Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BV2WAP014

- ► Formatting options
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Blast report description

Nucleotide Sequence (2097 letters)

RID <u>B8BV2WAP014</u> (Expires on 02-06 12:13 pm)

Query ID lcl|Query_148334

Description None **Molecule type** nucleic acid

Molecule type nucleic acid

Query Length 2097

Database Name nr

Description All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

excluding environmental samples from

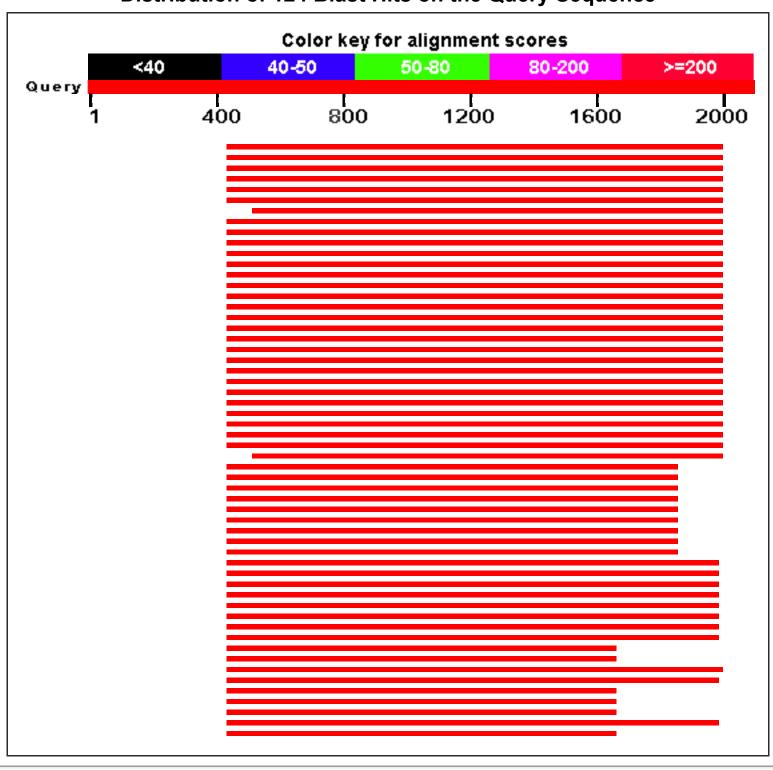
WGS projects

Program BLASTX 2.3.1+

□ Graphic Summary

No putative conserved domains have been detected

Distribution of 124 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
C3G ortholog, isoform F [Drosophila melanogaster]	769	769	74%	0.0	100%	NP_001138168.1
C3G ortholog, isoform H [Drosophila melanogaster]	768	768	74%	0.0	100%	NP_572350.2
RE10624p [Drosophila melanogaster]	766	766	74%	0.0	99%	AAQ22488.1
C3G ortholog, isoform I [Drosophila melanogaster]	761	761	74%	0.0	99%	NP_001259291.1
LOW QUALITY PROTEIN: uncharacterized protein Dsimw501_GD16179 [Drosophila simulans]	748	748	74%	0.0	97%	KMZ08542.1
uncharacterized protein Dere_GG17655, isoform B [Drosophila erecta]	716	716	74%	0.0	91%	XP_015010608.1
C3G ortholog, isoform D [Drosophila melanogaster]	714	714	70%	0.0	100%	NP_001138166.1
C3G, isoform I [Drosophila yakuba]	714	714	74%	0.0	91%	XP_015045493.1
uncharacterized protein Dere_GG17655, isoform A [Drosophila erecta]	714	714	74%	0.0	91%	XP_001978483.1
C3G, isoform A [Drosophila yakuba]	713	713	74%	0.0	91%	XP_002099940.1
C3G ortholog, isoform E [Drosophila melanogaster]	712	712	74%	0.0	90%	NP_001138167.1
IP03271p [Drosophila melanogaster]	712	712	74%	0.0	90%	ABF85718.1
C3G ortholog, isoform L [Drosophila melanogaster]	711	711	74%	0.0	90%	NP_001284966.1
C3G ortholog, isoform C [Drosophila melanogaster]	710	710	74%	0.0	90%	NP_788867.1
C3G ortholog, isoform K [Drosophila melanogaster]	710	710	74%	0.0	90%	NP_001259293.1
uncharacterized protein Dere_GG17655, isoform C [Drosophila erecta]	707	707	74%	0.0	90%	XP_015010609.1
guanine nucleotide exchange factor DC3G [Drosophila melanogaster]	707	707	74%	0.0	89%	AAC35280.1
C3G, isoform E [Drosophila yakuba]	707	707	74%	0.0	90%	XP_015045489.1
uncharacterized protein Dere_GG17655, isoform E [Drosophila erecta]	707	707	74%	0.0	90%	XP_015010611.1
C3G, isoform H [Drosophila yakuba]	706	706	74%	0.0	90%	XP_015045492.1
C3G, isoform C [Drosophila yakuba]	705	705	74%	0.0	90%	XP_015045487.1
uncharacterized protein Dere_GG17655, isoform H [Drosophila erecta]	673	673	74%	0.0	85%	XP_015010614.1
uncharacterized protein Dere_GG17655, isoform G [Drosophila erecta]	673	673	74%	0.0	85%	XP_015010613.1
uncharacterized protein Dere_GG17655, isoform F [Drosophila erecta]	672	672	74%	0.0	85%	XP_015010612.1
uncharacterized protein Dere_GG17655, isoform D [Drosophila erecta]	672	672	74%	0.0	85%	XP_015010610.1
C3G, isoform G [Drosophila yakuba]	664	664	74%	0.0	84%	XP_015045491.1
C3G, isoform D [Drosophila yakuba]	663	663	74%	0.0	84%	XP_015045488.1

C3G, Isoform F [Drosophila yakuba] 663 683 74% 0.0 84% XP_015045480.1 C3G ortholog, isoform G [Drosophila et al. 1975] 657 70% 0.0 90% NP_001188199.1 uncharacterized protein Dana_GF20837, 500rm K [Drosophila annanssae] uncharacterized protein Dana_GF20837, 537 583 583 67% 0.0 74% XP_01476975.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 537 583 583 67% 0.0 74% XP_01476975.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 537 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 532 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 532 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 532 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 532 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 532 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 532 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 532 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila annanssae] uncharacterized protein Dana_GF20837, 532 582 67% 0.0 74% XP_01476973.1 soform ID [Drosophila posudoboscura pseudoboscura pseudoboscura] pseudoboscura] uncharacterized protein Dana_GF20837, 534 573 73% 0.0 71% XP_01504128.1 soform ID [Drosophila pseudoboscura pseud	C3G, isoform B [Drosophila yakuba]	663	663	74%	0.0	84%	XP_015045486.1
melanogaskeri uncharacterized protein Dana GF20837, soform (Drosophila ananassae) 563	C3G, isoform F [Drosophila yakuba]	663	663	74%	0.0	84%	XP_015045490.1
Section Consembla anamassae Section Section Consembla anamassae Section Section Consembla anamassae Section S		657	657	70%	0.0	90%	NP_001138169.1
Solom	• = •	583	583	67%	0.0	74%	XP_014760976.1
	• = •	583	583	67%	0.0	74%	XP_014760975.1
Section Direct Description Descripti	·	583	583	67%	0.0	74%	XP_014760977.1
Isoform F [Drosophila ananassae] 902 909	• = •	582	582	67%	0.0	74%	XP_014760973.1
	·	582	582	67%	0.0	74%	XP_014760971.1
Isoform C [Drosophila ananasse] 992 362 67% 0.0 74% XP_01476978.1	•	582	582	67%	0.0	74%	XP_014760970.1
Isoform B [Drosophila ananassae]	·	582	582	67%	0.0	74%	XP_014760979.1
isoform A [Drosophila ananassae] 992 982 97% 0.0 74% AP_001994206.1 uncharacterized protein Dpse_GA16131, isoform C [Drosophila pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16131, isoform I [Drosophila pseudoobscura] uncharacterized protein Dpse_GA16131, isoform I [Drosophila pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16131, isoform D [Drosophila pseudoobscura] uncharacterized protein Dpse_GA16131, isoform D [Drosophila pseudoobscura] uncharacterized protein Dpse_GA16131, isoform E [Drosophila pseudoobscura] uncharacterized protein Dpse_GA16131, isoform E [Drosophila pseudoobscura pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16131, isoform E [Drosophila pseudoobscura pseudo	·	582	582	67%	0.0	74%	XP_014760978.1
isoform G [Drosophila pseudoobscura 576 576 576 73% 0.0 71% XP_015041262.1	·	582	582	67%	0.0	74%	XP_001964208.1
Isoform [Drosophila pseudoobscura 575 575 73% 0.0 71% XP_015041264.1	isoform G [Drosophila pseudoobscura	576	576	73%	0.0	71%	XP_015041262.1
Isoform D Drosophila pseudoobscura 575 575 73% 0.0 71% XP 015041259.1	isoform I [Drosophila pseudoobscura	575	575	73%	0.0	71%	XP_015041264.1
Isoform J [Drosophila pseudoobscura 574 574 73% 0.0 71% XP_015041265.1	isoform D [Drosophila pseudoobscura	575	575	73%	0.0	71%	XP_015041259.1
isoform E [Drosophila pseudoobscura pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16131, isoform F [Drosophila pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16131, isoform C [Drosophila pseudoobscura pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16131, isoform C [Drosophila pseudoobscura pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16131, isoform L [Drosophila pseudoobscura pseudoobscura pseudoobscura] uncharacterized protein Dana_GF20837, isoform I [Drosophila ananassae] uncharacterized protein Dana_GF20837, isoform G [Drosophila ananassae] uncharacterized protein Dana_GF20837, isoform G [Drosophila pseudoobscura pseudoobscura] uncharacterized protein Dana_GF20837, isoform G [Drosophila persimilis] 569 569 58% 0.0 81% XP_014760974.1 uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura pseudoobscura pseudoobscura pseudoobscura pseudoobscura pseudoobscura] uncharacterized protein Dpse_GA16545, 555 555 58% 5e-177 79% XP_015041258.1	isoform J [Drosophila pseudoobscura	574	574	73%	0.0	71%	XP_015041265.1
isoform F [Drosophila pseudoobscura 573 573 73% 0.0 71% XP_015041261.1 pseudoobscura] uncharacterized protein Dpse_GA16131, isoform C [Drosophila pseudoobscura 573 573 73% 0.0 71% XP_001355576.3 pseudoobscura] uncharacterized protein Dpse_GA16131, isoform L [Drosophila pseudoobscura 573 573 73% 0.0 71% XP_015041267.1 pseudoobscura] uncharacterized protein Dana_GF20837, isoform I [Drosophila ananassae] 569 569 58% 0.0 81% XP_014760974.1 uncharacterized protein Dana_GF20837, isoform G [Drosophila persimilis] 569 569 74% 0.0 68% XP_014760972.1 uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura 558 558 73% 3e-177 70% XP_015041258.1 pseudoobscura] uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura 558 558 558 73% 3e-177 70% XP_015041258.1 pseudoobscura] uncharacterized protein Dvir_GJ16545, 555 555 555 58% 5e-177 79% XP_015025478.1	isoform E [Drosophila pseudoobscura	574	574	73%	0.0	71%	XP_015041260.1
isoform C [Drosophila pseudoobscura 573 573 73% 0.0 71% XP_001355576.3 pseudoobscura] uncharacterized protein Dpse_GA16131, isoform L [Drosophila pseudoobscura 573 573 73% 0.0 71% XP_015041267.1 pseudoobscura] uncharacterized protein Dana_GF20837, isoform I [Drosophila ananassae] 569 569 58% 0.0 81% XP_014760974.1 uncharacterized protein Dana_GF20837, isoform G [Drosophila ananassae] 569 569 58% 0.0 81% XP_014760972.1 GL26876 [Drosophila persimilis] 569 569 74% 0.0 68% XP_002025124.1 uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura 558 558 73% 3e-177 70% XP_015041258.1 pseudoobscura] uncharacterized protein Dvir_GJ16545, 555 555 58% 5e-177 79% XP_015025478.1	isoform F [Drosophila pseudoobscura	573	573	73%	0.0	71%	XP_015041261.1
isoform L [Drosophila pseudoobscura 573 573 73% 0.0 71% XP_015041267.1 pseudoobscura] uncharacterized protein Dana_GF20837, isoform I [Drosophila ananassae] 569 569 58% 0.0 81% XP_014760974.1 uncharacterized protein Dana_GF20837, isoform G [Drosophila ananassae] 569 569 58% 0.0 81% XP_014760972.1 GL26876 [Drosophila persimilis] 569 569 74% 0.0 68% XP_002025124.1 uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura 558 558 73% 3e-177 70% XP_015041258.1 pseudoobscura] uncharacterized protein Dvir_GJ16545, 555 555 555 58% 5e-177 79% XP_015025478.1	isoform C [Drosophila pseudoobscura	573	573	73%	0.0	71%	XP_001355576.3
isoform I [Drosophila ananassae] uncharacterized protein Dana_GF20837, isoform G [Drosophila ananassae] GL26876 [Drosophila persimilis] uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura pseudoobscura] uncharacterized protein Dvir_GJ16545, 555 555 58% 58% 58% 58% 58% 58% 58% 58%	isoform L [Drosophila pseudoobscura	573	573	73%	0.0	71%	XP_015041267.1
isoform G [Drosophila ananassae] GL26876 [Drosophila persimilis] 569 569 74% 0.0 68% XP_002025124.1 uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura 558 558 73% 3e-177 70% XP_015025478.1 pseudoobscura] uncharacterized protein Dvir_GJ16545, 555 58% 58% 58% 58% 58% 58% 58%	·	569	569	58%	0.0	81%	XP_014760974.1
uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura 558 558 73% 3e-177 70% XP_015041258.1 pseudoobscura] uncharacterized protein Dvir_GJ16545, 555 58% 5e-177 79% XP_015025478.1	·	569	569	58%	0.0	81%	XP_014760972.1
isoform B [Drosophila pseudoobscura 558 558 73% 3e-177 70% XP_015041258.1 pseudoobscura] uncharacterized protein Dvir_GJ16545, 555 58% 5e-177 79% XP_015025478.1	GL26876 [Drosophila persimilis]	569	569	74%	0.0	68%	XP_002025124.1
- 550 55% 56% 56-177 79% XP 015025478.1	isoform B [Drosophila pseudoobscura	558	558	73%	3e-177	70%	XP_015041258.1
	• = •	555	555	58%	5e-177	79%	XP_015025478.1

uncharacterized protein Dvir_GJ16545, isoform F [Drosophila virilis]	555	555	58%	1e-176	79%	XP_002057080.2
uncharacterized protein Dvir_GJ16545, isoform E [Drosophila virilis]	555	555	58%	1e-176	79%	XP_015025481.1
uncharacterized protein Dpse_GA16131, isoform H [Drosophila pseudoobscura pseudoobscura]	558	558	73%	1e-176	70%	XP_015041263.1
uncharacterized protein Dvir_GJ16545, isoform D [Drosophila virilis]	554	554	58%	1e-176	79%	XP_015025480.1
uncharacterized protein Dvir_GJ16545, isoform C [Drosophila virilis]	554	554	58%	2e-176	79%	XP_015025479.1
uncharacterized protein Dwil_GK25837, isoform C [Drosophila willistoni]	542	542	58%	5e-172	81%	XP_002071502.2
uncharacterized protein Dwil_GK25837, isoform B [Drosophila willistoni]	543	543	58%	5e-172	81%	XP_015032709.1
C3G [Drosophila busckii]	515	515	58%	1e-164	77%	ALC49227.1
uncharacterized protein Dpse_GA16131, isoform K [Drosophila pseudoobscura pseudoobscura]	521	521	69%	7e-164	70%	XP_015041266.1
GM12551 [Drosophila sechellia]	485	578	44%	3e-159	98%	XP_002036724.1
uncharacterized protein Dvir_GJ16545, isoform G [Drosophila virilis]	501	501	54%	7e-158	77%	XP_015025477.1
GD16179 [Drosophila simulans]	466	466	53%	4e-153	96%	XP_002106330.1
uncharacterized protein Dmoj_Gl21607, isoform F [Drosophila mojavensis]	446	623	54%	2e-135	89%	XP_015016529.1
uncharacterized protein Dmoj_Gl21607, isoform B [Drosophila mojavensis]	447	624	54%	2e-135	89%	XP_015016526.1
uncharacterized protein Dmoj_Gl21607, isoform C [Drosophila mojavensis]	446	581	51%	4e-135	89%	XP_015016527.1
uncharacterized protein Dmoj_Gl21607, isoform D [Drosophila mojavensis]	445	580	51%	7e-135	89%	XP_015016528.1
uncharacterized protein Dmoj_Gl21607, isoform G [Drosophila mojavensis]	446	623	54%	9e-135	89%	XP_015016530.1
uncharacterized protein Dmoj_Gl21607, isoform H [Drosophila mojavensis]	446	623	54%	9e-135	89%	XP_015016531.1
uncharacterized protein Dmoj_Gl21607, isoform E [Drosophila mojavensis]	446	623	54%	9e-135	89%	XP_002010627.2
GH24527 [Drosophila grimshawi]	438	563	60%	3e-132	89%	XP_001992006.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X4 [Bactrocera dorsalis]	347	347	57%	2e-100	53%	XP_011207149.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X1 [Ceratitis capitata]	347	347	57%	5e-100	54%	XP_012158749.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X2 [Bactrocera dorsalis]	347	347	57%	6e-100	54%	XP_011207145.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X2 [Ceratitis capitata]	347	347	57%	8e-100	54%	XP_012158750.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X1 [Bactrocera dorsalis]	345	345	57%	1e-99	54%	XP_011207144.1
PREDICTED: guanine nucleotide- releasing factor 2-like [Musca domestica]	342	342	67%	1e-98	52%	XP_005190354.2
PREDICTED: guanine nucleotide- releasing factor 2 isoform X3 [Bactrocera	340	340	57%	8e-98	54%	XP_011207148.1

dorsalis]						
PREDICTED: guanine nucleotide- releasing factor 2 isoform X2 [Bactrocera oleae]	336	336	58%	2e-96	53%	XP_014101604.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X1 [Bactrocera oleae]	335	335	58%	4e-96	53%	XP_014101596.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X4 [Ceratitis capitata]	329	399	49%	8e-94	61%	XP_012158752.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X3 [Ceratitis capitata]	329	399	49%	1e-93	61%	XP_004529495.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X5 [Ceratitis capitata]	328	398	49%	1e-93	61%	XP_012158753.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X5 [Bactrocera cucurbitae]	318	391	49%	3e-90	60%	XP_011177585.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X6 [Bactrocera cucurbitae]	317	390	49%	3e-90	60%	XP_011177586.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X4 [Bactrocera cucurbitae]	318	392	49%	3e-90	60%	XP_011177584.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X3 [Bactrocera cucurbitae]	318	391	49%	4e-90	60%	XP_011177583.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X1 [Bactrocera cucurbitae]	318	391	49%	5e-90	60%	XP_011177581.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X2 [Bactrocera cucurbitae]	318	391	49%	6e-90	60%	XP_011177582.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X2 [Stomoxys calcitrans]	309	309	38%	3e-87	60%	XP_013109512.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X1 [Stomoxys calcitrans]	309	309	38%	4e-87	60%	XP_013109510.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X4 [Stomoxys calcitrans]	308	308	38%	5e-87	60%	XP_013109514.1
AAEL013817-PA [Aedes aegypti]	278	278	54%	1e-76	43%	XP_001664011.1
PREDICTED: guanine nucleotide- releasing factor 2 isoform X3 [Stomoxys calcitrans]	267	267	34%	6e-73	59%	XP_013109513.1
guanine-nucleotide exchange factor c3g [Culex quinquefasciatus]	263	263	54%	5e-71	40%	XP_001869397.1
AGAP000932-PA [Anopheles gambiae str. PEST]	251	292	43%	5e-67	51%	XP_309117.5
PREDICTED: guanine nucleotide- releasing factor 2-like isoform X2 [Apis dorsata]	201	201	53%	3e-50	39%	XP_006608566.1
PREDICTED: guanine nucleotide- releasing factor 2-like isoform X4 [Apis dorsata]	201	201	53%	3e-50	39%	XP_006608568.1
PREDICTED: guanine nucleotide- releasing factor 2-like isoform X3 [Apis dorsata]	201	201	53%	3e-50	39%	XP_006608567.1

□ <u>Alignments</u>

C3G ortholog, isoform F [Drosophila melanogaster]

Sequence ID: ref|NP_001138168.1| Length: 1468 Number of Matches: 1

▶ See 1 more title(s) Range 1: 157 to 676

Score		Expect Method	Identities	Positives	Gaps	Frame
769 bits	(1985)	0.0() Compositional matrix adjust	. 520/520(100%	%) 520/520(100%	%) 0/520(0%)	+2
Features	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI				
Sbjct	157	HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVIL RSTOTLETHVKDISNALKHFRDVIL				
Sbjct	217	RSTQTLETHVKDISNALKHFRDVIL				
Query	797	IMSSATLQVYQSLGKLIKLCDEVML IMSSATLQVYQSLGKLIKLCDEVML				
Sbjct	277	IMSSATLQVYQSLGKLIKLCDEVML				
Query	977	KLKEQDQCAFRYsgsglggigaaae KLKEQDQCAFRYSGSGLGGIGAAAE				
Sbjct	337	KLKEQDQCAFRYSGSGLGGIGAAAE				
Query	1157	IALTPKERDILEQHNVNPMRGSHST IALTPKERDILEQHNVNPMRGSHST	ESILRDTspppl	kpplpnrasnpp	plppkrrsqp	sa 1336
Sbjct	397	IALTPKERDILEQHNVNPMRGSHST				
Query	1337	sagtvgvgcssststsnqasPLPYA SAGTVGVGCSSSTSTSNQASPLPYA	OSHNISLNSDLI OSHNISLNSDLI	DCSSNISLLNYG DCSSNISLLNYG	VDRLSVRSRS	SPD 1516
Sbjct	457	SAGTVGVGCSSSTSTSNQASPLPYA				
Query	1517	ENSQCSFDSALNHSREEEDqqqqhq ENSQCSFDSALNHSREEEDQQQQHQ				
Sbjct	517	ENSQCSFDSALNHSREEEDQQQQHQ				
Query	1697	tgggiagvaggtggagegvaaaasg TGGGIAGVAGGTGGAGEGVAAAASG	dgeTNSNRHSNI	ESGFVSMREFRT	STOTTDYsvo	ss 1876
Sbjct	577	TGGGIAGVAGGTGGAGEGVAAAASG				
Query	1877	tkssssnseiafsisesTAVGSSSE TKSSSSNSEIAFSISESTAVGSSSE	YQQISQLVSHSQ YQQISQLVSHSQ	ORHI 1996 ORHI		
Sbjct	637	TKSSSSNSEIAFSISESTAVGSSSE				

C3G ortholog, isoform H [Drosophila melanogaster]

Sequence ID: ref|NP_572350.2| Length: 1571 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
768 bits	(1982)	0.0() Compositional matrix adjust.	520/520(100%)	520/520(100%	0) 0/520(0%)	+2
Feature	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKIS HKNSLKGTKLARRARSFKDDLIEKIS				
Sbjct	260	HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVILI RSTQTLETHVKDISNALKHFRDVILI				
Sbjct	320	RSTQTLETHVKDISNALKHFRDVILI				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLS IMSSATLQVYQSLGKLIKLCDEVMLS				
Sbjct	380	IMSSATLQVYQSLGKLIKLCDEVML				
Query	977	KLKEQDQCAFRYsgsglggigaaae: KLKEQDQCAFRYSGSGLGGIGAAAE:				
Sbjct	440	KLKEQDQCAFRYSGSGLGGIGAAAE				
Query	1157	IALTPKERDILEQHNVNPMRGSHSTI IALTPKERDILEQHNVNPMRGSHSTI	ESILRDTspppk	oplpnrasnppr	lppkrrsqp	sa 1336
Sbjct	500	IALTPKERDILEQHNVNPMRGSHSTI				

Query	1337	sagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	1516
Sbjct	560	SAĞTVĞVĞCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	619
Query	1517	ENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPLs	1696
Sbjct	620	ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPLS ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPLS	679
Query	1697	tgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqss	1876
Sbjct	680	TĞĞĞIAĞVAĞĞTĞĞAĞEĞVAAAASĞDĞETNSNRHSNESGFVSMREFRTSTQTTDYSVQSS TGGGIAGVAGGTGGAGEGVAAAASGDGETNSNRHSNESGFVSMREFRTSTQTTDYSVQSS	739
Query	1877	tkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996	
Sbjct	740	TKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI TKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI 779	

RE10624p [Drosophila melanogaster]

Sequence ID: gb|AAQ22488.1| Length: 1506 Number of Matches: 1

Range 1: 260 to 779

Score		Expect	Method		Identities	Positives	Gaps	Frame
766 bits((1978)	0.0()	Composition	nal matrix adjust.	519/520(99%)	519/520(99%)	0/520(0%)	+2
Features	S:							
Query	437			ARSFKDDLIEKIS ARSFKDDLIEKIS				
Sbjct	260			ARSFKDDLIEKIS				
Query	617			SNALKHFRDVILK SNALKHFRDVILK				
Sbjct	320			SNALKHFRDVILK SNALKHFRDVILK				
Query	797			GKLIKLCDEVMLS GKLIKLCDEVMLS				
Sbjct	380			KLIKLCDEVMLS				
Query	977	KLKE(ODOCAFRYS	gsglggigaaaei SSGLGGIGAAAEI	mgaVTASPGASV	PGTGVMRVSAA	ESAAQRTSI	PD 1156
Sbjct	440			SGLGGIGAAAEI SSGLGGIGAAAEI				
Query	1157	IALT]	PKERDILEQI	INVNPMRGSHSTE INVNPMRGSHSTE	SILRDTspppkp	plpnrasnppp	lppkrrsqp	sa 1336
Sbjct	500			INVNPMRGSHSTE INVNPMRGSHSTE				
Query	1337	sagt	vgvgcsssts	stsnqasPLPYAQ STSNQASPLPYAQ	SHNISLNSDLDC	SSNISLLNYGV	DRLSVRSRS	PD 1516
Sbjct	560			STSNQASPLPYAQ STSNQASPLPYAQ				
Query	1517	ENSO	CSFDSALNHS	SREEEDqqqqhqh SREEEDQQQQHQH	LRSFPKLAAMMD	EDMDKMVSYSA	AIDDKTQTP	Ls 1696
Sbjct	620			SREEEDQQQQHQH SREEEDQQQQQHQH				
Query	1697	tggg:	iagvaggtgo	gagegvaaaasgd SAGEGVAAAASGD	geTNSNRHSNES	GFVSMREFRTS	TOTTDYSVO	ss 1876
Sbjct	680			GAGEGVAAAASGD GAGEGVAAAASGD				
Query	1877			LSESTAVGSSSEY				
Sbjct	740			ISESTAVGSSSEY ISESTAVGSSSEY				

C3G ortholog, isoform I [Drosophila melanogaster]

Sequence ID: ref|NP_001259291.1| Length: 1414 Number of Matches: 1

See 1 more title(s) Range 1: 97 to 622

Score		Expect	Method	Identities	Positives	Gaps	Fram	e
761 bits(1965)	0.0()	Compositional matrix adjust.	519/526(99%)	519/526(98%)	6/526(1%)	+2	
Features	:							
Query	437		LKGTKLARRARSFKDDLIEKISI LKGTKLARRARSFKDDLIEKISI					616
Sbjct	97		LKGTKLARRARSFKDDLIEKISI					156
Query	617		TLETHVKDISNALKHFRDVILKF TLETHVKDISNALKHFRDVILKF					796
Sbjct	157		TLETHVKDISNALKHFRDVILK					216
Query	797	IMSS	ATLQVYQSLGKLIKLCDEVMLSE	EDSGECASLSNE	NVREVIDLLED.	AVRNLVTLA	.QG	976

Sbjct	217	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG	276
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQRTSLPD KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGASVPGTGVMRVSAAESAAQRTSLPD	1156
Sbjct	277	KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGASVPGTGVMRVSAAESAAQRTSLPD	336
Query	1157	IALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppkrrsqpsa	1336
Sbjct	337	IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPSA IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPSA	396
Query	1337	sagtvgvgcssststsngasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	1516
Sbjct	397	SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	456
Query	1517	ENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDK ENSOCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSY AAIDDK	1678
Sbjct	457	ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSY AAIDDK ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYKSTGYAGAAIDDK	516
Query	1679	TQTPLstgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTD	1858
Sbjct	517	TQTPLSTGGGIAGVAGGTGGAGEGVAAAASGDGETNSNRHSNESGFVSMREFRTSTQTTD TQTPLSTGGGIAGVAGGTGGAGEGVAAAASGDGETNSNRHSNESGFVSMREFRTSTQTTD	576
Query	1859	YsvqsstkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996	
Sbjct	577	YSVQSSTKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI YSVQSSTKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI 622	

LOW QUALITY PROTEIN: uncharacterized protein Dsimw501_GD16179 [Drosophila simulans]

Sequence ID: gb|KMZ08542.1| Length: 1559 Number of Matches: 1

Range 1: 280 to 799

Score		Expect	Method	Identities	Positives	Gaps	Frame
748 bits	(1932)	0.0()	Compositional matrix adjust.	502/520(97%)	504/520(96%)	0/520(0%)	+2
Features	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS				
Sbjct	280		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILKI				
Sbjct	340	RSTQ:	TLETHVKDISNALKHFRDVILKI TLETHVKDISNALKHFRDVILKI	KKLEVLPGNGTV KKLEVLPGNGTV	TLETIASMYSV	IQTYTLNEN	SA SA 399
Query	797		ATLQVYQSLGKLIKLCDEVMLSI				
Sbjct	400		AT QVYQSLGKLIKLCDEVMLSI ATQQVYQSLGKLIKLCDEVMLSI				
Query	977		QDQCAFRYsgsglggigaaaeir				
Sbjct	460		ODOCAFRYSĞSĞLĞĞIĞAAAEII QDQCAFRYSGSGLGGIGAAAEII				
Query	1157	IALT]	PKERDILEQHNVNPMRGSHSTE: PKERDILEQHNVNPMRGSHSTE:	SILRDTspppkp	plpnrasnppp	lppkrrsqp	sa 1336
Sbjct	520	IALT	PKERDILEQHNVNPMRGSHSTE:	SILRDTSPPPKP	PLPNRASNPPP:	LPPKRRSQP LPPKRRSQP	GA 579
Query	1337		vgvgcssststsnqasPLPYAQ				
Sbjct	580		VĞVĞCSSSTSTSNQASPLPYAQ: VGVGCSSSTSTSNQASPLPYAQ:				
Query	1517	ENSO	CSFDSALNHSREEEDqqqqhqhl	LRSFPKLAAMMD	EDMDKMVSYSA	AIDDKTQTP	Ls 1696
Sbjct	640		CSFDSALNHSREEED QQQ QHI CSFDSALNHSREEEDHQQQQQHI				
Query	1697	tggg:	iagvaggtggagegvaaaasgd	geTNSNRHSNES	GFVSMREFRTS'	TOTTDYsvq	ss 1876
Sbjct	700		+AĞV ĞĞTĞĞA EĞ AAAASĞ VAGVTGGTGGAAEGAAAAASGGI				
Query	1877		ssnseiafsisesTAVGSSSEY				
Sbjct	760		SSNSEIAFSISESTAVGSSSEY SSNSEIAFSISESTAVGSSSEY				

uncharacterized protein Dere_GG17655, isoform B [Drosophila erecta] Sequence ID: **ref|XP_015010608.1**| Length: 1470 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps	Frame
716 bits(1847)	0.0()	Compositional matrix adjust.	481/526(91%)	489/526(92%)	6/526(1%)	+2
Features:						

