Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BUBF5U014

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Blast report description

Nucleotide Sequence (1141 letters)

RID <u>B8BUBF5U014</u> (Expires on 02-06 12:12 pm)

Query ID lcl|Query_183521

Description None **Molecule type** nucleic acid **Query Length** 1141 **Database Name** nr

Description All non-redundant GenBank CDS

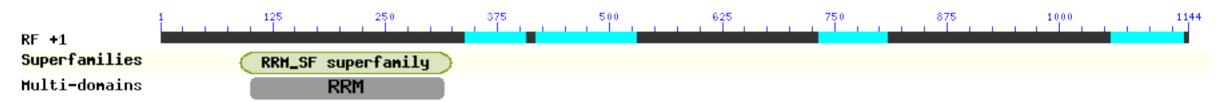
translations+PDB+SwissProt+PIR+PRF excluding

environmental samples from WGS projects

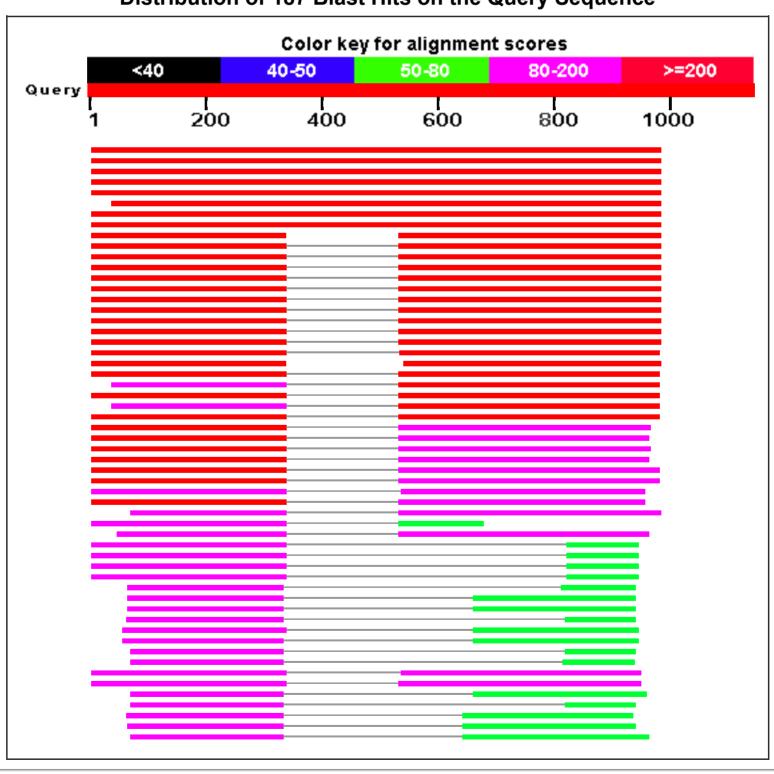
Program BLASTX 2.3.1+

□ Graphic Summary

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



Distribution of 187 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Description	Max score	Total score	Query	E value	Ident	Accession
RNA-binding protein 2, isoform A [Drosophila melanogaster]	449	449	85%	9e-154	100%	NP_524959.1
uncharacterized protein Dsimw501_GD17286, isoform C [Drosophila simulans]	447	447	85%	4e-153	99%	KMZ10169.1
RE23444p [Drosophila melanogaster]	443	443	85%	2e-151	99%	ADX35943.1
RNA-binding protein 2, isoform B [Drosophila melanogaster]	442	442	85%	3e-151	99%	NP_727982.1
uncharacterized protein Dere_GG17966, isoform B [Drosophila erecta]	442	442	85%	5e-151	98%	XP_015010732.1
RNA-binding protein 2, isoform E [Drosophila melanogaster]	423	423	82%	1e-143	100%	NP_001285331.1
uncharacterized protein Dana_GF19517, isoform B [Drosophila ananassae]	410	410	85%	7e-138	83%	XP_014759990.1
uncharacterized protein Dana_GF19517, isoform C [Drosophila ananassae]	409	409	85%	4e-137	86%	XP_014759991.1
GD17286 [Drosophila simulans]	238	238	39%	2e-72	99%	XP_002107116.1
RNA-binding protein 2, isoform C [Drosophila melanogaster]	239	471	68%	3e-71	100%	NP_996487.1
GM13442 [Drosophila sechellia]	238	469	68%	1e-70	99%	XP_002042252.1
RH12113p [Drosophila melanogaster]	236	469	68%	3e-70	99%	ABC86252.1
uncharacterized protein Dere_GG17966, isoform A [Drosophila erecta]	234	464	68%	2e-69	97%	XP_001977936.1
RNA-binding protein 2, isoform D [Drosophila melanogaster]	234	465	68%	5e-69	100%	NP_001285330.1
uncharacterized protein Dsimw501_GD17286, isoform B [Drosophila simulans]	234	465	68%	5e-69	100%	KMZ10168.1
uncharacterized protein Dana_GF19517, isoform A [Drosophila ananassae]	223	438	68%	1e-64	96%	XP_001966145.2
uncharacterized protein Dvir_GJ19028, isoform C [Drosophila virilis]	219	437	68%	4e-64	79%	XP_015026516.1
uncharacterized protein Dvir_GJ19028, isoform B [Drosophila virilis]	220	438	68%	6e-64	79%	XP_015026515.1
uncharacterized protein Dvir_GJ19028, isoform A [Drosophila virilis]	218	436	68%	2e-63	79%	XP_002055013.1
GH22433 [Drosophila grimshawi]	210	210	29%	2e-63	91%	XP_001997843.1
uncharacterized protein Dwil_GK25675 [Drosophila willistoni]	218	426	68%	3e-63	94%	XP_002071220.2
uncharacterized protein Dmoj_Gl21487 [Drosophila mojavensis]	213	213	29%	2e-62	91%	XP_002010838.2
uncharacterized protein Dpse_GA18178, isoform B [Drosophila pseudoobscura pseudoobscura]	214	422	68%	5e-62	82%	XP_003736162.1
uncharacterized protein Dpse_GA18178, isoform D [Drosophila pseudoobscura pseudoobscura]	214	399	65%	1e-61	82%	XP_015041559.1
uncharacterized protein Dpse_GA18178, isoform A [Drosophila pseudoobscura pseudoobscura]	214	422	68%	2e-61	82%	XP_001354678.2
uncharacterized protein Dpse_GA18178, isoform C [Drosophila pseudoobscura pseudoobscura]	214	399	65%	3e-61	82%	XP_015041558.1
GH24789 [Drosophila grimshawi]	202	202	38%	4e-60	76%	XP_001992509.1
GL20267 [Drosophila persimilis]	207	414	68%	9e-60	89%	XP_002023289.1
PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Bactrocera dorsalis]	202	349	67%	4e-58	90%	XP_011213861.1
PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Bactrocera cucurbitae]	202	355	66%	5e-58	89%	XP_011187272.1
PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Bactrocera dorsalis]	203	349	67%	7e-58	90%	XP_011213860.1

