BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ Formatting Results - CN9SU1M2015

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Blast report description

Nucleotide Sequence (2133 letters)

RID <u>CN9SU1M2015</u> (Expires on 02-23 13:13 pm)

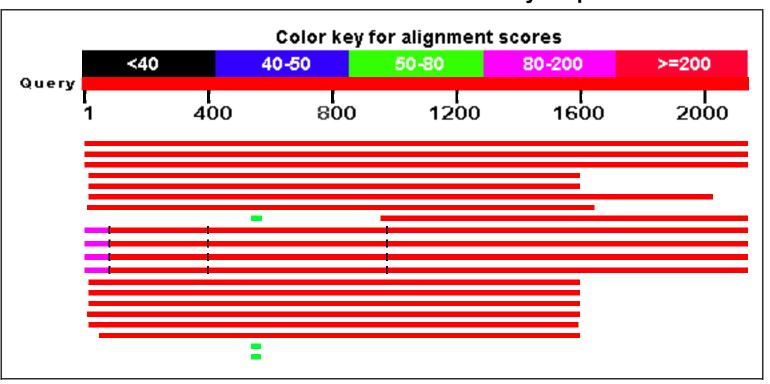
Description None **Description** Nucleotide collection (nt)

Molecule type nucleic acid Program BLASTN 2.3.1+

Query Length 2133

□ Graphic Summary

Distribution of 33 Blast Hits on the Query Sequence



$\begin{tabular}{ll} \hline \blacksquare \underline{Descriptions} \\ \hline \end{tabular}$

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Drosophila melanogaster LD24935 full insert cDNA	3871	3871	99%	0.0	99%	BT003258.1
Drosophila melanogaster pendulin (Pen), mRNA	3869	3869	99%	0.0	99%	NM_057693.5
Drosophila melanogaster pendulin (oho- 31) mRNA, complete cds	3862	3862	99%	0.0	99%	<u>U12269.1</u>
Drosophila sechellia GM17916 (Dsec\GM17916), mRNA	2697	2697	73%	0.0	98%	XM_002036391.1
Drosophila simulans GD23655 (Dsim\GD23655), mRNA	2647	2647	73%	0.0	97%	XM_002078829.1
Drosophila yakuba uncharacterized protein (Dyak\GE18896), mRNA	2534	2534	93%	0.0	90%	XM_002088987.2
Drosophila erecta uncharacterized protein (Dere\GG10083), mRNA	2495	2495	75%	0.0	94%	XM_001969358.2
Drosophila melanogaster LP03126 full length cDNA	2167	2167	55%	0.0	99%	AY061543.1
Drosophila melanogaster chromosome 2L	2139	3884	99%	0.0	99%	AE014134.6
Drosophila melanogaster clone BACR06G16, complete sequence	2139	3884	99%	0.0	99%	AC009744.8
Drosophila melanogaster DNA sequence (P1s DS00058 (D296), DS02068 (D297), and DS07249 (D318)), complete sequence	2139	3884	99%	0.0	99%	AC005734.1
D.melanogaster oho31 gene	1969	3723	99%	0.0	97%	X85752.1
Drosophila ananassae alpha Karyopherin-2 (Dana∖alphaKap2), mRNA	1594	1594	73%	0.0	85%	XM_001962998.2
Drosophila persimilis GL18958 (Dper\GL18958), mRNA	1328	1328	73%	0.0	82%	XM_002014394.1
Drosophila pseudoobscura pseudoobscura uncharacterized protein (Dpse\GA18440), mRNA	1314	1314	73%	0.0	82%	XM_001356277.3
Drosophila mojavensis uncharacterized protein (Dmoj\GI17589), mRNA	1194	1194	73%	0.0	80%	XM_002002782.2
Drosophila virilis alpha Karyopherin-2 (Dvir\alphaKap2), partial mRNA	1077	1077	73%	0.0	79%	XM_002057707.2
Drosophila willistoni uncharacterized protein (Dwil\GK18399), mRNA	898	898	72%	0.0	77%	XM_002074190.2
PREDICTED: Chinchilla lanigera karyopherin alpha 1 (importin alpha 5) (Kpna1), mRNA	56.5	56.5	1%	0.002	94%	XM_005386512.2
PREDICTED: Heterocephalus glaber karyopherin alpha 1 (importin alpha 5) (Kpna1), mRNA	54.7	54.7	1%	0.008	100%	XM_013068812.1
PREDICTED: Fukomys damarensis uncharacterized LOC104857895 (LOC104857895), mRNA	54.7	54.7	1%	0.008	100%	XM_010617966.1

□ <u>Alignments</u>

Drosophila melanogaster LD24935 full insert cDNA

Sequence ID: **gb|BT003258.1|** Length: 2505 Number of Matches: 1 Range 1: 275 to 2397

Query 788 AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGAT 847 Sbjct 1055 AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAACACCAAGAT 1114 Query 848 CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA 907 Sbjct 1115 CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA 1174 Query 908 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 967 Sbjct 1175 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1027 Sbjct 1235 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjct 1295 CAACAAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCCACCGTGCT 1147 Sbjct 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCCACCGTGCT 1414	Score		Expect	Identities	Gaps	Strand	Frame
Query 8 ************************************	3871 bit	s(2096)	0.0()	2114/2123(99%)	0/2123(0%)	Plus/Plus	
Sbjet 275 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Features	S:					
Query 68 CAACAGCATTAACAGCAGGACTCAGCCATGAGGTGAGCTGAGGTGAGCTGAGGTGAGCTGAGGTGAGCAGAGAGGATTAACAAGGAGGACCAGATTATACACGCGCGCAACATCAACAAGCAGGATCTAAC 187 Sbjet 395 CAAGTCCAAAAAGGAGCACCAGATTTTCAACCGCGCCAACATCAACAACGAGGATCTAAC 458 Sbjet 185 GTCGCCGCTCAAAAAGCCTCAATGGCCGTTGCACCTGTGCACTGTGCAGGAGAATACACCAGAGATACT 247 Sbjet 515 GCGGCCATGAACAGCCAAGGATCAGGAGCCCACTTCCTGGGCATGCAGTCTGCCCGCAA 307 Sbjet 515 GGGGCCATGAACAGCGAGGATCAGGAGCCCACTTCCTGGGCATGCAGTCTGCCCGCAA 754 Query 368 CATTGCAACCGGGGACCCAATCCACCCATCCACCTATCATCATCAGCCAGTGGTATTCTGCC 637 Sbjet 575 GATGCTCAGTCGGGGACCCAATCCACCCATCCACCTATCATCATCATCAGCCATGTATTCTGACCCCCTTC 227 Sbjet 575 GATGCTAACGATCCTCCTGCAGATTACCAACACTCAACTCAGCCTGGTTATCGAGCCCCTTC 427 Sbjet 535 CATTGCATACGATCTCTGCAGAATACCAACACTCAACTCAGCTGCTGTTATCGAACCAA 754 Query 488 TGCTGTGCCCAATTCCTGCCTCTTGCCCCACTTCCACTCCAACTCCATCTCATCTCACTCA	Query	8	aaaaaaaaaaa 	aaaaaTGAGTAAGGC 	GGATTCTAACTCACG	ACAGGGCTCCTA	CAAGGC 67
Sbjet 335 CAACACCATTAACACCCAGGACTCACCCATGACGTGACCATCAACTCCACTCCA 394 Query 128 CAACTCCAAAAAGGAGGACCCAGATGTTCAAGCGGCGCAACATCAACGACGAGGATCTAAC 187 Sbjet 395 CAAGTCCAAAAAGGAGGACCCAGATGTTCAAGCGGCGCACACATCAACGACGAGGATCTAC 454 Ouery 188 GTCGCCGCTCAAAGAGCTCAATGGCCAGTGCGCGGTGCACCTGTCCCGTGGACGAGATAGT 247 Ouery 248 GCCGGCCATCAACAGCGAGCATCAGGACCCCAGTTCCTGGGCATGCACTTCCCCCCCAA 307 Sbjet 515 GCCGGCCATCAACAGCGAGCAATCCACCCATCGACCTGATCATCTGCCCCTATTCTTCCCCCCAA 574 Query 308 GATGCTCAGTCGGGAACCCAATCCACCCATCGACCTGATCATCTGCCCATTGTTTTTCCC 367 Sbjet 535 CATTTGCATTACGTTCCTGCAGAATACCAACAACTCAATCGACTCAGTCAG	Sbjct	275	AAAAAAAAAAA	aaaaatgagtaaggc	ĠĠĀŦŦĊŦĀĀĊŦĊĀĊĠĀ	Acadddctccta	CAAGGC 334
Query 128 CAMGTCCAMANAGGAGGACCAGATGTTCAAGCGGCGACAATCAACGACGAGGATCTTAAC 187 Sbjet 395 CAMGTCCAMANAGGAGGACCAGATGTTCAAGCGGCGCAACATCAACGACGAGGATCTTAC 454 Query 188 GTCGCCCCTCAAAGGACTCAATGGCCAGTCGCCGGTGCAGCTGTCCCGTGGACCAGATAGT 247 Sbjet 515 GCGGCCATGAACAGCAGGATAGGACGCCAGTTCTCTGGGCATGCACCTGACCCCCCAA 574 Query 248 GCGGCCATGAACAGCAGGATCAGGACGCCAGTTCTTGGGCATGCAT	_			11111111111111			
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Query 188 CTGGCCGCTCAAAGAGCTCCAATGGCCAGTTCGCCGGTGCAGCTGTCCGTGGAGGAGATAGT 247 Sbjet 455 GTGGCCGCTCAAAGACCTCAATGGCCAGTTCGCGGGTGCAGCTTCCGTGGACGAGATAGT 514 Query 248 GGCGGCCATGAACAGCCAGGATCAGGACCGCCAGTTCTTGGGCATGCAGTCTGCCCGCAA 307 Sbjet 515 GGCGGCCATGAACAGCCAATCCACCCATCGACCTGATGATCGGCCATGGATTTTTGGCC 367 Query 308 GATGCTCAGTCGGGAACGCAATCCACCCATCGACCTATATCGCCCATGGATTTGAGGCGCGCTTC 427 Sbjet 535 CATTTGCATAGGCTTCCTGCCGAATACCAACACTCAATGCACATTTGAGGCAGTTTGAGCCGCGTTT 487 Sbjet 635 CATTTGCATACGCTTCCTGCCGAATACCAACACACAACTCAATGCACTTTGAGCAGTTTCGAGCCGCTTC 427 Sbjet 635 GGCGTTACCAACATCGCCTCTGGCACATCCGACCAAACCGCTGCGTTATCGAGCCGGTT 487 Sbjet 635 GGCGTTACCAACATGGCCTCTGGCCACTTCCAGTCCAAGTCCATGAACCTGGCGGAGGCGCGCGC				11111111111111			
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Query 248 GCGGGCCATGAACAGGGAAGGATCAGGAGCGCCAGTTCTGGGCATGCAGTCTGCCCGCAAA 307 Sbjet 515 GGGGGCCATGAACAGGGAAGGATCCACCCATGACTGTTCTGGGCATGCAGTCTGCCCGCAAA 574 Query 308 GATGCTCAGTCGGGAAGGCAATCCACCCATGACCTGATGATCGGCCATGGTATTGTGCC 367 Sbjet 575 GATGCTCAGTCGGGAAGGCAATCCACCCATCGACTGATGATGCGCCATGGATTTGAGGCCGCTTC 427 Sbjet 636 CATTTGCATACGCTTCCTGCAGAATACCAACAACTCAATGCTGCAGTTTGAGGCCGCTTC 694 Query 428 GGGGCTTACCAACATCGCCTCTTGGCACATCCGACCAAACGGCTGCGTTATGGAACACAA 764 Query 488 TGCTGTGCCGCATTTCGTGCCTCTTGCTCCAGTCCAAACGGCTGCGTTATTGAACACAAA 754 Sbjet 695 GCGCTTACCAACATTCGCCTCTTGCTCCAGTCCAAGTCCATGAACCTGGCGAACAGGC 547 Sbjet 755 TGCTGTGCCGCATTTCGTGGCTCTTGCTCCAGTCCAAGTCCATGAACCTGGCGAACAGGC 547 Sbjet 815 AGTCTGGGCTATTGGGCTACATTGCCGGGAGGGAGCCGCCGCCGCGCACATTCTCTCTTTTTT 667 Sbjet 815 AGTCTGGGCTAATTGCAGGAACATTGCCAGTGATCAACAATAGAACACCGCTCTTTTTTTT	_						
Query308GATGCTCAGTCGGGAACGCAATCCACCCATCGACCTGATGATCGGCCATGGTATTGTGCC367Sbjet575GATGCTCAGTCGGGACGCAATCCACCCATCGACCTGATGATCGCCATGGTATTGTGCC634Query368CATTTGCATACGCTTCCTGCAGAATACCAACAACTCAATGCTGAGTTTGAGGCCGCTTG427Sbjet635CATTTGCATACCATCGCCTCTGGCACATCCGACCAAACTCCAACGCGTTGGGTATCGAGCCCTTG694Query428GGCGCTTACCAACATCGCCTCTGGCACATCCGACCAAACGCCGTGCGTTATCGACACAA487Sbjet695GGCGCTTACCAACATCGCTCTGGCACATCCGACCAAACGCCCTCGGTAACCTGACCCAACACA754Query488TGCTGTGCCCGCATTTCGTGGCTCTCCTCCAGTCCAAGTCCATGAACCTGGCCGAGCAGGC814Sbjet815AGTCTGGGCTTTGGGCAACATTGCCGGCGAGGAGCCGCCGCCGCCGCGCACATTGTCATCCA607Query548AGTCTGGGCTTTGGGCAACATTGCCGGCGAGCGGAGCCCCCCCC		248	ĢĢÇĢĢÇÇAŢĢAA(Ҫ҅҇҅҄҅҅ҪҾҪҪ҄҅҅҄҅҅҄҅ҪҪ҄҅҅Ѻ҅Ҁ҄҅	 ĢÇĢÇÇĀĢŢŢСÇŢĢĢĢ(САТĢÇAĢТСТĢÇ	СССССАА 307
Sbjet 575 GATGCTCAGTCGGGGGCCAATCCACCCATCGACCTATATATCGCCATGGTATTCTCC Query 368 CATTTCCATACGCTTCCTGCAGAATACCAACAACTCAATGCTGCAGTTTGAGGCCGCTTG Sbjet 635 CATTTCCATACGCTTCCTGCAGAATACCAACAACTCAATGCTGCAGTTTGAGGCCGCTTG Query 428 GGCGCTTACCAACATCGCCTCTGGCACAATCCAACCACCTCGCTTATCGAACACAA Sbjet 695 GCCGCTTACCAACATCGCCTCTGGCACATCCGACCAAACGCGCTGCGTTATCGAACACAA Query 488 TGCTGTGCCGCATTTCGTGGCTCTCTCCAGTCCAAACGCCTGGCTATACGAACACAA Sbjet 755 TGCTGTGCCGCATTTCGTGGCTCTCCAGTCCAAGTCCATGAACCTGGCCGAGCAGGC Sbjet 815 AGTCTGGGCTCTGGGCAACATTGCCGGGGAGGGCGCGCCGCGCACATTTCTATCCA Query 608 CCACAACGTAATTGACGGAACTTTGCCAGCGGAGGAGCCGCCGCGCACATTTTTTT Sbjet 875 CCACAACGTAATTGACGGAACTTTGCCACTGATCAACAATAGAACACCCGCTCTCTTTTTT Sbjet 935 GCCCAACATCGTCTGGCTAATTGCCACTGATCAACAATAGAACACCCGCTCTCTTTTTT Sbjet 935 GCCAACATCGTCTGGCTGATCTCCACCTGTCCAGCAACACCCGCTCTCTTTTTT Query 728 CGATCAGGTGAAGCGGCTGTTCCCACCTGTGCCAGAACACAATCACTCCCCCCATT P34 Query 788 AGTGCTGGCCGAACGTTGCCCGTCCTGTCCCGGAACAACAATACAATCCACCCCCTTTT Sbjet 1055 AGTGCTGGCCGAACCTTTGCCCGTCTTTTTCCTACGCACAACTCAACAATCAAT	Sbjct	515	GGCGGCCATGAA		GCGCCAGTTTCTGGG(CCGCAA 574
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Sbjet 635 CATTTGCATACGCTTCCTGCAGAATACCAACAACTCAATGCTGCAGTTCGAGGCCGCTTG 694 Query 428 GGCGCTTACCAACATCGCCTCTGGCACATCCGACCAAACGCGCTGCGTTATCGAACACAA 487 Sbjet 695 GGCGCTTACCAACATCGCCTCTGGCACATCCGACCAAACGCGCTGCGTTATCGAACACAA 754 Query 488 TGCTGTGCCGCATTTCGTGGCTCTCCCAGTCCAAGTCCATGAACCTGGCCGACAGGC 547 Sbjet 755 TGCTGTGCCGCATTTCGTGGCTCTGCTCCAAGTCCATGAACCTGGCCGACAGGC 814 Query 548 AGTCTGGGCTCTGGGCAACATTGCCGGCGACGGC 6814 Query 548 AGTCTGGGCTCTGGGCAACATTGCCGGCGACGGACCGCCCCCCGCGCACATTGTCATCCA 607 Sbjet 815 AGTCTGGGCTCTGGGCAACATTGCCGGCGACGGACCGCCCCCCCGCACATTGTCATCCA 874 Query 608 CCACAACGTAATTGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTTT 667 Sbjet 875 CCACAACGTAATTGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTTT 934 Query 668 CCGCAACATCGTCTGGCTGATGTCCAACCTGTGCAGGAATAAGAATCCATCTCCGCCATT 727 Sbjet 935 GCCAACATCGTCTGGCTGATGTCCAACCTGTGCCAGGAATAAGAATCCATCTCCGCCATT 727 Sbjet 935 GCGAACATCGTCTGGCTGATGTCCAACCTGTGCCAGGAATAAGAATCCATCTCCGCCATT 727 Sbjet 935 GCGAACATCGTCTGGCTGATGTCCCACCTGTGCCAGAACAAGAATCCATCTCCGCCATT 727 Sbjet 950 CGATCAGGTGAAGCGGCTTGTGCCCGTCCTTGTCCGAGCTTCTGTTAGTCAGGACATCCA 1054 Query 788 AGTGCTGGCCGACGCCTGTGGCCTTCTTCTCTCTCTTGCTTAGTCAGGACATCCA 1054 Query 788 AGTGCTGGCCGACGCCTGCTGGGCTTTTTCCTACGTCACGGACGACTAAACACCAAGAT 1114 Query 848 CCAGGCTTGGTCGACCCTGCTGGCCTTTTTCCTACGTCACGGACGACGATAAACACCAAGAT 1114 Query 908 GCCGAGCATTATTTGGCCCGCCCTGGGCCTTGGCAACATTGTGACTGCAACATAGACCAAGAT 1124 Query 908 GCCGAGCATTATTTTGCCCCGCCCTCGCAGCGTTGGCAACATTGTGACTGCAACAATGACCA 1027 Sbjet 1175 CCCGAGCATTATTTTGCCCCGCCCTCGCAGCGTTTGCCAACATTGTGACTGCACAGATCA 1234 Query 968 ACAGACTGACTTGAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1224 Query 968 ACAGACTGACTTGAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1224 Query 1028 CAACAAAAGCAACATTGTGAACGAGGTTAACCAAGACTCAACAGCAGGTAA 1354 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGTTTACCAAGGCTGGCACCGTTGCAACATCACAGCAGGTAA 1354 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGTTTACCAAGGCTGGCACCGTCCTTCTACAGCACGTTGAATTGCAACAGCAGGTAA 1354 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGCACGGTTTTCCAGCAGCTGCCACCGTGCT 1147 Sbjet 1355 CCAGAAGCAG	Sbjct	575	gatgctcagtcg	ggydgggyyytggy	catcdacctdatdatc	cggccatggtat	पेर्विपेर्वेटेटे 634
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Sbjet 755 TGCTGTGCCGCATTTCGTGGCTCTGCTCCAGTCCAAGTCCATGAACCTGCCGGACAGTCCAGCCGCGCGCG							
Sbjet 815 AGTCTGGGCTACTGGGCAACATTGCCGGCGAGGCCGCCCGGCACATTGTCATCCA 874 Query 608 CCACAACGTAATTGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTTT 667 Sbjet 875 CCACAACGTAATTGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTTT 934 Query 668 GCGCAACATCGTCTGGCTGATGTCCAACCTGTGCAGGAATAAGAATCCATCTCCGCCATT 727 Sbjet 935 GCGCAACATCGTCTGGCTGATGTCCAACCTGTGCCGGAACAAGAATCCATCGCCGCCATT 994 Query 728 CGATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGGTTCTGCTTAGTCAGGACATCCA 787 Sbjet 995 CCATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA 1054 Query 788 AGTGCTGGCCGACGCCTGCTGGGCTTTTGTCCTACGTCACGGACGACAACAACAATCCA 1054 Sbjet 1055 AGTGCTGGCCGACGCCTGCTGGGCTTTTGTCCTACGTCACGGACGACGATAACACCAAGAT 1114 Query 848 CCAGGCTGTGGTCGACTCGGACGACGATGCACAGAACAACAACAACAA 1114 Query 908 GCCGAGCATTATTGTGCCCGCCCTGCCGCCCTGGTCAAACTGCTGCAAATGGACCA 1174 Query 908 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCACTCTGGAGGTTTACCAAGGCTGGGACCACAATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACCACAATCAACACA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGTTTACCAAGGCTGGGACCTCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCAACAGCAGGTAA 1354 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCAACAGCAGGTAA 1354 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCAACAGCAGGTAA 1354 Query 1028 CCAGAAGCAGATCCAGGCTGTGTATTCCAGCCAGCTTCCTCCAGCAGCTCCTTCTACACCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1028 CCAGAAGCAGATCCAGGCTGTGTATTCCAGCCGCCTCTCCAGCAGCTCCGCACCGTGCT 1147 Sbjct 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGTATTCCAGCCGCCGCACCTCTCCCAGCAGCTGCCTGC	_			11111111111111			
Query608CCACAACGTAATTGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTTT667Sbjet875CCACAACGTAATTGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTCT934Query668GCGCAACATCGTCTGGCTGATGTCCAACCTGTGCAGGAATAAGAATCCATCTCCGCCATT727Sbjet935GCGCAACATCGTCTGGCTGATGTCCAACCTGTGCCGGAACAAGAATCCATCGCCGCCATT994Query728CGATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA787Sbjet995CCATCAGGTGAACCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA1054Query788AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGAT847Sbjet1055AGTGCTGGCCGACGCCTGCTGGGCTTTTGTCCTACGTCACGGACGACGATAAACACCAAGAT1114Query848CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA907Sbjet1115CCAGGCTTGGTCGACTCGGACGCAGTGCCGCCCTGGTCAAACTGCTGCAAATGGACGA1174Query908GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA1234Query968ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA1027Sbjct1235ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA1294Query1028CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA1354Sbjct1295CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA1354Query1088CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1147Sbjct1355CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1414	Query	548	А ĢŢĊŢĢĢĢĊŢĊŢ¢	Ģ ĢĢÇ A AÇAŢŢĢÇÇĢĢ	ҀĢĄҀĢĢĄĢСÇĢСС	ССССБАСАТТСТ	САТССА 607
Sbjet 875 CCACAACGTAATTGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTTTTTCT 934 Query 668 GCGCAACATCGTCTGGCTGATGTCCAACCTGTGCAGGAATAAGAATCCATCTCCGCCATT 727 Sbjet 935 GCGCAACATCGTCTGGCTGATGTCCAACCTGTGCAGGAACAAGAATCCATCC	Sbjct	815	AGTCTGGGCTCT		CGACGGAGCCGCCGC		CATCCA 874
Query668GCGCAACATCGTCTGGCTGATGTCCAACCTGTGCAGGAATAAGAATCCATCTCCGCCATT727Sbjet935GCGCAACATCGTCTGGCTGATGTCCAACCTGTGCCGGAACAAGAATCCATCGCCGCCATT994Query728CGATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA787Sbjet995CGATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA1054Query788AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGAT847Sbjet1055AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAACACCAAGAT1114Query848CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA907Sbjet1115CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA1174Query908GCCGAGCATTATTGTGCCCGCCCTGGCCAGCGTTGGCAACATTGTGACTGGCACAGATCA967Sbjet1175GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA1234Query968ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA1227Sbjet1235ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA1294Query1028CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA1087Sbjet1295CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCACCAACATCACAGCAGGTAA1354Query1088CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1147Sbjet1355CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1414	Query	608	CCACAACGTAAT	TGACGGAATCTTGCC	ACTGATCAACAATGA(GACACCGCTCTC	TTTTTT 667
Sbjet 935 GCGAACATCGTCTGGCTGATGTCCAACCTGTGCCGGAACAAGAATCCATCGCCGCCATT 994 Query 728 CGATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA 787 Sbjet 995 CGATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA 1054 Query 788 AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCAGGACGACATCACAGAT 847 Sbjet 1055 AGTCCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCAGGACGACGATAATACCAAGAT 1114 Query 848 CCAGGCTGTGGTCGACTCGGACGCAGGCCTGGTCAAACTGCTGCAAATGGACGA 907 Sbjet 1115 CCAGGCTGTGGTCGACTCGGACGCAGTGCCGGCCTGGTCAAACTGCTGCAAATGGACGA 907 Sbjet 1175 GCCGAGCATTATTGTGCCCGCCCTGGCCAGCGTTGGCAACATTGTGACTGGCACAGATCA 967 Sbjet 1175 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCACACATCACAGCAGTAA 1087 Sbjet 1235 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCCT 1147 Sbjet 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTTCCAGCAGCTGCGCACCGTGCT 1414	Sbjct		ċċaċaaċĠtaat;	tĠĀĊĠĠĀĀŦĊŦŦĠĊĊ	Actgatcaacaatgac	SACACCGCTCTC	
Query728CGATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA787Sbjet995CGATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCA1054Query788AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGAT847Sbjet1055AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAACACCAAGAT1114Query848CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA907Sbjet1115CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCCCTGGTCAAACTGCTGCAAATGGACGA1174Query908GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA967Sbjet1175GCCGAGCATTATTGTGCCCGCCCTGCGCACCGTTGGCAACATTGTGACTGGCACAGATCA1234Query968ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA1027Sbjet1235ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA1294Query1028CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA1087Sbjet1295CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA1354Query1088CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1147Sbjet1355CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1414Sbjet1355CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1414	_			11111111111111			
Sbjet 995 CGATCAGGTGAAGCGCTGTTGCCCGTCCTGTCGAGCTTCTGCTTAGTCAGGACATCCA 1054 Query 788 AGTGCTGGCCGACGCTGCTGGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGAT 847 Sbjet 1055 AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGAT 1114 Query 848 CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCCCTGGTCAAACTGCTGCAAATGGACGA 907 Sbjet 1115 CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCCCTGGTCAAACTGCTGCAAATGGACGA 1174 Query 908 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 967 Sbjet 1175 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1027 Sbjet 1235 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjet 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Sbjet 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1147 Sbjet 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1414	_						
Query 788 AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGAT 847 Sbjet 1055 AGTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAACACCAAGAT 1114 Query 848 CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA 907 Sbjet 1115 CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA 1174 Query 908 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 967 Sbjet 1175 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1027 Sbjet 1235 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjet 1295 CAACAAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1147 Sbjet 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1147	_						
Query848CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTTGGTCAAACTGCTGCAAATGGACGA907Sbjet1115CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTTGGTCAAACTGCTGCAAATGGACGA1174Query908GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA967Sbjet1175GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA1234Query968ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA1027Sbjet1235ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA1294Query1028CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA1354Sbjet1295CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA1354Query1088CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1147Sbjet1355CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT1414	_						
Sbjet 1115 CCAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGA 1174 Query 908 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 967 Sbjet 1175 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1027 Sbjet 1235 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjet 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1147 Sbjet 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1414	_	1055	AGTGCTGGCCGA				 CAAGAT 1114
Query 908 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 967 Sbjct 1175 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1027 Sbjct 1235 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjct 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1147 Sbjct 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1414	Query	848	CCAGGCTGTGGT(CGACTCGGACGCAGT	GCCGCGCCTGGTCAA/	ACTGCTGCAAAT	GGACGA 907
Sbjet 1175 GCCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCA 1234 Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1027 Sbjet 1235 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjet 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCCTGC	Sbjct	1115	ccaggctgtggt	cgyctcggycgcygt	gccgcgcctggtcyy	Actectecaaat	GGACGA 1174
Query 968 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1027 Sbjct 1235 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjct 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCCTGC	_		GCCGAGCATTAT'	TGTGCCCGCCCTGCG 	CAGCGTTGGCAACATT	rgtgactggcac 	
Sbjct 1235 ACAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCA 1294 Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjct 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCCTGC	_						
Query 1028 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1087 Sbjct 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1147 Sbjct 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1414	_					GGACTCCTTCT	
Sbjct 1295 CAACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAA 1354 Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1147 Sbjct 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1414	_					JGGACTCCTTCT	
Query 1088 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1147 Sbjct 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1414	_			11111111111111			
Sbjct 1355 CCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCT 1414	_						
Query 1148 GGAGAAGGGTGATTTCAAGGCTCAAAAAAGAGGCTGCCTGGGCGGTGACAAACACACCACGAC 1207	-						 CGTGCT 1414
	Query	1148	GGAGAAGGGTGA'	TTTCAAGGCTCAAAA	AGAGGCTGCCTGGGC	GGTGACAAACAC	CACGAC 1207
Sbjct 1415 GGAGAAGGGTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGAC 1474	Sbjct	1415	GGAGAAGGGTGA'	tttcaaggctcaaaa	AdAddctdcctdddcc	GGTGACAAACAC	CACGAC 1474