Query	437	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGTKAPPTTEEVL	616
Sbjct	160	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHG+KAPPTTEEV HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGSKAPPTTEEVQ	219
Query	617	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA	796
Sbjct	220	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA	279
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG	976
Sbjct	280	IMS AT QVYQSLGKLIKLCDEVMLSEDSGEC SLSNENVREVIDLLEDAVRNLVTLAQG IMSCATQQVYQSLGKLIKLCDEVMLSEDSGECPSLSNENVREVIDLLEDAVRNLVTLAQG	339
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQRTSLPD	1156
Sbjct	340	KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPG SVPG G+MRVSAAESAAQRTSLPD KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGVSVPGAGIMRVSAAESAAQRTSLPD	399
Query	1157	IALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppkrrsqpsa	1336
Sbjct	400	IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQP A IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPGA	459
Query	1337	sagtvgvgc-ssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSP	1513
Sbjct	460	SAG SSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSP SAGAGSGIGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSP	519
Query	1514	DENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQ DENSQCSFDSALNHSREEED QQQQ Q LRSFPK+ AMMDEDMDK+VSYSAAI+DK Q	1684
Sbjct	520	DENSQCSFDSALNHSREEED QQQQ Q LRSFPK+ AMMDEDMDK+VSYSAAI+DK Q DENSQCSFDSALNHSREEEDHHHQQQQQQQLRSFPKMPAMMDEDMDKLVSYSAAIEDKMQ	579
Query	1685	TPLstgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTD	1858
Sbjct	580	TPL GG GV GGTGGA EG AAAA+G GETNSNR SNESGFVSMREFRTSTQTTD TPLPTGGVGGGGGVVGGTGGAVEGAAAAATGGGETNSNRLSNESGFVSMREFRTSTQTTD	639
Query	1859	YsvqsstkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996	
Sbjct	640	YS+QSSTKSSSSNS+IAFSISESTAVGSS EYQQISQ V HSQR I YSIQSSTKSSSSNSDIAFSISESTAVGSSGEYQQISQSVLHSQRQI 685	

C3G ortholog, isoform D [Drosophila melanogaster]

Sequence ID: ref|NP_001138166.1| Length: 1285 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 493

Score		Expect	Method		Identities	Positives	Gaps	Frame
714 bits	(1844)	0.0()	Compositiona	al matrix adjust.	493/493(100	%) 493/493(100%	%) 0/493(0%) +2
Features	S :							
Query	518					TOTLETHVKDISN		
Sbjct	1					TOTLETHVKDISN TOTLETHVKDISN		
Query	698					SSATLQVYQSLGK SSATLQVYQSLGK		
Sbjct	61					SSATLÖV TÖSLGK SSATLÖVYÖSLGK		
Query	878	DSGE	CASLSNENVR	EVIDLLEDAVRI	NLVTLAQGKLI JI.VTI.AQGKI.R	KEQDQCAFRYsgs KEQDQCAFRYSGS	glggigaaa	eim 1057 ETM
Sbjct	121					KEQDQCAFRYSGS		
Query	1058					TPKERDILEQHN TPKERDILEQHN		
Sbjct	181					LTPKERDILEÕHN		
Query	1238	ILRD	Tspppkpplp	nrasnppplpp NRASNPPPLPP	rrsqpsasac	gtvgvgcssstst TVGVGCSSSTST	sngasPLPY	AQS 1417
Sbjct	241					TVGVGCSSSTST		
Query	1418					SQCSFDSALNHSR SQCSFDSALNHSR		
Sbjct	301					SÕCSFDSALNHSR		
Query	1598	RSFP RSFP	KLAAMMDEDM	DKMVSYSAAIDI DKMVSYSAAIDI	OKTOTPLStgo	ggiagvaggtgga GGIAGVAGGTGGA	gegvaaaas GEGVAAAAS	gdg 1777
Sbjct	361	RSFP	KLAAMMDEDM	DKMVSYSAAIDI	OKTÕTPLSTGO	GIAGVAGGTGGA	GEGVAAAAS	GDG 420
Query	1778					ssssnseiafsis SSSSNSEIAFSIS		
Sbjct	421					SSSNSEIAFSIS		
Query	1958		LVSHSQRHI LVSHSQRHI	1996				
Sbjct	481		LVSHSQRHI	493				

Sequence ID: ref|XP_015045493.1| Length: 1460 Number of Matches: 1

▶ See 1 more title(s) Range 1: 155 to 668

Score		Expect Method	Identities	Positives	Gaps	Frame			
714 bits	(1843)	0.0() Compositional matrix adjust.	476/521(91%)	484/521(92%)	8/521(1%)	+2			
Features:									
Query	437	HKNSLKGTKLARRARSFKDDLIEKIS: HKNSLKGTKLARRARSFKDDLIEKIS:							
Sbjct	155	HKNSLKGTKLARRARSFKDDLIEKIS:							
Query	617	RSTQTLETHVKDISNALKHFRDVILK RSTQTLETHVKDISNALKHFRDVILK							
Sbjct	215	RSTQTLETHVKDISNALKHFRDVILK.							
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLS: IMS AT QVYQSLGKLIKLCDEVMLS:							
Sbjct	275	IMSCATQQVYQSLGKLIKLCDEVMLS							
Query	977	KLKEQDQCAFRYsgsglggigaaaeir KLKEQDQCAFRY GSGLGGIGAAAEI							
Sbjct	335	KLKEQDQCAFRYGGSGLGGIGAAAEI							
Query	1157	IALTPKERDILEQHNVNPMRGSHSTE							
Sbjct	395	IALTPKERDILEÕHNVNPMRGSHSTE							
Query	1337	sagtvgvgcssststsnqasPLPYAQ AG VGCSS TS S YAO	SHNISLNSDLDC HNISLN DLDC						
Sbjct	455	PAGAAVVGCSSLTSASYAQ							
Query	1517	ENSQCSFDSALNHSREEED-qqqqhq ENSQCSFDSALNHSREEED QQQQ Q		IDEDMDKMVSYS IDEDMDKMVSYS					
Sbjct	508	ENSQCSFDSALNHSREEEDHQQQQQQQ							
Query	1694	stgggiagvaggtggagegvaaaasg +TGG GV GGTGGA EG AAAA+G							
Sbjct	568	ATGGVGGGVVGGTGGAAEGAAAAATG							
Query	1874	stkssssnseiafsisesTAVGSSSE STKSSSSNSEIAFSISESTAVGSSSE							
Sbjct	628	STKSSSSNSEIAFSISESTAVGSSSE STKSSSSNSEIAFSISESTAVGSSSE							

uncharacterized protein Dere_GG17655, isoform A [Drosophila erecta]
Sequence ID: ref|XP_001978483.1| Length: 1575 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
714 bits	(1843)	0.0()	Compositional matrix adjust.	481/526(91%)	489/526(92%)	6/526(1%)	+2
Features	S :						
Query	437		LKGTKLARRARSFKDDLIEKISI LKGTKLARRARSFKDDLIEKISI				
Sbjct	265		LKGTKLARRARSFKDDLIEKISI LKGTKLARRARSFKDDLIEKISI				
Query	617		TLETHVKDISNALKHFRDVILKI TLETHVKDISNALKHFRDVILKI				
Sbjct	325		TLETHVKDISNALKHFRDVILKI				
Query	797		ATLQVYQSLGKLIKLCDEVMLSI AT OVYOSLGKLIKLCDEVMLSI				
Sbjct	385		ATQQVYQSLGKLIKLCDEVMLSI				
Query	977		QDQCAFRYsgsglggigaaaein QDQCAFRYSGSGLGGIGAAAEIN				
Sbjct	445		DDOCAFRISGSGLGGIGAAAEIN DDOCAFRYSGSGLGGIGAAAEIN				
Query	1157	IALT]	PKERDILEQHNVNPMRGSHSTES PKERDILEQHNVNPMRGSHSTES	SILRDTspppkp	plpnrasnppp	lppkrrsqp	sa 1336
Sbjct	505		PKERDILEQHNVNPMRGSHSTES				
Query	1337	sagt SAG	vgvgc-ssststsnqasPLPYAÇ SSSTSTSNQASPLPYAÇ				
Sbjct	565		GSGIGCSSSTSTSNQASPLPYAÇ				
Query	1514		QCSFDSALNHSREEEDqqqq QCSFDSALNHSREEED 0000				
Sbjct	625		QCSFDSALNHSREEEDHHHQQQ(QCSFDSALNHSREEEDHHHQQQ(Q Q LRSFPK+ QQQQLRSFPKMP			
Query	1685		-stgggiagvaggtggagegvaa	aaasgdgeTNSN	RHSNESGFVSM	REFRTSTOT	TD 1858
Sbjct	685	$ ext{TPL}$	ĞĞ ĞV ĞĞTĞĞA EĞ A <i>I</i> IGGVGGGGGVVGGTGGAVEGAA <i>I</i>				

Query 1859 YsvqsstkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996 YS+QSSTKSSSSNS+IAFSISESTAVGSS EYQQISQ V HSQR I Sbjct 745 YSIQSSTKSSSSNSDIAFSISESTAVGSSGEYQQISQSVLHSQRQI 790

C3G, isoform A [Drosophila yakuba]

Sequence ID: ref|XP_002099940.1| Length: 1567 Number of Matches: 1

▶ See 1 more title(s) Range 1: 262 to 775

					-	Frame
1841)	0.0()	Compositional matrix adjust.	476/521(91%)	484/521(92%)	8/521(1%)	+2
:						
437						
262	HKNS	LKGTKLARRARSFKDDLIEKISI	LMRTTNNTLGRS	HSPHSPRTKHG	SKAPPTTEE	V VQ 321
617	RSTO	TLETHVKDISNALKHFRDVILKI	KKLEVLPGNGTV	ILETIASMYSV	IOTYTLNEN	ISA 796
322	RSTQ:	TLETHVKDISNALKHFRDVILKI	KKLEVLPGNGTV KKLEVLPGNGTV	TLETTASMISV	IQTYTLNEN	ISA 381
797						
382						
977						
442						
1157	IALT]	PKERDILEQHNVNPMRGSHSTES	SILRDTspppkp	plpnrasnppp	lppkrrsqp	sa 1336
502						
1337						
562		AVVGCSSLTSASYAÕI	PHNISLNLDLDC	SSNISLLNYGV	DRLSVRSRS	SPD 614
1517						
615						
1694						
675						
1874						
735						
	437 262 617 322 797 382 977 442 1157 502 1337 562 1517 615 1694 675 1874	437 HKNST 617 RSTQ RSTQ 322 RSTQ 797 IMSS IMS IMS IMS IMS IMS IMS IMS IMS IMS	HKNSLKGTKLARRARSFKDDLIEKISI HKNSLKGTKLARRARSFKDDLIEKISI 162 HKNSLKGTKLARRARSFKDDLIEKISI 163 RSTQTLETHVKDISNALKHFRDVILKI RSTQTLETHVKDISNALKHFRDVILKI RSTQTLETHVKDISNALKHFRDVILKI RSTQTLETHVKDISNALKHFRDVILKI RSTQTLETHVKDISNALKHFRDVILKI RSTQTLETHVKDISNALKHFRDVILKI RSTQTLETHVKDISNALKHFRDVILKI RSTQTLETHVKDISNALKHFRDVILKI RSATLQVYQSLGKLIKLCDEVMLSI IMS AT QVYQSLGKLIKLCDEVMLSI IMS AT QVYQSLGKLIKLCDEVMLSI RKLKEQDQCAFRYSGSGLGGIGAAAEIN KLKEQDQCAFRYGGSGLGGIGAAAEIN KLKEQDQCAFRYGGSGLGGIGAAAEIN KLKEQDQCAFRYGGSGLGGIGAAAEIN LTPKERDILEQHNVNPMRGSHSTES IALTPKERDILEQHNVNPMRGSHSTES IALTPKERDILEQHNVNPMRGSHSTES IALTPKERDILEQHNVNPMRGSHSTES IALTPKERDILEQHNVNPMRGSHSTES IALTPKERDILEQHNVNPMRGSHSTES IALTPKERDILEQHNVNPMRGSHSTES IALTPKERDILEQHNVNPMRGSHSTES IALTPKERDILEQHNVNPMRGSHSTES ISSQCSFDSALNHSREEED-qqqqhql ENSQCSFDSALNHSREEED-qqqqhql ENSQCSFDSALNHSREEED-qqqqhql ENSQCSFDSALNHSREEED-qqqqhql ENSQCSFDSALNHSREEED-qqqqhql ENSQCSFDSALNHSREEED-qqqqhql ENSQCSFDSALNHSREEED-qqqqhql THGG GV GGTGGA EG AAAA+G TGG GV GGTGGA EG AAAA+G	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRS HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRS HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRS HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRS 617 RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV RSTOTLETHVKDISNALKHFRDVILKKKLEVLPGNGTV 797 IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNE IMS AT QVYQSLGKLIKLCDEVMLSEDSGECASLSNE 1MSCATQQVYQSLGKLIKLCDEVMLSEDSGECASLSNE RKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGSV KLKEQDQCAFRYGGSGLGGIGAAAEIMGAVTASPGSV KLKEQDQCAFRYGGSGLGGIGAAAEIMGAVTASPGSV KLKEQDQCAFRYGGSGLGGIGAAAEIMGAVTASPGVSV 1157 IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKP 1ALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKP 1337 SAGTVGVGCSSSTSSSSTSSILRDTSPPPKP 1337 SAGTVGVGCSSSTSSSSTSSILRDTSPPPKP 1337 SAGTVGVGCSSSTSSSSTSSILRDTSPPPKP 1517 ENSQCSFDSALNHSREEED-QQQQQQQLRSLSKMPTMM ENSQCSFDSALNHSREEED-QQQQQQQLRSLSKMPTMM 615 ENSQCSFDSALNHSREEEDHQQQQQQQQLRSLSKMPTMM 615 ENSQCSFDSALNHSREEEDHQQQQQQQQLRSLSKMPTMM 616 STKSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQ STKSSSSNSEIAFSISESTAVGSSSEYQQISQVSHSQ STKSSSSNSEIAFSISESTAVGSSSEYQQISQVSHSQ STKSSSSNSEIAFSISESTAVGSSSEYQQISQVSHSQ STKSSSSNSEIAFSISESTAVGSSSEYQQISQVSHSQ STKSSSSNSEIAFSISESTAVGSSSEYQQISQVSHSQ	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHG- HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPHTKHG- HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPHSPHTKHG- HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPSPHTKHG- HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSTSILAMYSV- RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILLETIASMYSV- RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILLETIASMYSV- RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILLETIASMYSV- RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILLETIASMYSV- RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVEVILLED- HMS AT QVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLED- RKLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGSVPGTGVMRVSAA- KLKEQDQCAFRYGGSGLGGIGAAAEIMGAVTASPGSVPGTGVMRVSAA- KLKEQDQCAFRYGGSGLGGIGAAAEIMGAVTASPGSVPGTGMRVSAA- KLKEQDQCAFRYGGSGLGGIGAAAEIMGAVTASPGVSVPGTGIMRVSAA- KLKEQDQCAFRYGGSGLGGIGAAAEIMGAVTASPGVSVPGTGIMRVSAA- HLTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPP- DIALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPP- BAGAVVGCSS TS S YAQ HNISLN DLDCSSNISLLNYGV- AG VGCSS TS S YAQ HNISLNSDLDCSSNISLNYGV- AG VGCSS TS S YAQ HNISLNSDLDCSSNISLNYGV	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGTKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGKAPPTTEE HKNSLKGTKLARRAFSFKDDLIEKISLLMRTTNNTLGRSHSPHSPHTKHGKKAPPTTEE HKNSLKGTKLARRAFSFKDDLIEKISLLMKHGSHSPTILETIASMYSVIQTYTLNEN RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNEN RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNEN RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNEN 1MS AT QVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLA 1MS AT QVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLEDAVRNLVTLA 1MS AT QVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLEDAVRNLVTLA 1MS AT QVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLEDAVRNLVTLA 1MS AT QVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLEDAVRNLVTLA 1MS AT QVYQSLGKLIKLCDEVMLSEDSGECASLS 1157 1ALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRSOP 1ALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRSOP 1ALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRSOP 1ALTPKERDLEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRSOP 1ALTPKERDILEQHNV

C3G ortholog, isoform E [Drosophila melanogaster]

Sequence ID: ref|NP_001138167.1| Length: 1417 Number of Matches: 1

Score		Expect	Method		Identities	Positives	Gaps	Frame	
712 bits	(1837)	0.0()	Composition	nal matrix adjust.	469/520(90%)	469/520(90%)	51/520(9%)	+2	
Features:									
Query	437			ARSFKDDLIEKIS ARSFKDDLIEKIS	, , _ , _ , _ , _ , _ , _ , _ , _ ,				
Sbjct	157			ARSFKDDLIEKIS					
Query	617			SNALKHFRDVILI SNALKHFRDVILI					
Sbjct	217			SNALKHFRDVILI SNALKHFRDVILI					
Query	797			GKLIKLCDEVMLS GKLIKLCDEVMLS					
Sbjct	277			GKLIKLCDEVMLS					
Query	977			gsglggigaaaei GSGLGGIGAAAEI					
Sbjct	337		~ ~	GSGLGGIGAAAE1			~		
Query	1157	IALT	PKERDILEQ	HNVNPMRGSHSTE HNVNPMRGSHSTE	ESILRDTspppk	oplpnrasnpp	plppkrrsqp	sa 1336	
Sbjct	397			HNVNPMRGSHSTE					

Query	1337	sagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	1516
Sbjct	457	SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	516
Query	1517	ENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPLS ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYS	1696
Sbjct	517	ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYS	564
Query	1697	tgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqss FVSMREFRTSTQTTDYSVQSS	1876
Sbjct	565	FVSMREFRTSTQTTDYSVQSS	585
Query	1877	tkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996	
Sbjct	586	TKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI TKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI 625	

IP03271p [Drosophila melanogaster]

Sequence ID: gb|ABF85718.1| Length: 1416 Number of Matches: 1

Range 1: 156 to 624

Score		Expect	Method	Identities	Positives	Gaps	Frame
712 bits	(1837)	0.0()	Compositional matrix adjust.	469/520(90%)	469/520(90%)	51/520(9%)	+2
Features	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS				
Sbjct	156		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK				
Sbjct	216		TLETHVKDISNALKHFRDVILK				
Query	797		ATLQVYQSLGKLIKLCDEVMLS ATLOVYOSLGKLIKLCDEVMLS				
Sbjct	276		ATLOVIOSLGKLIKLEDEVMLS				
Query	977	KLKE	QDQCAFRYsgsglggigaaaei QDQCAFRYSGSGLGGIGAAAEI	mgaVTASPGAS	VPGTGVMRVSA	AESAAQRTSLI	PD 1156
Sbjct	336		QDQCAFRYSGSGLGGIGAAAEI QDQCAFRYSGSGLGGIGAAAEI				
Query	1157	IALT	PKERDILEQHNVNPMRGSHSTE PKERDILEQHNVNPMRGSHSTE	SILRDTspppk	pplpnrasnpp	plppkrrsqps	sa 1336
Sbjct	396		PKERDILEQHNVNPMRGSHSTE				
Query	1337		.vgvgcssststsnqasPLPYAQ VGVGCSSSTSTSNQASPLPYAQ				
Sbjct	456		VGVGCSSSTSTSNQASPLPYAQ				
Query	1517	ENSO	CSFDSALNHSREEEDqqqqhqh CSFDSALNHSREEEDQQQQHQH	LRSFPKLAAMM	DEDMDKMVSYS	AAIDDKTQTPI	Ls 1696
Sbjct	516		CSFDSALNHSREEEDQQQQHQH				563
Query	1697	tggg	iagvaggtggagegvaaaasgd	lgeTNSNRHSNE	SGFVSMREFRT	STQTTDYsvqs STQTTDYSVQS	ss 1876
Sbjct	564						
Query	1877		ssnseiafsisesTAVGSSSEY SSNSEIAFSISESTAVGSSSEY				
Sbjct	585		SSNSEIAFSISESTAVGSSSEY				

C3G ortholog, isoform L [Drosophila melanogaster]

Sequence ID: ref|NP_001284966.1| Length: 1357 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Fram	<u>e</u>
711 bits	(1835) (0.0()	Compositional matrix adjust.	469/520(90%)	469/520(90%)	51/520(9%)	+2	
Features:								
Query	437		LKGTKLARRARSFKDDLIEKIS					616
Sbjct	97		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS					156
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK					796
Sbjct	157		TLETHVKDISNALKHFRDVILK					216
Query	797		ATLQVYQSLGKLIKLCDEVMLS ATLQVYQSLGKLIKLCDEVMLS					976

Sbjct	217	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG	276
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQRTSLPD	1156
Sbjct	277	KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGASVPGTGVMRVSAAESAAQRTSLPD KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGASVPGTGVMRVSAAESAAQRTSLPD	336
Query	1157	IALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppkrrsqpsa	1336
Sbjct	337	IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPSA IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPSA	396
Query	1337	sagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	1516
Sbjct	397	SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	456
Query	1517	ENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPLs	1696
Sbjct	457	ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYS ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYS	504
Query	1697	tgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqss	1876
Sbjct	505	FVSMREFRTSTQTTDYSVQSS FVSMREFRTSTQTTDYSVQSS	525
Query	1877	tkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996	
Sbjct	526	TKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI TKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI 565	

C3G ortholog, isoform C [Drosophila melanogaster]

Sequence ID: ref|NP_788867.1| Length: 1520 Number of Matches: 1

▶ See 1 more title(s) Range 1: 260 to 728

Score		Expect	Method		Identities	Positives	Gaps	Frame
710 bits((1833)	0.0()	Compositional ma	trix adjust.	469/520(90%)	469/520(90%)	51/520(9%)	+2
Features	S:							
Query	437		LKGTKLARRARSFK LKGTKLARRARSFK					
Sbjct	260		LKGTKLARRARSFK LKGTKLARRARSFK					
Query	617		TLETHVKDISNALK TLETHVKDISNALK					
Sbjct	320		TLETHVKDISNALK					
Query	797		ATLQVYQSLGKLIK ATLQVYQSLGKLIK					
Sbjct	380		ATLŐVYŐSLGKLIK ATLŐVYŐSLGKLIK					
Query	977	KLKE	QDQCAFRYsgsglg QDQCAFRYSGSGLG	gigaaaei GTGAAAET	mgaVTASPGAS\	VPGTGVMRVSA	AESAAQRTSL	PD 1156
Sbjct	440		QDQCAFRYSGSGLG					
Query	1157	IALT	PKERDILEQHNVNP PKERDILEQHNVNP	MRGSHSTE	SILRDTspppk	oplpnrasnpp	plppkrrsqp	sa 1336
Sbjct	500		PKERDILEÕHNVNP					
Query	1337	sagt	vgvgcssststsnq VGVGCSSSTSTSNQ	asPLPYAQ	SHNISLNSDLD	CSSNISLLNYG	VDRLSVRSRS	PD 1516
Sbjct	560		VGVGCSSSTSTSNQ VGVGCSSSTSTSNQ					
Query	1517	ENSO	CSFDSALNHSREEE CSFDSALNHSREEE	Dooonon	LRSFPKLAAMMI	DEDMDKMVSYS	AAIDDKTQTP	Ls 1696
Sbjct	620		CSFDSALNHSREEE					667
Query	1697	tggg	iagvaggtggageg		_	EMCMDEEDT(\overline{C}	CC
Sbjct	668					FVSMREFRT	STÕTTDYSVÕ	SS 688
Query	1877	tkss	ssnseiafsisesT SSNSEIAFSISEST	AVGSSSEY	QQISQLVSHSQI	RHI 1996		
Sbjct	689		SSNSEIAFSISEST SSNSEIAFSISEST					

C3G ortholog, isoform K [Drosophila melanogaster]

Sequence ID: ref|NP_001259293.1| Length: 1468 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps	Frame
710 bits(1833)	0.0()	Compositional matrix adjust	469/520(90%)	469/520(90%)	51/520(9%)	+2

Features	8:		
Query	437	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGTKAPPTTEEVL	616
Sbjct	157	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGTKAPPTTEEVL HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGTKAPPTTEEVL	216
Query	617	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA	796
Sbjct	217	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMISVIQTYTLNENSA	276
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG	976
Sbjct	277	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG	336
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQRTSLPD KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGASVPGTGVMRVSAAESAAQRTSLPD	1156
Sbjct	337	KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGASVPGTGVMRVSAAESAAQRTSLPD	396
Query	1157	IALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppkrrsqpsa IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPSA	1336
Sbjct	397	IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPSA	456
Query	1337	sagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	1516
Sbjct	457	SAGTVGVGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD	516
Query	1517	ENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPLs ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYS	1696
Sbjct	517	ENSQCSFDSALNHSREEEDQQQQHQHLRSFPKLAAMMDEDMDKMVSYS	564
Query	1697	tgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqss FVSMREFRTSTQTTDYSVQSS	1876
Sbjct	565	FVSMREFRTSTQTTDYSVQSS	585
Query	1877	tkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996 TKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI	
Sbjct	586	TKSSSSNSEIAFSISESTAVGSSSEYQQISQLVSHSQRHI 625	

uncharacterized protein Dere_GG17655, isoform C [Drosophila erecta] Sequence ID: **ref|XP_015010609.1**| Length: 1417 Number of Matches: 1

Score		Expect	Method		Identities	Positives	Gaps	Frame
707 bits	(1826)	0.0()	Composition	nal matrix adjust	480/532(90%)	488/532(91%)	12/532(2%)	+2
Features	S :							
Query	437				SLMRTTNNTLGR SLMRTTNNTLGR			
Sbjct	101				SLMRTTNNTLGR			
Query	617	RSTO	TLETHVKDIS	SNALKHFRDVIL	KKKLEVLPGNGT KKKLEVLPGNGT	VILETIASMYS'	VIOTYTLNEN	ISA 796
Sbjct	161				KKKLEVLPGNGT KKKLEVLPGNGT			
Query	797				SEDSGECASLSN SEDSGEC SLSN			
Sbjct	221				SEDSGEC SESN			
Query	977				imgaVTASPGAS IMGAVTASPG S			
Sbjct	281				IMGAVTASPGVS IMGAVTASPGVS			
Query	1157	IALT	PKERDILEQ	HNVNPMRGSHST	ESILRDTspppk ESILRDTSPPPK	pplpnrasnpp	plppkrrsqp	sa 1336
Sbjct	341				ESILRDTSPPPK.			
Query	1337	sagt SAG			AQSHNISLNSDL AQSHNISLNSDL			
Sbjct	401				AQSHNISLNSDL			
Query	1514		QCSFDSALNI OCSFDSALNI		qqhqhLRSFPKL QQ Q LRSFPK+			SAA 1666 AA
Sbjct	461				ŽÕQÕQLRSFPKM			
Query	1667		TOTPLsto	gggiagvaggtg GG GV GGTG	gagegvaaaasg GA EG AAAA+G	dgeTNSNRHSNI	ESGFVSMREF	'RT 1840
Sbjct	521				GAVEGAAAAATG			
Query	1841				isesTAVGSSSE ISESTAVGSS E			i
Sbjct	581				ISESTAVGSS E ISESTAVGSSGE			

guanine nucleotide exchange factor DC3G [Drosophila melanogaster] Sequence ID: **gb|AAC35280.1|** Length: 1383 Number of Matches: 1 Range 1: 122 to 590

Score		Expect Method	Identities	Positives	Gaps	Frame
707 bits	(1826)	0.0() Compositional matrix adjust.	465/520(89%)	466/520(89%)	51/520(9%)	+2
Feature	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKIS: HKNSLKGTKLARRARSFKDDLIEKIS:				
Sbjct	122	HKNSLKGTKLARRARSFKDDLIEKIS:				
Query	617	RSTQTLETHVKDISNALKHFRDVILK RSTOTLETHVKDISNALKHFRDVILK				
Sbjct	182	RSTQTLETHVKDISNALKHFRDVILK.				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLS: IMSSATLQVYQSLGKLIKLCDEVMLS:				
Sbjct	242	IMSSATLQVYQSLGKLIKLCDEVMLS:				
Query	977	KLKEQDQCAFRYsgsglggigaaaeir KLKEQDQCAF Y SGLGGIGAAAEI				
Sbjct	302	KLKEQDQCAFHYRRSGLGGIGAAAEI				
Query	1157	IALTPKERDILEQHNVNPMRGSHSTEIALTPKERDILEQHNVNPMRGSHSTE				
Sbjct	362	IALTPKERDILEÕHNVNPMRGSHSTE				
Query	1337	sagtvgvgcssststsnqasPLPYAQ SAGTVGVGCSSSTSTSNQASPLPYAQ	SHNISLNSDLD	CSSNISLLNYGV	DRLSVRSRS	PD 1516
Sbjct	422	SAGTVGVGCSSSTSTSNQASPLPYAQ				
Query	1517	ENSQCSFDSALNHSREEEDqqqqhqh: ENSQCSFDSALNHSREEEDQQQQHQH:			AAIDDKTQTP	Ls 1696
Sbjct	482	ENSQCSFDSALNHSREEEDQQQQHQH				529
Query	1697	tgggiagvaggtggagegvaaaasgd	geTNSNRHSNE	SGFVSMREFRTS FVSMREFRTS		
Sbjct	530			FVSMREFRTS	STÕTTDYSVÕ	SS 550
Query	1877	tkssssnseiafsisesTAVGSSSEY				
Sbjct	551	TKSSSSNSEIAFSISESTAVGSSSEY				