PREDICTED_exceptical translation relation based of the control	PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Bactrocera cucurbitae]	202	354	66%	9e-58	89%	XP_011187268.1
	•	201	346	68%	2e-57	89%	XP_014090168.1
	•	201	346	68%	3e-57	89%	XP_014090165.1
	•	199	346	65%	7e-57	88%	XP_012157029.1
PREDICTED: eukaryolic translation initiation factor 4H 190 342 82% 5e.53 95% XP_01187271.1	•	200	349	66%	1e-56	88%	XP_012157028.1
PREDICTED eulasyste translation mitiation factor 4H and softom XZ [Seatoners cubrillars] 150 342 62% 6e-53 95% XP_011187271.1 150 15	Rbp2 [Drosophila busckii]	195	378	62%	6e-55	73%	ALC49657.1
	hypothetical protein FF38_09267 [Lucilia cuprina]	192	253	42%	3e-54	83%	KNC26965.1
AAEL004010-PB (Aedes segypti) 155 222 39% 7e-40 67% XP_001648292.1 AAEL004010-PC (Redess segypti) 155 223 39% 8e-40 67% XP_00164829.1 AAEL004010-PC (Redess segypti) 155 223 39% 8e-40 67% XP_00164829.1 Iuncharacterized protein Dere, GC911771 [Drosophila 157 221 34% 3e-39 79% XP_00164829.1 Iuncharacterized protein Dayk_GE10899, isoform B 156 220 47% 6e-39 79% XP_001984180.1 [Drosophila yakuba] 156 220 47% 6e-39 79% XP_001984180.1 Iuncharacterized protein Dayk_GE10899, isoform A 156 220 47% 6e-39 79% XP_001984182.1 [Drosophila yakuba] 155 219 34% 8e-39 77% XP_00209432.1 Iuncharacterized protein Dayk_GE10899, isoform A 156 220 47% 6e-39 79% XP_00209432.1 Iuncharacterized protein Dayk_GE10899, isoform A 156 220 47% 6e-39 79% XP_00209432.1 Iuncharacterized protein Dayk_GE10899, isoform A 156 220 47% 6e-39 79% XP_00209432.1 Iuncharacterized protein Dayk_GE10899, isoform A 156 2219 34% 8e-39 77% XP_00209432.1 Iuncharacterized protein Dayk_GE10899, isoform A 156 216 49% 1e-38 74% XP_001387589.3 ECG1340, isoform A [Drosophila melanogaster] 153 215 33% 5e-38 77% XP_002020435.1 CG1340, isoform A [Drosophila melanogaster] 153 215 33% 5e-38 77% XP_002020435.1 Iuncharacterized protein Dana_GE2920 [Drosophila 154 219 33% 5e-38 77% XP_001984679.2 EREDICTED: eukaryotic translation initiation factor 4H 1soform XI (Stomovys calcitaris) 149 277 65% 1e-37 69% XP_01195840.1 EREDICTED: eukaryotic translation initiation factor 4H 1soform XI (Stomovys calcitaris) 151 216 49% 9e-37 77% XP_00203384.1 CG1340 [Drosophila simularis] 150 215 33% 5e-37 77% XP_00203384.1 CG1340 [Drosophila derized protein Drosophila virila] 149 281 65% 9e-37 77% XP_00203384.1 CG1340 [Drosophila derized protein Drosophila virila] 149 281 65% 9e-37 77% XP_00203384.1 CG1340 [Drosophila derized protein Drosophila virila] 149 281 65% 9e-37 77% XP_00203384.1 CG1340 [Drosophila derized protein Drosophila virila] 149 281 65% 9e-37 77% XP_00203384.1 CG1340 [Drosophila derized protein Drosophila virila] 149 281 65% 9e-37 77% XP_00203384.1 CG1340 [190	342	62%	5e-53	95%	XP_011187271.1
AREL004010-PC (Aedes aegyptii) 155 223 39% 8e-40 67% XP_001648293.1 AREL004010-PD (Aedes aegyptii) 155 223 39% 8e-40 67% XP_001648290.1 uncharacterized protein Dera_GC11771 [Drosophila erectal] uncharacterized protein Dyak_GE10899, isoform B 156 220 47% 8e-39 79% XP_001981180.1 uncharacterized protein Dyak_GE10899, isoform A 156 220 47% 8e-39 79% XP_001981180.1 uncharacterized protein Dyak_GE10899, isoform A 156 220 47% 8e-39 79% XP_00298492.1 [Drosophila yakuba] uncharacterized protein Dyak_GE10899, isoform A 156 220 47% 8e-39 79% XP_00209492.1 [Drosophila yakuba] uncharacterized protein Dyak_GE10899, isoform A 156 220 47% 8e-39 79% XP_00209492.1 [Uncharacterized protein Dyak_GE10899, isoform A 156 219 34% 8e-39 77% XP_00209492.1 [Uncharacterized protein Dyak_GE10899, isoform A 155 216 49% 1e-38 74% XP_001357599.3 [Seutodosporary pseudoosporary geodocosporary geo	AAEL004010-PA [Aedes aegypti]	155	222	39%	7e-40	67%	XP_001648291.1
AAEL004010-PD [Aedes aegypti] 155 223 39% 8e-40 67% XP_001848280.1 uncharacterized protein Dere_GG11771 [Drosophila erecta] 157 221 34% 3e-39 79% XP_001848160.1 erecta] uncharacterized protein Dyak_GE10899, isoform B [Drosophila yakuba] 156 220 47% 6e-39 79% XP_018049122.1 [Drosophila yakuba] 156 220 47% 6e-39 79% XP_018049122.1 [Drosophila yakuba] 155 219 34% 8e-39 77% XP_002099432.1 [Drosophila yakuba] 155 219 34% 8e-39 77% XP_002073592.2 willistori] 155 216 49% 1e-38 75% XP_001367599.3 [Statistical] 155 216 49% 1e-38 75% XP_001367599.3 [Statistical] 155 216 49% 1e-38 75% XP_001367599.3 [Statistical] 155 215 33% 5e-38 75% XP_001367599.3 [Statistical] 155 215 33% 5e-38 75% XP_001367599.3 [Statistical] 155 215 33% 5e-38 75% XP_001367699.3 [Statistical] 155 215 33% 5e-38 75% XP_00136640.1 [Statistical] 155 215 33% 5e-37 77% XP_002037394.1 [Statistical] 155 215 33% 5e-38 75% XP_00136658.1 [Statistical] 155 215 33% 5e-38 75% XP_00136658.1 [Statistical] 155 215 33% 5e-37 77% XP_002037394.1 [Statistical] 155 215 33% 5e-38 75% XP_00139658.1 [Statistical] 155 215 33% 5e-38 75% XP_00139658.1 [Statistical] 155 215 33% 5e-38	AAEL004010-PB [Aedes aegypti]	155	222	39%	7e-40	67%	XP_001648292.1
uncharacterized protein Dere _GG11771 [Drosophila erectal] uncharacterized protein Dyak_ GE10899, Isoform B 156 220 47% 6e-39 79% XP_015049122.1 NP_015049122.1 NP_01504912.1 NP_015049	AAEL004010-PC [Aedes aegypti]	155	223	39%	8e-40	67%	XP_001648293.1
renetal	AAEL004010-PD [Aedes aegypti]	155	223	39%	8e-40	67%	XP_001648290.1
Discophila yakuba 166 220 47% 68-39 79% XP_002099432.1 Uncharacterized protein Dyak_GE10899, isoform A 156 220 47% 68-39 79% XP_002099432.1 Uncharacterized protein Dyak_GE10899, isoform A 155 219 34% 88-39 77% XP_002073502.2 XP_002002073502.2 XP_002073502.2 XP_0020073502.2 XP_002073502.2 XP_0020073502.2 XP_	<u> </u>	157	221	34%	3e-39	79%	XP_001981160.1
Consophilal yakuba	• • • • • • • • • • • • • • • • • • • •	156	220	47%	6e-39	79%	XP_015049122.1
willistonal	, , =	156	220	47%	6e-39	79%	XP_002099432.1
Description	<u> </u>	155	219	34%	8e-39	77%	XP_002073502.2
CG1340, Isoform A [Drosophila melanogaster] 153 215 33% 5e-38 77% NP_651820.1 uncharacterized protein Dana_GF22920 [Drosophila ananassae] 154 219 33% 5e-38 78% XP_001964679.2 ananassae] PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Stomoxys calcitrans] 149 277 65% 1e-37 69% XP_013105640.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Stomoxys calcitrans] 149 281 65% 1e-37 69% XP_013105638.1 isoform X1 [Stomoxys calcitrans] 151 216 49% 2e-37 77% XP_002105546.1 GM12001 [Drosophila simulans] 150 215 33% 5e-37 77% XP_002105546.1 GM12001 [Drosophila sechellia] 150 215 33% 5e-37 77% XP_002037394.1 CG1340 [Drosophila sechellia] 149 221 49% 9e-37 73% ALC47603.1 uncharacterized protein Dvir_GJ24240 [Drosophila virilis] 148 218 49% 1e-36 75% XP_00204082.2 GH14211 [Drosophila girmshawi] 148 214 51% 2e-36 77% XP_0019495825.1 splicing factor [Anopheles darlingi] 145 215 40% 4e-36 60% ETN59545.1 AGAP003219-PB [Anopheles gambiae str. PEST] 146 213 39% 6e-36 61% XP_003438420.1 splicing factor [Culex quinquefasciatus] 145 217 61% 6e-36 67% XP_001848859.1 AGAP003219-PB [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_001848859.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] 143 273 65% 8e-36 60% XP_00191961.5 1 isoform X1 [Musca domestica] 143 273 65% 2e-35 60% XP_00191961.5 1 isoform X1 [Musca domestica] 140 197 40% 7e-35 59% XP_011343455.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Musca domestica] 140 197 40% 7e-35 59% XP_011343455.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Musca domestica] 140 197 40% 9e-35 59% XP_011343455.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Linepathema humile] 140 197 40% 9e-35 59% XP_011343455.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Linepathema humile] 140 197 40% 9e-35 59% XP_011343455.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Linepathema humile] 140 197 40%		155	216	49%	1e-38	74%	XP_001357599.3
uncharacterized protein Dana_GF22920 [Drosophila annassae] 154 219 33% 5e-38 78% XP_001964679.2 annassae] PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Stomoxys calcitrans] 149 277 66% 1e-37 69% XP_013105640.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Stomoxys calcitrans] 149 281 65% 1e-37 69% XP_013105638.1 GD21542 [Drosophila simulans] 151 216 49% 2e-37 77% XP_002105566.1 GM12901 [Drosophila sechellia] 150 215 33% 5e-37 77% XP_002037394.1 CG1340 [Drosophila busckii] 149 221 49% 9e-37 73% ALC47603.1 uncharacterized protein Dvir_GJ24240 [Drosophila virilis] 148 218 49% 1e-36 75% XP_002054082.2 GH14211 [Drosophila grimshawi] 148 214 51% 2e-36 77% XP_002954082.2 GH14211 [Drosophila grimshawi] 148 214 51% 2e-36 67% XP_00295451 s	GL13513 [Drosophila persimilis]	154	215	48%	1e-38	75%	XP_002020435.1
## PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Stomoxys calcitrans] PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Stomoxys calcitrans] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Stomoxys calcitrans] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Stomoxys calcitrans] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Stomoxys calcitrans] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Drosophila simulans] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H ilke isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H ilke isoform X2 [Musca domestica] ### PREDICTED: eukaryotic translation initiation factor 4H ilke isoform X2 [Linepathema humile] ### PREDICTED: eukaryotic translation initiation factor 4H ilke isoform X2 [Linepathema humile] ### PREDICTED: eukaryotic translation initiation factor 4H ilke isoform X2 [Linepathema humile] ### PREDICTED: eukaryotic translation initiation factor 4H ilke isoform X2 [Linepathema humile] ### PREDICTED: eukaryotic translation i	CG1340, isoform A [Drosophila melanogaster]	153	215	33%	5e-38	77%	NP_651820.1
Isoform X3 [Stomoxys calcitrans]	· · ·	154	219	33%	5e-38	78%	XP_001964679.2
isoform X1 [Stomoxys calcitrans] 149 261 69% 16-37 69% AP_UISI08636.1	•	149	277	65%	1e-37	69%	XP_013105640.1
GM12901 [Drosophila sechellia] 150 215 33% 5e-37 77% XP_002037394.1 CG1340 [Drosophila busckii] 149 221 49% 9e-37 73% ALC47603.1 uncharacterized protein Dvir_GJ24240 [Drosophila virilis] 148 218 49% 1e-36 75% XP_002054082.2 GH14211 [Drosophila grimshawi] 148 214 51% 2e-36 77% XP_001995925.1 splicing factor [Anopheles darlingi] 145 215 40% 4e-36 60% ETN59545.1 AGAP003219-PB [Anopheles gambiae str. PEST] 146 213 39% 6e-36 61% XP_003436420.1 splicing factor [Culex quinquefasciatus] 145 217 61% 6e-36 67% XP_001848859.1 AGAP003219-PA [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_001848859.1 AGAP003219-PA [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_001848859.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] 143 273 65% 8e-36 60% XP_005190145.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] 143 273 65% 2e-35 60% XP_001199144.1 isoform X1 [Musca domestica] 143 273 65% 2e-35 60% XP_011295194.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] 140 197 40% 7e-35 59% XP_011343457.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] 140 197 40% 9e-35 6e-34 6e-34 59% XP_01656940.1 PREDICTED: eukaryotic translation initiation factor 4H-like 150 1	•	149	281	65%	1e-37	69%	XP_013105638.1
CG1340 [Drosophila busckii] 149 221 49% 9e-37 73% ALC47603.1 uncharacterized protein Dvir_GJ24240 [Drosophila virilis] 148 218 49% 1e-36 75% XP_002054082.2 GH14211 [Drosophila grimshawi] 148 214 51% 2e-36 77% XP_00195925.1 splicing factor [Anopheles darlingi] 145 215 40% 4e-36 60% ETN59545.1 AGAP003219-PB [Anopheles gambiae str. PEST] 146 213 39% 6e-36 61% XP_003436420.1 splicing factor [Culex quinquefasciatus] 145 217 61% 6e-36 67% XP_001848859.1 AGAP003219-PA [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_312928.5 PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile]	GD21542 [Drosophila simulans]	151	216	49%	2e-37	77%	XP_002105546.1
uncharacterized protein Dvir_GJ24240 [Drosophila virilis] 148 218 49% 1e-36 75% XP_002054082.2 GH14211 [Drosophila grimshawi] 148 214 51% 2e-36 77% XP_001995925.1 splicing factor [Anopheles darlingi] 145 215 40% 4e-36 60% ETN59545.1 AGAP003219-PB [Anopheles gambiae str. PEST] 146 213 39% 6e-36 61% XP_003436420.1 splicing factor [Culex quinquefasciatus] 145 217 61% 6e-36 67% XP_001848859.1 AGAP003219-PA [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_001848859.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] 143 273 65% 8e-36 60% XP_005190146.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] 143 273 65% 2e-35 60% XP_0011295194.1 AGAP003219-PA-like protein [Anopheles sinensis] 137 137 25% 2e-35 63% KFB53209.1 <	GM12901 [Drosophila sechellia]	150	215	33%	5e-37	77%	XP_002037394.1
SH14211 [Drosophila grimshawi]	CG1340 [Drosophila busckii]	149	221	49%	9e-37	73%	ALC47603.1
splicing factor [Anopheles darlingi] 145 215 40% 4e-36 60% ETN59545.1 AGAP003219-PB [Anopheles gambiae str. PEST] 146 213 39% 6e-36 61% XP_003436420.1 splicing factor [Culex quinquefasciatus] 145 217 61% 6e-36 67% XP_001848859.1 AGAP003219-PA [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_312928.5 PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] 143 273 65% 8e-36 60% XP_005190146.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] 143 273 65% 1e-35 60% XP_005190145.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] 143 273 65% 2e-35 60% XP_011295194.1 AGAP003219-PA-like protein [Anopheles sinensis] 137 137 25% 2e-35 63% KFB53209.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] 140 197 40% 7e-35 59% XP_011343457.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] 137 194 65% 6e-34 61% XP_00556940.1	uncharacterized protein Dvir_GJ24240 [Drosophila virilis]	148	218	49%	1e-36	75%	XP_002054082.2
AGAP003219-PB [Anopheles gambiae str. PEST] 146 213 39% 6e-36 61% XP_003436420.1 splicing factor [Culex quinquefasciatus] 145 217 61% 6e-36 67% XP_001848859.1 AGAP003219-PA [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_312928.5 PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] 143 273 65% 8e-36 60% XP_005190146.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] 143 273 65% 1e-35 60% XP_005190145.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] 143 273 65% 2e-35 60% XP_011295194.1 AGAP003219-PA-like protein [Anopheles sinensis] 137 137 25% 2e-35 63% KFB53209.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] 140 197 40% 7e-35 59% XP_011343457.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] 148 149 4e-34 59% XP_012221230.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] 149 4e-34 59% XP_012221230.1	GH14211 [Drosophila grimshawi]	148	214	51%	2e-36	77%	XP_001995925.1
splicing factor [Culex quinquefasciatus] 145 217 61% 6e-36 67% XP_001848859.1 AGAP003219-PA [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_312928.5 PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] 143 273 65% 8e-36 60% XP_005190146.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] 143 273 65% 1e-35 60% XP_005190145.1 PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] 143 273 65% 2e-35 60% XP_011295194.1 AGAP003219-PA-like protein [Anopheles sinensis] 137 137 25% 2e-35 63% KFB53209.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] 140 197 40% 7e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] 140 197 40% 9e-35 59% XP_011343458.1 PREDICTED: eukaryotic translation initiation factor 4H-like isofo	splicing factor [Anopheles darlingi]	145	215	40%	4e-36	60%	ETN59545.1
AGAP003219-PA [Anopheles gambiae str. PEST] 145 211 39% 7e-36 61% XP_312928.5 PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] AGAP003219-PA-like protein [Anopheles sinensis] 137 137 25% 2e-35 63% KFB53209.1 PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile]	AGAP003219-PB [Anopheles gambiae str. PEST]	146	213	39%	6e-36	61%	XP_003436420.1
PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] AGAP003219-PA-like protein [Anopheles sinensis] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile]	splicing factor [Culex quinquefasciatus]	145	217	61%	6e-36	67%	XP_001848859.1
isoform X3 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] AGAP003219-PA-like protein [Anopheles sinensis] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile]	AGAP003219-PA [Anopheles gambiae str. PEST]	145	211	39%	7e-36	61%	XP_312928.5
isoform X2 [Musca domestica] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica] AGAP003219-PA-like protein [Anopheles sinensis] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile]	•	143	273	65%	8e-36	60%	XP_005190146.1
isoform X1 [Musca domestica] AGAP003219-PA-like protein [Anopheles sinensis] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile]	•	143	273	65%	1e-35	60%	XP_005190145.1
PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Linepithema humile]	•	143	273	65%	2e-35	60%	XP_011295194.1
isoform X1 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like 137 194 65% 6e-34 61% XP 006566940 1	AGAP003219-PA-like protein [Anopheles sinensis]	137	137	25%	2e-35	63%	KFB53209.1
isoform X2 [Cerapachys biroi] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like PREDICTED: eukaryotic translation initiation factor 4H-like 137 194 65% 6e-34 61% XP_006566940.1		140	197	40%	7e-35	59%	XP_011343457.1
isoform X1 [Linepithema humile] PREDICTED: eukaryotic translation initiation factor 4H-like 138 199 41% 4e-34 59% XP_012221230.1	•	140	197	40%	9e-35	59%	XP_011343458.1
1.37 194 00% 0P-34 01% XP 00000001	•	138	199	41%	4e-34	59%	XP_012221230.1
	•	137	194	65%	6e-34	61%	XP_006566940.1

