# **Basic Local Alignment Search Tool**

NCBI/ BLAST/ blastx/ Formatting Results - B8BJP379014

- ► Formatting options
- ▶ Download

Blast report description

#### **Nucleotide Sequence (2133 letters)**

**RID** <u>B8BJP379014</u> (Expires on 02-06 12:08 pm)

**Query ID** lcl|Query\_21893

**Description** None **Molecule type** nucleic acid **Query Length** 2133 **Database Name** nr

**Description** All non-redundant GenBank CDS

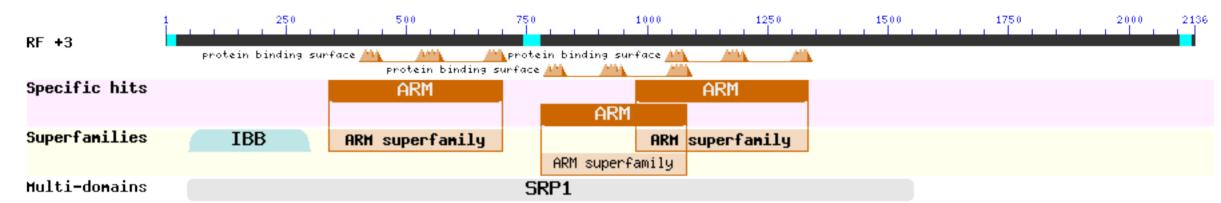
translations+PDB+SwissProt+PIR+PRF excluding

environmental samples from WGS projects

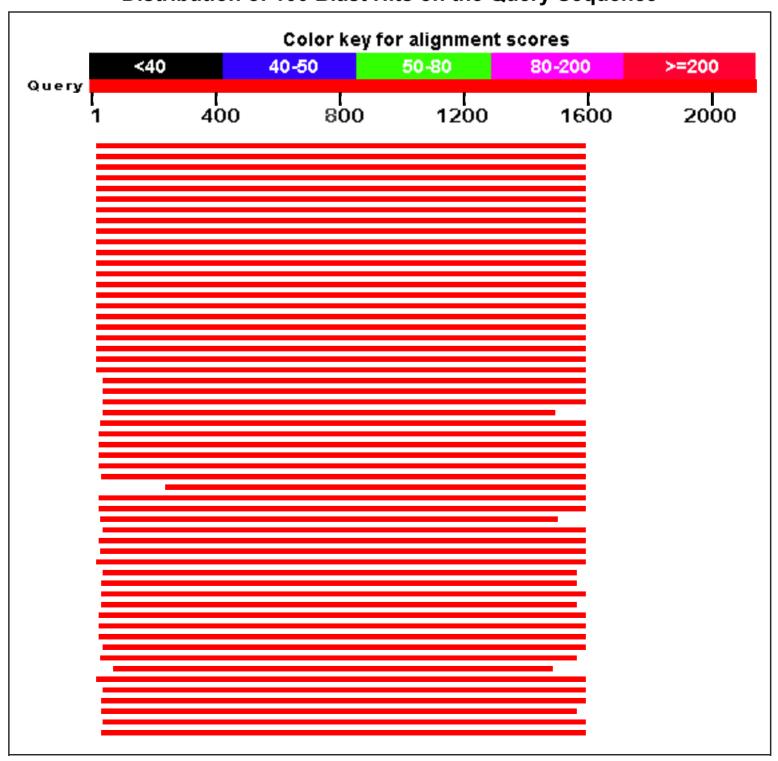
**Program** BLASTX 2.3.1+

# **□ Graphic Summary**

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



## Distribution of 100 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Description	Max 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	73%	0.0	57%	<u>XP_011305770.1</u>
PREDICTED: importin subunit alpha [Diachasma alloeum]	565	565	73%	0.0	56%	XP_015123786.1
PREDICTED: importin subunit alpha [Orussus abietinus]	551	551	73%	0.0	54%	XP_012276606.1
Importin subunit alpha-2 [Zootermopsis nevadensis]	546	546	73%	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	63%	0.0	63%	XP_001986958.1
PREDICTED: importin subunit alpha [Athalia rosae]	538	538	73%	0.0	54%	XP_012257423.1
PREDICTED: importin subunit alpha [Apis florea]	535	535	73%	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	73%	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%	<u>XP_014209910.1</u>
PREDICTED: importin subunit alpha [Cerapachys biroi]	530	530	71%	9e-178	53%	XP_011339385.1
PREDICTED: importin subunit alpha [Harpegnathos saltator]	529	529	71%	2e-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	71%	5e-177	53%	XP_014230579.1
Importin subunit alpha-2 [Habropoda laboriosa]	527	527	73%	2e-176	54%	KOC64063.1
PREDICTED: importin subunit alpha [Bombus impatiens]	524	524	73%	2e-175	54%	XP 003484488.1
PREDICTED: importin subunit alpha [Bombus terrestris]	524	524	73%	4e-175	54%	XP 003399525.1
PREDICTED: importin subunit alpha-1 [Strongylocentrotus	523	523	72%	4e-175	51%	XP 011662338.1
purpuratus]	020	020	7270	40 170	0170	<u>XI_011002000.1</u>
PREDICTED: importin subunit alpha [Megachile rotundata]	523	523	71%	6e-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%	5e-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%	4e-172	52%	XP_013787969.1
Importin subunit alpha-2 [Stegodyphus mimosarum]	515	515	72%	9e-172	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%	<u>XP_975293.1</u>
PREDICTED: importin subunit alpha [Monomorium pharaonis]	509	509	71%	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%	6e-168	67%	XP 001988308.1
PREDICTED: importin subunit alpha-1 [Atta cephalotes]	505	505	71%	8e-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	303	303	7 1 70	46-107	3170	
humile]	502	502	70%	1e-166	52%	<u>XP_012217870.1</u>
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%	8e-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						

mantelli]	499	499	71%	1e-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	71%	4e-165	50%	XP_009677268.1
PREDICTED: importin subunit alpha-1 [Tinamus guttatus]	498	498	71%	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	71%	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%	5e-165	50%	XP_010000998.1
PREDICTED: importin subunit alpha-1 [Manacus vitellinus]	498	498	71%	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%	9e-165	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%	1e-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

# ${\color{red} \bullet \underline{Alignments}}$

pendulin [Drosophila melanogaster]

Sequence ID: ref|NP\_477041.1| Length: 522 Number of Matches: 1

Score		Expect	Method		Identiti	es Po	ositives	Gaps	Frame
1051 bit	s(2717)	0.0()	Composition	al matrix adj	ust. 522/52	2(100%) 52	22/522(100%	%) 0/522(0%	) +3
Features	<b>S</b> :								
Query	24		SNSROGSYKA						
Sbjct	1		SNSRQGSYK <i>I</i> SNSRQGSYK <i>I</i>						
Query	204		PVQLSVDEIV PVQLSVDEIV						
Sbjct	61		PVQLSVDEIV						
Query	384		NSMLQFEAAV NSMLQFEAAV						
Sbjct	121		NSMLQFEAAV						
Query	564		GAAARDIVII GAAARDIVII						
Sbjct	181		GAAARDIVII						
Query	744	llpvl	sqlllsqDI(	)VLADACWA	LSYVTDDDN	TKIQAVVD	SDAVPRLVK	LLQMDEPS	IIV 923

Sbjct	241	LLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV LLPVLSQLLLSQDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV	300
Query	924	PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ	1103
Sbjct	301	PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ	360
Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD	1283
Sbjct	361	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD	420
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA	1463
Sbjct	421	TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA	480
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589	
Sbjct	481	IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 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 bit	ts(2707)	0.0()	Compositional matrix adjust.	521/522(99%)	521/522(99%)	0/522(0%)	+3
Feature	s:						
Query	24		DSNSRQGSYKANSINTQDSRMRI DSNSRQGSYKANSINTQDSRMRI				
Sbjct	1		DSNSRQGSYKANSINTQDSRMRI				
Query	204		SPVQLSVDEIVAAMNSEDQERQI SPVQ SVDEIVAAMNSEDQERQI				
Sbjct	61	LNGQS	SPVQPSVDEIVAAMNSEDQERQI	FLGMQSARKMLS	RERNPPIDLMI	GHGIVPICI	RF 120
Query	384		INSMLQFEAAWALTNIASGTSDO INSMLQFEAAWALTNIASGTSDO				
Sbjct	121		INSMLQFEAAWALTNIASGTSD(				
Query	564		OGAAARDIVIHHNVIDGILPLII OGAAARDIVIHHNVIDGILPLII				
Sbjct	181		OGAAARDIVIHHNVIDGILPLII				
Query	744	llpvl	sqlllsqDIQVLADACWALSY SQLLLSQDIQVLADACWALSY	VTDDDNTKIQAV	VDSDAVPRLVK	LLOMDEPSI	IV 923
Sbjct	241		LSQLLLSQDIQVLADACWALSY				
Query	924		SVGNIVTGTDQQTDVVIASGGLI SVGNIVTGTDQQTDVVIASGGLI				
Sbjct	301		SVGNIVTGTDQQTDVVIASGGL				
Query	1104		AGIFQQLRTVLEKGDFKAQKEA AGIFQQLRTVLEKGDFKAQKEA				
Sbjct	361		AGIFQQLRTVLEKGDFKAQKEA				
Query	1284		RTIKVVQTGLSNLFALAEKLGG' RTIKVVQTGLSNLFALAEKLGG'				
Sbjct	421		RTIKVVÕTGLSNLFALAEKLGG				
Query	1464		YFSNGDDEAEQELAPQEVNGALI YFSNGDDEAEQELAPQEVNGALI				
Sbjct	481		FSNGDDEAEQELAPQEVNGALI				

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

			_
1043 bit	s(2698)	0.0() Compositional matrix adjust. 518/522(99%) 520/522(99%) 0/522(0%) +3	<del></del>
Features	S:		
Query	24		203
Sbjct	1	MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE 6	60
Query	204	LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF 3 LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF	383
Sbjct	61		120
Query	384	LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG 5 LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKS+NLAEQAVWALG	563
Sbjct	121		180
Query	564	NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR 7 NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF+QVKR	743
Sbjct	181	<del>-</del>	240
Query	744	llpvlsqlllsqDiQVLADACWALSYVTDDDNTKiQAVVDSDAVPRLVKLLQMDEPSIIV 9 LLPVLSQLLLSQDiQVLADACWALSYVTDDDNTKiQAVVDSDAVPRLVKLLQMDEPSIIV	923
Sbjct	241	~ ~ ~ ~	300
Query	924	PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ 1 PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ	1103
Sbjct	301		360

Identities Positives

Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD	1283
Sbjct	361	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD	420
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA	1463
Sbjct	421	KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA	480
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589	
Sbjct	481	IIDTYFSN DDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 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 F	rame
1041 bit	s(2693)	0.0()	Compositional matrix adjust.	517/522(99%)	520/522(99%)	0/522(0%) +3	3
Features	s:						
Query	24		DSNSRQGSYKANSINTQDSRMR DSNSRQGSYKANSINTQDSRMR				
Sbjct	1		DSNSRQGS1KANSINTQDSKMRI DSNSRQGSYKANSINTQDSRMRI				
Query	204	LNGOS	SPVQLSVDEIVAAMNSEDQERQ SPVQLSVDEIVAAMNSEDQERQ	FLGMOSARKMLS	RERNPPIDLMI	GHGIVPICIRE	383
Sbjct	61		SPVQLSVDEIVAAMNSEDQERQ				
Query	384		INSMLQFEAAWALTNIASGTSDO INSMLQFEAAWALTNIASGTSDO				
Sbjct	121		INSMLQFEAAWALTNIASGTSD(				
Query	564		OGAAARDIVIHHNVIDGILPLI OGAAARDIVIHHNVIDGILPLI				
Sbjct	181		OGAAARDIVIHHNVIDGILPLI				
Query	744		sqlllsqDIQVLADACWALSY SOLLLSQDIQVLADACWALSY				
Sbjct	241		LSQLLLSQDIQVLADACWALSY				
Query	924		SVGNIVTGTDQQTDVVIASGGL: SVGNIVTGTDQQTDVVIASGGL:				
Sbjct	301		SVGNIVTGTDQQTDVVIASGGL				
Query	1104		AGIFQQLRTVLEKGDFKAQKEA AGIFQQLRTVLEKGDFKAQKEA				
Sbjct	361		AGIFQQLRTVLEKGDFKAQKEA				
Query	1284		RTIKVVQTGLSNLFALAEKLGG' RTIKVVQTGLSNLFALAEKLGG'				
Sbjct	421		RTIKVVÕIGLSNLFALAEKLGG'				
Query	1464		YFSNGDDEAEQELAPQEVNGALI YFSN DDEAEQELAPQEVNGALI				
Sbjct	481		FSNADDEAEQELAPQEVNGAL				

uncharacterized protein Dere\_GG10083 [Drosophila erecta]

Sequence ID: ref|XP\_001969394.1| Length: 522 Number of Matches: 1

Score	Expe	ct Method		Identities	Positives	Gaps	Frame
1040 bits(2	2689) 0.0()	Composition	al matrix adjust.	516/522(99%)	519/522(99%)	0/522(0%)	+3
Features:							
Query 2			ANSINTODSRMRF				
Sbjct 1			AN+INTQDSRMRF ANTINTQDSRMRF				
Query 2			/AAMNSEDQERQE /AAMNSEDQERQE				
Sbjct 6			/AAMNSEDOEROI /AAMNSEDQERQE				
Query 3			VALTNIASGTSDQ VALTNIASGTSDQ				
Sbjct 1			VALTNIASGISDŲ VALTNIASGISDŲ				
Query 5			HNVIDGILPLIN HNVIDGILPLIN	· ·		~	
Sbjct 1			HNVIDGILPLIN			~	
Query 7			QVLADACWALSY\				
Sbjct 2			QVLADACWALSY\ QVLADACWALSY\				
Query 9			QOTDVVIASGGLE				
Sbjct 3		-	QQTDVVIASGGLE QQTDVVIASGGLE	~		~ ~	~

Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD	1283
Sbjct	361	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVINTTTSGTPEQIVDLIEKYKILKPFIDLLD	420
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA	1463
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 bit	s(2661)	0.0()	Compositional matrix adjust.	515/524(98%)	517/524(98%)	2/524(0%)	+3
Features	s:						
Query	24		DSNSRQGSYKANSINTQDSRMRI DSNSRQGSYKANSINTQDSRMRI				
Sbjct	1		DSNSRQGSYKANSINTQDSRMRI DSNSRQGSYKANSINTQDSRMRI				
Query	204		SPVQLSVDEIVAAMNSEDQERQI SPVQLSVDEIVAAMNSEDQERQI				
Sbjct	61		SPVQLSVDEIVAAMNSEDQERQI				
Query	384	LONT- LONT	NNSMLQFEAAWALTNIASGT: NSMLQF AAWALTNIASGT:				
Sbjct	121		FITNSMLQFLAAWALTNIASGT				
Query	558		AGDGAAARDIVIHHNVIDGILPI AGDGAAARDIVIHHNVIDGILPI				
Sbjct	181		AGDGAAARDIVIHHNVIDGILPI				
Query	738		ovlsqlllsqDIQVLADACWALS				
Sbjct	241		PVLSÕLLLSÕDIÕVLADACWAL				
Query	918		RSVGNIVTGTDQQTDVVIASG LRSVGNIVTGTDQQTDVVIASG				
Sbjct	301		LRSVGNIVTGTDQQTDVVIASG				
Query	1098		IQAGIFQQLRTVLEKGDFKAQKI IQAGIFQQLRTVLEKGDFKAQKI				
Sbjct	361		Į Į AGIF Į ŽILTVLEKGDFKA Į KI				
Query	1278		OPRTIKVVOTGLSNLFALAEKLO OPRTIKVVOTGLSNLFALAEKLO				
Sbjct	421		PRTIKVVÕTGLSNLFALAEKLO				
Query	1458		OTYFSNGDDEAEQELAPQEVNGA OTYFSN DDEAEQELAPQEVNGA			9	
Sbjct	481		OTYFSNADDEAEQELAPQEVNGA				

uncharacterized protein Dyak\_GE18896 [Drosophila yakuba]

Sequence ID: ref|XP\_002089023.1| Length: 522 Number of Matches: 1

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	<b>S</b> :						
Query	24		DSNSRQGSYKANSINTQDSRMRI DSNSRQGSYKAN+INTQDSRMRI				
Sbjct	1		DSNSRQGS1KAN+INIQDSKMRF DSNSRQGSYKANTINTQDSRMRF				
Query	204		SPVQLSVDEIVAAMNSEDQERQI SPVQLSVDEIVAAMNSEDQERQI				
Sbjct	61		SPVQLSVDEIVAAMNSEDQERQI SPVQLSVDEIVAAMNSEDQERQI				
Query	384		NNSMLQFEAAWALTNIASGTSDQ NNSMLQFEAAWALTNIASGTSDQ				
Sbjct	121		NNSMLQFEAAWALTNIASGTSDÇ NNSMLQFEAAWALTNIASGTSDÇ				
Query	564		DGAAARDIVIHHNVIDGILPLIN DGAAARDIVIH+NVIDGILPLIN				
Sbjct	181		DGAAARDIVIHNNVIDGILPLIN				
Query	744		lsqlllsqDIQVLADACWALSY\ LSQLL SQDIQVLADACWALSY\				
Sbjct	241		LSQLLFSQDIQVLADACWALSY\				
Query	924		SVGNIVTGTDQQTDVVIASGGLI SVGNIVTGTDQQTDVVIASG LI				
Sbjct	301		SVGNIVTGTDQQTDVVIASG LE SVGNIVTGTDQQTDVVIASGALE				
Query	1104	AVIQ	AGIFQQLRTVLEKGDFKAQKEA <i>I</i>	AWAVTNTTTSGT	PEQIVDLIEKY	KILKPFIDL	LD 1283

# AV AGIF QLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKY ILKPFIDLLD AVEDAGIFHQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYHILKPFIDLLD 420 Query 1284 TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA KDPRTIKVVQTGLSN FALAEK G ENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA AKDPRTIKVVQTGLSNFFALAEKFNGIENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA 480 Query 1464 IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589 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	<b>3</b> :					
Query	24	MSKADSNSRQGSYKANSINTQDSRMRI				
Sbjct	1	MSKADSNSRQGSYK+N+INTQDSRMRI MSKADSNSRQGSYKSNTINTQDSRMRI				
Query	204	LNGQSPVQLSVDEIVAAMNSEDQERQI				
Sbjct	61	LNGQSPVQLSVDEIVAAMNSEDQERQI LNGQSPVQLSVDEIVAAMNSEDQERQI				
Query	384	LONTHNSMLQFEAAWALTNIASGTSDO				
Sbjct	121	LQNT N+MLQFEAAWALTNIASGTSDQ LQNTTNTMLQFEAAWALTNIASGTSDQ				
Query	564	NIAGDGAAARDIVIHHNVIDGILPLII				
Sbjct	181	NIAGDGA+ARDIVIHHNVIDGILPLII NIAGDGASARDIVIHHNVIDGILPLII				
Query	744	llpvlsqlllsqDIQVLADACWALSY				
Sbjct	241	LLPVLSÕLLLSÕDIÕVLADACWALSY LLPVLSÕLLLSÕDIÕVLADACWALSY	VTDDDN KIQAV VTDDDNNKIQAV	VDSDAVPRLVK. VDSDAVPRLVK.	LLEMDEPSI	IV 300
Query	924	PALRSVGNIVTGTDQQTDVVIASGGLI				
Sbjct	301	PALRSVGNIVTGTDQQTDVVIA+GGLI PALRSVGNIVTGTDQQTDVVIAAGGLI				
Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAZ AVIQAGIFQQLR VLEKGDFKAQKEAZ				
Sbjct	361	AVIQAGIFQQLRHVLEKGDFKAQKEA				
Query	1284	TKDPRTIKVVOTGLSNLFALAEKLGG'				
Sbjct	421	KDPRTIKVVQTGLSNLFALAEKLGG AKDPRTIKVVQTGLSNLFALAEKLGG				
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALI IIDTYFSNGDD EQELAPQEVNGALI				
Sbjct	481	IIDTYFSNGDDAVEQELAPQEVNGALI				

#### GL18958 [Drosophila persimilis]

Sequence ID: ref|XP\_002014430.1| Length: 522 Number of Matches: 1

Score		Expect	Method			Identities	Positives	Gaps	Fra	me
989 bits	(2556)	0.0()	Compositi	onal matr	rix adjust.	501/522(96%	b) 514/522(98°	%) 0/522(0%	) +3	
Features	<b>S</b> :									
Query	24						SKKEDOMFKRR			203
Sbjct	1						SKKEDOMFKRR SKKEDOMFKRR			60
Query	204						SRERNPPIDL SRERNPPIDL			383
Sbjct	61						LSRERNPPIDL			120
Query	384						/PHFVALLQSK /PHFVALLQS			563
Sbjct	121						PHFVALLQS			180
Query	564						NIVWLMSNLCR NIVWLMSNLCR			743
Sbjct	181						NIVWLMSNLCR			240
Query	744						AVVDSDAVPRL AVVDSDAVPRL			923
Sbjct	241						AVVDSDAVPRL			300
Query	924						KSNIVKEAAWT KSNIVKEAAWT			1103
Sbjct	301						KSNIVKEAAWT			360
Query	1104						GTPEQIVDLIE GTPEQIVDLIE			1283

```
Sbjct 361 AVIEAGIFQQLRNVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKFKILKPFIDLLD 420

Query 1284 TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA 1463
KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA AKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA 480

Query 1464 IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589
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	<b>3</b> :					
Query	24	MSKADSNSRQGSYKANSINTQDSRMRR				
Sbjct	1	M+K D+N+RQGSYK+N+INT DSRMRR MNKTDANTRQGSYKSNTINTLDSRMRR				
Query	204	LNGQSPVQLSVDEIVAAMNSEDQERQF LNGOSPVOLSVDEIVAAMNSEDQERQF				
Sbjct	61	LNGQSPVQLSVDEIVAAMNSEDQERQF				
Query	384	LQNTNNSMLQFEAAWALTNIASGTSDQ LQNT+N+MLQFEAAWALTNIASGTSDQ				
Sbjct	121	LÕNTSNTMLÕFEAAWALTNIASGTSDÕ				
Query	564	NIAGDGAAARDIVIHHNVIDGILPLIN NIAGDGAAARDIVI HNVIDGILPLIN				
Sbjct	181	NIAGDGAAARDIVI MNVIDGILPLIN				
Query	744	llpvlsqlllsqDIQVLADACWALSYV LLPVLSQLLLSQDIQVLADACWALSYV				
Sbjct	241	LLPVLSQLLLSQDIQVLADACWALSYV				
Query	924	PALRSVGNIVTGTDQQTDVVIASGGLP PALRSVGNIVTGTD QTDVVIA+GGLP				
Sbjct	301	PALRSVGNIVTGTDVQTDVVIAAGGLP				
Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAA AVI+AGIFQOLR VLEKGDFKAQKEAA				
Sbjct	361	AVIEAGIFQQLRNVLEKGDFKAQKEAA				
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGT KDPRTIKVVOTGLSNLFALAEKLGGT				
Sbjct	421	AKDPRTIKVVÕTGLSNLFALAEKLGGT				
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALE IIDTYFSNGDDEAEQELAPQEVNGALE				
Sbjct	481	IIDTYFSNGDDEAEQELAPQEVNGALE IIDTYFSNGDDEAEQELAPQEVNGALE				

uncharacterized protein Dmoj\_GI17589 [Drosophila mojavensis]
Sequence ID: ref|XP\_002002818.1| Length: 522 Number of Matches: 1

**Expect Method** 

#### ▶ See 1 more title(s) Range 1: 1 to 522

**Score** 

			10.0110.00			
954 bits	(2465)	0.0() Compositional matrix adjust.	466/523(89%)	495/523(94%)	2/523(0%) +3	
Feature	s:					
Query	24	MSKADSNSRQGSYKANSINTQDSRMRI				203
Sbjct	1	M+K+D+N+RQG YKAN++N QDSRMRI MNKSDANTRQGHYKANTLNMQDSRMRI				60
Query	204	LNGQSPVQLSVDEIVAAMNSEDQERQI LNGQSPV LSVDEIVAAMNSED ERQI				383
Sbjct	61	LNGQSPVLLSVDEIVAAMNSEDPERQI				120
Query	384	LQNTNNSMLQFEAAWALTNIASGTSDO				563
Sbjct	121	LQH-NNPLLQFEAAWALTNIASGTSD				179
Query	564	NIAGDGAAARDIVIHHNVIDGILPLII NIAGDG AARDIVI HNVIDGIL LII				743
Sbjct	180	NIAGDG AARDIVI HNVIDGIL LII NIAGDGPAARDIVIQHNVIDGILRLII				239
Query	744	<pre>ll-pvlsqlllsqDIQVLADACWALST LL + L+ +DIQVLADACWALST</pre>				920
Sbjct	240	LLPVLSQLLVYQEDIQVLADACWALS				299
Query	921	VPALRSVGNIVTGTDQQTDVVIASGGI VPALRSVGNIVTGTDQQTDVVIA+GGI				1100
Sbjct	300	VPALRSVGNIVTGTDQQTDVVIAAGGI				359
Query	1101	QAVIQAGIFQQLRTVLEKGDFKAQKEA QAVI AGIF Q+R VLEKGDFKAQKEA				1280
Sbjct	360	QAVI AGIF Q+K VLEKGDFKAQKEA				419

**Identities** 

**Positives** 

Gaps

Frame

```
DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY
+ KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEE+GGLDKLE LQQHENEEVYKKAY
EAKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEELGGLDKLEALQQHENEEVYKKAY
Query 1281
                                                                                                                                                                          1460
Sbjct
               420
                                                                                                                                                                            479
                            AIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF
A+IDTYFS GDDEAE+ELAPQEVNGALEFNATQPKAPEGGYTF
ALIDTYFSAGDDEAEKELAPQEVNGALEFNATQPKAPEGGYTF
Query
               1461
Sbjct
              480
                                                                                                                                    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	s:							
Query	24				RHEVTIELRKSK			
Sbjct	1				RHEVTIELRKSK RHEVTIELRKSK			
Query	204				FLGMQSARKMLS F+GMQ ARKMLS			
Sbjct	61				FVGMQQARKMLS			
Query	384	LONT	NNSMLQFEAAW	ALTNIASGTSDO	OTRCVIEHNAVE OTRCVIE NAVE	HFVALLQSKSM	NLAEQAVWA	LG 563
Sbjct	121				ŽTRCVIE NAVI ŽTRCVIEQNAVE			
Query	564				NNETPLSFLRNI NNETPLSFLRNI			
Sbjct	180				NNETPLSFLRNI			
Query	744				VTDDDNTKIQAV VTDDDN KIQAV			
Sbjct	240				VTDDDNNKIQAV			
Query	924				PRLGLLLQHNKS P+LGLLLOH+K			
Sbjct	300				PKLGLLLÕHSKO			
Query	1104				AWAVTNTTTSGT AWAVTNTTTSGT			
Sbjct	360	AVID	AGIFÕÕIRHVL	EKGDFKAÕKEA	AWAVTNTTTSGT	PEÕIVDLIEKY	KILKPFIDI	LD 419
Query	1284				renlclmveemorencerc			
Sbjct	420				renlclmveelo			
Query	1464				EFNATQPKAPEG EFNATQPKAPEG			
Sbjct	480				EFNATÕPKAPEG			

