   VP F++LL S   +++EQAV
Sbjct    121   LVAFLARTDCSPIQFEAAWALTNIASGTSDQTKAVVEGGGVPAFISLLASPHPHISEQAV    180

Query    552   WALGNIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPS    719
               WALGNIAGD+A RD+VI H  +  +L L+    +      +LRN+ W +SNLCRNKNP+
Sbjct    181   WALGNIAGDGSAYRDLVIKHGAVGPLLALLADPDLSTLATGYLRNVTWTLSNLCRNKNPA    240

Query    720   PPFDQVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQ    899
               PP D ++++LP L +LL   D +VLAD CWA+SY+TD  N +I  VV +  VPR+V+LL
Sbjct    241   PPLDAIQQILPTLVRLLHHDDREVLADTCWAVSYLTDGSNDRINVVVGTGLVPRIVQLLG    300

Query    900   MDEPSIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNIT    1079
                E +I+ P LR+VGNIVTGTD+QT VV+ +G L     LL H+K+NI KEAAWT+SNIT
Sbjct    301   CGELTIVTPCLRTVGNIVTGTDEQTQVVLDAGALSVFAELLTHHKNNIQKEAAWTLSNIT    360

Query    1080  AGNQKQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKIL    1259
               AG Q QIQ V+  G+   L  +L K D+K QKEA WAVTN T+ GT +QI+ L++   ++
Sbjct    361   AGRQDQIQEVVNHGLIPYLIEILRKADYKTQKEAIWAVTNYTSGGTIDQIIYLVQ-CSVI    419

Query    1260  KPFIDLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENE    1439
               +P  +LL  KD +T+ V+   +N+FA AEKLG TE LCLMVEE GGLD++E LQ HENE
Sbjct    420   EPLSNLLSVKDSKTVLVILDAFTNVFAAAEKLGETEKLCLMVEECGGLDRIEALQSHENE    479

Query    1440  EVYKKAYAIIDTYFSNGDDEAEQELAPQEVNGALEF    1547
               +VYK +  +I+ YFS  D E ++ LAP+  +    F
Sbjct    480   QVYKASAGLIEKYFSAEDGE-DESLAPETTSDGYTF    514
```


PREDICTED: importin subunit alpha-1 [Pseudopodoces humilis]

Sequence ID: **ref|XP_014111239.1|** Length: 529 Number of Matches: 1

▸ **See 2 more title(s)**
Range 1: 11 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
501 bits(1289)	4e-166()	Compositional matrix adjust.	258/509(51%)	355/509(69%)	9/509(1%)	+3

Features:

```
Query    42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKELNG-    212
               ++R   +K    ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  G
Sbjct    11    SARLNRFKNKGKDSTEMRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRGN    70

Query    213   QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN    392
               Q     SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + FL
Sbjct    71    QVSAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGR    130

Query    393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA    572
               + S +QFE+AWALTNIASGTS+QTR V+E  A+P F++LL S   +++EQAVWALGNIA
Sbjct    131   ADCSPIQFESAWALTNIASGTSEQTRAVVEGGAIPAFISLLASPHTHISEQAVWALGNIA    190

Query    573   GDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVK    740
               GDG+A RD+VI +  I+ +L L+    +      +LRN+ W +SNLCRNKNP PP D ++
Sbjct    191   GDGSAYRDLVIKYGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIDAIQ    250

Query    741   RllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSII    920
               +++LP L +LL   D +VLAD CWA+SY+TD  N +I  VV +  VP+LV+LL   E  I+
Sbjct    251   QILPTLVRLLHHDDPEVLADTCWAISYLTDGSNDRIEVVVKTGLVPQLVRLLGYSELPIM    310

Query    921   VPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQI    1100
               P+LR++GNIVTGTD+QT +VI SG L     LL H+K+NI KEAAWT+SNITAG Q QI
Sbjct    311   TPSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQI    370

Query    1101  QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL    1280
               Q V+  G+    L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++    +L+P ++LL
Sbjct    371   QRVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVLEPLLNLL    429

Query    1281  DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY    1460
                TKD +T+ V+   +SN+F  AEK+ TE LCLM+EE GGLD++E LQ HENE+VY+ +
Sbjct    430   STKDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDRIEALQSHENEQVYRASS    489

Query    1461  AIIDTYFSNGDDEAEQELAPQEVNGALEF    1547
               +II+ YFS  ++E +Q + P   +    F
Sbjct    490   TIIEKYFS-AEEEEDQNVVPDSTADSYTF    517
```


PREDICTED: importin subunit alpha-1-like [Cyprinodon variegatus]

Sequence ID: **ref|XP_015243393.1|** Length: 523 Number of Matches: 1
Range 1: 6 to 512

Score	Expect	Method	Identities	Positives	Gaps	Frame
500 bits(1288)	6e-166()	Compositional matrix adjust.	260/524(50%)	363/524(69%)	26/524(4%)	+3

Features:

```
Query    45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDE--DLTSPLKELN--G    212
               +R   +K    +  + R RR EV +ELRK+KK+DQMFKRRN++++   + TSPL+E N
```

```
Sbjct   6     ARLNKFKNKGKDVNELRRRRVEVNVELRKAKKDDQMFKRRNVSEDPDEATSPLQERNQNS   65

Query   213   QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN   392
              Q+     SVD+IVA +NSE++E Q   Q+ARK+LSR+++PPID MIG G++P  + FL
Sbjct   66    QAFQPWSVDKIVAGVNSENREAQLQATQAARKLLSRDKHPPIDQMIGAGLIPKFVAFLGL   125

Query   393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA   572
              ++   +QFEA+WALTNIASGTSDQT V++  A+P F++L+ S   +++EQAVWALGNIA
Sbjct   126   SDCHPIQFEASWALTNIASGTSDQTAAVVDGGAIPAFISLVTSPHQHISEQAVWALGNIA   185

Query   573   GDGAAARDIVIHHNVIDGILPLINNE-----TPLSFLRNIVWLMSNLCRNKNPSPPFDQV   737
              GDG+A RD VI H   I  +L L+       TP +LRN+ W +SNLCRNKNPSPP + +
Sbjct   186   GDGSALRDRVIKHGAITPLLSLLAVPDLAVFTP-GYLRNVTWTLSNLCRNKNPSPPIEAI   244

Query   738   KRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSI   917
              K++LP L +LL + D++VLADACWA+SY+TD  N +IQ VV++   +PRLVKLL  +E S+
Sbjct   245   KQILPALIRLLHNDDLEVLADACWAVSYLTDGSNDRIQVVVETGLIPRLVKLLGYEELSV   304

Query   918   IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ   1097
              + PALR++GNIVTGTD+QT  V+ +G L     LL+H K NI KEAAWT+SNITAG  Q
Sbjct   305   VTPALRALGNIVTGTDEQTQAVLDAGALTVFPQLLRHKKGNIQKEAAWTLSNITAGKDTQ   364

Query   1098  IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDL   1277
              IQ VI AG+   +  +L +GD+K QKEA WAVTN T+ GT +Q+V L++    +L+P ++L
Sbjct   365   IQEVINAGLVPYMVDLLVRGDYKTQKEAVWAVTNFTSGGTVQQVVYLVQA-NVLEPLLNL   423

Query   1278  LDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA   1457
              L +KD +T+ V+   ++N+F   +K+G ++ L LM+EE GGLDK+E LQ HENE +YK A
Sbjct   424   LSSKDSKTVLVILDAITNIFMAGDKIGESDKLSLMIEECGGLDKIEALQAHENEMIYKAA   483

Query   1458  YAIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              +I+ YFS  D+E +            +  P+A E GY F
Sbjct   484   LNLIEKYFSEEDEEVQ---------------SVVPEATEDGYAF   512
```

hypothetical protein D910_08772 [Dendroctonus ponderosae]

Sequence ID: **gb|ERL91442.1|** Length: 518 Number of Matches: 1
Range 1: 5 to 518

Score	Expect	Method	Identities	Positives	Gaps	Frame
500 bits(1287)	7e-166()	Compositional matrix adjust.	264/517(51%)	354/517(68%)	5/517(0%)	+3

Features:

```
Query   45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN--DEDLTSPLKELNGQS   218
              +R  S+K    + ++ R RR  TIELRK++K+DQ+ KRRNI+  DE+ TSP  E    S
Sbjct   5     NRIRSFKNKGKDCEEMRRRRIGQTIELRKARKDDQLLKRRNISSVDEEPTSPQLENEATS   64

Query   219   PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN   398
              PV +  +EI+  M + D+  Q    S RK+LSRERNPPID MI  G+VP C+ FL   +
Sbjct   65    PVHMKAEEIMYGMINPDESIQLQATLSCRKILSRERNPPIDQMIRLGVVPRCVDFLSKDH   124

Query   399   NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD   578
              N  LQFEA WALTNIASGTS+QT V+   A+P   LL+S  +++ EQAVWALGNIAGD
Sbjct   125   NPALQFEACWALTNIASGTSEQTAAVVHEGAIPKLQLLLKSPRIDVVEQAVWALGNIAGD   184

Query   579   GAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvl   758
              GA  RD+V+   V+   IL LIN +T +S +RN VW +SNLCRNKNP+P F++V+ +LP L
Sbjct   185   GALTRDMVLASGVLPEILRLINADTSISLMRNAVWAVSNLCRNKNPAPDFERVRPILPTL   244

Query   759   sqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRS   938
              + LL    D  VLAD CWALSY+TD  N +I+AV+++ + RLV+LL  +E +++ PALR+
Sbjct   245   ALLLSYTDKDVLADSCWALSYLTDGSNERIEAVLEAGLISRLVQLLTSNESTVLTPALRA   304

Query   939   VGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQA   1118
              VGNIVTG D QTDVVI +G L  L  LLQH + NIVKEAAWT+SNITAGN  QIQAVI A
Sbjct   305   VGNIVTGNDAQTDVVINAGVLHVLPKLLQHPRLNIVKEAAWTLSNITAGNSTQIEKVINA   364

Query   1119  GIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPR   1298
              GI     VL  GDFK+QKEAAW VTN T+ G+  Q++ L+E    +KP +LL++KD +
Sbjct   365   GIMPVILHVLSTGDFKSQKEAAWTVTNFTSGGSIPQLIKLVE-MGCIKPMCNLLNSKDYK   423