Query	1208	ATCTGGCACTCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTT	1267
Sbjct	1475	ATCTGGCACTCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTT	1534
Query	1268	TATCGATTTGCTGGACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATC	1327
Sbjct	1535	tatcgatttgctggacacaaaggatccgcgtaccatcaaggtggtgcagacgggcctatc	1594
Query	1328	CAATCTGTTTGCCCTGGCGGAGAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGA	1387
Sbjct	1595	caatctgtttgccctggcgagaaacttggtgcaccgagaacctatgcttgatggtcga	1654
Query	1388	GGAGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTA	1447
Sbjct	1655	ĠĠĀĠĀŦĠĠĠĊĠĠŦĊŦĀĠĀĊĀĀĠĊŦĠĠĀĀĀĊŦĊŦĠĊĀĠĊĀĠĊĀĊĠĀĠĀĀĊĠĀĠĠĀĠĠŦĊŦĀ	1714
Query	1448	CAAGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCA	1507
Sbjct	1715	caagaaggcctacgccatcattgacacatacttcagcaacgccgacgacgacgagcca	1774
Query	1508	AGAGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGC	1567
Sbjct	1775	AĠAĠĊŢĊĠĊĀĊĊŢĊĀĠĠĀĠĠŢĊĀĀĊĠĠĀĠĊĊĊŢĊĠĀĠŢŢĊĀĀŢĠĊĊĀĊĊĀĠĊĊĊĀĀĠĠĊ	1834
Query	1568	TCCCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAAACGCCGCTCACAC	1627
Sbjct	1835	tcccdaaggtgctacacgttctaatcgcccacccacacattccaaactcccccacac	1894
Query	1628	GCCTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCATTGTCAAACATACG	1687
Sbjct	1895	ĠĊĊŢŢĄĊĄĄĄĊŢĄĊĄĊĊŢŢĊĠĄĊĊĠĊĠĊŢĊĄĊĄĊĄĊŢĄŢĠĊĊĄŢŢĠŢĊĄĄĄĊĠŢĄĊĠ	1954
Query	1688	CATACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACA	1747
Sbjct	1955	ĊATACTCATCATCACATCTTACAAACATTCCCAAAACACTTTGGAGGTATGCATGGAAACA	2014
Query	1748	CAGGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAAATCCACTCGCATG	1807
Sbjct	2015	ĊÁĠĠĊĠĀĀŦĠĊĀŦŦĀĠĊŦŦĀĀĀĠŦĊĀŦĀĀŦŦĠĀĀŦĊĠĠĠŦŦĠĠĊĀĀĀĀŦĊĊĀĊŦĊĠĊĀŦĠ	2074
Query	1808	AATCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCACAGATTGCAGCAT	1867
Sbjct	2075	AATCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCACAGATTGCAGCAT	2134
Query	1868	GGATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCAGCTGCGCTGGCTG	1927
Sbjct	2135	ĠĠĂŦĊŦŦŦĊŦĠĠĊĀĠŦĠŦŦĊĊŦĊĠŦŦĊĀĊĠĀŦĠĊĀĀĊĊĠĊŦĊĠĠĠĊĀĠĊŦĠĊĠĊŦĠĠĊŦĠ	2194
Query	1928	GGATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCG	1987
Sbjct	2195	ĠĠĂŦĊĊĠŦĠĠĂŦĊĂŦĂĠŦĂŦŦŦĊĊĀĠĀĂŦĊĊĠŦĊŦĠŦĂĊĀĠĠĠĠĠĊĂĊĊŦŦĂŦĠŦŦŦĠĊĠ	2254
Query	1988	TGTACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTT	2047
Sbjct	2255	tgtactaggctttttattggatacgtttcgagctcatttcggatatatat	2314
Query	2048	AGTATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTCGCGCAAGCATTaca	2107
Sbjct	2315	AGTATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTCGCGCAAGCATTACA	2374
Query	2108	acaacaacaacaacaac 2130	
Sbjct	2375	ACAACAACAACAACAAC 2397	

Drosophila melanogaster pendulin (Pen), mRNA

Sequence ID: **ref|NM_057693.5|** Length: 2577 Number of Matches: 1 Range 1: 366 to 2487

Score		Expect	Identities	Gaps	Strand	Frame	
3869 bits	s(2095)	0.0()	2113/2122(99%)	0/2122(0%)	Plus/Plus		
Features	S:						
Query	9	aaaaaaaaaaa 	aaaaTGAGTAAGGCG	GATTCTAACTCACGAC	CAGGGCTCCTAC	AAGGCC	68
Sbjct	366	AAAAAAAAAA	AAAATGAGTAAGGCG	GATTCTAACTCACGAC	CAGGGCTCCTAC	AAGGCC	425
Query	69	AACAGCATTAAC	ACGCAGGACTCACGC	ATGCGCCGCCATGAGG	TGACCATCGAG	CTGCGC	128
Sbjct	426	AACAGCATTAAC	Acccaccaccaccaccaccaccaccaccaccaccaccacc	atgcgccgccatgagd	stdaccatcdad	ctgcgc	485
Query	129	AAGTCCAAAAAG	GAGGACCAGATGTTC.	AAGCGGCGCAACATC <i>I</i>	ACGACGAGGAT	CTAACG 	188
Sbjct	486	AAGTCCAAAAAG	daddaccadatdttc.	aagcggcgcaacatc <i>i</i>	rycgycgyggyt	ctaacc	545
Query	189	TCGCCGCTCAAA	GAGCTCAATGGCCAG'	TCGCCGGTGCAGCTG7	CCGTGGACGAG	ATAGTG 	248
Sbjct	546	tccccctcaaa	ĠĀĠĊŦĊĀĀŦĠĠĊĊĀĠ	tceccectect	rccetegege	Atagtg	605
Query	249	GCGGCCATGAAC	AGCGAGGATCAGGAG	CGCCAGTTCCTGGGC	TGCAGTCTGCC	CGCAAG	308

Sbjct	606	GCGGCCATGAACAGCGAGGATCAGGAGCGCCAGTTTCTGGGCATGCAGTCTGCCCGCAAG	665
Query Sbjct	309 666	ATGCTCAGTCGGGAACGCAATCCACCCATCGACCTGATGATCGGCCATGGTATTGTGCCC	368 725
Query	369	ATTTGCATACGCTTCCTGCAGAATACCAACAACTCAATGCTGCAGTTTGAGGCCGCTTGG	428
Sbjct	726	Atttgcatacgcttcctgcagaataccaacaactcaatgctgcagttcgaggccgcttgg	785
Query Sbjct	429 786	GCGCTTACCAACATCGCCTCTGGCACATCCGACCAAACGCGCTGCGTTATCGAACACAAT	488 845
Query	489	GCTGTGCCGCATTTCGTGGCTCTGCTCCAGTCCAAGTCCATGAACCTGGCCGAGCAGGCA	548
Sbjct	846	GCTGTGCCGCATTTCGTGGCTCTGCTCCAGTCCAAGTCCATGAACCTGGCCGAGCAGGCA	905
Query Sbjct	549 906	GTCTGGGCTCTGGGCAACATTGCCGGCGACGGAGCCGCCGCCGCGACATTGTCATCCAC	608 965
Query	609	CACAACGTAATTGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTTTG	668
Sbjct	966	cacaacgtaattgacggaatcttgccactgatcaacaatgagacaccgctctcttttctg	1025
Query Sbjct	669 1026	CGCAACATCGTCTGGCTGATGTCCAACCTGTGCAGGAATAAGAATCCATCTCCGCCATTC	728 1085
Query	729	GATÇAGGTGAAGÇGGÇTGTTGÇÇÇGTÇÇTGTÇGÇAGÇTTÇTGÇTTAGTÇAGGAÇATÇÇAA	788
Sbjct	1086	GATCAGGTGAAGCGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCAA	1145
Query	789 1146	GTGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGATC	848 1205
Sbjct Query	849	ÇAĢĢÇTĢTĢĢŢÇĢĄÇTÇĢĢĄÇĢÇAĢTĢÇÇĢÇĢÇÇTĢĢŢÇAAAÇTĢÇTĢÇAAATĢĢAÇĢAĢ	908
Sbjct	1206	CAGGCTGTGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGAG	1265
Query	909	CCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAA	968
Sbjct Query	1266 969	CCGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAA CAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCAC	1325 1028
Sbjct	1326	CAGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCAC	1385
Query	1029	AACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAAC	1088
Sbjct Query	1386 1089	ÁÁCÁÁÁÁGCÁÁCÁTTGTGÁÁGGÁGGCTGCCTGGÁCGGTCÁGCÁACÁTCÁCÁGCÁGGTÁÁC CAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTG	1445 1148
Sbjct	1446	CAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTG	1505
Query	1149	GAGAAGGGTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCCACGACA	1208
Sbjct Query	1506 1209	GAGAAGGGTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACA TCTGGCACTCCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTT	1565 1268
Sbjct	1566	TCTGGCACTCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTT	1625
Query	1269	ATCGATTTGCTGGACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCC	1328
Sbjct	1626 1329	ATCGATTTGCCCTGGCGGAGAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAG	1685 1388
Query Sbjct	1686	AATCTGTTTGCCCTGGCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAG	1745
Query	1389	GAGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTAC	1448
Sbjct	1746	ĠĀĠĀŦĠĠĠĊĠĠŦĊŦĀĠĀĊĀĀĠĊŦĠĠĀĀĀĊŦĊŦĠĊĀĠĊĀĠĊĀĊĠĀĠĀĀĊĠĀĠĠĀĠĠŦĊŦĀĊ	1805
Query Sbjct	1449 1806	AAGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAA	1508 1865
Query	1509	GAGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCT	1568
Sbjct	1866	GAGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCT	1925
Query Shict	1569 1926	CCCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAAACGCCGCTCACACG	1628 1985
Sbjct Query	1926	CCCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAAACTCCGCTCACACG CCTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCATTGTCAAACATACGC	1985
Sbjct	1986	CCTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCATTGTCAAACATACGC	2045
Query	1689	ATACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACAC	1748

Sbjct	2046	ATACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACAC	2105
Query	1749	AGGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAAATCCACTCGCATGA	1808
Sbjct	2106	AGGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAAATCCACTCGCATGA	2165
Query	1809	ATCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCACAGATTGCAGCATG	1868
Sbjct	2166	ATCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCACAGATTGCAGCATG	2225
Query	1869	GATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCAGCTGCGCTGGCTG	1928
Sbjct	2226	GATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCAGCTGCGCTGGCTG	2285
Query	1929	GATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCGT	1988
Sbjct	2286	GATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCGT	2345
Query	1989	GTACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTTA	2048
Sbjct	2346	GTACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTTA	2405
Query	2049	GTATTTATTTATGTATACAGGAAACGCTTTTTAATCCTCCACCTTCGCGCAAGCATTacaa	2108
Sbjct	2406	GTATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTCGCGCAAGCATTACAA	2465
Query	2109	caacaacaacaacaacaac 2130	
Sbjct	2466	CAACAACAACAACAAC 2487	

Drosophila melanogaster pendulin (oho-31) mRNA, complete cds

Sequence ID: **gb|U12269.1|DMU12269** Length: 2521 Number of Matches: 1 Range 1: 318 to 2435

Score		Expect	Identities	Gaps	Strand	Frame	
3862 bits	s(2091)	0.0()	2109/2118(99%)	0/2118(0%)	Plus/Plus		
Features	S :						
Query	10	aaaaaaaaaaa	aaaTGAGTAAGGCGG	ATTCTAACTCACGAC	AGGGCTCCTACA	AGGCCA	69
Sbjct	318	AAAAAAAAAAA	AAATGAGTAAGGCGGA	Attetaaeteaegaez	AGGGCTCCTACA	AGGCCA	377
Query	70	ACAGCATTAACA	.CGCAGGACTCACGCAT	GCGCCGCCATGAGG	rgaccatcgagc'	TGCGCA	129
Sbjct	378	Acaccattaaca	cecyeeycacecy	recececepter	rgyccytcgygc,	tgcgcy	437
Query	130	AGTCCAAAAAGG	AGGACCAGATGTTCAA	AGCGGCGCAACATCAZ	ACGACGAGGATC'	TAACGT	189
Sbjct	438	AGTCCAAAAAGG	AGGACCAGATGTTCAA	y de ce de caracter de la company de la comp	Acgacgaggatc	taacgt	497
Query	190	CGCCGCTCAAAG	AGCTCAATGGCCAGTO	CGCCGGTGCAGCTGT(CCGTGGACGAGA'	TAGTGG 	249
Sbjct	498	ĊĠĊĊĠĊŦĊĀĀĀĠ	AĠĊŦĊAAŦĠĠĊĊAĠŦĊ	ceccenteres	ccctccccccccccccccccccccccccccccccccccc	tagtgg	557
Query	250	CGGCCATGAACA	GCGAGGATCAGGAGCG	GCCAGTTCCTGGGCAT	FGCAGTCTGCCC(GCAAGA 	309
Sbjct	558	ĊĠĠĊĊĂŢĠĂĀĊĀ	ĠĊĠĀĠĠĀŢĊĀĠĠĀĠĊĊ	SCCAGTTCCTGGGCA:	rĠĊĀĠŦĊŦĠĊĊĊ	ĠĊĀĀĠĀ	617
Query	310	TGCTCAGTCGGG	AACGCAATCCACCCAT	CGACCTGATGATCG(GCCATGGTATTG' 	TGCCCA	369
Sbjct	618		ÄÄĊĠĊÄÄŤĊĊÄĊĊĊĀſ				677
Query	370		TCCTGCAGAATACCAA 				429
Sbjct	678		TCCTGCAGAATACCA <i>t</i>				737
Query	430		TCGCCTCTGGCACAT(489
Sbjct	738	CGCTTACCAACA			GCGTTATCGAAC.	ACAATG	797
Query	490		TCGTGGCTCTGCTCC <i>I</i>				549
Sbjct	798		ŢĊĠŢĠĠĊŢĊŢĠĊŢĊĊ <i>ŧ</i>				857
Query	550		GCAACATTGCCGGCGA				609
Sbjct	858		ĠĊĀĀĊĀŤŤĠĊĊĠĠĊĠź				917
Query	610		ACGGAATCTTGCCACT 				669 977
Sbjct	918 670		GGCTGATGTCCAACCT				729
Query	978		GGCTGATGTCCAACCT				1037
Sbjct	730		GGCTGATGTCCAACCT				1037 789
Query							1097
Sbjct	1038	ATCAGGTGAAGC	ĠĠĊŦĠŦŦĠĊĊĊĠŦĊĊſ	TGTCGCAGCTTCTGC'.	TAGTCAGGACA	TCCAAG	109/