C3G, isoform E [Drosophila yakuba]

Sequence ID: ref|XP_015045489.1| Length: 1409 Number of Matches: 1

Score		Expect	Method		Identities	Positives	Gaps	Frame
707 bits	(1824)	0.0()	Compositional	matrix adjust.	475/527(90%)	483/527(91%)	14/527(2%)	+2
Features	3 :							
Query	437				LMRTTNNTLGR			
Sbjct	98				LMRTTNNTLGRS LMRTTNNTLGRS			
Query	617				KKLEVLPGNGT			
Sbjct	158				KKLEVLPGNGT KKLEVLPGNGT			
Query	797				EDSGECASLSNI EDSGECASLSNI			
Sbjct	218				EDSGECASLSNI			
Query	977				mgaVTASPGAS			
Sbjct	278				MGAVTASPG SY MGAVTASPGVSY			
Query	1157	IALT	PKERDILEOHN	VNPMRGSHSTE	SILRDTspppk	oplpnrasnpp	olppkrrsqp	sa 1336
Sbjct	338				SILRDTSPPPKI SILRDTSPPPKI			
Query	1337		vgvgcssstst	snqasPLPYAQ	SHNISLNSDLD			
Sbjct	398	AG PAGA	VĞCSS TS AVVGCSSLTSA		HNISLN DLDO PHNISLNLDLDO			
Query	1517				hLRSFPKLAAM			
Sbjct	451		CSFDSALNHSR CSFDSALNHSR		QLRSLSKMPTMI	MDEDMDKMVSY MDEDMDKMVSYI	AA+ VSTGYAGAAV	_
Query	1676	KTQT	PLstgggiagv	aggtggagegv	aaaasgdgeTN	SNRHSNESGFV	SMREFRTSTQ	TT 1855

K QTPL+TGG GV GGTGGA EG AAAA+G GETNSNRHSNESGFVSMREFRTSTQTT KMQTPLATGGVGGGVVGGTGGAAEGAAAAATGGGETNSNRHSNESGFVSMREFRTSTQTT 570 Query 1856 DYsvqsstkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996 DYS+QSSTKSSSSNSEIAFSISESTAVGSSSEYQQISQ VSHSQRHI Sbjct 571 DYSIQSSTKSSSSNSEIAFSISESTAVGSSSEYQQISQSVSHSQRHI 617

uncharacterized protein Dere_GG17655, isoform E [Drosophila erecta]
Sequence ID: **ref|XP_015010611.1**| Length: 1442 Number of Matches: 1

▶ See 1 more title(s) Range 1: 126 to 657

Score		Expect	Method	Identities	Positives	Gaps	Frame
707 bits	(1824)	0.0()	Compositional matrix adjust.	480/532(90%)	488/532(91%)	12/532(2%)	+2
Features	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS				
Sbjct	126		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK				
Sbjct	186		TLETHVKDISNALKHFRDVILK				
Query	797		ATLQVYQSLGKLIKLCDEVMLS AT QVYQSLGKLIKLCDEVMLS				
Sbjct	246		AT QVIQSLGKLIKLCDEVMLS				
Query	977		QDQCAFRYsgsglggigaaaei QDQCAFRYSGSGLGGIGAAAEI				
Sbjct	306		QDQCAFRYSGSGLGGIGAAAEI QDQCAFRYSGSGLGGIGAAAEI				
Query	1157	IALT	PKERDILEQHNVNPMRGSHSTE PKERDILEQHNVNPMRGSHSTE	SILRDTspppk	pplpnrasnpp	olppkrrsqp	sa 1336
Sbjct	366	IALT	PKERDILEQHNVNPMRGSHSTE	SILRDTSPPPK	PPLPNRASNPPI	PLPPKRRSQP	GA 425
Query	1337	sagt SAG	vgvgc-ssststsnqasPLPYA SSSTSTSNQASPLPYA	QSHNISLNSDL	DCSSNISLLNY(GVDRLSVRSR	SP 1513
Sbjct	426		GSGIGCSSSTSTSNQASPLPYA				
Query	1514		QCSFDSALNHSREEEDqqq OCSFDSALNHSREEED OOC	qhqhLRSFPKL Q Q LRSFPK+	AAMMDEDMDKH	VSYS	AA 1666 AA
Sbjct	486		QCSFDSALNHSREEEDHHHQQQ	ÕQÕQLRSFPKM	PAMMDEDMDKL	VSYKSTGYAG	
Query	1667		TQTPLstgggiagvaggtgg	agegvaaaasg A EG AAAA+G	dgeTNSNRHSNI	ESGFVSMREF	RT 1840
Sbjct	546		MÕTPLPTGGVGGGGGVVGGTGG				
Query	1841		TDYsvqsstkssssnseiafsi TDYS+QSSTKSSSSNS+IAFSI				
Sbjct	606		TDYSIQSSTKSSSSNSDIAFSI				

C3G, isoform H [Drosophila yakuba]

Sequence ID: ref|XP_015045492.1| Length: 1466 Number of Matches: 1

Score		Expect Method	Identities	Positives	Gaps	Frame
706 bits	(1823)	0.0() Compositional matrix adjust.	475/527(90%)	483/527(91%)	14/527(2%)	+2
Features	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKIS HKNSLKGTKLARRARSFKDDLIEKIS				
Sbjct	155	HKNSLKGTKLARRARSFKDDLIEKIS				
Query	617	RSTQTLETHVKDISNALKHFRDVILK RSTQTLETHVKDISNALKHFRDVILK				
Sbjct	215	RSTQTLETHVKDISNALKHFRDVILK				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLS IMS AT QVYQSLGKLIKLCDEVMLS				
Sbjct	275	IMSCATQQVYQSLGKLIKLCDEVMLS				
Query	977	KLKEQDQCAFRYsgsglggigaaaei KLKEQDQCAFRY GSGLGGIGAAAEI				
Sbjct	335	KLKEQDQCAFRYGGSGLGGIGAAAEI				
Query	1157	IALTPKERDILEQHNVNPMRGSHSTE	SILRDTspppk	pplpnrasnppp	plppkrrsqp	sa 1336

Sbjct	395	IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQP A IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPGA	454
Query	1337	sagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD AG VGCSS TS S YAQ HNISLN DLDCSSNISLLNYGVDRLSVRSRSPD	1516
Sbjct	455	PAGAAVVGCSSLTSASYAQPHNISLNLDLDCSSNISLLNYGVDRLSVRSRSPD	507
Query	1517	ENSQCSFDSALNHSREEED-qqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDD ENSQCSFDSALNHSREEED QQQQ Q LRS K+ MMDEDMDKMVSY AA++D	1675
Sbjct	508	ENSQCSFDSALNHSREEED QQQQQQLRSLSKMPTMMDEDMDKMVSYKSTGYAGAAVED	567
Query	1676	KTQTPLstgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTT K QTPL+TGG GV GGTGGA EG AAAA+G GETNSNRHSNESGFVSMREFRTSTQTT	1855
Sbjct	568	KMQTPLATGGVGGGVVGGTGGAAEGAAAAATGGGETNSNRHSNESGFVSMREFRTSTQTT	627
Query	1856	DYsvqsstkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996 DYS+QSSTKSSSSNSEIAFSISESTAVGSSSEYQQISQ VSHSQRHI	
Sbjct	628	DYSIQSSTKSSSSNSEIAFSISESTAVGSSSEIQQISQ VSHSQRHI 674	

C3G, isoform C [Drosophila yakuba]

Sequence ID: ref|XP_015045487.1| Length: 1573 Number of Matches: 1

▶ See 1 more title(s) Range 1: 262 to 781

Score		Expect	Method	Identities	Positives	Gaps	Frame
705 bits((1820)	0.0()	Compositional matrix adjust.	475/527(90%)	483/527(91%)	14/527(2%)	+2
Features	S:						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct	262		LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK				
Sbjct	322		TLETHVKDISNALKHFRDVILK				
Query	797		ATLQVYQSLGKLIKLCDEVMLS AT QVYQSLGKLIKLCDEVMLS				
Sbjct	382		AT QVIQSLGKLIKLCDEVMLS ATQQVYQSLGKLIKLCDEVMLS				
Query	977	KLKE	QDQCAFRYsgsglggigaaaei QDQCAFRY GSGLGGIGAAAEI	mgaVTASPGASV	VPGTGVMRVSA	AESAAQRTSL	PD 1156
Sbjct	442	KLKE	QDQCAFRYGGSGLGGIGAAAEI QDQCAFRYGGSGLGGIGAAAEI	MGAVTASPGVSV	VPGTGIMRVSAZ VPGTGIMRVSAZ	AESAAQRTSL AESAAQRTSL	PD 501
Query	1157	IALT	PKERDILEQHNVNPMRGSHSTE PKERDILEQHNVNPMRGSHSTE	SILRDTspppk	oplpnrasnppr	olppkrrsqp	sa 1336
Sbjct	502		PKERDILEQHNVNPMRGSHSTE				
Query	1337	sagt AG	vgvgcssststsnqasPLPYAQ VGCSS TS S YAO	SHNISLNSDLDO HNISLN DLDO			
Sbjct	562		AVVGCSSLTSASYAQ	PHNISLNLDLD	CSSNISLLNYG\	DRLSVRSRS DRLSVRSRS	PD 614
Query	1517		CSFDSALNHSREEED-qqqqhq CSFDSALNHSREEED QQQQ Q		MDEDMDKMVSY- MDEDMDKMVSY	SAAI AA+	
Sbjct	615	ENSQ	CSFDSALNHSREEED QQQQ Q CSFDSALNHSREEEDHQQQQQQ				
Query	1676		PLstgggiagvaggtggagegv PL+TGG GV GGTGGA EG	aaaasgdgeTNS	SNRHSNESGFVS	SMREFRTSTO	TT 1855
Sbjct	675		PLATGGVGGGVVGGTGGAAEGA				
Query	1856		qsstkssssnseiafsisesTA QSSTKSSSSNSEIAFSISESTA			1996	
Sbjct	735		QSSTKSSSSNSETAFSTSESTA QSSTKSSSSNSETAFSTSESTA			781	

uncharacterized protein Dere_GG17655, isoform H [Drosophila erecta]
Sequence ID: ref|XP_015010614.1| Length: 1417 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
673 bits	(1736)	0.0()	Compositional matrix adjust.	443/524(85%)	449/524(85%)	55/524(10%)	+2
Feature	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS			_	
Sbjct	160		LKGTKLARRARSFKDDLIEKIS				
Query	617	RSTQ	TLETHVKDISNALKHFRDVILK	KKLEVLPGNGT	VILETIASMYS	VIQTYTLNEN	SA 796

		RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA	
Sbjct	220	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA	279
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG IMS AT QVYQSLGKLIKLCDEVMLSEDSGEC SLSNENVREVIDLLEDAVRNLVTLAQG	976
Sbjct	280	IMSCATQÕVYÕSLGKLIKLCDEVMLSEDSGECPSLSNENVREVIDLLEDAVRNLVTLAÕG	339
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQRTSLPD KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPG SVPG G+MRVSAAESAAQRTSLPD	1156
Sbjct	340	KLKEQDQCAFRYSGSGLGGIGAAAEIMGAVTASPGVSVPGAGIMRVSAAESAAQRTSLPD	399
Query	1157	IALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppkrrsqpsaIALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQP A	1336
Sbjct	400	IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPGA	459
Query	1337	sagtvgvgc-ssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSP SAG SSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSP	1513
Sbjct	460	SAGAGSGIGCSSSTSTSNQASPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSP	519
Query	1514	DENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQ DENSQCSFDSALNHSREEED QQQQ Q LRSFPK+ AMMDEDMDK+VSYS	1684
Sbjct	520	DENSQCSFDSALNHSREEEDHHHQQQQQQQLRSFPKMPAMMDEDMDKLVSYS	571
Query	1685	TPLstgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYs FVSMREFRTSTOTTDYS	1864
Sbjct	572	FVSMREFRTSTQTTDYS	588
Query	1865	vqsstkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996 +QSSTKSSSSNS+IAFSISESTAVGSS EYQQISQ V HSQR I	
Sbjct	589	IQSSTKSSSSNSTIAFSISESTAVGSS EIQQISQ V HSQK I IQSSTKSSSSNSDIAFSISESTAVGSSGEYQQISQSVLHSQRQI 632	

uncharacterized protein Dere_GG17655, isoform G [Drosophila erecta] Sequence ID: ref|XP_015010613.1| Length: 1462 Number of Matches: 1

▶ See 1 more title(s) Range 1: 160 to 632

Score		Expect Method	Identities	Positives	Gaps	Frame
673 bits	(1736)	0.0() Compositional matrix adjust.	443/524(85%)	449/524(85%) 55/524(10%)	+2
Features	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI				
Sbjct	160	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTOTLETHVKDISNALKHFRDVILIRSTOTLETHVKDISNALKHFRDVILI				
Sbjct	220	RSTQTLETHVKDISNALKHFRDVIL				
Query	797	IMSSATLQVYQSLGKLIKLCDEVML				
Sbjct	280	IMSCATQQVYQSLGKLIKLCDEVML				
Query	977	KLKEQDQCAFRYsgsglggigaaae KLKEQDQCAFRYSGSGLGGIGAAAE	imgaVTASPGAS	SVPGTGVMRVS	AAESAAQRTSL:	PD 1156
Sbjct	340	KLKEQDQCAFRYSGSGLGGIGAAAE				
Query	1157	IALTPKERDILEQHNVNPMRGSHST	ESILRDTsppp ESTLRDTSPPP	opplpnrasnp	oplppkrrsqp	sa 1336
Sbjct	400	IALTPKERDILEQHNVNPMRGSHST				
Query	1337	sagtvgvgc-ssststsnqasPLPYZ SAG SSSTSTSNQASPLPYZ				
Sbjct	460	SAGAGSGIGCSSSTSTSNÕASPLPY				
Query	1514	DENSQCSFDSALNHSREEEDqq DENSOCSFDSALNHSREEED 000	qqhqhLRSFPKI QQ Q LRSFPKH			TQ 1684
Sbjct	520	DENSQCSFDSALNHSREEEDHHHQQ				571
Query	1685	TPLstgggiagvaggtggagegvaa	aasgdgeTNSNF	RHSNESGFVSMI FVSMI	REFRTSTQTTD REFRTSTOTTD	Ys 1864 YS
Sbjct	572			FVSM	REFRTSTÕTTD	YS 588
Query	1865	vqsstkssssnseiafsisesTAVG +QSSTKSSSSNS+IAFSISESTAVG			996	
Sbjct	589	IQSSTKSSSSNSDIAFSISESTAVG	SSGEYÕÕISÕS!	/LHSQRQI 6	32	

uncharacterized protein Dere_GG17655, isoform F [Drosophila erecta] Sequence ID: ref|XP_015010612.1| Length: 1468 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
672 bits	(1734)	0.0()	Compositional matrix adjust.	443/524(85%)	449/524(85	%) 55/524(10	%) +2
Features	3:						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct	160		LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILF TLETHVKDISNALKHFRDVILF				
Sbjct	220		TLETHVKDISNALKHFRDVILI				
Query	797		ATLOVYOSLGKLIKLCDEVMLS AT OVYOSLGKLIKLCDEVMLS				
Sbjct	280		ATQQVYQSLGKLIKLCDEVMLS				
Query	977	KLKE	QDQCAFRYsgsglggigaaaei QDQCAFRYSGSGLGGIGAAAEI	mgaVTASPGAS	SVPGTGVMRV	SAAESAAQRT	SLPD 115
Sbjct	340		QDQCAFRYSGSGLGGIGAAAE1 QDQCAFRYSGSGLGGIGAAAE1				
Query	1157	IALT	PKERDILEQHNVNPMRGSHSTE PKERDILEQHNVNPMRGSHSTE	ESILRDTspppk	pplpnrasn	ppplppkrrs	sqpsa 133
Sbjct	400		PKERDILEQHNVNPMRGSHSTI				
Query	1337	sagt SAG	vgvgc-ssststsnqasPLPYA SSSTSTSNQASPLPYA	AQSHNISLNSDI	DCSSNISLI	NYGVDRLSVF	RSRSP 151
Sbjct	460		GSGIGCSSSTSTSNQASPLPY/				
Query	1514		QCSFDSALNHSREEEDqqc OCSFDSALNHSREEED OOC	qqhqhLRSFPKI QQ Q LRSFPK+	AMMDEDME	KMVSYSAAII	DDKTQ 168
Sbjct	520		QCSFDSALNHSREEEDHHHQQQ				571
Query	1685	TPLs	tgggiagvaggtggagegvaaa	aasgdgeTNSNF	RHSNESGFVS	MREFRTSTOT	TTDYs 186
Sbjct	572				r v s FVS	MREFRTSTQT MREFRTSTQT	TTDYS 588
Query	1865	vqss	tkssssnseiafsisesTAVGS	SSEYQQISQLV	SHSQRHI	1996	
Sbjct	589	TQSS IQSS	TKSSSSNS+IAFSISESTAVGS TKSSSSNSDIAFSISESTAVGS	SSGEYQQISQSV	LHSQRQI	632	

uncharacterized protein Dere_GG17655, isoform D [Drosophila erecta]
Sequence ID: **ref|XP_015010610.1**| Length: 1522 Number of Matches: 1

Score		Expect	Method		Identities	Positives	Gaps	Frame
672 bits	(1733)	0.0()	Compositional r	natrix adjust.	443/524(85%)	449/524(85%)) 55/524(10%)	+2
Features	S:							
Query	437		LKGTKLARRARS					
Sbjct	265		LKGTKLARRARS LKGTKLARRARS					
Query	617		TLETHVKDISNA TLETHVKDISNA					
Sbjct	325	RSTQ	TLETHVKDISNA	LKHFRDVILI	KKLEVLPGNGI	VILETIASMY	SVIQTYTLNEN	ISA 384
Query	797		ATLQVYQSLGKI AT QVYQSLGKI					
Sbjct	385		ATQQVYQSLGKI					
Query	977	KLKE	QDQCAFRYsgsg QDQCAFRYSGSG	lggigaaaei	LmgaVTASPGAS	SVPGTGVMRVS	AAESAAQRTSL	PD 1156
Sbjct	445		QDQCAFRYSGSG					
Query	1157	IALT	PKERDILEQHNV PKERDILEQHNV	NPMRGSHSTI	ESILRDTspppk	pplpnrasnp	oplppkrrsqp	sa 1336
Sbjct	505	IALT	PKERDILEÕHNV	NPMRGSHSTI	ESILRDTSPPPK	(PPLPNRASNP)	PPLPPKRRSQP	GA 564
Query	1337	sagt SAG	vgvgc-ssstst		AQSHNISLNSDI AQSHNISLNSDI			
Sbjct	565		GSGIGCSSSTST					
Query	1514		QCSFDSALNHSR OCSFDSALNHSR	EEEDqqq	qqhqhLRSFPKL QQ Q LRSFPK+	AAMMDEDMDKI	MVSYSAAIDDK	TQ 1684
Sbjct	625		QCSFDSALNHSR	EEEDHHHQQ(QQQQQLRSFPKM	IPAMMDEDMDK	LVSYS	676
Query	1685	TPLs	tgggiagvaggt	ggagegvaaa	aasgdgeTNSNR	RHSNESGFVSMI	REFRTSTOTTD REFRTSTOTTD	Ys 1864
Sbjct	677							
Query	1865	vgss	tkssssnseiaf TKSSSSNS+IAF	sisesTAVGS	SSSEYQQISQLV	SHSORHI 19	996	
Sbjct	694		TKSSSSNSTIAF				37	

C3G, isoform G [Drosophila yakuba]

Sequence ID: ref|XP_015045491.1| Length: 1409 Number of Matches: 1

▶ See 1 more title(s) Range 1: 155 to 617

Score		Expect Method	Identities	Positives	Gaps	Frame
664 bits	(1712)	0.0() Compositional matrix adjust.	437/521(84%	6) 441/521(84%) 59/521(11%)	+2
Features	S:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKIS HKNSLKGTKLARRARSFKDDLIEKIS				
Sbjct	155	HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVILI RSTQTLETHVKDISNALKHFRDVILI				
Sbjct	215	RSTQTLETHVKDISNALKHFRDVILI				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLS				
Sbjct	275	IMSCATQQVYQSLGKLIKLCDEVML				
Query	977	KLKEQDQCAFRYsgsglggigaaae: KLKEQDQCAFRY GSGLGGIGAAAE:				
Sbjct	335	KLKEQDQCAFRYGGSGLGGIGAAAE				
Query	1157	IALTPKERDILEQHNVNPMRGSHSTI IALTPKERDILEQHNVNPMRGSHSTI	ESILRDTsppp	okpplpnrasnp	pplppkrrsqps	sa 1336
Sbjct	395	IALTPKERDILEQHNVNPMRGSHSTI	ESILRDTSPPE	KPPLPNRASNP	PPLPPKRRSÕP(GA 454
Query	1337	sagtvgvgcssststsnqasPLPYAQ AG VGCSS TS S YAQ	OSHNISLNSDI O HNISLN DI	DCSSNISLLNY	GVDRLSVRSRSI GVDRLSVRSRSI	PD 1516
Sbjct	455	PAGAAVVGCSSLTSASYA	PHNISLNLDI	LDCSSNISLLNY	GVDRLSVRSRSI	PD 507
Query	1517	ENSQCSFDSALNHSREEED-qqqqho		AMMDEDMDKMVS MMDEDMDKMVS		PL 1693
Sbjct	508	ENSQCSFDSALNHSREEEDHQQQQQQ				556
Query	1694	stgggiagvaggtggagegvaaaas		DIZOMD DD		วิส
Sbjct	557			FVSMREF	RTSTÕTTDYSI	S 576
Query	1874	stkssssnseiafsisesTAVGSSSI STKSSSSNSEIAFSISESTAVGSSSI	EYOOISOLVSE	ISORHI 1996		
Sbjct	577	STKSSSSNSEIAFSISESTAVGSSSI				

C3G, isoform D [Drosophila yakuba]

Sequence ID: ref|XP_015045488.1| Length: 1454 Number of Matches: 1

Score		Expect	Method		Identities	Positives	Gaps	Frame
663 bits((1711) (0.0()	Compositiona	l matrix adjust.	437/521(84%)	441/521(84%)	59/521(11%)	+2
Features	S :							
Query	437		_		SLMRTTNNTLGF SLMRTTNNTLGF		_	
Sbjct	155		. —		SLMRTTNNTLGF			=
Query	617				KKKLEVLPGNGT KKKLEVLPGNGT			
Sbjct	215				KKKLEVLPGNG1			
Query	797				SEDSGECASLSN SEDSGECASLSN			
Sbjct	275				SEDSGECASLSN			
Query	977				imgaVTASPGAS IMGAVTASPG S			
Sbjct	335				IMGAVTASPGVS			
Query	1157	IALT	PKERDILEOHN	IVNPMRGSHST	ESILRDTspppk ESILRDTSPPPk	pplpnrasnpr	pplppkrrsqp	sa 1336
Sbjct	395				ESILRDTSPPP			
Query	1337	sagt AG	vgvgcssstst VGCSS TS		QSHNISLNSDLI Q HNISLN DLI			
Sbjct	455				QPHNISLNLDLI			

Query	1517	ENSQCSFDSALNHSREEED-qqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPL ENSQCSFDSALNHSREEED QQQQ Q LRS K+ MMDEDMDKMVSYS	1693
Sbjct	508	ENSÕCSFDSALNHSREEEDHÕÕÕÕQÕQLRSLSKMPTMMDEDMDKMVSYS	556
Query	1694	stgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqs FVSMREFRTSTQTTDYS+QS	1873
Sbjct	557	FVSMREFRTSTQTTDYSIQS	576
Query	1874	stkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996 STKSSSSNSEIAFSISESTAVGSSSEYQQISQ VSHSQRHI	
Sbjct	577	STKSSSSNSETAFSTSESTAVGSSSETQQTSQ VSHSQRHT STKSSSSNSETAFSTSESTAVGSSSEYQQTSQSVSHSQRHT 617	

C3G, isoform B [Drosophila yakuba]

Sequence ID: ref|XP_015045486.1| Length: 1460 Number of Matches: 1

▶ See 1 more title(s) Range 1: 155 to 617

Score		Expect Method	Identities	Positives	Gaps	Frame
663 bits	(1711)	0.0() Compositional matrix adjust.	437/521(84%)	441/521(84%)	59/521(11%)	+2
Features	S :					
Query	437	HKNSLKGTKLARRARSFKDDLIEKIS				
Sbjct	155	HKNSLKGTKLARRARSFKDDLIEKIS HKNSLKGTKLARRARSFKDDLIEKIS				
Query	617	RSTOTLETHVKDISNALKHFRDVILK RSTOTLETHVKDISNALKHFRDVILK				
Sbjct	215	RSTQTLETHVKDISNALKHFRDVILK	KKLEVLPGNGT	TVILETIASMYS	SVIQTYTLNEN	SA 274
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLS IMS AT QVYQSLGKLIKLCDEVMLS				
Sbjct	275	IMSCATQQVYQSLGKLIKLCDEVMLS				
Query	977	KLKEQDQCAFRYsgsglggigaaaei KLKEQDQCAFRY GSGLGGIGAAAEI				
Sbjct	335	KLKEQDQCAFRYGGSGLGGIGAAAEI				
Query	1157	IALTPKERDILEQHNVNPMRGSHSTE IALTPKERDILEQHNVNPMRGSHSTE	SILRDTspppk	rpplpnrasnpr	plppkrrsqp	sa 1336
Sbjct	395	IALTPKERDILEQHNVNPMRGSHSTE				
Query	1337	sagtvgvgcssststsnqasPLPYAQ AG VGCSS TS S YAO		CSSNISLLNYC		
Sbjct	455	PAGAAVVGCSSLTSASYAQ				
Query	1517	ENSQCSFDSALNHSREEED-qqqqhq ENSQCSFDSALNHSREEED QQQQ Q		MMDEDMDKMVSY MMDEDMDKMVSY		PL 1693
Sbjct	508	ENSQCSFDSALNHSREEEDHQQQQQQ				556
Query	1694	stgggiagvaggtggagegvaaaasg	dgeTNSNRHSN		RTSTQTTDYsv RTSTQTTDYS+	
Sbjct	557			FVSMREFF	RTSTÕTTDIST	QS 576
Query	1874	stkssssnseiafsisesTAVGSSSE STKSSSSNSEIAFSISESTAVGSSSE	YQQISQLVSHS	SORHI 1996		
Sbjct	577	STKSSSSNSEIAFSISESTAVGSSSE				

C3G, isoform F [Drosophila yakuba]

Sequence ID: ref|XP_015045490.1| Length: 1516 Number of Matches: 1

Score	E	xpect	Method	Identities	Positives	Gaps	Fram	e
663 bits(1710) 0	.0()	Compositional matrix adjust.	437/521(84%)	441/521(84%)	59/521(11%)	+2	_
Features:								
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS					616
Sbjct	262		LKGTKLARRARSFKDDLIEKIS					321
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK					796
Sbjct	322		TLETHVKDISNALKHFRDVILK					381
Query	797		ATLQVYQSLGKLIKLCDEVMLS AT QVYQSLGKLIKLCDEVMLS				~ -	976
Sbjct	382		ATQQVYQSLGKLIKLCDEVMLS					441

Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQRTSLPD KLKEQDQCAFRY GSGLGGIGAAAEIMGAVTASPG SVPGTG+MRVSAAESAAQRTSLPD	1156
Sbjct	442	KLKEQDQCAFRYGGSGLGGIGAAAEIMGAVTASPG SVPGTG+MRVSAAESAAQRTSLPD	501
Query	1157	IALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppkrrsqpsa	1336
Sbjct	502	IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQP A IALTPKERDILEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNPPPLPPKRRSQPGA	561
Query	1337	sagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD AG VGCSS TS S YAO HNISLN DLDCSSNISLLNYGVDRLSVRSRSPD	1516
Sbjct	562	AĞ VĞCSS TS S YAQ HNISLN DLDCSSNISLLNYGVDRLSVRSRSPD PAGAAVVGCSSLTSASYAQPHNISLNLDLDCSSNISLLNYGVDRLSVRSRSPD	614
Query	1517	ENSQCSFDSALNHSREEED-qqqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPL ENSQCSFDSALNHSREEED QQQQ Q LRS K+ MMDEDMDKMVSYS	1693
Sbjct	615	ENSQCSFDSALNHSREEED QQQQQQLRSLSKMPTMMDEDMDKMVSYS	663
Query	1694	stgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqs	1873
Sbjct	664	FVSMREFRTSTQTTDYS+QS FVSMREFRTSTQTTDYSIQS	683
Query	1874	stkssssnseiafsisesTAVGSSSEYQQISQLVSHSQRHI 1996	
Sbjct	684	STKSSSSNSEIAFSISESTAVGSSSEYQQISQ VSHSQRHI STKSSSSNSEIAFSISESTAVGSSSEYQQISQSVSHSQRHI 724	

C3G ortholog, isoform G [Drosophila melanogaster]

Sequence ID: ref|NP_001138169.1| Length: 1234 Number of Matches: 1

▶ See 3 more title(s) Range 1: 1 to 442

Score		Expect	Method		Identities	Positives	Gaps	Frame
657 bits	(1696)	0.0()	Compositiona	al matrix adjust.	442/493(90%)	442/493(89%)) 51/493(10%)	+2
Features	3 :							
Query	518			HSPRTKHGTKAI HSPRTKHGTKAI				
Sbjct	1			HSPRTKHGTKAI				
Query	698			TIASMYSVIQTY TIASMYSVIQTY				
Sbjct	61			TIASMYSVIQTY				
Query	878	DSGE	CASLSNENVR	EVIDLLEDAVRN EVIDLLEDAVRN	NLVTLAQGKLKE	QDQCAFRYsgs	sglggigaaae	im 1057
Sbjct	121			EVIDLLEDAVRI				
Query	1058			GVMRVSAAESA <i>A</i> GVMRVSAAESA <i>A</i>				
Sbjct	181			GVMRVSAAESAA				
Query	1238	ILRD	Tspppkpplp:	nrasnppplpp NRASNPPPLPP	krrsqpsasagt	vgvgcsssts	tsngasPLPYA	OS 1417
Sbjct	241			NRASNPPPLPP				
Query	1418			ISLLNYGVDRLS ISLLNYGVDRLS				
Sbjct	301			ISLLNYGVDRLS				
Query	1598		KLAAMMDEDMI KLAAMMDEDMI	DKMVSYSAAIDI	KTQTPLstggg	giagvaggtgga	agegvaaaasg	dg 1777
Sbjct	361		KLAAMMDEDMI					381
Query	1778	eTNS		SMREFRTSTOTT SMREFRTSTOTT				
Sbjct	382			SMREFRTSTQT1				
Query	1958		LVSHSQRHI LVSHSQRHI	1996				
Sbjct	430		LVSHSQRHI	442				

uncharacterized protein Dana_GF20837, isoform K [Drosophila ananassae] Sequence ID: **ref|XP_014760976.1|** Length: 987 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps	Frame
583 bits(1504)	0.0()	Compositional matrix adjust.	372/503(74%)	396/503(78%)	37/503(7%)	+2
Features:						