Query   1299  TIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTY   1478
              +  VV  GL N+ + A KLG T+ + +++EE GGLD +E LQ H+NE +Y KA +II+ Y
Sbjct   424   IVSVVLNGLDNILSAAHKLGETDKVAILIEECGGLDLIEALQAHDNENIYDKALSIIENY   483

Query   1479  FSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              FS    EA+   AP   +G + F +   + P+GG+ F
Sbjct   484   FSE-TQEADMP-APATQDGQITFASPPQEMPKGGFNF   518
```

PREDICTED: importin subunit alpha-1 [Cimex lectularius]

Sequence ID: **ref|XP_014253052.1|** Length: 521 Number of Matches: 1
Range 1: 10 to 520

Score	Expect	Method	Identities	Positives	Gaps	Frame
500 bits(1287)	9e-166()	Compositional matrix adjust.	262/516(51%)	359/516(69%)	6/516(1%)	+3

Features:

```
Query   45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN-DEDLTSPLKELNGQSP   221
              +R  ++K      ++++ R RR+EV+IELRK+KK+DQ+ KRRNI+ D++  SPL+E   SP
Sbjct   10    NRLSAFKNKGKDSEELRRRRNEVSIELRKAKKDDQLAKRRNIHIDDEPLSPLQESTSNSP   69

Query   222   VQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTNN   401
              +++++I A + S D+  Q    Q+ARK+LSRE+NPPID++I    VP I FL  ++N
Sbjct   70    -PITIEDIFAKLYSNDENVQLQATQAARKILSREKNPPIDVLID--AVPRFIEFLTYSHN   126
```

```
Query   402   SMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGDG   581
              LQFE+ WALTN+ASG S+QT  V+    A+P FVALL+S   +++AEQAVWALGNIAGDG
Sbjct   127   PTLQFESTWALTNVASGNSNQTMAVVNGGAIPKFVALLKSPHLHIAEQAVWALGNIAGDG   186

Query   582   AAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvls   761
              RD+V+H N +   IL LI  +T +  LRNIVW +SNLCRNKNP P F+ VK   LP L
Sbjct   187   PKTRDLVLHCNAMPAILELIKPDTSIPVLRNIVWTLSNLCRNKNPPPNFNTVKICLPYLC   246

Query   762   qlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRSV   941
              +LL   D +VL DACWALSY++D  N +IQAVVD+  V RLV+LL    + +++ PALR+V
Sbjct   247   KLLSYDDKEVLGDACWALSYLSDGTNGRIQAVVDTGIVARLVELLSSSDFTVLTPALRTV   306

Query   942   GNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQAG   1121
              GNIV+GTD QTD +I +GGL  L LLLQH K+N+VKEAAWT+SNITAGN +QI+ VI A
Sbjct   307   GNIVSGTDVQTDAIINAGGLQPLALLLQHPKNNMVKEAAWTISNITAGNVEQIEHVINAN   366

Query   1122  IFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPRT   1301
              I  L  VL KGD K+QKEAAWAVTN T+ G+P+Q+  LI  + ++   +LD+K+ +
Sbjct   367   ILPPLLDVLRKGDLKSQKEAAWAVTNLTSGGSPQQVASLI-CHGVIPHLCYILDSKECKI   425

Query   1302  IKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTYF   1481
              + +    L+N+  +A+    + LMV+E GG+DK+ E LQQHENE++Y K   IID YF
Sbjct   426   VNLALDALANILQVAQNNNELDRIALMVQESGGVDKIEDLQQHENEQIYNKCATIIDKYF   485

Query   1482  SNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              + D++ Q  P  N  LEF A     P+GG++F
Sbjct   486   NTLDEDDGQPYVPNLSNEQLEFCANT-SVPQGGFSF   520
```

importin subunit alpha-1 [Xenopus tropicalis]

Sequence ID: **ref|NP_001008155.1|** Length: 526 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 1 to 514

Score	Expect	Method	Identities	Positives	Gaps	Frame
500 bits(1287)	1e-165()	Compositional matrix adjust.	263/516(51%)	355/516(68%)	10/516(1%)	+3

Features:

```
Query   24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPL   197
              MS   ++ +R   +K     +T + R RR EV +ELRK+KK+DQM KRRN++    ++ TSPL
Sbjct   1     MSNNENAARLTRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTFPDEPTSPL   60

Query   198   KELN--GQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPI   371
              +E N  GQ+  Q SV+EIV + S  E Q   Q+ARK+LSRER PPID +I  G++P
Sbjct   61    QEKNQNGQTSTQWSVEEIVRGVASSSLEIQLQATQAARKLLSREREPPIDRIIQAGLIPK   120

Query   372   CIRFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAV   551
              + FL   T+ S +QFEAAWALTNIASGTSDQT+ V+E   VP F++LL S   +++EQAV
Sbjct   121   LVAFLARTDCSPIQFEAAWALTNIASGTSDQTKAVVEGGGVPAFISLLASPHPHISEQAV   180

Query   552   WALGNIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPS   719
              WALGNIAGDG+A RD+VI H  + +L L+     +       +LRN+ W +SNLCRNKNP+
Sbjct   181   WALGNIAGDGSAYRDLVIKHGAVGPLLALLADPDLSTLATGYLRNVTWTLSNLCRNKNPA   240

Query   720   PPFDQVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQ   899
              PP D ++++LP L +LL    D +VLAD CWA+SY+TD   N +I  VV +    VPR+V+LL
Sbjct   241   PPLDAIQQILPTLVRLLHHDDREVLADTCWAVSYLTDGSNDRINVVVGTGLVPRIVQLLG   300

Query   900   MDEPSIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNIT   1079
               E +I+ P LR+VGNIVTGTD+QT VV+ +G L    LL H+K+NI KEAAWT+SNIT
Sbjct   301   CGELTIVTPCLRTVGNIVTGTDEQTQVVLDAGALSVFAELLTHHKNNIQKEAAWTLSNIT   360

Query   1080  AGNQKQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKIL   1259
              AG Q QIQ V+  G+   L  +L K D++ QKEA WAVTN T+ GT +QI+ L++     ++
Sbjct   361   AGRQDQIQEVVNHGLIPYLIEILRKADYETQKEAIWAVTNYTSGGTIDQIIYLVQ-CSVI   419

Query   1260  KPFIDLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENE   1439
              +P   +LL  KD +T+ V+    +N+FA AEKLG TE LCLMVEE GGLD++E LQ HENE
Sbjct   420   EPLSNLLSVKDSKTVLVILDAFTNVFAAAEKLGETEKLCLMVEECGGLDRIEALQSHENE   479

Query   1440  EVYKKAYAIIDTYFSNGDDEAEQELAPQEVNGALEF   1547
              +VYK +  +I+ YFS  D E ++ LAP+ +    F
Sbjct   480   QVYKASAGLIEKYFSAEDGE-DESLAPETTSDGYTF   514
```

Importin subunit alpha-2 [Melipona quadrifasciata]

Sequence ID: **gb|KOX75105.1|** Length: 501 Number of Matches: 1
Range 1: 8 to 501

Score	Expect	Method	Identities	Positives	Gaps	Frame
499 bits(1284)	1e-165()	Compositional matrix adjust.	275/518(53%)	363/518(70%)	24/518(4%)	+3

Features:

```
Query   36    DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELNGQ   215
              D +SR+ S+K N   +++R RR E+++ELRK+KK+DQ+ KRRN+N+           +
Sbjct   8     DCHSRKASFKFN-YKHEEARRRRSEMSVELRKAKKDEQLQKRRNLNIGKESRNSASESNH   66

Query   216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
              S +   S+DEIV  M S D+  Q    Q+ RKMLSRE+NPPID MI   GIVP+C++FL
Sbjct   67    SSLSTSIDEIVNGMKSSDETIQLQATQACRKMLSREKNPPIDSMIQRGIVPLCVQFLDYH   126

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
              +N+ LQFEAAWALTN+ASGTS+QT  V++H A+   +ALL+S S N+AEQAVWALGNIAG
Sbjct   127   HNAALQFEAAWALTNVASGTSEQTHVVVKHGAIQKLIALLKSASPNVAEQAVWALGNIAG   186
```

```
Query  576   DGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv   755
             DG  ARD+V         +F RNIVW +SNLCRNKNP PPF+ V+   LPV
Sbjct  187   DGPVARDLV-------------------TFTRNIVWTLSNLCRNKNPPPFNVVRTALPV   227

Query  756   lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR   935
             L++LL + D  +LADACWALSY+TD  N KIQAVV+S  + +LV+LL   E +++ PALR
Sbjct  228   LNRLLSNDDKDILADACWALSYLTDGSNDKIQAVVESGVISKLVQLLNSAEVTVLTPALR   287

Query  936   SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ   1115
             +VGNIVTG D QTD +I++GGL  LGLLLQH++ NIVKEAAWT+SNITAG  +QIQ VI
Sbjct  288   AVGNIVTGNDTQTDAIISAGGLQYLGLLLQHHRVNIVKEAAWTISNITAGTMEQIQHVIS   347

Query  1116  AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP   1295
             AG+   L  VLE GDFK+QKEAAWAVTN TTSG+  Q+  L+E   +L PF +LL+ KD
Sbjct  348   AGLLPPLIHVLECGDFKSQKEAAWAVTNLTTSGSVVQLAQLVE-LGVLAPFCNLLEAKDW   406

Query  1296  RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT   1475
             +TI VV  GL+N+   A+++G  E + +M+EE+GGLDKLE LQ H+ E+VY+KA A+IDT
Sbjct  407   KTIIVVLDGLTNICNAADRMGEAERIAIMIEEVGGLDKLENLQHHDVEQVYQKATAMIDT   466

Query  1476  YFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
             +FS+ D + E  LA   + LEF  +    + G+ F
Sbjct  467   FFSDPDAQ-EPILATSAADTPLEFKPNE--TTQKGFNF   501
```

PREDICTED: importin subunit alpha-1 [Halyomorpha halys]

Sequence ID: **ref|XP_014270997.1|** Length: 517 Number of Matches: 1

Range 1: 7 to 507

Score	Expect	Method	Identities	Positives	Gaps	Frame
499 bits(1285)	1e-165()	Compositional matrix adjust.	270/505(53%)	360/505(71%)	5/505(0%)	+3

Features:

```
Query  36    DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND-EDLTSPLKELNG   212
             D  SR   +K    ++++ R RR+EV+IELRK+KK++Q+ KRRN++   ++ SPL + N
Sbjct  7     DVPSRFRKFKNRGKDSEEMRRRRNEVSIELRKAKKDEQLLKRRNMSSIDEPVSPLHDNNS   66

Query  213   QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN   392
             +  +  +++EI A M+S D++ QF+  QSARK LSRE+NPPID +  G+VP CI FL
Sbjct  67    R--MLTTIEEITAGMHSNDEQLQFIATQSARKTLSREKNPPIDTLIDSGLVPRCIEFLSY   124

Query  393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA   572
             ++N  LQFEAAWALTN+ASGTS QT  VI+  A+P  V+LL S   ++AEQAVWALGNIA
Sbjct  125   SHNPSLQFEAAWALTNVASGTSSQTLTVIKGGAIPKLVSLLSSPYPHVAEQAVWALGNIA   184

Query  573   GDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllp   752
             GDG+ ARD+V+       +L LI  +T +SFLRNIVW +SNLCRNKNP PPF  VK  LP
Sbjct  185   GDGSEARDMVLECLAMPALLELIKPDTSVSFLRNIVWSLSNLCRNKNPPPPFHMVKICLP   244

Query  753   vlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPAL   932
             L +LL    D +V+ D CWALSY+TD  N KIQAV+DS  VPRLV+LL   E S++ PAL
Sbjct  245   YLCKLLNYSDNEVITDTCWALSYLTDGPNDKIQAVIDSGVVPRLVQLLMSSEVSVLTPAL   304

Query  933   RSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVI   1112
             R+VGNIVTG D QTD +IA+GGL +L LLLQH +NIIKE+AWT+SNITAGN +QI+ VI
Sbjct  305   RTVGNIVTGNDSQTDYIIAAGGLQQLALLLQHTKANIIKESAWTISNITAGNTEQIEHVI   364

Query  1113  QAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKD   1292
              GI   L  VL+KGD+++QKEAAWA+TN T+ G+ EQ+  ++ +    + P   LLD++D
Sbjct  365   NNGILTPLLDVLKKGDYRSQKEAAWAITNLTSGGSLEQLATVV-RVGAIPPMCALLDSQD   423

Query  1293  PRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIID   1472
             +T+ V+  GLSNL   AEK G  E + +M+EE GGL+K+E LQ HENE+VY+K   II+
Sbjct  424   WKTVTVILDGLSNLLQAAEKTGEVERVAIMIEECGGLEKIEMLQHHENEQVYQKCSNIIE   483

Query  1473  TYFSNGDDEAEQELAPQEVNGALEF   1547
              +FS   +E E        + NG L F
Sbjct  484   QFFS-APEEDETLPTANDGNGHLNF   507
```

PREDICTED: importin subunit alpha-1 [Buceros rhinoceros silvestris]

Sequence ID: **ref|XP_010138696.1|** Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 12 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
499 bits(1286)	1e-165()	Compositional matrix adjust.	259/508(51%)	352/508(69%)	9/508(1%)	+3

Features:

```
Query  45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN--DEDLTSPLKELNG-Q   215
             +R    +K    +T + R RR EV +ELRK+KK+DQM KRRN++  DE  TSPL +  G Q
Sbjct  12    ARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSILPDDATSPLQENRGNQ   71

Query  216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
             SV+EIV   +NS + E Q   Q+ARK+LSRE+ PPID +   G++P   +  FL
Sbjct  72    VSAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGRA   131

Query  396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
             + S +QFE+AWALTNIASGTS+QT V++  A+P F++LL S   +++EQAVWALGNIAG
Sbjct  132   DCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAG   191

Query  576   DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
             DG+  RD+VI    I+ +L L+      +    FLRN+ W +SNLCRNKNP+PP + +++
Sbjct  192   DGSTYRDLVIKFGAIEPLLSLLAVPDLSSLASGFLRNVTWTLSNLCRNKNPAPPIEAIEQ   251
```

```
Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
              +LP L +LL   D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL    E  I+
Sbjct   252   ILPTLVRLLHHDDHEVLADTCWALSYLTDSSNDRIEVVVKTGLVPQLVKLLGCSELPIMT   311

Query   924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
              P+LR++GNIVTGTD+QT VVI SG L    LL H+K+NI KEAAWT+SNITAG Q QIQ
Sbjct   312   PSLRAIGNIVTGTDEQTQVVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQIQ   371

Query   1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
               VI G+   L +L KGDFK+QKEA WAVTN T+ GT +QIV L++    +++P ++LL
Sbjct   372   RVIDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLS   430

Query   1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
               KD RT+ V+    +SN+F  AEK+   TE LCLM+EE GGLD++E LQ HENE+VYK +
Sbjct   431   AKDSRTVLVILDAISNIFVAAEKINETEKLCLMIEECGGLDRIEALQSHENEQVYKASST   490

Query   1464  IIDTYFSNGDDEAEQELAPQEVNGALEF   1547
              +I+ YFS  ++E +Q + P+    + F
Sbjct   491   LIEKYFS-AEEEEDQNVVPESTAASYTF   517
```

PREDICTED: importin subunit alpha-1 [Apteryx australis mantelli]

Sequence ID: **ref|XP_013808591.1|** Length: 528 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 7 to 516

Score	Expect	Method	Identities	Positives	Gaps	Frame
499 bits(1286)	2e-165()	Compositional matrix adjust.	258/512(50%)	356/512(69%)	9/512(1%)	+3

Features:

```
Query   33    ADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-   203
              A++ +R    +K    +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E
Sbjct   7     ANAAARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQEN   66

Query   204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
               N Q     SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + F
Sbjct   67    RNNQVSAHWSVEEIVKGVNSNNTELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSF   126

Query   384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
              L   + S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S   +++EQAVWALG
Sbjct   127   LGRADCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALG   186

Query   564   NIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFD   731
              NIAGDG+  RD+VI    I+ +L L+      +LRN+ W +SNLCRNKNP+PP +
Sbjct   187   NIAGDGSTYRDLVIKFGAIEPLLTLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIE   246

Query   732   QVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEP   911
              +++++LP L +LL   D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL    E
Sbjct   247   AIEQILPTLVRLLHHNDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSEL   306

Query   912   SIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQ   1091
              I+ P+LR++GNIVTGTD+QT +VI SG L    LL H+K+NI KEAAWT+SNITAG Q
Sbjct   307   PIVTPSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQ   366

Query   1092  KQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFI   1271
               QIQ V+ G+   L VL KGDFK+QKEA WAVTN T+ GT +QIV L++    +++P +
Sbjct   367   DQIQQVVDHGLVPYLIGVLRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLL   425

Query   1272  DLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYK   1451
              +LL  KD +T+ V+    +SN+F  AEK+   TE LCLM+EE GGLDK+E LQ HENE+VYK
Sbjct   426   NLLSAKDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYK   485

Query   1452  KAYAIIDTYFSNGDDEAEQELAPQEVNGALEF   1547
              + ++I+ YFS  ++E +Q + P+    + F
Sbjct   486   ASSSLIEKYFS-AEEEEDQNVVPESTAASYTF   516
```

PREDICTED: importin subunit alpha-1 isoform X2 [Monodelphis domestica]

Sequence ID: **ref|XP_007482848.1|** Length: 528 Number of Matches: 1
Range 1: 12 to 528

Score	Expect	Method	Identities	Positives	Gaps	Frame
499 bits(1285)	2e-165()	Compositional matrix adjust.	264/522(51%)	358/522(68%)	12/522(2%)	+3

Features:

```
Query   45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQ   215
              +R    +K    ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E N Q
Sbjct   12    ARLNRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTFPDDATSPLQENRNNQ   71

Query   216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
                  SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + F L  T
Sbjct   72    GSALWSVEEIVKGINSNNLEVQLQATQAARKLLSREKQPPIDQIIEAGMIPKLVGFLGRT   131

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
              + + +QFE+AWALTNIASGTSDQT+ V++  A+P F+ALL S   +++EQAVWALGNIAG
Sbjct   132   DCNPIQFESAWALTNIASGTSDQTKAVVDGGAIPAFIALLASPQAHISEQAVWALGNIAG   191

Query   576   DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
              DG+A RD+VI +  ID +L L+      +LRN+ W +SNLCRNKNP+PP + +++
Sbjct   192   DGSAYRDLVIKYGAIDPLLALLAVPDISSLACGYLRNLTWTLSNLCRNKNPAPPIEAIEQ   251

Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
              +LP L +LL   D +VLAD CWA+SY+TD  N +I+ VV +  VP+LVKLL    E  I+
Sbjct   252   ILPTLVRLLHHDDPEVLADTCWAISYLTDGSNDRIEVVVKTGVVPQLVKLLGSGELPIVT   311
```

```
Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
             P+LR++GNIVTGTD+QT +VI SG L     LL H K+NI KEAAWT+SNITAG Q QIQ
Sbjct  312   PSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLTHPKTNIQKEAAWTMSNITAGRQDQIQ  371

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
               V+  G+   L +L KGDFK+QKEA WAVTN T+ GT EQIV L++   IL+P I+LL
Sbjct  372   QVVNHGLVPYLVGILSKGDFKSQKEAVWAVTNYTSGGTIEQIVYLVQN-GILEPLINLLS  430

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              KD + + V+    +SN+F  AEKL   TE LC+++EE GGLD++E LQ HENE VYK + +
Sbjct  431   AKDSKIVLVILDAISNIFLAAEKLNETEKLCILIEECGGLDRIEALQSHENEMVYKASSS  490

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF  1589
             +I+ YFS   +E +Q + P+ +     F   Q  AP G + F
Sbjct  491   LIEKYFSA--EEEDQNVVPESTSDGYTFQ-IQDGAP-GTFNF  528
```

karyopherin alpha-2 subunit like [Xenopus laevis]

Sequence ID: **ref|NP_001080433.1|** Length: 526 Number of Matches: 1

▸ **See 2 more title(s)**

Range 1: 1 to 514

Score	Expect	Method	Identities	Positives	Gaps	Frame
499 bits(1284)	3e-165()	Compositional matrix adjust.	257/516(50%)	356/516(68%)	10/516(1%)	+3

Features:

```
Query  24    MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPL  197
             MS  ++ +R    +K    ++ + R RR EV +ELRK+KK+DQM KRRN++    ++ TSPL
Sbjct  1     MSNNENGARLTRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTFPDEPTSPL  60