PREDICTED eularyotic translation initiation factor 4H-like acidor m.X 10 processoria quadroscelly acidoscelly acidoscelly acidom x 10 processoria quadroscelly acidom x 10 processoria quadroscell	PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Apis mellifera]	137	194	65%	8e-34	61%	XP_392894.1
RECOURT P. Company for translation inflation before 4H-like 136 192 40% 3e-33 61% XP_012247500.1 PREDICTED cularyotic translation inflation before 4H-like 136 198 41% 3e-33 59% XP_014470237.1 RECOURT P. Company for translation inflation before 4H-like 136 198 41% 3e-33 61% XP_01247500.2 XP_012477029.1 RECOURT P. Company for translation inflation factor 4H-like 136 198 41% 3e-33 61% XP_01247029.1 XP_	·	136	197	41%	2e-33	59%	XP_014470233.1
	·	136	196	40%	3e-33	58%	XP_011697818.1
		136	192	40%	3e-33	61%	XP_012247500.1
PREDICTE uskaryotic translation initiation factor 4H-like landom X2 [Wasmannia auropunctatis] 135 196 40% 3e-33 58% XP_011887819.1	_	136	196	41%	3e-33	59%	XP_014470237.1
Industry 1976 197		136	191	40%	3e-33	61%	XP_012170299.1
PREDICTED: exkaryotic translation initiation factor 4H-like 135 196 40% 4e-33 59% XP_01214442_1	_	135	196	40%	3e-33	58%	XP_011697819.1
Institution	_	137	194	35%	3e-33	67%	CAD55310.1
PREDICTED: eukaryotic translation initiation factor 4H-like tasform X2 [National State of the		135	196	40%	4e-33	59%	XP_012144422.1
PREDICTED: eukaryotic translation initiation factor 4H-like isoform X [Harpegnarhos salator] 134 194 41% 1e-32 57% XP_011142287.1 195 197	_	135	196	40%	6e-33	58%	XP_012532397.1
PREDICTED: eukaryotic translation initiation factor 4H-like soform X2 [Harpegnathos saltator] 134 135 268 60% 1e-32 71% XP_013105639.1	_	134	195	41%	1e-32	57%	XP_011142296.1
Institute Inst	·	134	194	41%	1e-32	57%	XP_011142297.1
Institute Inst		135	268	60%	1e-32	71%	XP_013105639.1
Solenopsis invictal	_	134	188	41%	2e-32	58%	XP_008217447.1
Isoform X2 [Vollenhovia emeryi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Vollenhovia emeryi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Vollenhovia emeryi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Nasonia vitripennis] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Nasonia vitripennis] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like lasoform X2 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Ceratosolen solmsi marchail] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pognomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchail] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Pognomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor		134	195	40%	2e-32	58%	XP_011162080.1
Isoform X1 [Vollenhovia emeryi] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Nasonia vitripennis] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pognomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation f	_	133	194	40%	2e-32	58%	XP_011866332.1
Isoform X4 [Nasonia vitripennis] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like [Atta cephalotes] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X		133	193	40%	3e-32	58%	XP_011866331.1
isoform X1 [Acromymex echinatior] PREDICTED: eukaryotic translation initiation factor 4H-like [Atta cephalotes] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X2 [Acromymex echinatior]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X2 [Acromymex echinatior]] PREDICTED: eukaryotic translation initiation factor 4H [soform X2 [Noistes dominula]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X2 [Ceratosolen solmsi marchali]] PREDICTED: eukaryotic translation initiation factor 4H [soform X1 [Polistes dominula]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X2 [Athalia rosae]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X2 [Athalia rosae]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X3 [Pogonomymex barbatus]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Ceratosolen solmsi marchali]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Ceratosolen solmsi marchali]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Ceratosolen solmsi marchali]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Athalia rosae]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Athalia rosae]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Pogonomymex barbatus]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Pogonomymex barbatus]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Pogonomymex barbatus]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Pogonomymex barbatus]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Pogonomymex barbatus]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Pogonomymex barbatus]] PREDICTED: eukaryotic translation initiation factor 4H-like [soform X4 [Pogonomymex barbatus]]		134	188	41%	3e-32	58%	XP_008217446.1
[Atta cephalotes] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Acromyrmex echinatior] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus]		133	191	40%	3e-32	58%	XP_011058247.1
isoform X2 [Acromymex echinatior] PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomymex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomymex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomymex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomymex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomymex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomymex barbatus]		133	191	40%	4e-32	58%	XP_012061221.1
isoform X2 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus]		132	190	40%	4e-32	58%	XP_011058248.1
isoform X2 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus]		132	188	39%	6e-32	59%	XP_015174166.1
isoform X1 [Polistes dominula] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus]		132	182	41%	8e-32	57%	XP_011494499.1
isoform X2 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H like isoform X4 [Pogonomyrmex barbatus]	-	132	189	39%	9e-32	59%	XP_015174165.1
isoform X3 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H 130 187 39% 2e-31 59% XP 014611152 1		132	183	39%	9e-32	60%	XP_012251403.1
isoform X1 [Ceratosolen solmsi marchali] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H 130 187 39% 2e-31 59% XP_014611152.1		132	192	41%	1e-31	57%	XP_011640375.1
isoform X1 [Athalia rosae] PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H 131 191 41% 1e-31 57% XP_011640376.1 PREDICTED: eukaryotic translation initiation factor 4H 130 187 39% 2e-31 59% XP_014611152.1	- I	132	183	41%	1e-31	57%	XP_011494498.1
isoform X4 [Pogonomyrmex barbatus] PREDICTED: eukaryotic translation initiation factor 4H 130 187 187 187 187 187 187 187 18	- · · · · · · · · · · · · · · · · · ·	132	183	39%	1e-31	60%	XP_012251395.1
130 107 39% 28-31 39% AF 0140111321	-	131	191	41%	1e-31	57%	XP_011640376.1
		130	187	39%	2e-31	59%	XP_014611152.1