Query	437	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGTKAPPTTEEVL HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPR+KHG K PP+ EEV	616
Sbjct	211	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRSKHGCKPPPSNEEVQ	270
Query	617	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA	796
Sbjct	271	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA	330
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG MSSAT QVYQSLGKLIKLCDEVMLS +S ECASLSNENVREVIDLLEDAVRNLVTLAQG	976
Sbjct	331	TMSSATQQVYQSLGKLIKLCDEVMLSGESDECASLSNENVREVIDLLEDAVRNLVTLAQG	390
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAA KLKEQDQC FRY G+GLGGIGAAAEIMGAVTASPG +V MRVSAA	1123
Sbjct	391	KLKEQDQC FRI G+GLGGIGAAAEIMGAVIASFG +V KLKEQDQCTFRYGGAGLGGIGAAAEIMGAVIASFGITVGSGGPGTGIGIGSVASMRVSAA	450
Query	1124	ESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnp ESA AQRTSLPDIALTPKERD LEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNP	1297
Sbjct	451	ESAVVAQRTSLPDIALTPKERDSLEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNP	510
Query	1298	pplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISL PP ++ + G SS+TSTSNQASPLPYAQSHNISLNSDLDCSSNISL	1468
Sbjct	511	PPLPPKRRSQQGGVTVGPGVGVGSSSSTTSTSNQASPLPYAQSHNISLNSDLDCSSNISL	570
Query	1469	LNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDM LNYGVD LSVRSRSPDENSQCSFDSALNHSREEED LR PK+ +D+DM	1639
Sbjct	571	LNYGVDHLSVRSRSPDENSQCSFDSALNHSREEEDQLRQMPKMPPALDQDMDGG	624
Query	1640	DKMVSYSAAIDDKTQTPLstgggiagvaggtggagegvaaaasgdgeTNSDK++SY + T ++ G G +G +G G G ++	1789
Sbjct	625	DKILSYKGEMASIPVTVMAGGQGGSGGSGHPDGGGGTTTTTVMAGGGESNTELRKAAAAL	684
Query	1790	NRHSNESGFVSMREFRTSTQT 1852 NRHSNESGFVSM+ +RTSTO+	
Sbjct	685	TINRHSNESGFVSMKSYRTSTQS 707	

uncharacterized protein Dana_GF20837, isoform J [Drosophila ananassae] Sequence ID: **ref|XP_014760975.1|** Length: 1614 Number of Matches: 1

Score		Expect	Method		Identities	Positives	Gaps	Frame
583 bits	(1502)	0.0()	Compositional	matrix adjust.	372/504(74%)	396/504(78%)	37/504(7%)	+2
Features	s:							
Query	437				LMRTTNNTLGR			
Sbjct	211				LMRTTNNTLGR LMRTTNNTLGR			
Query	617				KKLEVLPGNGT KKLEVLPGNGT			
Sbjct	271				KKLEVLPGNGT			
Query	797				SEDSGECASLSN S +S ECASLSN			
Sbjct	331				GESDECASLSN			
Query	977				mgaVTASPGAS MGAVTASPG +		-PGTGVMRVS MRVS	
Sbjct	391				MGAVTASPGIT			
Query	1124	ESA- ESA			HNVNPMRGSHS HNVNPMRGSHS			
Sbjct	451				HNVNPMRGSHS			
Query	1298		plppkrrsqps P ++ +		sststsnqasP SS+TSTSNQASP			
Sbjct	511	_			STTSTSNQASP			
Query	1469		VDRLSVRSRSP VD LSVRSRSP		LNHSREEEDqq	qqhqhLRSFPK LR PK		1639
Sbjct	571				LNHSREEED			GG 624
Query	1640	DKMV DK++	SYSAAIDDKTQ SY +	TPLstgggiag T ++ G G +6	vaggtggageg G +G G G		NS ++	1789
Sbjct	625				GSGHPDGGGGT	•	• •	AL 684
Query	1790		HSNESGFVSMR HSNESGFVSM+		1855			
Sbjct	685		HSNESGFVSMK		708			

▶ See 1 more title(s) Range 1: 89 to 586

Score		Expect Method	Identities	Positives	Gaps	Frame
583 bits	(1502)	0.0() Compositional matri	x adjust. 371/504(74%	5) 395/504(78%	37/504(7%)	+2
Feature	s:					
Query	437	HKNSLKGTKLARRARSFKDI HKNSLKGTKLARRARSFKDI				
Sbjct	89	HKNSLKGTKLARRARSFKDI				
Query	617	RSTQTLETHVKDISNALKHI RSTQTLETHVKDISNALKHI				
Sbjct	149	RSTQTLETHVKDISNALKHI				
Query	797	IMSSATLQVYQSLGKLIKLO MSSAT QVYQSLGKLIKLO				
Sbjct	209	TMSSATQQVYQSLGKLIKLO				
Query	977	KLKEQDQCAFRYsgsglgg: KLKEODOC FRY G+GLGG			PGTGVMRVS <i>I</i> MRVS <i>I</i>	
Sbjct	269	KLKEQDQC FRI G+GLGG				
Query	1124	ESAAQRTSLPDIALTPKI	ERDILEQHNVNPMRGSH ERD LEOHNVNPMRGSH			
Sbjct	329	ESAVVAQRTSLPDIALTPKI				
Query	1295	ppplppkrrsqpsasagt	tvgvgcssststsnqas SS+TSTSNOAS			
Sbjct	389	PPLPPKRRSQQGGVTVGPG				
Query	1469	LNYGVDRLSVRSRSPDENS(LNYGVD LSVRSRSPDENS(qqqhqhLRSFPI LR PI		163
Sbjct	449	LNYGVDHLSVRSRSPDENS				GG 502
Query	1640	DKMVSYSAAIDDKTQTPLst	tgggiagvaggtggage G G +G +G G G	gvaaaasgdge! G	rns ++	178
Sbjct	503	DKILSYKGEMASIPVTVMAC			• •	AL 562
Query	1790	NRHSNESGFVSMREFRTS				
Sbjct	563	TINRHSNESGFVSMKSYRTS				

uncharacterized protein Dana_GF20837, isoform H [Drosophila ananassae] Sequence ID: **ref|XP_014760973.1**| Length: 1561 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
582 bits	(1501)	0.0()	Compositional matrix adjust.	372/504(74%)	396/504(78%)	37/504(7%)	+2
Feature	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct	211		LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK				
Sbjct	271		TLETHVKDISNALKHFRDVILK				
Query	797		ATLQVYQSLGKLIKLCDEVMLS AT QVYQSLGKLIKLCDEVMLS				
Sbjct	331		ATQQVYQSLGKLIKLCDEVMLS				
Query	977		QDQCAFRYsgsglggigaaaei QDQC FRY G+GLGGIGAAAEI			-PGTGVMRVS MRVS	
Sbjct	391		QDQC FRI G+GLGGIGAAAEI QDQCTFRYGGAGLGGIGAAAEI				
Query	1124	ESA- ESA	-AQRTSLPDIALTPKERDILEQ				
Sbjct	451		VAQRTSLPDIALTPKERD LEQ VAQRTSLPDIALTPKERDSLEQ				
Query	1298	p P	plppkrrsqpsasagtvgvgcs P ++ + G S	sststsnqasPl S+TSTSNQASPl	LPYAOSHNISLI	NSDLDCSSNI	SL 1468
Sbjct	511		PKRRSQQGGVTVGPGVGVGSSS				
Query	1469		VDRLSVRSRSPDENSQCSFDSA VD LSVRSRSPDENSOCSFDSA		qqhqhLRSFPKI LR PK-		1639
Sbjct	571		VDHLSVRSRSPDENSQCSFDSA				GG 624
Query	1640	DKMV DK++	SYSAAIDDKTQTPLstgggiag SY + T ++ G G +G			\S	1789
Sbjct	625		SY + T ++ G G +G SYKGEMASIPVTVMAGGQGGSG			•	AL 684

Query 1790 --NRHSNESGFVSMREFRTSTQTT 1855 NRHSNESGFVSM+ +RTSTQ+ Sbjct 685 TINRHSNESGFVSMKSYRTSTQSV 708

uncharacterized protein Dana_GF20837, isoform F [Drosophila ananassae] Sequence ID: **ref|XP_014760971.1**| Length: 1576 Number of Matches: 1

▶ See 1 more title(s) kange 1: 211 to 708

Score		Expect	Method	Identities	Positives	Gaps	Frame
582 bits	(1501)	0.0()	Compositional matrix adjust	t. 372/504(74%)	396/504(78%)	37/504(7%)	+2
Features	S:						
Query	437		LKGTKLARRARSFKDDLIEKI LKGTKLARRARSFKDDLIEKI				
Sbjct	211		LKGTKLARRARSFKDDLIEKI LKGTKLARRARSFKDDLIEKI				
Query	617		TLETHVKDISNALKHFRDVII TLETHVKDISNALKHFRDVII				
Sbjct	271	RSTQ	TLETHVKDISNALKHFRDVII	KKKLEVLPGNGT	VILETIASMYS	/IQTYTLNEN	SA 330
Query	797		ATLQVYQSLGKLIKLCDEVMI AT QVYQSLGKLIKLCDEVMI				
Sbjct	331		AT QVIQDEGKEIKECDEVML ATQQVYQSLGKLIKLCDEVML				
Query	977	KLKE	QDQCAFRYsgsglggigaaae QDQC FRY G+GLGGIGAAAE	imgaVTASPGAS	V	-PGTGVMRVS MRVS	
Sbjct	391		ÖDÖC FRI GIGLGGIGAAAE ÕDÕCTFRYGGAGLGGIGAAAE				
Query	1124	ESA- ESA	-AQRTSLPDIALTPKERDILE AQRTSLPDIALTPKERD LE	OHNVNPMRGSHS	TESILRDTspp	okpplpnras	np 1297
Sbjct	451		VAQRTSLPDIALTPKERDSLE				
Query	1298	p P	plppkrrsqpsasagtvgvgc P ++ + G	ssststsnqasP SS+TSTSNQASP			
Sbjct	511		PKRRSQQGGVTVGPGVGVGSS	SSTTSTSNQASP	LPYAQSHNISLI	NSDLDCSSNI	SL 570
Query	1469		VDRLSVRSRSPDENSQCSFDS VD LSVRSRSPDENSQCSFDS		qqhqhLRSFPKI LR PK-		1639
Sbjct	571		VD LSVRSRSFDENSQCSFDS VDHLSVRSRSPDENSQCSFDS				GG 624
Query	1640	DKMV	SYSAAIDDKTQTPLstgggia SY + T ++ G G +	gvaggtggageg	vaaaasgdgeTi	NS	1789
Sbjct	625		SYKGEMASIPVTVMAGGQGGS				AL 684
Query	1790		HSNESGFVSMREFRTSTQTT	1855			
Sbjct	685		HSNESGFVSM+ +RTSTQ+ HSNESGFVSMKSYRTSTQSV	708			

uncharacterized protein Dana_GF20837, isoform E [Drosophila ananassae] Sequence ID: **ref|XP_014760970.1**| Length: 1584 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
582 bits	(1501)	0.0()	Compositional matrix adjust.	372/504(74%)	396/504(78%)	37/504(7%)	+2
Features	S :						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct	211		LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILK				
Sbjct	271		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK				
Query	797		ATLQVYQSLGKLIKLCDEVMLS AT QVYQSLGKLIKLCDEVMLS				
Sbjct	331		AT QVIQSLGKLIKLCDEVMLS ATQQVYQSLGKLIKLCDEVMLS				
Query	977		QDQCAFRYsgsglggigaaaei QDQC FRY G+GLGGIGAAAEI			-PGTGVMRVS MRVS	
Sbjct	391		QDQC FRI GTGLGGIGAAAEI QDQCTFRYGGAGLGGIGAAAEI				
Query	1124	ESA- ESA	-AQRTSLPDIALTPKERDILEQ AQRTSLPDIALTPKERD LEQ				
Sbjct	451	_~	VAQRTSLPDIALTPKERD LEQ VAQRTSLPDIALTPKERDSLEQ				

Query	1298	pplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISL PP ++ + G SS+TSTSNQASPLPYAQSHNISLNSDLDCSSNISL	1468
Sbjct	511	PPLPPKRRSQQGGVTVGPGVGVGSSSSTTSTSNQASPLPYAQSHNISLNSDLDCSSNISL	570
Query	1469	LNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDM LNYGVD LSVRSRSPDENSQCSFDSALNHSREEED LR PK+ +D+DM	1639
Sbjct	571	LNYGVD+LSVRSRSPDENSQCSFDSALNHSREEEDQLRQMPKMPPALDQDMDGG	624
Query	1640	DKMVSYSAAIDDKTQTPLstgggiagvaggtggagegvaaaasgdgeTNSDK++SY + T ++ G G +G +G G G ++	1789
Sbjct	625	DKILSYKGEMASIPVTVMAGGQGGSGGSGHPDGGGGTTTTTVMAGGGESNTELRKAAAAL	684
Query	1790	NRHSNESGFVSMREFRTSTQTT 1855 NRHSNESGFVSM+ +RTSTQ+	
Sbjct	685	TINRHSNESGFVSMKSYRTSTQSV 708	

uncharacterized protein Dana_GF20837, isoform C [Drosophila ananassae] Sequence ID: **ref|XP_014760979.1**| Length: 1537 Number of Matches: 1

▶ See 1 more title(s) Range 1: 134 to 631

Score		Expect	Method	Identities	Positives	Gaps	Frame
582 bits((1501)	0.0()	Compositional matrix adjust.	372/504(74%)	396/504(78%)	37/504(7%)	+2
Features	S:						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct	134		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK				
Sbjct	194		TLETHVKDISNALKHFRDVILK				
Query	797		ATLQVYQSLGKLIKLCDEVMLS AT QVYQSLGKLIKLCDEVMLS				
Sbjct	254		AT QVIQSEGREIRECDEVHES ATQQVYQSEGKLIKECDEVMLS				
Query	977		QDQCAFRYsgsglggigaaaei QDQC FRY G+GLGGIGAAAEI			-PGTGVMRVS MRVS	
Sbjct	314		QDQCTFRYGGAGLGGIGAAAEI				
Query	1124	ESA- ESA	-AQRTSLPDIALTPKERDILEQ AQRTSLPDIALTPKERD LEQ				
Sbjct	374		VAQRTSLPDIALTPKERDSLEQ				
Query	1298	p	plppkrrsqpsasagtvgvgcs P ++ + G S	sststsnqasPl S+TSTSNQASPl	LPYAQSHNISLI	NSDLDCSSNI	SL 1468
Sbjct	434	_	PKRRSQQGGVTVGPGVGVGSSS				
Query	1469		VDRLSVRSRSPDENSQCSFDSA VD LSVRSRSPDENSQCSFDSA		qqhqhLRSFPKI LR PK-		1639
Sbjct	494		VDHLSVRSRSPDENSQCSFDSA				GG 547
Query	1640	DKMV DK++	SYSAAIDDKTQTPLstgggiag SY + T ++ G G +G	vaggtggagegv +G G G		√S ++	1789
Sbjct	548		SYKGEMASIPVTVMAGGQGGSG				AL 607
Query	1790		HSNESGFVSMREFRTSTQTT HSNESGFVSM+ +RTSTQ+	1855			
Sbjct	608			631			

uncharacterized protein Dana_GF20837, isoform B [Drosophila ananassae] Sequence ID: **ref|XP_014760978.1**| Length: 1545 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
582 bits	(1501) (0.0()	Compositional matrix adjust.	372/504(74%)	396/504(78%)	37/504(7%)	+2
Features	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct	211		LKGTKLARRARSFKDDLIEKIS				-
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK				
Sbjct	271		TLETHVKDISNALKHFRDVILK				

Query	797	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG MSSAT QVYQSLGKLIKLCDEVMLS +S ECASLSNENVREVIDLLEDAVRNLVTLAQG	976
Sbjct	331	TMSSATQQVYQSLGKLIKLCDEVMLSGESDECASLSNENVREVIDLLEDAVRNLVTLAQG	390
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAA KLKEQDQC FRY G+GLGGIGAAAEIMGAVTASPG +V MRVSAA	1123
Sbjct	391	KLKEQDQCTFRYGGAGLGGIGAAAEIMGAVTASPGITVGSGGPGTGIGIGSVASMRVSAA	450
Query	1124	ESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnp ESA AQRTSLPDIALTPKERD LEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNP	1297
Sbjct	451	ESAVVAQRTSLPDIALTPKERDSLEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNP	510
Query	1298	pplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISL PP ++ + G SS+TSTSNQASPLPYAQSHNISLNSDLDCSSNISL	1468
Sbjct	511	PPLPPKRRSQQGGVTVGPGVGVGSSSSTTSTSNQASPLPYAQSHNISLNSDLDCSSNISL	570
Query	1469	LNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDM LNYGVD LSVRSRSPDENSQCSFDSALNHSREEED LR PK+ +D+DM	1639
Sbjct	571	LNYGVDHLSVRSRSPDENSQCSFDSALNHSREEEDQLRQMPKMPPALDQDMDGG	624
Query	1640	DKMVSYSAAIDDKTQTPLstgggiagvaggtggagegvaaaasgdgeTNSDK++SY + T ++ G G +G +G G G ++	1789
Sbjct	625	DKILSYKGEMASIPVTVMAGGQGGSGGSGHPDGGGGTTTTTVMAGGGESNTELRKAAAAL	684
Query	1790	NRHSNESGFVSMREFRTSTQTT 1855 NRHSNESGFVSM+ +RTSTQ+	
Sbjct	685	TINRHSNESGFVSMKSYRTSTÕSV 708	

uncharacterized protein Dana_GF20837, isoform A [Drosophila ananassae] Sequence ID: **ref|XP_001964208.1**| Length: 1507 Number of Matches: 1

▶ See 1 more title(s) Range 1: 211 to 708

Score		Expect	Method	Identities	Positives	Gaps	Frame
582 bits	(1500)	0.0()	Compositional matrix adjust	. 372/504(74%)	396/504(78%)	37/504(7%)	+2
Features	S :						
Query	437		LKGTKLARRARSFKDDLIEKI LKGTKLARRARSFKDDLIEKI				
Sbjct	211		LKGTKLARRARSFKDDLIEKI				
Query	617		TLETHVKDISNALKHFRDVIL TLETHVKDISNALKHFRDVIL				
Sbjct	271		TLETHVKDISNALKHFRDVIL				
Query	797		ATLQVYQSLGKLIKLCDEVML AT QVYQSLGKLIKLCDEVML				
Sbjct	331	TMSS	ATQQVYQSLGKLIKLCDEVML	SGESDECASLSN	ENVREVIDLLE	DAVRNLVTLA	QG 390
Query	977		QDQCAFRYsgsglggigaaae ODOC FRY G+GLGGIGAAAE			-PGTGVMRVS	
Sbjct	391		QDQCTFRYGGAGLGGIGAAAE				
Query	1124	ESA- ESA	-AQRTSLPDIALTPKERDILE AQRTSLPDIALTPKERD LE				
Sbjct	451		VAQRTSLPDIALTPKERDSLE				
Query	1298	p	plppkrrsqpsasagtvgvgc P ++ + G	ssststsnqasP SS+TSTSNQASP			
Sbjct	511		PKRRSQQGGVTVGPGVGVGSS				
Query	1469		VDRLSVRSRSPDENSQCSFDS		qqhqhLRSFPK LR PK		1639
Sbjct	571		VDHLSVRSRSPDENSQCSFDS				GG 624
Query	1640	DKMV DK++	SYSAAIDDKTQTPLstgggia SY + T ++ G G +	gvaggtggageg G +G G G		NS	1789
Sbjct	625		SYKGEMASIPVTVMAGGQGGS			• •	AL 684
Query	1790		HSNESGFVSMREFRTSTQTT HSNESGFVSM+ +RTSTO+	1855			
Sbjct	685		HSNESGFVSMKSYRTSTQSV	708			

uncharacterized protein Dpse_GA16131, isoform G [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041262.1|** Length: 1220 Number of Matches: 1

Score	Expect Method	Identities	Positives	Gaps	Frame
				=	

576 bits	(1484) (0.0() Compositional matrix adjust. 400/565(71%) 425/565(75%) 56/565(9%) +2	
Features	s:		
Query	437	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGTKAPPTTEE	610
Sbjct	193	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHG K PP+ EE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGAGVKPPPSNEE	252
Query	611	VLRSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYT-LNE V RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYT LNE	787
Sbjct	253	V KSIQILEINVKDISNALKHI KDVILKKKLEVLPGNGIVILEIIASMISVIQIII LNE VQRSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTPLNE	312
Query	788	NSAIMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTL NSAIMSSAT QVYQSLGKLIKLCDEVMLS++SGEC SLSN+NVREVIDLLEDAVRNLVTL	967
Sbjct	313	NSAIMSSATQQVYQSLGKLIKLCDEVMLSDESGECPSLSNDNVREVIDLLEDAVRNLVTL	372
Query	968	AQGKLKEQDQCAFRYsgsgl-ggigaaaeimgaVTASPGASVPGTGV AQGKLKEQDQCAFRYSG+ GGIGAAAEIMGAVTAS P VPGTG+	1105
Sbjct	373	AQGKLKEQDQCAFRYSGASGLGGIGAAAEIMGAVTASSTNAGSGGILPVGGVPGTGITGV	432
Query	1106	MRVSAAESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpp MR+SA ++AA ORTSLPDIAL+PKER ILE NVNPMRGSHSTESILRDT PP	1273
Sbjct	433	ASMRISAVDNAAVGQRTSLPDIALSPKERAILEHRNVNPMRGSHSTESILRDTSPP	488
Query	1274	<pre>lpnrasnppplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCS</pre>	1453
Sbjct	489	PKPPLPNRASNPPPLPPKRRSQPQAPPGGSSSSTSTSNQASPLPYAQSHNISLNSDLDCS	548
Query	1454	SNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDE SNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEED QQQ Q L+ KL M+E	1633
Sbjct	549	SNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDPQQQQQQLKQTVKLMEE	605
Query	1634	DMDKMVSYSAAIDDKTQTPLstgggiagvaggtggagegv D DKM+SY+ A QT L G G +G GG GE	1753
Sbjct	606	DADKMISYNAAGSASAAAQEMVMAQAPSNAÕTLLPGTGVPGPGPGASGAGAGAGAGGGGETN	665
Query	1754	aaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqsstkssssnseia + +NRHSNESGFVSM+ FRTSTO ++DYSVOSS KSSSSNSEIA	1909
Sbjct	666	TELRTATAVLTNNRHSNESGFVSMKSFRTSTÕSVSKRSSDYSVÕSSAKSSSSNSEIAISI	725

1984

750

uncharacterized protein Dpse_GA16131, isoform I [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041264.1**| Length: 1546 Number of Matches: 1

▶ See 1 more title(s) Range 1: 94 to 651

Query 1910 fsisesTAVGSSSEYQQISQLVSHS + +TA +SSEYQQISQ VSHS Sbjct 726 SESASATASAASSEYQQISQSVSHS

Score		Expect	Method	Identities	Positives	Gaps	Frame
575 bits	(1481)	0.0()	Compositional matrix adjust.	400/565(71%)	425/565(75%)	56/565(9%)	+2
Features	S:						
Query	437		LKGTKLARRARSFKDDLIEKIS				
Sbjct	94		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Query	611		TOTLETHVKDISNALKHFRDVI TOTLETHVKDISNALKHFRDVI				
Sbjct	154		TQTLETHVKDISNALKHFRDVI				
Query	788		MSSATLQVYQSLGKLIKLCDEV MSSAT QVYQSLGKLIKLCDEV				
Sbjct	214		MSSAT QVIQSLGKLIKLCDEV				
Query	968	AQGK	LKEQDQCAFRYsgsgl-ggiga LKEQDQCAFRYSG+ GGIGA	aaeimgaVTAS AAEIMGAVTAS	P(1105
Sbjct	274		LKEQDQCAFRYSGASGLGGIGA				GV 333
Query	1106		VSAAESAAQRTSLPDIALTP +SA ++AA QRTSLPDIAL+P				pp 1273 PP
Sbjct	334		ISAVDNAAVGÕRTSLPDIALSP				
Query	1274	lpnr	asnppplppkrrsqpsasagtv N PP + +		nqasPLPYAQS NQASPLPYAQS		
Sbjct	390	PKPP	LPNRASNPPPLPPKRRSQPQAP	PGGSSSSTSTS	NQASPLPYAQS:	HNISLNSDLD	CS 449
Query	1454		LLNYGVDRLSVRSRSPDENSQC LLNYGVDRLSVRSRSPDENSQC				DE 1633 +E
Sbjct	450	SNIS	LLNYGVDRLSVRSRSPDENSQC	SFDSALNHSRE	EEDPQQQQQQL:	KQTVKLM	
Query	1634	DMDK	MVSYSAAI M+SY+ A	DDKTQTPL QT L	stgggiag G G +G	vaggtggage G GG GE	gv 1753
Sbjct	507		MISYNAAGSASAAAQEMVMAQA				IN 566
Query	1754		sgdgeTNSNRHSNESGFVSMRE + +NRHSNESGFVSM+		TTDYsvqsstk ++DYSVQSS K		1909

Sbjct	567	TELRTATAVLTNNRHSNESGFVSMKS	FRTSTQSVSKRSSDYSVQSSAKSSSSNSEIAISI	626
Query	1910	fsisesTAVGSSSEYQQISQLVSHS + +TA +SSEYQQISQ VSHS	1984	
Sbjct	627		651	

uncharacterized protein Dpse_GA16131, isoform D [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041259.1|** Length: 1599 Number of Matches: 1

▶ See 1 more title(s) Range 1: 147 to 704

Score		Expect	Method	Identities	Positives	Gaps I	Frame
575 bits	(1481)	0.0()	Compositional matrix adjust	. 400/565(71%)	425/565(75%	5) 56/565(9%) +	<u> </u>
Features	S :						
Query	437		LKGTKLARRARSFKDDLIEKI				
Sbjct	147		LKGTKLARRARSFKDDLIEKI LKGTKLARRARSFKDDLIEKI				
Query	611		TQTLETHVKDISNALKHFRDV TQTLETHVKDISNALKHFRDV				
Sbjct	207		TÕTLETHVKDISNALKHFRDV				
Query	788		MSSATLQVYQSLGKLIKLCDE MSSAT QVYQSLGKLIKLCDE				
Sbjct	267		MSSATQQVYQSLGKLIKLCDE				
Query	968		LKEQDQCAFRYsgsgl-ggig LKEQDQCAFRYSG+ GGIG	aaaeimgaVTAS AAAEIMGAVTAS		PGASVPGTGV P VPGTG+	- 1105
Sbjct	327		LKEQDQCAFRYSGASGLGGIG				SV 386
Query	1106		VSAAESAAQRTSLPDIALT +SA ++AA ORTSLPDIAL+	PKERDILEQHNV PKER ILE NV			p 1273
Sbjct	387		ISAVDNAAVGQRTSLPDIALS				_
Query	1274	lpnr	asnppplppkrrsqpsasagt N PP + +			SHNISLNSDLDC SHNISLNSDLDC	
Sbjct	443	PKPP	LPNRASNPPPLPPKRRSQPQA				
Query	1454		LLNYGVDRLSVRSRSPDENSQ LLNYGVDRLSVRSRSPDENSQ				
Sbjct	503		LLNYGVDRLSVRSRSPDENSQ				
Query	1634		MVSYSAA M+SY+ A	IDDKTQTPL ÕT L	stgggiad G G +0		yv 1753
Sbjct	560		MISYNAAGSASAAAQEMVMAQ.				'N 619
Query	1754		sgdgeTNSNRHSNESGFVSMR + + NRHSNESGFVSM+	EFRTSTQ	TTDYsvqsstl ++DYSVQSS I	KSSSSNSEia	- 1909
Sbjct	620		TATAVLTNNRHSNESGFVSMK				SI 679
Query	1910		esTAVGSSSEYQQISQLVSHS +TA +SSEYOOISO VSHS	1984			
Sbjct	680		SATASAASSEYQQISQSVSHS	704			

uncharacterized protein Dpse_GA16131, isoform J [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041265.1|** Length: 1645 Number of Matches: 1

Score		Expect Method		Identities	Positives	Gaps	Frame
574 bits	(1480)	0.0() Composi	tional matrix adjust.	400/565(71%) 425/565(75%)	56/565(9%)	+2
Features	s:						
Query	437		RRARSFKDDLIEKIS RRARSFKDDLIEKIS				
Sbjct	193		RRARSFKDDLIEKIS				
Query	611		VKDISNALKHFRDVI VKDISNALKHFRDVI				
Sbjct	253		VKDISNALKHFRDVI				
Query	788		VYQSLGKLIKLCDEV VYQSLGKLIKLCDEV				
Sbjct	313		VYÕSLGKLIKLCDE\				
Query	968	AQGKLKEQDQC AQGKLKEQDQC	AFRYsgsgl-ggiga AFRYSG+ GGIGA	aaaeimgaVTA; AAAEIMGAVTA;		GASVPGTGV- VPGTG+	1105