Query  198   KELN--GQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPI  371
             +E N  GQ+  Q SV+EIV + +   + Q   Q+ARK+LSRER PPID +I  G++P
Sbjct  61    QEKNQNGQTSSQWSVEEIVRGVANPSLDIQLQATQAARKLLSREREPPIDRIIKAGLIPK  120

Query  372   CIRFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAV  551
               + FL +++ S +QFEAAWALTNIASGTSDQT+ V+E   VP F++LL S   +++EQAV
Sbjct  121   LVTFLAHSDCSPIQFEAAWALTNIASGTSDQTKAVVEGGGVPAFISLLASPHPHISEQAV  180

Query  552   WALGNIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPS  719
             WALGNIAGDG+A RD+VI H  + +L L+       +LRN+ W +SNLCRNKNP+
Sbjct  181   WALGNIAGDGSAYRDLVIKHGAVGPLLALLAGPDLSTLATGYLRNVTWTLSNLCRNKNPA  240

Query  720   PPFDQVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQ  899
             PP D ++++LP + +LL    D +VLAD CWA+SY+TD  N +I  VV +   V R+V+LL
Sbjct  241   PPLDAIQQILPTIVRLLHHDDREVLADTCWAVSYLTDGSNDRIDVVVRTGLVSRIVQLLA  300

Query  900   MDEPSIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNIT  1079
                E +++ P LR++GNIVTGTD+QT VV+ +G L    LL LL+H+K+NI KEAAWT+SNIT
Sbjct  301   CGELTVVTPCLRTIGNIVTGTDEQTQVVLDAGALSAFTELLTHHKNNIQKEAAWTLSNIT  360

Query  1080  AGNQKQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKIL  1259
             AG Q QIQ V+  G+    L  +L KGD+K QKEA WAVTN T+ GT +QI+ L++    I+
Sbjct  361   AGRQDQIQEVVNCGLIPYLVEILRKGDYKTQKEAIWAVTNYTSGGTIDQIIYLVQ-CGII  419

Query  1260  KPFIDLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENE  1439
             +P +LL  KD +T+ V+    +N+FA A+K+G TE LCLMVEE GGLD++E LQ HENE
Sbjct  420   EPLSNLLSVKDSKTVLVMLDAFTNIFAAADKIGETEKLCLMVEECGGLDRIEALQSHENE  479

Query  1440  EVYKKAYAIIDTYFSNGDDEAEQELAPQEVNGALEF  1547
             +VYK + A+I+ YFS   D E ++ LAP+     F
Sbjct  480   QVYKASAALIEKYFSAEDGE-DESLAPETTADGYAF  514
```

PREDICTED: importin subunit alpha-1 [Struthio camelus australis]

Sequence ID: **ref|XP_009677268.1|** Length: 528 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 7 to 516

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1283)	4e-165()	Compositional matrix adjust.	257/512(50%)	356/512(69%)	9/512(1%)	+3

Features:

```
Query  33    ADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-  203
             A++ +R    +K    +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E
Sbjct  7     ANTAARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQEN  66

Query  204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
              N Q    SV+EIV  +NS + Q   Q+ARK+LSRE  PPID +I  G++P  + F
Sbjct  67    RNNQVSAHWSVEEIVKGVNSNNTELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSF  126

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
             L   + S +QFE+AWALTNIASGTS+QT+ V++   A+P F++LL S   +++EQAVWALG
Sbjct  127   LGRADCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALG  186

Query  564   NIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFD  731
             NIAGDG+  RD+VI    I+ +L L+       +LRN+ W +SNLCRNKNP+PP +
Sbjct  187   NIAGDGSTYRDLVIKFGAIEPLLTLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIE  246

Query  732   QVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEP  911
             ++++LP L +LL    D +VLAD CWALSY+TD  N +I+ VV +   VP+LVKLL  +E
Sbjct  247   AIEQILPTLVRLLHHNDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCNEL  306

Query  912   SIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQ  1091
```

```
Sbjct  307   PIVTPSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLAHHKNNIQKEAAWTMSNITAGRQ   366
             I+ P+LR++GNIVTGTD+QT +VI SG L      LL H+K+NI KEAAWT+SNITAG Q

Query  1092  KQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFI   1271
             QIQ V+  G+   L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++   +++P +
Sbjct  367   DQIQRVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLL   425

Query  1272  DLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYK   1451
             +LL  KD +T+ V+  +SN+F  AEK+  TE LCLM+EE GGLDK+E LQ HENE+VYK
Sbjct  426   NLLTAKDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYK   485

Query  1452  KAYAIIDTYFSNGDDEAEQELAPQEVNGALEF   1547
              +  +I+ YFS  ++E +Q + P+    + F
Sbjct  486   ASSGLIEKYFS-AEEEEDQNVVPESTAASYTF   516
```

PREDICTED: importin subunit alpha-1 [Tinamus guttatus]

Sequence ID: **ref|XP_010216879.1|** Length: 528 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 7 to 516

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1283)	4e-165()	Compositional matrix adjust.	256/512(50%)	355/512(69%)	9/512(1%)	+3

Features:

```
Query  33    ADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-   203
             A++ +R   +K    +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E
Sbjct  7     ANAAARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQEN   66

Query  204   LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF   383
              N Q    SV+EIV  +NS + E Q    Q+AR++LSRE+ PPID +I  G++P  + F
Sbjct  67    RNNQVSAHWSVEEIVKGVNSNNTELQLQATQAARRLLSREKQPPIDNIIRAGLIPKFVSF   126

Query  384   LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG   563
             L  + +QFE+AWALTNIASGTS+QT+ V++   A+P F++LL S   +++EQAVWALG
Sbjct  127   LGRADCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAHISEQAVWALG   186

Query  564   NIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFD   731
             NIAGDG+  RD+VI    ID +L L+     +    +LRN+ W +SNLCRNKNP+PP +
Sbjct  187   NIAGDGSVYRDLVIKFGAIDPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIE   246

Query  732   QVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEP   911
              ++++LP L +LL    D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL   E
Sbjct  247   AIEQILPALVRLLHHDDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSEL   306

Query  912   SIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQ   1091
              I+ P+LR++GNIVTGTD+QT +VI SG L      LL H+K+NI KEAAWT+SNITAG Q
Sbjct  307   PIVTPSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQ   366

Query  1092  KQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFI   1271
             QIQ V+  G+   L  +L KGDFK+QKEA WAVTN T+ GT +QI+ L++   +++P +
Sbjct  367   DQIQRVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIIYLVQA-GVVEPLL   425

Query  1272  DLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYK   1451
             +LL  KD +T+ V+  +SN+F  AEK+  TE LCLM+EE GGLDK+E LQ HENE+VYK
Sbjct  426   NLLSAKDSKTVLVILDAISNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYK   485

Query  1452  KAYAIIDTYFSNGDDEAEQELAPQEVNGALEF   1547
              +  +I+ YFS  ++E +Q + P+    + F
Sbjct  486   ASSTLIEKYFS-AEEEEDQNVVPESTAASYTF   516
```

PREDICTED: importin subunit alpha-1 [Sturnus vulgaris]

Sequence ID: **ref|XP_014738197.1|** Length: 529 Number of Matches: 1

▸ **See 2 more title(s)**
Range 1: 11 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1283)	4e-165()	Compositional matrix adjust.	258/509(51%)	356/509(69%)	9/509(1%)	+3

Features:

```
Query  42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKELNG-   212
             ++R   +K    ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  G
Sbjct  11    SARLNRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRGN   70

Query  213   QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN   392
             Q    SV+EIV  +NS + E Q    Q+ARK+LSRE+ PPID +I  G++P  + FL
Sbjct  71    QVLAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGK   130

Query  393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA   572
             T+ S +QFE+AWALTNIASGTS+QT+ V++   A+P F++LL S   +++EQAVWALGNIA
Sbjct  131   TDCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIA   190

Query  573   GDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVK   740
             GDG+A RD+VI +  I+ +L L+         +LRN+ W +SNLCRNKNP+PP ++
Sbjct  191   GDGSAYRDLVIKYGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIQ   250

Query  741   RllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSII   920
             ++LP L +LL    D +VLAD CWA+SY+TD  N +I+ VV +  VP+LV+LL   E  I+
Sbjct  251   QILPTLVRLLHHDDPEVLADTCWAISYLTDGSNDRIEVVVKTGLVPQLVRLLGCSELPIM   310

Query  921   VPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQI   1100
              P+LR++GNIVTGTD+QT +VI SG L      LL H+K+NI KEAAWT+SNITAG Q QI
```

```
Sbjct   311  TPSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQI  370
Query  1101  QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL  1280
             Q VI  G+    L  VL KGDFK+QKEA WAVTN T+ GT +QIV L++    +L+P ++LL
Sbjct   371  QRVIDHGLVPYLIGVLRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVLEPLLNLL  429

Query  1281  DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY  1460
              TKD +T+ V+   +SN+F  AEK+  TE LCLM+EE GGLD++E LQ HENE+VY+ +
Sbjct   430  STKDSKTVLVILDAVSNIFMAAEKINETEKLCLMIEECGGLDRIEALQSHENEQVYRASS  489

Query  1461  AIIDTYFSNGDDEAEQELAPQEVNGALEF   1547
             II+ YFS  ++E +Q + P     + F
Sbjct   490  TIIEKYFS-AEEEEDQNVVPDSTADSYTF   517
```

PREDICTED: importin subunit alpha-1 [Corvus cornix cornix]

Sequence ID: **ref|XP_010405672.1|** Length: 529 Number of Matches: 1

Range 1: 11 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1283)	4e-165()	Compositional matrix adjust.	257/509(50%)	356/509(69%)	9/509(1%)	+3

Features:

```
Query    42  NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKELNG-  212
             ++R    +K     ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  G
Sbjct    11  SARLNRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRGN   70

Query   213  QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN  392
             Q      SV+EIV  +NS + Q    Q+ARK+LSRE+ PPID +I  G++P  + FL
Sbjct    71  QVLAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVLFLGR  130

Query   393  TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA  572
              + S +QFE+AWALTNIASGTS+QTR V++   A+P F++LL S   ++++EQAVWALGNIA
Sbjct   131  ADCSPIQFESAWALTNIASGTSEQTRAVVDGGAIPAFISLLASPHIHISEQAVWALGNIA  190