Query	790	TGCTGGCCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGATCC	849
Sbjct Query	1098 850	TĠĊŢĠĠĊĊĠĂĊĠĊĊŢĠĊŢĠĠĠĊŢŢŢĠŢĊĊŢĂĊĠŢĊĂĊĠĠĂĊĠĂĊĠĂŢĂĂĊĂĊĊĂĂĠĂŢĊĊ AGGCŢĠŢŢĠĠŢĊĠAĊŢĠĠĠĊŢŢŢĠŢĠĊĠĊĠĊĠŢĠŢĊĀĀĠŢŢĠĊŢĠĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠŎĠ	1157 909
Sbjct	1158	AGGCTGTGGTCGACTCGGACGCAGTGCCGCCCTGGTCAAACTGCTGCAAATGGACGAGC	1217
Query	910	CGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAAC	969
Sbjct	1218	CGAGCATTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAAC	1277
Query	970	AGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCACA	1029
Sbjct	1278	AGACTGACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCACA	1337
Query	1030	ACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACC	1089
Sbjct	1338 1090	ACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACC AGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGG	1397 1149
Query Sbjct	1398	AGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGG AGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGG	1457
Query	1150	AGAAGGGTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACAT	1209
Sbjct	1458	AGAAGGGTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACAT	1517
Query	1210	CTGGCACTCCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTA	1269
Sbjct	1518	ctggcactcccgaacagatcgtcgatctaattgagaagtacaaaatattgaagcctttta	1577
Query	1270	TCGATTTGCTGGACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCA	1329
Sbjct	1578	ŤĊĠĂŤŤŤĠĊŤĠĠĂĊĂĊĂĂĂĠĠĂŤĊĊĠĊĠŤĂĊĊĂŤŦĂĂĠĠŤĠĠŤĠĊĂĠĂĊĠĠĠĊĊŤĂŤĊĊĂ	1637
Query Sbjct	1330 1638	ATCTGTTTGCCCTGGCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGG 	1389 1697
Query	1390	AGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACA	1449
Sbjct	1698	AGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACA	1757
Query	1450	AGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAG	1509
Sbjct	1758	AGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAG	1817
Query	1510	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	1569
Sbjct	1818	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	1877
Query Sbjct	1570 1878	CCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAAACGCCGCTCACACGC	1629 1937
Query	1630	CTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCATTGTCAAACATACGCA	1689
Sbjct	1938		1997
Query	1690	TACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACACA	1749
Sbjct	1998	TACTCATCATCACCATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACACA	2057
Query	1750	GGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAAATCCACTCGCATGAA	1809
Sbjct	2058	ĠĠĊĠAĀŢĠĊĀŢŢĀĠĊŢŢĀĀĀĠŢĊĀŢĀĀŢŢĠĀĀŢĊĠĠĠŢŢĠĠĊĀĀĀĀŢĊĊĀĊŢĊĠĊĀŢĠĀĀ	2117
Query Sbjct	1810 2118	TCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCACAGATTGCAGCATGG	1869 2177
Query	1870	ATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCAGCTGCGCTGGCTG	1929
Sbjct	2178	ATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCAGCTGCGCTGGC	2237
Query	1930	ATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCGTG	1989
Sbjct	2238	ATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCGTG	2297
Query	1990	TACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTTAG	2049
Sbjct	2298	tactaggctttttattggatacgtttcgagctcatttcggatatatat	2357
Query	2050	TATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTCGCGCAAGCATTacaac	2109
Sbjct Query	2358 2110	TATTTATTTATGTATACAGGAAACGCTTTTTAATCCTCCACCTTCGCGCAAGCATTACAAC aacaacaacaacaacaac 2127	2417
Sbjct	2418	aacaacaacaacaac 2127 AACAACAACAACAAC 2435	
	0		

Drosophila sechellia GM17916 (Dsec\GM17916), mRNA

Sequence ID: **ref|XM_002036391.1|** Length: 1569 Number of Matches: 1 Range 1: 1 to 1568

Score		Expect	Identities	Gaps	Strand	Frame	
2697 bit	s(1460)	0.0()	1532/1568(98%)	0/1568(0%)	Plus/Plus		
Features	s:						
Query	24	aTGAGTAAGGCG	GATTCTAACTCACGAC	AGGGCTCCTACAAGG	GCCAACAGCATT	AACACG 	83
Sbjct	1		ĠĀŢŢĊŢĀĀĊŢĊĀĊĠĀĊ.		sccaacagcatt		60
Query Sbjct	84 61		ATGCGCCGCCATGAGG 				143 120
Query	144		AAGCGGCGCAACATCA				203
Sbjct	121			 ACGACGAGGATCTAA			180
Query	204	CTCAATGGCCAG	TCGCCGGTGCAGCTGT	CCGTGGACGAGATAG	TGGCGGCCATG	AACAGC	263
Sbjct	181	CTCAATGGCCAG	tcgccggtgcagctgt	ccgtggacgagatad	TGGCGGCCATG	AACAGC	240
Query	264		CGCCAGTTCCTGGGCA				323
Sbjct	241		ĊĠĊĊĂĠŦŦĊĊŦĠĠĠĊĂ				300
Query Sbjct	324 301		ATCGACCTGATGATCG 				383 360
Query	384		AACAACTCAATGCTGC				443
Sbjct	361	CTGCAGAATACC		 AGTTCGAGGCCGCCT		 AACATC	420
Query	444	GCCTCTGGCACA	TCCGACCAAACGCGCT	GCGTTATCGAACACA	ATGCTGTGCCG	CATTTC	503
Sbjct	421	GCCTCTGGCACC	tccgaccaaacgcgct	GCGTTATCGAACACA	ATGCTGTGCCG	CATTTC	480
Query	504	GTGGCTCTGCTC	CAGTCCAAGTCCATGA	ACCTGGCCGAGCAGG	CAGTCTGGGCT	CTGGGC 	563
Sbjct	481		ĊĀĠŦĊĊĀĀĠŦĊĊĀŦĊĀ				540
Query	564 541		GACGGAGCCGCCCC 				623 600
Sbjct Query	624		.CTGATCAACAATGAGA				683
Sbjct	601						660
Query	684	CTGATGTCCAAC	СТСТССАССАТАЛАСА	АТССАТСТСССССАТ	TCGATCAGGTG	ĄĄĢÇĢĢ	743
Sbjct	661	CTGATGTCCAAC	CTGTGCAGGAACAAGA	ATCCATCACCGCCAT	TCGAACAGGTG	AAGCGG	720
Query	744	CTGTTGCCCGTC	CTGTCGCAGCTTCTGC	TTAGTCAGGACATCC	CAAGTGCTGGCC	GACGCC 	803
Sbjct	721		ĊŢŢŢĊĊĊĂĀĊŢŢĊŢĠĊ				780
Query	804		TCCTACGTCACGGACG.				863 840
Sbjct Query	781 864		·TCCTACGTCACGGACG. ·CCGCGCCTGGTCAAAC				923
Sbjct	841		CCGCGCCTGGTCAAAC	11111111111111			900
Query	924	ССССССТССС	AGCGTTGGCAACATTG	ŢĢĄĊŢĢĢĊĄĊĄĢĄŢĊ	CAACAGACTGAC	GTTGTA	983
Sbjct	901	CCCGCCTGCGC	AGCGTTGGCAACATTG		CAACAGACTGAC		960
Query	984	ATTGCATCTGGA	GGTTTACCAAGGCTGG	GACTCCTTCTACAGC	CACAACAAAAGC	AACATT 	1043
Sbjct	961		ĠĠŦŦŦĀĊĊŦĀĠĠĊŦĠĠ				1020
Query	1044		GCCTGGACGGTCAGCA	111111 111111			1103
Sbjct	1021 1104		ĠĊĊŦĠĠĂĊĠĠŦĊĂĠĊĀ GCCGGCATCTTCCAGC.				1080 1163
Query Sbjct	104		GCCGGCATCTTCCAGC. GCCGGCATTTTCCAGC.				1140
Query	1164		ĠŖĠĠĊŦĠĊĊŦĠĠĠĊĠĠ				1223
Sbjct	1141	AAGGCACAAAAA			 \CATCTGGCACT	 CCCGAA	1200
Query	1224	CAGATCGTCGAT	CTAATTGAGAAGTACA	AAATATTGAAGCCTT	TTATCGATTTG	CTGGAC	1283
Sbjct	1201	cagategtagat	ctaattgagaagtaca	AAATATTGAAGCCTT	rttAtcGAtttG	ctggyc	1260

Query	1284	ACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGTTTGCCCTG	1343
Sbjct	1261	GCAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGTTTGCCCTG	1320
Query	1344	GCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGCGGTCTA	1403
Sbjct	1321	GCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGCGGTCTA	1380
Query	1404	GACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCCTACGCC	1463
Sbjct	1381	GACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCCTACGCC	1440
Query	1464	ATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAGAGCTCGCACCTCAG	1523
Sbjct	1441	ATCATCGACACTTACTTCAGCAACGCCGACGACGAGGCCGAGCAAGAGCTCGCACCTCAG	1500
Query	1524	GAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAGGTGGCTAC	1583
Sbjct	1501	GAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAGGGTGGCTAC	1560
Query	1584	ACGTTCTA 1591	
Sbjct	1561	ACGTTCTA 1568	

Drosophila simulans GD23655 (Dsim\GD23655), mRNA

Sequence ID: **ref|XM_002078829.1|** Length: 1575 Number of Matches: 1 Range 1: 1 to 1574

Score		Expect	Identities	Gaps	Strand	Frame	
2647 bit	s(1433)	0.0()	1528/1574(97%)	6/1574(0%)	Plus/Plus		
Features	s:						
Query	24	aTGAGTAAGGCG	GATTCTAACTCACGAC	AGGGCTCCTACAAGO	GCCAACAGCATT	AACACG	83
Sbjct	1	AtGAGTAAGGCG	GATTCTAACTCACGAC	agggctcctacaag	sccaacagcatt	AACACG	60
Query	84	CAGGACTCACGC	ATGCGCCGCCATGAGG	TGACCATCGAGCTGC	GCAAGTCCAAA	AAGGAG 	143
Sbjct	61	caggactcgcgc	Atgccccccatcacc	tgaccatcgagctgo	cgcaagtccaag	AAGGAG	120
Query	144	GACCAGATGTTC	AAGCGGCGCAACATCA	ACGACGAGGATCTAA	ACGTCGCCGCTC	AAAGAG 	203
Sbjct	121	ĠĀĊĊĀĠĀŦĠŦŦĊ	AAGCGGCGCAACATCA	Acgacgaggatctaz	ycetceccectco.	AAAGAG	180
Query	204	CTCAATGGCCAG	TCGCCGGTGCAGCTGT	CCGTGGACGAGATAC	TGGCGGCCATG	AACAGC 	263
Sbjct	181	ĊŦĊĀĀŦĠĠĊĊĀĠ	rtċĠċċĠĠtĠċAĠċtĠt	ĊĊĠŦĠĠĂĊĠĂĠĂŦĂĊ	stĠĠĊĠĠĊĊAtĠ <i>i</i>	AAĊAĠĊ	240
Query	264	GAGGATCAGGAG	CGCCAGTTCCTGGGCA	TGCAGTCTGCCCGC	AAGATGCTCAGT(CGGGAA 	323
Sbjct	241		ĊĠĊĊĂĠŤŤĊĊŤĠĠĠĊĀ				300
Query	324		ATCGACCTGATGATCG				383
Sbjct	301		ATĊĠĀĊĊŢĠĀŢĠĀŢĊĠ				360
Query	384	CTGCAGAATAC-	CAAC-AACTCAA				437
Sbjct	361			ŢĠĊŢĠĊĂĠŢŢĊĊŢĠĊ			420
Query	438		GGCACATCCGACCAAA				497
Sbjct	421	ÄÄĊÄŤĊĠĊĊŤĊŤ		CGCGCTGCGTTATC		GTGCCG	480
Query	498 481		CTGCTCCAGTCCAAGT 				557 540
Sbjct	558		GCCGGCGACGGAGCCG				617
Query Sbjct	541		GCCGGCGACGGAGCCG 				600
Query	618		TTGCCACTGATCAACA				677
Sbjct	601		TTGCCACTGATCAACA				660
Query	678		TCCAACCTGTGCAGGA				737
Sbjct	661					Î Î Î I Î	720
Query	738		ÇÇÇĞTCÇTĞTÇĞÇAĞÇ				797
Sbjct	721						780
Query	798	ĢĄCĢÇÇŢĢÇŢGG	- - - - - - - - - - - - - - - - - - -	ҪҪҪ҈ӒҪҪ҈Ӓ҅Ҫѽ҉҅҅҅҅҄Ҫ	\ÇÇAAGATCÇAG(ĢÇŢĢŢĢ	857
Sbjct	781					 GCTGTG	840
-							

Query	858	GTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATT	917
Sbjct	841	GTCGACTCCGACGCAGTGCCGCCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATT	900
Query	918	ATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAACAGACTGAC	977
Sbjct	901	ATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAACAGACTGAC	960
Query	978	GTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCACAACAAAAGC	1037
Sbjct	961	GTTGTAATTGCATCTGGAGGTTTACCTAGGCTGGGACTTCTTCTACAACAAAAAGC	1020
Query	1038	AACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACCAGAAGCAG	1097
Sbjct	1021	AACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACGGCAGGTAACCAGAAGCAG	1080
Query	1098	ATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGGAGAAGGGT	1157
Sbjct	1081	Atccadectedattcadeccedecatriticalectedecaccedectedectedadadadect	1140
Query	1158	GATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACATCTGGCACT	1217
Sbjct	1141	GATTTCAAGGCACAAAAAGAGGCTGCCTGGGCGGTAACAAACA	1200
Query	1218	CCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTATCGATTTG	1277
Sbjct	1201	cccdaacadatcdtgdatctaattdaaaadtacaaaatattdaadccttttatcdatttd	1260
Query	1278	CTGGACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGTTT	1337
Sbjct	1261	ctggacgcaaaggatccgcgtaccatcaaggtggtgcagacgggcctatccaatctgtt	1320
Query	1338	GCCCTGGCGGAGAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGC	1397
Sbjct	1321	ĠĊĊĊŦĠĠĊĠĠĀĠĀĀĀĀĊŦŦĠĠŦĠĠĊĀĊĊĠĀĠĀĀĊĊŦĀŦĠĊŦŦĠĀŦĠĠŦĊĠĀĠĀĠĀŦĠĠĠĊ	1380
Query	1398	GGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCC	1457
Sbjct	1381	ĠĠŦĊŦĀĠĀĊĀĀĠĊŦĠĠĀĀĀĊŦĊŦĠĊĀĠĊĀĠĊĀĊĠĀĠĀĠĠĀĠĠĀĠĠŦĊŦĀĊĀĀĠĀĀĠĠĊĊ	1440
Query	1458	TACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAGAGCTCGCA	1517
Sbjct	1441	taceccatcatcatceacacttacttcaecaacecceaceaceaceaeceae	1500
Query	1518	CCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAGGT	1577
Sbjct	1501	cctcaggaggtcaacggagccctcgagttcaatgccacccagccaaggctccaaggct	1560
Query	1578	GGCTACACGTTCTA 1591	
Sbjct	1561	ĠĠĊŦĀĊĀĊĠŤŤĊŤĀ 1574	

Drosophila yakuba uncharacterized protein (Dyak\GE18896), mRNA Sequence ID: ref|XM_002088987.2| Length: 2321 Number of Matches: 1 Range 1: 280 to 2303

Score		Expect	Identities	Gaps	Strand	Frame	
2534 bit	s(1372)	0.0()	1830/2043(90%)	64/2043(3%)	Plus/Plus		
Features	3:						
Query	21	aaaaTGAGTAAG	GCGGATTCTAACTC	ACGACAGGGCTCCTACA	AGGCCAACAGC.	ATTAAC	80
Sbjct	280	AAAATGAGTAAG	sdeddattetaaete	ecgacagggctcgtaca	AGGCCAACACC.	ATCAAC	339
Query	81	ACGCAGGACTCA	CGCATGCGCCGCCAT	GAGGTGACCATCGAGC	TGCGCAAGTCC.	AAAAAG 	140
Sbjct	340	ACGCAGGACTCG	scccatcccat	rgaggtgaccgtcgagd	TGCGCAAGGCC.	AAGAAG	399
Query	141	GAGGACCAGATO	GTTCAAGCGGCGCAAC	CATCAACGACGAGGATC	TAACGTCGCCG	CTCAAA	200
Sbjct	400	daddaccadatd	sttcaagcggcgcaad	catcaacgacgaggacd	tcycttcecce	ctcaaa	459
Query	201	GAGCTCAATGGC	CAGTCGCCGGTGCAG	GCTGTCCGTGGACGAGA	TAGTGGCGGCC.	ATGAAC	260
Sbjct	460	gygctcyyteg	ccyetcecceetecy	sctgtccgtggacgaga	tagtggcggcc.	AtGAAC	519
Query	261	AGCGAGGATCAG	GAGCGCCAGTTCCTC	GGCATGCAGTCTGCCC	GCAAGATGCTC.	AGTCGG 	320
Sbjct	520	AGCGAGGATCAG	sdadcdccadttcctd	sggcatgcagtctgccc	:GCAAGATGCTC.	AGTCGG	579
Query	321	GAACGCAATCCA	ACCCATCGACCTGATO	GATCGGCCATGGTATTG	TGCCCATTTGC.	ATACGC	380
Sbjct	580	gydcgcyytcc	scccatcgacctgatd	satcddccatddaattd	;tdddatttdd	ATACGC	639
Query	381	TTCCTGCAGAAT	ACCAACAACTCAATO	GCTGCAGTTTGAGGCCG	CTTGGGCGCTT.	ACCAAC	440
Sbjct	640	ttcctccaaaat	rtccaacaactcaatd	schdcadhhhdaddccd	ccteeecett	ACAAAC	699
Query	441	ATCGCCTCTGGC	CACATCCGACCAAAC	GCGCTGCGTTATCGAAC	CACAATGCTGTG	CCGCAT	500