#### 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	<del>)</del>
939 bits	(2426)	0.0()	Composition	nal matrix	adjust.	462/522(89%)	) 493/522(94%	) 0/522(0%)	+3	
Features	s:									
Query	24						KKEDOMFKRRN			203
Sbjct	1						KKEDQMFKRRN KKEDQMFKRRN			50
Query	204						SRERNPPIDLM			883
Sbjct	61						SRERNPPIDLM SRERNPPIDLM			20
Query	384						PHFVALLOSKS			63
Sbjct	121						PHF+ALLQSK PHFIALLQSKH			180
Query	564						IVWLMSNLCRN			743
Sbjct	181						IVWLMSNLCRN: IVWLMSNLCRN:			240
Query	744						VVDSDAVPRLV.		_	23
Sbjct	241						VV++DAVPRLV VVETDAVPRLV			300
Query	924						SNIVKEAAWTV			103
Sbjct	301						NIVKEAAWTV GNIVKEAAWTV			360
Query	1104						PEQIVDLIEK			283
Sbjct	361						+ EQIVDLIEK SSEQIVDLIEK			120

```
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	<b>S</b> :						
Query	24		DSNSRQGSYKANSINTQDSRMRI ++NSR SYK+NSINTQDSR+RI				
Sbjct	1		EANSRLSSYKSNSINTQDSRVRI				
Query	204		SPVQLSVDEIVAAMNSEDQERQI SPVQLSVDEIVAAMNSED ERQI				
Sbjct	61		SPVQLSVDEIVAAMNSEDSERQI				
Query	384	LONTI LON	NNSMLQFEAAWALTNIASGTSDO N MLQFEAAWALTNIASGTSDO				
Sbjct	121		ANPMLQFEAAWALTNIASGTSD(				
Query	564	NIAGI NIAGI	DGAAARDIVIHHNVIDGILPLII DG ARDIVI+H VIDGIL LII				
Sbjct	181		DG ARDIVI'H VIDGIL III DGPIARDIVINHGVIDGILRLII				
Query	744		lsqlllsqDIQVLADACWALSYV LS LLLS DIQVLADACWALSYV				
Sbjct	241		LSHLLLSTDIQVLADACWALSY				
Query	924		SVGNIVTGTDQQTDVVIASGGLI SVGNIVTGTDQQTDVVIASGGLI				
Sbjct	301		SVGNIVTGTDQQTDVVIASGGLI				
Query	1104	AVIQA AVI+	AGIFQQLRTVLEKGDFKAQKEA AGIF ++ VLE GDFKAQKEA				
Sbjct	361		AGIFNYIKQVLENGDFKAQKEAZ				
Query	1284		RTIKVVQTGLSNLFALAEKLGG' RTIKVVQTGL NLF LAEKLGG'				
Sbjct	421		RTIKVVÕIGL NIF LAEKIGG: RTIKVVÕTGLLNLFNLAEKLGG:				
Query	1464		YFSNGDDEAEQELAPQEVNGALI YF+ GD+ AEQELAPQEVNGALI				
Sbjct	481		YFNTGDEGAEQELAPQEVNGALI				

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	s:						
Query	24		DSNSRQGSYKANSINTQDSRMRI				
Sbjct	1		++N+RÖG +KA S+N Ö+SRMRI EANARQGQFKAKSLNLQESRMRI				
Query	204		SPVQLSVDEIVAAMNSEDQERQI SPVQL+VDEIVAAMNSED ERQI				
Sbjct	61		SPVQLTVDEIVAAMNSEDAERQI				
Query	384		NNSMLQFEAAWALTNIASGTSDONN MLOFEAAWALTNIASGT++0				
Sbjct	121		NN MLOFEAAWALTNIASGTAE(				
Query	564		DGAAARDIVIHHNVIDGILPLII DGA ARDIVI +NVIDGIL LI-				
Sbjct	181		DGA ARDIVI THVIDGIL LIT DGAIARDIVIQNNVIDGILSLIS				
Query	744		lsqlllsqDIQVLADACWALSY LSQLL SQDIQVLADACWALSY				
Sbjct	241		LSQLLTSQDIQVLADACWALSY				
Query	924		SVGNIVTGTDQQTDVVIASGGLI SVGNIVTGTDQQTDVVIA+GGLI				
Sbjct	301		SVGNIVTGTDQQTDVVIA+GGLI				
Query	1104		AGIFQQLRTVLEKGDFKAQKEA AGIF Q+R VLEKGDFKAQKEA				
Sbjct	361		AGIFHQIRQVLEKGDFKAQKEAZ				
Query	1284		RTIKVVQTGLSNLFALAEKLGG' RTIKVVQTGL+NLFALAEKLGG'				
Sbjct	421		RTIKVVQTGL+NLFALAEKLGG:				

Query 1464 IIDTYFSNGDDE-AEQELAPQEVNGALEFNATQPKAPEGGYTF Sbjct 481 IIDTYWPAGDDDAAEQELAPQEVNGALEFNTTQPKAPEGGYTF 1589 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	s:					
Query	24	MSKADSNSRQGSYKANSINTQDSRMRR MS+ D+ +RQG+YK+N+IN+ +SR+RR				
Sbjct	1	MSRMDA-TRQGAYKSNTINSNESRLRR				
Query	204	LNGQSPVQLSVDEIVAAMNSEDQERQF NGOSPVO++VDEIVAAM+S D ERQF				
Sbjct	60	SNGQSPVQ++VDEIVAAM+S D ERQF				
Query	384	LQNTNNSMLQFEAAWALTNIASGTSDQ LQN N+MLQFEAAWALTNIASGTS+Q				
Sbjct	120	LQNFENAMLQFEAAWALTNIASGTSEQ				
Query	564	NIAGDGAAARDIVIHHNVIDGILPLIN NIAGDGAAARDIVI HNVIDGIL L N				
Sbjct	180	NIAGDGAAARDIVI HNVIDGIL L'N NIAGDGAAARDIVIEHNVIDGILCLCN				
Query	744	llpvlsqlllsqDIQVLADACWALSYV LLPVLSQLL DIQVLADACWALSYV				
Sbjct	240	LLPVLSQLLCGTDIQVLADACWALSYV				
Query	924	PALRSVGNIVTGTDQQTDVVIASGGLP PALRSVGNIVTGTDQOTD VIA+GGLP				
Sbjct	300	PALRSVGNIVTGTDQQTD VIA GGLP				
Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAA AVI A IF O+R VLEKGDFK+OKEAA				
Sbjct	360	AVI A IF O'K VLEKGDEK OKEAA AVIDADIFSÕIRNVLEKGDEKSÕKEAA				
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGT KDPRTIKVV TGLSNLFALA++LGG				
Sbjct	420	AKDPRTIKVVLTGLSNLFALADRLGGA				
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALE I+D YFS+ D AE ELAPQEVNGALE				
Sbjct	480	IVDAYFSSADG-AESELAPQEVNGALE				

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
Feature	s:							
Query	24				RHEVTIELRKSK			
Sbjct	1				RHEVT+ELRKSK RHEVTVELRKSK			
Query	204				FLGMQSARKMLS F+GMQSARKMLS			
Sbjct	60				TVGMQSARKMLS TVGMQSARKMLS			
Query	384	LONTI LON			OTRCVIEHNAVP OTRCVIE NAVP			
Sbjct	120				TRCVIE NAVE TRCVIEQNAVP			
Query	564				NNETPLSFLRNI N ETPLSFLRNI			
Sbjct	180				NFETPLSFLRNI			
Query	744				/TDDDNTKIQAV /TDD+N KIQAV			
Sbjct	240				TDD-N KIOAV TDDENLKIÕAV			
Query	924				PRLGLLLQHNKS PRLG+LLQH+K			
Sbjct	300				PRLGVLLÕHSKC			
Query	1104	AVIQA AVI			AWAVTNTTTSGT AWAVTNTTTSGT			
Sbjct	360				AWAVTNTTTSGT AWAVTNTTTSGT			
Query	1284				TENLCLMVEEMG TENLCLMVEEMG			
Sbjct	420				TENLCLMVEEMG			
Query	1464		YFSNGDDEAEQE YF++G+D AE E		EFNATQPKAPEG EFNA APEG			
Sbjct	480				EFNAGHSNAPEG			

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()	Compositiona	al matrix adjust.	442/524(84%)	483/524(92%)	4/524(0%)	+3
Features	<b>S</b> :							
Query	24			ANSINTQDSRMRI NSINT +SR+RI				
Sbjct	1			SNSINTNESRLR				
Query	204			/AAMNSEDQERQI /AAM S D ERQI				
Sbjct	60			AAMQSTDPERQI				
Query	384	LQNTI LON		VALTNIASGTSD( VALTNIASGTS+(				
Sbjct	120			VALTNIASGTSE(				
Query	564		DGAAARDIVIH DGAAARDIVIH	HNVIDGILPLIN		NIVWLMSNLCR N VWLMSNLCR		
Sbjct	180			HKCIDGVLNMVI				
Query	738			DIQVLADACWALS				
Sbjct	240			DIQVLADACWALS				_
Query	918			DOQTDVVIASGO DOQTD VIA+GO				
Sbjct	300			TDÕÕTDAVIAAGO				
Query	1098			TVLEKGDFKAQKI VLEKGDFK+QKI				
Sbjct	360			VLEKGDFKSÕKI				
Query	1278			GLSNLFALAEKLO GLSNLFALAEKLO				
Sbjct	420			ELSNLFALAEKLO				
Query	1458			AEQELAPQEVNG <i>I</i> AE ELAPQEVNG <i>I</i>			9	
Sbjct	480			AESELAPÕEVNG <i>I</i>				

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()	Composition	al matrix adjust.	431/522(83%)	474/522(90%)	2/522(0%)	+3
Features	<b>S</b> :							
Query	24			ANSINTODSRMR				
Sbjct	1			+N+IN+Q+SRMRI SNAINSQESRMRI				
Query	204			VAAMNSEDQERQI V AMNS+D ERQI				
Sbjct	60			V AMNS ID EKO VTAMNS QDVER Q				
Query	384	LONTI LON		WALTNIASGTSDOWALTNIASGTS+0				
Sbjct	120			WALTNIASGTSE				
Query	564			HHNVIDGILPLII HNV++GIL LII				
Sbjct	180			QHNVVEGILGLII				
Query	744	llpv:	lsqlllsqDI	QVLADACWALSY QVLADACWALSY	VTDDDNTKIQAV	VDSDAVPRLVK	LLQMDEPSI LL DEPSI	
Sbjct	240			ŽVLADACWALSY				
Query	924			QQTDVVIASGGLI QTD VIA+GGLI				
Sbjct	300			LÕTDAVIAAGGL				
Query	1104	AVIQ AVI		LEKGDFKAQKEA LEKGDFK+QKEA				
Sbjct	360			LEKGDFKSÕKEA				
Query	1284			SNLFALAEKLGG' NLF LAEKLGG'				
Sbjct	420			GNLFVLAEKLGG				
Query	1464			QELAPQEVNGALI ELAPQEVNGALI				
Sbjct	480			AELAPQEVNGALI				

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	MSKADSNSRQGSYKANSINTQDSRMRR MSK+D+ SR SYK+NSIN+Q+SRMRR				
Sbjct	1	MSKSDT-SRLNSYKSNSINSQESRMRR				
Query	204	LNGQSPVQLSVDEIVAAMNSEDQERQF N QSP Q+S+DE+VA+MNS+D ERQF				
Sbjct	60	SNNQSPAQMSIDEMVASMNSQDVERQF				
Query	384	LQNTNNSMLQFEAAWALTNIASGTSDQ LQN N +LQFEAAWALTNIASGTS+Q				
Sbjct	120	LÕNHENPLLÕFEAAWALTNIASGTSEÕ				
Query	564	NIAGDGAAARDIVIHHNVIDGILPLIN NIAGDGAAARDIVI HNV+DGIL LIN				
Sbjct	180	NIAGDGAAARDIVIQHNVVDGILGLIN				
Query	744	llpvlsqlllsqDIQVLADACWALSYV LLPVLS+LLL +D QVLADACWALSYV				
Sbjct	240	LLPVLSRLLLGEDTQVLADACWALSYV				
Query	924	PALRSVGNIVTGTDQQTDVVIASGGLP PALRSVGNIVTGTDQOTD VIA+GGLP				
Sbjct	300	PALRSVGNIVTGTDQQTD VIA GGLP				
Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAA AVI AGIF +R VLEKGDFK+QKEAA				
Sbjct	360	AVINAGIFTPIRLVLEKGDFKSQKEAA				
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGT KDPRTIKVV GL NLF LAEKLGGT				
Sbjct	420	AKDPRTIKVVLMGLGNLFVLAEKLGGT				
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALE ++DTYF++G+D AE ELAPQEVNGALE				
Sbjct	480	LVDTYFNSGED-AEAELAPQEVNGALE				

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	s:					
Query	24	MSKADSNSRQGSYKANSINTQDSRMR MSKAD RQ +YK+NSINT +SR+R				
Sbjct	1	MSKADP-GRQNAYKSNSINTNESRLR				
Query	204	LNGQSPVQLSVDEIVAAMNSEDQERQ NGQSPVQ++VDEIVAAM S D ERQ				
Sbjct	60	SNGQSPVQMTVDEIVAAMQSADPERQ				
Query	384	LQNTNNSMLQFEAAWALTNIASGTSD LQN + +LQFEAAWALTNIASGTSD				
Sbjct	120	LQNFEHPLLQFEAAWALTNIASGTSD				
Query	564	NIAGDGAAARDIVIHHNVIDGILPLI NIAGDGAAARDIVI + IDGIL +I		NIVWLMSNLCR N VWLMSNLCR		
Sbjct	180	NIAGDGAAARDIVIQNKCIDGILNMI				
Query	738	KRllpvlsqlllsqDIQVLADACWAL KRLLPVLSQLL DIQVLADACWAL				
Sbjct	240	KRLLPVLSQLLCGTDIQVLADACWAL				
Query	918	IVPALRSVGNIVTGTDQQTDVVIASG IVPALRSVGNIVTGTDQQTD VIA+G				
Sbjct	300	IVPALRSVGNIVTGTDÕÕTDAVIAAG				
Query	1098	IQAVIQAGIFQQLRTVLEKGDFKAQK IQAVI A IF Q+R VLEKGDFK+QK				
Sbjct	360	IQAVIDADIFAQIRKVLEKGDFKSQK				
Query	1278	LDTKDPRTIKVVQTGLSNLFALAEKL LD KDPRTIKVV TG+SNLFALAEKL				
Sbjct	420	LDAKDPRTIKVVLTGVSNLFALAEKL				
Query	1458	YAIIDTYFSNGDDEAEQELAPQEVNG YAIID YFSNGD AE ELAPQEVNG			9	
Sbjct	480	YAIIDAYFSNGDG-AEAELAPQEVNG				

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 MSK D SR SYK++ + DSRMRRHEVT+ELRKSKKEDQ+FKRRNIN+ED+ SPLKE	203
Sbjct 1	MSKPDP-SRINSYKSSIRSATDSRMRRHEVTVELRKSKKEDQLFKRRNINEEDIVSPLKE	59
Query 204	LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF N QSPV +S+DE+V AM S+D ERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICI+F	383
Sbjct 60	NNVQSPVPMSIDEMVVAMKSDDIERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIQF	119
Query 384	LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG LQ T N +LQFEAAWALTNIASG SDQTRCVIE NAVP+FVALL+SKS+NLAEQAVWALG	563
Sbjct 120	LQKTENPLLQFEAAWALTNIASGNSDQTRCVIEQNAVPYFVALLRSKSINLAEQAVWALG	179
Query 564	NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR NIAGDGAAARDIVIH+NV+DG+L LIN TPLSFLRNIVWLMSNLCRNKNPSPPFD++KR	743
Sbjct 180	NIAGDGAAARDIVIHNNVVDGLLGLINQATPLSFLRNIVWLMSNLCRNKNPSPPFDEIKR	239
Query 744	llpvlsqlllsqDiQVLADACWALSYVTDDDNTKiQAVVDSDAVPRLVKLLQMDEPSIIV LLP++SQLLL D QVLADACWALSYVTDD+N KIQAVVD+ AV RLV LL DEPSIIV	923
Sbjct 240	LLPIISÕLLLGSDDÕVLADACWALSYVTDDENVKIÕAVVDTGAVERLVALLGTDEPSIIV	299
Query 924	PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ PALR+VGNIVTGTD QTD VIA+GGL LG+LLQ+ K NIVKEAAWT+SNITAGNQKQIQ	1103
Sbjct 300	PALRTVGNIVTGTDTÕTDAVIAAGGLQVLGVLLÕNPKGNIVKEAAWTISNITAGNÕKÕIÕ	359
Query 1104	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD AVI +G+F Q+R VLEKGDFK+QKEAAWAVTNTTTSGTPEQIVDLIEKY++LKPF DLLD	1283
Sbjct 360	AVIDSGVFAÕIRNVLEKGDFKSÕKEAAWAVTNTTTSGTPEÕIVDLIEKYQLLKPFCDLLD	419
Query 1284	TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA KDPRTIKVV TGL+NLF LA++LGGTENLCLM+EEMGGLDKLE LQ+HENEE+YKKAYA	1463
Sbjct 420	AKDPRTIKVVLTGLANLFVLADRLGGTENLCLMIEEMGGLDKLEKLÕEHENEEIYKKAYA	479
Query 1464	IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589 ++DTYF+N DD AE ELAPQEVNGALEFNA Q K PEGG+TF	
Sbjct 480	MVDTYFNNEDD-AENELAPÕEVNGALEFNAGÕSKTPEGGFTF 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	s:						
Query	42	NSRQ NSR	GSYKANSINTQDSRMRRHEVTI SYK + + R RRHEVT+1			LTSPLKELN +TSPL+E N	
Sbjct	10		ASYKHGVKSNAELRQRRHEVTV				
Query	216	SPVQ:	LSVDEIVAAMNSEDQERQFLGM L +EI+A +NS + +++F+ +6				
Sbjct	70		LKFEEILAYVNSGNAQKEFVAI				
Query	396		LQFEAAWALTNIASGTSDQTRCY LOFEAAWALTNIASGT++OT+				
Sbjct	130		LQFEAAWALTNIASGTTEQTKA'				
Query	576		ARDIVIHHNVIDGILPLI-NNE' ARDIV++ N ++ I+ L+ N '	TPLSFLRNIVWL T LSFLRNIVWL			
Sbjct	190		ARDIVLNFNSVESIIYLVQNTN				
Query	753	vlsq +LS+	lllsqDIQVLADACWALSYVTD LL +D QVLADACWALSYVTD			MDEPSIIVP + P+II P	
Sbjct	250		LLDHEDSQVLADACWALSYVTDI				
Query	933		NIVTGTDQQTDVVIASGGLPRLO NIVTG+D OTD V+A+G LP LO				VI 1112 V
Sbjct	310		NIVTGSDTÕTDAVLAAGALPFLO				
Query	1113	~	FQQLRTVLEKGDFKAQKEAAWA' F L VL KGDFK+QKEAAWA				
Sbjct	370		FHLLIEVLIKGDFKSÕKEAAWA:				
Query	1293		KVVQTGLSNLFALAEKLGGTEN +VV +G+SN+F AEK+GGTEN	LCLMVEEMGGLD LC + EE+G LD			
Sbjct	430		RVVLSGISNIFQFAEKIGGTEN				
Query	1473	TYFS:	NGDDEAEQELAPQEVNGALEFN + +D E AP+E +GALEFN	~	F 1589		
Sbjct	490		DAED-VNPECAPKEKDGALEFN		_		

# 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	е
654 bits	(1688)	0.0()	Compositional matrix adjust.	320/518(62%)	411/518(79%)	5/518(0%)	+3	
Features	<b>S</b> :							
Query	42	NSRQO N+R	GSYKANSINTQDSRMRRHEVTII +YK S T + R RRHEVT+F	~			~	218

Sbjct	8	NNRMAAYKHGSKTTTELRQRRHEVTVELRKSRKDDQLLKRRNINEDDGPTSPLQENNAQS	67
Query	219	PVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQNTN PV L +EI+ + S + ++F +Q+ARKMLSRE+NPPID +IG G+VPIC+++L+ ++	398
Sbjct	68	PVTLKYEEIMQFIRSGEPTKEFAAVQAARKMLSREKNPPIDKIIGLGMVPICVKYLEASD	127
Query	399	NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD LQFEAAWALTNIASGTSDQT+ VIE NA+P F+ LL S S+ +AEQAVWALGNIAGD	578
Sbjct	128	RPALQFEAAWALTNIASGTSDQTKVVIEANAIPRFINLLSSPSVTVAEQAVWALGNIAGD	187
Query	579	GAAARDIVIHHNVIDGILPLINN-ETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv G+ ARD V+ + ++ I+ L+ N TP+SFLRNIVWLMSNLCRNKNP+PPF++++ ++PV	755
Sbjct	188	GSKARDTVLEYKSVEAIISLVRNANTPISFLRNIVWLMSNLCRNKNPAPPFNRIEPMIPV	247
Query	756	<pre>lsqlllsqDiQvLADACWALSYVTDDDNTKiQAVVDSDAVPRLVKLLQMDEPSIIVPALR LS LL +D QvL+DACWALSYVTDDD+ K+++VV + AVP+LV+LL + P+II PALR</pre>	935
Sbjct	248	LSALLDHEDAQVLSDACWALSYVTDDDSVKLESVVTAGAVPKLVRLLGSNNPAIITPALR	307
Query	936	SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ SVGN+VTG D QTD VIA+G LP L LL H+K+ IVKEAAWTVSNITAGNQ QIQ V++	1115
Sbjct	308	SVGNVVTGNDTQTDAVIAAGSLPLLAGLLHHSKNTIVKEAAWTVSNITAGNQAQIQHVLE	367
Query	1116	AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP +GIF L VL KGDFK+QKEAAWAVTNTTT G+ EQIV L+EK+ ILKP+ DLL+ KD	1295
Sbjct	368	SGIFTDLVEVLAKGDFKSQKEAAWAVTNTTTGGSTEQIVLLLEKFHILKPYCDLLEAKDS	427
Query	1296	RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT RT++VV +G++N+F +A +GG EN+C M EE+G LDKLE LQ HENE++Y KA +I+T	1475
Sbjct	428	RTVRVVLSGITNIFQIAANVGGLENMCTMFEEIGALDKLEQLQNHENEDIYGKALQLIET	487
Query	1476	YFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589 YF + +DEA E AP+E NGALEFN T P+ GG++F	
Sbjct	488	YFCD-EDEANPECAPKEANGALEFNPTTPONGGFSF 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	<b>3</b> :						
Query	42	~	GSYKANSINTQDSRMRRHEVTI			TSPLKELNG TSPL+E N	
Sbjct	8	N+R NNRL	+YK S + + R RRHEVT+1 AAYKHGSKSNTELRQRRHEVTVI				
Query	219	PVQL:	SVDEIVAAMNSEDQERQFLGMQ; D+I+ + S E++F +O-	SARKMLSRERNP +ARKMLSRE+NP			TN 398
Sbjct	68		KFDDIMQYIRSGQPEKEFAAVQ				
Query	399		QFEAAWALTNIASGTSDQTRCV OFEAAWALTNIASGTS+OT+ V				
Sbjct	128		ÕFEAAWALTNIASGTSEÕTKAV				
Query	579	GAAAI	RDIVIHHNVIDGILPLINN-ET RDIV+ HN +D I+ L+ N T	PLSFLRNIVWLM	SNLCRNKNPSP	PFDQVKRll	pv 755
Sbjct	188		RDIVLEHNSVDAIIALVTNGNT				
Query	756	lsql LS L	llsqDIQVLADACWALSYVTDDI L +D QVL+DACWALSYVTDDI				
Sbjct	248		LDHEDAQVLSDACWALSYVTDDI	DVEKLĖSVVASG	AVPKLVRLLGT	NNPAIITPA	LR 307
Query	936		IVTGTDQQTDVVIASGGLPRLGI IVTG D+OTD VIA+ LP L				
Sbjct	308		IVTGNDKÕTDAVIAANALPLLTI				
Query	1116	AGIF	QQLRTVLEKGDFKAQKEAAWAV' L VL GDFK+QKEAAWAV'	INTTTSGTPEQI	VDLIEKYKILK	PFIDLLDTK	DP 1295
Sbjct	368		NVLIDVLANGDFKSQKEAAWAV	INTTTGGSTEÕI	IQLVEKYPIMK	PYCDLLEAK	DT 427
Query	1296		VVQTGLSNLFALAEKLGGTENL VV +G++N+F A ++GG ENL	CLMVEEMGGLDK C + EE+G LDK			
Sbjct	428		VV +G++N+F A ++GG END VVLSGVANIFQFASQIGGVENL				
Query	1476	YFSNO YF +	GDDEAEQELAPQEVNGALEFNA' +D E AP+EVNGALEFN '				
Sbjct	488		AED-VNPECAPKEVNGALEFNP				

## 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	<b>S</b> :						
Query	42	NSRQ0 N+R	GSYKANSINTQDSRMRRHEVTIE SYK S T + R RRHEVT+E				
Sbjct	8	-,	ASYKNASKTTTELRQRRHEVTVE				
Query	219	PVQL: PV L	SVDEIVAAMNSEDQERQFLGMQS +EI+ + S ++F +Q+	SARKMLSRERNP +ARKMLSRE+NP			

Sbjct	68	PVTLKFEEIMQYVKSGVPNKEFAAVQAARKMLSREKNPPIDKIIGLGMVPICVKFLEAAD	127
Query	399	NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD LQFEAAWALTNIASGTSDQT+ VI+ +A+P F+ LL S S+ +AEQAVWALGNIAGD	578
Sbjct	128	RPALQFEAAWALTNIASGTSDQTKAVIDAHAIPRFIDLLSSPSVTVAEQAVWALGNIAGD	187
Query	579	GAAARDIVIHHNVIDGILPLINN-ETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv G+ ARD V+ +N ++ I+ L+ N TP+SFLRNIVWLMSNLCRNKNP+PPF++++ ++PV	755
Sbjct	188	GSKARDNVLDYNSVEAIISLVRNPNTPISFLRNIVWLMSNLCRNKNPAPPFNRIEPMIPV	247
Query	756	lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR LS LL +D QVL+DACWALSYVTDDD K+++VV + VP+LV+LL + P+II PALR	935
Sbjct	248	LSVLLDHEDAQVLSDACWALSYVTDDDAVKLESVVAAGTVPKLVRLLGTNNPAIITPALR	307
Query	936	SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ SVGNIVTG D QTD VIA+G LP L LL+H K+ IVKEAAWTVSNITAGNQ QIQ V+	1115
Sbjct	308	SVGNIVTGNDTQTDAVIAAGALPLLANLLRHTKNTIVKEAAWTVSNITAGNQAQIQQVLN	367
Query	1116	AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP G+F L VL +GDFK+QKEAAWAVTNTTT G+ EQI+ L+EKY I+KP+ DLL+ KD	1295
Sbjct	368	WGVFNVLIDVLARGDFKSQKEAAWAVTNTTTGGSTEQIIQLVEKYPIMKPYCDLLEAKDS	427
Query	1296	RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT RT++VV TG++N+F +A +GG ENLC + EE+GGLDKLE LQ H+NE++Y+KA +I+T	1475
Sbjct	428	RTVRVVLTGVTNIFQIASNIGGVENLCTLFEEIGGLDKLE LQ HTNETTITKA TITI 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
Feature	s:						
Query	33		SRQGSYKANSINTQDSRMRRHE	VTIELRKSKKED V+IELRK+++D			LN 209
Sbjct	9	A S ATSA	SR +K+++++D+RRR+E SRLAKFKYHN-KSEDARRRNE				
Query	210		VQLSVDEIVAAMNSEDQERQFL + +SVDEIV+ M +D Q	GMQSARKMLSRE O+ RKMLSRE		GIVPICIRF GIVP C+ F	
Sbjct	68		ILMSVDEIVSGMTCDDPHLQLQ				
Query	390	NTNN + N	SMLQFEAAWALTNIASGTSDQT LOFEAAWALTN+ASGTS+OT				
Sbjct	128		PALQFEAAWALTNVASGTSEQT				
Query	570		AAARDIVIHHNVIDGILPLINN A RD+V+ H + ++ LI	ETPLSFLRNIVW E+ LSF+RNIVW			749
Sbjct	188		PATROLVLQHECMPILISLIQP				_
Query	750	pvls P LS	${f qlllsqDIQVLADACWALSYVT} \ {f LL} \ {f D} \ {f VLAD+CWALSY+T}$				
Sbjct	248		SLLDFTDGDVLADSCWALSYLT				
Query	930		GNIVTGTDQQTDVVIASGGLPR GNIVTG D OTD +I +GGL +				
Sbjct	308		GNIVTGNDTÕTDAIINAGGLDK				
Query	1110	IQAG I AG	IFQQLRTVLEKGDFKAQKEAAW I L VLE GDFK+QKEAAW			LKPFIDLLD L PF +LLD	
Sbjct	368		IISPLIEVLEIGDFKSÕKEAAW				
Query	1290		IKVVQTGLSNLFALAEKLGGTE + VV GL+N+ A K+G E	NLCLMVEEMGGI N+ +MVEE+GGI			
Sbjct	427		VMVVLDGLTNILNAANKMGQIE				
Query	1470		SNGDDEAEQELAPQEVNGALEF S+GDDE OELAP+ + F	NATQPKAPEGGY A+ AP+GG+			
Sbjct	487		STGDDE QELAF SDGDDE-NQELAPEANDEQFNF				

PREDICTED: importin subunit alpha [Fopius arisanus]

Sequence ID: ref|XP\_011305770.1| Length: 520 Number of Matches: 1

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	<b>S</b> :						
Query	30	KADSI +A+ I	NSRQGSYKANSINTQDSRMRRHE NSR +K N+ T+D+R RR+E			NDEDLTSPL E L SP	KE 203
Sbjct	5		NSRLAKFK-NNFKTEDARRRRNE		~	~-	DH 63
Query	204		SPVQLSVDEIVAAMNSEDQERQF SP+ +S+DEIVA MNS D+ Q		RERNPPIDLMIORE++PPID+MI		
Sbjct	64		SPIGMSIDEIVAGMNSPDEVLÕI				_

Query	384	LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG L +N LQFEA+WALTN+ASGTS+QT V + A+P V LL+S + N+AEQAVWALG	563
Sbjct	122	LSYHHNPALQFEASWALTNVASGTSEQTMIVASNGAIPKLVELLKSPATNVAEQAVWALG	181
Query	564	NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKR NIAGDG +ARD V+	743
Sbjct	182	NIAGDG TARD VT THE LITTS TRNIVW TSNLCRNKNP P FT VK NIAGDGPSARDQVLEEQCMPLLLNLIKTDTSVSFTRNIVWTISNLCRNKNPPPSFEIVKL	241
Query	744	llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV LPVL++LL +D +LAD CWALSY+TD +N KIQAVVDS VP+LV LL E S++	923
Sbjct	242	ALPVLNRLLTGEDPDILADTCWALSYLTDGENFKIQAVVDSGVVPKLVALLASPEASVLT	301
Query	924	PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ PALR+VGNIVTG D QTD +I +GGLP L LL+H + NIVKEAAWT+SNITAGN +QIQ	1103
Sbjct	302	PALRAVGNIVIG D QID TI TGGLP L LLTH T NIVKEAAWITSNIIAGN TQIQ PALRAVGNIVTGNDTQTDAIINAGGLPNLKGLLEHKRVNIVKEAAWTISNITAGNHEQIQ	361
Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD	1283
Sbjct	362	VI AGI L VL GDFKAQKEAAWAVTN T+ G+ Q+V LI+ + +LKPF ++L ${ t HVINAGILPPLVHVLATGDFKAQKEAAWAVTNLTSGGSIPQLVQLIQ-HGVLKPFCNILQ}$	420
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA	1463
Sbjct	421	KD + I VV GL+N+ AEK+G E + LM+EE+ GLDKLE LQ HENE++Y+KA + AKDQKAIIVVLDGLTNILNAAEKMGQLEQVALMIEEVRGLDKLEDLQHHENEKIYQKAAS	480
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589	
Sbjct	481	+IDT+FS + E+ Q +AP V+G L+F++T AP+GG+ F 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()	Compositiona	al matrix adjust.	291/522(56%)	382/522(73%	) 8/522(1%)	+3
Features	s:							
Query	30				EVTIELRKSKKE			
Sbjct	5	+A+ [ EANH]			EV++ELRK++++ EVSVELRKARRD		I E L SP IEPEPLKSPI	
Query	204	~	~	~ ~	FLGMQSARKMLS	RERNPPIDLM RE++PPID+M		
Sbjct	64		SP+ +S+DEIV SPIGMSIDEIV		LQATQACRKMLS			
Query	384				QTRCVIEHNAVP OT V + A+P			
Sbjct	122				ÕTMIVASNGAIP			
Query	564	NIAG:		HNVIDGILPLI + +L LI	NNETPLSFLRNI	VWLMSNLCRN		
Sbjct	182				KTDTSVSFTRNI			
Query	744		lsqlllsqDIÇ L++LL D		VTDDDNTKIQAV +TD +N KIQAV			
Sbjct	242				LTDGENYKIÕAV			
Query	924	PALR	SVGNIVTGTDQ	OTDVVIASGGL	PRLGLLLQHNKS P L LL+H +	NIVKEAAWTV	SNITAGNOKO	QIQ 1103
Sbjct	302				PNĽKRĽĽEHKRV			
Query	1104	AVIQ. VI			AWAVTNTTTSGT AWAVTN T+ G+			
Sbjct	362				AWAVTNLTSGGS			
Query	1284				TENLCLMVEEMG E + +M+EE+G			
Sbjct	421				LEQVAMMIEEVG			
Query	1464			)ELAPQEVNGAL ) +AP+ V+G	EFNATQPKAPEG F+ T AP+G	GYTF 1589 G+ F		
Sbjct	481				NFHPTD-SAPQG			

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
Feature	s:						
Query	30		NSRQGSYKANSINTQDSRMRRHI				
Sbjct	5	+ + EGEH	+SR +K NS + R RR+1 SSRLAKFKFNS-KHDEVRRRRN1			+T PL 7VTEPLSP	
Query	210	~	VQLSVDEIVAAMNSEI + V +I++ MNS				
Sbjct	62	~-	PDMKSSVGLMDVTQIISNMNSS				
Query	369	ICIR C+	FLQNTNNSMLQFEAAWALTNIA; FL +N LOFEAAWALTN+A;				
Sbjct	122		FLSYNDNPPLQFEAAWALTNVA:				

Query	549	VWALGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPF	728
Sbjct	182	VWALGNIAGDG RD+V+ H+ + +L LI +TP+SF RN+VW +SNLCRNKNP PPF VWALGNIAGDGPVPRDLVLGHDALPLLLELIKPDTPVSFTRNLVWTLSNLCRNKNPPPPF	241
Query	729	DQVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDE VK LPVL++LL D VLADACWALSY++D +N KI+AVV+S +P+LV+LL E	908
Sbjct	242	QTVKAALPVLNRLLSYADNDVLADACWALSYLSDGENEKIEAVVNSGVIPKLVELLASAE	301
Query	909	PSIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGN +I+ PALR+VGNIVTG D QTD VI +GGL LG LL H + NI+KEAAW +SNI AGN	1088
Sbjct	302	VTILTPALRAVGNIVTGNDVÕTDAVITAGGLKHLGALLHHKRVNIIKEAAWAISNIAAGN	361
Query	1089	QKQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPF QIQ +I AG+	1268
Sbjct	362	HNÕIÕHIINAGLLPSLIHVLQKGDFKSÕKEAAWAITNFTSGGTVQÕLAQLIQ-LGILEPF	420
Query	1269	IDLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVY +L+ KD + I V+ GL+N+ A+K+G E + +M+EE+GGLDKLE LQQH+N+EVY	1448
Sbjct	421	CSMLEAKDWKIILVILDGLTNILNAADKIGEVERVAMMIEEVGGLDKLEALQQHDNDEVY	480
Query	1449	KKAYAIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589 +K A+IDT++S+G E + LAP LEF T+ AP+GG+ F	
Sbict	481	OKVMAMIDTFYSDGYTE-DNNLAPATEEEOLEFOPTE-AAPOGGFOF 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()	Composition	al matrix adjus	t. 283/525(54%	%) 373/525(71%	) 10/525(1%)	) +3
Features	s:							
Query	30					RKSKKEDOMFKRI		
Sbjct	5		+SRQ S+ SSRQNRLTSF			RK++K+DQ+ KRI RKARKDDQLLKRI		PL LPL 64
Query	198					RKMLSRERNPPII		
Sbjct	65					RK LSRER+PPII RKALSRERSPPII		
Query	378	RFLQ FL				INAVPHFVALLQS		
Sbjct	124					IGAVPKLVQLLG		
Query	558		AGDGAAARDI AGDG+ ARD+			SFLRNIVWLMSNI SFLRN+VW +SNI		~
Sbjct	184					SFLRNVVWTLSNI		
Query	735		lpvlsqllls LPV ++LL		ALSYVTDDDNI ALSY+TD N	TKIQAVVDSDAVI	PRLVKLLQMD: PRLV+LL	EPS 914
Sbjct	244					KIQAV+D+ VI KIQAVIDTGIVI		
Query	915					QHNKSNIVKEAZ L+H + NI+KEAZ		
Sbjct	304					LRHPRLNIMKEA		
Query	1095			RTVLEKGDFKA VL GDF++		TTTSGTPEQIVDI + G+ +O+	LIEKYKILKP: +++ +LKP:	
Sbjct	364					MSGGSVQQLAT:		
Query	1275		KDPRTIKVVQ KD + + VV			NVEEMGGLDKLE' N+EE GGLDKLE		
Sbjct	423					MIEECGGLDKLE		
Query	1455		IDTYFSNGDD ID+YFS D		NGALEFNATQE NG L+FN	PKAPEGGYTF :	1589	
Sbjct	483				NG L+FN NGQLDFNTD		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
Feature	s:					
Query	39	SNSRQGSYKANSINTQDSRMRRHEVT				=
Sbjct	8	+NSR +K ++R RR EV- ANSRISKFKFQG-KFDEARRRTEVS	-+ELRK+ K++Q SVELRKAHKDNQ			Q QK 64
Query	216	SPV-QLSVDEIVAAMNSEDQERQFLO	T		GIVPICIRFL GIVP+C+ FL	
Sbjct	65	SPVFNMSIDEIIAGMTSEDDQAMLQA				
Query	393	TNNSMLQFEAAWALTNIASGTSDQTF +N MLQFEA WALTN+ASGTS+QT-				
Sbjct	125	HHNPMLQFEACWALTNVASGTSEQT				
Query	573	GDGAAARDIVIHHNVIDGILPLINNE GDG AARD+V+ + ++ LI E	TPLSFLRNIVW T LSF+RNIVW		~	lp 752
Sbjct	185	GDGPAARDLVLKEGSLSLLIALITPE				
Query	753	vlsqlllsqDIQVLADACWALSYVTI	DDDNTKIQAVVD	SDAVPRLVKLL(	QMDEPSIIVP.	AL 932

Sbjct	245	+L++LL D VL DACWALSY+TD N $+IQ$ V $+DS$ VP $+LV+LL$ E $+++$ PAL LLNRLLSYPDKDVLGDACWALSYLTDGTNERIQTVLDSGVVPKLVELLGSSEVTVLTPAL	304
Query	933	RSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVI R+VGNIVTG D QTD +I++G L LG LL H + N+VKEAAWT+SNITAGN +QIQ +I	1112
Sbjct	305	RAVGNIVIG D QID TITTE L LG LL H T NTVKEAAWITSNIIAGN TQIQ TI RAVGNIVIGNDLQIDTIISAGALNYLGALLIHKRVNLVKEAAWIISNIIAGNDQQIQRII	364
Query	1113	QAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKD	1292
Sbjct	365	AG+ L VL GDFK+QKEAAWA+TN T+ GT Q+ L++ +L PF +LL++KD DAGLLPLLIQVLHMGDFKSQKEAAWAITNLTSGGTVPQLALLVQ-LGVLTPFCNLLESKD	423
Query	1293	PRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIID	1472
Sbjct	424	+ + VV GL+N+ AEK+G + + L++EE+GGLDKLE LQ HENE VY+KA +ID WKCVLVVLDGLNNILNAAEKMGEVDRVALVIEEIGGLDKLEALQTHENENVYQKAVHMID	483
Query	1473	TYFSNGDDEAEQELAP-QEVNGALEFNATQPKAPEGGYTF 1589	
Sbjct	484	T+FS+G EA+ LAP ++G LEF AT AP+GG+ F TFFSDGEADPNLAPTTNMDGQLEFQATT-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	s:						
Query	243		MNSEDQERQFLGMQSARKMLSRI +NS+D +RO LGM+ ARK+ I	ERNPPIDLMIGH E NPPIDLMIGH			
Sbjct	23		TNSTD TRO LGMT ARRT I INSKDPQRQLLGMELARKLACNI				
Query	423		TNIASGTSDOTRCVIEHNAVPHI TNIA+GTS OT+CVI+ NAVP				
Sbjct	83		TNIAAGTSGQTQCVIDENAVPLI				
Query	603		VIDGILPLINNETPLSFLRNIV VI GILPLIN PLS LR IV			pvlsqllls P+LS+LL+S	
Sbjct	143		VIGGILPLINKGMPLSLLRKIV				
Query	783		ADACWALSYVTDDDNTKIQAVVI + ACWAL VT DD K+QAV+I	OSDAVPRLVKLL O+ VPRLV LL		LRSVGNIVI LR VG IV	
Sbjct	202		SCACWALCSVTHDDKLQAVII				
Query	963		DVVIASGGLPRLGLLLQHNKSNI DVVIA+G L LG LL+H+ NI				
Sbjct	260		DVVIAAGVLQPLGQLLEHSDRNI				
Query	1143	VLEK	GDFKAQKEAAWAVTNTTTSGTPI + KA+K+AA AV+NTT SGT I			DPRTIKVVÇ DP TI VVÇ	
Sbjct	320		NNIKARKQAACAVSNTTISGTYI				
Query	1323		FALAEKLGGTENLCLMVEEMGGI F LA+ LG +++ LM E++GGI				EA 1502
Sbjct	380		FDLAKNLGDPKDIFLMFEQLGGI				
Query	1503	EQEL. EO +	APQEVNGALEFNATQPKAPEGGY +N +EFNATQP+ P+GGY				
Sbjct	440		INDGVEFNATQPRKPDGG				

PREDICTED: importin subunit alpha [Athalia rosae]

Sequence ID: ref|XP\_012257423.1| Length: 521 Number of Matches: 1

Score		Expect Method		Identities	Positives	Gaps	Frame
538 bits	(1387)	0.0() Composition	onal matrix adjust.	282/521(54%)	373/521(71%)	5/521(0%)	+3
Features	s:						
Query	30		NSINTQDSRMRRH	EVTIELRKSKKE E +ELRK +K+			
Sbjct	5		NASKPEDARRRN				
Query	207		VAAMNSEDQERQF + M+S+D+ Q				
Sbjct	64		IIGMSSKDETIÕL				
Query	387		.WALTNIASGTSDQ .WALTN+ASGTS+Q				
Sbjct	124		WALTNVASGTSEQ				
Query	567	IAGDGAAARDIVI IAGDG ARD+V+	HHNVIDGILPLIN + + +L LI	NETPLSFLRNIV +T ++ RNIV			
Sbjct	184		ANKALPLLLDLIK				
Query	747	lpvlsqlllsqDI LPVL++LL D	QVLADACWALSYV +LADACWALSY+				
Sbjct	244		DILADACWALSYL				_
Query	927		QQTDVVIASGGLP QTD +IA+GGL		IVKEAAWTVSN IVKEAAWT+SN		~

Sbjct	304	ALRAVGNIVTGTDVQTDAIIAAGGLRHLVGLLQHERLNIVKEAAWTISNITAGNVDQIQQ	363
Query	1107	VIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDT VI+AG+ L VL+ GDFK+OKEAAWAVTN T+ G+ +O+ L++ L P LLD	1286
Sbjct	364	$ ext{VI+AG+} \qquad  ext{L} \qquad  ext{VL+} \qquad  ext{GDFK+QKEAAWAVTN} \qquad  ext{T+} \qquad  ext{L} \qquad  ext{P} \qquad  ext{LLD} \  ext{VIEAGLLPPLLHVLQSGDFKSQKEAAWAVTNLTSGGSVQQLAQLVQ-LGALDPLCALLDA}$	422
Query	1287	KDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAI	1466
Sbjct	423	KD +T+ VV GL+N+ A+K+G E + +M+EE+GGLDKLE LQ H NE+VY+KA A+ KDWKTVLVVLDGLTNILTAAQKMGEVERVAVMIEEVGGLDKLENLQHHVNEQVYQKAMAM	482
Query	1467	IDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589	
Sbjct	483	$ ext{I+TYFS+G+ E E +AP +G LEF T PEGG+ F} \\  ext{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 F	-rame_
535 bits	(1379)	1e-179()	Compositional matrix adjust.	285/521(55%)	385/521(73%)	6/521(1%) +	-3
Features	s:						
Query	30		ISRQGSYKANSINTQDSRMRRHI -SR+ ++K N+ +++R RR I	EVTIELRKSKKE E+++ELRK++K+		DEDLTSPLKE ++ +P+ E	
Sbjct	5		ISRKANFKFNN-KHEEARRRRSI				
Query	207		PVQLSVDEIVAAMNSEDQERQFI P+ +S++EIV M S DQ Q		ERNPPIDLMIG E+NPPID+MI	HGIVPICIRF GIVP C+ F	
Sbjct	64		PISVSIEEIVNGMKSSDÕTIÕL				
Query	387		ISMLQFEAAWALTNIASGTSDQ I+ LQFEAAWALTN+ASGTS+Q				
Sbjct	123		IAALQFEAAWALTNVASGTSEQ				
Query	567		GAAARDIVIHHNVIDGILPLIN G AARD+V+ ++ + +L LI	NETPLSFLRNIV +T ++F RNIV			746
Sbjct	183		PAARDLVLGYDAMPLLLELIKI				'A 242
Query	747		qlllsqDIQVLADACWALSYV -+LL + D +LADACWALSY+				
Sbjct	243		IRLLSNNDKDILADACWALSYL				
Query	927		GNIVTGTDQQTDVVIASGGLPI GNIVTG D OTD +I++GGL				
Sbjct	303		GNIVTGNDMQTDAIISAGGLQI				
Query	1107	VIQAG VI AG	GIFQQLRTVLEKGDFKAQKEAAV G+ L VLE GDFK+OKEAAV			ILKPFIDLLD +L PF +LL+	
Sbjct	363		SLLPLLIHVLESGDFKSQKEAAV				
Query	1287	KDPRT KD +T	TIKVVQTGLSNLFALAEKLGGTI TI VV GL+N+F AEK+G I	ENLCLMVEEMGG E + +M+EE+GG			
Sbjct	422		TIIVVLDGLTNIFNAAEKMGEII				
Query	1467	IDTYF ID +F	SNGDDEAEQELAPQEVNGALEI S + E P +G LEI				
Sbjct	482		SEPEAEESTLTTPTAADGQLEI				

PREDICTED: importin subunit alpha [Polistes canadensis]

Sequence ID: ref|XP\_014609001.1| Length: 531 Number of Matches: 1

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	s:						
Query	36	DSNSR D NSR	QGSYKANSINTQDSRMRRHEVT ++K NS +++R RR E++				
Sbjct	14		IANFKFNS-KHEEARRRRSEIS	IELRK+KKE+Q IELRKAKKENQ			N -N 71
Query	210	GQSPV P	QLSVDEIVAAMNSEDQERQFLG S+++IVA M S D+ O	MQSARKMLSRE: +Q+ RKMLSRE		GIVPICIRF GIVP CIRF	
Sbjct	72	_	SSSIEDIVANMLSSDETIQLQA				
Query	390	NTNNS: +N	MLQFEAAWALTNIASGTSDQTR LQFEA+WALTN+ASGTS+QT				
Sbjct	132		ALQFEASWALTNVASGTSEQTY				
Query	570	AGDGA AGDG	AARDIVIHHNVIDGILPLINNE RD+V+ + ++ +L LI +	TPLSFLRNIVW			11 749
Sbjct	192		VTRDLVLANGLLPVLLSLIKPD				AL 251
Query	750		lllsqDIQVLADACWALSYVTD LL + D +LADACWALSY+TD				
Sbjct	252		LLSNTDKDILADACWALSYLTD				
Query	930		NIVTGTDQQTDVVIASGGLPRL NIVTG D QTD +I++GGL L				
Sbjct	312		NIVIG D QID IIIIGGL L NIVTGNDVQTDAIISAGGLNHL				

Query	1110	IQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTK 1 I A + + L VL GD+K+QKEAAWA+TN T+ + + I LI+ IL PF +LLD+K	1289
Sbjct	372		130
	312	IMANVERTEQVERVODIRDQREAMATINETOCOVRETATETQT-OTEOTICNEEDOR 4	:50
Query	1290	DPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAII 1	1469
2 1		D +T+ VV GLSN+ + K+G E + LM+EE GGLDK+E LÕÕ+ENE+VY++A AII	
Sbjct	431		190
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()	Composition	al matrix adjust.	282/519(54%)	372/519(71%	) 10/519(1%)	+3
Features	s:							
Query	42	NSRQC NSR		QDSRMRRHEVTII ++R +R EVTII				GQ 215
Sbjct	9			DEARRKRTEVTI				-K 64
Query	216		-LSVDEIVAA +S+DEI+	MNSEDQERQFLG	MQSARKMLSREF Q+ RKMLS+E+		GIVPICIRFL GI+P+CI+FL	
Sbjct	65			MQSTDELVÕLEA'				
Query	393			TNIASGTSDQTRO		/ALLQSKSMNL / LL+S MN+		
Sbjct	125			IN ASGISTOI INVASGISEÕIL				
Query	573	GDGAA GDG		VIDGILPLINNE' + I+ L+N E'	TPLSFLRNIVWI TP+SF+RNIVW			
Sbjct	185			ALPHIILLLNPE'				
Query	753	vlsql +L++I		ADACWALSYVTD ADACWALSY+TD				
Sbjct	245			ADACWALSYLTD				
Query	933			DVVIASGGLPRLO D +IA+GGL L				
Sbjct	305			DSIIAAGGLNYL				
Query	1113	QAGIF AG+		GDFKAQKEAAWA` GDFK+QKEAAWA			LKPFIDLLDT L PF +LL++	
Sbjct	365			GDFKSQKEAAWA				
Query	1293		(VVQTGLSNL: VV GL ++	FALAEKLGGTEN: +AEK+ +	LCLMVEEMGGLI + LM+EE+GGLI			
Sbjct	424			LNVAEKMEEVDK				
Query	1473			APQEVNGALEFN + E G LEF				
Sbjct	484			STNE-EGQLEFQ				

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	s:						
Query	30		SRQGSYKANSINTQDSRMRRHE SR+ ++K N+ +++R RR E	VTIELRKSKKE			
Sbjct	5		SRKANFKFNN-KHEEARRRRSE				
Query	207		VQLSVDEIVAAMNSEDQERQFL + +S++EIV M S DQ Q		ERNPPIDLMIGI E+NPPID+MI	HGIVPICIR	
Sbjct	64		ISVSIEEIVNGMKSSDÕTIÕLQ				
Query	387		SMLQFEAAWALTNIASGTSDQT + LQFEAAWALTN+ASGTS+QT				
Sbjct	123		AALQFEAAWALTNVASGTSEQT				
Query	567		AAARDIVIHHNVIDGILPLINN AARD+V+ ++ + +L LI	ETPLSFLRNIV +T ++F RNIV			Rl 746
Sbjct	183		PAARDLVLGYDAMPLLLELIKP				TA 242
Query	747		qlllsqDIQVLADACWALSYVT +LL + D +LADACWALSY+T				
Sbjct	243		RLLSNNDKDILADACWALSYLT				
Query	927		GNIVTGTDQQTDVVIASGGLPR GNIVTG D OTD +I++GGL				
Sbjct	303		GNIVTGNDMQTDAIISAGGLQH				
Query	1107	VIQAG VI AG	IFQQLRTVLEKGDFKAQKEAAW + L VLE GDFK+OKEAAW		~	ILKPFIDLL: +L PF +LL:	
Sbjct	363		LLPLLIHVLESGDFKSQKEAAW				
Query	1287	KDPRT	IKVVQTGLSNLFALAEKLGGTE	NLCLMVEEMGG	LDKLETLQQHEI	NEEVYKKAY.	AI 1466

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 F	rame
533 bits	(1373)	1e-178()	Compositional matrix adjust.	281/520(54%)	372/520(719	%) 6/520(1%) +	3
Features	s:						
Query	36		QGSYKANSINTQDSRMRRHEVI				
Sbjct	14	+ NSR ERNSR	t ++K NS +++R RR E++ LIANFKFNS-KHEEARRRSEIS	-+ELRK+KKE+Q SVELRKAKKENQ		+E+ S L E AEEEEASVLTEN	
Query	210	GQSPV O P	QLSVDEIVAAMNSEDQERQFLO S+++I+A M S D O	MOSARKMLSRE +O+ RKMLSRE		HGIVPICIRFL GIVP+CI FL	
Sbjct	73		SSSIEDIIANMLSFDVTIQLQA				
Query	390	NTNNS +N	MLQFEAAWALTNIASGTSDQTF LOFEA+WALTN+ASGTS+OT				
Sbjct	132		ALQFEASWALTNVASGISTQI				
Query	570	AGDGA AGDG	AARDIVIHHNVIDGILPLINNE RD+V+ + ++ +L LI +	TPLSFLRNIVW T ++F RNIVW			1 749 L
Sbjct	192		VTRDLVLANGLLPVLLSLIKPI				
Query	750	pvlsq PVL++	lllsqDIQVLADACWALSYVTI LL D +LADACWALSY+TI				
Sbjct	252		LLSHTDKDILADACWALSYLTI				
Query	930		NIVTGTDQQTDVVIASGGLPRI				
Sbjct	312		NIVIG D QID +1++GGL I NIVTGNDVQTDAIISAGGLNHI				
Query	1110	IQAGI I A +	FQQLRTVLEKGDFKAQKEAAWA + L VL GD+K+QKEAAWA			XILKPFIDLLDT +L PF +LLD+	
Sbjct	372		LRPLCQVLGGGDYKSQKEAAWA				
Query	1290	DPRTI D + +	KVVQTGLSNLFALAEKLGGTEN VV GLSN+ + K+G E+			ENEEVYKKAYAI ENE+VY++A A+	
Sbjct	431		LVVLDGLSNILEASAKMGEIE				
Query	1470	DTYFS DTYFS	NGDDEAEQELAPQEVNGALEFN DE A L+F				
Sbjct	491		ENDQEFNAIDAKVSEGTELQF1		_		

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	3:						
Query	24		SN-SRQGSYKANSINTQDSRMF				
Sbjct	1		N SR +K + ++R F MNASRISKFKFQG-KSDEARRF	R EV++ELRK+ RAEVSVELRKA			PLS 58
Query	201		SPVQLSVDEIVAAMNSEDQERÇ SPV +++DE++ M S+++ +		SRERNPPIDLM S ++NPPID M		
Sbjct	59		SPVNMTIDEVLCGMQSDNEMVF				
Query	381		NNSMLQFEAAWALTNIASGTSI N++MLQFE+ WALTN+ASGTS+				
Sbjct	119		NSTMLQFESCWALTNVASGTSE				
Query	561	GNIAG GNIAG	DGAAARDIVIHHNVIDGILPLI DG ARD+V+ +I+ ++ L+		IVWLMSNLCRN IVW +SNLCRN		
Sbjct	179		DGPGARDLVLKEGIINLLVSLV				
Query	741		lsqlllsqDIQVLADACWALSY L++LL D ++L+D CWALSY				
Sbjct	239		LNRLLNYNDKEILSDTCWALSY				_
Query	921		SVGNIVTGTDQQTDVVIASGGI +VGNIVTG+D OTD VIA G I				
Sbjct	299		AVGNIVTGSDIQTDTVIAHGAL				
Query	1101	QAVIQ O VI	AGIFQQLRTVLEKGDFKAQKEA A I L V+ +GDFK++KEA				)LL 1280 )LL
Sbjct	359		ANIIPPLINVMHQGDFKSKKEA				
Query	1281		RTIKVVQTGLSNLFALAEKLGG R I +V GL+ + AEK+G	TENLCLMVEEM T+ + LM+EE+			
Sbjct	418		RCISIVLDGLNYILTAAEKMGE				
Query	1461	AIIDT	YFSNGDDEAEQELAPQ-EVNGA	LEFNATQPKAP	EGGYTF 158	9	

+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) kange 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	<b>S</b> :						
Query	45	~	YKANSINTQDSRMRRHEVTIEI +K + +++R RR+ +++EI				SP 221 SP
Sbjct	10		FKFHG-KHEEARRRNAMSVEI				
Query	222		DEIVAAMNSEDQERQFLGMQSA +EIV +N+ D+ OFL O+	ARKMLSRERNPP RK+LSRE+NPP			NN 401 +N
Sbjct	69		EEIVDGINASDESMQFLATQTO				
Query	402		'EAAWALTNIASGTSDQTRCVIE 'EAAW LTNIASGTS+QT+ VI+				
Sbjct	128		EAAWVLTNIASGTSEQTQNVIK				
Query	582		) 	SFLRNIVWLMSN -FLRNIVW +SN			
Sbjct	188		LVLGHDAMLLLLDLIKPDIPVI				•
Query	762	qllls +LL	qDIQVLADACWALSYVTDDDNT D VLAD CWALSY+TD N			PSIIVPALR +I+ PALR	
Sbjct	248		DDDDVLADTCWALSYLTDGSND				
Query	942		GTDQQTDVVIASGGLPRLGLLI G D OTD +IA+GGLP LG LI				
Sbjct	308		GDDAQTDTIIAAGGLPHLGALI				
Query	1122		RTVLEKGDFKAQKEAAWAVTNT VL+ GD+KAQKEAAWAVTN			IDLLDTKDP +LLD KD	RT 1301
Sbjct	368	LLPSL	VEVLQFGDYKAQKEAAWAVTNI	TSGGTIQÕLIE	LVNA-GVLQPF		
Query	1302	IKVVQ I VV	TGLSNLFALAEKLGGTENLCLM G++N+ A+K+G + + +M	NVEEMGGLDKLE N+EE GGLDKLE			
Sbjct	427		DGITNILHAADKMGQMDQVAIM				
Query	1482	SNGDD S +	EAEQELAPQEVNGALEFNATQ E + +G +EFN +	1559			
Sbjct	487		ETLTSEVKENADGQVEFNVKE	512			

PREDICTED: importin subunit alpha [Harpegnathos saltator]

Sequence ID: ref|XP\_011146718.1| Length: 517 Number of Matches: 1

Score		Expect	Method		Identities	Positives	Gaps	Frame
529 bits	(1363)	2e-177()	Compositiona	al matrix adjust.	281/507(55%)	364/507(71%)	5/507(0%)	+3
Features	<b>3</b> :							
Query	39	SNSRQ SN R	GSYKANSINT	QDSRMRRHEVTI	ELRKSKKEDOM ELRK+KK++Q+		TSPLKELNG L	
Sbjct	8			DEARRRNIVSI			_	S SIS 65
Query	219			EDQERQFLGMQS D+ Q Q+			PICIRFLQN P C+ L	TN 398
Sbjct	66	PNFSS	IDDIVAGMNS	PDETVQLQATQT	CRKLLSREKHP	PIT MI GIVE PIETMINCGIVE		
Query	399			ASGTSDQTRCVI ASGT++QT+ VI				
Sbjct	126			ASGTTEQTOVVI ASGTTEQTQVVI				
Query	579		DIVIHHNVID	GILPLINNETPL +L LI +T +	SFLRNIVWLMS: SF+RNIVW +S			ovl 758
Sbjct	186			LLLDLIKPDTSV				
Query	759	sqlll ++LL		CWALSYVTDDDN CWALSY+TD N			EPSIIVPAL E +++ PAL	
Sbjct	246			CWALSYLTDGSN				
Query	939			IASGGLPRLGLL I +GGL LG L				
Sbjct	306			I FGGL LG L IIAGGLTHLGNL				
Query	1119	GIFQQ GI	LRTVLEKGDF	KAQKEAAWAVTN KAQKEAAWAVTN	TTTSGTPEQIV	DLIEKYKILKP:	FIDLLDTKD DLL TKD	PR 1298
Sbjct	366			KAQKEAAWAVIN KAQKEAAWAVTN				
Query	1299	TIKVV TI V+		AEKLGGTENLCL AEKLG E + +				
Sbjct	425			AEKLG E + + AEKLGQVEQIAI				
Query	1479		DEAEQELAPQ E E ELAP	EVNGALEFNATQ +G LEF A++				

Sbjct 485 FS-GDGEQE-ELAPAANDGQLEFKASE 509

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	<b>S</b> :						
Query	39	SNSRQ ++ R	GSYKANSINTQDSRMRRHEVTI +K N+ +++R RR+ +++			TSPLKELNG L N	~
Sbjct	14		IAEFKFNN-RHEEARRRNALSV				S VS 72
Query	219		SVDEIVAAMNSEDQERQFLGMQ S+DEIV +NS ++ Q + Q			VPICIRFLQ VP CI L	NT 395
Sbjct	73		SIDEIVDGINSSNETTÕLIATÕ				CD 132
Query	396		QFEAAWALTNIASGTSDQTRCV QFEAAW LTNIASGTS+QT+ V				
Sbjct	133		QFEAAWVLTNIASGTSEQTQSV				
Query	576		RDIVIHHNVIDGILPLINNETE RD ++ H+ + +L LI +	PLSFLRNIVWLM ++F+RNIVW +			pv 755 PV
Sbjct	193		RDFILRHDALSLLLDLIKPDVS				
Query	756		lsqDIQVLADACWALSYVTDDI S DI VLAD CWALSY+TD			DEPSIIVPA E +++ PA	
Sbjct	253		NSTDIDVLADTCWALSYLTDGS				
Query	936		VTGTDQQTDVVIASGGLPRLGI VTG D OTD VI++GGLP LG				~
Sbjct	313		VTGDDLÕTDAVISAGGLPHLGA				
Query	1116	AGIFQ A +	QLRTVLEKGDFKAQKEAAWAV1 L VL+ GD+KAQKEAAWA+1			PFIDLLDTK PF +LL+TK	
Sbjct	373		PLINVLQFGDYKAQKEAAWAII				
Query	1296	RTIKV I V	VQTGLSNLFALAEKLGGTENLO V GL+N+ A+K+G + L	CLMVEEMGGLDK: +M+EE+GGLDK			
Sbjct	432		VLDGLTNILHAAQKMGEVDRLA				
Query	1476		DDEAEQELAPQEVNGALEFNAT D E ++ + ++G LEFN T		1589		
Sbjct	492		DVEEAILISKEHIDGHLEFNVI		528		

PREDICTED: importin subunit alpha-1 [Trichogramma pretiosum]
Sequence ID: ref|XP\_014230579.1| Length: 517 Number of Matches: 1

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	s:						
Query	39		GSYKANSINTQDSRMRRHEVTI				NG 212
Sbjct	7	+NSR NNSRL	+K + ++R RR E+++ SKFKFQG-KSDEARRRTEISV			L+ P E PLSPPPGE-	-K 63
Query	213		LSVDEIVAAMNSEDQERQFLGM +S+DEI+A M S D+ +	OSARKMLSRER O+ RKMLSRER		IVPICIRFI +VP+CI FI	
Sbjct	64		MSIDEITA M S DT MSIDEITAGMTSGDEVTKLQAT				
Query	393		LQFEAAWALTNIASGTSDQTRO LQFEA WALTN+ASGTS+QT+				
Sbjct	124	HDSPL	LÕFEACWALTNVASGTSEÕTQV	VVVKHGAIPKLV	ALLKSSAINVA	EQAVWALGN EQAVWALGN	IA 183
Query	573	GDGAA GDG	ARDIVIHHNVIDGILPLINNET RD+V++ + ++ L+ ET	PLSFLRNIVWL			
Sbjct	184		PRDLVLNEGALTMLIQLLTPET				
Query	753	vlsql +L+++	llsqDIQVLADACWALSYVTDI L D VL DACW LSY+TD			MDEPSIIVP E +++ P	
Sbjct	244		LTYNDKDVLGDACWTLSYLTDG				
Query	933		IVTGTDQQTDVVIASGGLPRLG	GLLLQHNKSNIV LL+H + NIV			
Sbjct	304		IVTGNDSÕTDAIISAGALRYFI				
Query	1113	QAGIF AG+	QQLRTVLEKGDFKAQKEAAWAV L VL+ GDFK+QKEAAWA+			KPFIDLLDT PF +LLD	
Sbjct	364		PPLIEVLQTGDFKSQKEAAWAI				
Query	1293	PRTIK + +	VVQTGLSNLFALAEKLGGTENI V+ GL+N+ A K+G EN+	CLMVEEMGGLD + +++EE+GGLD			
Sbjct	423		VILDGLTNILNTAMKMGELENI				
Query	1473	TYFSN ++FS	GDDEAEQELAPQEVNGALEFNA + E +P NG L+F A				
Sbjct	483		-EKEEPDMPSPSTENGQLQFQF				

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	<b>S</b> :						
Query	30		SRQGSYKANSINTQDSRMRRHI +R+ ++K N +++R +R+	EVTIELRKSKKE E++IELRK++K+		DEDLTSPLKI ++L SP++	
Sbjct	5		NRKANFKYN-YKQEEARRKRN				
Query	207	NGQSP N SP	VQLSVDEIVAAMNSEDQERQFI + S++EIV M S D+ O		ERNPPIDLMIG E+NPPID MI	HGIVPICIR	
Sbjct	64		ISTSIEEIVNGMQSSDETIQL				
Query	387		SMLQFEAAWALTNIASGTSDQ' +LOFEAAWALTN+ASGTS+Q'				
Sbjct	123		DLLQFEAAWALTNVASGTSEQ				
Query	567	IAGDG IAGDG	AAARDIVIHHNVIDGILPLIN ARD+V+ H + +L LI	NETPLSFLRNIV +T ++F RNIV			Rl 746
Sbjct	183		PVARDLVLGHAAMPILLELIK				TA 242
Query	747		qlllsqDIQVLADACWALSYV' +LL + D +LADACWALSY+'				
Sbjct	243		RLLSNSDKDILADACWALSYL				
Query	927		GNIVTGTDQQTDVVIASGGLPI GNIVTG D OTD +I++GGL				
Sbjct	303		GNIVTGNDTQTDAIISAGGLQI				
Query	1107	VIQAG VI AG	IFQQLRTVLEKGDFKAQKEAAI + L +LE GDFK+QKEAAI			ILKPFIDLL: +L PF +LL:	
Sbjct	363		LIPPLIHILESGDFKSQKEAA				
Query	1287		IKVVQTGLSNLFALAEKLGGT + VV GL+N+ AEK+G		LDKLETLQQHE LDKLE LQ HE		
Sbjct	422		VVVVLDGLTNILNAAEKMGEV				
Query	1467	IDTYF ID +F	SNGDDEAEQELAPQEVNGALE				
Sbjct	482		SEADAE-ESTLTPTAGDAQLE				

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 F	rame
524 bits	(1350)	2e-175()	Compositional matrix adjust	. 282/521(54%)	378/521(72%)	7/521(1%) +	-3
Features	s:						
Query	30		JSRQGSYKANSINTQDSRMRRH -SR+ ++K N +++R RR+	EVTIELRKSKKE E+++ELRK++K+		DEDLTSPLKE ++ S + E	
Sbjct	5		ISRKANFKFN-YKHEEARRRRN				
Query	207		PVQLSVDEIVAAMNSEDQERQF + S+DEIV M S D+ +		ERNPPIDLMIG E++PPID MI	HGIVPICIRF GIVP+C+ F	
Sbjct	63		SLLSSIDEIVTGMKSLDETIRL				
Query	387		ISMLQFEAAWALTNIASGTSDQ I+ LOFEAAWALTN+ASGTS+O				
Sbjct	122		TALQFEAAWALTNVASGTSEQ				
Query	567		GAAARDIVIHHNVIDGILPLIN GA ARD+V+ + + +L LI	NETPLSFLRNIV +T ++F RNIV			1 746
Sbjct	182		SAMARDLVLGTDAMPLLLELIK				'A 241
Query	747	lpvls LPVL+	sqlllsqDIQVLADACWALSYV -+LL + D +LADACWALSY+	TDDDNTKIQAVV TD N KIÕAVV	DSDAVPRLVKLD +P+LV+L	LQMDEPSIIV L E +++	
Sbjct	242		IRLLSNSDKDILADACWALSYL				P 301
Query	927		GNIVTGTDQQTDVVIASGGLP GNIVTG D QTD +I +GGL				
Sbjct	302	ALRSV	GNIVTGNDAÕTDAIIQAGGLQ	YLGLLLÕHHRLN	IVKEAAWTISN	ITAGNMEÕIÕ	E 361
Query	1107	VIQAG VI A	GIFQQLRTVLEKGDFKAQKEAA + L VLE GDFK+QKEAA			ILKPFIDLLD +L PF +LL+	
Sbjct	362		LLPPLIHVLECGDFKSÕKEAA				
Query	1287	KDPRT KD +T	TIKVVQTGLSNLFALAEKLGGT TI VV GLSN+ + AEK+G				
Sbjct	421		TIVVLDGLSNICSAAEKMGEV				
Query	1467	IDTYF IDT+F	SNGDDEAEQELAPQEVNGALE S + + P +G LE		YTF 1589 + F		
Sbjct	481		SEPEAQESTLATPTIADGQLE				

PREDICTED: importin subunit alpha [Bombus terrestris]

Sequence ID: ref|XP\_003399525.1| Length: 519 Number of Matches: 1

#### ▶ See 1 more title(s) Range 1: 5 to 519

Score		Expect	Method	Identities	Positives	Gaps I	Frame
524 bits	(1349)	4e-175()	Compositional matrix adjust.	282/521(54%)	380/521(72%)	7/521(1%) +	-3
Features	<b>S</b> :						
Query	30		SRQGSYKANSINTQDSRMRRHE SR+ ++K N +++R RR+E	EVTIELRKSKKE E+++ELRK++K+			_
Sbjct	5		SRKANFKFN-YKHEEARRRRNE				
Query	207	NGQSP	VQLSVDEIVAAMNSEDQERQFI + S+DEIV M S D+ +		ERNPPIDLMIG E++PPID MI	HGIVPICIRE GIVP+C+ E	
Sbjct	63	-SDHL	LLSSIDEIVNGMKSLDETIRLÇ				
Query	387		SMLQFEAAWALTNIASGTSDQ7 + LQFEAAWALTN+ASGT++Q7				
Sbjct	122		NALQFEAAWALTNVASGTTEQT				
Query	567		AAARDIVIHHNVIDGILPLINN A ARD+V+ + + +L LI	NETPLSFLRNIV +T ++F RNIV			746
Sbjct	182		AMARDLVLGTDAMPLLLELIKE				'A 241
Query	747		qlllsqDIQVLADACWALSYVT				
Sbjct	242		RLLSNSDKDILADACWALSYLT				
Query	927		GNIVTGTDQQTDVVIASGGLPF GNIVTG D OTDV+I +GGL				
Sbjct	302		GNIVTGNDAQTDVIIQAGGLQY				
Query	1107	VIQAG VI A	GIFQQLRTVLEKGDFKAQKEAAV + L VLE GDFK+QKEAAV			ILKPFIDLLD +L PF +LL+	
Sbjct	362		LLPPLIHVLECGDFKSQKEAAV				
Query	1287		'IKVVQTGLSNLFALAEKLGGTE 'I VV GLSN+ + AEK+G +	ENLCLMVEEMGG + + +M+EE+GG			
Sbjct	421		TIVVLDGLSNICSAAEKMGEVI				
Query	1467	IDTYF IDT+F	SNGDDEAEQELAPQEVNGALEFS + + P +G LEF				
Sbjct	481		SEPEAQESTLATPAVADGQLE				

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 I	Frame
523 bits	(1348)	4e-175()	Compositional matrix adjust.	265/517(51%)	359/517(69%)	3/517(0%) +	-3
Features	s:						
Query	42		SYKANSINTQDSRMRRHEVTIE ++K S ++ + R RR+EV++E				
Sbjct	6		AFKNKSKDSSELRRRRNEVSVE				
Query	219		VDEIVAAMNSEDQERQFLGMQS + +I A++S D OF +O+	SARKMLSRERNP -AR+MLSRER P			
Sbjct	65		IPDICKAISSSDSSTÕFNAVÕT				
Query	399		FEAAWALTNIASGTSDQTRCVI FEAAWALTNIASGT +OT+ V+			AVWALGNIAG AVWALGNIAG	
Sbjct	125		FEAAWALTNIASGTPEQTKAVV				
Query	579		DIVIHHNVIDGILPLINNETPI D+V H ++ +L L TP+	SFLRNIVWLMS FLRN+ W +S		FDQVKRllpv + V +LPV	
Sbjct	185		DVVTRHGILQPLLELYQPTTPV				
Query	759	sqlll L+	sqDIQVLADACWALSYVTDDDN D +++ADACWALSY+TD N				
Sbjct	245		HCDKEIVADACWALSYLTDGSN				
Query	939		TGTDQQTDVVIASGGLPRLGLI TGTD+QT VI S LP I	LQHNKSNIVKE LOH K NI KE			
Sbjct	305		TGTDEÕTQSVIDSQSLPLFVAL				
Query	1119	~ ~	LRTVLEKGDFKAQKEAAWAVTN L VLEKGD+K+OKEA WAVTN			FIDLLDTKDP DLL+ K+	
Sbjct	365		LVGVLEKGDYKSÕKEACWAVTN				
Query	1299	TIKVV T+V+	QTGLSNLFALAEKLGGTENLCI N+ + AEKL E +CI	MVEEMGGLDKL M+EE GGLDK+			
Sbjct	424		LDAFKNILSAAEKLEQLETVCI				
Query	1479		DEAEQELAPQEVNGALEFNATC +E + +G EF+ C	PKAPEGGYTF AP+GG+ F	1589		
Sbjct	484		EEDVKVAPSTNESGTYEFSGQÇ		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) 6e-175() Compositional matrix adjust. 284/510(56%) 374/510(73%) 7/510(1%) +3							
Feature	s:						
Query	36	DSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKELN D +R+ S+K N ++R RR+E ++ELRK++K++Q+FKRRN I E TS + N	209				
Sbjct	6	DDCARKSSFKFN-YKHDEARRRNEASVELRKARKDEQLFKRRNLSIGKEQQTSTDEN	62				
Query	210	GQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQ S + S+++IV M S D+ Q Q+ RKMLSRE+NPPID MI GIVP C+ FL	389				
Sbjct	63	SHSRLSTSINDIVNDMKSSDETIQLQATQACRKMLSREKNPPIDNMIKQGIVPRCVEFLD	122				
Query	390	NTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNI +N LQFEAAWALTN+ASGT++QT+ V++H A+P VALL+S S N+AEQAVWALGNI	569				
Sbjct	123	YNHNPALQFEAAWALTNVASGTTEQTQFVVKHGAIPKLVALLKSASPNVAEQAVWALGNI	182				
Query	570	AGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRll AGDG ARD+V+ H+ + +L LI +T ++F RNIVW +SNLCRNKNP PPF+ V+ L	749				
Sbjct	183	AGDGPMARDLVLGHDTMPLLLELIKPDTSVTFTRNIVWTLSNLCRNKNPPPPFEIVRTAL	242				
Query	750	<pre>pvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPA PVL++LL + D +LADACWALSY+TD N KIQAVVDS +P+LV+LL + E +++ PA</pre>	929				
Sbjct	243	PVLNRLLSNTDKDILADACWALSYLTDGSNDKIQAVVDSGIIPKLVELLALPEVTVLTPA	302				
Query	930	LRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAV LR+VGNIVTG D QTD +IA+GGL LGLLLQH++ NIVKEAAWT+SNITAGN +QIQ V	1109				
Sbjct	303	LRAVGNIVTGNDSÕTDAIIAAGGLQHLGLLLÕHHRINIVKEAAWTISNITAGNMEÕIÕHV	362				
Query	1110	IQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTK I AG+ L VL+ GDFK+QKEAAWAVTN T+ G+ +O+ L++ +L PF LL+ K	1289				
Sbjct	363	INAGLLPPLIHVLQCGDFKSQKEAAWAVTNLTSGGSVQQLAQLVQ-LGVLAPFCKLLEAK	421				
Query	1290	DPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAII + +T+ VV GL+N+ AEK+G E + LM+EE+GG+DKLE LQ HE E+VY+KA A+I	1469				
Sbjct	422	EWKTVLVVLDGLTNILNAAEKMGEVERVALMIEEVGGIDKLEDLÕHHEVEQVYQKAIAMI	481				

uncharacterized protein Dwil\_GK23224 [Drosophila willistoni]

Sequence ID: ref|XP\_002074732.1| Length: 491 Number of Matches: 1

DTYFSNGDDEAEQELAPQEVNGALEFNATO 1559 DT+FS+GD E E L P +G LEF + DTFFSDGDVE-EAVLPPTATDGQLEFKTAE 510

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

1470

482

Query

Sbjct

Score		Expect	Method		Identities	Positives	Gaps	Frame
519 bits(	(1337)	9e-174()	Compositiona	al matrix adjust.	271/471(58%)	349/471(74%)	9/471(1%)	+3
Features	<b>3</b> :							
Query	78	NTQDS ++ D		IELRKSKKEDQM ++LR+S+ +	IFKRRNINDEDL -++ + D D		PVQLSVDEI P O SV+E+	
Sbjct	6			VQLRRSRTNSDV				
Query	252			SARKMLSRERNE ARKMLSRE NE			NSMLQFEAA + M+O+EAA	
Sbjct	60			VARKMLSRETNE				
Query	432			IEHNAVPHFVAL I++ AVP VA		AVWALGNIAGD AVWAL NIAGD		
Sbjct	120			IDNGAVPILVAT				
Query	612		ILPLINNETPI	LSFLRNIVWLMS	NLCRNKNPSPP NLCR K+P			
Sbjct	180			QAFLRNIVWLIA				
Query	792			N-TKIQAVVDSD + +KIQAVVD+				
Sbjct	240			OVSKIQAVVDTG				
Query	969			LLLQHNKSNIVK LL+H KS+IVK				VL 1148 +L
Sbjct	300			NLLEHPKSSIVK				_
Query	1149			INTTTSGTPEQI INTT++GT ÕI			RTIKVVQTG + +V+TG	
Sbjct	360			INTT++GT QI INTTSTGTQIQI				
Query	1329	NLFAL +LF+L		CLMVEEMGGLDK ++++++GGL K				
Sbjct	420			GILIDDLGGLKK			+ FI 470	

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

Sequence ID: ref|XP\_013403921.1| Length: 521 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
518 bits	(1335)	5e-173()	Compositional matrix adjust.	282/527(54%)	369/527(70%)	11/527(2%)	+3
Features	s:						
Query	24	MSKAD	SNSRQGSYKANSINTQDSRMRI	RHEVTIELRKSK	KEDQMFKRRN-	-INDEDLTS	PL 197

Sbjct	1	M ++ +R +YK + D R RR+EV++ELRK+KK+DQ+ KRRN I DE TSPL MPSQENTARLKAYKNKGRDVDDLRRRRNEVSVELRKNKKDDQLLKRRNVAITDEP-TSPL	59
Query	198	KELNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICI +E + V LS+ EIV +++ D ++Q + Q+ARKMLSRERNPPID +I G++P +	377
Sbjct	60	QEQKQNVGLSLQEIVDSIHGTDPQKQMIATQAARKMLSRERNPPIDSIIQSGVIPRLV	117
Query	378	RFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWA FL+ + LQFEAAWALTN+ASGTS QT+ V+ NAV F+ALL S N++EQAVWA	557
Sbjct	118	EFLRYNDRPELQFEAAWALTNVASGTSTQTKAVVNANAVVPFIALLTSPHHNVSEQAVWA	177
Query	558	LGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQV +GNIAGDG RD VI ++ +L L+ + SFLRN+ W +SN+CRNKNP PPF V	737
Sbjct	178	VGNIAGDGPEMRDYVIKCGAVEPLLSLVKPQIETSFLRNVTWTISNMCRNKNPPPPFATV	237
Query	738	KRllpvlsqlllsqDiQvLADACWALSYVTDDDNTKiQAVVDSDAVPRLVKLLQMDEPSI K+ LP LSQLLL D +VL+DACWALSY+TD N KIQ V++S VPRLV+LL EPSI	917
Sbjct	238	KQCLPTLSQLLLHTDKEVLSDACWALSYLTDGTNDKIQEVLNSGVVPRLVELLASPEPSI	297
Query	918	IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ + PALR+VGNIVTG D QT VI +G +P LLL H+KS+I KEAAWTVSNITAGN +Q	1097
Sbjct	298	VTPALRAVGNIVTGDDGQTQAVIDAGAVPVFNLLLTHSKSSIQKEAAWTVSNITAGNTQQ	357
Query	1098	IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDL IQAV+ AG+	1277
Sbjct	358	IQAVLDAGVIPNVVNLLVKGDFKTQKEAVWAVTNLTSGGTVEQIVHLVQ-CGVLRPLCNL	416
Query	1278	LDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA L K+ + I V+ L N+ A+KLG +E +C+M+EE+ G++K+E LQQHENE+VYK A	1457
Sbjct	417	LTAKEAKVILVILDALQNILNAADKLGQSEAVCIMIEEVEGMEKIENLQQHENEQVYKAA	476
Query	1458	YAIIDTYFSNGDDEAEQELAPQEVNGALEFN-ATQPKAPEGGYTF 1589 Y II+ YF D+ ++ LAP E + EF ATO P GG++F	
Sbjct	477	YGIIEKYFGGDGDDEDESLAPTCSENSNNFEFQPATQVPAGGFSF 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()	Composition	al matrix adjust.	274/518(53%)	356/518(68%)	6/518(1%)	+3
Features	s:							
Query	45			SRMRRHEVTIEI R RR EV +EI			TSPLKELNG SPL+E N	QS 218
Sbjct	8			MRRRRTEVNVEL				
Query	219			EDQERQFLGMQS D+ ++ +	SARKMLSRERNP: -ARK+LSRERNP:			TN 398
Sbjct	67			GDENKEITATHA				
Query	399			ASGTSDQTRCVI ASGTSDQT+ V+			AVWALGNIA AVWALGNIA	
Sbjct	127			ASGTSDÕTKAVV				
Query	579		DIVIHHNVID D VI +I	GILPLINNETPI +L LI +T	SFLRNIVWLMS: +FLRN+ W +S		FDQVKRllp V++LLP	
Sbjct	187			PLLTLIKPDTSA				
Query	759			CWALSYVTDDDN CWALSY+TD N			EPSIIVPAL E ++I P L	
Sbjct	247			CWALSYLTDGPN				
Query	939			IASGGLPRLGLI +A+G P L I				
Sbjct	307			LAAGACPLLAKI				
Query	1119	GIFQQ + +		KAQKEAAWAVTN K OKEAAWA+TN				
Sbjct	367			KCQKEAAWAITN				
Query	1299			AEKLGGTENLCI AEK+G E + I				
Sbjct	426			AEKMGELEKVSI				
Query	1479		DEAEQELAPQ DE + ELAP	EV-NGALEFNAT +G EFN +		1589		
Sbjct	486			TSQSGNYEFNNS		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	Fram	<u>e</u>
517 bits(1	1332) 2	2e-172()	Compositional matrix adjust.	275/518(53%)	361/518(69%)	8/518(1%)	+3	
Features:								
Query	39		GSYKANSINTQDSRMRRHEVTI ++K + ++R RR+ V	ELRKSKKEDOMI ELRK+KK++O+		SPLKELNG	QS 2	218
Sbjct	16		ANFKYTN-RLDEARRRRNIVYT			LNLS-CEA	is '	73
Query	219	~	VDEIVAAMNSEDQERQFLGMQS +++IVAAM S D+ O O+	ARKMLSRERNPI RK+LSRE++PI			TN :	398
Sbjct	74		IEDIVAAMKSPDETLQLQATQT				нн :	133

Query	399	NSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGD N LQFEAAWALTN+ASGTS+QT+ VI++ AVP V LL+S S N+AEQAVWALGNIAGD	578
Sbjct	134	NVALQFEAAWALTNVASGTSEQTQVVIKYGAVPRLVVLLKSPSANVAEQAVWALGNIAGD	193
Query	579	GAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvl G ARD+++ H+ + +L LI +T ++F+RNIVW +SNLCRNKNP PPFD VK LP L	758
Sbjct	194	GPPARDLILAHDAVPLLLDLIKPDTSVTFMRNIVWTLSNLCRNKNPPPPFDIVKTALPAL	253
Query	759	sqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRS ++LL S D +LAD CWALSY+TD N KIQAV+DS VP+LV LL E +++ PALR+	938
Sbjct	254	NRLLTSPDRDILADTCWALSYLTDGSNDKIQAVLDSGVVPQLVSLLTSQEATVLTPALRT	313
Query	939	VGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQA VGNIVTG D QTD +I +GGL L LL H++ NI+KEAAW +SNITAGN +QIQ VI A	1118
Sbjct	314	VGNIVIG D QID +1 +GGL L LL H++ NI+KEAAW +5NIIAGN +QIQ VI A VGNIVTGDDAQTDSIILAGGLKHLCNLLSHSRKNIMKEAAWAISNITAGNTEQIQHVINA	373
Query	1119	GIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPR GI L VL+ GD KAQKEAAWAVTN T+ G+ +Q+ DL++ +L P +LL KD	1298
Sbjct	374	GI L VL+ GD KAQKEAAWAVTN T+ G+ +Q+ DL++ +L P +LL KD GILPPLIQVLDSGDLKAQKEAAWAVTNLTSGGSYQQLADLVQA-GVLPPLCNLLAAKDWS	432
Query	1299	TIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTY T VV GL+N+ AEK + + LM+EE+GGLDKLE LO H+NE++Y+K+ A+IDT+	1478
Sbjct	433	T VV GL+N+ AEK + + LM+EE+GGLDKLE LQ H+NE++Y+K+ A+IDT+ TTVVVLDGLTNILNTAEKCNQVDQIALMIEEIGGLDKLEALQHHKNEQIYQKSMAMIDTF	492
Query	1479	FSNGDDEAEQELAPQEVN-GALEFNATQPKAPEGGYTF 1589	
Sbjct	493	FS DE LAP + G LEF A P++ +TF FSGDEEHASLAPAANDEGQLEFKAPESTSTDFTF 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
Feature	s:						
Query	39		QGSYKANSINTQDSRMRRHEVTI ++K N+ +++R+R+ +++			TSPLKELN- +S L +	GQ 215
Sbjct	8		ANFKFNN-RHEEARVRRNALS				VS 66
Query	216	SPVQI S	SVDEIVAAMNSEDQERQFLGMQ S++EIV +NS ++ O +C	QSARKMLSRERN O+ RK+LSRER+		VPICIRFLQ VP+CI+FL	
Sbjct	67		STTETV TNS TT Q TÇ SIEEIVNHLNSSNETLQLTAIÇ				
Query	396		QFEAAWALTNIASGTSDQTRCV QFE W LTNIASGTS QT+ V				
Sbjct	127		QFEVTWVLTNIASGTSVQTQNV				
Query	576		ARDIVIHHNVIDGILPLINNETI ARD+V+ H+ + ++ LI +TI	PLSFLRNIVWLM P++F RNIVW +			
Sbjct	187		ARDLVLGHDALPRLVDLIKPDTI				
Query	756	lsqll ++LI	lsqDIQVLADACWALSYVTDDI D VLAD CWALSY+TD			DEPSIIVPA E +I+ PA	
Sbjct	247		SYTDRDVLADTCWALSYLTDG				
Query	936		VTGTDQQTDVVIASGGLPRLGI VTG D QTD VI++GGL G	LLLQHNKSNIVK LL++ ++NIVK			
Sbjct	307		VTGNDAQTDAVISAGGLSHFGA				
Query	1116		QQLRTVLEKGDFKAQKEAAWAV1 ) L +L+ GD+KAQKEAAWAV1			PFIDLLDTK PF +LL++K	
Sbjct	367		PLIQILQFGDYKAQKEAAWAVI				
Query	1296		VVQTGLSNLFALAEKLGGTENLO VV GL+N+ AEK+G + L	CLMVEEMGGLDK +M+E++GGLDK			
Sbjct	426		VLDGLTNILHAAEKVGQVDKLA				
Query	1476		DDEAEQELAPQEVNGALEFN DEE++NEFN	NATQ 1559 N T+			
Sbjct	486		D E E T T N T N T T N T T N T T N T T N T T N T T N T T N T T N T N T T N				

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 Fra	ame
516 bits	(1328)	4e-172()	Compositional matrix adjust.	267/518(52%)	357/518(68%)	4/518(0%) +3	
Features	s:						
Query	42	NSRQG ++R	SYKANSINTODSRMRRHEVTIE +K + ++ R RR E +E			rsplkelngos rspl e n	218
Sbjct	5		HFKNRGKDVEEMRRRRTEANVE				64
Query	219		SVDEIVAAMNSEDQERQFLGMQ S++EIV ++S+D+ F Q	SARKMLSRERNI SARK+LSRERNI			395
Sbjct	65	•	SMEEIVQGISSQDETLNFQAAQ				124
Query	396		QFEAAWALTNIASGTSDQTRCV OFEAAWALTNIASG SDOTRCV				575
Sbjct	125		QFEAAWALTNIASGNSDQTRCV				184
Query	576	DGAAA	RDIVIHHNVIDGILPLINNETP	LSFLRNIVWLM	SNLCRNKNPSPI	PFDQVKRllpv	755

		DG RD++I H ++ +L LI +++P SFLRN+ W +SNLCRNKNP PPF+ VK+ LP	
Sbjct	185	DGPDCRDLIIRHGIMKPLLDLIKSDSPASFLRNVTWTLSNLCRNKNPPPPFEVVKQSLPT	244
Query	756	lsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR L QL+ D +V+ADACW LSY+TD N KIQ V+D+ VPRL +LL +DE SI+ P+LR	935
Sbjct	245	LRQLIYHNDKEVVADACWXLSYLTDGTNEKIQEVIDAGVVPRLCELLDVDEVSILTPSLR	304
Query	936	SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ +VGNIVTG D QT VI LP LL + K NI KEAAW +SN+TAGN QIQ+VI	1115
Sbjct	305	AVGNIVTGNDAÕTQHVIDCQALPPFRKLLCNKKINIQKEAAWMISNVTAGNDSÕIÕSVID	364
Query	1116	AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP +G+ + L VL +GD+K+QKEA WAV N T+ GT EQIV L++ ++ P D+L DP	1295
Sbjct	365	SGLVEPLIEVLAQGDYKSQKEATWAVANFTSGGTLEQIVYLVQA-GVVPPLCDMLKISDP	423
Query	1296	RTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDT + + V+ L+N+ A+KLG E + L++EE+GG+DK+E LQQHEN +VY A I+	1475
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)	9e-172()	Compositional matrix adjust.	269/519(52%)	353/519(68%	) 10/519(1%)	+3
Features	s:						
Query	39	SNSRQ S +R	QGSYKANSINTQDSRMRRHEVT +K + + R RR EV				GQ 215
Sbjct	3		IKCFKNKGRDQEAMRRRRTEVN				58
Query	216		LSVDEIVAAMNSEDQERQFLGM ++V+EI+ + S D + OF G			IVPICIRFLQ VPI + FL	NT 395
Sbjct	59		ITVEEIMRGIKSNDPQLQFAGA				TS 117
Query	396		LOFEAAWALTNIASGTSDOTRC LOFEA WALTNIASG S OTR			EQAVWALGNI EOAVWALGNI	
Sbjct	118		LOFEACWALTNIASG S OIR LOFEACWALTNIASGNSSQTRA				
Query	576	DGAA <i>I</i> DG	ARDIVIHHNVIDGILPLINNET RD VI VI ++ L+		MSNLCRNKNPS +SN+CRNKNPS		
Sbjct	178		LRDEVIRSGVIKPLINLLKPNI				
Query	756	lsql] + LI	llsqDIQVLADACWALSYVTDD D++V+ DACWALSY+TD				
Sbjct	238		LSDSDLEVVTDACWALSYLTDG				
Query	936		IVTGTDQQTDVVIASGGLPRLG IVTG D QT VI +G L L			AGNQKQIQAV AGN +QIQAV	
Sbjct	298		IVTGDDVQTQAVIDAGALEPLR				
Query	1116		QQLRTVLEKGDFKAQKEAAWAV Q+ VL +GD+K QKEA WAV				
Sbjct	358		OT VL TGDTK OKEA WAV SQIVDVLNEGDYKCQKEAIWAV				DP DP 416
Query	1296	RTIK\ + + \	/VQTGLSNLFALAEKLGGTENL /V LSN+ + K+ E +				
Sbjct	417		/V LSN+ + K+ E + /VLDALSNILHASAKMNAVETV		K+E LQ HEN KIENLQHHENS		
Query	1476		GDDEAEQELAPQ-EVNGALEFN D+E O+LAPO E +G EFN				
Sbjct	477	YFSN YFSN-	D+E Q+LAPQ E +G EFN DEEELQDLAPQVEGSGTYEFN-				

importin alpha [Culex quinquefasciatus]

Sequence ID: ref|XP\_001847920.1| Length: 459 Number of Matches: 1

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	<b>S</b> :						
Query	414		ALTNIASGTSDQTRCVIEHNAV				
Sbjct	67		/ALTNIASGTS+QT+ VI+ AV /ALTNIASGTSEQTKAVIDAGAV				
Query	594		HNVIDGILPLINN-ETPLSFLR				
Sbjct	127		+N ++ I L+ N +T LSFLR YNSVESINYLVQNADTQLSFLR				
Query	771		QVLADACWALSYVTDDDNTKIQ QVLADACWALSYVTDDD KI+				
Sbjct	187		QVLADACWALSIVIDDD KIT QVLADACWALSYVTDDDAVKIE				
Query	951		QQTDVVIASGGLPRLGLLLQHN QTD VIA+G LP LG LL+++				~
Sbjct	247		TÕTDAVIAAGSLPALGKLLRNS				-
Query	1131	QLRTV	LEKGDFKAQKEAAWAVTNTTTS	GTPEQIVDLIE	KYKILKPFIDLI	LDTKDPRTI	KV 1310