Query   573  GDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVK  740
             GDG+A RD+VI +  I+ +L L+       +  +LRN+ W +SNLCRNKNP+PP + ++
Sbjct   191  GDGSAYRDLVIKYGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIQ  250

Query   741  RllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSII  920
             ++LP L +LL    D +VLAD CWA+SY+TD  N +I+ VV +  VP+LV+LL    E  I+
Sbjct   251  QILPTLVRLLHHDDPEVLADTCWAISYLTDGSNDRIEVVVKTGLVPQLVRLLGCSELPIM  310

Query   921  VPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQI  1100
              P+LR++GNIVTGTD+QT +VI SG L     LL HNK+NI KEAAWT+SNITAG Q QI
Sbjct   311  TPSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLSHNKNNIQKEAAWTMSNITAGRQDQI  370

Query  1101  QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL  1280
             Q V+  G+    L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++    +L+P ++LL
Sbjct   371  QRVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVLEPLLNLL  429

Query  1281  DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY  1460
              TKD +T+ V+   +SN+F  AEK+   TE LCL++EE GGLD++E LQ HENEEVY+ +
Sbjct   430  STKDSKTVLVILDAVSNIFLAAEKINETEKLCLIIEECGGLDRIEALQSHENEEVYRASS  489

Query  1461  AIIDTYFSNGDDEAEQELAPQEVNGALEF   1547
             II+ YFS  ++E +Q + P       + F
Sbjct   490  TIIEKYFS-AEEEEDQSVVPGSTANSYTF   517
```

Importin subunit alpha-1 [Cathartes aura]

Sequence ID: **gb|KFP51772.1|** Length: 529 Number of Matches: 1

Range 1: 12 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1283)	4e-165()	Compositional matrix adjust.	257/508(51%)	354/508(69%)	9/508(1%)	+3

Features:

```
Query    45  SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQ  215
             +R    +K     +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  + Q
Sbjct    12  ARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRSNQ   71

Query   216  SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT  395
                   SV+EIV  +NS + Q    Q+ARK+LSRE+ PPID +I  G++P  + FL
Sbjct    72  VSAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGRA  131

Query   396  NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG  575
              + S +QFE+AWALTNIASGTS+QT+ V++   A+P F++LL S   +++EQAVWALGNIAG
Sbjct   132  DCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAG  191

Query   576  DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
             DG+A RD+VI       I+ +L L+       +  +LRN+ W +SNLCRNKNP+PP + +++
Sbjct   192  DGSAYRDLVIKFGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIEQ  251

Query   744  llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
             +LP L +LL    D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL    E  I+
Sbjct   252  ILPTLVRLLHHDDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSELPIMT  311

Query   924  PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
             P+LR++GNIVTGTD+QT +VI SG L     LL H+K+NI KEAAWT+SNITAG Q QIQ
Sbjct   312  PSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQIQ  371

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
              V+  G+    L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++    +++P ++LL
Sbjct   372  RVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLS  430
```

```
Query  1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              KD +T+ V+    +SN+F  AEK+   TE LCLM+EE GGLDK+E LQ HENE+VYK +
Sbjct  431    AKDSKTVLVILDAISNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYKASST  490

Query  1464   IIDTYFSNGDDEAEQELAPQEVNGALEF  1547
              +I+ YFS ++E +Q +AP+   +   F
Sbjct  491    LIEKYFS-AEEEEDQNVAPESTAASYAF  517
```

PREDICTED: importin subunit alpha-1 [Leptosomus discolor]

Sequence ID: **ref|XP_009948935.1|** Length: 528 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 7 to 516

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1283)	4e-165()	Compositional matrix adjust.	258/512(50%)	355/512(69%)	9/512(1%)	+3

Features:

```
Query  33     ADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-  203
              A++ +R    +K     +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E
Sbjct  7      ANTAARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQEN  66

Query  204    LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF  383
                N Q     SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + F
Sbjct  67     RNNQVSAHWSVEEIVRGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSF  126

Query  384    LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG  563
              L   S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S   +++EQAVWALG
Sbjct  127    LGRADCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALG  186

Query  564    NIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFD  731
              NIAGDG+  RD+VI     I+ +L L+      +   +LRN+ W +SNLCRNKNP+PP +
Sbjct  187    NIAGDGSTYRDLVIKFGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIE  246

Query  732    QVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEP  911
              +++++LP L +LL    D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL    E
Sbjct  247    AIEQILPTLVRLLHHDDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSEL  306

Query  912    SIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQ  1091
              I+ P+LR++GNIVTGTD+QT +VI SG L    LL H+K+NI KEAAWT+SNITAG Q
Sbjct  307    PIMTPSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQ  366

Query  1092   KQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFI  1271
                QIQ V+ G+   L +L KGDFK+QKEA WAVTN T+ GT +QIV L++   +++P +
Sbjct  367    DQIQRVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLL  425

Query  1272   DLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYK  1451
              +LL   KD +T+ V+    +SN+F  AEK+   TE LCLMVEE GGLDK+E LQ HENE+VYK
Sbjct  426    NLLSAKDSKTVLVILDAISNIFLAAEKINETEKLCLMVEECGGLDKIEALQSHENEQVYK  485

Query  1452   KAYAIIDTYFSNGDDEAEQELAPQEVNGALEF  1547
              +  +I+ YFS ++E +Q + P+   +   F
Sbjct  486    ASSTLIEKYFS-AEEEEDQNVVPESTAASYTF  516
```

PREDICTED: importin subunit alpha-1 [Pelodiscus sinensis]

Sequence ID: **ref|XP_006110655.1|** Length: 529 Number of Matches: 1
Range 1: 12 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1282)	5e-165()	Compositional matrix adjust.	257/508(51%)	357/508(70%)	9/508(1%)	+3

Features:

```
Query  45     SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIN--DEDLTSPLKE-LNGQ  215
              +R    +K     +T + R RR EV +ELRK+KK+DQM KRRN+    D TSPL+E LN Q
Sbjct  12     ARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSILPDDATSPLQENRNNQ  71

Query  216    SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT  395
              +     SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + FL  T
Sbjct  72     ATAHWSVEEIVKGINSNNLELQLQATQAARKLLSREKQPPIDHIIRAGLIPKFVAFLGRT  131

Query  396    NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG  575
              + S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S   +++EQAVWALGNIAG
Sbjct  132    DCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAG  191

Query  576    DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
              DG+A RD+VI +  ID +L L+        +LRNI W +SNLCRNKNP+PP D +++
Sbjct  192    DGSAYRDLVIKYGAIDPLLALLAVPDLSSLASGYLRNITWTLSNLCRNKNPAPPIDAIEQ  251

Query  744    llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
              +LP L +LL    D +VLAD CWA+SY+TD  N +I+ VV +  VP+LVKLL    E  I+
Sbjct  252    ILPTLLRLLHHDDHEVLADTCWAISYLTDGSNDRIEVVVKTGLVPLVKLLGCGEPIMT  311

Query  924    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
              P+LR++GNIVTGTD+QT +VI SG L    LL H+K+NI KEAAWT+SNITAG  + QIQ
Sbjct  312    PSLRAIGNIVTGTDEQTQIVIESGALGVFPSLLSHHKNNIQKEAAWTLSNITAGRRDQIQ  371

Query  1104   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
              V++ G+   L +L+KGDFK+QKEA WAVTN T+ GT +Q+V L++   +++P ++LL
Sbjct  372    RVVEHGLVPYLIGILKKGDFKSQKEAVWAVTNYTSGGTIDQVVFLVQA-GVVEPLLNLLS  430

Query  1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
              KD +T+ V+    ++N+F  AEK+   TE LCLM+EE GGLDK+E LQ HENE+VYK +
Sbjct  431    AKDSKTVLVILDAITNIFLAAEKIDETERLCLMIEECGGLDKIEALQSHENEQVYKASSN  490
```

```
Query  1464    IIDTYFSNGDDEAEQELAPQEVNGALEF    1547
               +I+ YFS  ++E +Q + P    + F
Sbjct  491     LIEKYFS-AEEEEDQNVLPDSTADSYNF    517
```

PREDICTED: importin subunit alpha-1 [Chaetura pelagica]

Sequence ID: **ref|XP_010000998.1|** Length: 527 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 11 to 523

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1282)	6e-165()	Compositional matrix adjust.	260/516(50%)	356/516(68%)	10/516(1%)	+3

Features:

```
Query  48      RQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQS    218
               R  +K   +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  + Q
Sbjct  11      RLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRSNQV    70

Query  219     PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN    398
                  SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + FL   +
Sbjct  71      SAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGRAD    130

Query  399     NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD    578
                S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S    +++EQAVWALGNIAGD
Sbjct  131     CSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAGD    190

Query  579     GAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl    746
               G+A RD+VI     I+ +L L+    +      +LRN+ W +SNLCRNKNP+PP + ++++
Sbjct  191     GSAYRDLVIKFGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIEQI    250

Query  747     lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP    926
               LP L +LL    D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL    E   I+ P
Sbjct  251     LPTLVRLLHHDDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSELPIMTP    310

Query  927     ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA    1106
               +LR++GNIVTGTD+QT +VI SG L     LL H+KSNI KEAAWT+SNITAG Q QIQ
Sbjct  311     SLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKSNIQKEAAWTMSNITAGRQDQIQR    370

Query  1107    VIQAGIFQQLRTVLEKGDFKAQKEAAWAVNTTTSGTPEQIVDLIEKYKILKPFIDLLDT    1286
               V+  G+    L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++   +++P ++LL
Sbjct  371     VVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLSA    429

Query  1287    KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI    1466
               KD +T+ V+   +SN+F  AEK+   TE LCLM+EE GGLDK+E LQ HENE+VYK + +
Sbjct  430     KDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYKASSTL    489

Query  1467    IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPE    1574
               I+ YFS  ++E +Q + P+    + F    Q  AP+
Sbjct  490     IEKYFS-AEEEEDQNVVPESTAASYTFQ-IQGNAPD    523
```

PREDICTED: importin subunit alpha-1 [Manacus vitellinus]

Sequence ID: **ref|XP_008920062.1|** Length: 528 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 7 to 516

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1281)	7e-165()	Compositional matrix adjust.	258/512(50%)	358/512(69%)	9/512(1%)	+3

Features:

```
Query  33      ADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKEL    206
               A++ +R   +K     ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E
Sbjct  7       ANTPARLNRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQEN    66

Query  207     NG-QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF    383
                G Q      SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + F
Sbjct  67      KGNQVLAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSF    126