Sbjct	700	ATCGCCTCCGGCACCAAACGCGCTGCGTCATCGAACACAATGCTGTGCCGCAT	759
Query	501	TTCGTGGCTCTGCTCCAGTCCAAGTCCATGAACCTGGCCGAGCAGGCAG	560
Sbjct	760	ŤŤĊĠŤĠĠĊŤĊŤĠĊŤĠĊÁĠŤĊĊÁÁĠŤĊĊÁCCÁÁĊĊŤĠĠĊĊĠÁĠĊÁĠĠĊÁĠŤĊŤĠĠĠĊŤĊŤĠ	819
Query Sbjct	561 820	GGCAACATTGCCGGCGACGGAGCCGCCGCCCGCGACATTGTCATCCACCACAACGTAATT	620 879
Query	621	GACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTTTTGCGCAACATCGTC	680
Sbjct	880	GACGGAATCTTACCTCTGATCAACAATGAGACGCCACTTTCTTT	939
Query	681	ŢĢĢĊŢĢĄŢĢŢĊĊĄĄĊĊŢĢŢĢĊĄĠĠĄĄŢĄĄĠĄĄŢĊĊĄŢĊŢĊĊĢĊĊĄŢŢĊĠĄŢĊĄĠĠŢĠĄĄĠ	740
Sbjct	940	TGGCTGATGTCTAACCTGTGCAGAAACAAGAATCCCTCGCCGCCGTTTGAGCAGGTGAAG	999
Query	741	CGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCAAGTGCTGGCCGAC	800
Sbjct	1000	cgctctctccccccccccccccccccccccccccccccc	1059
Query	801	GCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGATCCAGGCTGTGGTC	860
Sbjct	1060	GCCTGCTGGGCTTTGTCCTACGTCACAGACGACGATAACAGCAAGATTCAGGCAGTGGTC	1119 920
Query Sbjct	861 1120	GACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATTATT	1179
Query	921	GTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAACAGACTGACGTT	980
Sbjct	1180	GTGCCCGCCTTGCGCAGCGTTGGCAACATTGTGACCGGCACAGATCAACAGACTGATGTT	1239
Query	981	GTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCACAACAAAAGCAAC	1040
Sbjct	1240	GTAATCGCATCTGGAGCTTTACCTTTGCTGGGACTTCTTCTGCAGCACAAAAAGAGTAAC	1299
Query	1041	ATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACCAGAAGCAGATC	1100
Sbjct	1300	ÄŤŤĠŤĊĂĂĠĠĂĀĠĊŤĠĊĊŤĠĠĂĊĠĀŤĊĂĠĊĂĠĊĂĠĊĀĠĊĀĠĠŤĂĀĊĊĀĠĀĀĠĊĀĠĀŤĊ	1359
Query Sbjct	1101 1360	CAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGGAGAAGGGTGAT	1160 1419
Query	1161	TTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCCACGACATCTGGCACTCCC	1220
Sbjct	1420	TTTAAGGCCCAGAAAGAGGCAGCCTGGGCGGTGACAAACACCACGACATCTGGCACTCCT	1479
Query	1221	Ģ ĄĄÇĄĢĄŢÇĢŢĊĢĄŢĊŢĄĄŢŢĢĄĢĄĄĢŢĄĊĄĄĄĄŢĄŢŢĢĄĄĢĊĊŢŢŢŢĄŢĊĢĄŢŢŢĢĊŢĢ	1280
Sbjct	1480	GAACAGATCGTGGATCTAATTGAGAAGTACCATATATTGAAGCCGTTTATCGATCTGCTG	1539
Query	1281	GACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGTTT-GC	1339
Sbjct	1540	ĠAĊGĊAAAĠĠATĊĊĠĊĠTAĊTATĊAAĠĠTĠĠTĠĊAĠAĊĠĠĠĊĊTATĊĊAA-ĊTTTTTCĠĊ	1598
Query	1340	CCTGGCGGAGAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGCGG	1399
Sbjct Query	1599 1400	CCTGGCGGAGAAATTCAATGGCATCGAGAACCTATGCTTGATGGTCGAGGAGATGGGCGG TCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCCTA	1658 1459
Sbjct	1659	CCTAGATAAGCTGGAAACACTGCAGCAGCACGAAAACGAGGAGGTCTACAAGAAGGCCTA	1718
Query	1460	ҪҪҪҪ҅ӒҭҪ҅Ӓ҅҅ҬҬ҅҅҄҄҄҄ӒҪӒҪӒҬӒҪҬҬҪӒҪҪӒӒҪ҅Ҫ҄ҪҪҪ҄ӒҪҪӒҪҪӒҪҪӒ҅ҪҪӒ҅ҪҪӒ҅҅ҪӒӒҪӒ҅҅Ҫ҅҅҅҅ҀӒҪҪ	1519
Sbjct	1719	CGCCATCATCGACACTTACTTCAGCAACGCGACGACGAGCCGAGCAAGAACTTGCGCC	1778
Query	1520	TCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAGGTGG	1579
Sbjct	1779	tcaggaggtcaaccagagccccaggagttcaatgccaccaggccaaggctcagggtgg	1838
Query	1580	CTACACGTTCTA-A-TCGCCCACCCCACACATTCCAAACGCCGCTCACACGCCTTAC	1634
Sbjct	1839	ĊŦĂĊĂĊĠŦŦĊŦĂĠĂĊŦAAŦĊĠĊĊĊĂ——ĊĊĂĊĂŦĂŦŦŦĊĂĂĂĊĠĊĊĠĊŦĊĂĊĂĊĠĊĊŦŦĂĊ AAAC—A—ACTA—C——————ACCTTCGACCGCGCTCACACACTATGCCATTGTCA—AA—C	1896 1682
Query Sbjct	1635 1897	AAAC-A-ACTA-CACCTTCGACCGCGCTCACACACTATGCCATTGTCA-AA-C	1956
Query	1683	-ATACG-CATAC-TCATCATCACATCTTAC-AAACATTCCCAAACACTTTG	1729
Sbjct	1957	TATGCCATTGTCAAACATACGCACCATCACATCTCACCACGAACATTCCCAAACAC-TTG	2015
Query	1730	GAGGTATGCATGGAAACACAGGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTG	1789
Sbjct	2016	GAGGTATGCATGGAAACACAGACGAATGCATTAGCTTAAA-TCATAATTGAATCAGGTTG	2074
Query	1790	GCA-A-A-ATCCACTCGCATGAATCCCCATTTAACATACCCGTATTCCTC	1836
Sbjct	2075	dcggagaccacccgtacccatctatgcatgaat-cccatttcaacattcttc	2133
Query	1837	GCGTTAGACTAGACTTCACAGATTGCAGCATGGATCTTTCTG-GCAGTGTTCCTCGTTCA	1895

Sbjct	2134	GCATTGGAGTTCACAGATTGCAGCATGAATCTC-CGGTGCAGTATTTCACGTTCA	2187
Query	1896	CGATGCAACCGCTCGGGCAGCTGCGCTGGCTGGGATCCGTGGATCATAGTATTTCCAGAA	1955
Sbjct	2188	GGATGCAACCGCTCGGGCAGCTGTGCTGGCTGGGATCA-TGG-TT-GT-TGCCCAGAA	2241
Query	1956	TCCGTCTGTACAGGGGCACCTTATGTTTGCGTGTACTAGGCTTTTTATTGGATACGTTT	2015
Sbjct	2242	TCCGTCTGTACAGGGTGC-CCTTCTGATTGCGTGTGCTCGGCTTTTTATTGGATACGTTT	2300
Query	2016	CGA 2018	
Sbjct	2301	CGA 2303	

Drosophila erecta uncharacterized protein (Dere\GG10083), mRNA Sequence ID: **ref|XM_001969358.2|** Length: 1701 Number of Matches: 1 Range 1: 73 to 1695

Score		Expect	Identities	Gaps	Strand	Frame	
2495 bit	s(1351)	0.0()	1535/1625(94%)	7/1625(0%)	Plus/Plus		
Feature	S :						
Query	19	aaaaaa TGAGT A	AGGCGGATTCTAACTC	CACGACAGGGCTCCT	ACAAGGCCAACA	GCATTA	78
Sbjct	73	AAAAAATGAGTA	AGGCGGATTCTAACTC	CGCGACAGGGCTCGT	ACAAGGCCAACA	.ccatca	132
Query	79	ACACGCAGGACT	CACGCATGCGCCGCC	ATGAGGTGACCATCGA	AGCTGCGCAAGT	CCAAAA	138
Sbjct	133	y y y y y y y y y y y y y y y y y y y	rcecechtechtechtech	\rdaddtdaccatcd <i>i</i>	Agctgcgcaagt	ccaaga	192
Query	139	AGGAGGACCAGA	ATGTTCAAGCGGCGCA <i>I</i>	ACATCAACGACGAGGA 	ATCTAACGTCGC	CGCTCA	198
Sbjct	193	AĠĠĀĠĠĀĊĊĀĠĀ		ACATCAACGACGAGG <i>i</i>		ĊĠĊŢĊĀ	252
Query	199		GCCAGTCGCCGGTGC <i>I</i>				258
Sbjct	253		ĠĊĊĂĠŤĊĠĊĊĠĠŤĠĊ <i>Ĭ</i>				312
Query	259 313	ACAGCGAGGATC ACAGCGAAGATC	AGGAGCGCCAGTTCCT 				318 372
Sbjct Query	319		CACCCATCGACCTGAT			CCATAC	378
Sbjct	373		CGCCATCGACCTGA			GCATAC	432
Query	379		АТАССААСААСТСААТ			TTAÇÇA	438
Sbjct	433		 ATACCAACAACTCAAT	 GCTGCAGTTCGAGG(CCGCCTGGGCGC	 TTACCA	492
Query	439	АСАТСССТСТС	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	СССССТСССТТАТССР	AACACAATGCTG	ŢĢÇÇĢÇ	498
Sbjct	493	ACATCGCCTCC	GTACCTCCGACCAAA	cgcgctgcgttatcg	AACACAATGCTG	TGCCGC	552
Query	499	ATTTCGTGGCTC	TGCTCCAGTCCAAGTC	CCATGAACCTGGCCG	AGCAGGCAGTCT	GGGCTC	558
Sbjct	553	Atttcctccc	tgctccagtccaagtc	ctaccaacctggccg	AGCAGGCAGTCT	qqqqtq	612
Query	559	TGGGCAACATTG	CCGGCGACGGAGCCGC	CCGCCCGCGACATTGT	CATCCACCACA	ACGTAA 	618
Sbjct	613		;ċċĠĠċĠÀċĠĠÀĠċċĠċ				672
Query	619		TGCCACTGATCAACA?				678
Sbjct	673		TĠĊĊŦĊŦĠĂŦĊĂĂĊĂŹ				732
Query	679 733		CCAACCTGTGCAGGA <i>I</i> CCAACCTGTGCAGGA <i>I</i>				738 792
Sbjct Query	739		CCCAACCIGIGCAGGAA CCCGTCCTGTCGCAGCT				798
Sbjct	793		CCGTTCTGTCCCAGC				852
Query	799		CTTTGTCCTACGTCA				858
Sbjct	853	ACGCCTGCTGGG			 GCAAGATCCAAG	 CAGTGG	912
Query	859	ҭСĢĄҪҭҪĢĢĄҪĢ	; ;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	ӷҪѧѧѧҪҭҫҪҭҫҪѧѧѧҁ	ГĢĢĄÇĢĄĢÇÇĢĄ	.ĢÇ <u>А</u> ŢŢĄ	918
Sbjct	913	TTGACTCGGACG	CAGTGCCGCGCCTGG1	rcaaactgctgcaaa	rggacgagccga	.GCATTA	972
Query	919	TTGTGCCCGCCC	TGCGCAGCGTTGGCA	ACATTGTGACTGGCA(CAGATCAACAGA	CTGACG	978
Sbjct	973	TTGTGCCCGCCC	TGCGCAGCGTTGGCA	ACATTGTGACCGGCA	CAGATCAACAGA	.ctgacg	1032
Query	979	TTGTAATTGCAT	CTGGAGGTTTACCAAC	GGCTGGGACTCCTTC	TACAGCACAACA	AAAGCA 	1038
Sbjct	1033	ttgtaatcgcat	rctggaggtttacctac	gen in the second se	rgcagcacaaca	AGAGTA	1092

Query	1039	ACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACCAGAAGCAGA	1098
Sbjct	1093	ACATTGTCAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACCAGAAGCAGA	1152
Query	1099	TCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGGAGAAGGGTG	1158
Sbjct	1153	tccaacccctcattcaccccccatctttcaccacctcccccc	1212
Query	1159	ATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACATCTGGCACTC	1218
Sbjct	1213	ATTTCAAGGCCCAGAAAGAGGCAGCCTGGGCGGTGACAAACACCACGACGTCTGGAACTC	1272
Query	1219	CCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTTATCGATTTGC	1278
Sbjct	1273	ccgaacagatcgtagatctaattgaaaagtacaaaatattgaagccgtttatcgatctgc	1332
Query	1279	TGGACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGTTTG	1338
Sbjct	1333	tegatecaaaegatecegeatactateaaegtegtegtegeaegeetateeaatectatee	1392
Query	1339	CCCTGGCGGAGAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGCG	1398
Sbjct	1393	ccctgccgagaaaacttgctgccaccgagaacttatgcttaatgctcgagagaga	1452
Query	1399	GTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCCT	1458
Sbjct	1453	ĠŦĊŦĀĠĀŦĀĀĠĊŦĠĠĀĀĀĊŦĊŦĠĊĀĠĊĀĠĊĀĊĠĀĠĀĀĊĠĀĀĠĀĠĠŦĀŦĀĊĀĀĠĀĀĠĠĊĊŦ	1512
Query	1459	ACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAGAGCTCGCAC	1518
Sbjct	1513	AcGCCATCATCGACACTTACTTCAGCAACGCCGACGACGAGGCCGAGCAAGAACTCGCTC	1572
Query	1519	CTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAGGTG	1578
Sbjct	1573	ctcaggaggtraacggagcgctcgagttcaatgccactcagcccaaggctccgagggtg	1632
Query	1579	GCTACACGTTCTA-A-TCGCCCACCCCACACATTCCAAACGCCGCTCACACGCCTTA	1633
Sbjct	1633	ĠĊŦĂĊĂĊĠŦŦĊŦĀĠĀĊŦĀĀŦĊĠĊĊĊĀ——ĊĊĀĊĀŦĀŦŦĊĊĀŦĀĊĠĊĊĠĊŦĊĀĊĀĊĠĊĊŦŦĀ	1690
Query	1634	CAAAC 1638	
Sbjct	1691	CAAAC 1695	

Drosophila melanogaster LP03126 full length cDNA

Sequence ID: **gb|AY061543.1**| Length: 1284 Number of Matches: 1 Range 1: 1 to 1176

Score		Expect	Identities	Gaps	Strand	Frame	
2167 bits	s(1173)	0.0()	1175/1176(99%)	0/1176(0%)	Plus/Plus		
Features	s:						
Query	955	CTGGCACAGATC	AACAGACTGACGTTGT	AATTGCATCTGGAGG	GTTTACCAAGGC	TGGGAC	1014
Sbjct	1	ctggcacagatc	AACAGACTGACGTTGT	AATTGCATCTGGAGG	STTTACCAAGGC	TGGGAC	60
Query	1015	TCCTTCTACAGC	ACAACAAAAGCAACAT	TGTGAAGGAGGCTGC	CTGGACGGTCA	GCAACA	1074
Sbjct	61	teettetaeage	Acaacaaaagcaacat	tgtgaaggaggctgd	ctggacggtca	GCAACA	120
Query	1075	TCACAGCAGGTA	ACCAGAAGCAGATCCA	GGCTGTGATTCAGGC	CGGCATCTTCC	AGCAGC	1134
Sbjct	121	tcacagcaggta	Accadaadcadatcca	ggctgtgattcaggc	ccgcatcttcc	AGCAGC	180
Query	1135	TGCGCACCGTGC	TGGAGAAGGGTGATTT	CAAGGCTCAAAAAGA	GGCTGCCTGGG	CGGTGA	1194
Sbjct	181	tececyccetec	tggagaagggtgatt	caaggctcaaaaaga	ʹͼͼϲͱͼϲϲͱͼͼͼ	ÇĞĞTĞA	240
Query	1195	CAAACACCACGA	CATCTGGCACTCCCGA	ACAGATCGTCGATCT	AATTGAGAAGT	ACAAAA 	1254
Sbjct	241	caaacaccacga	ĊAŦĊŦĠĠĊAĊŦĊĊĊĠA	Acagatcgtcgatct	rAATTGAGAAGT	yçyyyy	300
Query	1255	TATTGAAGCCTT	TTATCGATTTGCTGGA	CACAAAGGATCCGCG	TACCATCAAGG	TGGTGC	1314
Sbjct	301	tattgaagcctt	††A†¢ĠA†††Ġ¢†ĠĠA	ĊĀĊĀĀĀĠĠĀŦĊĊĠĊĠ	staccatcaagg	tĠĠtĠĊ	360
Query	1315	AGACGGGCCTAT	CCAATCTGTTTGCCCT	GGCGGAGAAACTTGG	TGGCACCGAGA	ACCTAT	1374
Sbjct	361	AGACGGGCCTAT	ccaatctgtttgccct	ĠĠĊĠĠĀĠĀĀĀĊŦŦĠĊ	stggcaccgaga	ACCTAT	420
Query	1375	GCTTGATGGTCG	AGGAGATGGGCGGTCT	AGACAAGCTGGAAAC	TCTGCAGCAGC	ACGAGA 	1434
Sbjct	421	ĠĊŦŦĠĂŦĠĠŦĊĠ	AĠĠĀĠĀŦĠĠĠĊĠĠŦĊŦ	AĠĀĊĀĀĠĊŦĠĠĀĀĀĊ	ctctgcagcagc	AĊĠĀĠĀ	480
Query	1435	ACGAGGAGGTCT	ACAAGAAGGCCTACGC	CATCATTGACACATA	CTTCAGCAACG	GCGACG	1494
Sbjct	481	AĊĠĀĠĠĀĠĠ ŦĊŦ	<u> AĊAAĠAAĠĠĊĊ</u> ŦAĊĠĊ	ĊĀŢĊĀŢŢĠĀĊĀĊĀŢĀ	\ctrcagcaacd	ĠĊĠÀĊĠ	540

Query	1495	ACGAGGCCGAGCAAGAGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCA	1554
Sbjct	541	ACGAGGCCGAGCAAGAGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCA	600
Query	1555	CCCAGCCCAAGGCTCCCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAA	1614
Sbjct	601	cccadcccaaddctcccaaddtacctacacdttctaatcdcccacacaca	660
Query	1615	ACGCCGCTCACACGCCTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCAT	1674
Sbjct	661	Actcccctcacacccttacaaacaactacaccttccacccccc	720
Query	1675	TGTCAAACATACGCATACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGT	1734
Sbjct	721	†G†CÁÁÁCÁTÁCGCÁTÁCTCÁTCÁTCÁCÁTCTTÁCÁÁÁCÁTTCCCÁÁÁCÁCTTTGGÁGGT	780
Query	1735	ATGCATGGAAACACAGGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAA	1794
Sbjct	781	ATGCATGGAAACACAGGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAA	840
Query	1795	ATCCACTCGCATGAATCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCA	1854
Sbjct	841	ATCCACTCGCATGAATCCCCATTTAACATACCGTATTCCTCGCGTTAGACTAGACTTCA	900
Query	1855	CAGATTGCAGCATGGATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCA	1914
Sbjct	901	ĊĀĠĀŢŢĠĊĀĠĊĀŢĠĠĀŢĊŢŢŢĊŢĠĠĊĀĠŢĠŢŢĊĊŢĊĠŢŢĊĀĊĠĀŢĠĊĀĀĊĊĠĊŢĊĠĠĠĊĀ	960
Query	1915	GCTGCGCTGGCTGGGATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCA	1974
Sbjct	961	ĠĊŦĠĊĠĊŦĠĠĊŦĠĠĠĂŦĊĊĠŦĠĠĂŦĊĂŦĂĠŦĂŦŦŦĊĊĀĠĀĀŦĊĊĠŦĊŦĠŦĀĊĀĠĠĠĠĠĊĀ	1020
Query	1975	CCTTATGTTTGCGTGTACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATA	2034
Sbjct	1021	ĊĊŢŢĸŢĠŢŢŢĠĊĠŢĠŢĸĊŢĸĠĠĊŢŢŢŢŢĸŢŢĠĠĸŢĸĊĠŢŢŢĊĠĸĠĊŢĊĸŢŢŢĊĠĠĸŢĸŢĸ	1080
Query	2035	TTTTAGGCTGTTTAGTATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTCG	2094
Sbjct	1081	†††††åĠĠĊ†Ġ†††åĠţĂţ††å†å†å†å†åĊÅĠĠĂĂĂĊĠĊ†††åA†ĊĊ†ĊĊĂĊĊ††ĊĠ	1140
Query	2095	CGCAAGCATTacaacaacaacaacaacaacaac 2130	
Sbjct	1141	ĊĠĊĀĀĠĊĀŦŦĀĊĀĀĊĀĀĊĀĀĊĀĀĊĀĀĊĀĀĊĀĀĊ 1176	

Drosophila melanogaster chromosome 2L

Sequence ID: **gb|AE014134.6|** Length: 23513712 Number of Matches: 4 Range 1: 10058845 to 10060005

Score		Expect	Identities	Gaps	Strand	Frame
2139 bits	s(1158)	0.0()	1160/1161(99%)	0/1161(0%)	Plus/Plus	
Features pendulir						
Query	970	AGACTGAC	GTTGTAATTGCATCTG	GAGGTTTACCAAGGC	TGGGACTCCTT	CTACAGCACA
Sbjct	10058845	AGACTGAC	GTTGTAATTGCATCTG	GAGGTTTACCAAGGC	rtgggactcctt	CTACAGCACA
Query	1030	ACAAAAGC	AACATTGTGAAGGAGG	GCTGCCTGGACGGTCA	GCAACATCACA	GCAGGTAACC
Sbjct	10058905	ACAAAAGC	AACATTGTGAAGGAGG	ctgcctggacggtca	.GCAACATCACA	.GCAGGTAACC
Query	1090	AGAAGCAG	ATCCAGGCTGTGATTC	CAGGCCGGCATCTTCC	AGCAGCTGCGC	ACCGTGCTGG
Sbjct	10058965	AGAAGCAG	ATCCAGGCTGTGATTC	AGGCCGGCATCTTCC	AGCAGCTGCGC	ACCGTGCTGG
Query	1150	AGAAGGGT	GATTTCAAGGCTCAAA	AAGAGGCTGCCTGGG	CGGTGACAAAC	ACCACGACAT
Sbjct	10059025	AGAAGGGT	GATTTCAAGGCTCAAA	AAGAGGCTGCCTGGG	CGGTGACAAAC	ACCACGACAT
Query	1210	CTGGCACT	CCCGAACAGATCGTCG	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	'ACAAAATATTG	AAGCCTTTTA
Sbjct	10059085	CTGGCACT	CCCGAACAGATCGTCG	SATCTAATTGAGAAGT	ACAAAATATTG	BAAGCCTTTTA
Query	1270	TCGATTTG	CTGGACACAAAGGATC	CGCGTACCATCAAGG	TGGTGCAGACG	GGCCTATCCA
Sbjct	10059145	TCGATTTG	CTGGACACAAAGGATC	CGCGTACCATCAAGG	TGGTGCAGACG	GGCCTATCCA
Query	1330	ATCTGTTT	GCCCTGGCGGAGAAAC	CTTGGTGGCACCGAGA	ACCTATGCTTG	ATGGTCGAGG
Sbjct	10059205	ATCTGTTT	GCCCTGGCGGAGAAAC	TTGGTGGCACCGAGA	ACCTATGCTTG	ATGGTCGAGG
Query	1390	AGATGGGC	GGTCTAGACAAGCTGG	SAAACTCTGCAGCAGC	:ACGAGAACGAG	GAGGTCTACA
Sbjct	10059265	AGATGGGC	GGTCTAGACAAGCTGG	SAAACTCTGCAGCAGC	ACGAGAACGAG	GAGGTCTACA
Query	1450	AGAAGGCC	TACGCCATCATTGACA	CATACTTCAGCAACG	GCGACGACGAG	GCCGAGCAAG
Sbjct	10059325	AGAAGGCC	TACGCCATCATTGACA	ACATACTTCAGCAACG	GCGACGACGAG	GCCGAGCAAG