RNA-binding protein 2, isoform A [Drosophila melanogaster]

Sequence ID: ref|NP_524959.1| Length: 325 Number of Matches: 1

See 1 more title(s) Range 1: 1 to 325

Score		Expect	Method		Identities	Positives	Gaps	Frame
449 bits	(1155)	9e-154()	Compositiona	l matrix adjust.	325/325(100)%) 325/325(100%) 0/325(0%) -	⊦ 1
Features	S :							
Query	7					POGLVOGDVIKIFO		
Sbjct	1					PQGLVQGDVIKIFQ PQGLVQGDVIKIFQ		
Query	187					SAPLRIDIADRRK SAPLRIDIADRRK		
Sbjct	61					SAPLRIDIADRRK		
Query	367	gnggm	trgdggrdgFQ	Krgpprqggss	qsysrggpgt	ggggreggggsgn GGGGREGGGGSGN	rgdsrDRPAN	546
Sbjct	121					GGGGREGGGGSGN		
Query	547					ORYNNFNRHRDRER ORYNNFNRHRDRER		
Sbjct	181					ORYNNFNRHRDRER		
Query	727	RPsggr	ntglgggsggs	gglgvgggssm	gAIDDNERPF	RLQLKPRTIAAPIN RLQLKPRTIAAPIN	AVAETKOSAS	906
Sbjct	241	RPSGGI	MTGLGGGSGGS	GGLGVGGGSSM	GAIDDNERPF	RLQLKPRTIAAPIN	AVAETKOSAS	300
Query	907		KPREEKLKELQ KPREEKLKELQ	~	981			
Sbjct	301		KPREEKLKELQ		325			

uncharacterized protein Dsimw501_GD17286, isoform C [Drosophila simulans]

Sequence ID: gb|KMZ10169.1| Length: 325 Number of Matches: 1

Range 1: 1 to 325

Score		Expect	Method	Identities	Positives	Gaps Fr	ame
447 bits	(1151)	4e-153()	Compositional matrix adjust.	324/325(99%)	325/325(100%)	0/325(0%) +1	
Features	s:						
Query	7		SYEHARSGFGGDRASKQLPTEP				186
Sbjct	1		GYEHARSGFGGDRASKQLPTEP: GYEHARSGFGGDRASKQLPTEP:				60
Query	187		OQFKGFCYVEFETLDNLERALE OQFKGFCYVEFETLDNLERALE				366
Sbjct	61		OOFKGFCYVEFETLDNLERALE OOFKGFCYVEFETLDNLERALE				120
Query	367	gnggmt	rgdggrdgFQKrgpprqggss TRGDGGRDGFQKRGPPRQGGSS	qsysrggpgtgg	ggreggggggnr	gdsrDRPAN	546
Sbjct	121		rgdggrdgrokkgpproggss rgdggrdgrokkgpproggss				180
Query	547		SFNNDDRPFERNQDRDRGQREG SFNNDDRPF+RNQDRDRGQREG				726
Sbjct	181		SFNNDDRPFDRNQDRDRGQREG				240
Query	727		ntglgggsggsgglgvgggssm MTGLGGGSGGSGGLGVGGGSSM				906
Sbjct	241		ATGLGGGSGGSGGLGVGGGSSM				300
Query	907		KPREEKLKELQQNVNHNGDN KPREEKLKELQQNVNHNGDN	981			
Sbjct	301			325			