Query  384     LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG    563
               L    S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S    +++EQAVWALG
Sbjct  127     LGRAECSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALG    186

Query  564     NIAGDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFD    731
               NIAGDG+A RD+VI +  I+ +L L+    +       +LRN+ W +SNLCRNKNP+PP +
Sbjct  187     NIAGDGSAYRDLVIKYGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIE    246

Query  732     QVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEP    911
               +++++LP L +LL    +D +VLAD CWA+SY+TD  N +I+ VV +  VP+LV+LL    E
Sbjct  247     AIQQILPTLVRLLHHEDPEVLADTCWAISYLTDGSNDRIEVVVKTGLVPQLVRLLGCSEL    306

Query  912     SIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQ    1091
                I+ P+LR++GNIVTGTD+QT +VI SG L     LL H+K+NI KEAAWT+SNITAG Q
Sbjct  307     PIMTPSLRAIGNIVTGTDEQTQLVIDSGALAVFPSLLSHHKNNIQKEAAWTMSNITAGRQ    366

Query  1092    KQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVNTTTSGTPEQIVDLIEKYKILKPFI    1271
                QIQ V+  G+    L  +L KGDFK+QKEAAWAVTN T+ GT +QIV L++    +L+P +
Sbjct  367     DQIQRVVDHGLVPYLIGILRKGDFKSQKEAAWAVTNYTSGGTIDQIVYLVQA-GVLEPLL    425

Query  1272    DLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYK    1451
               +LL TKD +T+ V+   +SN+F  AEK+   TE LCLM+EE GGLDK+E LQ HENE+VY+
Sbjct  426     NLLTTKDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYR    485

Query  1452    KAYAIIDTYFSNGDDEAEQELAPQEVNGALEF    1547
```

```
              +    II+ YFS   ++E +Q + P      + F
Sbjct  486    ASSTIIEKYFS-AEEEEDQNVVPDATADSYTF   516
```

PREDICTED: importin subunit alpha-1 [Picoides pubescens]

Sequence ID: **ref|XP_009900980.1|** Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 12 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1281)	8e-165()	Compositional matrix adjust.	256/508(50%)	355/508(69%)	9/508(1%)	+3

Features:

```
Query  45     SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQ   215
              +R    +K     +T + R RR EV +ELRK+KK+DQ+ KRRN++    +D TSPL+E  + Q
Sbjct  12     ARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQILKRRNVSTFPDDATSPLQENRSNQ   71

Query  216    SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
                V  SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + FL
Sbjct  72     VSVHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGRA   131

Query  396    NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
              + S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S    +++EQAVWALGNIAG
Sbjct  132    DCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAG   191

Query  576    DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
              DG+A RD+VI +  I+ +L L+      +  +LRN+ W +SNLCRNKNP+PP + +++
Sbjct  192    DGSAYRDLVIKYGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIEQ   251

Query  744    llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
              +LP L +LL    D +VLAD CWA+SY+TD  N +I+ VV +  VP+LVKLL    E  I+
Sbjct  252    ILPTLVRLLHHDDHEVLADTCWAISYLTDGSNDRIEIVVKTGLVPQLVKLLGCSELPIMT   311

Query  924    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
              P+LR++GNIVTGTD+QT +VI SG L    LL H+K+NI KEAAWT+SNITAG Q QIQ
Sbjct  312    PSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQIQ   371

Query  1104   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
               V+  G+    L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++    +++P ++LL
Sbjct  372    RVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLS   430

Query  1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
               KD +T+ V+    +SN+F  AEK+   TE LCLM+EE GGLDK+E LQ HENEEVYK +
Sbjct  431    AKDSKTVLVILDAISNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEEVYKASST   490

Query  1464   IIDTYFSNGDDEAEQELAPQEVNGALEF   1547
              +I+ YFS   ++E +Q + P+      + F
Sbjct  491    LIEKYFS-AEEEEDQNVVPESTAASYTF   517
```

PREDICTED: importin subunit alpha-1 [Caprimulgus carolinensis]

Sequence ID: **ref|XP_010165233.1|** Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 13 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1281)	8e-165()	Compositional matrix adjust.	256/507(50%)	351/507(69%)	9/507(1%)	+3

Features:

```
Query  48     RQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQS   218
              R    +K     +T + R RR E+ +ELRK+KK+DQM KRRN++    +D TSPL+E  + Q
Sbjct  13     RLNRFKNKGKDTTEMRRRRIEINVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRSNQV   72

Query  219    PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN   398
                 SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + FL   +
Sbjct  73     SAHWSVEEIVKGINSNNMELQLQATQAARKLLSREKQPPIDSIIRAGLIPRFVSFLGRAD   132

Query  399    NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD   578
               S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S    +++EQAVWALGNIAGD
Sbjct  133    CSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAGD   192

Query  579    GAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl   746
              G+  RD+VI    I+ +L L+      +  +LRN+ W +SNLCRNKNP+PP + ++++
Sbjct  193    GSTYRDLVIKFGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIEQI   252

Query  747    lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP   926
              LP L +LL    D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL    E SI+ P
Sbjct  253    LPTLVRLLHHDDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSELSIMTP   312

Query  927    ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA   1106
              +LR++GNIVTGTD+QT VVI SG L    LL H+K+NI KEAAWT+SNITAG Q QIQ
Sbjct  313    SLRAIGNIVTGTDEQTQVVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQIQR   372

Query  1107   VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT   1286
              V+  G+    L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++    +++P ++LL
Sbjct  373    VVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTTDQIVYLVQA-GVVKPLLNLLSA   431

Query  1287   KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI   1466
              KD +T+ V+    +SN+F  AEK+   TE LCLM+EE GGLDK+E LQ HENE+VYK +  +
Sbjct  432    KDSKTVLVILDAISNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYKASSTL   491

Query  1467   IDTYFSNGDDEAEQELAPQEVNGALEF   1547
              I+ YFS  ++E +  + P+      + F
```

```
Sbjct    492    IEKYFS-AEEEEDHNVVPESTAASYTF    517
```

PREDICTED: importin subunit alpha-1 [Ornithorhynchus anatinus]

Sequence ID: **ref|XP_001509792.1|** Length: 529 Number of Matches: 1

▸ **See 2 more title(s)**
Range 1: 12 to 529

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1281)	8e-165()	Compositional matrix adjust.	259/522(50%)	356/522(68%)	11/522(2%)	+3

Features:

```
Query    45     SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQ    215
                +R    +K      ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  N Q
Sbjct    12     ARLNRFKNKGKDSSEMRRRRIEVNVELRKAKKDDQMLKRRNVSTFPDDATSPLQENRNNQ    71

Query    216    SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT    395
                   SV+EIV  +NS + E Q    Q+ARK+LS+E+ PPID +I  G++P  + FL  +
Sbjct    72     GSAHWSVEEIVRGINSNNLELQLQATQAARKLLSKEKQPPIDSIIRAGMIPKLVSFLGRS    131

Query    396    NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG    575
                + S +QFE+AWALTNIASGTSDQT+ V++   F++LL S   +++EQAVWALGNIAG
Sbjct    132    DCSPIQFESAWALTNIASGTSDQTKAVVDGGGIPAFISLLASPHSHISEQAVWALGNIAG    191

Query    576    DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR    743
                DG+A RD+VI +  ID +L L     +      +LRN+ W +SNLCRNKNP+PP D +++
Sbjct    192    DGSAYRDLVIKYGAIDPLLALFAVPDISSLACGYLRNLTWALSNLCRNKNPAPPIDAIEQ    251

Query    744    llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV    923
                +LP L +LL    D VLAD CWA+SY+TD  N +I+ VV +  VP+LVKLL    E  I+
Sbjct    252    ILPTLVRLLHHDDQDVLADTCWAISYLTDGSNDRIEVVVKTGVVPQLVKLLGSGELPIVT    311

Query    924    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ    1103
                P+LR++GNIVTGTD+QT +VI +G L      LL H K+NI KEAAWT+SNITAG Q QIQ
Sbjct    312    PSLRAIGNIVTGTDEQTQIVIEAGALAVFPSLLTHPKTNIQKEAAWTMSNITAGRQDQIQ    371

Query    1104   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD    1283
                 V+  G+   L  +L KGDFK+QKEA WAVTN T+ GT EQIV L++    I++P I+LL
Sbjct    372    QVVNHGLVPYLVEILSKGDFKSQKEAVWAVTNYTSGGTIEQIVYLVQS-GIMEPLINLLT    430

Query    1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA    1463
                 KD + + V+   ++N+F  AEKLG TE LC+M+EE GGLD++E LQ HENE +YK + +
Sbjct    431    AKDSKIVLVILDAITNIFLAAEKLGETEKLCIMIEECGGLDRIEALQSHENELIYKASSS    490

Query    1464   IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    1589
                +I+ YFS  ++E +Q + P+  +     F  Q   PG + F
Sbjct    491    LIEKYFS-AEEEEDQNVVPESTSDGYAFQ-IQDNTP-GTFNF    529
```

Importin subunit alpha-1 [Corvus brachyrhynchos]

Sequence ID: **gb|KFO62143.1|** Length: 529 Number of Matches: 1
Range 1: 12 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1281)	8e-165()	Compositional matrix adjust.	257/508(51%)	355/508(69%)	9/508(1%)	+3

Features:

```
Query    45     SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKELNG-Q    215
                +R    +K      ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  G Q
Sbjct    12     ARLNRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRGNQ    71

Query    216    SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT    395
                   SV+EIV  +NS + E Q    Q+ARK+LSRE+ PPID +I  G++P   + FL
Sbjct    72     VLAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVLFLGRA    131

Query    396    NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG    575
                + S +QFE+AWALTNIASGTS+QTR V++   A+P F++LL S    ++++EQAVWALGNIAG
Sbjct    132    DCSPIQFESAWALTNIASGTSEQTRAVVDGGAIPAFISLLASPHIHISEQAVWALGNIAG    191

Query    576    DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR    743
                DG+A RD+VI +  I+ +L L+     +    +LRN+ W +SNLCRNKNP+PP + +++
Sbjct    192    DGSAYRDLVIKYGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIQQ    251

Query    744    llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV    923
                +LP L +LL    D +VLAD CWA+SY+TD  N +I+ VV +  VP+LV+LL    E  I+
Sbjct    252    ILPTLVRLLHHDDPEVLADTCWAISYLTDGSNDRIEVVVKTGLVPQLVRLLGCSELPIMT    311