Sbjct	373	AQGKLKEQDQCAFRYSGASGLGGIGAAAEIMGAVTASSTNAGSGGILPVGGVPGTGITGV	432
Query	1106	MRVSAAESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpp	1273
Sbjct	433	MR+SA ++AA QRTSLPDIAL+PKER ILE NVNPMRGSHSTESILRDT PP ASMRISAVDNAAVGQRTSLPDIALSPKERAILEHRNVNPMRGSHSTESILRDTSPP	488
Query	1274	lpnrasnppplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCS	1453
Sbjct	489	N PP + + G SSSTSTSNQASPLPYAQSHNISLNSDLDCS PKPPLPNRASNPPPLPPKRRSQPQAPPGGSSSSTSTSNQASPLPYAQSHNISLNSDLDCS	548
Query	1454	SNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDE	1633
Sbjct	549	SNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEED QQQ Q L+ KL M+E SNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDPQQQQQQLKQTVKLMEE	605
Query	1634	DMDKMVSYSAAIDDKTQTPLstgggiagvaggtggagegv	1753
Sbjct	606	D DKM+SY+ A QT L ĞĞ +Ğ ĞĞĞĞE DADKMISYNAAGSASAAAQEMVMAQAPSNAQTLLPGTGVPGPGPGASGAGAGAGGGGETN	665
Query	1754	aaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqsstkssssnseia	1909
Sbjct	666	+ +NRHSNESGFVSM+ FRTSTQ ++DYSVÕSS KSSSSNSEIA TELRTATAVLTNNRHSNESGFVSMKSFRTSTQSVSKRSSDYSVQSSAKSSSSNSEIAISI	725
Query	1910	fsisesTAVGSSSEYQQISQLVSHS 1984	
Sbjct	726	+ +TA +SSEYQQISQ VSHS SESASATASAASSEYQQISQSVSHS 750	

uncharacterized protein Dpse_GA16131, isoform E [Drosophila pseudoobscura pseudoobscura] Sequence ID: ref|XP_015041260.1| Length: 1605 Number of Matches: 1

▶ See 1 more title(s) Range 1: 193 to 750

Score		Expect Method		Identities	Positives	Gaps	Frame
574 bits	(1479)	0.0() Compositional	matrix adjust.	400/565(71%)	425/565(75%)	56/565(9%)	+2
Features	S :						
Query	437	HKNSLKGTKLARRARS HKNSLKGTKLARRARS					
Sbjct	193	HKNSLKGTKLARRARS					
Query	611	VLRSTQTLETHVKDIS V RSTQTLETHVKDIS					
Sbjct	253	V RSTOTLETHVKDIS					
Query	788	NSAIMSSATLQVYQSL NSAIMSSAT QVYQSL					
Sbjct	313	NSAIMSSAT QVIQSL					
Query	968	AQGKLKEQDQCAFRYS AOGKLKEODOCAFRYS		aaeimgaVTAS AAEIMGAVTAS	P Р		1105
Sbjct	373	AQGKLKEQDQCAFRYS			-		GV 432
Query	1106	MRVSAAESAAQR MR+SA ++AA OR		KERDILEQHNV			pp 1273 PP
Sbjct	433	ASMRISAVDNAAVGÕR					
Query	1274	lpnrasnppplppkrr N PP	sqpsasagtv + +		nqasPLPYAQS NQASPLPYAQS		
Sbjct	489	PKPPLPNRASNPPPLP					
Query	1454	SNISLLNYGVDRLSVR SNISLLNYGVDRLSVR					DE 1633 +E
Sbjct	549	SNISLLNYGVDRLSVR					_
Query	1634	DMDKMVSYS D DKM+SY+	AAI A	DDKTQTPL QT L	stgggiag G G +G		gv 1753
Sbjct	606	DADKMISYNAAGSASA					TN 665
Query	1754	aaaasgdgeTNSNRHS	NESGFVSMRE NESGFVSM+		TTDYsvqsstk ++DYSVQSS K		1909
Sbjct	666	TELRTATAVLTNNRHS	NESGFVSMKS	FRTSTÕSVSKR	SSDYSVÕSSAK	SSSSNSEIAI	SI 725
Query	1910	fsisesTAVGSSSEYQ + +TA +SSEYQ	QISQLVSHS OISO VSHS	1984			
Sbjct	726	SESASATASAASSEYÕ		750			

uncharacterized protein Dpse_GA16131, isoform F [Drosophila pseudoobscura pseudoobscura] Sequence ID: ref|XP_015041261.1| Length: 1590 Number of Matches: 1

Score	Expect Method	Identities	Positives	Gaps	Frame

573 bits((1478) (0() Compositional matrix adjust. 400/565(71%) 425/565(75%) 56/565(9%) +2
Features	S:	
Query	437	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGTKAPPTTEE 610
Sbjct	193	HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHG K PP+ EE HKNSLKGTKLARRARSFKDDLIEKISLMRTTNNTLGRSHSPHSPRTKHGAGVKPPPSNEE 252
Query	611	VLRSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYT-LNE 787 V RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYT LNE
Sbjct	253	V ROIQIDEINVRDISNALKHIRDVILKKKLEVLPGNGTVILETIASHISVIQITI ENE VQRSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTPLNE 312
Query	788	NSAIMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTL 967 NSAIMSSAT QVYQSLGKLIKLCDEVMLS++SGEC SLSN+NVREVIDLLEDAVRNLVTL
Sbjct	313	NSAIMSSATQQVYQSLGKLIKLCDEVMLSDESGECPSLSNDNVREVIDLLEDAVRNLVTL 372
Query	968	AQGKLKEQDQCAFRYsgsgl-ggigaaaeimgaVTASPGASVPGTGV 1105 AOGKLKEODOCAFRYSG+ GGIGAAAEIMGAVTAS P VPGTG+
Sbjct	373	AQGKLKEQDQCAFRYSGASGLGGIGAAAEIMGAVTASSTNAGSGGILPVGGVPGTGITGV 432
Query	1106	MRVSAAESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpp 1273 MR+SA ++AA QRTSLPDIAL+PKER ILE NVNPMRGSHSTESILRDT PP
Sbjct	433	ASMRISAVDNAAVGQRTSLPDIALSPKERAILEHRNVNPMRGSHSTESILRDTSPP 488
Query	1274	lpnrasnppplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCS 1453 N PP + + G SSSTSTSNOASPLPYAOSHNISLNSDLDCS
Sbjct	489	PKPPLPNRASNPPPLPPKRRSQPQAPPGGSSSSTSTSNQASPLPYAQSHNISLNSDLDCS 548
Query	1454	SNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDE 1633 SNISLLNYGVDRLSVRSRSPDENSOCSFDSALNHSREEED 000 0 L+ KL M+E
Sbjct	549	SNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDPQQQQQLKQTVKLMEE 605
Query	1634	DMDKMVSYSAAIDDKTQTPLstgggiagvaggtggagegv 1753 D DKM+SY+ A OT L G G +G G GE
Sbjct	606	DADKMISYNAAGSASAAAQEMVMAQAPSNAQTLLPGTGVPGPGPGASGAGAGAGGGGETN 665
Query	1754	aaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqsstkssssnseia 1909 + +NRHSNESGFVSM+ FRTSTQ ++DYSVQSS KSSSSNSEIA
Sbjct	666	TELRTATAVLTNNRHSNESGFVSMKSFRTSTÕSVSKRSSDYSVÕSSAKSSSSNSEIAISI 725
Query	1910	fsisesTAVGSSSEYQQISQLVSHS 1984 + +TA +SSEYQQISQ VSHS
Sbjct	726	SESASATASAASSEYÕÕISÕSVSHS 750

uncharacterized protein Dpse_GA16131, isoform C [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_001355576.3|** Length: 1550 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
		•				•	
573 bits	(1478)	0.0()	Compositional matrix adjust.	400/565(71%)	425/565(75%)	56/565(9%)	+2
Features	S :						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct	193		LKGTKLARRARSFKDDLIEKIS:				
Query	611		TQTLETHVKDISNALKHFRDVI TQTLETHVKDISNALKHFRDVI				
Sbjct	253		TQTLETHVKDISNALKHFRDVI				
Query	788		MSSATLQVYQSLGKLIKLCDEV MSSAT QVYQSLGKLIKLCDEV				
Sbjct	313		MSSATQQVYQSLGKLIKLCDEV				
Query	968		LKEQDQCAFRYsgsgl-ggiga LKEODOCAFRYSG+ GGIGA		P(P	GASVPGTGV- VPGTG+	1105
Sbjct	373		LKEQDQCAFRYSGASGLGGIGA				GV 432
Query	1106		VSAAESAAQRTSLPDIALTP +SA ++AA ORTSLPDIAL+P				pp 1273 PP
Sbjct	433		ISAVDNAAVGQRTSLPDIALSP.				
Query	1274	lpnr	asnppplppkrrsqpsasagtv N PP + +	gvgcssststsi G SSSTSTSN	nqasPLPYAQSI NQASPLPYAQSI	HNISLNSDLD	CS 1453
Sbjct	489	PKPP:	LPNRASNPPPLPPKRRSQPQAP				
Query	1454		LLNYGVDRLSVRSRSPDENSQC LLNYGVDRLSVRSRSPDENSOC				DE 1633 +E
Sbjct	549		LLNYGVDRLSVRSRSPDENSQC				
Query	1634		MVSYSAAI M+SY+ A		stgggiagv G G +G	aggtggage G GG GE	gv 1753
Sbjct	606		MISYNAAGSASAAAQEMVMAQA				TN 665
Query	1754	aaaa	sgdgeTNSNRHSNESGFVSMRE	FRTSTQ	TTDYsvqsstks	ssssnseia-	1909

Sbjct	666	+ +NRHSNESGFVSM+ FRTSTQ ++DYSVQSS KSSSSNSEIA TELRTATAVLTNNRHSNESGFVSMKSFRTSTQSVSKRSSDYSVQSSAKSSSSNSEIAISI	725
Query	1910	fsisesTAVGSSSEYQQISQLVSHS 1984 + +TA +SSEYQQISQ VSHS	
Sbjct	726	SESASATASAASSEYQQISQSVSHS 750	

uncharacterized protein Dpse_GA16131, isoform L [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041267.1|** Length: 1598 Number of Matches: 1

▶ See 1 more title(s) Range 1: 193 to 750

Score		Expect	Method	Identities	Positives	Gaps	Frame
573 bits	(1477)	0.0()	Compositional matrix adjust.	400/565(71%)	425/565(75%)	56/565(9%)	+2
Features	S:						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct	193		LKGTKLARRARSFKDDLIEKIS				
Query	611		TQTLETHVKDISNALKHFRDVI TQTLETHVKDISNALKHFRDVI				
Sbjct	253		TÕTLETHVKDISNALKHFRDVI				
Query	788		MSSATLQVYQSLGKLIKLCDEV MSSAT QVYQSLGKLIKLCDEV				
Sbjct	313		MSSATQQVYQSLGKLIKLCDEV				
Query	968		LKEQDQCAFRYsgsgl-ggiga LKEODOCAFRYSG+ GGIGA	aaeimgaVTAS AAEIMGAVTAS	P(P	GASVPGTGV- VPGTG+	1105
Sbjct	373		LKEQDQCAFRYSGASGLGGIGA				GV 432
Query	1106		VSAAESAAQRTSLPDIALTP +SA ++AA QRTSLPDIAL+P				pp 1273 PP
Sbjct	433		ISAVDNAAVGÕRTSLPDIALSP				
Query	1274	lpnr	asnppplppkrrsqpsasagtv N PP + +		nqasPLPYAQSI NQASPLPYAQSI		
Sbjct	489	PKPP	LPNRASNPPPLPPKRRSQPQAP				
Query	1454		LLNYGVDRLSVRSRSPDENSQC LLNYGVDRLSVRSRSPDENSQC				DE 1633 +E
Sbjct	549		LLNYGVDRLSVRSRSPDENSQC				
Query	1634		MVSYSAAI M+SY+ A	DDKTQTPL	stgggiag G G +G	vaggtggage G GG GE	gv 1753
Sbjct	606		MISYNAAGSASAAAQEMVMAQA				
Query	1754		sgdgeTNSNRHSNESGFVSMRE + +NRHSNESGFVSM+		TTDYsvqsstks		1909
Sbjct	666		TATAVLTNNRHSNESGFVSMKS				SI 725
Query	1910		esTAVGSSSEYQQISQLVSHS +TA +SSEYQQISQ VSHS	1984			
Sbjct	726		SATASAASSEYQQISQSVSHS	750			

uncharacterized protein Dana_GF20837, isoform I [Drosophila ananassae] Sequence ID: **ref|XP_014760974.1**| Length: 1551 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
569 bits	(1466) (0.0()	Compositional matrix adjust.	348/427(81%)	362/427(84%)	25/427(5%)	+2
Features	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS				
Sbjct	211		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				-
Query	617		TLETHVKDISNALKHFRDVILK TLETHVKDISNALKHFRDVILK				
Sbjct	271		TLETHVKDISNALKHFRDVILK				
Query	797		ATLQVYQSLGKLIKLCDEVMLS AT QVYQSLGKLIKLCDEVMLS				
Sbjct	331		ATQQVYQSLGKLIKLCDEVMLS				
Query	977	KLKE	QDQCAFRYsgsglggigaaaei	mgaVTASPGAS	J	-PGTGVMRVS	AA 1123

Sbjct	391	KLKEQDQC FRY G+GLGGIGAAAEIMGAVTASPG +V MRVSAA KLKEQDQCTFRYGGAGLGGIGAAAEIMGAVTASPGITVGSGGPGTGIGIGSVASMRVSAA	450
Query	1124	ESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnp ESA AQRTSLPDIALTPKERD LEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNP	1297
Sbjct	451	ESA AQRISLPDIALIPKERD LEQHNVNPMRGSHSTESILRDISPPRPPLPNRASNP ESAVVAQRTSLPDIALTPKERDSLEQHNVNPMRGSHSTESILRDTSPPPKPPLPNRASNP	510
Query	1298	pplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISL PP ++ + G SS+TSTSNQASPLPYAQSHNISLNSDLDCSSNISL	1468
Sbjct	511	PP ++ + G SS+TSTSNQASPLPYAQSHNISLNSDLDCSSNISL PPLPPKRRSQQGGVTVGPGVGVGSSSSTTSTSNQASPLPYAQSHNISLNSDLDCSSNISL	570
Query	1469	LNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDM LNYGVD LSVRSRSPDENSOCSFDSALNHSREEED LR PK+ +D+DM	1639
Sbjct	571	LNYGVDHLSVRSRSPDENSQCSFDSALNHSREEED LR PK+ +D+DM LNYGVDHLSVRSRSPDENSQCSFDSALNHSREEEDQLRQMPKMPPALDQDMDGG	624
Query	1640	DKMVSYS 1660	
Sbjct	625	DK++SYS DKILSYS 631	

uncharacterized protein Dana_GF20837, isoform G [Drosophila ananassae] Sequence ID: **ref|XP_014760972.1**| Length: 1444 Number of Matches: 1

See 1 more title(s) Range 1: 211 to 631

Score		Expect M	ethod		Identities	Positives	Gaps	Frame
569 bits	(1466)	0.0() Co	ompositional	matrix adjust.	348/427(81%)	362/427(84%)	25/427(5%)	+2
Features	S:							
Query	437				LMRTTNNTLGR: LMRTTNNTLGR:			
Sbjct	211				LMRTTNNTLGR			
Query	617				KKLEVLPGNGT' KKLEVLPGNGT'			
Sbjct	271				KKLEVLPGNGT			
Query	797				EDSGECASLSNI +S ECASLSNI			
Sbjct	331	TMSSAT	QQVYQSLGK.	LIKLCDEVMLS	GESDECASLSNI	ENVREVIDLLEI	DAVRNLVTLA DAVRNLVTLA	QG 390
Query	977	KLKEOD	QCAFRYsgs	glggigaaaei:	mgaVTASPGAS\ MGAVTASPG +\	J	-PGTGVMRVS MRVS	_
Sbjct	391				MGAVTASPGIT			
Query	1124				HNVNPMRGSHS' HNVNPMRGSHS'			
Sbjct	451				HNVNPMRGSHS!			
Query	1298	ppl	ppkrrsqps		sststsnqasPl S+TSTSNQASPl			
Sbjct	511				STTSTSNÕASPI			
Query	1469			DENSQCSFDSA DENSQCSFDSA	LNHSREEEDqq	qqhqhLRSFPKI LR PKH		1639
Sbjct	571				LNHSREEED		MPPALDQDMD	GG 624
Query	1640	DKMVSY DK++SY						
Sbjct	625	DKILSY						

GL26876 [Drosophila persimilis]

Sequence ID: ref|XP_002025124.1| Length: 1526 Number of Matches: 1

Score	E	Expect	Method	Identities	Positives	Gaps	Frame
569 bits	(1466) 0	0.0()	Compositional matrix adjust.	394/578(68%)	420/578(72%)	65/578(11%)	+2
Features	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS				
Sbjct	187		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS			_	
Query	611		TQTLETHVKDISNALKHFRDVI TQTLETHVKDISNALKHFRDVI				
Sbjct	247		TQTLETHVKDISNALKHFRDVI				
Query	788	NSAI	MSSATLQVYQSLGKLIKLCDEV	MLSEDSGECAS	LSNENVREVID	LLEDAVRNLV	TL 967

		NSAIMSSAT QVYQSLGKLIKLCDEVMLS++SGEC SLSN+NVREVIDLLEDAVRNLVTL	
Sbjct	307	NSAIMSSATQQVYQSLGKLIKLCDEVMLSDESGECPSLSNDNVREVIDLLEDAVRNLVTL	366
Query	968	AQGKLKEQDQCAFRYsgsglggigaaaeimg-aVTASPGASVPGTGV AQGKLKEQDQCAFRYSGS G AA + AVTAS P VPGTG+	1105
Sbjct	367	AQGKLKEQDQCAFRYSGSSGLGGIGAAAEIMGAVTASSTNAGGVGSGGILPVGGVPGTGI	426
Query	1106	MRVSAAESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTsppp MR+SA E+AA QRTSLPDIAL+PKER ILE NVNPMRGSHSTESILRDT	1264
Sbjct	427	TGVASMRISAVENAAVGQRTSLPDIALSPKERAILEHRNVNPMRGSHSTESILRDT	482
Query	1265	kpplpnrasnppplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDL PP N PP + + G SSSTSTSNQASPLPYAQSHNISLNSDL	1444
Sbjct	483	SPPPKPPLPNRASNPPPLPPKRRSQPQAPPGGSSSSTSTSNQASPLPYAQSHNISLNSDL	542
Query	1445	DCSSNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAM DCSSNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEED QQQ Q L+ +	1624
Sbjct	543	DCSSNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDPQQQQQQLKQTLKL	599
Query	1625	MDEDMDKMVSYSAAIDDKTQTPLstgggiagvaggtggag M+ED DK++SY A QT L G G +G G G	1744
Sbjct	600	MEEDADKLISYKAAGSASAAAQEMVMAQAPSNAQTLLPGTGVPGPGPGASGAGAGAGGGG	659
Query	1745	egvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQTTDYsvqsstkssssnseia E + +NRHSNESGFVSM+ FRTSTQ ++DYSVQSS KSSSSNSEIA	1909
Sbjct	660	ETNTELRTATAALTNNRHSNESGFVSMKSFRTSTQSVSKRSSDYSVQSSAKSSSSNSEIA	719
Query	1910	fsisesTAVGSSSEYQQISQLVSHSQRHI 1996 + +TA +SSEYQQISQ VSHS Q+HI	
Sbjct	720	ISISESASATASAASSEYQQISQSVSHSSHRSQQQQHI 757	

uncharacterized protein Dpse_GA16131, isoform B [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041258.1**| Length: 1479 Number of Matches: 1

558 bits(143	37) 3e-177()	Compositional matrix adjust.	381/545(70%)	402/545(73%)	\ 87/5 <u>45(15%</u>) +	2
Features:				10_10_10_10_1) 01/3 1 3(13/0) 1	·Z
i caluics.						
Query 43		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Sbjct 19		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS				
Query 61		TOTLETHVKDISNALKHFRDVI TÕTLETHVKDISNALKHFRDVI				
Sbjct 25		TQTLETHVKDISNALKHFRDVI				
Query 78		MSSATLQVYQSLGKLIKLCDEV MSSAT QVYQSLGKLIKLCDEV				
Sbjct 31		MSSATQQVYQSLGKLIKLCDEV				
Query 96		LKEQDQCAFRYsgsgl-ggiga LKEODOCAFRYSG+ GGIGA	aaeimgaVTAS AAEIMGAVTAS	I	PGASVPGTGV VPGTG+	- 1105
Sbjct 37		LKEQDQCAFRYSGASGLGGIGA				V 432
Query 11		VSAAESAAQRTSLPDIALTP +SA ++AA QRTSLPDIAL+P				
Sbjct 43		ISAVDNAAVGQRTSLPDIALSP				
Query 12	74 lpnr	asnppplppkrrsqpsasagtv N PP + +			SHNISLNSDLDC SHNISLNSDLDC	
Sbjct 48	9 PKPP	LPNRASNPPPLPPKRRSQPQAP				
Query 14		LLNYGVDRLSVRSRSPDENSQC LLNYGVDRLSVRSRSPDENSQC				
Sbjct 54	9 SNIS	LLNYGVDRLSVRSRSPDENSQC	SFDSALNHSRE	EEDPQQQQQQI	LKQTVKLME	
Query 16		MVSYSAAIDDKTQTPLstgggi M+SYS	agvaggtggag	egvaaaasgd	geTNSNRHSNES	G 1813
Sbjct 60	6 DADKI	MISYS				- 614
Query 18		REFRTSTQTTDYsvqss + FRTSTO ++DYSVOSS	tkssssnseia KSSSSNSEIA			
Sbjct 61		KSFRTSTQSVSKRSSDYSVQSS				
Query 19	70 LVSH					
Sbjct 67						

▶ See 1 more title(s) Range 1: 116 to 526

Score		Expect	Method	Identities	Positives	Gaps	Frame
555 bits	(1429)	5e-177()	Compositional matrix adjust.	328/417(79%)	353/417(84%)	15/417(3%)	+2
Features	s:						
Query	437		.KGTKLARRARSFKDDLIEKIS .KGTKLARRARSFKDDLIEKIS				
Sbjct	116		KGTKLARRARSFKDDLIEKIS				•
Query	617		LETHVKDISNALKHFRDVILK				
Sbjct	176		LETHVKDISNALKHFRDVI K LETHVKDISNALKHFRDVIHK				
Query	797		TLOVYOSLGKLIKLCDEVMLS				
Sbjct	236		AT QVYQSLGKLIKLCDEVMLS ATQQVYQSLGKLIKLCDEVMLS				
Query	977		DOCAFRYsgsglggigaaaeir				
Sbjct	296		DOC FRYSG+GLGGIGAAA+II DOCTFRYSGAGLGGIGAAADII			AA + QRTS AAAAVVQRTS	
Query	1154		PKERDILEQHNVNPMRGSHST				-
Sbjct	356		'PKERDILEQ NVNPMRGSHST' 'PKERDILEQSNVNPMRGSHST'				P+ PQ 415
Query	1316		sasagtvgvgcssststsnqa	SPLPYAOSHNIS	SLNSDLDCSSN	ISLLNYGVDR	LS 1495
Sbjct	416	+ SQLAN	+ ++ ++ +++ +S	SPLPYAQSHNIS SPLPYAQSHNIS			
Query	1496		SPDENSQCSFDSALNHSREEED				1660
Sbjct	476		SPDENSQCSFDSALNHSREEE+ SPDENSQCSFDSALNHSREEEE	L+ E QLQKPE		D+DK++SYS DVDKLISYS	526

uncharacterized protein Dvir_GJ16545, isoform F [Drosophila virilis]
Sequence ID: ref|XP_002057080.2| Length: 1405 Number of Matches: 1

See 1 more title(s) Range 1: 151 to 561

	Expect	Method		Identities	Positives	Gaps	Frame
(1429)	1e-176()	Compositional	matrix adjust.	328/417(79%)	353/417(84%)	15/417(3%)	+2
S:							
437							
151							
617							
211							
797							
271							
977	KLKEO	DOCAFRYSGS	glggigaaaeir	mgaVTASPGA-S	SVPGTGVMRVS		
331							
1154	DIALT	'PKERDILEOHN	IVNPMRGSHSTI	ESILRDTspppk	xpplpnrasn		pk 1315 P+
391							-
1316							
451							
1496							1660
511							561
	3: 437 151 617 211 797 271 977 331 1154 391 1316 451 1496	(1429) 1e-176() s: 437	(1429) 1e-176() Compositional (1429) 1e-176() Compositional (1429) 1e-176() Compositional (1437	(1429) 1e-176() Compositional matrix adjust. 3: 437	(1429) 1e-176() Compositional matrix adjust. 328/417(79%) 3: 437	(1429) 1e-176() Compositional matrix adjust. 328/417(79%) 353/417(84%) 3: 437	(1429) 1e-176() Compositional matrix adjust. 328/417(79%) 353/417(84%) 15/417(3%) 15/417(3%) 1

uncharacterized protein Dvir_GJ16545, isoform E [Drosophila virilis]
Sequence ID: ref|XP_015025481.1| Length: 1406 Number of Matches: 1

Score		Expect	Method		Identities	Positives	Gaps	Frame
555 bits	(1429)	1e-176()	Compositional	matrix adjust.	328/417(79%)	353/417(84%)	15/417(3%)	+2
Features	S:							
Query	437				LMRTTNNTLGRS			
Sbjct	151				LMRTTNNTLGRS LMRTTNNTLGRS			
Query	617				KKLEVLPGNGT\ KKLEVLPGNGT\			
Sbjct	211				KKLEVLPGNGT\ KKLEVLPGNGT\			
Query	797				EDSGECASLSNE E SGECASLSNE			
Sbjct	271				EKSGECASLSNE			
Query	977	KLKEO	DOC FRYSGS	lggigaaaei	mgaVTASPGA-S MG VTA+ A S	SVPGTGVMRVS	AAESAAQRTS AA + ORTS	
Sbjct	331				MGVVTAASAAGS			
Query	1154				ESILRDTsppp ESILRDTSPPP			pk 1315 P+
Sbjct	391				ESILRDISPPP			-
Query	1316	rrsqp +	sasagtvgvgc + ++		SPLPYAQSHNIS SPLPYAQSHNIS			
Sbjct	451	•			SPLPYAQSHNIS SPLPYAQSHNIS			
Query	1496		PDENSQCSFDS PDENSQCSFDS		qqqqhqhLRSFI L+ I			1660
Sbjct	511				QLQKPI		D+DK++SYS DVDKLISYS	561

uncharacterized protein Dpse_GA16131, isoform H [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041263.1**| Length: 1574 Number of Matches: 1

Score		Expect	Method			ldentit	ies	Positi	ves	Gaps	Fra	me
558 bits	(1438)	1e-176()) Compositio	nal matri	x adjust.	381/54	5(70%)	402/54	15(73%	b) 87/545(1	15%) +2	
Feature	s:											
Query	437		LKGTKLARR <i>I</i> LKGTKLARR <i>I</i>									610
Sbjct	193		LKGTKLARR <i>I</i>								PP+ EE PPSNEE	252
Query	611		TQTLETHVKI TQTLETHVKI									787
Sbjct	253		TQTLETHVKI TQTLETHVKI									312
Query	788		MSSATLQVY(MSSAT QVY(967
Sbjct	313		MSSAT QVIÇ MSSATQQVYÇ									372
Query	968	AQGKI	LKEQDQCAFI LKEODOCAFI	RYsgsgl	-ggiga	aaeimo AAEIMO	Javtas			PGASVPGT		1105
Sbjct	373		LKEQDQCAFI						SGGIL			432
Query	1106		VSAAESAA +SA ++AA								pppkpp PP	1273
Sbjct	433		ISAVDNAAVO									488
Query	1274	lpnra	asnppplpp N PP	krrsqps +		gvgcss	sststs	ngasP	LPYAC	SHNISLNS SHNISLNS	SDLDCS	1453
Sbjct	489	PKPPI	LPNRASNPPI	•	•							548
Query	1454		LLNYGVDRLS LLNYGVDRLS								AAMMDE M+E	1633
Sbjct	549		LLNYGVDRLS									605
Query	1634		MVSYSAAIDI M+SYS	OKTQTPL	stgggi	agvag	gtggag	gegvaa	aasgd	geTNSNR	HSNESG	1813
Sbjct	606	DADKI	MISYS									614
Query	1814		REFRTSTQ + FRTSTO		Ysvqss YSVQSS				isesT + +T		ZQQISQ ZQQISQ	1969
Sbjct	615		KSFRTSTÕS\									674
Query	1970	LVSHS VSHS										
Sbjct	675	SVSH										

uncharacterized protein Dvir_GJ16545, isoform D [Drosophila virilis]
Sequence ID: **ref|XP_015025480.1**| Length: 1413 Number of Matches: 1

▶ See 1 more title(s) Range 1: 151 to 561

Score		Expect	Method	Identities	Positives	Gaps	Frame
554 bits	(1428)	1e-176()	Compositional matrix adjust.	328/417(79%)	353/417(84%)	15/417(3%)	+2
Feature	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS				
Sbjct	151		LKGTKLARRARSFKDDLIEKISI LKGTKLARRARSFKDDLIEKISI				
Query	617		TLETHVKDISNALKHFRDVILKI TLETHVKDISNALKHFRDVI KI				
Sbjct	211		TLETHVKDISNALKHFRDVI KI				
Query	797		ATLQVYQSLGKLIKLCDEVMLSI AT QVYQSLGKLIKLCDEVMLSI				
Sbjct	271		ATQQVYQSLGKLIKLCDEVMLSI				
Query	977	KLKEC	QDQCAFRYsgsglggigaaaeir QDQC FRYSG+GLGGIGAAA+IN	mgaVTASPGA-S	SVPGTGVMRVSA	AESAAQRTS A + ORTS	
Sbjct	331		DDQCTFRYSGAGLGGIGAAADII				
Query	1154	DIALT	TPKERDILEQHNVNPMRGSHSTI TPKERDILEQ NVNPMRGSHSTI	ESILRDTspppk	pplpnrasn		pk 1315 P+
Sbjct	391		TPKERDILEQSNVNPMRGSHSTI			•	
Query	1316	rrsqr +	osasagtvgvgcssststsnqas + ++ ++ +S S	SPLPYAQSHNIS			
Sbjct	451	•	NANASTNTNTNPTTTSHSSQAN				
Query	1496		SPDENSQCSFDSALNHSREEED SPDENSQCSFDSALNHSREEE+	qqqqhqhLRSFI L+ I		MDKMVSYS HDK++SYS	1660
Sbjct	511		SPDENSQCSFDSALNHSREEEE-				561

uncharacterized protein Dvir_GJ16545, isoform C [Drosophila virilis]
Sequence ID: ref|XP_015025479.1| Length: 1414 Number of Matches: 1