```
L VL KGDFK+QKEAAWA+TNTTT G+ EQI+ L+EKY ++KP+ DLLD KD RT++V
Sbjct 307
                     VLVEVLIKGDFKSQKEAAWAITNTTTGGSTEQIIHLVEKYPVMKPYCDLLDAKDSRTVRV
                                                                                                                          366
                    VQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTYFSNG 1490
V +G++N+F +AEK+GG ENLC + EE+G LDKLE LQ HENEEVYKKA+ +I+TYF++
VLSGIANIFQIAEKIGGAENLCTLFEEIGALDKLEALQNHENEEVYKKAFQLIETYFTDA 426
                                                                                                                        1490
Query
          1311
Sbjct
          367
                    DDEAEQELAPQEVNGALEFNATQPKAPEG
+D E AP+EVNGALEFN + + G
ED-VNPECAPKEVNGALEFNPSAAQQQSG
          1491
                                                                      1577
Query
Sbjct
           427
```

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	<b>3</b> :						
Query	45		YKANSINTQDSRMRRHEVTIEI +K + ++ R RR TIEI	.RKSKKEDOMFK .RK+KKEDO+ K			SP 221
Sbjct	5		FKNKGKDCEEMRRRRAGQTIEI				SL 64
Query	222	VQLSV + +S	DEIVAAMNSEDQERQFLGMQSA +EI+ M S D+ OF O+	ARKMLSRERNPP RKMLSRERNPP		~	NN 401 +N
Sbjct	65		EEILMGMMSPDENLÕFKATÕAC				
Query	402		EAAWALTNIASGTSDQTRCVIE EA WALTNIASGTS+QT V++		QSKSMNLAEQA S +++ EQA		
Sbjct	125		EACWALTNIASGTSEÕTAAVVQ		SSNRIDVVEÕA	IWAIGNIAG	DG 184
Query	582		IVIHHNVIDGILPLINNETPLS +V+++ V+ ++ LI T LS	SFLRNIVWLMSN S LRN VW++SN			
Sbjct	185		LVLNYGVLPSLINLIKPNTTLS				
Query	762	qllls +LL	qDIQVLADACWALSYVTDDDNT D VLAD CWALSY+TD N			PSIIVPALR +++ PALR	
Sbjct	245		DDKDVLADTCWALSYLTDGSNE				
Query	942		GTDQQTDVVIASGGLPRLGLLI G D OTD+VI +G L + LI				
Sbjct	305		GNDHQTDMVINAGALDCMIRLI				
Query	1122		RTVLEKGDFKAQKEAAWAVTNT VL+ GDFK+OKEAAWAVTN			IDLLDTKDP: +LL++KD	
Sbjct	365		LHVLQTGDFKSQKEAAWAVTNE				
Query	1302	IKVVQ I VV	TGLSNLFALAEKLGGTENLCLM GL+N+ + A KL E + +M	NEEMGGLDKLE N+EE GGLD +E			
Sbjct	424		EGLNNILSAAAKLNQAEKVAIM				
Query	1482	SNGDD ++G++	EAEQELAPQEVNGALEFNATQE +A E+ A A O				
Sbjct	484	_	GVTVTVANGEIQFATPNMADQQ				

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 I	-rame
509 bits	(1310)	5e-169()	Compositional matrix adjust.	267/508(53%)	363/508(71%)	4/508(0%) +	-3
Features	<b>S</b> :						
Query	42		SYKANSINTQDSRMRRHEVTIE ++K N+ +++RMRR+ +++E				
Sbjct	30		++K N+ +++RMRR+ +++E NFKFNN-KPEEARMRRNALSVE			L E S PNLSEEAIVS	
Query	222	VQ-LS	VDEIVAAMNSEDQERQFLGMQS +DEIV +NS D+ Q +Q+	ARKMLSRERNP	PIDLMIGHGIVI	PICIRFLONT	N 398
Sbjct	89		IDEIVNHINSSDETLQLAAIQT				
Query	399		FEAAWALTNIASGTSDQTRCVI				
Sbjct	149		FE AW LTNIASGTS QT+ V+ FEVAWVLTNIASGTSVQTQNVV			AVWALGNIAG AVWALGNIAG	
Query	579		DIVIHHNVIDGILPLINNETPL D+V+ H+ + ++ LI +TP+				
Sbjct	209		DLVLGHDALPLLIDLIKPDTPI				
Query	759	_	sqDIQVLADACWALSYVTDDDN				
Sbjct	269	+ LL NCLLS	D VLAD CWALSY+TD N YTDRDVLADTCWALSYLTDGAN			E +I+ PALR EGAILTPALR	
Query	939		TGTDQQTDVVIASGGLPRLGLL				
Sbjct	329		TG D QTD VI +GGL LG L TGDDAQTDAVIFAGGLSHLGAL				
Query	1119		LRTVLEKGDFKAQKEAAWAVTN				R 1298
Sbjct	389		L VL+ GD+KAQKEAAWAVTN LIHVLQFGDYKAQKEAAWAVTN			F +LL++KD FCNLLESKDW	N 447
Query	1299	TIKVV	'QTGLSNLFALAEKLGGTENLCL	MVEEMGGLDKL	ETLQQHENEEVY	/KKAYAIIDT	Y 1478

I VV GL+N+ AEK+G E L +M+EE+GGLDK+E LQ HENE+VY+++ AIIDT+
Sbjct 448 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 I	Frame
507 bits	(1306)	1e-168()	Compositional matrix adjust.	265/512(52%)	363/512(70%)	9/512(1%) +	<u></u>
Feature	s:						
Query	36		QGSYKANSINTQDSRMRRHEVT + ++K N+ +++R+RR+ ++				
Sbjct	7		KANFKFNN-KHEEARIRRNALS	-+ELRK+KK+DQ SVELRKAKKDDQ		L +L+ QELSDLSN	
Query	216	SPVQ- + V	LSVDEIVAAMNSEDQERQF LS+DEIV +NS D+ Q		RERNPPIDLMI RE+NPPI+ +I		RF 383
Sbjct	64	. •	TPTLSIDEIVNHINSSDETLÕI				AL 123
Query	384	~	NSMLQFEAAWALTNIASGTSDQ N LQFE AW LTNIASGTS Q			NLAEQAVWAI +AEOAVWAI	
Sbjct	124		N LOFE AW LINIASGIS Q NVALQFEVAWVLTNIASGISLQ				
Query	564	NIAGD NIAGD	GAAARDIVIHHNVIDGILPLIN G ARD+V+ H+ + +L LI				
Sbjct	184		GPYARDLVLGHDALPLLLDLIK				
Query	744	llpvl +LP+	sqlllsqDIQVLADACWALSYV ++LL D VLAD CWALSY+				
Sbjct	244		NRLLSYTDRDVLADTCWALSYI				
Query	924		VGNIVTGTDQQTDVVIASGGLF VGNIVTG D OTD VI +GGL				
Sbjct	304		VGNIVTGDDAÕTDAVILAGGLS				
Query	1104	AVIQA VI A	GIFQQLRTVLEKGDFKAQKEAA G+ L VL+ GD+K+QKEAA			KILKPFIDLI +L PF +LI	
Sbjct	364		GLLSPLIEVLQFGDYKSÕKEAA				
Query	1284	TKDPR +KD	TIKVVQTGLSNLFALAEKLGGT + VV GL+N+ AEK+G	ENLCLMVEEMG E L +++EE G			
Sbjct	423		IVIVVLDGLTNILHAAEKIGQV				
Query	1464	IIDTY IID +	FSNGDDEAEQELAPQE-VNGAI FS D E OE G +	EFNAT 1556 EFN T			
Sbjct	483		FSQKDVEETLTSEVQENCEGQI				

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 F	rame
507 bits	(1306)	1e-168()	Compositional matrix adjust.	268/522(51%)	365/522(69%)	11/522(2%) +	3
Features	<b>S</b> :						
Query	39		QGSYKANSINTQDSRMRRHEVT ++K N+ +++R+R+ ++-				
Sbjct	8	S+ R SHGRI	ANFKFNN-KHEEARIRRNTLS				
Query	219		SVDEIVAAMNSEDQERQFLGM S+DEIV +NS D+ Q L +0			IVPICIRFLQN' +VP CI+ L +	395
Sbjct	67		SIDEIVNYINSSDETLÕLLAI(				126
Query	396		QFEAAWALTNIASGTSDQTRC				
Sbjct	127		QFEVAWVLTNIASGIS+QI+ QFEVAWVLTNIASGISEQTQN				
Query	576		ARDIVIHHNVIDGILPLINNET ARD+V+ H+ + +L LI ET	PLSFLRNIVWLN ++F+RNIVW +			
Sbjct	187		ARDLVLEHDALPLLLNLIKPET;				
Query	756	lsqll ++LI	lsqDIQVLADACWALSYVTDDI D VLAD CWALSY+TD		OAVPRLVKLLQI +P+LV+LL	MDEPSIIVPALI + +I+ PALI	
Sbjct	247		INCTDQDVLADTCWALSYLTDG:				
Query	936		VTGTDQQTDVVIASGGLPRLG VTG D QTD VI +GGL LG				2 1115
Sbjct	307		VTGDDAQTDAVILAGGLSYLG				1 366
Query	1116	AGIFQ AG+	QLRTVLEKGDFKAQKEAAWAV L VL+ GD+KAOKE AWA+-			KPFIDLLDTKDI PF +LL+ KD	2 1295
Sbjct	367		SPLIEVLQVGDYKAQKEVAWAI				<b>425</b>
Query	1296		VVQTGLSNLFALAEKLGGTENLO				1475
Sbjct	426		VV GL+N+ AEK+G E L VVLDGLTNILHAAEKIGQVERLA	M+EE GGLDH IMIEEAGGLDH			A 485
Query	1476	YFSNG	GDDEAEQELAPQEVNGALI	EFNATQPKAPE(	GGYTF 1589		

PREDICTED: importin subunit alpha [Vollenhovia emeryi]

Sequence ID: ref|XP\_011877264.1| Length: 523 Number of Matches: 1

Range 1: 8 to 514

	Expect Me	ethod	Identities	Positives	Gaps	Frame
(1305)	1e-168() Co	mpositional matrix adjust.	266/516(52%)	360/516(69%)	18/516(3%)	+3
<b>S</b> :						
39						209
8		FKFNN-KHEEARRRRTTLS	VELRKAKKDDQ1	+ KRRN++ LSKRRNLD		SD 60
210	GQSPV					
61	QAASSPT					
381						
121						
561						
181						
741						
241						
921						QI 1100
301						_
1101						
361						
1281						
420						
1461				1559		
480				514		
	39 8 210 61 381 121 561 181 741 241 921 301 1101 361 1281 420 1461	(1305) 1e-168() Co S: 39 SNSRQGS S R + 8 SQGRMAN 210GQSPV SP 61 QAASSPT 381 FLQNTNN L + +N 121 LLDSEHN 561 GNIAGDG GNIAGDG GNIAGDG GNIAGDG 181 GNIAGDG 181 GNIAGDG 181 GNIAGDG 181 GNIAGDG 181 GNIAGDG 301 TPALRTV 921 VPALRSV PALR+V 301 TPALRTV 1101 QAVIQAG Q+ I AG 361 QSAISAG 1281 DTKDPRT +TKD 420 ETKDWNV 1461 AIIDTYF AI+D +F	(1305) 1e-168() Compositional matrix adjust.  S:  39	(1305) 1e-168() Compositional matrix adjust. 266/516(52%)  3:  39	(1305) 1e-168() Compositional matrix adjust. 266/516(52%) 360/516(69%)  S:  39	(1305) 1e-168() Compositional matrix adjust. 266/516(52%) 360/516(69%) 18/516(3%) 65:  39

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 F	rame
505 bits	(1301)	6e-168()	Compositional matrix adjust.	269/524(51%)	354/524(67%)	6/524(1%) +	3
Features	s:						
Query	24		SNSRQGSYKANSINTQDSRMRF				
Sbjct	1		- ++R +YK + D R RE RDTRLKNYKNKGKDCDDLRRRE	RNETSVELRKAK	KHDQ+ KRRN+ KDDQLSKRRNL	D+ SPLK TLTDV-SPLK	
Query	204	LNGQS N O	SPVQL-SVDEIVAAMNSEDQERQ L + +I+ ++ S+DOE+				
Sbjct	60		PAAPLMPMSDIIKSIKSQDQEKW				
Query	381		NNSMLQFEAAWALTNIASGTSI +N LOFEAAWALTNIASGTS		PHFVALLQSKS F+ LL S	MNLAEQAVWA N+AEOAVWA	
Sbjct	120		DNPDLQFEAAWALTNIASGTS				
Query	561	GNIAG	DGAAARDIVIHHNVIDGILPLI DG RD++I + +L LI	NNETPLSFLRN + +TP++FLRN			
Sbjct	180		GDGPELRDLLIKEGCLPPLLSLI				
Query	741		lsqlllsqDIQVLADACWALSY				
Sbjct	240		L+QL+ + D ++L+DACWALSY LAQLIHTADKEILSDACWALSY				
Query	921		RSVGNIVTGTDQQTDVVIASGGI R++GNIVTG D OT V + I		SNIVKEAAWTV +++ KEA WT+		
Sbjct	300		RTIGNIVTG D Q1 V + RTIGNIVTGDDSQTQVALDHNMI				
Query	1101	QAVIQ Q V+	AGIFQQLRTVLEKGDFKAQKEA + + L KGDFK QKEA			YKILKPFIDL + P L	
Sbjct	360		CQLLPLIVDCLAKGDFKTQKE				
Query	1281		PRTIKVVQTGLSNLFALAEKLGG P+ I VV  + N+ A+				
Sbjct	419		P+ I VV		GGL K+ETLQ GGLTKIETLQN		
Query	1461		YFSNGDDEAEQELAPQEV-NGA	~		9	
Sbjct	479	II+ FIIEK	+FS +DE QELAP+ G FFSEEEDEV-QELAPESTEQGN		GG++F NGGFSF 520		

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)	6e-168()	Compositional matrix adjust.	274/412(67%)	326/412(79%)	2/412(0%)	) +3
Features	s:						
Query	207		VQLSVDEIVAAMNSEDQERQFI VQLS+D+IV A+NSED E+QFI		ERNPPIDLMIGI + PIDLMIG		RFL 386
Sbjct	5		VQLS+D+IV A+NSED E+QFI VQLSIDQIVVAVNSEDPEQQFI				
Query	387		SMLQFEAAWALTNIASGTSDQT + LQFEAAWALTNI SGT++QT				
Sbjct	64		NRLQFEAAWALTNITSGTTEQT				
Query	567		AAARDIVIHHNVIDGILPLINN AAARDIVI HNVIDGILPLI+N			PSPPFDQVI PSPPF OV-	
Sbjct	124		AAARDIVI HNVIDGILPLIFN			~	
Query	747		qlllsqDIQVLADACWALSYVT Q+LLSQDI +L DAC +L V				
Sbjct	184		QMLLSQDI +L DAC +L V QMLLSQDIPILIDACSSLVNVA				
Query	927		GNIVTGTDQQTDVVIASGGLPR				
Sbjct	244		GNI GTDQQTD +I++GGL + GNIAFGTDQQTDSLISAGGLTK				
Query	1107		IFQQLRTVLEKGDFKAQKEAAW				
Sbjct	304		IFQQ+R +LEKG+ KAQK AAW IFQQIRHLLEKGNVKAQKNAAW			I+KP+IDLI IIKPYIDLI	
Query	1287		TIKVVQTGLSNLFALAEKLGGT				9
Sbjct	364	_	I VV GL LF TETT GI IINVVLLGLEKLFRFSEQICGT				
_		P	I VV GL LF +E++ GT	ENLCLMVE++	GLDKL+ L H	ΕΕ	9

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 F	rame
505 bits	(1300)	8e-168()	Compositional matrix adjust.	263/512(51%)	363/512(70%)	9/512(1%) +	3
Features	<b>S</b> :						
Query	36		QGSYKANSINTQDSRMRRHEVT	TIELRKSKKEDQ -+ELR++KK+DO			~
Sbjct	7		KANFKFNN-KHEEARIRRNALS				
Query	216	SPVQ- + V	LSVDEIVAAMNSEDQERQE LS++EIV +NS D+ O		RERNPPIDLMI RE+NPPI+ +I		F 383
Sbjct	64		TPTLSINEIVNHINSSDETLÕI				L 123
Query	384	~	NSMLQFEAAWALTNIASGTSDQ N LQFE AW LTNIASGTS Q			NLAEQAVWAL +AEOAVWAL	
Sbjct	124		NIALÕFEVAWVLTNIASGTSLÕ	TQNVVKYGAIP	KLVKLLKSTSP		
Query	564	NIAGD NIAGD	GAAARDIVIHHNVIDGILPLIN G ARD+V+ H+ + +L LI		VWLMSNLCRNK VW +SNLCRNK		R 743
Sbjct	184		GPYARDLVLGHDALPLLLDLI				P 243
Query	744	llpvl +LP+	sqlllsqDIQVLADACWALSYV ++LL D VLAD CWALSY				V 923
Sbjct	244		NRLLSYTDRDVLADTCWALSYI				т 303
Query	924		VGNIVTGTDQQTDVVIASGGLE VGNIVTG D OTD VI +GGL				~
Sbjct	304		VGNIVTGDDAÕTDAVILAGGLS				
Query	1104	AVIQA VI A	.GIFQQLRTVLEKGDFKAQKEA <i>F</i> .G+ L VL+ GD+K+QKEA <i>F</i>			KILKPFIDLL +L PF +LL	
Sbjct	364		GLLSPLIEVLQFGDYKSQKEA				
Query	1284	TKDPR +KD	TIKVVQTGLSNLFALAEKLGGT I VV GL+N+ AEK+G	ENLCLMVEEMG E L +++EE G			
Sbjct	423		VIIVVLDGLTNILHAAEKIGQ\	ĒKLAILIĒĒAG	GLDKIEALÕHH	QNEQVYQKSM	A 482
Query	1464	IIDTY IID +	FSNGDDEAEQELAPQE-VNGAI FS D E QE G H	EFNAT 1556 EFN T			
Sbjct	483		FSQKDIEETLTSEVÕENYEGQI				

importin subunit alpha-1 [Danio rerio]

Sequence ID: ref|NP\_001002335.1| Length: 525 Number of Matches: 1

▶ See 1 more title(s) kange 1: 1 to 514

Score Expect Method Identities Positives Gaps Frame

503 bits	(1296) 4	4e-167() Compositional matrix adjust. 262/516(51%) 356/516(68%) 10/516(1%) +3	
Features	s:		
Query	24	MSKADSNS-RQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSP MS A+ N+ R +K + + R RR EV +ELRK+KK++Q+ KRRN++ ++ TSP	194
Sbjct	1	MSAANENTARLTQFKNKGKDATELRRRRIEVNVELRKAKKDEQILKRRNVSSFPDEATSP	60
Query	195	LKELNGQSPVQ-LSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPI L+E + Q +V+EIV +NS + E Q Q+ARK+LSRER+PPID +I G++P	371
Sbjct	61	L+E+Q+V+EIV+NS+EQQ+ARK+LSRER+PPID+IG+PPID+QE+PPID+IG+PPIDRIISAGLIPK	120
Query	372	CIRFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAV + FL ++ +OFEAAWALTNIASGTSDOT V++ A+P F++L+ S +++EOAV	551
Sbjct	121	+ FL ++ +QFEAAWALTNIASGTSDQT V++ A+P F++L+ S +++EQAV FVGFLSLVDSPPIQFEAAWALTNIASGTSDQTSAVVQGGAIPAFISLISSPHAHISEQAV	180
Query	552	WALGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPS	719
Sbjct	181	WALGNIAGDG+ RD VI H I +L L+ + P +LRN+ W +SNLCRNKNP+ WALGNIAGDGSGYRDRVIKHGAIPPLLALLAVPDLSVFPAGYLRNVTWTLSNLCRNKNPA	240
Query	720	PPFDQVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQ PP + VK++LP L LL D +VLAD CWA+SY+TD N +I+ VV++ VPRLV+LL	899
Sbjct	241	PP + VK++LP L LL D +VLAD CWA+SY+TD N +I+ VV++ VPRLV+LL PPLEAVKQILPTLICLLQHSDKEVLADTCWAISYLTDGPNDRIEVVVNAGVVPRLVQLLA	300
Query	900	MDEPSIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNIT	1079
Sbjct	301	E SI+ P+LRS+GNIVTGTD+QT V+ +G LP LL+H KSNI KEA+WT+SNIT SGELSIVTPSLRSIGNIVTGTDEQTQAVLEAGALPMFPALLRHQKSNIQKEASWTLSNIT	360
Query	1080	AGNQKQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKIL	1259
Sbjct	361	AG QIQ VI AGI L VL +GD+K QKEA WAVTN T+ GT EQ+V L++ +L $AGRDYQIQEVINAGIVPYLVEVLRRGDYKTQKEAVWAVTNYTSGGTVEQVVYLVQA-NVL$	419

KPFIDLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENE 143 +P ++LL TKD TI V+ ++N+F EK+G E LCLM+EE GGLDK+E LQ HENE EPLLNLLSTKDSTTILVILDAITNIFLAGEKIGEVEKLCLMIEECGGLDKIEALQSHENE 479

1547

1439

PREDICTED: importin subunit alpha-1 [Linepithema humile]

Sequence ID: ref|XP\_012217870.1| Length: 520 Number of Matches: 1

EVYKKAYAIIDTYFSNGDDEAEQELAPQEVNGALEF VYK + +I+ YFS G++E ++ +AP+ + F MVYKASLNLIEKYFS-GEEEGDECVAPEATDDGYAF

# ▶ See 1 more title(s) Range 1: 9 to 508

1260

1440

420

480

Query

Sbjct

Query

Sbjct

Score		Expect	Method	Identities	Positives	Gaps I	Frame
502 bits	(1292)	1e-166()	Compositional matrix adjust.	264/507(52%)	353/507(69%)	12/507(2%) +	+3
Features	s:						
Query	45	SRQGS +R+	SYKANSINTQDSRMRRHEVTIE +K N+ + +++R RR+ ++E	LRKSKKEDOMFI LRK+KK+DO+ 1		~	- 215
Sbjct	9		FKFNNKH-EEARRRNAASVE			KE N Q KESNPQIE	E 62
Query	216	-SPVÇ	QLSVDEIVAAMNSEDQERQFLGI S+DE++ ++ S D+ + L			GIVPICIRFLO GIVP CI L	N 392
Sbjct	63	•	FSLDELIQSIKSSDETTRLLA				Y 122
Query	393	TNNSN +N	/// /// /// // // // // // // // // //		VALLQSKSMNL V LL+S+S N+		
Sbjct	123		PLQFEAAWVLTNIASGTSVQTQ				
Query	573	GDGA <i>I</i> GDG	AARDIVIHHNVIDGILPLINNE ARD V+ + + +L LI +	PLSFLRNIVWI ++FLRNIVW			
Sbjct	183		TARDFVLTNEAMPQLLELIRPD				
Query	753		lllsqDIQVLADACWALSYVTD LL + D VLAD CWALSY++D				
Sbjct	243		LLTNTDQDVLADTCWALSYLSD				
Query	933		NIVTGTDQQTDVVIASGGLPRLO				
Sbjct	303		NIVIG D QID VITTG LF LO NIVIGDDAQTDAVISAGALPHLO				
Query	1113	QAGII A +	FQQLRTVLEKGDFKAQKEAAWAY L VL+ GD+KAQKEAAWAY			LKPFIDLLDTK L F +LLD+K	
Sbjct	363		LTPLVEVLQFGDYKAQKEAAWA				
Query	1293		KVVQTGLSNLFALAEKLGGTEN VV GLSNL A K+G N	LCLMVEEMGGLI L +++EE+G LI			
Sbjct	422		IVVLDGLSNLLHTAAKMGEETN				
Query	1473	TYFSI YF+	NGDDEAEQELAPQ-EVNGALEFI D E L P+ E N L+F-				
Sbjct	482		EKDTEEVGTLTPKVEDNNQLQF				

PREDICTED: importin subunit alpha-1 isoform X2 [Xenopus tropicalis] Sequence ID: ref|XP\_012821933.1| Length: 526 Number of Matches: 1

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	s:		
Query	24	MSKADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPL MS ++ +R +K +T + R RR EV +ELRK+KK+DQM KRRN++ ++ TSPL	197
Sbjct	1	MSNNENAARLTRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTFPDEPTSPL	60
Query	198	KELNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPI +E N GQ+ Q SV+EIV + S E Q Q+ARK+LSRER PPID +I G++P	371
Sbjct	61	QEKNQNGÕTSTÕWSVEEIVRGVASSSLEIÕLQATÕAARKLLSREREPPIDRIIQAGLIPK	120
Query	372	CIRFLQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAV + FL T+ S +QFEAAWALTNIASGTSDQT+ V+E VP F++LL S +++EQAV	551
Sbjct	121	LVAFLARTDCSPIQFEAAWALTNIASGTSDQTKAVVEGGGVPAFISLLASPHPHISEQAV	180
Query	552	WALGNIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPS WALGNIAGDG+A RD+VI H + +L L+ + +LRN+ W +SNLCRNKNP+	719
Sbjct	181	WALGNIAGDGSAYRDLVIKHGAVGPLLALLADPDLSTLATGYLRNVTWTLSNLCRNKNPA	240
Query	720	PPFDQVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQ PP D ++++LP L +LL D +VLAD CWA+SY+TD N +I VV + VPR+V+LL	899
Sbjct	241	PPLDAIQQILPTLVRLLHHDDREVLADTCWAVSYLTDGSNDRINVVVGTGLVPRIVQLLG	300
Query	900	MDEPSIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNIT E +I+ P LR+VGNIVTGTD+QT VV+ +G L LL H+K+NI KEAAWT+SNIT	1079
Sbjct	301	CGELTIVTPCLRTVGNIVTGTDEQTQVVLDAGALSVFAELLTHHKNNIQKEAAWTLSNIT	360
Query	1080	AGNQKQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKIL AG Q QIQ V+ G+ L +L K D+K QKEA WAVTN T+ GT +QI+ L++ ++	1259
Sbjct	361	AGRÕDÕIÕEVVNHGLIPYLIEILRKADYKTÕKEAIWAVTNYTSGGTIDÕIIYLVQ-CSVI	419
Query	1260	KPFIDLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENE +P +LL KD +T+ V+ +N+FA AEKLG TE LCLMVEE GGLD++E LO HENE	1439
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	s:						
Query	42	~	SYKANSINTQDSRMRRHEVTIE				_
Sbjct	11	++R SARLN	+K ++ + R RR EV +E RFKNKGKDSTEMRRRRIEVNVE				G GN 70
Query	213	QSPVQ Q	LSVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E Q	IQSARKMLSRER Q+ARK+LSRE+			~
Sbjct	71		WSVEEIVKGVNSNNMELÕLQAT				
Query	393		LQFEAAWALTNIASGTSDQTRO +QFE+AWALTNIASGTS+QTR			EQAVWALGN EOAVWALGN	
Sbjct	131		TÖFESAWALTNIASGTSEÖTRA				
Query	573		ARDIVIHHNVIDGILPLIN RD+VI + I+ +L L+		IVWLMSNLCRNI + W +SNLCRNI		
Sbjct	191		YRDLVIKYGAIEPLLSLLAVPI				
Query	741		lsqlllsqDIQVLADACWALSY L +LL D +VLAD CWA+SY				II 920 I+
Sbjct	251		LVRLLHHDDPEVLADTCWAISY				
Query	921		SVGNIVTGTDQQTDVVIASGGI ++GNIVTGTD+QT +VI SG I		SNIVKEAAWTV: +NI KEAAWT+:		
Sbjct	311	TPSLR	AIGNIVTGTDEQTQIVIDSGAI	LAVFPSLLSHHK			
Query	1101	~ ~	AGIFQQLRTVLEKGDFKAQKEA G+ L +L KGDFK+QKEA			YKILKPFID +L+P ++	
Sbjct	371		HGLVPYLIGILRKGDFKSQKE				
Query	1281		RTIKVVQTGLSNLFALAEKLGG +T+ V+ +SN+F AEK+		GGLDKLETLQQI GGLD++E LQ I		
Sbjct	430		KTVLVILDAVSNIFLAAEKINE				
Query	1461	AIIDT II+	YFSNGDDEAEQELAPQEVNGAI YFS ++E +O + P +	EF 1547 F			
Sbjct	490		YFS-AEEEEDÕNVVPDSTADSY				

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

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

500 bits(1288) 6e-166() Compositional matrix adjust. 260/524(50%) 363/524(69%) 26/524(4%) +3

Features:

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

Sbjct	6	ARLNKFKNKGKDVNELRRRRVEVNVELRKAKKDDQMFKRRNVSEDPDEATSPLQERNQNS	65
Query	213	QSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRFLQN Q+ SVD+IVA +NSE++E Q Q+ARK+LSR+++PPID MIG G++P + FL	392
Sbjct	66	QAFQPWSVDKIVAGVNSENREAQLQATQAARKLLSRDKHPPIDQMIGAGLIPKFVAFLGL	125
Query	393	TNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIA ++ +QFEA+WALTNIASGTSDQT V++ A+P F++L+ S +++EQAVWALGNIA	572
Sbjct	126	SDCHPIQFEASWALTNIASGTSDQTAAVVDGGAIPAFISLVTSPHQHISEQAVWALGNIA	185
Query	573	GDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQV GDG+A RD VI H I +L L+ TP +LRN+ W +SNLCRNKNPSPP + +	737
Sbjct	186	GDG+A RD VI H I +L L+ TP +LRN+ W +SNLCRNKNPSPP + + GDGSALRDRVIKHGAITPLLSLLAVPDLAVFTP-GYLRNVTWTLSNLCRNKNPSPPIEAI	244
Query	738	KRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSI K++LP L +LL + D++VLADACWA+SY+TD N +IQ VV++ +PRLVKLL +E S+	917
Sbjct	245	KQILPALIRLLHNDDLEVLADACWAYSYLTDGSNDRIQVVVETGLIPRLVKLLGYEELSV	304
Query	918	IVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQ + PALR++GNIVTGTD+OT V+ +G L LL+H K NI KEAAWT+SNITAG O	1097
Sbjct	305	VTPALRALGNIVTGTDEQTQAVLDAGALTVFPQLLRHKKGNIQKEAAWTLSNITAGKDTQ	364
Query	1098	IQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDL IO VI AG+	1277
Sbjct	365	IQ VI AG+ + +L +GD+K QKEA WAVTN T+ GT +Q+V L++ +L+P ++L IQEVINAGLVPYMVDLLVRGDYKTQKEAVWAVTNFTSGGTVQQVVYLVQA-NVLEPLLNL	423
Query	1278	LDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKA	1457
Sbjct	424	L +KD +T+ V+ ++N+F +K+G ++ L LM+EE GGLDK+E LQ HENE +YK A LSSKDSKTVLVILDAITNIFMAGDKIGESDKLSLMIEECGGLDKIEALQAHENEMIYKAA	483
Query	1458	YAIIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589	
Sbjct	484	+I+ YFS D+E + + P+A E GY F LNLIEKYFSEEDEEVQSVVPEATEDGYAF 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
Feature	s:						
Query	45		SYKANSINTODSRMRRHEVTIEI				~
Sbjct	5		S+K + ++ R RR TIEI SFKNKGKDCEEMRRRRIGQTIEI	LRK++K+DQ+ K LRKARKDDQLLK			S TS 64
Query	219	PVQLS PV +	SVDEIVAAMNSEDQERQFLGMQS +EI+ M + D+ O	SARKMLSRERNP S RK+LSRERNP		PICIRFLON P C+ FL	TN 398
Sbjct	65		KAEEIMYGMINPDESIQLQATLS				•
Query	399		FEAAWALTNIASGTSDOTRCV FEA WALTNIASGTS+OT V-			AVWALGNIA AVWALGNIA	
Sbjct	125		FEACWALTNIASGTSEÕTAAV				
Query	579		RDIVIHHNVIDGILPLINNETPI RD+V+ V+ IL LIN +T -	LSFLRNIVWLMS +S +RN VW +S			
Sbjct	185		RDMVLASGVLPEILRLINADTS				
Query	759	sqlll + LL	sqDIQVLADACWALSYVTDDD1 D VLAD+CWALSY+TD 1			EPSIIVPAL	
Sbjct	245		SYTDKDVLADSCWALSYLTDGSI				
Query	939		TGTDQQTDVVIASGGLPRLGLI TG D QTDVVI +G L L I				~
Sbjct	305		TGNDAQTDVVINAGVLHVLPKI				
Query	1119		LRTVLEKGDFKAQKEAAWAVTI + VL GDFK+OKEAAW VTI				
Sbjct	365		ILHVLSTGDFKSQKEAAWTVTI				
Query	1299		OTGLSNLFALAEKLGGTENLCI GL N+ + A KLG T+ + -				
Sbjct	424		ZLNGLDNILSAAHKLGETDKVA				
Query	1479	FSNGD FS	DEAEQELAPQEVNGALEFNAT( EA+ AP +G + F +	QPKAPEGGYTF + P+GG+ F	1589		
Sbjct	484		QEADMP-APATQDGQITFASPI		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)	8e-166()	Compositional matrix adjust.	262/516(51%)	359/516(69%)	6/516(1%)	+3
Features	3:						
Query	45	~	YKANSINTQDSRMRRHEVTIEL +K ++++ R RR+EV+IEL				SP 221
Sbjct	10		FKNKGKDSEELRRRRNEVSIEL				~ -
Query	222		DEIVAAMNSEDQERQFLGMQSA ++I A + S D+ O O+A	RKMLSRERNPP RK+LSRE+NPP			NN 401
Sbjct	70		EDIFAKLYSNDENVQLQATQAA				

Query	402	SMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALGNIAGDG LQFE+ WALTN+ASG S+QT V+ A+P FVALL+S +++AEQAVWALGNIAGDG	581
Sbjct	127	PTLQFESTWALTNVASGNSNQTMAVVNGGAIPKFVALLKSPHLHIAEQAVWALGNIAGDG	186
Query	582	AAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpvls RD+V+H N + IL LI +T + LRNIVW +SNLCRNKNP P F+ VK LP L	761
Sbjct	187	PKTRDLVLHCNAMPAILELIKPDTSIPVLRNIVWTLSNLCRNKNPPPNFNTVKICLPYLC	246
Query	762	qlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALRSV +LL D +VL DACWALSY++D N +IQAVVD+ V RLV+LL + +++ PALR+V	941
Sbjct	247	KLLSYDDKEVLGDACWALSYLSDGTNGRIQAVVDTGIVARLVELLSSSDFTVLTPALRTV	306
Query	942	GNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQAG GNIV+GTD QTD +I +GGL L LLLQH K+N+VKEAAWT+SNITAGN +QI+ VI A	1121
Sbjct	307	GNIVSGTDVQTDAIINAGGLQPLALLLQHPKNNMVKEAAWTISNITAGNVEQIEHVINAN	366
Query	1122	IFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDPRT I L VL KGD K+QKEAAWAVTN T+ G+P+Q+ LI + ++ +LD+K+ +	1301
Sbjct	367	ILPPLLDVLRKGDLKSQKEAAWAVIN IT GTPTQT LI T TT TLDTKT T ILPPLLDVLRKGDLKSQKEAAWAVTNLTSGGSPQQVASLI-CHGVIPHLCYILDSKECKI	425
Query	1302	IKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYAIIDTYF + + L+N+ +A+ + + LMV+E GG+DK+E LQQHENE++Y K IID YF	1481
Sbjct	426	+ + L+N+ +A+ + + LMV+E GG+DK+E LQQHENE++Y K IID YF VNLALDALANILQVAQNNNELDRIALMVQESGGVDKIEDLQQHENEQIYNKCATIIDKYF	485
Query	1482	SNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589	
Sbjct	486	+ D++ Q P N LEF A P+GG++F 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	t. 263/516(51%)	355/516(68%)	) 10/516(1%)	+3
Features	s:						
Query	24		DSNSRQGSYKANSINTQDSRMI				
Sbjct	1		++ +R +K +T + R I ENAARLTRFKNKGKDTTEMRRI	RR EV +ELRK+1 RRIEVNVELRKA			
Query	198		GQSPVQLSVDEIVAAMNSEI GO+ O SV+EIV + S		RKMLSRERNPP RK+LSRER PP		
Sbjct	61	+Ε Ν QEKNÇ	GQ+ Q SV+EIV + S QNGQTSTQWSVEEIVRGVASS				_
Query	372		LQNTNNSMLQFEAAWALTNIAS L T+ S +OFEAAWALTNIAS				
Sbjct	121		LARTDCSPIQFEAAWALTNIAS				
Query	552		NIAGDGAAARDIVIHHNVIDG NIAGDG+A RD+VI H + -	ILPLINNE' +L L+ +		LMSNLCRNKN +SNLCRNKN	
Sbjct	181		NIAGDG'A KD'VI II NIAGDGSAYRDLVIKHGAVGPI				
Query	720		QVKRllpvlsqlllsqDIQVLA ++++LP L +LL D +VLA	ADACWALSYVTDI AD CWA+SY+TD			
Sbjct	241		AIQQILPTLVRLLHHDDREVLA				
Query	900		SIIVPALRSVGNIVTGTDQQTI +I+ P LR+VGNIVTGTD+OT		GLLLQHNKSNI LL H+K+NI		
Sbjct	301		TIVTPCLRTVGNIVTGTDEÕT(				
Query	1080		KQIQAVIQAGIFQQLRTVLEKO OIO V+ G+ L +L K				IL 1259
Sbjct	361		OŽIŽEVVNHGLIPYLIEILRKA				
Query	1260		OLLDTKDPRTIKVVQTGLSNLI +LL KD +T+ V+ +N+I	FALAEKLGGTENI FA AEKLG TE I			
Sbjct	420		NLLSVKDSKTVLVILDAFTNVI				
Query	1440	EVYKI +VYK	XAYAIIDTYFSNGDDEAEQELA + +I+ YFS D E ++ LA		1547		
Sbjct	480		ASAGLIEKYFSAEDGE-DESLA		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	<b>S</b> :						
Query	36		RQGSYKANSINTQDSRMRRHEVT R+ S+K N +++R RR E++	TIELRKSKKEDÇ ++ELRK+KK++Ĉ		LTSPLKELN	~
Sbjct	8		RKASFKFN-YKHEEARRRRSEMS				
Query	216	SPVQI S +	SVDEIVAAMNSEDQERQFLGMQ S+DEIV M S D+ O	)SARKMLSRERN )+ RKMLSRE+N		VPICIRFLQ	NT 395
Sbjct	67	-	TSIDEIVNGMKSSDETIÕLQATÇ				YH 126
Query	396		QFEAAWALTNIASGTSDQTRC\ LOFEAAWALTN+ASGTS+OT \	/IEHNAVPHFVA /++H A+ +A			
Sbjct	127		LQFEAAWALTNVASGTSEQTHV\			~	

Query 576	DGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFDQVKRllpv DG ARD+V +F RNIVW +SNLCRNKNP PPF+ V+ LPV	755
Sbjct 187	DG ARD+V +F RNIVW +SNLCRNKNP PPF+ V+ LPV DGPVARDLVTFTRNIVWTLSNLCRNKNPPPPFNVVRTALPV	227
Query 756	lsqlllsqDiQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIVPALR	935
Sbjct 228	L++LL + D +LADACWALSY+TD N KIQAVV+S + +LV+LL E +++ PALR LNRLLSNDDKDILADACWALSYLTDGSNDKIQAVVESGVISKLVQLLNSAEVTVLTPALR	287
Query 936	SVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQAVIQ	1115
Sbjct 288	+VGNIVTG D QTD +I++GGL LGLLLQH++ NIVKEAAWT+SNITAG +QIQ VI AVGNIVTGNDTQTDAIISAGGLQYLGLLLQHHRVNIVKEAAWTISNITAGTMEQIQHVIS	347
Query 1116	AGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLDTKDP AG+ L VLE GDFK+QKEAAWAVTN TTSG+ Q+ L+E +L PF +LL+ KD	1295
Sbjct 348	AGLLPPLIHVLECGDFKSQKEAAWAVTNLTTSGSVVQLAQLVE-LGVLAPFCNLLEAKDW	406
Query 1296		1475
Sbjct 407	+TI VV GL+N+ A+++G E + +M+EE+GGLDKLE LQ H+ E+VY+KA A+IDT KTIIVVLDGLTNICNAADRMGEAERIAIMIEEVGGLDKLENLQHHDVEQVYQKATAMIDT	466
Query 1476		
Sbjct 467	+FS+ D + E LA + LEF + + G+ F FFSDPDAQ-EPILATSAADTPLEFKPNETTQKGFNF 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
Feature	s:						
Query	36		QGSYKANSINTQDSRMRRHEVI				
Sbjct	7	D SR DVPSR	t +K ++++ R RR+EV+ FRKFKNRGKDSEEMRRRRNEVS			+ SPL + EPVSPLHDN	
Query	213	QSPVQ + +	LSVDEIVAAMNSEDQERQFLGM +++EI A M+S D++ QF+			SIVPICIRFL S+VP CI FL	
Sbjct	67		TTIEEITAGMHSNDEQLÕFIAT				
Query	393		ILQFEAAWALTNIASGTSDQTRO LOFEAAWALTN+ASGTS OT			AEQAVWALGN AEOAVWALGN	
Sbjct	125		LÕFEAAWALTNVASGTSSÕTLI				
Query	573		ARDIVIHHNVIDGILPLINNET ARD+V+ + +L LI +T	PLSFLRNIVWL +SFLRNIVW			lp 752 LP
Sbjct	185		ARDMVLECLAMPALLELIKPDI				
Query	753	vlsql L +L	llsqDIQVLADACWALSYVTDI L D +V+ D CWALSY+TD			MDEPSIIVP E S++ P	
Sbjct	245		LNYSDNEVITDTCWALSYLTDO				
Query	933		IIVTGTDQQTDVVIASGGLPRLO				
Sbjct	305		IVTGNDSQTDYIIAAGGLQQLA				
Query	1113	QAGIF GI	'QQLRTVLEKGDFKAQKEAAWA\ L VL+KGD+++QKEAAWA+			KPFIDLLDT	
Sbjct	365		TPLLDVLKKGDYRSQKEAAWAI				
Query	1293	PRTIK +T+		CLMVEEMGGLD - +M+EE GGL+			ID 1472 I+
Sbjct	424	_	VILDGLSNLLQAAEKTGEVER				_
Query	1473	TYFSN +FS	IGDDEAEQELAPQEVNGALEF +E E + NG L F	1547			
Sbjct	484		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	~	YKANSINTQDSRMRRHEVTIEL +K +T + R RR EV +EL				-Q 215	
Sbjct	12		FKNKGKDTTEMRRRRIEVNVEL					
Query	216	~	SVDEIVAAMNSEDQERQFLGMQ SV+EIV +NS + E Q Q	SARKMLSRERNI +ARK+LSRE+ I			NT 395	
Sbjct	72		SVEEIVKGVNSNNMELQLQATQ				RA 131	
Query	396		QFEAAWALTNIASGTSDQTRCV QFE+AWALTNIASGTS+QT+ V			AVWALGNI AVWALGNI		
Sbjct	132		QFESAWALTNIASGTSEQTKAV					
Query	576		RDIVIHHNVIDGILPLIN RD+VI I+ +L L+		VWLMSNLCRNKN W +SNLCRNKN			
Sbjct	192		RDLVIKFGAIEPLLSLLAVPDL					

Query	744	llpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEPSIIV +LP L +LL D +VLAD CWALSY+TD N +I+ VV + VP+LVKLL E I+	923
Sbjct	252	ILPTLVRLLHHDDHEVLADTCWALSYLTDSSNDRIEVVVKTGLVPQLVKLLGCSELPIMT	311
Query	924	PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ	1103
Sbjct	312	P+LR++GNIVTGTD+QT $VVI$ $SG$ $L$ $LL$ $H+K+NI$ $KEAAWT+SNITAG$ $Q$ $QIQ$ $PSLRAIGNIVTGTDEQTQVVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQIQ$	371
Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD	1283
Sbjct	372	VI G+ L +L KGDFK+QKEA WAVTN T+ GT +QIV L++ +++P ++LL RVIDHGLVPYLIGILRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVVEPLLNLLS	430
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA	1463
Sbjct	431	KD RT+ V+ +SN+F AEK+ TE LCLM+EE GGLD++E LQ HENE+VYK + AKDSRTVLVILDAISNIFVAAEKINETEKLCLMIEECGGLDRIEALQSHENEQVYKASST	490
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALEF 1547	
Sbjct	491	+I+ YFS ++E +Q + P+ + F LIEKYFS-AEEEEDQNVVPESTAASYTF 517	

PREDICTED: importin subunit alpha-1 [Apteryx australis mantelli]
Sequence ID: ref|XP\_013808591.1| Length: 528 Number of Matches: 1

**Expect Method** 

# ▶ See 1 more title(s) Range 1: 7 to 516

Score

499 bits	(1286)	1e-165() Compositional matrix adjust. 258/512(50%) 356/512(69%) 9/512(1%) +3	
Feature	s:		
Query	33	ADSNSRQGSYKANSINTQDSRMRRHEVTIELRKSKKEDQMFKRRNINDEDLTSPLKE-	203
Sbjct	7	A++ +R +K +T + R RR EV +ELRK+KK+DQM KRRN++ +D TSPL+E ANAAARLNRFKNKGKDTTEMRRRRIEVNVELRKAKKDDQMLKRRNVSTLPDDATSPLQEN	66
Query	204	LNGQSPVQLSVDEIVAAMNSEDQERQFLGMQSARKMLSRERNPPIDLMIGHGIVPICIRF N O SV+EIV +NS + E O Q+ARK+LSRE+ PPID +I G++P + F	383
Sbjct	67	N Q SV+EIV +NS + E Q Q+ARK+LSRE+ PPID +I G++P + F RNNQVSAHWSVEEIVKGVNSNNTELQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSF	126
Query	384	LQNTNNSMLQFEAAWALTNIASGTSDQTRCVIEHNAVPHFVALLQSKSMNLAEQAVWALG L + S +QFE+AWALTNIASGTS+QT+ V++ A+P F++LL S +++EQAVWALG	563
Sbjct	127	LGRADCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHTHISEQAVWALG	186
Query	564	NIAGDGAAARDIVIHHNVIDGILPLINNETPLSFLRNIVWLMSNLCRNKNPSPPFD NIAGDG+ RD+VI I+ +L L+ + +LRN+ W +SNLCRNKNP+PP +	731
Sbjct	187	NIAGDGSTYRDLVIKFGAIEPLLTLLAVPDLSSLASGYLRNVTWTLSNLCRNKNPAPPIE	246
Query	732	QVKRllpvlsqlllsqDIQVLADACWALSYVTDDDNTKIQAVVDSDAVPRLVKLLQMDEP ++++LP L +LL D +VLAD CWALSY+TD N +I+ VV + VP+LVKLL E	911
Sbjct	247	AIEQILPTLVRLLHHNDHEVLADTCWALSYLTDGSNDRIEVVVKTGLVPQLVKLLGCSEL	306
Query	912	SIIVPALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQ I+ P+LR++GNIVTGTD+OT +VI SG L LL H+K+NI KEAAWT+SNITAG O	1091
Sbjct	307	PIVTPSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLSHHKNNIQKEAAWTMSNITAGRQ	366
Query	1092	KQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFI QIQ V+ G+ L VL KGDFK+QKEA WAVTN T+ GT +QIV L++ +++P +	1271
Sbjct	367	DÕIÕQVVDHGLVPYLIGVLRKGDFKSÕKEAVWAVTNYTSGGTIDÕIVYLVQA-GVVEPLL	425
Query	1272	DLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYK +LL KD +T+ V+ +SN+F AEK+ TE LCLM+EE GGLDK+E LO HENE+VYK	1451
Sbjct	426	NLLSAKDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYK	485
Query	1452	KAYAIIDTYFSNGDDEAEQELAPQEVNGALEF 1547 + ++I+ YFS ++E +O + P+	
Sbjct	486	ASSSLIEKYFS-AEEEEDQNVVPESTAASYTF 516	

Identities

Gaps

**Frame** 

**Positives** 

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	s:						
Query	45	_ ~	SYKANSINTQDSRMRRHEVTIE:				=
Sbjct	12	+R ARLNF	+K ++ + R RR EV +E RFKNKGKDSTEMRRRRIEVNVE				Q NQ 71
Query	216	SPVQI	LSVDEIVAAMNSEDQERQFLGM				NT 395
Sbjct	72	GSALV	SV+EIV +NS + E Q VSVEEIVKGINSNNLEVQLQAT	Q+ARK+LSRE+ QAARKLLSREKÇ			RT 131
Query	396		LOFEAAWALTNIASGTSDQTRC				
Sbjct	132		-QFE+AWALTNIASGTSDQT+  QFESAWALTNIASGTSDQTKA			EQAVWALGNI. EQAVWALGNI.	
Query	576		ARDIVIHHNVIDGILPLIN				
Sbjct	192		RD+VI + ID +L L+ RDLVIKYGAIDPLLALLAVPD		+ W +SNLCRNK TWTLSNLCRNK		
Query	744		sqlllsqDIQVLADACWALSY				
Sbjct	252		L +LL D +VLAD CWA+SY LVRLLHHDDPEVLADTCWAISY				

Query	924	PALRSVGNIVTGTDQQTDVVIASGGLPRLGLLLQHNKSNIVKEAAWTVSNITAGNQKQIQ P+LR++GNIVTGTD+QT +VI SG L LL H K+NI KEAAWT+SNITAG Q QIQ	1103
Sbjct	312	PSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLTHPKTNIQKEAAWTMSNITAGRQDQIQ	371
Query	1104	AVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLLD	1283
Sbjct	372	V+ $G+$ $L$ $+L$ $KGDFK+QKEA$ $WAVTN$ $T+$ $GT$ $EQIV$ $L++$ $IL+P$ $I+LL$ $QVVNHGLVPYLVGILSKGDFKSQKEAVWAVTNYTSGGTIEQIVYLVQN-GILEPLINLLS$	430
Query	1284	TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA	1463
Sbjct	431	KD + + V+	490
Query	1464	IIDTYFSNGDDEAEQELAPQEVNGALEFNATQPKAPEGGYTF 1589	
Sbjct	491	+I+ YFS +E +Q + P+ + F Q AP G + F LIEKYFSAEEEDQNVVPESTSDGYTFQ-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	<b>S</b> :						
Query	24		OSNSRQGSYKANSINTQDSRMR -+ +R +K ++ + R R	RHEVTIELRKSI R EV +ELRK+I			
Sbjct	1		ENGARLTRFKNKGKDSTEMRRR				
Query	198	KELN- +E N	GOSPVOLSVDEIVAAMNSED GO+ O SV+EIV + +		RKMLSRERNPP: RK+LSRER PP:		
Sbjct	61		ONGÕTSSÕWSVEEIVRGVANPS				
Query	372		QNTNNSMLQFEAAWALTNIAS L +++ S +OFEAAWALTNIAS				
Sbjct	121		LAHSDCSPIQFEAAWALTNIAS				
Query	552		NIAGDGAAARDIVIHHNVIDGI NIAGDG+A RD+VI H + +	LPLINNET		LMSNLCRNKN +SNLCRNKN	
Sbjct	181		VIAGDG'A KD'VI II VIAGDGSAYRDLVIKHGAVGPL				
Query	720		QVKRllpvlsqlllsqDIQVLA ++++LP + +LL				
Sbjct	241		AIQQILPTIVRLLHHDDREVLA				
Query	900		SIIVPALRSVGNIVTGTDQQTD -++ P LR++GNIVTGTD+OT			VKEAAWTVSN KEAAWT+SN	
Sbjct	301		TVVTPCLRTIGNIVTGTDEQTQ				
Query	1080		KQIQAVIQAGIFQQLRTVLEKG QIQ V+ G+ L +L KG				IL 1259 I+
Sbjct	361		OŽIŽEVVNCGLIPYLVEILRKG				
Query	1260		DLLDTKDPRTIKVVQTGLSNLF -LL KD +T+ V+ +N+F	ALAEKLGGTENI A A+K+G TE I			
Sbjct	420		ILLSVKDSKTVLVMLDAFTNIF				
Query	1440		XAYAIIDTYFSNGDDEAEQELA + A+I+ YFS D E ++ LA		1547		
Sbjct	480		ASAALIEKYFSAEDGE-DESLA		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	s:						
Query	33	ADSNS A++ +	RQGSYKANSINTQDSRMRRHEV R +K +T + R RR EV			-EDLTSPLK +D TSPL+	
Sbjct	7		RLNRFKNKGKDTTEMRRRRIEV				
Query	204	LNGQS N O	PVQLSVDEIVAAMNSEDQERQF SV+EIV +NS + E O	LGMQSARKMLS Q+ARK+LS			RF 383
Sbjct	67		SAHWSVEEIVKGVNSNNTELÕL				_
Query	384		NSMLQFEAAWALTNIASGTSDQ S +QFE+AWALTNIASGTS+Q			NLAEQAVWA +++EOAVWA	
Sbjct	127		CSPIQFESAWALTNIASGTSEQ				
Query	564	NIAGD NIAGD	GAAARDIVIHHNVIDGILPLIN G+ RD+VI I+ +L L+		LRNIVWLMSNLO LRN+ W +SNLO		
Sbjct	187		GSTYRDLVIKFGAIEPLLTLLA				
Query	732		lpvlsqlllsqDIQVLADACWA LP L +LL D +VLAD CWA				
Sbjct	247		LPTLVRLLHHNDHEVLADTCWA				
Query	912	SIIVP	ALRSVGNIVTGTDQQTDVVIAS	GGLPRLGLLLQ	HNKSNIVKEAAV	WTVSNITAG	NQ 1091

Sbjct	307	I+ P+LR++GNIVTGTD+QT +VI SG L LL H+K+NI KEAAWT+SNITAG Q PIVTPSLRAIGNIVTGTDEQTQIVIDSGALSVFPSLLAHHKNNIQKEAAWTMSNITAGRQ	366
Query	1092	KQIQAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFI QIQ V+ G+ L +L KGDFK+QKEA WAVTN T+ GT +QIV L++ +++P +	1271
Sbjct	367	DÕIÕRVVDHGLVPYLIGILRKGDFKSÕKEAVWAVTNYTSGGTIDÕIVYLVQA-GVVEPLL	425
Query	1272	DLLDTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYK +LL KD +T+ V+ +SN+F AEK+ TE LCLM+EE GGLDK+E LQ HENE+VYK	1451
Sbjct	426	NLLTAKDSKTVLVILDAVSNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYK	485
Query	1452	KAYAIIDTYFSNGDDEAEQELAPQEVNGALEF 1547	
Sbjct	486	+ +I+ YFS ++E +Q + P+ + F 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()	Compositiona	al matrix adjust.	256/512(50%)	355/512(69%)	9/512(1%)	+3
Features	<b>S</b> :							
Query	33			NTQDSRMRRHEV				
Sbjct	7	A++ + ANAAA		+T + R RR EV DTTEMRRRRIEV			+D TSPL+ PDDATSPLQ	
Query	204	LNGQS N Q	PVQLSVDEIV. SV+EIV	AAMNSEDQERQF	LGMQSARKMLS O+AR++LS			RF 383
Sbjct	67			KGVNSNNTĒLÕI				
Query	384			ALTNIASGTSDÇ ALTNIASGTS+Ç			NLAEQAVWA +++EOAVWA	
Sbjct	127			ALTNIASGTSEÕ				
Query	564	NIAGD NIAGD		HNVIDGILPLIN ID +L L+		LRNIVWLMSNLO LRN+ W +SNLO		
Sbjct	187			FGAIDPLLSLLA				
Query	732		lpvlsqllls LP L +LL	qDIQVLADACWA	LSYVTDDDNTK LSY+TD N +			EP 911 E
Sbjct	247			DDHEVLADTCWA				_
Query	912			GTDQQTDVVIAS GTD+OT +VI S		HNKSNIVKEAA H+K+NI KEAA		
Sbjct	307			GTDEÕTQIVIDS				
Query	1092			RTVLEKGDFKAÇ +L KGDFK+Ç				
Sbjct	367			IGILRKGDFKSÇ				•
Query	1272		KDPRTIKVVQ KD +T+ V+	TGLSNLFALAEK +SN+F AEK		EEMGGLDKLET: EE GGLDK+E :		
Sbjct	426			DAISNIFLAAEK				
Query	1452			EAEQELAPQEVN E +O + P+	IGALEF 1547 + F			
Sbjct	486			EEDÕNVVPESTA				

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	<b>S</b> :						
Query	42	NSRQG ++R	SYKANSINTQDSRMRRHEVTIE +K ++ + R RR EV +E			LTSPLKELNO TSPL+E	
Sbjct	11		RFKNKGKDSTEMRRRRIEVNVE				_
Query	213		LSVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E Q		NPPIDLMIGHG		QN 392
Sbjct	71	Q QVLAH	WSVEEIVKGVNSNNMELQLQAT				GK 130
Query	393		LQFEAAWALTNIASGTSDQTRC +QFE+AWALTNIASGTS+QT+			EQAVWALGN EÕAVWALGN	
Sbjct	131		IQFESAWALTNIASGTSEQTKA			~	
Query	573		ARDIVIHHNVIDGILPLIN RD+VI + I+ +L L+		IVWLMSNLCRNI + W +SNLCRNI		
Sbjct	191		YRDLVIKYGAIEPLLSLLAVPD				
Query	741		lsqlllsqDIQVLADACWALSY L +LL D +VLAD CWA+SY				II 920 I+
Sbjct	251		LVRLLHHDDPEVLADTCWAISY				
Query	921		SVGNIVTGTDQQTDVVIASGGI ++GNIVTGTD+QT +VI SG I		SNIVKEAAWTV: +NI KEAAWT+;		

Sbjct	311	TPSLRAIGNIVTGTDEQTQIVIDSGALAVFPSLLSHHKNNIQKEAAWTMSNITAGRQDQI	370
Query	1101	QAVIQAGIFQQLRTVLEKGDFKAQKEAAWAVTNTTTSGTPEQIVDLIEKYKILKPFIDLL	1280
Sbjct	371	Q VI G+ L VL KGDFK+QKEA WAVTN T+ GT +QIV L++ +L+P ++LL QRVIDHGLVPYLIGVLRKGDFKSQKEAVWAVTNYTSGGTIDQIVYLVQA-GVLEPLLNLL	429
Query	1281	DTKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAY	1460
Sbjct	430	TKD +T+ V+ +SN+F AEK+ TE LCLM+EE GGLD++E LQ HENE+VY+ + STKDSKTVLVILDAVSNIFMAAEKINETEKLCLMIEECGGLDRIEALQSHENEQVYRASS	489
Query	1461	AIIDTYFSNGDDEAEQELAPQEVNGALEF 1547	
Sbjct	490	II+ YFS ++E +Q + P + F 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	s:						
Query	42		SYKANSINTQDSRMRRHEVTIE				G- 212
Sbjct	11	++R SARLN	+K ++ + R RR EV +E RFKNKGKDSTEMRRRRIEVNVE			TSPL+E ATSPLQENR	GN 70
Query	213		LSVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E Q	IQSARKMLSRER Q+ARK+LSRE+		IVPICIRFL ++P + FL	
Sbjct	71	Q QVLAH	WSVEEIVKGVNSNNMELQLQAT				
Query	393		LQFEAAWALTNIASGTSDQTRC +QFE+AWALTNIASGTS+OTR			EQAVWALGN EOAVWALGN	
Sbjct	131		PIQFESAWALTNIASGTSEQTRA				
Query	573		ARDIVIHHNVIDGILPLIN RD+VI + I+ +L L+		IVWLMSNLCRNI + W +SNLCRNI		
Sbjct	191		YRDLVIKYGAIEPLLSLLAVPD				
Query	741	_	lsqlllsqDIQVLADACWALSY L +LL D +VLAD CWA+SY			~	II 920 I+
Sbjct	251		LVRLLHHDDPEVLADTCWAISY				_
Query	921		SVGNIVTGTDQQTDVVIASGGI ++GNIVTGTD+OT +VI SG I				
Sbjct	311		AIGNIVTGTDEQTQIVIDSGAI				
Query	1101	QAVIQ O V+	AGIFQQLRTVLEKGDFKAQKEA G+ L +L KGDFK+OKEA			YKILKPFID +L+P ++	
Sbjct	371		HGLVPYLIGILRKGDFKSQKEA				
Query	1281		RTIKVVQTGLSNLFALAEKLGG +T+ V+ +SN+F AEK+		GGLDKLETLQQI GGLD++E LO I		
Sbjct	430		KTVLVILDAVSNIFLAAEKINE				
Query	1461	AIIDT II+	YFSNGDDEAEQELAPQEVNGAI YFS ++E +O + P +	LEF 1547			
Sbjct	490		YFS-AEEEEDQSVVPGSTANSY	-			

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	s:						
Query	45	~	YKANSINTQDSRMRRHEVTIEL				~
Sbjct	12		+K +T + R RR EV +EL FKNKGKDTTEMRRRRIEVNVEL				Q NQ 71
Query	216	_	SVDEIVAAMNSEDQERQFLGMQ SV+EIV +NS + E Q Q				NT 395
Sbjct	72		SVEEIVKGVNSNNMELQLQATQ				RA 131
Query	396		QFEAAWALTNIASGTSDQTRCV OFE+AWALTNIASGTS+OT+ V			QAVWALGNI OAVWALGNI	
Sbjct	132		QFESAWALTNIASGTS+QTKAV				
Query	576	DGAAA DG+A	RDIVIHHNVIDGILPLIN RD+VI I+ +L L+		VWLMSNLCRNK		
Sbjct	192		RDLVIKFGAIEPLLSLLAVPDL				
Query	744	llpvl +LP L	sqlllsqDIQVLADACWALSYV +LL D +VLAD CWALSY+				
Sbjct	252		VRLLHHDDHEVLADTCWALSYL				-
Query	924	PALRS	VGNIVTGTDQQTDVVIASGGLP	RLGLLLQHNKS	NIVKEAAWTVS	NITAGNOKO	IQ 1103
Sbjct	312		+GNIVTGTD+QT +VI SG L IGNIVTGTDEQTQIVIDSGALS				
Query	1104	AVIQA V+	GIFQQLRTVLEKGDFKAQKEAA				
Sbjct	372	•	G+ L +L KGDFK+QKEA GLVPYLIGILRKGDFKSQKEAV			+++P ++L: GVVEPLLNL:	