RE23444p [Drosophila melanogaster]

Sequence ID: gb|ADX35943.1| Length: 326 Number of Matches: 1

Range 1: 3 to 326

Score		Expect	Method		Identities	Positives	Gaps	Frame
443 bits	(1139)	2e-151()	Compositional matrix	adjust.	324/325(99%)	324/325(99%)	1/325(0%)	+1
Features	s:							
Query	7		YEHARSGFGGDRASKO					
Sbjct	3		YEHA SGFGGDRASKO YEHA-SGFGGDRASKO					
Query	187		QFKGFCYVEFETLDNL QFKGFCYVEFETLDNL					
Sbjct	62		OFKGFCYVEFETLDNL					
Query	367	gnggmt	.rgdggrdgFQKrgppr 'RGDGGRDGFQKRGPPR	qggssq	sysrggpgtgg sysrccpcrcc	ggreggggsgni GGREGGGGSGNI	rgdsrDRPA	N 546
Sbjct	122		'RGDGGRDGFQKRGPPR					
Query	547		FNNDDRPFERNODRDR FNNDDRPFERNODRDR					
Sbjct	182		FNNDDRPFERNQDRDR					

Query 727 RPsggmtglgggsggsgglgvgggssmgAIDDNERPRLQLKPRTIAAPINAVAETKQSAS 906 RPSGGMTGLGGGSGGSGGLGVGGGSSMGAIDDNERPRLQLKPRTIAAPINAVAETKQSAS Sbjct 242 RPSGGMTGLGGGSGGSGGLGVGGGSSMGAIDDNERPRLQLKPRTIAAPINAVAETKQSAS 301

Query 907 IFGNAKPREEKLKELQQNVNHNGDN 981 IFGNAKPREEKLKELQQNVNHNGDN 326

RNA-binding protein 2, isoform B [Drosophila melanogaster]

Sequence ID: ref|NP_727982.1| Length: 324 Number of Matches: 1

▶ See 1 more title(s) Range 1: 1 to 324

Score		Expect	Method	Identities	Positives	Gaps	Frame
442 bits	(1138)	3e-151()	Compositional matrix adjust.	324/325(99%)	324/325(99%)	1/325(0%)	+1
Features	s:						
Query	7		YEHARSGFGGDRASKQLPTEPI				
Sbjct	1		YEHA SGFGGDRASKQLPTEPI YEHA-SGFGGDRASKQLPTEPI				
Query	187		QFKGFCYVEFETLDNLERALE				
Sbjct	60		QFKGFCYVEFETLDNLERALE QFKGFCYVEFETLDNLERALE				
Query	367	gnggmt	.rgdggrdgFQKrgpprqggss 'RGDGGRDGFQKRGPPRQGGSS(qsysrggpgtgg	ggreggggggni	rgdsrDRPAN	546
Sbjct	120		RGDGGRDGFQKRGPPRQGGSS(
Query	547		FNNDDRPFERNQDRDRGQREGSFNNDDRPFERNQDRDRGQREGS				
Sbjct	180		FNNDDRPFERNQDRDRGQREG				
Query	727	RPsggm	tglgggsggsgglgvgggssm TGLGGGSGGSGGLGVGGGSSM	GAIDDNERPRLO	LKPRTIAAPINA	AVAETKOSAS	906
Sbjct	240		TGLGGGSGGSGGLGVGGGSSM				
Query	907		PREEKLKELQQNVNHNGDN S	981			
Sbjct	300			324			

uncharacterized protein Dere_GG17966, isoform B [Drosophila erecta] Sequence ID: **ref|XP_015010732.1|** Length: 325 Number of Matches: 1

▶ See 3 more title(s) Range 1: 1 to 325

Score		Expect	Method	Identities	Positives	Gaps	Frame
442 bits(1137)	5e-151()	Compositional matrix adjust.	320/325(98%)	324/325(99%)	0/325(0%)	+1
Features	s:						
Query	7		SYEHARSGFGGDRASKQLPTEPI				
Sbjct	1		YEHAR GFGGDRASKQLPTEP YEHARGGFGGDRASKQLPTEP				
Query	187		OOFKGFCYVEFETLDNLERALE				
Sbjct	61		OFKGFCYVEFETLDNLERALE OFKGFCYVEFETLDNLERALE				
Query	367	gnggmt	rgdggrdgFQKrgpprqggss RGDGGRDGFQKRGPPRQGGSS	qsysrggpgtgg	ggreggggggni	rgdsrDRPA	N 546
Sbjct	121		RGDGGRDGFQKRGPPRQGGSS(
Query	547		FNNDDRPFERNQDRDRGQREG FNNDDRPF+RNQDRDRGQREG				
Sbjct	181		FNNDDRFF TRNODRDRGQREG FNNDDRPFDRNQDRDRGQREG				
Query	727	RPsggm	ntglgggsggsgglgvgggssm N+GLGGGSGGSGGLGVGGGSSM	gAIDDNERPRLO	LKPRTIAAPINA	AVAETKOSA	S 906
Sbjct	241		ISGLGGGSGGSGGLGVGGGSSM				
Query	907		PREEKLKELQQNVNHNGDN S PREEKLKELQQNVNHNGDN	981			
Sbjct	301			325			

RNA-binding protein 2, isoform E [Drosophila melanogaster]

Sequence ID: ref|NP_001285331.1| Length: 317 Number of Matches: 1

See 1 more title(s)

Range 1: 5 to 317

Score Expect Method Identities Positives Gaps Frame

Feature	es:		
Query	43	GFGGDRASKQLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLVKDRETDQFKGFC GFGGDRASKQLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLVKDRETDQFKGFC	222
Sbjct	5	GFGGDRASKQLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLVKDRETDQFKGFC	64
Query	223	YVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKNdrpgggvgggnggmtrgdggr YVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKNDRPGGGVGGGNGGMTRGDGGR	402
Sbjct	65	YVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKNDRPGGGVGGGNGGMTRGDGGR	124
Query	403	dgFQKrgpprqggssqsysrggpgtggggreggggsgnrgdsrDRPANRGRYGSFNNDDR DGFQKRGPPRQGGSSQSYSRGGPGTGGGGREGGGGSGNRGDSRDRPANRGRYGSFNNDDR	582
Sbjct	125	DGFQKRGPPRQGGSSQSYSRGGPGTGGGGREGGGGSGNRGDSRDRPANRGRYGSFNNDDR	184
Query	583	PFERNQDRDRGQREGSYGNQSRDGDRYNNFNRHRDRERTHYNPNQQSERPsggmtglggg PFERNQDRDRGQREGSYGNQSRDGDRYNNFNRHRDRERTHYNPNQQSERPSGGMTGLGGG	762
Sbjct	185	PFERNQDRDRGQREGSYGNQSRDGDRYNNFNRHRDRERTHYNPNQQSERPSGGMTGLGGG	244
Query	763	sggsgglgvgggssmgAIDDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL SGGSGGLGVGGGSSMGAIDDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL	942
Sbjct	245	SGGSGGLGVGGGSSMGAIDDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL	304
Query	943	KELQQNVNHNGDN 981 KELQQNVNHNGDN	
Sbjct	305	KELQQNVNHNGDN 317	

uncharacterized protein Dana_GF19517, isoform B [Drosophila ananassae] Sequence ID: **ref|XP_014759990.1|** Length: 369 Number of Matches: 1

▶ See 1 more title(s) Range 1: 44 to 369

Score		Expect	Method	Identities	Positives	Gaps	Frame
410 bits	(1054)	7e-138()	Compositional matrix adjust.	272/328(83%)	278/328(84%)	5/328(1%) -	+1
Features	s:						
Query	7		YEHARSGFGGDRASKQLPTEPF				
Sbjct	44		YEHARSGFGG+R KOLPTEPE YEHARSGFGGERHMKOLPTEPE				
Query	187		QFKGFCYVEFETLDNLERALEC QFKGFCYVEFETLDNLERALEC				
Sbjct	104		QFKGFCYVEFETLDNLERALEC				
Query	367	gnggmt GNGG	rgdggrdgFQKrgpprqggssc DGGRDGFQK P + G +	ısysrggpgtgg GG	ggreggggsgn: GG GG	rgdsrDRPAN G DRPAN	
Sbjct	164		GRDGGRDGFQK-RGPPRQGGAT				•
Query	547		FNNDDRPFERNQDR-DRGQREG FNNDDR FERNQDR DRGQREG				
Sbjct	223		FNNDDR-FERNQDRGDRGQREG				
Query	724	ERPs ERP	ggmtglgggsggsgglgvgggs G G GG GG GG	smgAIDDNERP	RLQLKPRTIAAI	PINAVAETKO	897
Sbjct	282		IGGGGAGGIGGGGGGGAGGGGS				
Query	898		NAKPREEKLKELQQNVNHNGDN NAKPREEKLKELQQNVNHNGDN				
Sbjct	342		NAKPREEKLKELQQNVNHNGDN				

uncharacterized protein Dana_GF19517, isoform C [Drosophila ananassae] Sequence ID: **ref|XP_014759991.1**| Length: 376 Number of Matches: 1