▶ See 1 more title(s) kange 1: 151 to 561

Score		Expect	Method		Identities	Positives	Gaps	Frame
554 bits	(1427)	2e-176()	Compositional	matrix adjust.	328/417(79%)	353/417(84%)	15/417(3%)	+2
Features	S :							
Query	437				LMRTTNNTLGRS			
Sbjct	151				LMRTTNNTLGRS LMRTTNNTLGRS			
Query	617				KKLEVLPGNGT\ KKLEVLPGNGT\			
Sbjct	211				KKLEVLPGNGT\ KKLEVLPGNGT\			
Query	797				EDSGECASLSNE E SGECASLSNE			
Sbjct	271				EKSGECASLSNE			
Query	977				mgaVTASPGA-S MG VTA+ A S		AAESAAQRTS AA + ORTS	
Sbjct	331				MGVVTAASAAGS			
Query	1154	DIALT	'PKERDILEQHN	VNPMRGSHSTI	ESILRDTsppp ESILRDTSPPP	mpplpnrasn-		pk 1315 P+
Sbjct	391				ESILRDTSPPP			-
Query	1316				SPLPYAQSHNIS			
Sbjct	451				SPLPYAQSHNIS			
Query	1496		SPDENSQCSFDS SPDENSQCSFDS		qqqqhqhLRSFI L+ I		OMDKMVSYS O+DK++SYS	1660
Sbjct	511		SPDENSÕCSFDS			PSRTLHHQLDDI		561

▶ See 1 more title(s) Range 1: 128 to 556

Score		Expect	Metho	d	Identities	Positives	Gaps	Frame
542 bits	(1396)	5e-172()	Compo	ositional matrix adjust.	349/429(81%)	363/429(84%)	21/429(4%)	+2
Features	S :							
Query	437			ARRARSFKDDLIEKIS ARRARSFKDDLIEKIS				
Sbjct	128			ARRARSFKDDLIEKIS				
Query	614			VKDISNALKHFRDVILI VKDISNALKHFRDVILI				
Sbjct	188			VKDISNALKHFRDVILI VKDISNALKHFRDVILI				
Query	794			YQSLGKLIKLCDEVML QSLGKLIKLCDEVML				
Sbjct	248			SÕSLGKLIKLCDEVML				
Query	974			FRYsgsglggigaaae FRY G GLGGIGAAAE			IRVSAA IRVS AA	
Sbjct	308			FRYGGPGLGGIGAAAE:				-
Query	1130			ALTPKERDILEQHNVNI ALTPKERDILEQ N NI				
Sbjct	368			ALTPKERDILEQSNGN				
Query	1310	pkrrs PKRRS	qpsas	agtvgvgcssststsno G S++ STSNo	qasPLPYAQSHN QASPLPY QSHN	NISLNSDLDCSS	SNISLLNYGV SN SLLNYGV	DR 148
Sbjct	428			TGGGNSSSSTTASTSN				
Query	1490			NSQCSFDSALNHSREE NSOCSFDS+LNHSR+E		SFPKLAAMM + M		DE 163 D+
Sbjct	488			NSQCSFDSSLNHSRDE				_
Query	1634	DMDKM D+DK+		1660				
Sbjct	548	DVDKI		556				

uncharacterized protein Dwil_GK25837, isoform B [Drosophila willistoni] Sequence ID: **ref|XP_015032709.1**| Length: 1448 Number of Matches: 1

▶ See 1 more title(s) Range 1: 128 to 556

Score		Expect	Metho	d		Identities	Positiv	es Gaps	Fı	rame
543 bits	(1399)	5e-172()	Compo	sitional m	atrix adjust	. 349/429(8	1%) 363/429	9(84%) 21/429	9(4%) +2	2
Feature	s:									
Query	437							PRTKHGT-KAP		
Sbjct	128							PR KHG+ K F PRAKHGSAKPF		
Query	614							ASMYSVIQTY ASMYSVIO+Y		
Sbjct	188							ASMYSVIQSY ASMYSVIQSY		
Query	794							/IDLLEDAVRN /IDLLEDAVRN		
Sbjct	248							/IDLLEDAVRN		
Query	974	GKLKE	ODOCA	FRYsgsg]	lggigaaae LGGIGAAAE	imgaVTAS	PGASVPGT S T	GVMRVS MRVS	AAES	
Sbjct	308							ISVANMRVSAD		
Query	1130							opkpplpnras PPKPPLPNR S		
Sbjct	368							PREPLENK		
Query	1310	pkrrs PKRRS		agtvgvgo G	cssststsn	qasPLPYA	OSHNISLNSI	DLDCSSNISLI DLDCSSN SLI	NYGVDR	1489
Sbjct	428			_				DLDCSSNFSLI		
Query	1490				SALNHSREE S+LNHSR+E		nLRSFPKLA <i>l</i> L+ +	MM M	DE D+	
Sbjct	488							JOMKSTAAKQS		
Query	1634	DMDKM D+DK+		1660						
Sbjct	548	DYDKI		556						

C3G [Drosophila busckii]

Sequence ID: **gb|ALC49227.1|** Length: 1099 Number of Matches: 1 Range 1: 105 to 530

Score		Expect	Met	hod				ldent	ities		Positi	ves	(Gaps		Frai	ne
515 bits	(1327)	1e-164()	Con	npositio	nal ma	itrix ac	djust.	327/4	27(77	7%) 3	353/42	27(82	%) 2	21/427	7(4%)	+2	
Features	s:																
Query	437			KLARR <i>I</i> KLARR <i>I</i>													613
Sbjct	105			KLARR <i>I</i>													164
Query	614			THVKDI THVKDI													793
Sbjct	165			THVKD1													224
Query	794			OVYOSI ÕVYÕSI													973
Sbjct	225			QV 1051 QVYQSI													284
Query	974			CAFRYS						GAS\ A		SVM				-RV	1114
Sbjct	285			SAFRYS									SLRS	SDAA	AAAV	7AA	344
Query	1115	SAAES +AA		RTSLPI RTSLPI				-EQHN + ++									1288
Sbjct	345			RTSLPI													404
Query	1289			krrsqr KRRSQI		gtvgv		sstst + +									1468
Sbjct	405			KRRSQI		AAQS <i>I</i>											463
Query	1469			SVRSRS									PKLA PK				1636
Sbjct	464			SVRSRS SVRSRS							Q QLQLQ			M PIMLR		DED DED	523
Query	1637	MDKMV		1657													
Sbjct	524	+DK++ LDKLI		530													

uncharacterized protein Dpse_GA16131, isoform K [Drosophila pseudoobscura pseudoobscura] Sequence ID: ref|XP_015041266.1| Length: 1426 Number of Matches: 1

▶ See 1 more title(s) kange 1: 1 to 531

Score		Expect	Method		Identities	Positives	Gaps	Frame
521 bits	(1342)	7e-164()) Compositional mat	trix adjust.	375/538(70	%) 399/538(74%	o) 56/538(10 ⁹	%) +2
Features	S :							
Query	518		NNTLGRSHSPHSPRI NNTLGRSHSPHSPRI			RSTQTLETHVKD RSTQTLETHVKD		
Sbjct	1		NNTLGRSHSPHSPRI NNTLGRSHSPHSPRI					
Query	692		EVLPGNGTVILETI <i>I</i> EVLPGNGTVILETI <i>I</i>					
Sbjct	61		EVLPGNGTVILETI <i>F</i> EVLPGNGTVILETI <i>F</i>					
Query	869		SGECASLSNENVREV					
Sbjct	121		SGEC SLSN+NVRE\ SGECPSLSNDNVRE\					
Query	1046		gaVTAS	PGASVP	GTGV			
Sbjct	181		GAVTAS GAVTASSTNAGSGG]				QRTSLPDIA QRTSLPDIA	
Query	1175		LEQHNVNPMRGSHS7					gtvg 1354
Sbjct	241	ER II ERAII	LE NVNPMRGSHS7 LEHRNVNPMRGSHS7			$egin{array}{ll} ext{N} & ext{PP} \ ext{PPLPNRASNPPP} \end{array}$	+ + LPPKRRSQP(QAPP 296
Query	1355	vgcss	sststsngasPLPY	AOSHNISL	NSDLDCSSN	ISLLNYGVDRLS	VRSRSPDEN:	SQCS 1534
Sbjct	297		SSTSTSNÕASPLPY <i>I</i> SSTSTSNÕASPLPY <i>I</i>					
Query	1535		LNHSREEEDqqqqh					
Sbjct	357		LNHSREEED QQQ (LNHSREEEDPQQQQ(DKM+SY+ DKMISYNAAGSA		A AQAP 413
Query	1673		TPLstgggi					
Sbjct	414		T L G G TLLPGTGVPGPGPG <i>I</i>		GG GE GGGGETNTE		HSNESGFVSI HSNESGFVSI	
Query	1835	RTST	QTTDYsvqss	stkssssn	seiafs	isesTAVGSSSE	YQQISQLVSI	HS 1984

GM12551 [Drosophila sechellia]

Sequence ID: ref|XP_002036724.1| Length: 596 Number of Matches: 2

▶ See 1 more title(s) Range 1: 266 to 527

Score		Expect	Method	Identities	Positives	Gaps	Frame
485 bits	(1249)	3e-159()	Compositional matrix adjust.	258/262(98%)	259/262(98%)	0/262(0%)	+2
Features	S :						
Query	437		KGTKLARRARSFKDDLIEKIS KGTKLARRARSFKDDLIEKIS				
Sbjct	266		KGTKLARRARSFKDDLIEKIS				
Query	617		LETHVKDISNALKHFRDVILK LETHVKDISNALKHFRDVILK				
Sbjct	326		LETHVKDISNALKHFRDVILK				
Query	797		TLQVYQSLGKLIKLCDEVMLSI T QVYQSLGKLIKLCDEVMLSI				
Sbjct	386		TQQVYQSLGKLIKLCDEVMLS				
Query	977		DQCAFRYsgsglggigaaaeir DQCAFRYSGSGLGGIGAAAEI				
Sbjct	446		DÕCAFRYSGSGLGGIGAAAEII				
Query	1157		KERDILEQHNVNPMRGS 123 KERDILEQHNVNPMRGS	22			
Sbjct	506		KERDILEQHNVNPMRGS 52	7			

Range 2: 528 to 575

Score	Expect Method	Identities	Positives	Gaps	Frame
93.2 bits(230)	3e-16() Compositional matrix adjust.	45/48(94%)	45/48(93%)	0/48(0%)	+3
Features:					
Query 122	TAPKVSCATRVHRRSHRYPIGPVIRRRCI TAPKVSCATRVHRRSHRYPIGPV RRRCI			1367	
Sbjct 528	TAPKVSCATRVHRRSHRYPIGPVTRRRC			575	

uncharacterized protein Dvir_GJ16545, isoform G [Drosophila virilis]
Sequence ID: **ref|XP_015025477.1**| Length: 1237 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 384

Score		Expect	Method	Identities	Positives	Gaps	Frame
501 bits	(1289)	7e-158()	Compositional matrix adjust.	301/390(77%)	326/390(83%)	15/390(3%)	+2
Features	S:						
Query	518		INTLGRSHSPHSPRTKHGTKAPI INTLGRSHSPHSPR+KHG+K PI				
Sbjct	1		INTLGRSHSPHSPRSKHGSKPPI				
Query	698		.PGNGTVILETIASMYSVIQTY1 .PGNGTVILETIASMYSVIQ+Y1				
Sbjct	61		PGNGTVILETIASMYSVIQSYT				
Query	878		ASLSNENVREVIDLLEDAVRNI ASLSNENVREVIDLLEDAVRNI				
Sbjct	121		CASLSNENVREVIDLLEDAVRNI				
Query	1058		ASPGA-SVPGTGVMRVSAAESA	AQRTSLPDIALT QRTSLPDIALT			
Sbjct	181		A+ A SV G +AA + ASAAGSVTGLRTPADAAAAAV\				
Query	1235		Tspppkpplpnrasnp				
Sbjct	241		TSPPPKPPLPNRASN TSPPPKPPLPNRASNPPPLPPF		+ ++ IANASTNTNTNE	++++ +S TTTSHSSQA	S NS 300
Query	1397	PLPYA	QSHNISLNSDLDCSSNISLLNY	/GVDRLSVRSRS	SPDENSQCSFDS	SALNHSREEE	Dq 1576

Sbjct	301	PLPYAQSHNISLNSDLDCSSN SLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEE+ PLPYAQSHNISLNSDLDCSSNFSLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEE-	359
Query	1577	qqqhqhLRSFPKLAAMMDEDMDKMVSYS 1660 L+ P L +D+D+DK++SYS	
Sbjct	360	QLQKPPSRTLHHQLDDDVDKLISYS 384	

GD16179 [Drosophila simulans]

Sequence ID: ref|XP_002106330.1| Length: 491 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 377

Score		Expect	Method		Identities	Positives	Gaps	Frame
466 bits((1198)	4e-153()	Compositional ma	atrix adjust.	361/377(96%)	362/377(96%)	0/377(0%)	+2
Features	s:							
Query	866		SGECASLSNENVRI SGECASLSNENVRI					
Sbjct	1		SGECASLSNENVRI					
Query	1046		aVTASPGASVPGTO AVTASPG SVPG (
Sbjct	61		AVTASPG SVPG (AVTASPGVSVPGA					
Query	1226	STESI	LRDTspppkpplp: LRDTSPPPKPPLP:	nrasnpppl	ppkrrsqpsas	agtvgvgcsss	tstsngasP	LP 1405
Sbjct	121		LRDTSPPPKPPLPI					
Query	1406		NISLNSDLDCSSN: NISLNSDLDCSSN:					
Sbjct	181		NISLNSDLDCSSN:					
Query	1586	hqhLR	SFPKLAAMMDEDMI SFPKLAAMMDEDMI	DKMVSYSAA	IDDKTQTPLst	gggiagvaggt	ggagegvaa	aa 1765
Sbjct	241		SFPKLAAMMDEDMI SFPKLAAMMDEDMI					
Query	1766	sgdge	TNSNRHSNESGFV:	SMREFRTST	QTTDYsvqsst	kssssnseiaf	sisesTAVG	SS 1945
Sbjct	301		TNSNR SNESGEV.					
Query	1946		ISOLVSHSORHI	1996				
Sbjct	361		ISQ VSHSQRHI ISQSVSHSQRHI	377				

uncharacterized protein Dmoj_Gl21607, isoform F [Drosophila mojavensis] Sequence ID: **ref|XP_015016529.1|** Length: 1500 Number of Matches: 3

▶ See 1 more title(s) Range 1: 113 to 387

Score		Expect	Method	Identities	Positives	Gaps	Frame
446 bits	(1148)	2e-135()	Compositional matrix adjust.	246/275(89%)	252/275(91%)	3/275(1%)	+2
Features	S :						
Query	437		KGTKLARRARSFKDDLIEKISL KGTKLARRARSFKDDLIEKISL				
Sbjct	113		KGTKLARRARSFKDDLIEKISL				
Query	617		LETHVKDISNALKHFRDVILKK LETHVKDISNALKHFRDVIL+K				
Sbjct	173		LETHVKDISNALKHFRDVILRK				
Query	797		TLQVYQSLGKLIKLCDEVMLSE T QVYQSLGKLIKLCDEVMLSE				
Sbjct	233		TQQVYQSLGKLIKLCDEVMLSE				
Query	977		DQCAFRYsgsglggigaaaeim DQC FRYSG GLGGIGAAA+IM			SAAESAAQR +AA + AOR	
Sbjct	293		DOC FRISG GLGGIGAAA+IM DOCTFRYSGGGLGGIGAAADIM				
Query	1148		LTPKERDILEOHNVNPMRGSHS		252		
Sbjct	353		LTPKERDILEQ NVNPMRGSHS LTPKERDILEQSNVNPMRGSHS		87		

Score		Expect	Method	Identities	Positives	Gaps	Frame
134 bits	(337)	8e-29()	Compositional matrix adjust.	66/88(75%)	74/88(84%)	0/88(0%)	+2
Features	S :						
Query	1397		AQSHNISLNSDLDCSSNISLLNYGV AQSHNISLNSDLDCSSN SLLNYGV				
Sbjct	473		AQSHNISLNSDLDCSSN SLLNIGV AQSHNISLNSDLDCSSNFSLLNYGV				
Query	1577		qhLRSFPKLAAMMDEDMDKMVSYS + +D+D+DK++SY+	1660			
Sbjct	533	Q+ LQKPI	PSRTLHHQQHQQLDDDVDKLISYT	560			

Range 3: 633 to 654

Score		Expect	Method		Identities	Positives	Gaps	Frame
42.7 bits	(99)	1.9()	Compositional matrix adj	ust.	19/22(86%)	20/22(90%)	0/22(0%)	+2
Features	s:							
Query	1787		SNESGFVSMREFRTSTQT SNESGFVSM FRTSTO+	1852				
Sbjct	633		SNESGFVSMMSFRTSTQS	654				

uncharacterized protein Dmoj_Gl21607, isoform B [Drosophila mojavensis] Sequence ID: **ref|XP_015016526.1|** Length: 1537 Number of Matches: 3

▶ See 1 more title(s) Range 1: 150 to 424

Score		Expect	Method	Identities	Positives	Gaps	Frame
447 bits	(1149)	2e-135()	Compositional matrix adjust.	246/275(89%)	252/275(91%)	3/275(1%)	+2
Features	S :						
Query	437		KGTKLARRARSFKDDLIEKISL KGTKLARRARSFKDDLIEKISL				
Sbjct	150		KGTKLARRARSFKDDLIEKISL				
Query	617		LETHVKDISNALKHFRDVILKK LETHVKDISNALKHFRDVIL+K				
Sbjct	210		LETHVKDISNALKHFRDVILRK				
Query	797		TLQVYQSLGKLIKLCDEVMLSE T QVYQSLGKLIKLCDEVMLSE				
Sbjct	270		TQQVYQSLGKLIKLCDEVMLSE				
Query	977		DQCAFRYsgsglggigaaaeim DQC FRYSG GLGGIGAAA+IM			SAAESAAQR' +AA + AOR'	
Sbjct	330		DÕCTFRYSGGGLGGIGAAATIM				
Query	1148		LTPKERDILEQHNVNPMRGSHS LTPKERDILEQ NVNPMRGSHS		252		
Sbjct	390		LTPKERDILEQSNVNPMRGSHS		24		

Range 2: 510 to 597

Score		Expect	Method	Identities	Positives	Gaps	Frame	<u>e</u>
134 bits	(337)	8e-29()	Compositional matrix adjust.	66/88(75%)	74/88(84%)	0/88(0%)	+2	
Features:								
Query	1397		AQSHNISLNSDLDCSSNISLLNYG AQSHNISLNSDLDCSSN SLLNYG					1576
Sbjct	510		AQSHNISLNSDLDCSSNFSLLNYG AQSHNISLNSDLDCSSNFSLLNYG					569
Query	1577	qqqha	qhLRSFPKLAAMMDEDMDKMVSYS + +D+D+DK++SY+	1660				
Sbjct	570	~	PSRTLHHQQHQQLDDDVDKLISYT	597				

Range 3: 670 to 691

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.7 bits(99)	2.0()	Compositional matrix adjust.	19/22(86%)	20/22(90%)	0/22(0%)	+2

Features:

Query	1787	SNRHSNESGFVSMREFRTSTQT	1852
_		SNRHSNESGFVSM FRTSTQ+	
Sbjct	670	SNRHSNESGFVSMMSFRTSTQS	691

uncharacterized protein Dmoj_Gl21607, isoform C [Drosophila mojavensis] Sequence ID: **ref|XP_015016527.1|** Length: 1546 Number of Matches: 2

▶ See 1 more title(s) Range 1: 248 to 522

Score		Expect Method	Identities	Positives	Gaps I	Frame
446 bits	(1147)	4e-135() Compositional matrix adjus	t. 246/275(89%)	252/275(91%)	3/275(1%) +	+2
Features	3 :					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI: HKNSLKGTKLARRARSFKDDLIEKI:				
Sbjct	248	HKNSLKGTKLARRARSFKDDLIEKI;				
Query	617	RSTQTLETHVKDISNALKHFRDVILIRSTQTLETHVKDISNALKHFRDVIL				
Sbjct	308	RSTQTLETHVKDISNALKHFRDVILI				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLS				
Sbjct	368	IMSSATQQVYQSLGKLIKLCDEVML				
Query	977	KLKEQDQCAFRYsgsglggigaaae: KLKEQDQC FRYSG GLGGIGAAA+	imgaVTASPGA		SAAESAAQRT +AA + AORT	
Sbjct	428	KLKEQDQCTFRYSGGGLGGIGAAAD:				
Query	1148	LPDIALTPKERDILEQHNVNPMRGSI LPDIALTPKERDILEQ NVNPMRGSI		252		
Sbjct	488	LPDIALTPKERDILEQSNVNPMRGSI		22		

Range 2: 608 to 695

Score		Expect	Method	Identities	Positives	Gaps	Frame	_
135 bits	(339)	4e-29()	Compositional matrix adjust.	67/88(76%)	74/88(84%)	0/88(0%)	+2	_
Features	S :							
Query	1397		AQSHNISLNSDLDCSSNISLLNYGV AQSHNISLNSDLDCSSN SLLNYGV					576
Sbjct	608		AQSHNISLNSDLDCSSNFSLLNYG AQSHNISLNSDLDCSSNFSLLNYG					67
Query	1577	qqqho	qhLRSFPKLAAMMDEDMDKMVSYS + +D+D+DK++SYS	1660				
Sbjct	668	~	PSRTLHHQQHQQLDDDVDKLISYS	695				

uncharacterized protein Dmoj_Gl21607, isoform D [Drosophila mojavensis] Sequence ID: **ref|XP_015016528.1|** Length: 1554 Number of Matches: 2

▶ See 1 more title(s) Range 1: 248 to 522

Score		Expect	Method	Identities	Positives	Gaps	Frame
445 bits((1145)	7e-135()	Compositional matrix adjust.	246/275(89%)	252/275(91%)	3/275(1%)	+2
Features	S:						
Query	437		KGTKLARRARSFKDDLIEKISI				
Sbjct	248		KGTKLARRARSFKDDLIEKISI KGTKLARRARSFKDDLIEKISI				
Query	617		LETHVKDISNALKHFRDVILKI LETHVKDISNALKHFRDVIL+I				
Sbjct	308		LETHVKDISNALKHFRDVILRE				
Query	797		TLQVYQSLGKLIKLCDEVMLSI T QVYQSLGKLIKLCDEVMLSI				
Sbjct	368		TQQVYQSLGKLIKLCDEVMLSI				
Query	977		DOCAFRYsgsglggigaaaein DOC FRYSG GLGGIGAAA+IN			SAAESAAQR +AA + AQR	

Sbjct	428	KLKEQDQCTFRYSGGGLGGIGAAADIMGAVTAASTAGGSVPGLHTPADAAAAAAVAQRTS			
Query	1148	LPDIALTPKERDILEQHNVNPMRGSHSTESILRDT LPDIALTPKERDILEQ NVNPMRGSHSTESILRDT	1252		
Sbjct	488	LPDIALTPKERDILEÖ NVNFMRGSHSTESILRDT	522		

Range 2: 608 to 695

Score		Expect Method Ide	entities	Positives	Gaps	Frame
134 bits	(338)	5e-29() Compositional matrix adjust. 67/	(88(76%)	74/88(84%)	0/88(0%)	+2
Features	S :					
Query	1397	PLPYAQSHNISLNSDLDCSSNISLLNYGVDRI PLPYAQSHNISLNSDLDCSSN SLLNYGVDRI				
Sbjct	608	PLPYAQSHNISLNSDLDCSSNFSLLNYGVDRI				
Query	1577	111 1	560			
Sbjct	668	Q+ + +D+D+DK++SYS LQKPPSRTLHHQQHQQLDDDVDKLISYS 69)5			

uncharacterized protein Dmoj_Gl21607, isoform G [Drosophila mojavensis] Sequence ID: **ref|XP_015016530.1|** Length: 1635 Number of Matches: 3

▶ See 1 more title(s) Range 1: 248 to 522

Score	E	Expect	Method	Identities	Positives	Gaps	Frame
446 bits(1	147) 9	e-135()	Compositional matrix adjust.	246/275(89%)	252/275(91%)	3/275(1%)	+2
Features:							
Query 4	137		KGTKLARRARSFKDDLIEKISL KGTKLARRARSFKDDLIEKISL				
Sbjct 2	248		KGTKLARRARSFKDDLIEKISL KGTKLARRARSFKDDLIEKISL				
Query 6	517		LETHVKDISNALKHFRDVILKK LETHVKDISNALKHFRDVIL+K				
Sbjct 3	308		LETHVKDISNALKHFRDVILRK LETHVKDISNALKHFRDVILRK				
Query 7	797		TLQVYQSLGKLIKLCDEVMLSE T QVYQSLGKLIKLCDEVMLSE				
Sbjct 3	368		TQQVYQSLGKLIKLCDEVMLSE				
Query 9	977		DQCAFRYsgsglggigaaaeim DQC FRYSG GLGGIGAAA+IM			SAAESAAQRT AA + AORT	
Sbjct 4	128		DOC FRISG GLGGIGAAA IM DOCTFRYSGGGLGGIGAAADIM				
Query 1	1148		LTPKERDILEQHNVNPMRGSHS LTPKERDILEQ NVNPMRGSHS		252		
Sbjct 4	188		LTPKERDILEQ NVNFMRGSHS LTPKERDILEQSNVNPMRGSHS		22		

Range 2: 608 to 695

Score		Expect	Method	Identities	Positives	Gaps	Frame	
134 bits	(336)	1e-28()	Compositional matrix adjust.	66/88(75%)	74/88(84%)	0/88(0%)	+2	
Features	s:							
Query	1397		AQSHNISLNSDLDCSSNISLLNYG					6
Sbjct	608		AQSHNISLNSDLDCSSN SLLNYG AQSHNISLNSDLDCSSNFSLLNYG					
Query	1577	0+ qqqh	qhLRSFPKLAAMMDEDMDKMVSYS + +D+D+DK++SY+	1660				
Sbjct	668	~	PSRTLHHQQHQQLDDDVDKLISYT	695				

Range 3: 768 to 789

Score	Expect	Method		Identities	Positives	Gaps	Frame
42.7 bits(9	99) 2.0()	Compositional matrix ac	ljust.	19/22(86%)	20/22(90%)	0/22(0%)	+2
Features:							
Query 1		HSNESGFVSMREFRTSTOT HSNESGFVSM FRTSTO+	1852				

Sbjct 768 SNRHSNESGFVSMMSFRTSTQS 789

uncharacterized protein Dmoj_Gl21607, isoform H [Drosophila mojavensis] Sequence ID: **ref|XP_015016531.1**| Length: 1634 Number of Matches: 3

▶ See 1 more title(s) Range 1: 248 to 522

Score		Expect	Method	Identities	Positives	Gaps	Frame
446 bits	(1147)	9e-135()	Compositional matrix adjust.	246/275(89%)	252/275(91%)	3/275(1%)	+2
Features	S :						
Query	437		KGTKLARRARSFKDDLIEKISL KGTKLARRARSFKDDLIEKISL				
Sbjct	248		KGTKLARRARSFKDDLIEKISL				
Query	617		LETHVKDISNALKHFRDVILKK				
Sbjct	308		LETHVKDISNALKHFRDVIL+K LETHVKDISNALKHFRDVILRK				
Query	797		TLQVYQSLGKLIKLCDEVMLSE				
Sbjct	368		T QVYQSLGKLIKLCDEVMLSE TQQVYQSLGKLIKLCDEVMLSE				
Query	977		DQCAFRYsgsglggigaaaeim				
Sbjct	428		DQC FRYSĞ ĞLĞĞIĞAAA+IM DQCTFRYSGGGLGGIGAAADIM			-AA + AQR' AAAAAVAQR'	
Query	1148		LTPKERDILEQHNVNPMRGSHS		252		
Sbjct	488		LTPKERDILEQ NVNPMRGSHS LTPKERDILEQSNVNPMRGSHS		22		

Range 2: 608 to 696

Score		Expect	Method	Identities	Positives	Gaps	Frame	_
134 bits	(336)	1e-28()	Compositional matrix adjust.	66/89(74%)	74/89(83%)	0/89(0%)	+2	_
Features	s:							
Query	1397		AQSHNISLNSDLDCSSNISLLNYG AQSHNISLNSDLDCSSN SLLNYG					576
Sbjct	608		AQSHNISLNSDLDCSSNFSLLNYG					57
Query	1577	qqqha	qhLRSFPKLAAMMDEDMDKMVSYSA + +D+D+DK++SY -					
Sbjct	668	~	+ +D+D+DK++SY - PSRTLHHQQHQQLDDDVDKLISYK					

Range 3: 767 to 788

Score		Expect	Method		Identities	Positives	Gaps	Frame
42.7 bits	s(99) 2	2.0()	Compositional matrix ac	ljust.	19/22(86%)	20/22(90%)	0/22(0%)	+2
Features	S :							
Query	1787		SNESGFVSMREFRTSTQT SNESGFVSM FRTSTQ+	1852				
Sbjct	767		SNESGFVSMMSFRTSTQS	788				

uncharacterized protein Dmoj_Gl21607, isoform E [Drosophila mojavensis] Sequence ID: **ref|XP_002010627.2**| Length: 1627 Number of Matches: 3

▶ See 1 more title(s) Range 1: 248 to 522

Score		Expect	Method	Identities	Positives	Gaps	Frame	1
446 bits	(1147) 9	9e-135()	Compositional matrix adjust.	246/275(89%)	252/275(91%)	3/275(1%)	+2	
Features	S :							
Query	437		KGTKLARRARSFKDDLIEKISL KGTKLARRARSFKDDLIEKISL				_	16
Sbjct	248		KGTKLARRARSFKDDLIEKISL					07

Query	617	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA RSTQTLETHVKDISNALKHFRDVIL+KKLEVLPGNGTVILETIASMYSVIQ+YTLNENSA	796
Sbjct	308	RSTQTLETHVKDISNALKHFRDVILRKKLEVLPGNGTVILETIASMYSVIQSYTLNENSA	367
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG IMSSAT QVYQSLGKLIKLCDEVMLSE S ECASLSNENVREVIDLLEDAVRNLVTLAQG	976
Sbjct	368	IMSSATQQVYQSLGKLIKLCDEVMLSEKSTECASLSNENVREVIDLLEDAVRNLVTLAQG	427
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGV-MRVSAAESAAQRTS KLKEQDQC FRYSG GLGGIGAAA+IMGAVTA+ G SVPG +AA + AQRTS	1147
Sbjct	428	KLKEQDQCTFRYSGGGLGGIGAAADIMGAVTAASTAGGSVPGLHTPADAAAAAAAAAAQRTS	487
Query	1148	LPDIALTPKERDILEOHNVNPMRGSHSTESILRDT 1252	
Sbict	488	LPDIALTPKERDILEQ NVNPMRGSHSTESILRDT LPDIALTPKERDILEOSNVNPMRGSHSTESILRDT 522	