```
TKDPRTIKVVQTGLSNLFALAEKLGGTENLCLMVEEMGGLDKLETLQQHENEEVYKKAYA 1463
KD +T+ V+ +SN+F AEK+ TE LCLM+EE GGLDK+E LQ HENE+VYK +
AKDSKTVLVILDAISNIFLAAEKINETEKLCLMIEECGGLDKIEALQSHENEQVYKASST 490
Query 1284
Sbjct 431
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	s:						
Query	33	ADSNS A++ +	RQGSYKANSINTQDSRMRRHEV R +K +T + R RR EV			-EDLTSPLK +D TSPL+	
Sbjct	7		RLNRFKNKGKDTTEMRRRRIEV				
Query	204	LNGQS N Q	PVQLSVDEIVAAMNSEDQERQF SV+EIV +NS + E O	LGMQSARKMLS Q+ARK+LS			RF 383
Sbjct	67		SAHWSVEEIVRGVNSNNMELQI				_
Query	384		NSMLQFEAAWALTNIASGTSDC S + OFE+AWALTNIASGTS+C			NLAEQAVWA +++EOAVWA	
Sbjct	127		CSPIQFESAWALTNIASGTSEQ				
Query	564	NIAGD NIAGD	GAAARDIVIHHNVIDGILPLIN G+ RD+VI I+ +L L+		LRNIVWLMSNLO		
Sbjct	187		GSTYRDLVIKFGAIEPLLSLLA				
Query	732		lpvlsqlllsqDIQVLADACWA				EP 911 E
Sbjct	247		LPTLVRLLHHDDHEVLADTCWA				
Query	912		ALRSVGNIVTGTDQQTDVVIAS +LR++GNIVTGTD+QT +VI S		HNKSNIVKEAAI H+K+NI KEAAI		
Sbjct	307		SLRAIGNIVTGTDEQTQIVIDS				
Query	1092		.VIQAGIFQQLRTVLEKGDFKAÇ V+ G+ L +L KGDFK+C				
Sbjct	367		VVDHGLVPYLIGILRKGDFKSQ				
Query	1272		KDPRTIKVVQTGLSNLFALAEK KD +T+ V+ +SN+F AEK		EEMGGLDKLETI EE GGLDK+E 1		
Sbjct	426		KDSKTVLVILDAISNIFLAAEK				
Query	1452		IDTYFSNGDDEAEQELAPQEVN I+ YFS ++E +O + P+	IGALEF 1547 + F			
Sbjct	486		IEKYFS-AEEEEDQNVVPESTA				