Query	1510	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	1569
Sbjct	10059385	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	10059444
Query	1570	CCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAAACGCCGCTCACACGC	1629
Sbjct	10059445	ccdaaggtggctacacgttctaatcgcccaccccacacattccaaactccgctcacacgc	10059504
Query	1630	CTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCATTGTCAAACATACGCA	1689
Sbjct	10059505	cttacaaacaactacaccttcgaccgcgctcacacactatgccattgtcaaacatacgca	10059564
Query	1690	TACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACACA	1749
Sbjct	10059565	TACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACACA	10059624
Query	1750	GGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAAATCCACTCGCATGAA	1809
Sbjct	10059625	GGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAAATCCACTCGCATGAA	10059684
Query	1810	TCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCACAGATTGCAGCATGG	1869
Sbjct	10059685	tccccatttaacatacccctattcctccccttacactacacttcacacacttccc	10059744
Query	1870	ATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCAGCTGCGCTGGCTG	1929
Sbjct	10059745	Atctttctgccagtgttcctcgttcacgatgcaaccgctcggcagctagct	10059804
Query	1930	ATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCGTG	1989
Sbjct	10059805	Atccctcctcatactattccacaatccctctctctacacccctctctctacccccc	10059864
Query	1990	TACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTTAG	2049
Sbjct	10059865	tactaggctttttattggatacgtttcgagctcatttcggatatatat	10059924
Query	2050	TATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTCGCGCAAGCATTacaac	2109
Sbjct	10059925	tatttatttatgtatacaggaaacgcttttaatcctccaccttccccccaagcattacaac	10059984
Query	2110	aacaacaacaacaacaac 2130	
Sbjct	10059985	AACAACAACAACAAC 10060005	

Range 2: 10058195 to 10058769

Score		Expect	Identities	Gaps	Strand	Frame	
1024 bit	ts(554)	0.0()	568/575(99%)	0/575(0%)	Plus/Plus		
Feature penduli							
Query	397	ACAACTCA	ATGCTGCAGTTTGAGG	GCCGCTTGGGCGCT	TACCAACATCGC	CTCTGGCACAT	456
Sbjct	10058195	Acactca	Atectecaettceaed	sccectteeecet	tyccyycytcgc	cttctggcacat	10058254
Query	457	CCGACCAA	ACGCGCTGCGTTATCG	GAACACAATGCTGT(GCCGCATTTCGT	GGCTCTGCTCC	516
Sbjct	10058255	CCGACCAA	accccctcccttatcc	saacacaatgctgto	gccccatttcct	reecte	10058314
Query	517	AGTCCAAG	TCCATGAACCTGGCCG	GAGCAGGCAGTCTG(GGCTCTGGGCAA	CATTGCCGGCG	576
Sbjct	10058315	AGTCCAAG	tccatgaacctgccc	sygcygcygtctgo	gecteteeery	rcyttecceece	10058374
Query	577	ACGGAGCC	GCCGCCGCGACATTC	TCATCCACCACAA(CGTAATTGACGG	AATCTTGCCAC	636
Sbjct	10058375	Acgdadcc	ccccccccccccccccccccccccccccccccccccc	stcatccaccacaa	cgtaattgacg	saatetteeeae	10058434
Query	637	TGATCAAC	AATGAGACACCGCTC7	CTTTTTTGCGCAA(CATCGTCTGGCT	GATGTCCAACC	696
Sbjct	10058435	TGATCAAC	aatgagacacccctt	rcttttctgcgcaac	catestets	rgatgtccaacc	10058494
Query	697	TGTGCAGG	AATAAGAATCCATCTC	CGCCATTCGATCA(GGTGAAGCGGCT 	GTTGCCCGTCC	756
Sbjct	10058495	tgtgccgg	AACAAGAATCCATCGC	ccccattccatcac	ĠĠŦĠĂĂĠĊĠĠĊŦ	rettecccetcc	10058554
Query	757	TGTCGCAG	CTTCTGCTTAGTCAGO	GACATCCAAGTGCT(GGCCGACGCCTG	CTGGGCTTTGT	816
Sbjct	10058555	tĠtċĠċAĠ	ĊŦŦĊŦĠĊŦŦĂĠŦĊĀĠĊ	SACATCCAAGTGCTG	ĠĠĊĊĠĂĊĠĊĊŦĠ	cteccette	10058614
Query	817	CCTACGTC	ACGGACGACGATAATA	ACCAAGATCCAGGC	TGTGGTCGACTC 	GGACGCAGTGC	876
Sbjct	10058615	cctacctc	acggacgacgataac <i>i</i>	ACCAAGATCCAGGC:	tĠtĠĠtĊĠĂĊtĊ	ddacdcadddc	10058674
Query	877	CGCGCCTG	GTCAAACTGCTGCAAA	ATGGACGAGCCGAG(CATTATTGTGCC	CGCCCTGCGCA	936
Sbjct	10058675	ҁҿҁҿҁҁҭҿ	gtcaaactgctgcaa <i>t</i>	vtęęyceyęceyę vtęęycey	cattattetec	cecctece	10058734
Query	937	GCGTTGGC	AACATTGTGACTGGC	ACAGATCAACAG	971		
Sbjct	10058735	gcgttgc	AACATTGTGACTGGC/	acagatcaacag	10058769		

Range 3: 10057819 to 10058134

Score		Expect	Identities		Gaps	Strand	Frame	
573 bits	(310)	5e-159()	314/316(9	9%)	0/316(0%)	Plus/Plus		
Feature penduli	s: n							
Query	85	AGGACTC	ACGCATGCGC	CGCCATGA	GGTGACCATC	GAGCTGCGCAAGT	CCAAAAAGGAGG	144
Sbjct	10057819	AGGACTC	ACGCATGCGC	CGCCATGA	.GGTGACCATC	GAGCTGCGCAAGT(CCAAAAAGGAGG	100578
Query	145	ACCAGATO	GTTCAAGCGG	CGCAACAT	CAACGACGAG	GATCTAACGTCGC	CGCTCAAAGAGC	204
Sbjct	10057879	Accadato	GTTCAAGCGG	cccaacat	CAACGACGAGG	gatetaaegtege	cdctcaaadadc	100579
Query	205	TCAATGG(CCAGTCGCCG	GTGCAGCT	GTCCGTGGAC	GAGATAGTGGCGG	CCATGAACAGCG	264
Sbjct	10057939	tcaatgg	ccagtcgccg	ĠŦĠĊĀĠĊŦ	ĠŦĊĊĠŦĠĠĀĊ	gagatagtgggg	ccatgaacagcg	100579
Query	265	AGGATCA(GAGCGCCAG	TTCCTGGG	CATGCAGTCTC	GCCGCAAGATGC'	CAGTCGGGAAC	324
Sbjct	10057999	AĠĠĀŦĊĀŒ	GAGCGCCAG	ҭҭҵҭҁ҅ҭ҅ҁҁҁ	catecaetct	scccdcaadatdc:	rcagtcgggagc	100580
Query	325	GCAATCC	ACCCATCGAC	CTGATGAT	CGGCCATGGT	ATTGTGCCCATTT(GCATACGCTTCC	384
Sbjct	10058059	ĠĊĀĀŦĊĊ <i>ī</i>	Acccatcgac	ĊϮĠĂϮĠĂϮ	ĊĠĠĊĊĂŦĠĠŦź	Artgrgcccartr	ĠĊĀŦĀĊĠĊŦŦĊĊ	100583
Query	385	TGCAGAA	TACCAACAA	400				
Sbjct	10058119	†ĠĊĀĠĀĀ:	raccaacaa	1005813	4			

Range 4: 10057682 to 10057760

Score		Expect	Identities	Gaps	Strand	Frame	
147 bits	s(79)	1e-30()	79/79(100%)	0/79(0%)	Plus/Plus		
Feature penduli							
Query	9	aaaaaaa	aaaaaaaaa TGA G	TAAGGCGGATTCTAAC	TCACGACAGGG	CTCCTACAAGGCC	68
Sbjct	10057682	AAAAAA	AAAAAAAAAATGAG	TAAGGCGGATTCTAAC	TCACGACAGGG	CTCCTACAAGGCC	10057741
Query	69	AACAGC <i>I</i>	ATTAACACGCAGG	87			
Sbjct	10057742	AACAGC <i>I</i>	ATTAACACGCAGG	10057760			

Drosophila melanogaster clone BACR06G16, complete sequence Sequence ID: **gb|AC009744.8|** Length: 179038 Number of Matches: 4

Range 1: 167754 to 168914

Score		Expect	Identities	Gaps	Strand	Frame	_
2139 bit	ts(1158)	0.0()	1160/1161(99%)	0/1161(0%)	Plus/Plus		_
Feature	s:						
Query	970	AGACTGACGT	TGTAATTGCATCTGGA	GGTTTACCAAGGCTG	GGACTCCTTCT	TACAGCACA	1029
Sbjct	167754	AGACTGACGT	rtgtaattgcatctgga	ggtttaccaaggctd	GGACTCCTTC	racagcaca	167813
Query	1030	ACAAAAGCAA	CATTGTGAAGGAGGCT	GCCTGGACGGTCAGC	CAACATCACAGO	CAGGTAACC	1089
Sbjct	167814	ACAAAAGCAA	CATTGTGAAGGAGGCT	GCCTGGACGGTCAG	CAACATCACAGO	CAGGTAACC	167873
Query	1090	AGAAGCAGAT	CCAGGCTGTGATTCAG	GCCGGCATCTTCCAG	GCAGCTGCGCAC	CCGTGCTGG	1149
Sbjct	167874	AGAAGCAGAT	ccaggctgtgattcag	gccgcatcttccad	scadctdcdcad	ccgtgctgg	167933
Query	1150	AGAAGGGTGA	TTTCAAGGCTCAAAAA	GAGGCTGCCTGGGC	GTGACAAACAC	CCACGACAT	1209
Sbjct	167934	AGAAGGGTGA	tttcaaggctcaaaaa	gyggctgcctgggcg	GTGACAAACA	CCACGACAT	167993
Query	1210	CTGGCACTCC	CGAACAGATCGTCGAT	CTAATTGAGAAGTAC	CAAAATATTGA <i>I</i>	AGCCTTTTA	1269
Sbjct	167994	CTGGCACTCC	cdaacadatcdtcdat	ctaattgagaagtad	CAAAATATTGAZ	AGCCTTTTA	168053
Query	1270	TCGATTTGCT	GGACACAAAGGATCCG	CGTACCATCAAGGTO	GTGCAGACGG	GCCTATCCA	1329
Sbjct	168054	tcgatttgct	dgacacaaaaggatccg	cgtaccatcaaggtd	GTGCAGACGG	Scctatcca	168113
Query	1330	ATCTGTTTGC	CCTGGCGGAGAACTT(GGTGGCACCGAGAAC	CCTATGCTTGAT	TGGTCGAGG	1389

Sbjct	168114	ATCTGTTTGCCCTGGCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGG	168173
Query	1390	AGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACA	1449
Sbjct	168174	AGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACA	168233
Query	1450	AGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAG	1509
Sbjct	168234	AGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAG	168293
Query	1510	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	1569
Sbjct	168294	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	168353
Query	1570	CCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAAACGCCGCTCACACGC	1629
Sbjct	168354	ccdaaggtggctacacgttctaatcgcccaccccacacattccaaactccgctcacacgc	168413
Query	1630	CTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCATTGTCAAACATACGCA	1689
Sbjct	168414	cttacaaacaactacaccttcgaccgcgctcacacactatgccattgtcaaacatacgca	168473
Query	1690	TACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACACA	1749
Sbjct	168474	tactcatcatcatcttacaaacattcccaaacatttggaggtatgcatggaaacaca	168533
Query	1750	GGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAAATCCACTCGCATGAA	1809
Sbjct	168534	ĠĠĊĠĂĂŦĠĊĂŦŦĂĠĊŦŦĂĂĂĠŦĊĂŦĂĂŦŦĠĂĂŦĊĠĠĠŦŦĠĠĊĂĂĂĂŦĊĊĂĊŦĊĠĊĀŦĠĀĀ	168593
Query	1810	TCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCACAGATTGCAGCATGG	1869
Sbjct	168594	tcccatttaacatacccgtattcctcgcgttagactagacttcacagattgcagcatgg	168653
Query	1870	ATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCAGCTGCGCTGGCTG	1929
Sbjct	168654	Atctttctgccagtgttcctcgttcacgatgcaaccgctcggcagctagct	168713
Query	1930	ATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCGTG	1989
Sbjct	168714	Atccctcctcctcctcctccccccccccccccccccccc	168773
Query	1990	TACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTTAG	2049
Sbjct	168774	TACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTTAG	168833
Query	2050	TATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTCGCGCAAGCATTacaac	2109
Sbjct	168834	tatttatttatgtatacaggaaacgcttttaatcctccaccttcccccccaccattaccacc	168893
Query	2110	aacaacaacaacaac 2130	
Sbjct	168894	AACAACAACAACAACAAC 168914	

Range 2: 167104 to 167678

Score		Expect	Identities	Gaps	Strand	Frame	
1024 bit	s(554)	0.0()	568/575(99%)	0/575(0%)	Plus/Plus		
Features	s:						
Query	397	ACAACTCAAT	GCTGCAGTTTGAGGC	CGCTTGGGCGCTTAG	CCAACATCGCC'	PCTGGCACAT	456
Sbjct	167104	ACAGCTCAAT	GCTGCAGTTCGAGGC	cectteeecetta	CCAACATCGCC'	rctggcacat	16716
Query	457	CCGACCAAAC	GCGCTGCGTTATCGA	ACACAATGCTGTGC	CGCATTTCGTG	GCTCTGCTCC	516
Sbjct	167164	ccdaccaaac	gcgctgcgttatcga	acacaatgctgtgc	ccatttcctc	Schchechcc	1672
Query	517	AGTCCAAGTC	CATGAACCTGGCCGA	GCAGGCAGTCTGGG	CTCTGGGCAAC	ATTGCCGGCG	576
Sbjct	167224	AGTCCAAGTC	catgaacctggccga	gcyggcyggcyggc	ctctgggcaac,	ATTGCCGGCG	16728
Query	577	ACGGAGCCGC	CGCCGCGACATTGT	CATCCACCACAACG	FAATTGACGGAZ	ATCTTGCCAC	636
Sbjct	167284	acggagccgc	ċĠċċċĠċĠAċAተተĠϮ	catccaccacaacg;	taattgacgga	Atcttgccac	1673
Query	637	TGATCAACAA	TGAGACACCGCTCTC	TTTTTTGCGCAACA'	TCGTCTGGCTG	ATGTCCAACC	696
Sbjct	167344	†ga†caacaa	tgagacacccctctc	ttttctgcgcaaca:	tcgtctggctg	Atgtccaacc	1674
Query	697	TGTGCAGGAA	TAAGAATCCATCTCC	GCCATTCGATCAGG'	TGAAGCGGCTG'	TTGCCCGTCC	756
Sbjct	167404	†Ġ†ĠĊCĠĠAA	.caagaatccatcgcc	ĠĊĊĀŢŢĊĠĀŢĊĀĠĠſ	rgaagcggctg:	rtgccccttcc	1674
Query	757	TGTCGCAGCT	TCTGCTTAGTCAGGA	CATCCAAGTGCTGG(CCGACGCCTGC'	rgggctttgt 	816
Sbjct	167464	tgtcgcagct	rctgcttagtcagga	catccaagtgctgc	ccepccic contraction contracti	rĠĠĠĊϮϮϮĠϮ	1675
Query	817	CCTACGTCAC	GGACGACGATAATAC	CAAGATCCAGGCTG'	TGGTCGACTCG(GACGCAGTGC	876
Sbjct	167524	cctacctcac	ggacgacgataacac	caagatccaggctg:	tĠĠtĊĠĂĊtĊĠ	gacecaetec gacecaetec	1675

Query	877	CGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGA		936
_	167584	CGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGA		167643
Query	937	GCGTTGGCAACATTGTGACTGGCACAGATCAACAG		
Shict	167644	GCGTTGGCAACATTGTGACTGGCACAGATCAACAG	167678	

Range 3: 166728 to 167043

Score		Expect	Identities	Gaps	Strand	Frame	
573 bits((310)	5e-159()	314/316(99%)	0/316(0%)	Plus/Plus		_
Features	s:						
Query	85	AGGACTCAC	GCATGCGCCGCCAT	GAGGTGACCATCGAGC	CTGCGCAAGTCC <i>A</i>	AAAAGGAGG	144
Sbjct	166728	AGGACTCAC	GCATGCGCCGCCAT	GAGGTGACCATCGAGC	CTGCGCAAGTCCA	AAAAGGAGG	166787
Query	145	ACCAGATGT	rcaagcggcgcaac	ATCAACGACGAGGATC	TAACGTCGCCGC	TCAAAGAGC	204
Sbjct	166788	ACCAGATGT:	rcaadcddcdcaac	Atcaacdacdaddatc	ctaacgtcgccgc	tcaaagagc	166847
Query	205	TCAATGGCC	AGTCGCCGGTGCAG	CTGTCCGTGGACGAGA	ATAGTGGCGGCCA	TGAACAGCG	264
Sbjct	166848	†caatggcc2	agtcgccggtgcag	ctetcceteeace	vtygtggcggccy	tgaacagcg	166907
Query	265	AGGATCAGG	AGCGCCAGTTCCTG	GGCATGCAGTCTGCCC	GCAAGATGCTCA	GTCGGGAAC	324
Sbjct	166908	AGGATCAGG	AGCGCCAGTTTCTG	ggcatgcagtctgccc	cgcaagatgctca	GTCGGGAGC	166967
Query	325	GCAATCCAC	CCATCGACCTGATG	ATCGGCCATGGTATTC	TGCCCATTTGCA	TACGCTTCC	384
Sbjct	166968	GCAATCCAC	ccatcgacctgatg	Atceeccateetate	stdddattddd	tacccttcc	167027
Query	385	TGCAGAATA	CCAACAA 400				
Sbjct	167028	tdcadaata	ccaacaa 16704	3			

Range 4: 166591 to 166669

Score		Expect	Identities	Gaps	Strand	Frame	
147 bits	s(79)	1e-30()	79/79(100%) 0/79(0%	(b) Plus/Plus		_
Feature	s:						
Query	9	aaaaaaaa	aaaaaaa TGAG	TAAGGCGGATTCT <i>F</i>	AACTCACGACAGGGC	TCCTACAAGGCC	68
Sbjct	166591	AAAAAAAA	AAAAAAAATGAG	taaddcddattcta	AACTCACGACAGGGC	tcctacaaggcc	166650
Query	69	AACAGCATT	TAACACGCAGG	87			
Sbjct	166651	AACAGCAT	raacacgcagg	166669			

Drosophila melanogaster DNA sequence (P1s DS00058 (D296), DS02068 (D297), and DS07249 (D318)), complete sequence Sequence ID: **gb|AC005734.1|AC005734** Length: 155335 Number of Matches: 4 Range 1: 23418 to 24578

Score		Expect	Identities	Gaps	Strand	Frame	
2139 bit	ts(1158)	0.0()	1160/1161(99%)	0/1161(0%)	Plus/Plus		
Feature	s:						
Query	970	AGACTGACGT	rgtaattgcatctggag	GTTTACCAAGGCTGO	GGACTCCTTCT <i>P</i>	ACAGCACA	1029
Sbjct	23418	AGACTGACGT	rgtaattgcatctggag	GTTTACCAAGGCTG	GACTCCTTCT <i>I</i>	ACAGCACA	23477
Query	1030	ACAAAAGCAAG	CATTGTGAAGGAGGCTG	CCTGGACGGTCAGC	AACATCACAGC <i>I</i>	AGGTAACC	1089
Sbjct	23478	ACAAAAGCAA	CATTGTGAAGGAGGCTG	CCTGGACGGTCAGC	AACATCACAGC <i>I</i>	AGGTAACC	23537
Query	1090	AGAAGCAGATO	CCAGGCTGTGATTCAGG	CCGGCATCTTCCAGO	CAGCTGCGCACC	CGTGCTGG	1149
Sbjct	23538	AGAAGCAGATO	ccaddctdtdattcadd	cceecatcttcceec	CAGCTGCGCAC	cgtgctgg	23597
Query	1150	AGAAGGGTGAT	TTTCAAGGCTCAAAAAG	AGGCTGCCTGGGCG(GTGACAAACAC 	CACGACAT	1209
Sbjct	23598	AGAAGGGTGAT	rttcaaggctcaaaaag	add a dae a da	GTGACAAACAC	cacdacat	23657
Query	1210	CTGGCACTCCC	CGAACAGATCGTCGATC	TAATTGAGAAGTAC <i>I</i>	AAAATATTGAA(CCTTTTA	1269

Sbjct	23658	CTGGCACTCCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTA	23717
Query	1270	TCGATTTGCTGGACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCA	1329
Sbjct	23718	tcgatttgctggacacaaaggatccgcgtaccatcaaggtggtgcagacgggcctatcca	23777
Query	1330	ATCTGTTTGCCCTGGCGGAGAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGG	1389
Sbjct	23778	ATCTGTTTGCCCTGGCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGG	23837
Query	1390	AGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACA	1449
Sbjct	23838	AGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACA	23897
Query	1450	AGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAG	1509
Sbjct	23898	AGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAG	23957
Query	1510	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	1569
Sbjct	23958	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	24017
Query	1570	CCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAAACGCCGCTCACACGC	1629
Sbjct	24018	ccdaadgtgctacacgttctaatcgccacccacacattcaaactccacacaca	24077
Query	1630	CTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCATTGTCAAACATACGCA	1689
Sbjct	24078	ĊŢŢŖĊĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸ	24137
Query	1690	TACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACACA	1749
Sbjct	24138	TACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGTATGCATGGAAACACA	24197
Query	1750	GGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAAAATCCACTCGCATGAA	1809
Sbjct	24198	ĠĠĊĠĂĂŢĠĊĂŢŢĂĠĊŢŢĂĂĂĠŢĊĂŢĂĂŢŢĠĂĂŢĊĠĠĠŢŢĠĠĊĂĂĂĂŢĊĊĂĊŢĊĠĊĀŢĠĀĀ	24257
Query	1810	TCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTCACAGATTGCAGCATGG	1869
Sbjct	24258	TĊĊĊĊĂŢŢŢĂĂĊĂŢĂĊĊĊĠŢĂŢŢĊĊŢĊĠĊĠŢŢĂĠĂĊŢĀĠĂĊŢŢĊĂĊĂĠĂŢŢĠĊĂĠĊĂŢĠĠ	24317
Query	1870	ATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGCAGCTGCGCTGGCTG	1929
Sbjct	24318	ÄŤĊŤŤŤĊŤĠĠĊĂĠŤĠŤŤĊĊŤĊĠŤŤĊĂĊĠĂŤĠĊĂĂĊĊĠĊŤĊĠĠĠĊĂĠĊŤĠĊĠĊŤĠĠĊŤĠ	24377
Query	1930	ATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCGTG	1989
Sbjct	24378	ATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGCACCTTATGTTTGCGTG	24437
Query	1990	TACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTTAG	2049
Sbjct	24438	TACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATATATTTTAGGCTGTTTAG	24497
Query	2050	TATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTCGCGCAAGCATTacaac	2109
Sbjct	24498	TĂTTTĂTTĂTĠTĂTĂĊĂĠĠĂĂĂĊĠĊŤŤŤŤĂĂŤĊĊŤĊĊĂĊĊŤŤĊĠĊĠĊĂĂĠĊĂŤŤĂĊĂĂĊ	24557
Query	2110	aacaacaacaacaacaac 2130	
Sbjct	24558	AACAACAACAACAAC 24578	