Query    924    PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ    1103
                P+LR++GNIVTGTD+QT +VI SG L      LL HNK+NI KEAAWT+SNITAG Q QIQ
Sbjct    312    PSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLSHNKNNIQKEAAWTMSNITAGRQDQIQ    371

Query    1104   AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD    1283
                 V+  G+   L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++     +L+P ++LL
Sbjct    372    RVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVLEPLLNLLS    430

Query    1284   TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA    1463
                TKD +T+ V+   +SN+F  AEK+  TE LCL++EE GGLD++E LQ HENEEVY+ +
Sbjct    431    TKDSKTVLVILDAVSNIFLAAEKINETEKLCLIIEECGGLDRIEALQSHENEEVYRASST    490

Query    1464   IIDTYFSNGDDEAEQELAPQEVNGALEF    1547
                II+ YFS  ++E +Q + P      + F
Sbjct    491    IIEKYFS-AEEEEDQSVVPGSTANSYTF    517
```

PREDICTED: importin subunit alpha-1 [Serinus canaria]

Sequence ID: **ref|XP_009092579.1|** Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 11 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
497 bits(1280)	1e-164()	Compositional matrix adjust.	258/509(51%)	355/509(69%)	9/509(1%)	+3

Features:

```
Query   42    NSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKELNG-  212
              ++R   +K   ++ + R RR EV +ELRK+KK+DQM KRRN++   +D TSPL+E  G
Sbjct   11    SARLNRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENKGN   70

Query   213   QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN  392
              Q    SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P   + FL
Sbjct   71    QVLAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGR  130

Query   393   TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA  572
              + S +QFE+AWALTNIASGTS+QTR V++  A+P F++LL S   +++EQAVWALGNIA
Sbjct   131   ADCSPIQFESAWALTNIASGTSEQTRAVVDGGAIPAFISLLASPHTHISEQAVWALGNIA  190

Query   573   GDGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVK  740
              GDG+A RD+VI +  I+ +L L+        +LRN+ W +SNLCRNKNP+PP + ++
Sbjct   191   GDGSAYRDLVIKYGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIQ  250

Query   741   RllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSII  920
              ++LP L +LL    D +VLAD CWA+SY+TD  N +I+ VV +  VP+LV+LL    E  I+
Sbjct   251   QILPTLVRLLHHDDPEVLADTCWAISYLTDGSNDRIEVVVKTGLVPQLVRLLGCSELPIM  310

Query   921   VPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQI  1100
               P+LR++GNIVTGTD+QT VVI SG L    LL H+K+NI KEAAWT+SNITAG Q QI
Sbjct   311   TPSLRAIGNIVTGTDEQTQVVIDSGALAVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQI  370

Query   1101  QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL  1280
              Q V+  G+    L  VL KGDFK +QKEA WAVTN T+ GT +QIV L++   +L+P ++LL
Sbjct   371   QRVVDHGLVPYLIGVLRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVLEPLLNLL  429

Query   1281  DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY  1460
               TKD +T+ V+   +SN+F  AEK+  TE LCLM+EE GGLD++E LQ HENE+VY+ +
Sbjct   430   STKDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDRIEALQSHENEQVYRASS  489

Query   1461  AIIDTYFSNGDDEAEQELAPQEVNGALEF   1547
              II+ YFS ++E +Q + P    + F
Sbjct   490   TIIEKYFS-AEEEEDQNVVPDSTADSYTF   517
```


PREDICTED: importin subunit alpha-1 [Tyto alba]

Sequence ID: **ref|XP_009970687.1|** Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**
Range 1: 12 to 525

Score	Expect	Method	Identities	Positives	Gaps	Frame
497 bits(1280)	1e-164()	Compositional matrix adjust.	259/517(50%)	357/517(69%)	10/517(1%)	+3

Features:

```
Query   45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQ  215
              +R   +K    +T + R RR EV +ELRK+KK+DQM KRRN++   +D TSPL+E  + Q
Sbjct   12    ARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRSNQ   71

Query   216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT  395
                   SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P   + FL
Sbjct   72    VSAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDSIIRAGLIPKFVSFLGRA  131

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG  575
              + S +QFE+AWALTNIASGTS+QTR V++  A+P F+ LL S   +++EQAVWALGNIAG
Sbjct   132   DCSPIQFESAWALTNIASGTSEQTRAVVDGGAIPAFILLLASPHTHISEQAVWALGNIAG  191

Query   576   DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
              DG+  RD+VI    I+ +L L+        +LRN+ W +SNLCRNKNP+PP + +++
Sbjct   192   DGSTYRDLVIKFGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIEQ  251

Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
              +LP L +LL    D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL    E  I+
Sbjct   252   ILPTLVRLLHHDDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSELPIMT  311

Query   924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
               P+LR++GNIVTGTD+QT +VI SG L    LL H+K+NI KEAAWT+SNITAG Q QIQ
Sbjct   312   PSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQIQ  371

Query   1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
               V+  G+    L  +L KGDFK +QKEA WAVTN T+ GT +QIV L+Q   +L+P ++LL
Sbjct   372   RVVDHGLVPYLIGILKKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLS  430

Query   1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
               KD +T+ V+   +SN+F  AEK+  TE LCLM+EE GGLDK+E LQ HENE+VYK +
Sbjct   431   AKDSKTVLVILDAISNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYKASST  490

Query   1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPE   1574
              +I+ YFS ++E +Q + P+     + F+ Q AP+
Sbjct   491   LIEKYFS-AEEEEDQNVVPESTAASYTFH-IQGNAPD   525
```

PREDICTED: importin subunit alpha-1 [Aptenodytes forsteri]

Sequence ID: ref|XP_009285978.1| Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 13 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
497 bits(1280)	1e-164()	Compositional matrix adjust.	257/507(51%)	352/507(69%)	9/507(1%)	+3

Features:

```
Query  48    RQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQS  218
             R +K   +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  + Q
Sbjct  13    RLNRFKNKGKDTTEMRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRSNQV   72

Query  219   PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN  398
              SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + FL   +
Sbjct  73    SAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGRAD  132

Query  399   NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD  578
              S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S   +++QAVWALGNIAGD
Sbjct  133   CSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAGD  192

Query  579   GAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl  746
             G+  RD+VI   I+ +L L+  +    +LRN+ W +SNLCRNKNP+PP + ++++
Sbjct  193   GSTYRDLVIKFGAIEPLLSLLAIPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIEQI  252

Query  747   lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP  926
             LP L +LL   D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL   E  I+ P
Sbjct  253   LPTLVRLLHHDDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSELPIMTP  312

Query  927   ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA  1106
             +LR++GNIVTGTD+QT +VI SG L      LL HNK+NI KEAAWT+SNITAG Q QIQ
Sbjct  313   SLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHNKNNIQKEAAWTMSNITAGRQDQIQQ  372

Query  1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT  1286
             V+  G+   L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++  +++P ++LL
Sbjct  373   VVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLSA  431

Query  1287  KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI  1466
             KD +T+ V+   +SN+F  AEK+  TE LCLM+EE GGLDK+E LQ HENE+VYK + +
Sbjct  432   KDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYKASSTL  491

Query  1467  IDTYFSNGDDEAEQELAPQEVNGALEF     1547
             I+ YFS  ++E +Q +AP+    + F
Sbjct  492   IEKYFS-AEEEEDQNVAPESTAASYTF     517
```

PREDICTED: importin subunit alpha-1 [Nipponia nippon]

Sequence ID: ref|XP_009465206.1| Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 12 to 525

Score	Expect	Method	Identities	Positives	Gaps	Frame
497 bits(1280)	1e-164()	Compositional matrix adjust.	259/517(50%)	356/517(68%)	10/517(1%)	+3

Features:

```
Query  45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQ  215
             +R  +K    +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  + Q
Sbjct  12    ARLNRFKNKGKDTTEMRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRSNQ   71

Query  216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT  395
              SV+EIV  +NS + E Q   Q+ARK+LSRE+ PPID +I  G++P  + FL
Sbjct  72    VSAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGRA  131

Query  396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG  575
             + S +QFE+AWALTNIASGTS+QT+ V++  A+P F++LL S   +++EQAVWALGNIAG
Sbjct  132   DCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAG  191

Query  576   DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR  743
             DG+  RD+VI   I+ +L L+  +    +LRN+ W +SNLCRNKNP+PP + +++
Sbjct  192   DGSTYRDLVIKFGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIEQ  251

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV  923
             +LP L +LL    D +VLAD CWALSY+TD  N +I+ VV +  VP+LVKLL   E  I+
Sbjct  252   ILPTLVRLLHHDDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSELPIMT  311

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ  1103
             P+LR++GNIVTGTD+QT +VI SG L      LL H+KSNI KEAAWT+SNITAG Q QIQ
Sbjct  312   PSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKSNIQKEAAWTMSNITAGRQDQIQ  371

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD  1283
              V+  G+   L  +L KGDFK+QKEA WAVTN T+ GT +QIV L++  +++P ++LL
Sbjct  372   RVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLS  430

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA  1463
             KD +T+ V+   +SN+F  AEK+  TE LCLM+EE GGLDK+E LQ HENE+VYK +
Sbjct  431   AKDSKTVLVILDAISNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYKASST  490

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPE    1574
             +I+ YFS  ++E +Q +AP+    + F  Q AP+
Sbjct  491   LIEKYFS-AEEEEDQNVVPESTAASYTFQ-IQGNAPD   525
```

PREDICTED: importin subunit alpha-5-like [Chelonia mydas]

Sequence ID: **ref|XP_007062787.1|** Length: 519 Number of Matches: 1

Range 1: 6 to 519

Score	Expect	Method	Identities	Positives	Gaps	Frame
497 bits(1279)	1e-164()	Compositional matrix adjust.	261/521(50%)	356/521(68%)	10/521(1%)	+3

Features:

```
Query  36    DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDL---TSPLKEL    206
             + + R   +K    +T    R +R EV +ELRK+KK++Q+ KRRNI+    +    SP +E
Sbjct  6     EQDERMRFKNKGKDTAAMRRQRMEVNVELRKAKKDEQILKRRNISFSSMGESLSPEQE-     64

Query  207   NGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFL    386
             +   QLS++EIV A+N  + E      Q+AR+MLSR+RNPP++ +I  GI+P  + FL
Sbjct  65    KKNATAQLSLEEIVQAVNGNNPELHLKATQTARRMLSRQRNPPLNQIIEAGIIPKLVEFL    124