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 I	Frame
498 bits	(1282)	5e-165()	Compositional matrix adjust.	257/508(51%)	357/508(70%)	9/508(1%) +	-3
Features	3:						
Query	45		YKANSINTQDSRMRRHEVTIEL +K +T + R RR EV +EL			TSPLKE-LNG TSPL+E N	~
Sbjct	12		FKNKGKDTTEMRRRRIEVNVEL				
Query	216		SVDEIVAAMNSEDQERQFLGMQ SV+EIV +NS + E O O	SARKMLSRERNI +ARK+LSRE+			IT 395 Т
Sbjct	72		SVEEIVKGINSNNLELÕLQATÕ				_
Query	396		QFEAAWALTNIASGTSDQTRCV OFE+AWALTNIASGTS+OT+ V			QAVWALGNIA DAVWALGNIA	
Sbjct	132		QFESAWALTNIASGTSEQTKAV				
Query	576		RDIVIHHNVIDGILPLIN RD+VI + ID +L L+		VWLMSNLCRNKI W +SNLCRNKI		
Sbjct	192		RDLVIKYGAIDPLLALLAVPDL				
Query	744	llpvl +LP L	sqlllsqDIQVLADACWALSYV +LL D +VLAD CWA+SY+				
Sbjct	252		LRLLHHNDHEVLADTCWAISYL				
Query	924		VGNIVTGTDQQTDVVIASGGLP +GNIVTGTD+QT +VI SG L				
Sbjct	312		IGNIVTGTDEQTQIVIESGALG				
Query	1104	AVIQA V++	GIFQQLRTVLEKGDFKAQKEAA G+ L +L+KGDFK+QKEA			KILKPFIDLI +++P ++LI	
Sbjct	372	•	GLVPYLIGILKKGDFKSQKEAV				
Query	1284		TIKVVQTGLSNLFALAEKLGGT T+ V+ ++N+F AEK+ T	ENLCLMVEEMGO E LCLM+EE GO			A 1463
Sbjct	431		TVLVILDAITNIFLAAEKIDET				SN 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 I	Frame_
498 bits	(1282)	5e-165()	Compositional matrix adjust.	260/516(50%)	356/516(68%)	10/516(1%) +	-3
Features	<b>3</b> :						
Query	48		KANSINTQDSRMRRHEVTIEL				S 218
Sbjct	11		-K +T + R RR EV +EL KNKGKDTTEMRRRRIEVNVEL			TSPL+E + Q TSPLQENRSNQ	v 70
Query	219		SVDEIVAAMNSEDQERQFLGMQ SV+EIV +NS + E Q Q	SARKMLSRERNI +ARK+LSRE+ I			N 398
Sbjct	71		SVEEIVKGVNSNNMELÕLQATÕ.				
Query	399		FEAAWALTNIASGTSDQTRCV FE+AWALTNIASGTS+OT+ V			QAVWALGNIAG QAVWALGNIAG	
Sbjct	131	CSPIÇ	PESAWALTNIASGIS OT V PESAWALTNIASGISEQTKAV	VDGGAIPAFIS	LLASPHTHISE	QAVWALGNIAG QAVWALGNIAG	D 190
Query	579	GAAAR G+A R	RDIVIHHNVIDGILPLIN RD+VI I+ +L L+		VWLMSNLCRNKI W +SNLCRNKI		
Sbjct	191		RDLVIKFGAIEPLLSLLAVPDL				
Query	747	lpvls LP L	qlllsqDIQVLADACWALSYV +LL D +VLAD CWALSY+				
Sbjct	251		RLLHHDDHEVLADTCWALSYL				_
Query	927		GNIVTGTDQQTDVVIASGGLP: -GNIVTGTD+OT +VI SG L	RLGLLLQHNKSI LL H+KSI			
Sbjct	311		GNIVTGTDEQTQIVIDSGALS				
Query	1107	VIQAG V+ G	GIFQQLRTVLEKGDFKAQKEAA G+ L +L KGDFK+QKEA			KILKPFIDLLD +++P ++LL	T 1286
Sbjct	371		SLVPYLIGILRKGDFKSÕKEAV	WAVTNYTSGGT:	IDÕIVYLVQA-		A 429
Query	1287	KDPRT KD +T	TIKVVQTGLSNLFALAEKLGGT T+ V+ +SN+F AEK+ T	ENLCLMVEEMGO E LCLM+EE GO			I 1466
Sbjct	430		VLVILDAVSNIFLAAEKINET				
Query	1467	IDTYF I+ YF	SNGDDEAEQELAPQEVNGALE S ++E +O + P+ +		1574		
Sbjct	490		S-AEEEEDÕNVVPESTAASYT		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()	Compositiona	l matrix adjust.	258/512(50%)	358/512(69%)	9/512(1%)	+3
Feature	s:							
Query	33	ADSNS A++ +			TIELRKSKKED +ELRK+KK+D		-EDLTSPLK +D TSPL+	
Sbjct	7				NVELRKAKKDD			
Query	207			AMNSEDQERQF +NS + E O	LGMOSARKMLS	RERNPPIDLMI RE+ PPID +I		
Sbjct	67	G Q KGNQV	SV+EIV LAHWSVEEIVK		QTARKTLS: QATQAARKLLS:			F SF 126
Query	384				TRCVIEHNAVP T+ V++ A+P			
Sbjct	127	L LGRAE			TKAVVDGGAIP.		+++EQAVWA HISEQAVWA	
Query	564				NETPLSF			
Sbjct	187		G+A RD+VI + GSAYRDLVIKY		+ +; VPDLSSLASGY:	LRN+ W +SNL LRNVTWTLSNL		
Query	732	QVKR1	lpvlsqllls	DIQVLADACWA	LSYVTDDDNTK +SY+TD N +	IQAVVDSDAVP	RLVKLLQMD	
Sbjct	247				ISYLTDGSNDR			E EL 306
Query	912				GGLPRLGLLLQ G L LL			
Sbjct	307				GALAVFPSLLS			
Query	1092				KEAAWAVTNTT			
Sbjct	367		V+ G+ L VVDHGLVPYLI		KEAAWAVTN T KEAAWAVTNYT			
Query	1272		KDPRTIKVVQT KD +T+ V+	GLSNLFALAEK +SN+F AEK	LGGTENLCLMV	EEMGGLDKLET: EE GGLDK+E :		
Sbjct	426				INETEKLCLMI			
Query	1452	KAYAI	IDTYFSNGDDE	CAEQELAPQEVN	GALEF 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	<b>S</b> :						
Query	45	~	SYKANSINTQDSRMRRHEVTIE: +K +T + R RR EV +E				~
Sbjct	12	+R ARLNR	RFKNKGKDTTEMRRRRIEVNVE:				Q NQ 71
Query	216		SVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E Q				NT 395
Sbjct	72		SVEETVKGVNSNNMELÕLQAT				RA 131
Query	396		QFEAAWALTNIASGTSDQTRC			QAVWALGNI QAVWALGNI	
Sbjct	132		QFESAWALTNIASGTSEQTKA				
Query	576		RDIVIHHNVIDGILPLIN RD+VI + I+ +L L+		VWLMSNLCRNK W +SNLCRNK		
Sbjct	192		RDLVIKYGAIEPLLSLLAVPD				
Query	744	llpvl +LP L	.sqlllsqDIQVLADACWALSY L +LL D +VLAD CWA+SY				IV 923
Sbjct	252		VRLLHHDDHEVLADTCWAISY				MT 311
Query	924		SVGNIVTGTDQQTDVVIASGGL: -+GNIVTGTD+OT +VI SG L				
Sbjct	312		IGNIVTGTDEÕTQIVIDSGAL				
Query	1104	~	GIFQQLRTVLEKGDFKAQKEA G+ L +L KGDFK+OKEA			KILKPFIDL +++P ++L	
Sbjct	372	-	IGLVPYLIGILRKGDFKSQKEA				
Query	1284		RTIKVVQTGLSNLFALAEKLGG T+ V+ +SN+F AEK+ '	TENLCLMVEEMG TE LCLM+EE G			
Sbjct	431		TVLVILDAISNIFLAAEKINE				
Query	1464	IIDTY +I+ Y	TFSNGDDEAEQELAPQEVNGALT TFS ++E +Q + P+ +	EF 1547 F			
Sbjct	491		FS-AEEEEDÕNVVPESTAASY				