Range 2: 22768 to 23342

Score		Expect	Identities	Gaps	Strand	Frame	
1024 bit	s(554)	0.0()	568/575(99%)	0/575(0%)	Plus/Plus		
Features	s:						
Query	397	ACAACTCAATG	CTGCAGTTTGAGGCC	GCTTGGGCGCTTAC	CAACATCGCCTC	TGGCACAT	456
Sbjct	22768	ACAGCTCAATG	CTGCAGTTCGAGGCC	GCTTGGGCGCTTAC	CAACATCGCCTC	TGGCACAT	2282
Query	457	CCGACCAAACG	CGCTGCGTTATCGAA	CACAATGCTGTGCC	GCATTTCGTGGC	TCTGCTCC	516
Sbjct	22828	ccdaccaaacd	ccctcccttatccaa	.cacaatgctgtgcc	ĠĊĀŦŦŦĊĠŦĠĠĊ	tctcctcc	2288
Query	517	AGTCCAAGTCC	ATGAACCTGGCCGAG	CAGGCAGTCTGGGC	TCTGGGCAACAT	TGCCGGCG	576
Sbjct	22888	AdtccAAdtcc	atgaacctgcccac	ċdddddddddddddddddddddddddddddddddddddd	tctcccat	tgccgccg	2294
Query	577	ACGGAGCCGCC	GCCCGCGACATTGTC	ATCCACCACAACGT.	AATTGACGGAAT 	CTTGCCAC	636
Sbjct	22948	yçegyeççeçç	ĠĊĊĠĊĠĀĊĀŦŦĠŦĊ	Atccaccacaacgt.	AATTGACGGAAT	cttgccyc	2300
Query	637	TGATCAACAAT	GAGACACCGCTCTCT	TTTTTGCGCAACAT	CGTCTGGCTGAT	GTCCAACC	696
Sbjct	23008	tgatcaacaat	dadacaccdctctct	tttctgcgcaacat	cetcteecteat	gtccaacc	2306
Query	697	TGTGCAGGAAT	AAGAATCCATCTCCG	CCATTCGATCAGGT	GAAGCGGCTGTT 	GCCCGTCC	756
Sbjct	23068	tgtgccggaac	AAGAATCCATCGCCG	ccattcgatcaggt	GAAGCGGCTGTT	ccccctcc	2312

Query	757	TGTCGCAGCTTCTGCTTAGTCAGGACATCCAAGTGCTGGCCGACGCCTGCTGGGCTTTGT	816
Sbjct	23128	TGTCGCAGCTTCTGCTTAGTCAGGACATCCAAGTGCTGGCCGACGCCTGCTGGGCTTTGT	23187
Query	817	CCTACGTCACGGACGACGATAATACCAAGATCCAGGCTGTGGTCGACTCGGACGCAGTGC	876
Sbjct	23188	CCTACGTCACGGACGATAACACCAAGATCCAGGCTGTGGTCGACTCGGACGCAGTGC	23247
Query	877	CGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATTATTGTGCCCGCCC	936
Sbjct	23248	CGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATTATTGTGCCCGCCC	23307
Query	937	GCGTTGGCAACATTGTGACTGGCACAGATCAACAG 971	
Shict	23308	GCGTTGGCAACATTGTGACTGGCACAGATCAACAG 23342	

Range 3: 22392 to 22707

Score		Expect	Identities	Gaps	Strand	Frame	
573 bits	(310)	5e-159()	314/316(99%)	0/316(0%)	Plus/Plus		<u> </u>
Features	s:						
Query	85	AGGACTCACGO	CATGCGCCGCCATG	AGGTGACCATCGAGCT	GCGCAAGTCCAA	AAAGGAGG	144
Sbjct	22392	AGGACTCACGC	catececcectate	AGGTGACCATCGAGC1	rdddadddddad	AAAGGAGG	22451
Query	145	ACCAGATGTTO	CAAGCGGCGCAACA	rcaacgacgaggatci	TAACGTCGCCGCT	CAAAGAGC	204
Sbjct	22452	ACCAGATGTT	caagcggcgcaaca:	rcaacdacdaddatci	raacgtcgccgct	CAAAGAGC	22511
Query	205	TCAATGGCCAC	GTCGCCGGTGCAGC	rgtccgtggacgaga1	AGTGGCGGCCAT	GAACAGCG	264
Sbjct	22512	tcaatggccac	etcecceetecyec.	teteegteeaegaeat	ragtggcggccat	GAACAGCG	22571
Query	265	AGGATCAGGAC	GCGCCAGTTCCTGG(GCATGCAGTCTGCCC	CAAGATGCTCAG	TCGGGAAC	324
Sbjct	22572	aggatcaggad	gcgccygttrctgc	gcatecaetctecce	scaagatgctcag	tcgggagc	22631
Query	325	GCAATCCACCC	CATCGACCTGATGAT	rcggccatggtattg7	GCCCATTTGCAT	ACGCTTCC	384
Sbjct	22632	gcaatccacc	catcgacctgatgar	tcgccatgctattct	rdcccatttdcat	ACGCTTCC	22691
Query	385	TGCAGAATACO	CAACAA 400				
Sbjct	22692	tgcagaatacc	caacaa 22707				

Range 4: 22255 to 22333

Score		Expect	Identities		Gaps	Strand	Frame	
147 bits	(79)	1e-30()	79/79(100°	%)	0/79(0%)	Plus/Plus		
Feature	s:							
Query	9	aaaaaaaaa	aaaaaaa TGA G	TAAGGC(GATTCTAACTC	CACGACAGGGCTC	CTACAAGGCC	68
Sbjct	22255	AAAAAAAAA		TAAGGC	GATTCTAACTC	CACGACAGGGCTC	CTACAAGGCC	22314
Query	69	AACAGCATTA	AACACGCAGG	87				
Sbjct	22315	AACAGCATT	AACACGCAGG	22333				

D.melanogaster oho31 gene

Sequence ID: **emb|X85752.1|** Length: 3862 Number of Matches: 4 Range 1: 2085 to 3247

Score		Expect	Identities	Gaps	Strand	Frame	
1969 bit	ts(1066)	0.0()	1145/1177(97%)	30/1177(2%)	Plus/Plus		
Feature	s:						
Query	970	AGACTGACGTT(GTAATTGCATCTGGAGG	TTTACCAAGGCTGGG	SACTCCTTCTAC	AGCACA	1029
Sbjct	2085	AGACTGACGTT	TAATTGCATCTGGAGG	TTTACCAAGGCTGGG	ACTCCTTCTAC	AGCACA	2144
Query	1030	ACAAAAGCAACA	ATTGTGAAGGAGGCTGC	CTGGACGGTCAGCAA	CATCACAGCAG	GTAACC	1089
Sbjct	2145	ACAAAAGCAACA	Atteteaaeeaeetee	ctggacggtcagcaa	CATCACAGCAG	GTAACC	2204
Query	1090	AGAAGCAGATCO	CAGGCTGTGATTCAGGC	CGGCATCTTCCAGCA	GCTGCGCACCG	TGCTGG	1149

Sbjct	2205	AGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGG	2264
Query	1150	AGAAGGGTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACAT	1209
Sbjct	2265	AGAAGGGTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACAT	2324
Query	1210	CTGGCACTCCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTA	1269
Sbjct	2325	CTGGCACTCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTA	2384
Query	1270	TCGATTTGCTGGACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCA	1329
Sbjct	2385	tcgatttgctggacacaaaggatccgcgtaccattaaggtggtgcagacgggcctatcca	2444
Query	1330	ATCTGTTTGCCCTGGCGGAGAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGG	1389
Sbjct	2445	Atctgtttgccctggcgagaaacttggtgccaccgagaacctatgcttgatggtcgagg	2504
Query	1390	AGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACA	1449
Sbjct	2505	AGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACA	2564
Query	1450	AGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAG	1509
Sbjct	2565	AGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAG	2624
Query	1510	AGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTC	1569
Sbjct	2625	AĠĊŦĊĠĊAĊĊŦĊĀĠĠĀĠĠŦĊĀĀĊĠĠĀĠĊĊĊŦĊĠĀĠŦŦĊĀĀŦĠĊĊĀĊĊĊĀĠĊĊĊĀĀĠĠĊŦĊ	2684
Query	1570	CCGAAGGTGGCTACACGTTCTAATCGCCCACCCCACACATTCCAAACGCCGCTCACACGC	1629
Sbjct	2685	ĊĊĠAĠĠĠŦĠĠĊŦĂĊĂĊĠŦŦĊŦĂĂŦĊĠĊĊĊĂĊĊĊĊĂĊĂĊĂŦŦĊĊĂĂĂĊĠĊĊĠĊŦĊĂĊĂĊĠĊ	2744
Query	1630	CTTACAAACAACTACACCTTCGACCGCGCTCACACACTATGCCATTGTCAAACATACGCA	1689
Sbjct	2745	ĊŢŢŖĊĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸĸ	2804
Query	1690	TACTCATCATCACATCTTACAAACATTCCCAAACACTTTGGAGGT	1734
Sbjct	2805	TACTCATCATCACATCTTACAAACATTCGCGTTAGACTAGACCCCAAAACACTTTGGAGGT	2864
Query	1735	ATGCATGGAAACAC-AGGCGAATGCATTAGCTTAAAGTCATAATTGAATCGGGTTGGCAA	1793
Sbjct	2865	ATĠĊĀŢĠĠĀĀĀĊĀĊĀĀĠĠĊĠĀĀŢĠĊĀŢŢĀĠĊŢŢĀĀĀĠŢĊĀŢĀĀŢŢĠĀĀŢĊĠĠĠŢŢĠĠĊĀĀ	2924
Query	1794	AATCCACTCGCATGAATCCCCATTTAACATACCCGTATTCCTCGCGTTAGACTAGACTTC	1853
Sbjct	2925	AATCCACTCGCATGAATCCCCATTTAACATACCCGTATTCCTTTCT	2970
Query	1854	ACAGATTGCAGCATGGATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGC	1913
Sbjct	2971	ACAGATTGCAGCATGGATCTTTCTGGCAGTGTTCCTCGTTCACGATGCAACCGCTCGGGC	3030
Query	1914	AGCTGCGCTGGCTGGATCCGTGGATCATAGTATTTCCAGAATCCGTCTGTACAGGGGGC	1973
Sbjct	3031	AĠĊŢĠĊĠĊŢĠĠĊŢĠĠĠĀŢĊĊĠŢĠĠĀŢĊĀŢĀĠŢĀŢŢŢĊĊĀĠĀĀŢĊĊĠŢĊŢĠŢĀĊĀĠĠĠĠĊ	3090
Query	1974	ACCTTATGTTTGCGTGTACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATAT	2033
Sbjct	3091	ACCTTATGTTTGCGTGTACTAGGCTTTTTATTGGATACGTTTCGAGCTCATTTCGGATAT	3150
Query	2034	ATTTTAGGCTGTTTAGTATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTC	2093
Sbjct	3151	ATTTTAGGCTGTTTAGTATTTATTTATGTATACAGGAAACGCTTTTAATCCTCCACCTTC	3210
Query	2094	GCGCAAGCATTacaacaacaacaacaacaacaac 2130	
Sbjct	3211	ĠĊĠĊŔŔĠĊŔŤŤŔĊŔŔĊŔŔĊŔŔĊŔŔĊŔŔĊŔŔĊŔŔĊ	

Range 2: 1444 to 2018

Score		Expect	Identities	Gaps	Strand	Frame	
1024 bits(554)		0.0()	568/575(99%)	0/575(0%)	Plus/Plus		
Feature	s:						
Query	397	ACAACTCAATGC	TGCAGTTTGAGGCCGC	CTTGGGCGCTTACC	AACATCGCCTCT	GGCACAT	456
Sbjct	1444	ACAGCTCAATGC	tgcagtttgaggccgd	cttgggcgcttacc	aacatcdcctct	GGCACAT	1503
Query	457	CCGACCAAACGC	GCTGCGTTATCGAAC <i>I</i>	ACAATGCTGTGCCG	CATTTCGTGGCT	CTGCTCC	516
Sbjct	1504	ccdaccaaacdc	GCTGCGTTATCGAACA	Acaatgctgtgccg	catttcctcct	ctdctcc	1563
Query	517	AGTCCAAGTCCA	TGAACCTGGCCGAGC <i>I</i>	AGGCAGTCTGGGCT	CTGGGCAACATT	GCCGGCG	576
Sbjct	1564	AGTCCAAGTCCA	tgyycctggccgygci	/ggcyg4c4gggc4	çtççççyyçytı	.qcqqqqq	1623
Query	577	ACGGAGCCGCCG	CCCGCGACATTGTCAT	CCACCACAACGTA	ATTGACGGAATC	TTGCCAC	636
Sbjct	1624	yçegyeççeçç	cccccacacattcat	tccyccycyycety	AttGACGGAAtC	ttgccyc	1683

Query	637	TGATCAACAATGAGACACCGCTCTCTTTTTTTGCGCAACATCGTCTGGCTGATGTCCAACC	696
Sbjct	1684	TGATCAACAATGAGACACCGCTCTCTTTTCTGCGCAACATCGTCTGGCTGATGTCCAACC	1743
Query	697	TGTGCAGGAATAAGAATCCATCTCCGCCATTCGATCAGGTGAAGCGGCTGTTGCCCGTCC	756
Sbjct	1744	TGTGCCGAAACAAGAATCCATCGCCGCCATTCGATCAGGTGAAGCGGCTGTTGCCCGTCC	1803
Query	757	TGTCGCAGCTTCTGCTTAGTCAGGACATCCAAGTGCTGGCCGACGCCTGCTGGGCTTTGT	816
Sbjct	1804	TGTCGCAGCTTCTGCTTAGTCAGGACATCCAAGTGCTGGCCGACGCCTGCTGGGCTTTGT	1863
Query	817	CCTACGTCACGGACGACGATAATACCAAGATCCAGGCTGTGGTCGACTCGGACGCAGTGC	876
Sbjct	1864	CCTACGTCACGGACGATAACACCAAGATCCAGGCTGTGGTCGACTCGGACGCAGTGC	1923
Query	877	CGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATTATTGTGCCCGCCC	936
Sbjct	1924	CGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATTATTGTGCCCGCCC	1983
Query	937	GCGTTGGCAACATTGTGACTGGCACAGATCAACAG 971	
Sbjct	1984	GCGTTGGCAACATTGTGACTGGCACAGATCAACAG 2018	

Range 3: 1069 to 1384

Score		Expect	Identities	Gaps	Strand	Frame	
584 bits(316)		2e-162()	316/316(100%)	0/316(0%)	Plus/Plus		
Features	S :						
Query	85	AGGACTCACGC	ATGCGCCGCCATGAG	GTGACCATCGAGCTGC	CGCAAGTCCAAA	AAGGAGG	144
Sbjct	1069	AGGACTCACGC	ATGCGCCGCCATGAG	GTGACCATCGAGCTGC	CGCAAGTCCAAA	AAGGAGG	1128
Query	145	ACCAGATGTTC	AAGCGGCGCAACATC	AACGACGAGGATCTAA	CGTCGCCGCTC	CAAAGAGC	204
Sbjct	1129	Accadatettc	aagcggcgcaacatc	AACGACGAGGATCTAA	rcetceccectc	AAAGAGC	1188
Query	205	TCAATGGCCAG'	rcgccggtgcagctg	TCCGTGGACGAGATAG	TGGCGGCCATG	SAACAGCG	264
Sbjct	1189	tcaatggccag;	rcecceetecy	tccctccaccacacacacacacacacacacacacacaca	rtggcggccatd	SAACAGCG	1248
Query	265	AGGATCAGGAG	CGCCAGTTCCTGGGC	ATGCAGTCTGCCCGC	AGATGCTCAGT	CGGGAAC	324
Sbjct	1249	AddAtcAddAdd	ceccycles	atgcagtctgccccc	Adatdctcadt	ccccccccccccccccccccccccccccccccccccccc	1308
Query	325	GCAATCCACCC	ATCGACCTGATGATC	GGCCATGGTATTGTGC	CCATTTGCATA	CGCTTCC	384
Sbjct	1309	gcyy4ccyc	AtcGAcctGAtGAtc	deckateetattee	ccatttgcata	rçêç44çç	1368
Query	385	TGCAGAATACC	AACAA 400 				
Sbjct	1369	tgcagaatacc	AACAA 1384				

Range 4: 933 to 1010

Score		Expect	Identitie	S	Gaps	Strand	Frame	
145 bits	(78)	5e-30()	78/78(10	00%)	0/78(0%)	Plus/Plus		
Features	S :							
Query	10	aaaaaaaaaa	aaaaTGAG	TAAGGCG	GATTCTAACTCAG	CGACAGGGCTCCT	ACAAGGCCA	69
Sbjct	933	AAAAAAAAAA	AAAATGAG	TAAGGCG	GATTCTAACTCA	CGACAGGGCTCCT	ACAAGGCCA	992
Query	70	ACAGCATTAAC	ACGCAGG	87				
Sbjct	993	ACAGCATTAAC	ACGCAGG	1010				

Drosophila ananassae alpha Karyopherin-2 (Dana\alphaKap2), mRNA Sequence ID: **ref|XM_001962998.2|** Length: 2631 Number of Matches: 1 Range 1: 281 to 1851

Score		Expect	Identities	Gaps	Strand	Frame	
1594 bit	s(863)	0.0()	1335/1571(85%)	0/1571(0%)	Plus/Plus		
Features	S :						
Query	21	aaaaTGAGTAA 	GGCGGATTCTAACTCAG	CGACAGGGCTCCTAC	AAGGCCAACAGC	ATTAAC	80