▶ See 1 more title(s) Range 1: 44 to 376

Score		Expect	Method	Identities	Positives	Gaps	Frame
409 bits	(1050)	4e-137()	Compositional matrix adjust.	286/334(86%) 292/334(87%)	10/334(2%)	-1
Features	s:						
Query	7		GYEHARSGFGGDRASKQLPTEPI				
Sbjct	44		GYEHARSGFGG+R KQLPTEPI GYEHARSGFGGERHMKQLPTEPI				
Query	187		OOFKGFCYVEFETLDNLERALE(
Sbjct	104		OGFKGFCYVEFETLDNLERALE OGFKGFCYVEFETLDNLERALE				
Query	367	gnggmt	rgdggrdgFQKrgppi DGGRDGFQKR G	rqggssqsysr	ggpgtggggre	ggggsgnrgds	528
Sbjct	164		IGRDGGRDGFQKRGPPRQGGAT(
Query	529		IRGRYGSFNNDDRPFERNODR-I IRGRYG+FNNDDR FERNODR I				
Sbjct	224		IRGRYGNFNNDDR-FERNQDRGI				
Query	706	NPNQQS NPNOOS	SERPsggmtglgggsggsgg SERP G G GG GG GG	lgvgggssmgA	.IDDNERPRLQLI .IDD ERPRLQLI	KPRTIAAPINA	879
Sbjct	283		SERPSGGIGGGGAGGIGGGGGG				
Query	880)SASIFGNAKPREEKLKELQQN\)SASIFGNAKPREEKLKELQQN\		1		
Sbjct	343		SASIFGNAKPREEKLKELQQN SASIFGNAKPREEKLKELQQN		6		

GD17286 [Drosophila simulans]

Sequence ID: ref|XP_002107116.1| Length: 256 Number of Matches: 1

▶ See 1 more title(s) Range 1: 107 to 256

Score		Expect Method	Identities	Positives	Gaps	Frame
238 bits	(608)	2e-72() Compositional matrix adjust.	149/150(99%)	150/150(100%)	0/150(0%)	+1
Feature	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNODRD				
Sbjct	107	DRPANRGRYGSFNNDDRPF+RNQDRD DRPANRGRYGSFNNDDRPFDRNQDRD				
Query	712	NQQSERPsggmtglgggsggsgglgv NQQSERPSGGMTGLGGGSGGSGGLGV				
Sbjct	167	NQQSERPSGGMTGLGGGSGGSGGLGV				
Query	892	KQSASIFGNAKPREEKLKELQQNVNH KOSASIFGNAKPREEKLKELQONVNH				
Sbjct	227	KQSASIFGNAKPREEKLKELQQNVNH				

RNA-binding protein 2, isoform C [Drosophila melanogaster]

Sequence ID: ref|NP_996487.1| Length: 358 Number of Matches: 2

▶ See 2 more title(s) Range 1: 209 to 358

Score		Expect Method	Identities	Positives	Gaps	Frame
239 bits	(609)	3e-71() Compositional matrix adjust.	150/150(100%)	150/150(100%)	0/150(0%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNODRD DRPANRGRYGSFNNDDRPFERNODRD				
Sbjct	209	DRPANRGRYGSFNNDDRPFERNQDRD				
Query	712	NQQSERPsggmtglgggsggsgglgv NQOSERPSGGMTGLGGGSGGSGGLGV	gggssmgAIDDN	ERPRLOLKPRTIA	AAPINAVAE	T 891
Sbjct	269	NQQSERPSGGMTGLGGGSGGSGGLGV				
Query	892	KQSASIFGNAKPREEKLKELQQNVNE KQSASIFGNAKPREEKLKELQQNVNE				
Sbjct	329	KQSASIFGNAKPREEKLKELQQNVNE				

Range 2: 1 to 111

Score		Expect	Method	Identities	Positives	Gaps	Frame
232 bits	(591)	2e-68()	Compositional matrix adjust.	111/111(100%)	111/111(100%)	0/111(0%)	+1
Features	s:						
Query	7		GGYEHARSGFGGDRASKQLPTEF GGYEHARSGFGGDRASKQLPTEF				
Sbjct	1		GGYEHARSGFGGDRASKOLPTEF				
Query	187		TDQFKGFCYVEFETLDNLERALE TDQFKGFCYVEFETLDNLERALE				
Sbjct	61		TDQFKGFCYVEFETLDNLERALE				

GM13442 [Drosophila sechellia]

Sequence ID: ref|XP_002042252.1| Length: 358 Number of Matches: 2

▶ See 2 more title(s) kange 1: 209 to 358

Score		Expect Method	Identities	Positives	Gaps	Frame
238 bits	(606)	1e-70() Compositional matrix adjust.	149/150(99%)	150/150(100%)	0/150(0%)	+1
Feature	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD				
Sbjct	209	DRPANRGRYGSFNNDDRPF+RNQDRD DRPANRGRYGSFNNDDRPFDRNQDRD				
Query	712	NQQSERPsggmtglgggsggsgglgv NQQSERPSGGMTGLGGGSGGSGGLGV	gggssmgAIDDN	IERPRLOLKPRTI	AAPINAVAE	T 891
Sbjct	269	NQQSERPSGGMTGLGGGSGGSGGLGV				
Query	892	KQSASIFGNAKPREEKLKELQQNVNH KQSASIFGNAKPREEKLKELQQNVNH				

Range 2: 1 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame
231 bits	(590)	2e-68() Compositional matrix adjust.	111/111(100%)	111/111(100%)	0/111(0%)	+1
Features	S :					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTE MAGRGGYEHARSGFGGDRASKQLPTE				
Sbjct	1	MAGRGGYEHARSGFGGDRASKQLPTE:				
Query	187	KDRETDQFKGFCYVEFETLDNLERALI KDRETDQFKGFCYVEFETLDNLERALI				
Sbjct	61	KDRETDQFKGFCYVEFETLDNLERAL				

RH12113p [Drosophila melanogaster]

Sequence ID: gb|ABC86252.1| Length: 358 Number of Matches: 2

Range 1: 209 to 358

Score		Expect	Method	Identities	Positives	Gaps	Frame
236 bits	(603)	3e-70()	Compositional matrix adjust.	149/150(99%)	149/150(99%)	0/150(0%)	+1
Features	3:						
Query	532		IRGRYGSFNNDDRPFERNQDRDR IRGRYGSFNNDDRPFERNODRDR				
Sbjct	209		IRGRYGSFNNDDRPFERNQDRDR				
Query	712		RPsggmtglgggsggsgglgvg				
Sbjct	269		ERPSGGMTGLGGGSGGSGGLGVG ERPSGGMTGLGGGSGGSGGLGVG				
Query	892		SIFGNAKPREEKLKELQQNVNHN				
Sbjct	329		SIFGNAKPREEKLKELQQNVNHN SIFGNAKPREEKLKELQQNVNHN				

Range 2: 1 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame
232 bits	(591)	2e-68() Compositional matrix adjust.	111/111(100%)	111/111(100%)	0/111(0%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTE MAGRGGYEHARSGFGGDRASKQLPTE				
Sbjct	1	MAGRGGYEHARSGFGGDRASKQLPTE				
Query	187	KDRETDQFKGFCYVEFETLDNLERAL				
Sbjct	61	KDRETDQFKGFCYVEFETLDNLERALI KDRETDQFKGFCYVEFETLDNLERALI				

uncharacterized protein Dere_GG17966, isoform A [Drosophila erecta]
Sequence ID: ref|XP_001977936.1| Length: 358 Number of Matches: 2

▶ See 3 more title(s) Range 1: 209 to 358

Score	t	Expect Method	identities	Positives	Gaps	Frame
234 bits(597) 2	2e-69() Compositional matrix adjust.	146/150(97%)	150/150(100%)	0/150(0%)	+1
Features	:					
Query	532	DRPANRGRYGSFNNDDRPFERNODRDF DRPANRGRYG+FNNDDRPF+RNODRDF				
Sbjct	209	DRPANRGRYGNFNNDDRPFDRNQDRDF	~ ~			
Query	712	NQQSERPsggmtglgggsggsgglgvg NOOSERPSGGM+GLGGGSGGSGGLGVG				
Sbjct	269	NQQSERPSGGMSGLGGGSGGSGGLGVG				
Query	892	KQSASIFGNAKPREEKLKELQQNVNHN KOSASIFGNAKPREEKLKELOONVNHN				
Sbjct	329	KQSASIFGNAKPREEKLKELQQNVNHN				