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	<b>3</b> :						
Query	48		KANSINTQDSRMRRHEVTIELF K +T + R RR E+ +ELF			SPLKE-LNG SPL+E +	
Sbjct	13		KNKGKDTTEMRRRRIEINVELF				
Query	219		VDEIVAAMNSEDQERQFLGMQS V+EIV +NS + E Q Q+				TN 398
Sbjct	73		VEEIVKGINSNNMELQLQATQA	ARKTLSREKQP	PID +1 G++. PIDSIIRAGLI	PRFVSFLGR	AD 132
Query	399		FEAAWALTNIASGTSDQTRCVI FE+AWALTNIASGTS+QT+ V+			AVWALGNIA AVWALGNIA	
Sbjct	133		FESAWALTNIASGIS+QI+ V+ FESAWALTNIASGISEQTKAVV				
Query	579		DIVIHHNVIDGILPLINND+VI I+ +L L+ +		WLMSNLCRNKN W +SNLCRNKN		
Sbjct	193		DLVIKFGAIEPLLSLLAVPDLS				
Query	747	lpvls LP L	qlllsqDIQVLADACWALSYVT +LL D +VLAD CWALSY+T		DSDAVPRLVKL: + VP+LVKL:		
Sbjct	253		RLLHHDDHEVLADTCWALSYLT				
Query	927		GNIVTGTDQQTDVVIASGGLPF GNIVTGTD+OT VVI SG L				
Sbjct	313		GNIVTGTD+QT VVI SG L GNIVTGTDEQTQVVIDSGALSV				
Query	1107		IFQQLRTVLEKGDFKAQKEAAW + L +L KGDFK+QKEA W			ILKPFIDLL ++KP ++LL	
Sbjct	373		LVPYLIGILRKGDFKSQKEAVW				
Query	1287	KDPRT KD +T	TIKVVQTGLSNLFALAEKLGGTE T+ V+ +SN+F AEK+ TE	NLCLMVEEMGG: LCLM+EE GG:			
Sbjct	432		+ V+ +SN+F AEK+ TE VLVILDAISNIFLAAEKINETE				+ TL 491
Query	1467	IDTYF I+ YF	SNGDDEAEQELAPQEVNGALEE S ++E + + P+ + E				