Sbjct	281	AAAATGAGTAAGGCGGATTCCAACTCCCGTCAGGGATCCTACAAATCCAACACCATCAAC	340
Query	81	ACGCAGGACTCACGCATGCGCCCCATGAGGTGACCATCGAGCTGCGCAAGTCCAAAAAG	140
Sbjct	341	Actcaggactcgcgcatgcgtcgccatgaggtgaccattgagctgcgcaagtcgaagaag	400
Query	141	GAGGACCAGATGTTCAAGCGCGCCAACATCAACGACGAGGATCTAACGTCGCCGCTCAAA	200
Sbjct	401	ĠĂĠĠĂŢĊĀĠĂŢĠŢŢĊĀĀĀĊĠĀĊĠĀĀĠĀŢĊĀĀĊĠĀĊĠĀĠĠĀŢĊŢŢĀĊĊŢĊĠĊĊĊŢĊĀĀĠ	460
Query	201	GAGCTCAATGGCCAGTCGCCGGTGCAGCTGTCCGTGGACGAGATAGTGGCGGCCATGAAC	260 520
Sbjct Query	461 261	GAGCTGAACGGGCAGTCCCCGGTGCAGCTATCGGTGGACGAGATCGTGGCGGCTATGAAC AGCGAGGATCAGGAGCGCCAGTTCCTGGGCATGCAGTCTGCCCGCAAGATGCTCAGTCGG	320
Sbjct	521	AGCGAGGACCAGGAGCGCCAGTTCCTGGGAATGCAGTCCGCCCGC	580
Query	321	ĢĀАÇĢÇĀĀTÇÇĀÇÇĢĀŢCĢĀCÇŢĢĀŢĢĀŢСĢĢСÇĀTĢĢTĀŢTĢŢĢÇÇĀŢŢŢĢÇĀŢĀÇĢÇ	380
Sbjct	581	GAGCGCAACCCGCCCATTGATCTGATGATTGGACACGGCATCGTTCCCATTTGCATCCGC	640
Query	381	TTCCTGCAGAATACCAACAACTCAATGCTGCAGTTTGAGGCCGCTTGGGCGCTTACCAAC	440
Sbjct	641	ttcctgcagaacaccaccaaccatgttgcagttcgaggctgcctgggctctcaccaac	700
Query	441	ATCGCCTCTGGCACATCCGACCAAACGCGCTGCGTTATCGAACACAATGCTGTGCCGCAT	500
Sbjct	701	ATTĠĊĊŦĊĊĠĠĊAĊĊŦĊĊĠAĊĊAGAĊĊĊĠĊŦĠŦĠŦĊAŦŦĠAGĊAĊAAĊĠĊAĠŦĊĊĊŦĊAĊ	760
Query	501	TTCGTGGCTCTGCTCCAGTCCAAGTCCATGAACCTGGCCGAGCAGCAGTCTGGGCTCTG	560 820
Sbjct Query	761 561	TTĊĠŦĠĠĊŦĊŦĠĊŦĊĊĂĠŦĊĊĂĂĠŦĊĊĂŦĊĂĀŦĊŦĠĠĊĊĠĂĠĊĂĠĠĊĀĠŦĊŦĠĠĠĊŦĊŦĠ GGCAACATTGCCGGCGACGGAGCCGCCGCCGCGACATTGTCATCCACCACAACGTAATT	620
Sbjct	821	GCAACATTGCCGGCGACGCCCAGTGCCCGCGACATTGTTATCCATCACAACGTGATC	880
Query	621	ĢĄCĢĢĄĄŢCTŢĢÇÇĄÇŢĢĄŢÇĄĄÇĄĄTĢĄĢĄÇĄÇÇĢÇŢÇŢŢŢŢŢŢŢŢŢĢÇĢÇĄĄÇĄŢCĢŢÇ	680
Sbjct	881	GATGGCATTCTGCCGCTGATCAACAACGAGACGCCGCTCTCCTTTCTGCGCAACATTGTC	940
Query	681	TGGCTGATGTCCAACCTGTGCAGGAATAAGAATCCATCTCCGCCATTCGATCAGGTGAAG	740
Sbjct	941	TGGTTGATGTCGAATCTGTGCCGCAACAAGAACCCATCGCCGCCGTTCGAGCAGGTGCGG	1000
Query	741	CGGCTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCAAGTGCTGGCCGAC	800
Sbjct	1001	ĊĠĠĊŦĠŦŦĠĊĊAĠŦĊĊŦĠŦĊĠĊĀAĊŦĠŦŦĠĊŦŦĀĠĊĊĀĠĠĀŦĀŦĊĊĀĠĠŦĠĊŦĠĠĊĊĠĀĊ	1060
Query	801 1061	GCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGATCCAGGCTGTGGTC	860 1120
Sbjct Query	861	GACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATTATT	920
Sbjct	1121		1180
Query	921	ĢŢĠÇÇĊĢĊĊŢĠĊĢĊĄĠĊĢŢŢĠĢĊĄĄĊĄŢŢĠŢĠĄĊŢĠĢĊĄĊĄĠĄŢĊĄĄĊĄĠĄĊŢĠĄĊĠŢŢ	980
Sbjct	1181	GTCCCAGCTCTTCGTAGTGTGGGCAACATTGTGACTGGAACAGATCAACAGACTGATGTG	1240
Query	981	GTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCACAACAAAAGCAAC	1040
Sbjct	1241	GTTATTGCCGCCGGAGGATTACCCAGATTGGGTCTTCTCTTGCAACACAGCAAGAGCAAC	1300
Query	1041	ATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACCAGAAGCAGATC	1100
Sbjct	1301	ÁTTGTTÁÁGGÁGGCAGCCTGGÁCAGTGÁGCÁÁCÁTCÁCGGCTGGCÁÁCCÁAÁÁGCÁGÁTC	1360
Query Sbjct	1101 1361	CAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGGAGAAGGGTGAT	1160 1420
Query	1161	TTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACATCTGGCACTCCC	1220
Sbjct	1421	TTCAAGGCCCAGAAGGAAGCTGCATGGGCAGTGACCAACACCACCTCTGGCACTCCC	1480
Query	1221	ĢĄАÇĄĢĄŢĊĢĄŢĊŢĄĄŢŢĢĄĢĄĄĢŢĄĊĄĄĄĄŢАТŢĢĄĄĢĊĊŢŢŢŢĄŢĊĢĄŢŢŢĠĊŢĢ	1280
Sbjct	1481	GAGCAGATTGTAGATCTGATTGAGAAGTTCAAGATCCTGAAGCCATTCATCGATCTTCTG	1540
Query	1281	GACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGTTTGCC	1340
Sbjct	1541	ĠAĊĠĊĊĀĀĠĠĀŦĊĊĠĊĠĀĀĊĊĀŦĊĀĀĀĠŦĠĠŦĠĊĀĠĀĊĊĠĠŦĊŦĠŦĊĊĀĀŦĊŦĠŦŦĊĠĊĊ	1600
Query	1341	CTGGCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGCGGT	1400
Sbjct	1601 1401	CTGGCCGAGAAGCTGGGCGGTACCGAGAACCTGTGCCTAATGGTCGAAGAGATGGGTGGC CTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCCTAC	1660 1460
Query Sbjct	1661	CTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCCTAC	1460
Query	1461	GCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAGAGCTCGCACCT	1520
Sbjct	1721	GCATAATAGACACCTACTTCAGCAACGGCGACGACGGGTTGAGCAGGAGCTGGCCCA	1780

Query	1521	CAGGAGGTCAACG	GAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAGGTGGC	1580
Sbjct	1781	caggaggttaacg	degecetegyatteyecseeyeese	1840
Query	1581	TACACGTTCTA 	1591	
Sbjct	1841	TATACATTCTA	1851	

Drosophila persimilis GL18958 (Dper\GL18958), mRNA

Sequence ID: **ref|XM_002014394.1|** Length: 1569 Number of Matches: 1 Range 1: 1 to 1568

Score		Expect	Identities	Gaps	Strand	Frame
1328 bit	ts(719)	0.0()	1285/1568(82%)	0/1568(0%)	Plus/Plus	
Feature	s:					
Query	24	аТĢАСТААСС	ССССТАТТСТААСТСАССА	СА ĢĢĢ ÇŢÇÇŢĄСĄĄĢ	GÇÇAAÇAGCATTA	AACACG 83
Sbjct	1	ATGAATAAAA	CGGATGCAAACACTCGT	CAGGGCTCCTATAAG	TCCAACACAATC	AACACG 60
Query	84	CAGGACTCACO	GCATGCGCCGCCATGAG	GTGACCATCGAGCTG	CGCAAGTCCAAA	AAGGAG 143
Sbjct	61	CAGGACTCGC	scardedredecardad	Gtraccatrgagrtg	cccaactccaaa	AAGGAG 120
Query	144	GACCAGATGTT	CAAGCGGCGCAACATC	AACGACGAGGATCTA	ACGTCGCCGCTC	AAAGAG 20:
Sbjct	121	ĠATĊAĠAŦĠŦſ	rcaagcgrcgcaacatc	<u> AAĊĠĀĊĠĀĀĠĀCĊŦ</u> C	AcctcccctG	AAAGAA 180
Query	204	CTCAATGGCC#	AGTCGCCGGTGCAGCTG 	TCCGTGGACGAGATA	GTGGCGGCCATGA	AACAGC 26:
Sbjct	181	ттааатсст	\drcdccddrdcadctd	†¢GĠ†ĠĠAŢĠAĠAŤŢ	ĠŦĠĠĊĠĠĊĊĀŦĠ	AACAGC 240
Query	264		AGCGCCAGTTCCTGGGC 			
Sbjct	241		AGCGCCAGTTCATGGGT			
Query	324		CCATCGACCTGATGATC			
Sbjct	301 384		CCÁTTGÁTCTAÁTGÁTT CCAACAACTCAATGCTG			
Query Sbjct	361		CCACCACTCAATGCTG			
Query	444		CATCCGACCAAACGCGC			
Sbjct	421	GCCTCGGGAAG		TGTGTCATCGAGCAC		
Query	504	ĢŢĠĢĊŢĊŢĠĊŢ	rcçagtçcaagtçcatg	ĄĄCÇŢĠĢÇĊĢĄĢĊĄĢ	GÇAGTCTGGGÇT(СТĢĢĢС 563
Sbjct	481	GTTGCCCTGCT		AATCTTGCTGAGCAG	 GCCGTATGGGCT:	 TGGGT 540
Query	564	AAÇATTGÇÇĞÇ	GCGACGGAGCCGCCGCC	ССССВАСАТТСТСАТС	САССАСААССТА	ATTGAC 623
Sbjct	541	AACATAGCCG	GCGATGGAGCCGCTGCT	CGCGACATTGTAATC	CAACATAATGTC	ATCGAT 600
Query	624	GGAATCTTGC	CACTGATCAACAATGAG	ACACCGCTCTCTTT	TTGCGCAACATC	GTCTGG 683
Sbjct	601	GGTATTTTGCC	egetgattaacaacgaa	Acgcccctrtcattt	ttgcggaacatro	STTTGG 660
Query	684	CTGATGTCCA	ACCTGTGCAGGAATAAG	AATCCATCTCCGCCA	TTCGATCAGGTGA	AAGCGG 743
Sbjct	661	ctdatdtcta	Arctgtgccgcaacaag	AATCCTTCGCCGCCC	tttgaacaagtg	ACACGC 720
Query	744	CTGTTGCCCGT	PCCTGTCGCAGCTTCTG 	CTTAGTCAGGACATC	CAAGTGCTGGCC	
Sbjct	721		rrctgtcgcagcttttg			
Query	804		FGTCCTACGTCACGGAC			
Sbjct	781		rĠŦĊAŦAŦĠŦĊĀĊĊĠĀŦ			
Query	864		rgccgcgcctggtcaaa 			
Sbjct	841 924		TTCCTAGACTAGTGÁÁÁ SCAGCGTTGGCAACATT			
Query Sbjct	901		GCAGCGTTGGCAACATT 			
Query	984		GAGGTTTACCAAGGCTG			
Sbjct	961					AACATT 10
Query	1044		CTĢÇCTĢĢAÇGĢTCAĢC			
Sbjct	1021			11111 11111111		
,						

Query	1104	GCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGGAGAAGGGTGATTTC	1163
Sbjct	1081	GCAGTTATTGAAGCTGGCATCTTCCAACAACTACGCAACGTGCTCGAGAAGGGCGATTTT	1140
Query	1164	AAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACATCTGGCACTCCCGAA	1223
Sbjct	1141	AAGGCACAAAAAGAGGCCGCATGGGCAGTGACCAACACGACAACATCGGGCACCCCAGAG	1200
Query	1224	CAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTATCGATTTGCTGGAC	1283
Sbjct	1201	CAGATTGTGGATCTGATTGAGAAGTTCAAAATATTGAAGCCATTCATCGACTTGCTCGAT	1260
Query	1284	ACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGTTTGCCCTG	1343
Sbjct	1261	GCTAAAGATCCACGCACCATCAAAGTTGTGCAGACTGGCTTGTCCAACCTCTTTGCGCTG	1320
Query	1344	GCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGCGGTCTA	1403
Sbjct	1321	GCCGAGAAACTGGGCGGTACTGAGAACCTCTGTCTCATGGTCGAAGAGATGGGCGGATTG	1380
Query	1404	GACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCCTACGCC	1463
Sbjct	1381	GATAAACTGGAAACATTGCAGCAACACGAGAACGAAGAGGTGTACAAGAAGGCGTACGCA	1440
Query	1464	ATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAGAGCTCGCACCTCAG	1523
Sbjct	1441	ATTATCGATACCTACTTCAGCAATGGCGACGACGAGGCCGAGCAAGAGCTCGCCCCAG	1500
Query	1524	GAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAGGTGGCTAC	1583
Sbjct	1501	GAAGTGAATGGAGCCCTCGAATTTAATGCAACTCAGCCTAAGGCTCCAGAGGGTGGTTAC	1560
Query	1584	ACGTTCTA 1591	
Sbjct	1561	ACATTCTA 1568	

Drosophila pseudoobscura pseudoobscura uncharacterized protein (Dpse\GA18440), mRNA Sequence ID: **ref|XM_001356277.3**| Length: 2341 Number of Matches: 1 Range 1: 222 to 1790

Score		Expect	Identities	Gaps	Strand	Frame	
1314 bits	s(711)	0.0()	1283/1569(82%)	0/1569(0%)	Plus/Plus		
Features	S :						
Query	24	aTGAGTAAGGC	GGATTCTAACTCACGA	CAGGGCTCCTACAAGG	GCCAACAGCATT	TAACACG	83
Sbjct	222	ATGAATAAAAC	GGATGCAAACACTCGT	CAGGGCTCCTATAAG	rccaacacaato	CAACACG	281
Query	84	CAGGACTCACG	CATGCGCCGCCATGAG	GTGACCATCGAGCTG(CGCAAGTCCAA <i>I</i>	AAAGGAG	143
Sbjct	282	credacteses	catecerceccateae	gtraccatrgagrtg	CGCAAGTCCAA	AAAGGAG	341
Query	144	GACCAGATGTT	CAAGCGGCGCAACATC	AACGACGAGGATCTA	ACGTCGCCGCTC	CAAAGAG	203
Sbjct	342	GATCAGATGTT	CAAGCGTCGCAACATC	AACGACGAAGACCTC	AcctcGcccct	GAAAGAA	401
Query	204	CTCAATGGCCA	GTCGCCGGTGCAGCTG	TCCGTGGACGAGATA(GTGGCGGCCATG	GAACAGC	263
Sbjct	402	TTAAATGGCCA	.gtcgccggtgcagctg	tegetegateagatro	STGGCGGCCAT	SAACAGC	461
Query	264	GAGGATCAGGA	GCGCCAGTTCCTGGGC.	ATGCAGTCTGCCCGC	AAGATGCTCAGT	TCGGGAA	323
Sbjct	462	GAGGATCAGGA	.dcdccadttcatdddt	Atgcagtcggcacggz	AAGATGCTGAG1	rcccdag	521
Query	324	CGCAATCCACC	CATCGACCTGATGATC	GGCCATGGTATTGTG(CCCATTTGCATA	ACGCTTC	383
Sbjct	522	CGCAATCCACC	CATTGATCTAATGATT	GGCCATGGCATCGTT	CCATATGCATA	ACGATTT	581
Query	384	CTGCAGAATAC	CAACAACTCAATGCTG	CAGTTTGAGGCCGCT	rgggcgcttaco	CAACATC	443
Sbjct	582	CTTCAAAACAC	cagcaataccatgttg	cagtttgaggcagcc:	rgggctttgac <i>i</i>	AAACATT	641
Query	444	GCCTCTGGCAC	ATCCGACCAAACGCGC	TGCGTTATCGAACACA	ATGCTGTGCC	CATTTC	503
Sbjct	642	dcctcgggaac	Atctgaccagacacgc	tgtgtcatcgagcacı	AATGCGGTGCCG	SCATTTT	701
Query	504	GTGGCTCTGCT	CCAGTCCAAGTCCATG	AACCTGGCCGAGCAG	GCAGTCTGGGCT	TCTGGGC	563
Sbjct	702	gtrgccctgct	GCAGTCGAACTCTATC	AATCTTGCTGAGCAG	SCCGTATGGGCT	rttgggt	761
Query	564	AACATTGCCGG	CGACGGAGCCGCCGCC	CGCGACATTGTCATC	CACCACAACGTA	AATTGAC	623
Sbjct	762	AACATAGCCGG	CGATGGGGCCGCTGCT	cccacattctaatc	CAACATAATGTO	CATCGAT	821
Query	624	GGAATCTTGCC	ACTGATCAACAATGAG	ACACCGCTCTCTTTT	TTGCGCAACATO	CGTCTGG	683
Sbjct	822	GGTATTTTGCC	gctgattaacaacgaa	Acccccctrtcattt	rtgcggaacati	rgtctgg	881
Query	684	CTGATGTCCAA	CCTGTGCAGGAATAAG	AATCCATCTCCGCCA	TTCGATCAGGT	GAAGCGG	743

Sbjct	882	TTGATGTCGAATCTGTGCCGCAACAAGAATCCTTCGCCGCCCTTTGAACAAGTGACACGC	941
Query	744	CTGTTGCCCGTCCTGTCGCAGCTTCTGCTTAGTCAGGACATCCAAGTGCTGGCCGACGCC	803
Sbjct	942	TTGCTGCCAGTTCTGTCGCAGCTTTTGCTTAGTCAAGATATTCAGGTTTTTGGCCGACGCC	1001
Query	804	TGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGATCCAGGCTGTGGTCGAC	863
Sbjct	1002	TGCTGGGCTTTGTCATATGTCACCGATGATGACAACCACAAGATTCAGGCGGTAGTGGAC	1061
Query	864	TCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCATTATTGTG	923
Sbjct	1062	TCGGATGCAGTTCCTAGACTAGTGAAACTTTTGCAAATGGATGAGCCCAGCATAATTGTG	1121
Query	924	CCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAACAGACTGACGTTGTA	983
Sbjct	1122	CCAGCACTGCGCAGTGTGGGAAACATTGTCACCGGCACAGATGTACAGACCGATGTTGTT	1181
Query	984	ATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCACAACAAAAGCAACATT	1043
Sbjct	1182	ATTGCTGCGGGTGGCTTGCCCCGACTGGGTCTGCTGCTGCAGCACAACAAGAGCAACATT	1241
Query	1044	GTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACCAGAAGCAGATCCAG	1103
Sbjct	1242	GTCAAGGAGGCTGCTTGGACTGTAAGTAACATAACAGCAGGTAATCAGAAGCAAATCCAA	1301
Query	1104	GCTGTGATTCAGGCCGGCATCTTCCAGCAGCTGCGCACCGTGCTGGAGAAGGGTGATTTC	1163
Sbjct	1302	GCAGTTATTGAAGCTGGAATCTTCCAACAACTACGCAACGTGCTCGAGAAGGGCGATTTT	1361
Query	1164	AAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCCACGACATCTGGCACTCCCGAA	1223
Sbjct	1362	AAGGCACAAAAAGAGGCCGCATGGGCAGTGACCAACACGACAACATCGGGCACCCCAGAG	1421
Query	1224	CAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTATCGATTTGCTGGAC	1283
Sbjct	1422	cagatretegatregatregatregatregatregatrega	1481
Query	1284	ACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGTTTGCCCTG	1343
Sbjct	1482	GCTAAAGATCCACGCACCATCAAAGTTGTGCAGACTGGCTTGTCCAACCTCTTTGCGCTG	1541
Query	1344	GCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGCGGTCTA	1403
Sbjct	1542	dccdadaaactgddcddractdadaacctctdtctctctctctdtcatddtcdaadadatdddcddattg	1601
Query	1404	GACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCCTACGCC	1463
Sbjct	1602	GATAAACTGGAAACATTGCAGCAACACGAGAACGAAGAGGTGTACAAGAAGGCGTACGCA	1661
Query	1464	ATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAGAGCTCGCACCTCAG	1523
Sbjct	1662	ATTATCGATACCTACTTCAGCAATGGCGACGACGAGGCCGAGCAAGAGCTCGCCCCAG	1721
Query	1524	GAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAGGTGGCTAC	1583
Sbjct	1722	GAAGTGAATGGAGCCCTCGAATTTAATGCAACTCAGCCTAAGGCTCCAGAGGGTGGTTAC	1781
Query	1584	ACGTTCTAA 1592	
Sbjct	1782	ACATTCTAA 1790	

Drosophila mojavensis uncharacterized protein (Dmoj\GI17589), mRNA Sequence ID: **ref|XM_002002782.2|** Length: 2697 Number of Matches: 1 Range 1: 217 to 1789

Score		Expect	Identities	Gaps	Strand	Frame	
1194 bits(646)		0.0()	1268/1577(80%)	8/1577(0%)	Plus/Plus		
Feature	s:						
Query	20	aaaaaTGAGT <i>I</i>	AAGGCGGATTCTAACTC	ACGACAGGGCTCCTA	CAAGGCCAACAG	GCATTAA	79
Sbjct	217	AAACATGAATA	AATCGGATGCAAACAC	TCGCCAGGGCCACTA	CAAGGCCAACA	CTCTTAA	276
Query	80	CACGCAGGACT	CACGCATGCGCCGCCA	TGAGGTGACCATCGA	GCTGCGCAAGT	CCAAAAA	139
Sbjct	277	cardcaddaci	rcececatecerceca	tgaggtgaccatcga	GCTGCGCAAGT	CAAAGAA	336
Query	140	GGAGGACCAG <i>I</i>	ATGTTCAAGCGGCGCAA	CATCAACGACGAGGA	TCTAACGTCGC	CGCTCAA 	199
Sbjct	337	ddaddaddad	rtgttcaagcgccgcaa	catcaargargagga	CCTAACCTCAC	CGTTGAA	396
Query	200	AGAGCTCAATO	GCCAGTCGCCGGTGCA	GCTGTCCGTGGACGA	GATAGTGGCGG(CCATGAA 	259
Sbjct	397	GĠAAĊŦĊAAŦĊ	seccaetcecce	ĠĊŦĠŦĊĠĠŦĠĠĀĊĠĀ	AATCGTCGCTG	ccatgaa	456
Query	260	CAGCGAGGATO	CAGGAGCGCCAGTTCCT	GGGCATGCAGTCTGC 	CCGCAAGATGC'	TCAGTCG	319