Range 2: 1 to 111

Score	Expect	Metnoa	identities	Positives	Gaps	Frame
230 bits(586)	7e-68()	Compositional matrix adjust.	110/111(99%)	110/111(99%)	0/111(0%)	+1
Features:						

Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLV MAGRGGYEHAR GFGGDRASKQLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLV	186
Sbjct	1	MAGRGGYEHARGGFGGDRASKÕLPTEPPFIAFVGNLPÕGLVÕGDVIKIFÕDFEVKYVRLV	60
Query	187	KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN 339 KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN	
Sbjct	61	KDRETDÕFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN 111	

RNA-binding protein 2, isoform D [Drosophila melanogaster]

Sequence ID: ref|NP_001285330.1| Length: 388 Number of Matches: 2

▶ See 1 more title(s) Range 1: 1 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame
234 bits	(597)	5e-69() Compositional matrix adjust.	111/111(100%)	111/111(100%)	0/111(0%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKOLPTE				
Sbjct	1	MAGRGGYEHARSGFGGDRASKQLPTE MAGRGGYEHARSGFGGDRASKQLPTE				
Query	187	KDRETDQFKGFCYVEFETLDNLERAL KDRETDQFKGFCYVEFETLDNLERAL				
Sbjct	61	KDRETDQFKGFCYVEFETLDNLERAL				

Range 2: 209 to 388

Score	E	Expect Method	Identities	Positives	Gaps	Frame
231 bits(588) 9	e-68() Compositional matrix adjust.	150/180(83%)	150/180(83%)	30/180(16%)	+1
Features	:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD DRPANRGRYGSFNNDDRPFERNODRD				
Sbjct	209	DRPANRGRYGSFNNDDRPFERNQDRD	~ ~			
Query	712	NQQSERPsggmtglgggsggsgglgv NQOSERPSGGMTGLGGGSGGSGGLGV				- 819
Sbjct	269	NQQSERPSGGMTGLGGGSGGSGGLGV		FRHFKKPISRI	SNMCQSRVSQ	L 328
Query	820	DNERPRLQLKPRTIAAPINA DNERPRLOLKPRTIAAPINA				
Sbjct	329	AVPRTNDNERPRLQLKPRTIAAPINA	~		~ ~	

uncharacterized protein Dsimw501_GD17286, isoform B [Drosophila simulans]

Sequence ID: gb|KMZ10168.1| Length: 385 Number of Matches: 2

Range 1: 1 to 111

Score		Expect	Method	Identities	Positives	Gaps	Frame
234 bits	(596)	5e-69()	Compositional matrix adjust.	111/111(100%)	111/111(100%)	0/111(0%)	+1
Features	S :						
Query	7		GGYEHARSGFGGDRASKQLPTEF GGYEHARSGFGGDRASKQLPTEF				
Sbjct	1		GGYEHARSGFGGDRASKOLPTEF				
Query	187		TDQFKGFCYVEFETLDNLERALE TDQFKGFCYVEFETLDNLERALE				
Sbjct	61		TDQFKGFCYVEFETLDNLERALE				

Range 2: 209 to 385

Score		Expect Method	Identities	Positives	Gaps	Frame
231 bits	(588) 9	9e-68() Compositional matrix adjust.	149/177(84%)	150/177(84%)	27/177(15%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRI DRPANRGRYGSFNNDDRPF+RNODRI				
Sbjct	209	DRPANRGRYGSFNNDDRPFDRNQDRI				
Query	712	NQQSERPsggmtglgggsggsgglgv NQQSERPSGGMTGLGGGSGGSGGLGV				- 819
Sbjct	269	NQQSERPSGGMTGLGGGSGGSGGLGV	GGGSSMGAIDH	IQKPISSTFSNN	MCQSRVSQLDA	P 328
Query	820	DNERPRLQLKPRTIAAPINAVAE DNERPRLQLKPRTIAAPINAVAE				981
Sbjct	329	CIYDNERPRLÖLKPRTIAAPINAVAE				385

Sequence ID: ref|XP_001966145.2| Length: 412 Number of Matches: 2

▶ See 1 more title(s) Range 1: 44 to 154

Score		Expect Method	Identities	Positives	Gaps	Frame
223 bits	(569)	1e-64() Compositional matrix adjust.	107/111(96%)	108/111(97%)	0/111(0%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEP MAGRGGYEHARSGFGG+R KOLPTEP	PFIAFVGNLPQO PFIAFVGNLPQO			
Sbjct	44	MAGRGGYEHARSGFGGERHMKQLPTEP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALE KDRETDQFKGFCYVEFETLDNLERALE				
Sbjct	104	KDRETDOFKGFCYVEFETLDNLERALE				

Range 2: 261 to 412

Score		Expect Method	Identities	Positives	Gaps	Frame
214 bits(5	545)	3e-61() Compositional matrix adjust.	130/153(85%)	133/153(86%)	4/153(2%)	+1
Features:						
Query	532	DRPANRGRYGSFNNDDRPFERNQDR-D DRPANRGRYG+FNNDDR FERNQDR D				
Sbjct	261	DRPANRGRYGNFNNDDR-FERNQDRGD				
Query	709	PNQQSERPsggmtglgggsggsgglgv PNOOSERPSGG+ G G G G G		DDNERPRLQLKP DD ERPRLOLKP		
Sbjct	320	PNQQSERPSGGIGGGGAGGIGGGGGGG				
Query	883	AETKQSASIFGNAKPREEKLKELQQNV AETKOSASIFGNAKPREEKLKELQONV				
Sbjct	380	AETKOSASTFONAKPREEKLKELQQNV AETKQSASTFGNAKPREEKLKELQQNV				

uncharacterized protein Dvir_GJ19028, isoform C [Drosophila virilis]

Sequence ID: ref|XP_015026516.1| Length: 325 Number of Matches: 2

▶ See 1 more title(s) Range 1: 177 to 325

Score		Expect Method	Identities	Positives	Gaps	Frame
219 bits(559) 4	4e-64() Compositional matrix adjust.	118/150(79%)	126/150(84%)	1/150(0%)	+1
Features	:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRDR DRPANRGRYG+FNND+R F+RNODRDR				
Sbjct	177	DRPANRGRYGNFNNDER-FDRNQDRDR				
Query	712	NQQSERPsggmtglgggsggsgglgvg		ERPRLQLKPRTI. ERPRLOLKPRTI.		
Sbjct	236	NQQQERPSGVAMGAIGNNSMRQDSNMT.		~		
Query	892	KQSASIFGNAKPREEKLKELQQNVNHN KOSASIFGNAKPREEKLKELQON+NHN				
Sbjct	296	KÕSASIFGNAKPREEKLKELÕÕNMNHN				

Range 2: 1 to 111

Score	E	xpect	Method	Identities	Positives	Gaps	Fram	ne
217 bits(5	553) 36	e-63()	Compositional matrix adjust.	102/111(92%)	106/111(95%)	0/111(0%)	+1	
Features:								
Query			GYEHARSGFGGDRASKOLPTEPI GYEHAR GFGG+R KO+PTEPI					186
Sbjct			GYEHARGGFGGERHVKOMPTEPE					50
Query			DOFKGFCYVEFETLDNLERALECTOFKGFCYVEFETLDNLERALEC					
Sbjct			DOFKGFCYVEFETLDNLERALEC					

uncharacterized protein Dvir_GJ19028, isoform B [Drosophila virilis] Sequence ID: ref|XP_015026515.1| Length: 352 Number of Matches: 2

▶ See 1 more title(s) Range 1: 204 to 352

Score	Expect	Method	Identities	Positives	Gaps	Frame
220 bits(560)	6e-64()	Compositional matrix adjust.	118/150(79%)	126/150(84%)	1/150(0%)	+1

Features: Ouery DRPANRGRYGSFNNDDRPFERNQDRDRGQREGSYGNQSRDGDRYNNFNRHRDRERTHYNP 532 711 DRPANRGRYG+FNND+R F+RNQDRDRGQREGSYGNQSRDGDRYNNF+RHRDRERTHYNP Sbjct 204 DRPANRGRYGNFNNDER-FDRNQDRDRGQREGSYGNQSRDGDRYNNFSRHRDRERTHYNP 262 712 891 Query NÕÕQERPSGVAMGAIGNNSMRQDSNMTANNLDIVADDTERPRLÕLKPRTIAAPINAVAET Sbjct 263 322 KQSASIFGNAKPREEKLKELQQNVNHNGDN KQSASIFGNAKPREEKLKELQQN+NHNGDN 892 Query 981 KÕSASIFGNAKPREEKLKELÕÕNMNHNGDN Sbjct 323 352 Range 2: 1 to 111 Score **Expect Method** Identities **Positives Frame** Gaps 218 bits(554) 3e-63() Compositional matrix adjust. 102/111(92%) 106/111(95%) 0/111(0%) +1 Features: Query 7 ${\tt MAGRGGYEHARSGFGGDRASKQLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLV}$ 186 MAGRGGYEHAR GFGG+R KÕ+PTEPPFIA+VGNLPÕGLVÕGDV+KIF DFEVK VRLV MAGRGGYEHARGGFGGERHVKQMPTEPPFIAYVGNLPÕGLVÕGDVMKIFNDFEVKNVRLV Sbjct 1 60 KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN Query 187 339 Sbjct 61 KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN 111 uncharacterized protein Dvir GJ19028, isoform A [Drosophila virilis] Sequence ID: ref|XP 002055013.1| Length: 332 Number of Matches: 2 See 1 more title(s) Range 1: 204 to 332 Score **Expect Method** Identities **Positives** Gaps Frame 218 bits(555) 2e-63() Compositional matrix adjust. 119/150(79%) 124/150(82%) 21/150(14%) +1 Features: DRPANRGRYGSFNNDDRPFERNQDRDRGQREGSYGNQSRDGDRYNNFNRHRDRERTHYNP 711 Query 532 DRPANRGRYG+FNND+R F+RNQDRDRGQREGSYGNQSRDGDRYNNF+RHRDRERTHYNP Sbjct 204 DRPANRGRYGNFNNDER-FDRNQDRDRGQREGSYGNQSRDGDRYNNFSRHRDRERTHYNP 262 891 Query 712 NÕÕQERPSGVAMG----AIDDTERPRLQLKPRTIAAPINAVAET Sbjct 263 302