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	s:						
Query	45	~	SYKANSINTQDSRMRRHEVTIE +K ++ + R RR EV +E				~
Sbjct	12	+R ARLNI	RFKNKGKDSSEMRRRRIEVNVE				Q NQ 71
Query	216	SPVQI	LSVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E O				NT 395
Sbjct	72	GSAHV	NSVEEIVRGINSNNLELQLQAT				
Query	396		LQFEAAWALTNIASGTSDQTRC +QFE+AWALTNIASGTSDQT+			EQAVWALGNI EQAVWALGNI	
Sbjct	132		IQFESAWALTNIASGTSDQTKA				
Query	576		ARDIVIHHNVIDGILPLIN RD+VI + ID +L L		IVWLMSNLCRNI + W +SNLCRNI		
Sbjct	192		YRDLVIKYGAIDPLLALFAVPD				
Query	744		lsqlllsqDIQVLADACWALSY L +LL D VLAD CWA+SY				IV 923
Sbjct	252		LVRLLHHDDQDVLADTCWAISY				•
Query	924		SVGNIVTGTDQQTDVVIASGGL ++GNIVTGTD+QT +VI +G L				
Sbjct	312		AIGNIVTGTDEÕTQIVIEAGAL.				
Query	1104	~	AGIFQQLRTVLEKGDFKAQKEA G+ L +L KGDFK+OKEA			YKILKPFIDL I++P I+L	
Sbjct	372	•	HGLVPYLVEILSKGDFKSÕKEA				
Query	1284		RTIKVVQTGLSNLFALAEKLGG + + V+ ++N+F AEKLG	TENLCLMVEEMO			
Sbjct	431		KIVLVILDAITNIFLAAEKLGE				
Query	1464	IIDTY +I+	YFSNGDDEAEQELAPQEVNGAL YFS ++E +O + P+ +		GGYTF 1589 G + F		
Sbjct	491		YFS-AEEEEDQNVVPESTSDGY				