Query  387   QNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGN    566
             +N  LQFEAAWALTNIASGTSDQTR V+E  AVP FVALL S  M+++EQ+VWALGN
Sbjct  125   SRNDNVTLQFEAAWALTNIASGTSDQTRAVVEAGAVPAFVALLSSPHMHISEQSVWALGN    184

Query  567   IAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRl    746
             IAGDG   RD +IH+NVI  +L L++   TP+ FLRNI W +SNLCRNKNP PP + VK++
Sbjct  185   IAGDGPMYRDSLIHNNVIPPLLALVSPSTPVGFLRNITWTLSNLCRNKNPYPPLEAVKQI    244

Query  747   lpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVP    926
             LPVL +LL  +D +L+D CWA+SY+TD  N +I  VV++  +PRLV+L+   E S++ P
Sbjct  245   LPVLIRLLKHEDKDILSDTCWAVSYLTDGSNDRIHVVVETGILPRLVELMGSPELSVVTP    304

Query  927   ALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQA    1106
             ALR++GN+VTGTD+QT + I +G L  L  LLQH K  I KEAAWT+SNI AG   QIQ
Sbjct  305   ALRAIGNVVTGTDEQTQMAIDAGVLAVLPQLLQHPKPTIQKEAAWTLSNIAAGPCHQIQQ    364

Query  1107  VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT    1286
             +I  G+    L  +L+KG+FKAQKEA WAV N TT GT +Q+V+L++ Y +LKP ++LL
Sbjct  365   LITCGLLPPLVELLDKGEFKAQKEAVWAVANFTTGGTVQQVVELVQ-YGVLKPLLNLLSA    423

Query  1287  KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI    1466
             +D +TI V+    +SNLF  AEKL  TE LC +VEE+GGL+K+E LQ H+N  VY+ A  +
Sbjct  424   RDGKTILVILDTISNLFLAAEKLEETEKLCFLVEELGGLEKIEALQTHDNTMVYRAALGL    483

Query  1467  IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF    1589
             I+ YF++ ++  Q  + QE      F+  +P      YTF
Sbjct  484   IEKYFASEENPNLQPESDQE-RPTFNFSTEKPDF----YTF    519
```

PREDICTED: importin subunit alpha-1 [Chelonia mydas]

Sequence ID: **ref|XP_007055158.1|** Length: 529 Number of Matches: 1

▸ **See 1 more title(s)**

Range 1: 12 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
497 bits(1280)	1e-164()	Compositional matrix adjust.	256/508(50%)	355/508(69%)	9/508(1%)	+3

Features:

```
Query  45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQ    215
             +R   +K    +T + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  N Q
Sbjct  12    ARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRNNQ    71

Query  216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT    395
             +    SV+EIV   +NS + E Q    Q+ARK+LSRE+ PPID +I  G++P   + FL
Sbjct  72    ATAHWSVEEIVKGINSNNLELQLQATQAARKLLSREKQPPIDHIIRAGLIPKFVSFLGRA    131

Query  396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG    575
             + S +QFE+AWALTNIASGTS+QT+ V++   A+P F++LL S   +++EQAVWALGNIAG
Sbjct  132   DCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALGNIAG    191

Query  576   DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR    743
             DG+A RD+VI +   ID +L L+    +    +LRN+ W +SNLCRNKNP PP + +++
Sbjct  192   DGSAYRDLVIKYGAIDPLLALLAVPDISSLASGYLRNLTWTLSNLCRNKNPAPPIEAIEQ    251

Query  744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV    923
             +LP L +LL    D +VLAD CWA+SY+TD  N +I  VV +  VP+LVKLL   E I+
Sbjct  252   ILPTLVRLLHHDDHEVLADTCWAISYLTDGSNDRIEVVVKTGLVPQLVKLLGCGELPIMT    311

Query  924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ    1103
             P+LR++GNIVTGTD QT +VI SG L    LL H+K+NI KEAAWT+SNITAG + QIQ
Sbjct  312   PSLRAIGNIVTGTDDQTQIVIESGALTVFPSLLSHHKNNIQKEAAWTMSNITAGRRDQIQ    371

Query  1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD    1283
              V+  G+    L  +L+KGDFK+QKEA WAVTN T+ GT +QIV L++     +++P ++LL
Sbjct  372   QVVDHGLVPYLIGILKKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLS    430

Query  1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA    1463
              KD +T+ V+   ++N+F  AEK+G TE LCLM+EE GGLDK+E LQ HENE VYK + +
Sbjct  431   AKDSKTVLVILDAITNIFLAAEKIGETERLCLMIEECGGLDKIEALQSHENELVYKASSS    490

Query  1464  IIDTYFSNGDDEAEQELAPQEVNGALEF    1547
             +I+ YFS  ++E +Q + P     + F
Sbjct  491   LIEKYFS-AEEEEDQNVVPDSTVDSYTF    517
```

PREDICTED: importin subunit alpha-1 isoform X1 [Monodelphis domestica]

Score	Expect	Method	Identities	Positives	Gaps	Frame
499 bits(1285)	2e-164()	Compositional matrix adjust.	264/522(51%)	358/522(68%)	12/522(2%)	+3

Features:

```
Query   45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKE-LNGQ   215
              +R    +K     ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E   N Q
Sbjct   79    ARLNRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTFPDDATSPLQENRNNQ    138

Query   216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
                  SV+EIV  +NS + E Q    Q+ARK+LSRE+ PPID +I  G++P  + FL  T
Sbjct   139   GSALWSVEEIVKGINSNNLEVQLQATQAARKLLSREKQPPIDQIIEAGMIPKLVGFLGRT    198

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
              + + +QFE+AWALTNIASGTSDQT+ V++  A+P F+ALL S   +++EQAVWALGNIAG
Sbjct   199   DCNPIQFESAWALTNIASGTSDQTKAVVDGGAIPAFIALLASPQAHISEQAVWALGNIAG    258

Query   576   DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
              DG+A RD+VI +   ID +L L+    +     +LRN+ W +SNLCRNKNP+PP + +++
Sbjct   259   DGSAYRDLVIKYGAIDPLLALLAVPDISSLACGYLRNLTWTLSNLCRNKNPAPPIEAIEQ    318

Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
              +LP L +LL    D +VLAD CWA+SY+TD  N +I+ VV +   VP+LVKLL    E  I+
Sbjct   319   ILPTLVRLLHHDDPEVLADTCWAISYLTDGSNDRIEVVVKTGVVPQLVKLLGSGELPIVT    378

Query   924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
              P+LR++GNIVTGTD+QT +VI SG L    LL H K+NI KEAAWT+SNITAG Q QIQ
Sbjct   379   PSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLTHPKTNIQKEAAWTMSNITAGRQDQIQ    438

Query   1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
               V+  G+    L +L KGDFK+QKEA WAVTN T+ GT EQIV L++    IL+P I+LL
Sbjct   439   QVVNHGLVPYLVGILSKGDFKSQKEAVWAVTNYTSGGTIEQIVYLVQN-GILEPLINLLS    497

Query   1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
               KD + + V+   +SN+F  AEKL   TE LC+++EE GGLD++E LQ HENE VYK + +
Sbjct   498   AKDSKIVLVILDAISNIFLAAEKLNETEKLCILIEECGGLDRIEALQSHENEMVYKASSS    557

Query   1464  IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF   1589
              +I+ YFS   +E +Q + P+  +    F   Q AP G + F
Sbjct   558   LIEKYFS--AEEEDQNVVPESTSDGYTFQ-IQDGAP-GTFNF   595
```

PREDICTED: LOW QUALITY PROTEIN: importin subunit alpha-1-like [Corvus brachyrhynchos]

Score	Expect	Method	Identities	Positives	Gaps	Frame
498 bits(1283)	2e-164()	Compositional matrix adjust.	257/508(51%)	355/508(69%)	9/508(1%)	+3

Features:

```
Query   45    SRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNIND--EDLTSPLKELNG-Q   215
              +R    +K     ++ + R RR EV +ELRK+KK+DQM KRRN++    +D TSPL+E  G Q
Sbjct   58    ARLNRFKNKGKDSTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQENRGNQ    117

Query   216   SPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNT   395
                  SV+EIV  +NS + E Q    Q+ARK+LSRE+ PPID +I  G++P  + FL
Sbjct   118   VLAHWSVEEIVKGVNSNNMELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVLFLGRA    177

Query   396   NNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAG   575
              + S +QFE+AWALTNIASGTS+QTR V++  A+P F++LL S   ++++EQAVWALGNIAG
Sbjct   178   DCSPIQFESAWALTNIASGTSEQTRAVVDGGAIPAFISLLASPHIHISEQAVWALGNIAG    237

Query   576   DGAAARDIVIHHNVIDGILPLIN----NETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR   743
              DG+A RD+VI +   I+ +L L+        +LRN+ W +SNLCRNKNP+PP + +++
Sbjct   238   DGSAYRDLVIKYGAIEPLLSLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIEAIQQ    297

Query   744   llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV   923
              +LP L +LL    D +VLAD CWA+SY+TD  N +I+ VV +   VP +LV+LL    E  I+
Sbjct   298   ILPTLVRLLHHDDPEVLADTCWAISYLTDGSNDRIEVVVKTGLVPQLVRLLGCSELPIMT    357

Query   924   PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ   1103
              P+LR++GNIVTGTD+QT +VI SG L    LL HNK+NI KEAAWT+SNITAG Q QIQ
Sbjct   358   PSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLSHNKNNIQKEAAWTMSNITAGRQDQIQ    417

Query   1104  AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD   1283
               V+  G+    L +L KGDFK+QKEA WAVTN T+ GT +QIV L++    +L+P ++LL
Sbjct   418   RVVDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVLEPLLNLLS    476

Query   1284  TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA   1463
              TKD +T+ V+    +SN+F  AEK+   TE LCL++EE GGLD++E LQ HENEEVY+ +
Sbjct   477   TKDSKTVLVILDAVSNIFLAAEKINETEKLCLIIEECGGLDRIEALQSHENEEVYRASST    536

Query   1464  IIDTYFSNGDDEAEQELAPQEVNGALEF   1547
              II+ YFS  ++E +Q + P     + F
Sbjct   537   IIEKYFS-AEEEDQSVVPGSTANSYTF   563
```