Range 2: 608 to 695

Score		Expect	Method	Identities	Positives	Gaps	Frame	<u>e</u>
134 bits(336)	1e-28()	Compositional matrix adjust.	66/88(75%)	74/88(84%)	0/88(0%)	+2	
Features:								
Query	1397		AQSHNISLNSDLDCSSNISLLNYG AQSHNISLNSDLDCSSN SLLNYG					1576
Sbjct	608		AQSHNISLNSDLDCSSNFSLLNYG					667
Query	1577	o+ qqqh	qhLRSFPKLAAMMDEDMDKMVSYS + +D+D+DK++SY+	1660				
Sbjct	668	~	PSRTLHHQQHQQLDDDVDKLISYT	695				

Range 3: 768 to 789

Score		Expect	Method		Identities	Positives	Gaps	Frame
42.7 bits	s(99) 2	2.0()	Compositional matrix adj	ust.	19/22(86%)	20/22(90%)	0/22(0%)	+2
Features	3 :							
Query	1787		SNESGFVSMREFRTSTOT	1852				
Sbjct	768		SNESGFVSM FRTSTQ+ SNESGFVSMMSFRTSTQS	789				

GH24527 [Drosophila grimshawi]

Sequence ID: ref|XP_001992006.1| Length: 1545 Number of Matches: 2

▶ See 1 more title(s) Range 1: 244 to 518

Score	I	Expect	Method	Identities	Positives	Gaps	Frame
438 bits(1126) 3	Be-132()	Compositional matrix adjust.	246/275(89%)	251/275(91%)	3/275(1%)	+2
Features	:						
Query	437		KGTKLARRARSFKDDLIEKISL				
Sbjct	244		KGTKLA+RARSFKDDLIEKISL KGTKLAKRARSFKDDLIEKISL				
Query	617		LETHVKDISNALKHFRDVILKK LETHVKDISNALKHFRDVILKK				
Sbjct	304		LETHVKDISNALKHFRDVILKK LETHVKDISNALKHFRDVILKK				
Query	797		TLQVYQSLGKLIKLCDEVMLSE T QVYQSLGKLIKLCDEVMLSE				
Sbjct	364		TQQVYQSLGKLIKLCDEVMLSE				
Query	977		DQCAFRYsgsglggigaaaeim DQCAFRY GSGLGGIGAAA+IM			SAAESAAQR +AA + AQR	
Sbjct	424		DQCAFRYGGSGLGGIGAAATIM DQCAFRYGGSGLGGIGAAADIM				
Query	1148		LTPKERDILEQHNVNPMRGSHS LTPKERDILEQ N NPMRGSHS		252		
Sbjct	484		LTPKERDILEQ N NFMRGSHS LTPKERDILEQSNSNPMRGSHS		18		

Range 2: 576 to 727

Score Expect Method Id	dentities Positives	Gaps	Frame
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124 bits(312) 9e-26() Compositional matrix adjust. 78/157(50%) 98/157(62%) 14/157(8%) +2									
Feature	s:								
Query	1397	PLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEEDq PLPYAQ+HNIS+NSDLDCSSN+SLLN+GVDRLSVRSRSPDENSQCS DSALNHSREEE++	1576						
Sbjct	576	PLPYAQTHNISINSDLDCSSNLSLLNFGVDRLSVRSRSPDENSQCS DSALNHSREEEEE	635						
Query	1577	qqqhqhLRSFPKLAAMMDEDMDKMVSYSAAIDDKTQTPLstgggiagvagg OO + + + +D+DK++SY+ + + + + + G G	1729						
Sbjct	636	Q Q + + + +D+DK++SY+ + + + + + G G HLQLQLQKPPTRQQQQQQQMHHHLAVDDVDKLISYTTSSSQMAVTFGPGSRPGA	690						
Query	1730	tggagegvaaaasgdgeTNSNRHSNESGFVSMREFRT 1840							
Sbjct	691	E ++NRHSNESGFVSM FRT VLTTAEASTELRKVSTPLSNNRHSNESGFVSMMSFRT 727							

PREDICTED: guanine nucleotide-releasing factor 2 isoform X4 [Bactrocera dorsalis]

Sequence ID: ref|XP_011207149.1| Length: 1355 Number of Matches: 1

Range 1: 127 to 501

Score	Ex	kpect Method	Identities	Positives	Gaps	Frame
347 bits((891) 2e	-100() Compositional matrix adju	st. 230/430(53%) 269/430(62%)	81/430(18%)	+2
Features	3:					
Query	437	HKNSLKGTKLARRARSFKDDLIE			_	
Sbjct	127	HKNSLKGTKLARRARSFKDDLIE HKNSLKGTKLARRARSFKDDLIE			K P T EE+ SMKPPTTAEEL	
Query	617	RSTQTLETHVKDISNALKHFRDV				
Sbjct	186	+ L+THVKDISNALKHFRDV AAESPLQTHVKDISNALKHFRDV				
Query	797	IMSSATLQVYQSLGKLIKLCDEVI				
Sbjct	246	++ SAT QVYQSLGKL+KLCDEVI VLLSATQQVYQSLGKLVKLCDEVI			A LS +NV+E LKALLSEDNVKE	
Query	926	IDLLEDAVRNLVTLAQGKLKEQDO	QCAFRYsgsglgg	igaaaeimga V		
Sbjct	306	+DLL +AVRNL TLA KLKE++- VDLLGEAVRNLATLAHQKLKERE	T A TIT ENALKYAPDNAVA	A AALANNG	A+V AAVSLNH	+ IL 356
Query	1106	MRVSAAESAAQRTSLPDIALTPKI M + E A QRTSLPDI LTPKI				
Sbjct	357	MHLPEVAGQRTSLPDITLTPK				
Query	1286	asnppplppkrrsqpsasagtvg	vgcssststsnqa	SPLPYAOSHNIS O	SLNSDLD SLN SD D	C 1450
Sbjct	415	PPPLPPKRR		NQQQQP	SLNNKSINSDFD)W 442
Query	1451	SSNISLLNYGVDRLSVRSRSS SS+ISL NYG D LSV S S	PDEN-SQCSFDSA PDEN SQCS DS		qqhqhLRSFPKL	A 1618
Sbjct	443	SSTISL NIG D LSV S S. S	PDEN SQCS DS PDENSSQCSLDSE	LNHSREEGNGYI	ND	491
Query	1619	AMMDEDMDKM 1648 +++D D+DK+				
Sbjct	492	SLLDNDVDKL 501				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X1 [Ceratitis capitata]

Sequence ID: ref|XP_012158749.1| Length: 1499 Number of Matches: 1

Range 1: 128 to 530

Score	Ex	pect	Method	Identities	Positives	Gaps	Frame
347 bits	(890) 5e-	-100()	Compositional matrix adjust.	231/431(54%)	278/431(64%)	55/431(12%)	+2
Features	s:						
Query	437		LKGTKLARRARSFKDDLIEKIS				
Sbjct	128		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS			K PPT EE SMKPPPTAEE	•
Query	617		TLETHVKDISNALKHFRDVILF +LE HVKDISNALKHFRDVILF				
Sbjct	187		SLENHVKDISNALKHFRDVIL				
Query	797		ATLQVYQSLGKLIKLCDEVML- AT OVYOSLGKL+KLCDEVML				898
Sbjct	247		ATQQVYQSLGKLVKLCDEVMLI		GGADGDGVGDG	SNAQTERQQLK	TL 306
Query	899		NVREVIDLLEDAVRNLVTLAQONV+E++DLL DAVRNL TL+Q				SP 1078 S
Sbjct	307		NVKEIVDLLGDAVRNLATLSÕÇ				-

Query	1079	GASVPGTGVMRVSAAESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTsp A+V +MR+ E A QRTSLPDI LTPKERDILE+ N NP+R SHSTESILRDTSP	1258
Sbjct	366	-AAVSHNHLMRL-PVEVAGQRTSLPDITLTPKERDILEKTNSNPIRASHSTESILRDTSP	423
Query	1259	ppkpplpnrasnppplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNS	1438
Sbjct	424	PPKPPLPNRPPPLPPKRRNQQQNQQQLLSNNKSMNSDLEW	463
Query	1439	DLDCSSNISLLNYGVDRLSVRSRSPDEN-SQCSFDSALNHSREEEDqqqqhqhLRSFPKL + D S ++Y + LSV S SPDEN SOCS DS LNHSREEE+ + R	1615
Sbjct	464	NSDISLGNYGVDY-MSNLSVHSHSPDENSSQCSLDSELNHSREEEELKALGLGNRLN	519
Query	1616	AAMMDEDMDKM 1648 +M+D D+DK+	
Sbjct	520	DSMLDNDVDKL 530	

PREDICTED: guanine nucleotide-releasing factor 2 isoform X2 [Bactrocera dorsalis]

Sequence ID: ref|XP_011207145.1| Length: 1448 Number of Matches: 1

▶ See 1 more title(s) Range 1: 122 to 496

Score	E	xpect	Method	Identities	Positives	Gaps	Frame
347 bits	(889) 6e	: -100()) Compositional matrix adjust.	233/430(54%)	273/430(63%)	81/430(18%)	+2
Features	S:						
Query	437		SLKGTKLARRARSFKDDLIEKI SLKGTKLARRARSFKDDLIEKI			_	
Sbjct	122		SLKGTKLARRARSFKDDLIEKI SLKGTKLARRARSFKDDLIEKI			K P T EE- SMKPPTTAEEI	
Query	617	RSTÇ +	QTLETHVKDISNALKHFRDVIL +THVKDISNALKHFRDVI+				
Sbjct	181	•	SPLQTHVKDISNALKHFRDVII				
Query	797		SATLQVYQSLGKLIKLCDEVML SAT OVYOSLGKL+KLCDEVML		E	-CASLSNENVRI A LS +NV+I	
Sbjct	241		SAT QVIQSLGKL*KLCDEVML SATQQVYQSLGKLVKLCDEVML		VEDNLQDEHQQI		
Query	926	IDLI	LEDAVRNLVTLAQGKLKEQDQC L +AVRNL TLA KLKE+++	AFRYsgsglgg:	igaaaeimgaV	TASPGASVPGT(A+ GA+V	GV 1105
Sbjct	301	VDLI	LGEAVRNLATLAHQKLKEREEN	ALKY	APDNAVAĀAI		
Query	1106	MRVS M +	SAAESAAQRTSLPDIALTPKER E A QRTSLPDI LTPKER	DILEQHNVNPMI	RGSHSTESILRI	OTspppkpplpr	nr 1285
Sbjct	352		PEVAGQRTSLPDITLTPKER				
Query	1286		opplppkrrsqpsasagtvgvg PP				
Sbjct	410	PPPI	PP LPPKRR		NQQQQPS	SLNNKSINSDFI	OW 437
Query	1451		ISLLNYGVDRLSVRSRSPD ISL NYG D LSV S SPD	EN-SQCSFDSAI EN SQCS DS I		qqhqhLRSFPKI	LA 1618
Sbjct	438		ISL NIG D LSV S SFD ISLGNYGADYISNLSVHSHSPD	ENSSÕCSLDSEI	LNHSREEGNGY	ND	486
Query	1619		DEDMDKM 1648 D D+DK+				
Sbjct	487		DNDVDKL 496				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X2 [Ceratitis capitata]

Sequence ID: ref|XP_012158750.1| Length: 1495 Number of Matches: 1

Range 1: 124 to 526

Score	E	Expect	Method	Identities	Positives	Gaps	Frame
347 bits	(889) 8	Be-100()	Compositional matrix adjust.	231/431(54%)	278/431(64%)	55/431(12%)	+2
Features	S :						
Query	437		LKGTKLARRARSFKDDLIEKIS LKGTKLARRARSFKDDLIEKIS			HGTKAPPTTEE K PPT EE	
Sbjct	124		LKGTKLARRARSFKDDLIEKIS				
Query	617		TLETHVKDISNALKHFRDVILI +LE HVKDISNALKHFRDVILI				
Sbjct	183		SLENHVKDISNALKHFRDVILI				
Query	797		ATLQVYQSLGKLIKLCDEVML- AT OVYOSLGKL+KLCDEVML				898
Sbjct	243		ATQQVYQSLGKLVKLCDEVMLI		SGGADGDGVGDO	SNAQTERQQLK	TL 302
Query	899		NVREVIDLLEDAVRNLVTLAQO NV+E++DLL DAVRNL TL+Q				SP 1078

Sbjct	303	LSEDNVKEIVDLLGDAVRNLATLSQQKLKEREENAFKYAPSNIDAAATSNNVNVNNNSS-	361
Query	1079	GASVPGTGVMRVSAAESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTSP A+V +MR+ E A ORTSLPDI LTPKERDILE+ N NP+R SHSTESILRDTSP	1258
Sbjct	362	A+V +MR+ E A QRTSLPDI LTPKERDILE+ N NP+R SHSTESILRDTSP -AAVSHNHLMRL-PVEVAGQRTSLPDITLTPKERDILEKTNSNPIRASHSTESILRDTSP	419
Query	1259	ppkpplpnrasnppplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNS PPKPPLPNR PP ++ +S N L	1438
Sbjct	420	PPKPPLPNRPPPLPPKRRNQQQNQQQLLSNNKSMNSDLEW	459
Query	1439	DLDCSSNISLLNYGVDRLSVRSRSPDEN-SQCSFDSALNHSREEEDqqqqhqhLRSFPKL + D S ++Y + LSV S SPDEN SOCS DS LNHSREEE+ + R	1615
Sbjct	460	NSDISLGNYGVDY-MSNLSVHSHSPDENSSQCSLDSELNHSREEEELKALGLGNRLN	515
Query	1616	AAMMDEDMDKM 1648 +M+D D+DK+	
Sbjct	516	DSMLDNDVDKL 526	

PREDICTED: guanine nucleotide-releasing factor 2 isoform X1 [Bactrocera dorsalis]

Sequence ID: ref|XP_011207144.1| Length: 1453 Number of Matches: 1

Range 1: 127 to 501

Score	E	xpect Method	Identities	Positives	Gaps	Frame
345 bits	(886) 16	e-99() Compositional matrix adjust.	232/430(54%)	273/430(63%)	81/430(18%)	+2
Features	S :					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI			_	
Sbjct	127	HKNSLKGTKLARRARSFKDDLIEKI			K P T EE+ SMKPPTTAEEI	
Query	617	RSTQTLETHVKDISNALKHFRDVIL + L+THVKDISNALKHFRDVI+				
Sbjct	186	AAESPLQTHVKDISNALKHFRDVII	RSKLEVLPGNA	TVILETIASMY	TVIÕSYALDKHS	SN 245
Query	797	IMSSATLQVYQSLGKLIKLCDEVML ++ SAT OVYOSLGKL+KLCDEVML			-CASLSNENVRE A LS +NV+E	
Sbjct	246	VLLSATQQVYQSLGKLVKLCDEVML				
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC	AFRYsgsglgg	igaaaeimgaV	TASPGASVPGTO	¥ 1105
Sbjct	306	+DLL +AVRNL TLA KLKE+++ VDLLGEAVRNLATLAHQKLKEREEN	ALKY	APDNAVAAA	LANNGAAVSLNE	iL 356
Query	1106	MRVSAAESAAQRTSLPDIALTPKER M + E A QRTSLPDI LTPKER				
Sbjct	357	MHLPEVAGQRTSLPDITLTPKER				
Query	1286	asnppplppkrrsqpsasagtvgvg				
Sbjct	415	PPPLPPKRR		NŎQQQP	SLNNKSINSDFI	OW 442
Query	1451	SSNISLLNYGVDRLSVRSRSPD SS+ISL NYG D LSV S SPD	EN-SQCSFDSA	LNHSREEEDqq	qqhqhLRSFPKI	LA 1618
Sbjct	443	SSDISLGNYGADYISNLSVHSHSPD	ENSSÕCSLDSE	LNHSREEGNGY	ND	491
Query	1619	AMMDEDMDKM 1648 +++D D+DK+				
Sbjct	492	SLLDNDVDKL 501				

PREDICTED: guanine nucleotide-releasing factor 2-like [Musca domestica] Sequence ID: **ref|XP_005190354.2|** Length: 1303 Number of Matches: 1

Range 1: 53 to 482

Score	E	xpect Method	Identities	Positives	Gaps	Frame
342 bits	(877) 16	e-98() Compositional matrix adjust.	247/477(52%)	292/477(61%)	52/477(10%)	+2
Features	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI				
Sbjct	53	HKNSLKGTK ARRARSFKDDLI HKNSLKGTKFARRARSFKDDLI			H K PPT EE HKNKPPPTAEE	•
Query	617	RSTQTLETHVKDISNALKHFRDVII +S+Q+L+ HVKDI+NALKHF+DVII				
Sbjct	108	KSSQSLDIHVKDITNALKHFKDVII				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMI + SAT QV +SLGKLIKLCDEVMI			EDAVRNLVTLA +AVRNL TLA	
Sbjct	168	TLLSATQQVQKSLGKLIKLCDEVMI				
Query	977	KLKEQDQCAFRYsgsglggigaaae LKE+ F+Y A F			AAESAAQRTSI E A QRTSI	
Sbjct	228	SLKERRDFTFQYDVNATE				

Query	1157	IALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppkrrsqpsa I LTPKERDILE+ NPM S+STE+ILRD+SPPPKPPLPNR+ NPPPLPPK+	1336
Sbjct	280	ITLTPKERDILEKTTSNPMHASYSTENILRDSSPPPKPPLPNRSHNPPPLPPKKN	334
Query	1337	sagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLSVRSRSPD +Q N SL ++ D S N S GVD L+VRS SPD	1516
Sbjct	335	SQPVNQSL-TNYDTSINSSDAELGVDHLTVRSCSPD	369
Query	1517	EN-SQCSFDSALNHSREEEDqqqqhqhLRSF-PKLAAMMDEDMDKMVSYSAAIDDKTQTP EN SOCS D SR+EE+ + + + + + A K AA + P	1690
Sbjct	370	ENSSQCSLDQSRDEEEYHEFNLAYKNLAEGIGAGGGGACGKDNGIKAATTRSAENP	425
Query	1691	LstgggiagvaggtggagegvaaaasgdgeTNSNRHSNESGFVSMREFRTSTQT 18 + + N++RHSNESGF S RTSTO+	52
Sbjct	426	IESNIIQKSGKCDLSGGVITEFDEEIGKTELRKVNNHRHSNESGFHSNCSIRTSTQS 48	2

PREDICTED: guanine nucleotide-releasing factor 2 isoform X3 [Bactrocera dorsalis]

Sequence ID: ref|XP_011207148.1| Length: 1404 Number of Matches: 1

Range 1: 78 to 452

Score	E	xpect Method	Identities	Positives	Gaps	Frame
340 bits	(873) 8e	e-98() Compositional matrix adjust.	230/425(54%)	276/425(64%)	71/425(16%)	+2
Features	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI				
Sbjct	78	HKNSLKGTKLARRARSFKDDLIEKI			K P T EE SMKPPTTAEE	
Query	617	RSTQTLETHVKDISNALKHFRDVII + L+THVKDISNALKHFRDVI+				
Sbjct	137	AAESPLQTHVKDISNALKHFRDVII				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMI ++ SAT QVYQSLGKL+KLCDEVMI		E		
Sbjct	197	VLLSATQQVYQSLGKLVKLCDEVML				
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC	CAFRYsgsglgg	igaaaeimgaV	TASPGASVPGT	GV 1105
Sbjct	257	+DLL +AVRNL TLA KLKE+++ VDLLGEAVRNLATLAHQKLKEREEN	IALKY	APDNAVAAA	LANNGAAVSLN	н <mark>ь</mark> 307
Query	1106	MRVSAAESAAQRTSLPDIALTPKER M + E A QRTSLPDI LTPKER				
Sbjct	308	M + E A QRTSLPDI LTPKER MHLPEVAGQRTSLPDITLTPKER				
Query	1286	asnppplppkrrsqpsasagtvgvg	cssststsnqa	SPLPYAQSHNI	SLNSDLDCSSN	IS 1465
Sbjct	366	PP ++ Q PPPLPPKRRNQQQQ		PSLNNKSI	NSDFDWSSD	IS 398
Query	1466	LLNYGVDRLSVRSRSPDEN-SC L NYG D LSV S SPDEN SC	CSFDSALNHSR	EEEDqqqqhqh		
Sbjct	399	L NYG D LSV S SPDEN SQ LGNYGADYISNLSVHSHSPDENSSQ	CS DS LNHSR CSLDSELNHSR	EEGNGYND	+++; SLL:	DN 447
Query	1634	DMDKM 1648				
Sbjct	448	D+DK+ DVDKL 452				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X2 [Bactrocera oleae]

Sequence ID: ref|XP_014101604.1| Length: 1418 Number of Matches: 1

Range 1: 78 to 462

Score	E	xpect Method	Identities	Positives	Gaps	Frame
336 bits	(862) 2	e-96() Compositional matrix adjust.	226/425(53%)	275/425(64%)	59/425(13%)	+2
Features	S :					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI			HGTKAPPTTEE K P T EE	
Sbjct	78	HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVII + L+THVKDISNALK+FRDVI				
Sbjct	137	AAESPLQTHVKDISNALKYFRDVIF				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMI ++ SAT QVYQSLGKL+KLCDEVMI			-CASLSNENVR A LS +NV+	
Sbjct	197	VLLSATQQVYQSLGKLVKLCDEVML				
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC +DLL DAVRNL TLA KLKE+++	AFRYsgsglgg	igaaaeimgaV'	TASPGASVPGT A+ GA+V	GV 1105
Sbjct	257	VDLLADAVRNLATLAHQKLKEREEN				

Query	1106	MRVSAAESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnr M + A QRTSLPDI LTPKERDILE+ N NP+R SHSTESILRDTSPPPKPPLPNR	1285
Sbjct	308	MHLPDVAGQRTSLPDITLTPKERDILEKTNSNPIRASHSTESILRDTSPPPKPPLPNR	365
Query	1286	asnppplppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISL-NSDLDCSSNI PP ++ O S + ++	1462
Sbjct	366		410
Query	1463	SLLNYGVDRLSVRSRSPDEN-SQCSFDSALNHSREEEDqqqqhqhLRSFPKLAAMMDEDM SV S SPDEN SQCS DS LNHSREEE+ + R +++D D+	1639
Sbjct	411	SVHSHSPDENSSQCSLDSELNHSREEEELKSLGLGNRYNDSLLDNDV	457
Query	1640	DKMVS 1654	
Sbjct	458	DK+ S DKLNS 462	

PREDICTED: guanine nucleotide-releasing factor 2 isoform X1 [Bactrocera oleae]

Sequence ID: ref|XP_014101596.1| Length: 1462 Number of Matches: 1

Range 1: 122 to 506

Score	E	xpect Method	Identities	Positives	Gaps	Frame
335 bits	(860) 46	e-96() Compositional matrix adjust.	226/425(53%)	275/425(64%)	59/425(13%)	+2
Features	S :					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI			HGTKAPPTTEEV K P T EE-	
Sbjct	122	HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVII + L+THVKDISNALK+FRDVI				
Sbjct	181	AAESPLQTHVKDISNALKYFRDVII				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMI ++ SAT QVYQSLGKL+KLCDEVMI			-CASLSNENVRI A LS +NV+1	
Sbjct	241	VLLSATQQVYQSLGKLVKLCDEVMI				
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQQ	CAFRYsgsglgg	igaaaeimgaV	TASPGASVPGT(GV 1105
Sbjct	301	+DLL DAVRNL TLA KLKE+++ VDLLADAVRNLATLAHQKLKEREEN	IALKY	APDNAVATT	LANNGATVSHNI	HL 351
Query	1106	MRVSAAESAAQRTSLPDIALTPKEF M + + A QRTSLPDI LTPKEF				
Sbjct	352	MHLPDVAGQRTSLPDITLTPKER				
Query	1286	asnppplppkrrsqpsasagtvgvg	gcssststsnqa	SPLPYAQSHNI	SL-NSDLDCSSI	NI 1462
Sbjct	410	PP ++ Q S + ++ PPPLPPKRRNQQQQQSLNNKSINSI)	FDWSSDI	SLGNYGADYISI	NL 454
Query	1463	SLLNYGVDRLSVRSRSPDEN-SQCS SV S SPDEN SQCS				
Sbjct	455	SVHSHSPDENSSQCS				
Query	1640	DKMVS 1654 DK+ S				
Sbjct	502	DKT S DKLNS 506				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X4 [Ceratitis capitata]

Sequence ID: **ref|XP_012158752.1|** Length: 1450 Number of Matches: 2

Range 1: 79 to 372

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
329 bits	(843) 86	e-94() Compositional matrix adjust.	183/298(61%)	217/298(72%)	30/298(10%)	+2
Feature	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI			HGTKAPPTTEE K PPT EE	
Sbjct	79	HKNSLKGTKLARRARSFKDDLIEKI				•
Query	617	RSTQTLETHVKDISNALKHFRDVII +S +LE HVKDISNALKHFRDVII				
Sbjct	138	KSASSLENHVKDISNALKHFRDVII				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMI ++ SAT QVYQSLGKL+KLCDEVMI				898
Sbjct	198	VLLSATQQVYQSLGKLVKLCDEVML			GNAQTERQQLK	TL 257
Query	899	LSNENVREVIDLLEDAVRNLVTLAC LS +NV+E++DLL DAVRNL TL+C				SP 1078
Sbjct	258	LSEDNVKEIVDLLGDAVRNLATLSQ				
Query	1079	GASVPGTGVMRVSAAESAAQRTSLF	DIALTPKERDI	LEQHNVNPMRG	SHSTESILRDT	1252

Score		Expect	Method		Identities	Positives	Gaps	Frame
70.5 bits	(171)	7e-09()	Compositional mat	rix adjust.	43/78(55%)	53/78(67%)	7/78(8%)	+2
Features) :							
Query	1427		LDCSSNISLLNYGVI					hqh 1594
Sbjct	407)L+ +S+ISL NYGVI)LEWNSDISLGNYGVI			S DS LNHSR SLDSELNHSR		GLG 466
Query	1595	LRSFP R	KLAAMMDEDMDKM +M+D D+DK+	1648				
Sbjct	467		DSMLDNDVDKL	481				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X3 [Ceratitis capitata]

Sequence ID: ref|XP_004529495.1| Length: 1491 Number of Matches: 2

Range 1: 128 to 421

Score	E	xpect Method	Identities	Positives	Gaps	Frame
329 bits	(843) 1e	e-93() Compositional matrix adjust.	183/298(61%)	217/298(72%)	30/298(10%)	+2
Features	S :					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI				
Sbjct	128	HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVII +S +LE HVKDISNALKHFRDVII				
Sbjct	187	KSASSLENHVKDISNALKHFRDVII				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMI ++ SAT QVYQSLGKL+KLCDEVMI				898
Sbjct	247	VLLSATQQVYQSLGKLVKLCDEVML			GNAQTERQQLK	TL 306
Query	899	LSNENVREVIDLLEDAVRNLVTLAÇ LS +NV+E++DLL DAVRNL TL+Ç				SP 1078
Sbjct	307	LSEDNVKEIVDLLGDAVRNLATLSÕ				
Query	1079	GASVPGTGVMRVSAAESAAQRTSLF A+V +MR+ E A ÖRTSLF		LEQHNVNPMRG		
Sbjct	366	-AAVSHNHLMRL-PVEVAGQRTSLF				

Range 2: 456 to 530

Score		Expect Method	Identities	Positives	Gaps	Frame
70.1 bits	s(170)	8e-09() Compositional matrix	adjust. 43/78(55%)	53/78(67%)	7/78(8%)	+2
Features	s:					
Query	1427	SLNSDLDCSSNISLLNYGVD- S+NSDL+ +S+ISL NYGVD				hqh 1594
Sbjct	456	SMNSDLEWNSDISLGNYGVDY				GLG 515
Query	1595	LRSFPKLAAMMDEDMDKM 1 R +M+D D+DK+	648			
Sbjct	516		30			

PREDICTED: guanine nucleotide-releasing factor 2 isoform X5 [Ceratitis capitata]

Sequence ID: **ref|XP_012158753.1|** Length: 1397 Number of Matches: 2 Range 1: 128 to 421

Score	Exp	pect Method	Identities	Positives	Gaps	Frame)
328 bits	(842) 1e-9	93() Compositional matrix adjust.	183/298(61%)	217/298(72%)	30/298(10%)	+2	_
Features	s:						
Query		HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI			HGTKAPPTTEE K PPT EF		516
Sbjct		HKNSLKGTKLARRARSFKDDLIEKI			-SMKPPPTAEE	VA 1	186

Query	7 617	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA +S +LE HVKDISNALKHFRDVILK KLEVLPGN TVILETIASMY+VIQ+Y L+++S	796
Sbjct	187	KSASSLENHVKDISNALKHFRDVILKSKLEVLPGNATVILETIASMYTVIQSYALDKHSP	246
Query	7 797	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECAS++ SAT QVYQSLGKL+KLCDEVML + G+ S	898
Sbjct	247	VLLSATQQVYQSLGKLVKLCDEVMLIHAARRGDDESSGGADGDGVGDGNAQTERQQLKTL	306
Query	7 899	LSNENVREVIDLLEDAVRNLVTLAQGKLKEQDQCAFRYsgsglggigaaaeimgaVTASP LS +NV+E++DLL DAVRNL TL+Q KLKE+++ AF+Y+ S + + + + + + + S	1078
Sbjct	307	LSEDNVKEIVDLLGDAVRNLATLSQQKLKEREENAFKYAPSNIDAAATSNNVNVNNNSS-	365
Query	1079	GASVPGTGVMRVSAAESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDT A+V +MR+ E A QRTSLPDI LTPKERDILE+ N NP+R SHSTESILRDT	1252
Sbjct	366		421

Range 2: 456 to 530

Score		Expect Method	Identities	Positives	Gaps	Frame
69.7 bits	s(169)	1e-08() Compositional matrix adjust.	43/78(55%)	53/78(67%)	7/78(8%)	+2
Features	S :					
Query	1427	SLNSDLDCSSNISLLNYGVDRLSVR S+NSDL+ +S+ISL NYGVD LSV	SRSPDEN-SQC S SPDEN SQC			hqh 1594
Sbjct	456	SHNSDLEWNSDISLGNYGVDYMSNLSVH				GLG 515
Query	1595	LRSFPKLAAMMDEDMDKM 1648 R +M+D D+DK+				
Sbjct	516	R +M+D D+DK+ NRLNDSMLDNDVDKL 530				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X5 [Bactrocera cucurbitae]