Sbjct	457	TAGTGAGGATCCGGAACGCCAATTCGTGGGCATGCAGCAGGCACGCAAGATGCTCAGTCG	516
Query	320	GGAACGCAATCCACCCATCGACCTGATGATCGGCCATGGTATTGTGCCCCATTTGCATACG	379
Sbjct	517	CGAACGTAATCCACCTATTGATGTGATGATTAGCCATGGCATTGTGCCTATCTGCATTCG	576
Query	380	CTTCCTGCAGAATACCAACAACTCAATGCTGCAGTTTGAGGCCGCTTGGGCGCTTACCAA	439
Sbjct	577	cttccttcagcacaacaacc-ctctattgcaatttgaggccgcctgggctttgaccaa	633
Query	440	CATCGCCTCTGGCACATCCGACCAAACGCGCTGCGTTATCGAACACAATGCTGTGCCGCA	499
Sbjct	634	ĊATĊĠĊATĊGĠĠĊAĊATĊGĠATĊAGAĊĠĊĠTTĠĊĠŤŤATĊĠAAĊAGAATĠĊCĠŤĠĊĊĠĊA	693
Query	500	TTTCGTGGCTCTGCTCCAGTCCAAGTCCATGAACCTGGCCGAGCAGGCAG	559
Sbjct	694	TTTCATAGCACTGCTGCAGTCGAAGTCGCTTAATCTGGCCGAGCAGGCCGTCTGGGCCCT	753
Query	560 754	GGGCAACATTGCCGGCGACGGAGCCGCCGCCCGCGACATTGTCATCCACCACAACGTAAT	619 813
Sbjct Query	620	TGACGGAATCTTGCCACTGATCAACAATGAGACACCGCTCTCTTTTTTTGCGCAACATCGT	679
Sbjct	814	CGATGCCATTTTGCGTTTAATCAATAATGAGACGCCGCTGTCGTTTCTCCGCAACATTGT	873
Query	680	CTGGCTGATGTCCAACCTGTGCAGGAATAAGAATCCATCTCCGCCATTCGATCAGGTGAA	739
Sbjct	874	TTGGCTGATGTCGAATTTGTGCCGCAACAAGAATCCGTCGCCGCCCTTTGACCAGGTGAA	933
Query	740	ĢÇĢGÇŢĢŢŢĢÇÇCĢŢCÇŢĢŢÇĢÇĄĢCŢTÇŢĢCŢ—ŢĄGTÇĄĢĢĄC—ĄŢCCĄ—Ą—ĢŢĢÇŢĢĢ	795
Sbjct	934	GCGCCTGTTGCCGGTGCTGTCGCAGTTGCTGGTCTAC-CAGGAGGATATACAGGTGCTGG	992
Query	796	CCGACGCCTGCTGGGCTTTGTCCTACGTCACGGACGACGATAATACCAAGATCCAGGCTG	855
Sbjct	993	ccdardcctgrtgggccttgtcctargtgacggacgargaaaacaacaagatacaggcgg	1052
Query	856	TGGTCGACTCGGACGCAGTGCCGCGCCTGGTCAAACTGCTGCAAATGGACGAGCCGAGCA	915
Sbjct	1053	†CĠŤĊĠĂŦĂĊĠĀĀŦĠĊĀĠŤĠĊĊĊĠŦĊŤĠĠŤĠCĀĀĊŤĠĊŤĠĊĀĠĀCŦĠĀŦĠĀĠĊĊĊĀĠĊĀ	1112
Query	916	TTATTGTGCCCGCCCTGCGCAGCGTTGGCAACATTGTGACTGGCACAGATCAACAGACTG	975
Sbjct	1113 976	ŤCÁŤŤĠŤĠĊĊĠĠĊAĊŤĠAĠĠĂĠĊĠŤĠĠĠĊĂĂĊĂŤŤĠŤĊĂĊĊĠĠAĂĊĠĠĂŤĊĂĠĊĂĠĂĊĊĠ ACGTTGTAATTGCATCTGGAGGTTTACCAAGGCTGGGACTCCTTCTACAGCACAAAAA	11721035
Query Sbjct	1173	ACGITGIAATIGCATCIGGAGGITTACCAAGGCIGGACICCITCIACAGCACAACAAAA	1232
Query	1036	GCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACATCACAGCAGGTAACCAGAAGC	1095
Sbjct	1233	GCAACATTGTGAAGGAGGCTGCCTGGACCGTGAGCAACATCACGGCTGGCAATCAGAAAC	1292
Query	1096	ĄĢĄŢĊÇĄĢĢÇŢĢŢĠĄŢTĊĄĠĢÇĊĢĢÇĄŢÇŢŢĊĊĄĢÇĄĠĊŢĠÇĢÇACĊĢŢĢĊŢĠĢĄĢĄĄĠĢ	1155
Sbjct	1293	AGATTCAGGCTGTCATCGATGCGGGCATCTTTGTGCAAATACGCCATGTGCTCGAGAAAG	1352
Query	1156	GTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTGACAAACACCACGACATCTGGCA	1215
Sbjct	1353	GCGATTTCAAGGCACAAAAGGAGGCCGCCTGGGCTGTGACCAATACCACCACTTCGGGCA	1412
Query	1216	CTCCCGAACAGATCGTCGATCTAATTGAGAAGTACAAAATATTGAAGCCTTTTATCGATT	1275
Sbjct	1413	ĊAĊĊĠĀGĊĀĠĀŢŢĠŢĊĠĀŢĊŢĠĀŢĊĠĀĠĀĀĠŢĀĊĀĀGĀŢĀĊŢŢĀĀĠĊĊĀŢŢĀŢŢĠĀŢŢ	1472
Query	1276	TGCTGGACACAAAGGATCCGCGTACCATCAAGGTGGTGCAGACGGGCCTATCCAATCTGT	1335
Sbjct	1473	ŤĠĊŤĊĠĂĠĠĊĊĂĂĀĠĂŤĊĊĀĊĠĀĀĊĊĂŤĊĂĀĀĠŤĠĠŤŦĊĀĠĀĊŦĠĠŦŦŤĠŤĊĊĂĀŤĊŤĠŤ	1532
Query	1336 1533	TTGCCCTGGCGGAGAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGG	1395 1592
Sbjct Query	1396	GCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGG	1455
Sbjct	1593	GCGGTCTCGACAAACTGGAAGCATTGCAGCACGAGAACGAGGAGGTCTACAAGAAGG	1652
Query	1456	ÇÇŢĄCĢÇÇAŢCĄŢŢĢĄCĄÇĄŢĄÇŢŢÇĄĢCAACĢĢÇĢĄÇĢĄÇĢĄĢĢÇÇĢĄGCĄAĢĄĢÇŢCĢ	1515
Sbjct	1653		1712
Query	1516	CACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAG	1575
Sbjct	1713	CGCCACAGGAGTCAATGGCGCACTGGAGTTTAACGCCACACAGCCTAAGGCGCCGGAGG	1772
Query	1576	GTGGCTACACGTTCTAA 1592	
Sbjct	1773	GCGGCTATACCTTCTAA 1789	

Range 1: 312 to 1874

Score		Expect	Identities	Gaps	Strand	Frame	
1077 bit	s(583)	0.0()	1245/1572(79%)	15/1572(0%)	Plus/Plus		_
Features	3:						
Query	24		CGGATTCTAACTCACG.				82
Sbjct	312		ċĠĠĀŦĠĊĀĀĠĊĀĊĀĊĠ				370
Query	83		CGCATGCGCCGCCATG.				142
Sbjct Query	371 143		CGCATGCGTCGCCATG. FTCAAGCGGCGCAACA'				430 202
Sbjct	431		TTTAAGCGCCGTAACA	111111 11 11111			490
Query	203	ĢСŢСĄĄŢĢĢC(; САĢŢÇGÇÇĢĢŢĢÇAĢС	ŢĠŢĊĊĠŢĠĠŖĊĠŖĠŖŢ	AGTGGCGGCCAT	: Г Ģ ААСАG	262
Sbjct	491	GTTAAATGGAG	CAGTCACCGGTGCTGC	TATCGGTTGATGAGAT	TGTGGCGGCTAT	GAACAG	550
Query	263	CGAGGATCAGG	GAGCGCCAGTTCCTGG	GCATGCAGTCTGCCCG	CAAGATGCTCAG	TCGGGA	322
Sbjct	551		ĠAAĊĠĊĊAAŤŤĊGŤĠĠ				610
Query	323		CCATCGACCTGATGA' 	1111 11111 11111			382
Sbjct	611		CCATTGATCTTATGA'				670 441
Query Sbjct	383 671	CCTGCAGAATZ	ACCAACAACTCAATGC' 	TGCAGTTTGAGGCCGC TGCAGTTTGAGGCTGC			726
Query	442		CĄCĄTÇCGĄCCĄAĄCG				50
~ Sbjct	727	TTGCATCGGG	 FACATCGGAGCAGACG	 CGTTGCGTCATTGAGC	 AGAATGCTGTGC	 CCCATT	780
Query	502	TCGT-G-GCTC	CTGCTCCAGTCCAAGT	CCATGAACCTGGCCGA	GCAGGCAGTCTG	GGCTCT	559
Sbjct	787	TCATTGAGCT	bctccagtcgaagt	CGCTTAATCTTGCCGA	ACAGGCCGTTTG	GGCGTT	844
Query	560	GGGCAACATT(GCCGGCGACGGAGCCG	CCGCCCGCGACATTGT	CATCCACCACAA	CGTAAT	61
Sbjct	845		ecedecedacede de la companya del companya del companya de la compa				90
Query	620		FTGCCACTGATCAACA	111111 11 11 11			67
Sbjct Query	905 680		CTĠĊGTTTAĂTĊĂĂTĂ. FCCAACCTGTGCAGGA.				964 739
Query Sbjct	965		rccaaccigigcagga 				10:
Query	740		ÇÇCĞTCÇTĞTÇĞÇAĞC'				799
Sbjct	1025	GCGTCTGCTGC		TGCTGGTCAGCCAGGA		GGCCGA	10
Query	800	CGCCTGCTGG	GCTTTGTCCTACGTCA	CGGACGACGATAATAC	CAAGATCCAGGC	TGTGGT	85
Sbjct	1085	TGCGTGCTGG	GCGCTGTCGTATGTGA	CAGATGATGACAACAA	CAAGATACAAGC	GGTGGT	11
Query	860		GCAGTGCCGCGCCTGG'				91
Sbjct	1145		ĠĊĀĠŢĠĊĊĀĊĠĊĊŢŢĠ				120
Query Shict	920 1205		CTGCGCAGCGTTGGCA 				97: 12:
Sbjct Query	980		CTGCGCAGTGTCGGTA CCTGGAGGTTTACCAA				10
Sbjct	1265		GCTGGTGGCTTGCCCA				13
Query	1039		GGAGGCTGCCTGGACG				10
Sbjct	1324	ATATAGTTAA		 GTGAGCAACATTACGG	CCGGTAATCAGA	AACAGA	13
Query	1099	TCCAGGCTGT	GATTCAGGCCGGCATC	TTCCAGCAGCTGCG-C	ACCGTGCTGGAG	SAAGGGT	11
Sbjct	1384	TTCAGGCAGT	catcgacdcgdgtatc	ttccagcagatacgtc	AT-GTATTGGAA	ryygggc	14
Query	1158		CTCAAAAAGAGGCTGC				12
Sbjct	1443		ĊAĊĀĀĀĀĀĀĠĀĠĠĊĊĠĊ				15
Query	1218		FCGTCGATCTAATTGA 	11111111			12
Sbjct Query	1503 1278		PTGTAGATCTCATTGA AGGATCCGCGTACCAT				150 130
zact l	12/0					ĭ†ĭ††	₁ J .

Query	1338	GCCCTGGCGGAGAAACTTGGTGGCACCGAGAACCTATGCTTGATGGTCGAGGAGATGGGC	1397
Sbjct	1623	GCTCTCGCCGAGAAGCTGGGTGGCACGGAGAATCTATGCCTGATGGTCGAGGAACTAGGT	1682
Query	1398	GGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAGAACGAGGAGGTCTACAAGAAGGCC	1457
Sbjct	1683	GGCCTCGACAAGCTGGAAGCTTTGCAGCAGCACGAAAACGAAGAAGTCTATAAGAAGGCC	1742
Query	1458	TACGCCATCATTGACACATACTTCAGCAACGGCGACGACGAGGCCGAGCAAGAGCTCGCA	1517
Sbjct	1743	TATGCCATAATAGATACTTATTTCAACACTGGTGACGATGAGGCCGAGCAGGAGCTAGCG	1802
Query	1518	CCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCCACCCAGCCCAAGGCTCCCGAAGGT	1577
Sbjct	1803	CCGCAGGAGGTAAATGGTGCACTGGAGTTTAATGCCACGCAGCCCAAGGCGCCGGAGGGC	1862
Query	1578	GGCTACACGTTC 1589	
Sbjct	1863	GGTTATACCTTC 1874	

Drosophila willistoni uncharacterized protein (Dwil\GK18399), mRNA Sequence ID: **ref|XM_002074190.2|** Length: 2095 Number of Matches: 1 Range 1: 61 to 1596

Score		Expect	Identities	Gaps	Strand	Frame	
898 bits	(486)	0.0()	1189/1539(77%)	6/1539(0%)	Plus/Plus		
Feature	s:						
Query	57	TCCTACAAGO	GCCAACAGCATTAACAC	GCAGGACTCACGCAT(GCGCCGCCATGA	GGTGACC	116
Sbjct	61	TCCTACAAG	rcgaactcaatcaacac	GCAGGACTCGCGTGT	GCGTCGTCATGA	GGTGACC	120
Query	117	ATCGAGCTG	CGCAAGTCCAAAAAGGA(GGACCAGATGTTCAA(GCGGCGCAACAT	CAACGAC	176
Sbjct	121	ATAGAGCTTC	cgcaagtccaaaaagga	ggaccagatgttcaa	gcgccgcaacat	CAACGAT	180
Query	177	GAGGATCTA	ACGTCGCCGCTCAAAGA(GCTCAATGGCCAGTC	GCCGGTGCAGCT(GTCCGTG	236
Sbjct	181	GAAGATCTG	ycctceccectyyddy	dccadatddacdatc'	rccactccact	gtcegte	240
Query	237	GACGAGATA(GTGGCGGCCATGAACAG(CGAGGATCAGGAGCG(CCAGTTCCTGGG(CATGCAG	296
Sbjct	241	ĠĀĊĠĀĀĀŤŦŒ	ĠŦĠĠĊŦĠĊĊĂŦĠĂĀĊĀĠ	ĊĠĀĠĠĀŢŢĊĠĠĀĠĊĠ [,]	rċAĠϮϮτGϮĠĠĠ	AÁTĠĊÁA	300
Query	297	TCTGCCCGC	AAGATGCTCAGTCGGGA? 	ACGCAATCCACCCAT(CGACCTGATGAT(CGGCCAT	356
Sbjct	301	ŤĊĠĠĊŦĊĠĊ <i>Ĭ</i>	\AĠATĠTTGAĠTĊĠĠĠA(GĊĠTĀĀCĊĊĀĊĊTĀϮ'	rĠATTTĠATĠAT;	ГĠĠTĊÀŤ	360
Query	357		CCCATTTGCATACGCTT(416
Sbjct	361		CCGATTTGTATCAGATT(420
Query	417		rgggcgcttaccaacat(476
Sbjct	421		ÌĠĠĠĊŦĊŤĠĂĊĊĂĂŦĂŤ! \ATGCTGTGCCGCATTT!				480 535
Query Sbjct	477 481		ATGCTGTGCCGCATTT 				539
Query	536		GCAGTCTGGGCTCTGG				595
Sbjct	540		GCTGTCTGGGCTTTGG				599
Query	596		CCACCACAACGTAATTG				655
Sbjct	600		AAATCATGGTGTCATCG				659
Query	656	GÇŢĊŢĊŢŢŢ	TTTGÇÇÇAAÇATCGTCT(ĢĢÇŢĠĄŢĢŢÇĊĄĄCC'	ŢĢŢĢÇAĢGĄĄŢĄ.	ĄĢĄĄTÇÇ	715
Sbjct	660	ACTTTCGTT(CCTCCGCAACATTGTTT	 GGCTTATGTCGAATT'		 AGAACCC	719
Query	716	AŢÇŢÇÇÇÇ <i>I</i>	\ ŢŢĊĢĄŢĊĄĠĢŢĢĄĄĠĊ	ĢGCŢĢTŢĢÇÇÇGŢCÇ'	ŢĠŢĊĠĊŖĠĊŢŢĊ'	ГСТТАС	775
Sbjct	720	GTCGCCACCT	rttgagcaagtgaaac	 GTTTGCTGCCCATTC'	 		779
Query	776	ŢĊĀĢĢĀĊĀŢĊ	ССААĢТБСТĢĢССĢАСĢ	, ССТССТССТССТТТСТТТСТТСТТСТТТСТТТСТТТТСТТТТ	, ССТАСĢТСАСG	ĄCĢĄCĢĄ	835
Sbjct	780	TACGGATAT	rcaagttttggccgatg	CCTGTTGGGCCCTGT	CCTATGTGACAG	 ATGATGA	839
Query	836	TAATACCAA	GATCCAGGCTGTGGTCG	ACTCGGACGCAGTGC	CGCGCCTGGTCA	AACTGCT	895
Sbjct	840	TAACAACAA	GATTCAGGCTGTCGTGG	ATACGGATGCGGTAC	CCAGGTTGGTTA	ACTTGTT	899
Query	896	GCAAATGGA(CGAGCCGAGCATTATTG'	TGCCCGCCCTGCGCA	GCGTTGGCAACA'	TTGTGAC	955
Sbjct	900	GCAAATGGAT	rgagccaagtattatag	tecceecctece	GTGTGGGTAATA'	tagtgac	959
Query	956	TGGCACAGAT	rcaacagactgacgttg:	TAATTGC-ATCTGGA	GGTTTACCAAGG(CTGGGAC	1014

Sbjct	960	GGGCACAGATCAACAGACTGACGTGGTCATTGCTAGC-GGTGGCCTACCTAGATTGGGCC	1018
Query	1015	TCCTTCTACAGCACAAAAGCAACATTGTGAAGGAGGCTGCCTGGACGGTCAGCAACA	1074
Sbjct	1019	TGTTGCTGCAGCACTCGAAAAGCAACATTGTTAAAGAGGCCGCCTGGACAGTAAGCAATA	1078
Query	1075	TCACAGCAGGTAACCAGAAGCAGATCCAGGCTGTGATTCAGGCCGGCATCTTCCAGCAGC	1134
Sbjct	1079	TTACTGCTGGTAACCAGAAGCAGATTCAGGCCGTCATTGAAGCCGGAATTTTCAATTATA	1138
Query	1135	TGC-GCACCGTGCTGGAGAAGGGTGATTTCAAGGCTCAAAAAGAGGCTGCCTGGGCGGTG	1193
Sbjct	1139	traagcaa-gtcctggaaaarggtgatttraaggctcagaaggaagctgcctgggctgtr	1197
Query	1194	ACAAACACCACGACATCTGGCACTCCCGAACAGATCGTCGATCTAATTGAGAAGTACAAA	1253
Sbjct	1198	ACCAATACCACAACTTCGGGAACTCCTGAGCAGATCGTAGATCTCATTGAGAAGTACAAG	1257
Query	1254	ATATTGAAGCCTTTTATCGATTTGCTGGACACAAAGGATCCGCGTACCATCAAGGTGGTG	1313
Sbjct	1258	Atcttgaaaccctttatcgatcttttggacgctaaggatccacgtaccatttaaggtgtc	1317
Query	1314	CAGACGGGCCTATCCAATCTGTTTGCCCTGGCGGAGAACTTGGTGGCACCGAGAACCTA	1373
Sbjct	1318	ĊAĠAĊŦĠĠAĊŦŦŦŦĠĀĀŦĊŦĠŦŦĊAAŦĊŦĊĠĊŦĠĀĠĀĀĀĊŦĠĠĠŦĠĠĊĀĊĊĠĀAĀĀŦĊŦŦ	1377
Query	1374	TGCTTGATGGTCGAGGAGATGGGCGGTCTAGACAAGCTGGAAACTCTGCAGCAGCACGAG	1433
Sbjct	1378	tgcctgatggtcgaagaaatgggtggattggataaattggaagccctccagcagcatgaa	1437
Query	1434	AACGAGGAGGTCTACAAGAAGGCCTACGCCATCATTGACACATACTTCAGCAACGGCGAC	1493
Sbjct	1438	AAĊĠĀĠĠĀĀĠŦĊŦĀŦĀĀĠĀĀĀĠĊĊŦĀŦĠĊĊĀŦŦĀŦŦĠĀŦĀĊĊŦĀĊŦŦĊĀĀŦĀĊŦĠĠĊĠĀŦ	1497
Query	1494	GACGAGGCCGAGCAAGAGCTCGCACCTCAGGAGGTCAACGGAGCCCTCGAGTTCAATGCC	1553
Sbjct	1498	ĠAAĠĠŦĠĊŦĠAAĊĀĠĠĀĠŦŦĠĠĊŦĊĊAĊĀĠĠĀAĠŦAĀĀŦĠĠĀĠĊŦŦŦĀĠĀĀŦŦŦĀĀŦĠĊŦ	1557
Query	1554	ACCCAGCCCAAGGCTCCCGAAGGTGGCTACACGTTCTAA 1592	
Sbjct	1558	ACTCAACCCAAGGCTCCGAAGGGGGCTACACCTTTTAA 1596	

PREDICTED: Chinchilla lanigera karyopherin alpha 1 (importin alpha 5) (Kpna1), mRNA

Sequence ID: **ref|XM_005386512.2|** Length: 5328 Number of Matches: 1 Range 1: 979 to 1014

Score		Expect	Identities	Gaps	Strand	Frame
56.5 bits(30)		0.002()	34/36(94%)	0/36(0%)	Plus/Plus	
Features	S:					
Query	543	CAGGCAGTCTGG	GCTCTGGGCAACAT	TGCCGGCGAC	578	
Sbjct	979	caddcadtctdd	gctctgggcaacat	TGCTGGAGAC	1014	

PREDICTED: Heterocephalus glaber karyopherin alpha 1 (importin alpha 5) (Kpna1), mRNA

Sequence ID: ref|XM_013068812.1| Length: 4219 Number of Matches: 1

Range 1: 758 to 786

Score		Expect	Identities	Gaps	Strand	Frame	
54.7 bits(29)		0.008()	29/29(100%)	0/29(0%)	Plus/Plus		_
Features	s:						
Query	543	CAGGCAGTCTGGGCTCTGGGCAACATTGC		571			
Sbjct	758	caggcagtctggg	CTCTGGGCAACATTGC	786			

PREDICTED: Fukomys damarensis uncharacterized LOC104857895 (LOC104857895), mRNA

Sequence ID: ref|XM_010617966.1| Length: 5544 Number of Matches: 1

Range 1: 2351 to 2379

Score	Expect	Identities	Gaps	Strand	Frame
54.7 bits(29)	0.008()	29/29(100%)	0/29(0%)	Plus/Plus	

Features:

Query 543 CAGGCAGTCTGGGCTCTGGGCAACATTGC 571
Sbjct 2351 CAGGCAGTCTGGGCTCTGGGCAACATTGC 2379