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 Fra	ame
498 bits	(1281)	8e-165()	Compositional matrix adjust.	257/508(51%)	355/508(69%)	9/508(1%) +3	
Features	s:						
Query	45	~	YKANSINTQDSRMRRHEVTIEL			~	215
Sbjct	12		+K       ++ + + R RR EV +EL FKNKGKDSTEMRRRRIEVNVEL			TSPL+E G Q TSPLQENRGNQ	71
Query	216		SVDEIVAAMNSEDQERQFLGMQ				39!
Sbjct	72		SV+EIV +NS + E Q Q SVEEIVKGVNSNNMELQLQATQ	+ARK+LSRE+ 1 AARKLLSREKQ1			13
Query	396		QFEAAWALTNIASGTSDQTRCV				57
Sbjct	132		QFE+AWALTNIASGTS+QTR V QFESAWALTNIASGTSEQTRAV			QAVWALGNIAG QAVWALGNIAG	19
Query	576		RDIVIHHNVIDGILPLIN				74
Sbjct	192		RD+VI + I+ +L L+ RDLVIKYGAIEPLLSLLAVPDL		W +SNLCRNK FWTLSNLCRNK		25
Query	744		sqlllsqDIQVLADACWALSYV				92
Sbjct	252	+LP L ILPTL	+LL <sup>-</sup> D +VLAD CWA+SY+ VRLLHHDDPEVLADTCWAISYL				31
Query	924		VGNIVTGTDQQTDVVIASGGLP +GNIVTGTD+OT +VI SG L				11
Sbjct	312		IGNIVTGTDEQTQIVIDSGALA				37
Query	1104		GIFQQLRTVLEKGDFKAQKEAA G+ L +L KGDFK+OKEA			KILKPFIDLLD +L+P ++LL	128
Sbjct	372		GLVPYLIGILRKGDFKSQKEAV				43
Query	1284	TKDPR'	TIKVVQTGLSNLFALAEKLGGT T+ V+ +SN+F AEK+ T	ENLCLMVEEMGOE LCL++EE GO			14
Sbjct	431		TYLVILDAVSNIFLAAEKINET				49
Query	1464		FSNGDDEAEQELAPQEVNGALE FS ++E +O + P +	F 1547			
Sbjct	491	II+ Y	FS ++E +Q + P + FS-AEEEEDOSVVPGSTANSYT				

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)	9e-165()	Compositional matrix adjust.	258/509(51%)	355/509(69%)	9/509(1%)	+3
Feature	s:						
Query	42	NSRQG ++R	SYKANSINTQDSRMRRHEVTIE +K ++ + R RR EV +E				G- 212
Sbjct	11		RFKNKGKDSTEMRRRRIEVNVE				_
Query	213	= ~	LSVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E Q	IQSARKMLSRER O+ARK+LSRE+		IVPICIRFLO	QN 392
Sbjct	71	Q QVLAH	WSVEEIVKGVNSNNMELÕLQAT				GR 130
Query	393		LQFEAAWALTNIASGTSDQTRO +QFE+AWALTNIASGTS+QTR			EQAVWALGN EQAVWALGN	
Sbjct	131		TÖFESAWALTNIASGTSEÖTRA				
Query	573		ARDIVIHHNVIDGILPLIN RD+VI + I+ +L L+		IVWLMSNLCRNI + W +SNLCRNI		
Sbjct	191		YRDLVIKYGAIEPLLSLLAVPI				
Query	741		lsqlllsqDIQVLADACWALSY L +LL D +VLAD CWA+SY				II 920 I+
Sbjct	251		LVRLLHHDDPEVLADTCWAIS				
Query	921		SVGNIVTGTDQQTDVVIASGGI ++GNIVTGTD+QT VVI SG I				
Sbjct	311		AIGNIVTGTDEQTQVVIDSGAI				
Query	1101	QAVIQ Q V+	AGIFQQLRTVLEKGDFKAQKE G+ L VL KGDFK+QKE			YKILKPFID: +L+P ++	
Sbjct	371		HGLVPYLIGVLRKGDFKSQKE				
Query	1281		RTIKVVQTGLSNLFALAEKLGO +T+ V+ +SN+F AEK+		GGLDKLETLQQI GGLD++E LQ I		
Sbjct	430		KTVLVILDAVSNIFLAAEKINE				
Query	1461	AIIDT II+	YFSNGDDEAEQELAPQEVNGAI YFS ++E +O + P +	LEF 1547			
Sbjct	490		YFS-AEEEEDÕNVVPDSTADS	_			

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 I	Frame
497 bits	(1280)	1e-164()	Compositional matrix adjust.	259/517(50%)	357/517(69%)	) 10/517(1%) +	-3
Features	s:						
Query	45		SYKANSINTQDSRMRRHEVTIE +K +T + R RR EV +E				
Sbjct	12	+R ARLNF	RFKNKGKDTTEMRRRRIEVNVE				
Query	216	SPVQI	SVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E Q	QSARKMLSRERI Q+ARK+LSRE+		IVPICIRFLQN ++P + FL	т 395
Sbjct	72	VSAHV	VSVEEIVKGVNSNNMELÕLQAT				A 131
Query	396		QFEAAWALTNIASGTSDQTRC OFE+AWALTNIASGTS+QTR			EQAVWALGNIA EQAVWALGNIA	
Sbjct	132		Į Į ETAWALINIASGIS Į Į TRA				
Query	576	DGAA <i>F</i> DG+	ARDIVIHHNVIDGILPLIN RD+VI I+ +L L+		IVWLMSNLCRN: + W +SNLCRN:		
Sbjct	192		RDLVIKFGAIEPLLSLLAVPD				
Query	744		lsqlllsqDIQVLADACWALSY L +LL				
Sbjct	252		LVRLLHHDDHEVLADTCWALSY				
Query	924		SVGNIVTGTDQQTDVVIASGGL ++GNIVTGTD+OT +VI SG L				
Sbjct	312		AIGNIVTGTDEÕTQIVIDSGAL				
Query	1104	~	AGIFQQLRTVLEKGDFKAQKEA G+ L +L+KGDFK+OKEA			YKILKPFIDLL +++P ++LL	
Sbjct	372	RVVDE	HGLVPYLIGILKKGDFKSÕKEA				
Query	1284		RTIKVVQTGLSNLFALAEKLGG +T+ V+ +SN+F AEK+	TENLCLMVEEMOTE LCLM+EE			A 1463
Sbjct	431		KTVLVILDAISNIFLAAEKINE				т 490
Query	1464	IIDTY +I+ Y	/FSNGDDEAEQELAPQEVNGAL /FS ++E +Q + P+ +	EFNATQPKAPE F+ O AP+	1574		
Sbjct	491		ZFS-AEEEEDÕNVVPESTAASY		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
Feature	s:						
Query	48	~	KANSINTQDSRMRRHEVTIELF				~
Sbjct	13		K +T + R RR EV +ELF KNKGKDTTEMRRRRIEVNVELF			SPL+E + ( SPLQENRSN(	
Query	219	~	VDEIVAAMNSEDQERQFLGMQS				
Sbjct	73		V+EIV +NS + E Q Q+ VEEIVKGVNSNNMELQLQATQ <i>P</i>	-ARK+LSRE+ P AARKLLSREKQP			+ AD 132
Query	399		FEAAWALTNIASGTSDOTRCVI FE+AWALTNIASGTS+OT+ V+				
Sbjct	133		FESAWALTNIASGTS+QT+ V+			AVWALGNIAO AVWALGNIAO	
Query	579		DIVIHHNVIDGILPLINND+VI I+ +L L+ +		WLMSNLCRNKN W +SNLCRNKN		
Sbjct	193		DLVIKFGAIEPLLSLLAIPDLS				
Query	747	lpvls LP L	qlllsqDIQVLADACWALSYVT +LL D +VLAD CWALSY+T				
Sbjct	253		RLLHHDDHEVLADTCWALSYLT				
Query	927		GNIVTGTDQQTDVVIASGGLPF GNIVTGTD+OT +VI SG L				
Sbjct	313		GNIVIGID-OI +VI SG L GNIVIGIDEQTQIVIDSGALSV				
Query	1107	VIQAG V+ G	IFQQLRTVLEKGDFKAQKEAAW + L +L KGDFK+QKEA W			ILKPFIDLLI +++P ++LL	от 128
Sbjct	373		LVPYLIGILRKGDFKSQKEAV	VAVIN IT GI VAVTNYTSGGTI	DQIVYLVQA-G		SA 431
Query	1287	KDPRT KD +T	IKVVQTGLSNLFALAEKLGGTE + V+ +SN+F AEK+ TE	ENLCLMVEEMGG E LCLM+EE GG			AI 146
Sbjct	432		VLVILDAVSNIFLAAEKINETE				
Query	1467	IDTYF I+ YF	SNGDDEAEQELAPQEVNGALER S ++E +O +AP+ + E				
Sbjct	492		S-AEEEEDQNVAPESTAASYTE				

PREDICTED: importin subunit alpha-1 [Nipponia nippon]

Sequence ID: ref|XP\_009465206.1| Length: 529 Number of Matches: 1

#### ▶ See 1 more title(s) kange 1: 12 to 525

Score		Expect	Method	Identities	Positives	Gaps	Frame
497 bits	s(1280)	1e-164()	Compositional matrix adjust.	259/517(50%)	356/517(68%)	10/517(1%)	+3
Feature	s:						
Query	45	SRQGS +R	SYKANSINTODSRMRRHEVTIE +K +T + R RR EV +E				
Sbjct	12		RFKNKGKDTTEMRRRRIEVNVE				Q NQ 71
Query	216	SPVQI	SVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E Q	QSARKMLSRERN O+ARK+LSRE+			NT 395
Sbjct	72	VSAHW	VSVEEIVKGVNSNNMELQLQAT				RA 131
Query	396		QFEAAWALTNIASGTSDQTRC			EQAVWALGNIA EQAVWALGNIA	
Sbjct	132		IQFESAWALTNIASGIS+QI+				
Query	576	DGAAA DG+	ARDIVIHHNVIDGILPLIN RD+VI I+ +L L+		IVWLMSNLCRNI W +SNLCRNI		
Sbjct	192		RDLVIKFGAIEPLLSLLAVPD				
Query	744	llpvl +LP I	sqlllsqDIQVLADACWALSY L +LL D +VLAD CWALSY				
Sbjct	252		LYRLLHHDDHEVLADTCWALSY				
Query	924		SVGNIVTGTDQQTDVVIASGGLI -+GNIVTGTD+QT +VI SG L				
Sbjct	312		AIGNIVTGTDEQTQIVIDSGAL				
Query	1104	AVIQA V+	AGIFQQLRTVLEKGDFKAQKEA G+ L +L KGDFK+QKEA			KILKPFIDLI +++P ++L	
Sbjct	372	•	G+ L +L KGDFK+QKEA IGLVPYLIGILRKGDFKSQKEA'				
Query	1284		RTIKVVQTGLSNLFALAEKLGG'	renlclmveemore lclm+ee			YA 1463
Sbjct	431		-T+ V+ +SN+F AEK+ ' KTVLVILDAISNIFLAAEKINE'				ST 490
Query	1464		YFSNGDDEAEQELAPQEVNGALI		1574		
Sbjct	491	+I+ Y LIEKY	YFS ++E +Q + P+ + YFS-AEEEEDQNVVPESTAASY'		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 adju	st. 261/521(50%	) 356/521(68%	6) 10/521(1%)	+3
Features	s:						
Query	36	DSNSF + + F	RQGSYKANSINTQDSRMRRHI R +K +T R +R I	EVTIELRKSKKED EV +ELRK+KK++			
Sbjct	6	_	RMRKFKNKGKDTAAMRRQRMI				
Query	207	NGQSI +	PVQLSVDEIVAAMNSEDQER( OLS++EIV A+N + E		SRERNPPIDLM: SR+RNPP++ +:		
Sbjct	65		TAQLSLEEIVQAVNGNNPELI				
Query	387	QNTNN +N	ISMLQFEAAWALTNIASGTSI I LQFEAAWALTNIASGTSI			MNLAEQAVWAL M+++EO+VWAL	
Sbjct	125		IVTLÕFEAAWALTNIASGTSI				
Query	567	IAGDO IAGDO	GAAARDIVIHHNVIDGILPLI G RD +IH+NVI +L L-		VWLMSNLCRNI W +SNLCRNI		
Sbjct	185		SPMYRDSLIHNNVIPPLLALV				
Query	747	lpvls LPVL	sqlllsqDIQVLADACWALS +LL +D +L+D CWA+S				
Sbjct	245		RLLKHEDKDILSDTCWAVS				
Query	927		/GNIVTGTDQQTDVVIASGGI -GN+VTGTD+QT + I +G 1				7
Sbjct	305		GNVVTGTDEÕTQMAIDAGVI				
Query	1107	VIQAC +I C	GIFQQLRTVLEKGDFKAQKEA G+ L +L+KG+FKAQKEA				
Sbjct	365		GLLPPLVELLDKGEFKAQKE				
Query	1287	KDPRT +D +T	TIKVVQTGLSNLFALAEKLGO TI V+ +SNLF AEKL	GTENLCLMVEEMOTE LC +VEE+O			AI 1466 +
Sbjct	424		TILVILDTISNLFLAAEKLE				
Query	1467		FSNGDDEAEQELAPQEVNGAI F++ ++ O + OE	LEFNATQPKAPEG F+ +P	GYTF 1589 YTF		
Sbjct	484		FASEENPNLÕPESDÕE-RPTI				

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
Feature	s:						
Query	45		YKANSINTQDSRMRRHEVTIEL				
Sbjct	12		+K +T + R RR EV +EL RFKNKGKDTTEMRRRRIEVNVEL				Q NQ 71
Query	216		SVDEIVAAMNSEDQERQFLGMQ SV+EIV +NS + E Q Q	SARKMLSRERNI +ARK+LSRE+			NT 395
Sbjct	72		SVEEIVKGINSNNLELÕLQATÕ				RA 131
Query	396		QFEAAWALTNIASGTSDQTRCV QFE+AWALTNIASGTS+QT+ V			QAVWALGNIA QAVWALGNIA	
Sbjct	132		QFESAWALTNIASGTSEQTKAV				
Query	576		RDIVIHHNVIDGILPLIN RD+VI + ID +L L+		VWLMSNLCRNKI W +SNLCRNKI		
Sbjct	192		RDLVIKYGAIDPLLALLAVPDI				
Query	744	llpvl +LP L	sqlllsqDIQVLADACWALSYV +LL D +VLAD CWA+SY+				
Sbjct	252		VRLLHHDDHEVLADTCWAISYL				
Query	924		VGNIVTGTDQQTDVVIASGGLP +GNIVTGTD QT +VI SG L	RLGLLLQHNKS			
Sbjct	312		IGNIVTGTDDÕTQIVIESGALT				
Query	1104		GIFQQLRTVLEKGDFKAQKEAA G+ L +L+KGDFK+QKEA	WAVTNTTTSGTI	PEQIVDLIEKY	KILKPFIDLI +++P ++LI	
Sbjct	372		GLVPYLIGILKKGDFKSQKEAV				
Query	1284		TIKVVQTGLSNLFALAEKLGGT T+ V+ ++N+F AEK+G T	ENLCLMVEEMGOE LCLM+EE GO			
Sbjct	431		VLVILDAITNIFLAAEKIGET				
Query	1464	IIDTY +I+ Y	FSNGDDEAEQELAPQEVNGALE FS ++E +O + P +	F 1547 F			
Sbjct	491		FS-AEEEEDÕNVVPDSTVDSYT				

Sequence ID: **ref|XP\_001379295.3|** Length: 595 Number of Matches: 1 Range 1: 79 to 595

Score		Expect	Method	Identities	Positives	Gaps	Frame
499 bits	(1285)	1e-164()	Compositional matrix adjust.	264/522(51%)	358/522(68%	) 12/522(2%)	+3
Features	s:						
Query	45	SRQGS +R	SYKANSINTQDSRMRRHEVTIE +K ++ + R RR EV +E				
Sbjct	79		RFKNKGKDSTEMRRRRIEVNVE				Q NQ 138
Query	216	SPVQI	LSVDEIVAAMNSEDQERQFLGM SV+EIV +NS + E Q	QSARKMLSRER Q+ARK+LSRE+		SIVPICIRFLQI S++P + FL	NT 395 T
Sbjct	139	GSALV	VSVEEIVKGINSNNLEVÕLQAT				
Query	396		LQFEAAWALTNIASGTSDQTRC HQFE+AWALTNIASGTSDQT+			EQAVWALGNI. EQAVWALGNI.	
Sbjct	199		IÕFESAWALTNIASGTSDÕTKA				
Query	576		ARDIVIHHNVIDGILPLIN RD+VI + ID +L L+		IVWLMSNLCRN + W +SNLCRN		
Sbjct	259		RDLVIKYGAIDPLLALLAVPD				
Query	744	llpvl +LP I	lsqlllsqDIQVLADACWALSY L +LL				
Sbjct	319		LVRLLHHDDPEVLADTCWAISY				
Query	924		SVGNIVTGTDQQTDVVIASGGL ++GNIVTGTD+OT +VI SG L				
Sbjct	379		AIGNIVTGTDEÕTQIVIDSGAL				
Query	1104	~	AGIFQQLRTVLEKGDFKAQKEA G+ L +L KGDFK+QKEA			YKILKPFIDL: IL+P I+L:	
Sbjct	439	-	IGLVPYLVGILSKGDFKSÕKEA				
Query	1284		RTIKVVQTGLSNLFALAEKLGG + + V+	TENLCLMVEEMO			
Sbjct	498		KDSKIVLVILDAISNIFLAAEKLN				
Query	1464	IIDTY +I+ Y	/FSNGDDEAEQELAPQEVNGAL /FS +E +O + P+ +	EFNATQPKAPE			
Sbjct	558		ZFSAEEEDÕNVVPESTSDGY				

PREDICTED: LOW QUALITY PROTEIN: importin subunit alpha-1-like [Corvus brachyrhynchos]

Sequence ID: **ref|XP\_008635795.1|** Length: 575 Number of Matches: 1 Range 1: 58 to 563

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							+3
Features	<b>S</b> :						
Query	45		SYKANSINTQDSRMRRHEVTIEL +K ++ + R RR EV +EL RFKNKGKDSTEMRRRRIEVNVEL	RK+KK+DÕM K	RRN++ +D'	TSPL+E G Ç	
Sbjct	58						
Query	216		SVDEIVAAMNSEDQERQFLGMQ SV+EIV +NS + E O O	SARKMLSRERNI +ARK+LSRE+			NT 395
Sbjct	118		SVEETVKGVNSNNMELQLQATQ				RA 177
Query	396		QFEAAWALTNIASGTSDQTRCV			QAVWALGNI OAVWALGNI	
Sbjct	178		QFESAWALTNIASGTSEQTRAV				
Query	576		RDIVIHHNVIDGILPLIN RD+VI + I+ +L L+		VWLMSNLCRNK W +SNLCRNK		
Sbjct	238		YRDLVIKYGAIEPLLSLLAVPDL				
Query	744	llpvl +LP L	.sqlllsqDIQVLADACWALSYV .+LL D +VLAD CWA+SY+				
Sbjct	298		LVRLLHHDDPEVLADTCWAISYL				•
Query	924		SVGNIVTGTDQQTDVVIASGGLP ++GNIVTGTD+OT +VI SG L		NIVKEAAWTVS NI KEAAWT+S		
Sbjct	358		IGNIVTGTDEQTQIVIDSGALA				
Query	1104	~	QAGIFQQLRTVLEKGDFKAQKEAA G+ L +L KGDFK+QKEA DHGLVPYLIGILRKGDFKSQKEAV	WAVTN T+ GT	+ÕIV L++	+L+P $++LL$	
Sbjct	418						
Query	1284		PRTIKVVQTGLSNLFALAEKLGGTI +T+ V+ +SN+F AEK+ TI SKTVLVILDAVSNIFLAAEKINETI	E LCL++EE GO	GLD++E LQ̃HI	ENEEVY+ +	YA 1463
Sbjct	477						ST 536
Query	1464	II+ YFS ++E +Q̄ +	FSNGDDEAEQELAPQEVNGALE				
Sbjct	537		FS ++E +Q + P + FS-AEEEEDQSVVPGSTANSYT	F F 563			