Sequence ID: **ref|XP_011177585.1|** Length: 1378 Number of Matches: 2 Range 1: 127 to 404

Score	E	Expect Method	Identities	Positives	Gaps	Frame
318 bits	(816) 3	e-90() Compositional matrix adjust.	176/292(60%)	207/292(70%)	34/292(11%)	+2
Feature	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI			HGTKAPPTTEE K P T EF	
Sbjct	127	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVII				
Sbjct	186	+ L+THVKDISNALKHFRDVI AAESPLQTHVKDISNALKHFRDVIF				
Query	797	IMSSATLQVYQSLGKLIKLCDEVML				
Sbjct	246	++ +AT QVYQSLGKL+KLCDEVML VLMTATQQVYQSLGKLVKLCDEVML		ED+ GE VEDNLQGEHQQI	LS +NV+ LKTLLSEDNVK	_
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC +DLL DAVRNL +LA KLKE+++			TASPGASVPGT TA+ S P	G- 1102
Sbjct	306	VDLLTDAVRNLASLAHQKLKEREES				'SH 353
Query	1103	VMRVSAAESAAQRTSLPDIALTP				
Sbjct	354	+M $+$ E A QRTSLPDI LTP NHLMHL-PVEVAGQRTSLPDITLTP				

Range 2: 432 to 508

Score		Expect Method	Identities	Positives	Gaps	Frame
72.8 bits	s(177)	1e-09() Compositional matrix adjust	. 45/80(56%)	53/80(66%)	7/80(8%)	+2
Features	3:					
Query	1421	NISLNSDLDCSSNISLLNYGVDR				
Sbjct	432	N S+NSDLD SS+ISL NYG D NKSINSDLDWSSDISLGNYGADYISN				
Query	1589	qhLRSFPKLAAMMDEDMDKM 1648 R +M+D D+DK+				
Sbjct	492	LGNRFNDSMLDNDVDKL 508				

Sequence ID: **ref|XP_011177586.1|** Length: 1207 Number of Matches: 2 Range 1: 127 to 404

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
317 bits	(813) 36	e-90() Compositional matrix adjust.	176/292(60%)	207/292(70%)	34/292(11%)	+2
Features	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI				
Sbjct	127	HKNSLKGTKLARRARSFKDDLIEKI			K P T EE- SMKPPTTAEE!	
Query	617	RSTQTLETHVKDISNALKHFRDVII				
Sbjct	186	+ L+THVKDISNALKHFRDVI AAESPLQTHVKDISNALKHFRDVIF				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMI				
Sbjct	246	++ +AT QVYQSLGKL+KLCDEVMI VLMTATQQVYQSLGKLVKLCDEVMI		ED+ GE VEDNLQGEHQQI	LS +NV+1 KTLLSEDNVKI	
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC		2		G- 1102
Sbjct	306	+DLL DAVRNL +LA KLKE+++ VDLLTDAVRNLASLAHQKLKEREES		_	TA+ S P TAALTNSTPAV:	SH 353
Query	1103	VMRVSAAESAAQRTSLPDIALTF				
Sbjct	354	+M $+$ E A QRTSLPDI LTF NHLMHL-PVEVAGQRTSLPDITLTF				

Range 2: 431 to 508

Score		Expect Method	Identities	Positives	Gaps	Frame
72.8 bits	(177)	1e-09() Compositional matrix adjust.	45/81(56%)	54/81(66%)	7/81(8%)	+2
Features	S :					
Query	1418	HNISLNSDLDCSSNISLLNYGVDRL +N S+NSDLD SS+ISL NYG D L	SVRSRSPDEN- SV S SPDEN			
Sbjct	431	NNKSINSDLDWSSDISLGNYGADYISNL				
Query	1586	hqhLRSFPKLAAMMDEDMDKM 1648 R +M+D D+DK+				
Sbjct	491	GLGNRFNDSMLDNDVDKL 508				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X4 [Bactrocera cucurbitae]

Sequence ID: **ref|XP_011177584.1|** Length: 1430 Number of Matches: 2 Range 1: 80 to 357

Score	Ex	kpect Method	Identities	Positives	Gaps	Frame
318 bits(816) 3e	e-90() Compositional matrix adjust.	176/292(60%)	207/292(70%)	34/292(11%)	+2
Features	:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI			HGTKAPPTTEE K P T EE	
Sbjct	80	HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVIL + L+THVKDISNALKHFRDVI				
Sbjct	139	AAESPLQTHVKDISNALKHFRDVIF				
Query	797	IMSSATLQVYQSLGKLIKLCDEVML ++ +AT QVYQSLGKL+KLCDEVML		SEDSGECAS- ED+ GE	LSNENVR LS +NV+	
Sbjct	199	VLMTATQQVYQSLGKLVKLCDEVML				
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC +DLL DAVRNL +LA KLKE+++			ГАSPGASVPGT ГА+ S P	G- 1102
Sbjct	259	VDLLTDAVRNLASLAHQKLKEREES				SH 306
Query	1103	VMRVSAAESAAQRTSLPDIALTP +M + E A QRTSLPDI LTP				
Sbjct	307	NHLMHL-PVEVAGQRTSLPDITLTP				

Range 2: 385 to 461

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.2 bits(178)	1e-09()	Compositional matrix adjust.	46/80(58%)	54/80(67%)	7/80(8%)	+2
Footures:						

Query	1421	NISLNSDLDCSSNISLLNYGVDRLSVRSRSPDEN-SQCSFDSALNHSREEEDqqqqh	1588
Sbjct	385	N S+NSDLD SS+ISL NYG D LSV S SPDEN SQCS DS LNHSREEE+ + NKSINSDLDWSSDISLGNYGADYISNLSVHSHSPDENSSQCSLDSELNHSREEEELKALG	444
Query	1589	qhLRSFPKLAAMMDEDMDKM 1648 R F +M+D D+DK+	
Sbict	445	LGNR-FNDSMLDNDVDKL 461	

PREDICTED: guanine nucleotide-releasing factor 2 isoform X3 [Bactrocera cucurbitae]

Sequence ID: **ref|XP_011177583.1|** Length: 1469 Number of Matches: 2 Range 1: 127 to 404

Score	E	expect Method	Identities	Positives	Gaps	Frame
318 bits	(815) 4	e-90() Compositional matrix adjust.	176/292(60%)	207/292(70%)	34/292(11%)	+2
Feature	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI				
Sbjct	127	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI			K P T EE SMKPPTTAEE	
Query	617	RSTQTLETHVKDISNALKHFRDVIL + L+THVKDISNALKHFRDVI				
Sbjct	186	AAESPLQTHVKDISNALKHFRDVIF				
Query	797	IMSSATLQVYQSLGKLIKLCDEVML ++ +AT QVYQSLGKL+KLCDEVML		SEDSGECAS- ED+ GE	LSNENVR LS +NV+	
Sbjct	246	VLMTATQQVYQSLGKLVKLCDEVML				_
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC +DLL DAVRNL +LA KLKE+++			TASPGASVPGT TA+ S P	G- 1102
Sbjct	306	VDLLTDAVRNLASLAHQKLKEREES		-		SH 353
Query	1103	VMRVSAAESAAQRTSLPDIALTP +M + E A ORTSLPDI LTP				
Sbjct	354	NHLMHL-PVEVAGQRTSLPDITLTP				

Range 2: 432 to 508

Score		Expect Method	Identities	Positives	Gaps	Frame
72.8 bits	s(177)	1e-09() Compositional matrix adj	ust. 46/80(58%)	54/80(67%)	7/80(8%)	+2
Features	S :					
Query	1421	NISLNSDLDCSSNISLLNYGVD				
Sbjct	432	N S+NSDLD SS+ISL NYG D NKSINSDLDWSSDISLGNYGADYI				
Query	1589	<u> </u>	548			
Sbjct	492	R F +M+D D+DK+ LGNR-FNDSMLDNDVDKL 5(8			

PREDICTED: guanine nucleotide-releasing factor 2 isoform X1 [Bactrocera cucurbitae]

Sequence ID: **ref|XP_011177581.1|** Length: 1477 Number of Matches: 2

Range 1: 127 to 404

Score	E	xpect Method	Identities	Positives	Gaps	Frame
318 bits	(815) 56	e-90() Compositional matrix adjust.	176/292(60%)	207/292(70%)	34/292(11%)	+2
Features	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI				
Sbjct	127	HKNSLKGTKLARRARSFKDDLIEKI				=
Query	617	RSTQTLETHVKDISNALKHFRDVII + L+THVKDISNALKHFRDVI				
Sbjct	186	AAESPLQTHVKDISNALKHFRDVIF				
Query	797	IMSSATLQVYQSLGKLIKLCDEVML ++ +AT QVYQSLGKL+KLCDEVML			LSNENVR LS +NV+	
Sbjct	246	VLMTATQQVYQSLGKLVKLCDEVML				_
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC +DLL DAVRNL +LA KLKE+++		9	TASPGASVPGT TA+ S P	G- 1102
Sbjct	306	VDLLTDAVRNLASLAHQKLKEREES				'SH 353
Query	1103	VMRVSAAESAAQRTSLPDIALTP	KERDILEQHNV	NPMRGSHSTES:	ILRDT 1252	

Range 2: 432 to 508

Score		Expect Method	Identities	Positives	Gaps	Frame
72.8 bits	(177)	1e-09() Compositional matrix adjust.	46/80(58%)	54/80(67%)	7/80(8%)	+2
Features	S:					
Query	1421	NISLNSDLDCSSNISLLNYGVDRI				
Sbjct	432	N S+NSDLD SS+ISL NYG D I NKSINSDLDWSSDISLGNYGADYISNI	LSV S SPDEN S LSVHSHSPDENSS			
Query	1589	qhLRSFPKLAAMMDEDMDKM 1648 R F +M+D D+DK+				
Sbjct	492	LGNR-FNDSMLDNDVDKL 508				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X2 [Bactrocera cucurbitae]

Sequence ID: ref|XP_011177582.1| Length: 1472 Number of Matches: 2

Range 1: 122 to 399

Score	Е	xpect Method	Identities	Positives	Gaps	Frame
318 bits	(815) 6	e-90() Compositional matrix adjust.	176/292(60%)	207/292(70%)	34/292(11%)	+2
Features	s:					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKGTKLARRARSFKDDLIEKI			HGTKAPPTTEE K P T EE	
Sbjct	122	HKNSLKGTKLARRARSFKDDLIEKI				
Query	617	RSTQTLETHVKDISNALKHFRDVII + L+THVKDISNALKHFRDVI	KKKLEVLPGNG	TVILETIASMY	SVIQTYTLNEN	ISA 796
Sbjct	181	AAESPLQTHVKDISNALKHFRDVIF				
Query	797	IMSSATLQVYQSLGKLIKLCDEVMI ++ +AT QVYQSLGKL+KLCDEVMI		SEDSGECAS- ED+ GE	LSNENVF LS +NV+	
Sbjct	241	VLMTATQQVYQSLGKLVKLCDEVML				_
Query	926	IDLLEDAVRNLVTLAQGKLKEQDQC +DLL DAVRNL +LA KLKE+++			TASPGASVPGT TA+ S P	G- 1102
Sbjct	301	VDLLTDAVRNLASLAHQKLKEREES				7SH 348
Query	1103	VMRVSAAESAAQRTSLPDIALTF +M + E A QRTSLPDI LTF				?
Sbjct	349	NHLMHL-PVEVAGQRTSLPDITLTE				

Range 2: 427 to 503

Score		Expect Method	Identities	Positives	Gaps	Frame
72.8 bits	s(177)	1e-09() Compositional matrix adjust.	46/80(58%)	54/80(67%)	7/80(8%)	+2
Features	3 :					
Query	1421	NISLNSDLDCSSNISLLNYGVDRL N S+NSDLD SS+ISL NYG D L	SVRSRSPDEN-S SV S SPDEN S			
Sbjct	427	NKSINSDLD SS+13L NIG D L				
Query	1589	qhLRSFPKLAAMMDEDMDKM 1648 R F +M+D D+DK+				
Sbjct	487	LGNR-FND-SMLDNDVDKL 503				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X2 [Stomoxys calcitrans]

Sequence ID: **ref|XP_013109512.1|** Length: 1272 Number of Matches: 1 Range 1: 55 to 307

Score)	Expect	Method	Identities	Positives	Gaps	Frame	_
309 b	its(791)	3e-87()	Compositional matrix adjust.	163/270(60%)	202/270(74%)	17/270(6%)	+2	_
Featu	res:							
Quer	y 437		SLKGTKLARRARSFKDDLIEKIS SLKG KLARRARSFKD+L +++			_		16
Sbjc [.]	t 55		SLKGNKLARRARSFKDELFDRLY					12

Query	617	RSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTLNENSA +S+Q+L+THVKDI+NALK+F+DVILK KLEVLPGNGT+IL+T ASM+SVIQ Y LNEN+	796
Sbjct	113	KSSQSLDTHVKDITNALKYFKDVILKNKLEVLPGNGTIILDTTASMFSVIQAYALNENNT	172
Query	797	IMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLVTLAQG + SAT QVY+SLGKLIKLCDEVMLSEDS EC SLS +NVRE++DLLE+AV+NL LAQ	976
Sbjct	173	SLLSATQQVYKSLGKLIKLCDEVMLSEDSEECVSLSGDNVREIVDLLEEAVKNLAILAQQ	232
Query	977	KLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQRTSLPD +L+E+ + A + +A+P ++ +MR S E + QRTSLPD	1156
Sbjct	233	RLQEKKERATEKEEENPSATP-TNITHNRLMRPS-VEGSVQRTSLPD	277
Query	1157	IALTPKERDILEQHNVNPMRGSHSTESILR 1246 I LT ERDI+ + NPM GS STE+ILR	
Sbjct	278	IPLTSDERDIIAKSTSNPMHGSFSTENILR 307	

PREDICTED: guanine nucleotide-releasing factor 2 isoform X1 [Stomoxys calcitrans]

Sequence ID: ref|XP_013109510.1| Length: 1273 Number of Matches: 1

Range 1: 55 to 307

Score	E	xpect Method	Identities	Positives	Gaps	Frame
309 bits	(791) 46	e-87() Compositional matrix adjust.	163/270(60%)	202/270(74%)	17/270(6%)	+2
Features	S :					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKG KLARRARSFKD+L +++				
Sbjct	55	HKNSLKGNKLARRARSFKDELFDRL				
Query	617	RSTQTLETHVKDISNALKHFRDVIL: +S+Q+L+THVKDI+NALK+F+DVIL:				
Sbjct	113	KSSQSLDTHVKDITNALKYFKDVIL				
Query	797	IMSSATLQVYQSLGKLIKLCDEVML + SAT QVY+SLGKLIKLCDEVML				
Sbjct	173	SLLSATQQVYKSLGKLIKLCDEVML				
Query	977	KLKEQDQCAFRYsgsglggigaaae +L+E+ + A +			AESAAQRTSL E + ORTSL	
Sbjct	233	RLQEKKERATEK				
Query	1157	IALTPKERDILEQHNVNPMRGSHSTI I LT ERDI+ + NPM GS ST				
Sbjct	278	IPLTSDERDIIAKSTSNPMHGSFST				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X4 [Stomoxys calcitrans]

Sequence ID: ref|XP_013109514.1| Length: 1264 Number of Matches: 1

Range 1: 55 to 307

Score	E	xpect Method	Identities	Positives	Gaps	Frame
308 bits	(790) 5e	e-87() Compositional matrix adjust.	163/270(60%)	202/270(74%)	17/270(6%)	+2
Features	S :					
Query	437	HKNSLKGTKLARRARSFKDDLIEKI HKNSLKG KLARRARSFKD+L +++				
Sbjct	55	HKNSLKGNKLARRARSFKDELFDRL				
Query	617	RSTQTLETHVKDISNALKHFRDVILI +S+Q+L+THVKDI+NALK+F+DVILI				
Sbjct	113	KSSQSLDTHVKDITNALKYFKDVIL				
Query	797	IMSSATLQVYQSLGKLIKLCDEVML + SAT QVY+SLGKLIKLCDEVML				~
Sbjct	173	SLLSATQQVYKSLGKLIKLCDEVML				~
Query	977	KLKEQDQCAFRYsgsglggigaaae. +L+E+ + A +	imgaVTASPGAS +A+P +	SVPGTGVMRVSA	AESAAQRTSL E + ORTSL	PD 1156
Sbjct	233	RLQEKKERATEK				
Query	1157	IALTPKERDILEQHNVNPMRGSHSTI I LT ERDI+ + NPM GS STI				
Sbjct	278	IPLTSDERDIIAKSTSNPMHGSFST				

Sequence ID: ref|XP_001664011.1| Length: 1131 Number of Matches: 1

▶ See 1 more title(s) Range 1: 18 to 356

070 hito/744						
2/8 DIIS(/11)) 1e-76()	Compositional matrix adjust.	171/397(43%)	234/397(58%)	76/397(19%)	+2
Features:						
Query 43		SLKGTKLARRARSFKDDLIEKI S++G KLARRARSFKDD +EKI			HGTKAPPTT G ++ +	-E 607
Sbjct 18		SIRGNKLARRARSFKDDFLEKI	= -		_	GD 77
Query 608		RSTQTLETHVKDISNALKH ST Q L HV+ + NAL H				
Sbjct 78		GSTKPVQDLAYHVRQVKNALTH:				
Query 779		NSAIMSSATLQVYQSLGKLIKL NS+ + +AT VY SLG L+KL				
Sbjct 138		NSSALINATNHVYMSLGNLLKL				
Query 959		AQGKLKEQDQCAFRYsgsglgg. A K+ ++	-	- · ~ ·		
Sbjct 198	3 ANT	A K+ ++ ANEKISDK		-AAGGTGSNSSN	NTLQRPAVDIA	SQ 231
Query 113	39 RTS	LPDIALTPKERDILEQHNVNPMILPDI LTP+ERDILEQ ++ +1	RGSHSTESILR	DTspppkpplpr	nrasnppplpp	kr 1318
Sbjct 232		LPDIPLTPRERDILEQTSLKTV		DS		269
Query 13	19 rsq	psasagtvgvgcssststsnqa	SPLPYAQ			G- 1480
Sbjct 270)	SPPPKPPLPDRGQDP			_	•
Query 148		LSVRSRSPDENSQCSF	DSALNHSREEE DSALNHSREEE			
Sbjct 320		MSLRSRSPEDNSSLLSASAGSL				

PREDICTED: guanine nucleotide-releasing factor 2 isoform X3 [Stomoxys calcitrans]

Sequence ID: **ref|XP_013109513.1|** Length: 1192 Number of Matches: 1 Range 1: 1 to 226

Score	Е	xpect Met	hod	Identities	Positives	Gaps	Frame
267 bits	(683) 6	e-73() Com	positional matrix adjust.	144/243(59%)	178/243(73%)	17/243(6%)	+2
Feature	s:						
Query	518		LGRSHSPHSPRTKHGTKA LGRSHSP SPR K+ K				
Sbjct	1		LGRSHSPQSPRNKNKL				
Query	698		NGTVILETIASMYSVIQT				
Sbjct	59		NGTIILDTTASMFSVIQA				
Query	878		LSNENVREVIDLLEDAVR			glggigaaae +	
Sbjct	119		LSGDNVREIVDLLEEAVK				
Query	1058	gaVTASP +A+P	GASVPGTGVMRVSAAESA ++ +MR S E +	AQRTSLPDIALT QRTSLPDI LT		VNPMRGSHSI NPM GS SI	
Sbjct	166		-TNITHNRLMRPS-VEGS				
Query	1238		46				
Sbjct	224	ILR ILR 22	6				

guanine-nucleotide exchange factor c3g [Culex quinquefasciatus]

Sequence ID: ref|XP_001869397.1| Length: 1397 Number of Matches: 1

▶ See 1 more title(s) Range 1: 104 to 449

Score	Ex	pect	Method	Identities	Positives	Gaps	Fram	. <u>е</u>
263 bits	(673) 5e	-71()	Compositional matrix adjust.	162/402(40%)	227/402(56%)	79/402(19%)	+2	
Features	S:							
Query	437		SLKGTKLARRARSFKDDLIEKI S++G KLARRARSFKDD +EKI			HGTKAPPT		601
Sbjct	104		SIRGNKLARRARSFKDDFLEKI			SAGGGGAGGGV	'GG	163

Query	602	TEEVLRSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSV ++++L S+ Q L HV+ + NAL HF+DVILK KLE+LPGNGTV+LE +A++++	763
Sbjct	164	NRKSDDLLASSKPVQDLNYHVRQVKNALTHFKDVILKNKLEMLPGNGTVVLELVANVHTA	223
Query	764	IQTYTLNENSAIMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLED +Q+YTLNENS+ + +AT VY SLG L+KLCDEV+L+ D+ C SLS ENV+E+++L+E+	943
Sbjct	224	LOSYTLNENSSALINATNHVYMSLGNLLKLCDEVLLTADNENCPSLSKENVKEIVELVEN	283
Query	944	AVRNLVTLAQGKLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAA AV NLV LA K+ ++ A	1123
Sbjct	284	AVNNLVNLANEKISDKAAGSGSGNHHSSNTLQRPAV	319
Query	1124	ESAAQRTSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppp + A QRTSLPDI LTP+ERDILEQ ++ +R SHSTESILRD+	1303
Sbjct	320	DIAGORTSLPDIPLTPRERDILEQTSLKTVRASHSTESILRDS	362
Query	1304	lppkrrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNIS + PLP ++++H+ SD D +	1465
Sbjct	363	SPPPKPPLPDRAQDPPPLPPKRKSQHSKNHSFHETSDADSTFLGG	407
Query	1466	LLNYGVDRLSVRSRSPDENSQCSFDSALNHSREEED 1573 +DR+S+RSRSP++N S S DSALNHSREE++	
Sbjct	408	GCGGALDRMSLRSRSPEDNSSLLSASAGSLDSALNHSREEDE 449	

AGAP000932-PA [Anopheles gambiae str. PEST]

Sequence ID: ref|XP_309117.5| Length: 1262 Number of Matches: 2

▶ See 1 more title(s) Range 1: 19 to 284

Score	E	xpect Method	Identities	Positives	Gaps	Frame	
251 bits(640) 5	e-67() Compositional matrix adjust.	139/273(51%)	188/273(68%)	8/273(2%)	+2	
Features:							
Query	437	HKNSLKGTKLARRARSFKDDLIEKIS HK S++G KLARRARSFKDD +EKIS		SHSPHSP-RTKH H P + R	GTKAPPTTE TK TT+		
Sbjct	19	HKGSIRGNKLARRARSFKDDFLEKIS				_	
Query	614	LRSTQTLETHVKDISNALKHFRDVIL + Q L HV+ + NAL HF+DVIL					
Sbjct	79	AKPVQDLNYHVRQVKNALTHFKDVIL					
Query	794	AIMSSATLQVYQSLGKLIKLCDEVML + +AT V+ SLG L+KLCDEV+L					
Sbjct	139	SAFINATNHVHVSLGNLLKLCDEVLL					
Query	974	GKLKEQDQCAFRYsgsglggigaaae KL D+ A G G G G +	imgaVTASPGAS G T P ++		AESAAQRTS + +ORTS		
Sbjct	199	EKLSDRKAIGTGGGGGPGTGVSGT					
Query	1154	DIALTPKERDILEQHNVNPMRGSHST DI LTP+ERDILEQ ++ +R SHST	ESILRDT 125	52			
Sbjct	252	DIPLTPRERDILEQTSLKTVRASHST		1			

Range 2: 359 to 395

Score		Expect	Method	Identities	Positives	Gaps	Frame
41.6 bits	s(96) 4	1.5()	Compositional matrix adjust.	21/37(57%)	28/37(75%)	6/37(16%)	+2
Features	S :						
Query	1481		SVRSRSPDENSQCSFDSA S+RSRSP++N S S DSA	ALNHSREEED ALNHSREE++	1573		
Sbjct	359		SLRSRSPEDNCSLLSASAGSLDSA		395		

PREDICTED: guanine nucleotide-releasing factor 2-like isoform X2 [Apis dorsata]

Sequence ID: **ref|XP_006608566.1|** Length: 1243 Number of Matches: 1 Range 1: 72 to 409

Score	Expe	ect Method	Identities	Positives	Gaps	Fram	e
201 bits(51	0) 3e-50	O() Compositional matrix adjust.	152/392(39%)	208/392(53%)	72/392(18%)	+2	
Features:							
Query 4		GTKLARRARSFKDDLIEKISLMRT G KLARRARSFK+D +EK+S MR+		TLGRSHSPHSPF R+ SP SPF		TE T+	607
Sbjct 72		GGKLARRARSFKEDFLEKLSHMRS					131

Query	608	EVLRSTQTLETHVKDISNALKHFRDVILKKKLEVLPGNGTVILETIASMYSVIQTYTL	781
Sbjct	132	L + L HV+ + AL HF+DV+LKKKLE+LPGNGT+IL+ I ++++V+++Y L ATLDKNPLRDLHIHVRQVQLALLHFKDVVLKKKLEMLPGNGTIILDHITTIHTVLKSYLL	191
Query	782	NENSAIMSSATLQVYQSLGKLIKLCDEVMLSEDSGECASLSNENVREVIDLLEDAVRNLV	961
Sbjct	192	ENS+ + SAT QVYQ+L +L+KLCD+V+L D + ++L ENV +I L+EDAV+NLV YENSSTLGSATNQVYQALAQLLKLCDDVLLHGDQSSALDTENVTHIIGLVEDAVKNLV	249
Query	962	TLAQGKLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQR	1141
Sbjct	250	LA K+ + + A AV S S G G +E QR DLANEKIANRQKPASELTPQR	282
Query	1142	TSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppk	1315
Sbjct	283	SLPDI LTP+ER ILEQ + +R SHS+ESILRD+ NSLPDIPLTPRERQILEQTAATTSLVRSSHSSESILRDS	321
Query	1316	rrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLS	1495
Sbjct	322	S P S S+ +P P LD S + L +D +SSPPPKPPLPERTNVCLSEENSSSGTPPPLPPKRRTRAQQLLDESEGLLASSLDGVS	377
Query	1496	VRSRSPDENSQCSFDSALNHSREEED 1573	
Sbjct	378	+RSRSP++ S S DSALNHSR+E++ LRSRSPEDSSSLLSASAGSLDSALNHSRDEDE 409	

PREDICTED: guanine nucleotide-releasing factor 2-like isoform X4 [Apis dorsata]

Sequence ID: **ref|XP_006608568.1**| Length: 1235 Number of Matches: 1 Range 1: 72 to 409

Score	E	xpect Method	Identities	Positives	Gaps Fr	ame
201 bits	(510) 36	e-50() Compositional matrix adjust.	152/392(39%)	208/392(53%)	72/392(18%) +2	<u> </u>
Feature	s:					
Query	452	KGTKLARRARSFKDDLIEKISLMRT				
Sbjct	72	+G KLARRARSFK+D +EK+S MR+ RGGKLARRARSFKEDFLEKLSHMRS		R+ SP SP: GATRAASPSSP:		
Query	608	EVLRSTQTLETHVKDISNALKHF L + L HV+ + AL HF				
Sbjct	132	ATLDKNPLRDLHIHVRQVQLALLHF				
Query	782	NENSAIMSSATLQVYQSLGKLIKLC ENS+ + SAT QVYQ+L +L+KLC				
Sbjct	192	YENSSTLGSATNQVYQALAQLLKLC				
Query	962	TLAQGKLKEQDQCAFRYsgsglggi	gaaaeimgaVT.	ASPGASVPGTG	VMRVSAAESAAQR	1141
Sbjct	250	LA K+ + + A DLANEKIANRQKPA	AVA	TSNRTSGYG	SELTPQR	282
Query	1142	TSLPDIALTPKERDILEQHNVNF SLPDI LTP+ER ILEO +	MRGSHSTESIL: +R SHS+ESIL:		pnrasnppplppk	1315
Sbjct	283	NSLPDIPLTPRERQILEQTAATTSI	VRSSHSSESIL	RDS		321
Query	1316	rrsqpsasagtvgvgcssststsnc	asPLPYAQSHN +P P		NISLLNYGVDRLS + L +D +S	
Sbjct	322	SPPPKPPLPERTNVCLSEENSSS				
Query	1496	VRSRSPDENSQCSFDSALN +RSRSP++ S S DSALN	HSREEED 15	73		
Sbjct	378	LRSRSPEDSSSLLSASAGSLDSALN		9		

PREDICTED: guanine nucleotide-releasing factor 2-like isoform X3 [Apis dorsata]

Sequence ID: **ref|XP_006608567.1|** Length: 1237 Number of Matches: 1 Range 1: 72 to 409

Score	I	Expect Method	Identities	Positives	Gaps	Frame
201 bits	(510) 3	Be-50() Compositional matrix adjust.	152/392(39%)	208/392(53%)	72/392(18%)	+2
Feature	s:					
Query	452	KGTKLARRARSFKDDLIEKISLMRT +G KLARRARSFK+D +EK+S MR+			_	
Sbjct	72	RGGKLARRARSFKEDFLEKLSHMRS		10. 01 01.		-
Query	608	EVLRSTQTLETHVKDISNALKHE L + L HV+ + AL HE				
Sbjct	132	ATLDKNPLRDLHIHVRQVQLALLHE				
Query	782	NENSAIMSSATLQVYQSLGKLIKLC ENS+ + SAT OVYO+L +L+KLC				
Sbjct	192	YENSSTLGSATNQVYQALAQLLKLO				

Query	962	TLAQGKLKEQDQCAFRYsgsglggigaaaeimgaVTASPGASVPGTGVMRVSAAESAAQR LA K+ + + A AV S S G G +E QR	1141
Sbjct	250	DLANEKIANRQKPASELTPQR	282
Query	1142	TSLPDIALTPKERDILEQHNVNPMRGSHSTESILRDTspppkpplpnrasnppplppk	1315
Sbjct	283	SLPDI LTP+ER ILEQ + +R SHS+ESILRD+ NSLPDIPLTPRERQILEQTAATTSLVRSSHSSESILRDS	321
Query	1316	rrsqpsasagtvgvgcssststsnqasPLPYAQSHNISLNSDLDCSSNISLLNYGVDRLS	1495
Sbjct	322	S P S S + +P P LD S + L +D +SSPPPKPPLPERTNVCLSEENSSSGTPPPLPPKRRTRAQQLLDESEGLLASSLDGVS	377
Query	1496	VRSRSPDENSQCSFDSALNHSREEED 1573	
Sbjct	378	+RSRSP++ S S DSALNHSR+E++ LRSRSPEDSSSLLSASAGSLDSALNHSRDEDE 409	