Query 892 KQSASIFGNAKPREEKLKELQQNVNHNGDN KQSASIFGNAKPREEKLKELQQN+NHNGDN Sbjct 303 KQSASIFGNAKPREEKLKELQQNMNHNGDN

Range 2: 1 to 111

Score		Expect	Method	Identities	Positives	Gaps	Fram	e
217 bits	(553)	3e-63()	Compositional matrix adjust.	102/111(92%)	106/111(95%)	0/111(0%)	+1	
Features	S:							
Query	7		GGYEHARSGFGGDRASKQLPTEPI GGYEHAR GFGG+R KQ+PTEPI					86
Sbjct	1		GGYEHARGGFGGERHVKQMPTEPI					0
Query	187		PDQFKGFCYVEFETLDNLERALEC					
Sbjct	61		rdof kgf civer eitdniekale(rdofkgfcyvefetldniekale(

981

332

GH22433 [Drosophila grimshawi]

Sequence ID: ref|XP_001997843.1| Length: 113 Number of Matches: 1

▶ See 1 more title(s) kange 1: 1 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame
210 bits	(534)	2e-63() Compositional matrix adjust.	101/111(91%)	105/111(94%)	0/111(0%)	+1
Feature	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTE MAGRGGYEHAR GFGG+R KOLPTE	PPFIAFVGNLPQOPFIA+VGNLPQO			
Sbjct	1	MAGRGGYEHARGGFGGERHVKQLPTE				
Query	187	KDRETDQFKGFCYVEFETLDNLERAL KDR+TD FKGFCYVEFETLDNLERAL				
Sbjct	61	KDRDTDMFKGFCYVEFETLDNLERAL				

uncharacterized protein Dwil_GK25675 [Drosophila willistoni]

Sequence ID: ref|XP_002071220.2| Length: 351 Number of Matches: 2

See 1 more title(s)

Range 1: 1 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame
218 bits	(554)	3e-63() Compositional matrix adjust.	104/111(94%)	106/111(95%)	0/111(0%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEP: MAGRGGYEHAR GFGG+R KOLPTEP:				
Sbjct	1	MAGRGGYEHAR GFGGFR KOLPTEP: MAGRGGYEHARGGFGGERHVKQLPTEP:	PF+AFVGNLPQG PFLAFVGNLPQG			
Query	187	KDRETDQFKGFCYVEFETLDNLERALE KDRETDQFKGFCYVEFETLDNLERALE				
Sbjct	61	KDRETDQFKGFCYVEFETLDNLERALE				

Range 2: 212 to 349

Score	E	Expect Method	Identities	Positives	Gaps	Frame
208 bits(530) 1	e-59() Compositional matrix adjust.	120/148(81%)	129/148(87%)	10/148(6%)	+1
Features	:					
Query	535	RPANRGRYGSFNNDDRPFERNQDRDRO +PANRGRYG+FNNDDR F+RNODRDRO				
Sbjct	212	KPANRGRYGNFNNDDR-FDRNQDRDRO				
Query	715	QQSERPsggmtglgggsggsgglgvgg OOS+RP GGS G G G	ggssmgAIDDNE G++MGAIDD E	RPRLQLKPRTI	AAPINAVAET AAPTNAVA+T	K 894
Sbjct	271	ÕÕSDRPSGGGSSGGGGGS				
Query	895	QSASIFGNAKPREEKLKELQQNVNHNO OSASIFGNAKPREEKLKEL+ONVNHNO				
Sbjct	322	QSASIFGNAKPREEKLKELEQNVNHNC				

uncharacterized protein Dmoj_GI21487 [Drosophila mojavensis]

Sequence ID: ref|XP_002010838.2| Length: 251 Number of Matches: 1

▶ See 1 more title(s) kange 1: 1 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame
213 bit	s(541)	2e-62() Compositional matrix adjust.	101/111(91%)	106/111(95%)	0/111(0%)	+1
Feature	es:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEP MAGRGGYEHAR GFGG+R KOLPTEP	PFIAFVGNLPQG PFIA+VGNLPQG			
Sbjct	1	MAGRGGYEHARGGFGGERHVKQLPTEP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALE				
Sbjct	61	KDRETDQFKGFCYVEFETLDNLERALE KDRETDQFKGFCYVEFETLDNLERALE				

uncharacterized protein Dpse_GA18178, isoform B [Drosophila pseudoobscura pseudoobscura] Sequence ID: ref|XP_003736162.1| Length: 335 Number of Matches: 2

See 1 more title(s) Range 1: 178 to 334

Score		Expect Method	Identities	Positives	Gaps	Frame
214 bits	(545)	5e-62() Compositional matrix adjust.	130/158(82%)	138/158(87%)	10/158(6%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNODRD				
Sbjct	178	DRPANRGRYG+FNNDDR FERNQDRD				
Query	712	NQQSERPsggmtglggg NOOSERP G +G GG	sggsgglgvggg SG GG G GGG			
Sbjct	237	NQQSERPSGGLGGGGGGLGGSGGLGG				
Query	865	APINAVAETKQSASIFGNAKPREEKLI APINAVAETKQSASIFGNAKPREEKLI				
Sbjct	297	APINAVAETKOSASIFGNAKPREEKLI APINAVAETKOSASIFGNAKPREEKLI				

Score		Expect Method	Identities	Positives	Gaps	Frame
207 bits	(527)	2e-59() Compositional matrix adjust.	99/111(89%)	104/111(93%)	0/111(0%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPI MAGRGGYEHAR GFGG+R K LPTEPI				
Sbjct	1	MAGRGGYEHARGGFGGERQMKVLPTEPI				
Query	187	KDRETDQFKGFCYVEFETLDNLERALECKDRETD FKGFCYVEFETL+NLERALE				
Sbjct	61	KDRETDMFKGFCYVEFETLENLERALE				

uncharacterized protein Dpse_GA18178, isoform D [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041559.1**| Length: 369 Number of Matches: 2

▶ See 1 more title(s) Range 1: 212 to 368

Score		Expect Method	Identities	Positives	Gaps	Frame
214 bits(5	546) 1	le-61() Compositional matrix adjust.	130/158(82%)	138/158(87%)	10/158(6%)	+1
Features:						
Query !	532	DRPANRGRYGSFNNDDRPFERNODRDF				
Sbjct :	212	DRPANRGRYG+FNNDDR FERNQDRDF DRPANRGRYGNFNNDDR-FERNQDRDF				
Query	712	NQQSERPsggmtglgggs NOOSERP G +G GGS	sggsgglgvggg SG GG G GGG			
Sbjct :	271	NQQSERPSGGLGGGGGGLGGSGLGGS				
Query	865	APINAVAETKQSASIFGNAKPREEKLI APINAVAETKOSASIFGNAKPREEKLI				
Sbjct :	331	APINAVAETKOSASIFGNAKPREEKLI				

Range 2: 47 to 145

Score		Expect	Method	identities	Positives	Gaps	Frai	me
184 bits(467)	3e-50()	Compositional matrix adjust.	88/99(89%)	93/99(93%)	0/99(0%)	+1	
Features	:							
Query	43	GFGGDF GFGG+F	RASKQLPTEPPFIAFVGNLPQGLVÇ R K LPTEPPF+AFVGNLPQGLVÇ					222
Sbjct	47		ROMKVLPTEPPFLAFVGNLPOGLVÇ					106
Query	223		TLDNLERALECDGRIKLDDLSAPLF TL+NLERALE DGRIKLDDLSAPLF		339			
Sbjct	107		TLENLERALEFDGRIKLDDLSAPLF		145			

uncharacterized protein Dpse_GA18178, isoform A [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_001354678.2**| Length: 368 Number of Matches: 2

▶ See 1 more title(s) Range 1: 211 to 367

Score		Expect Method	Identities	Positives	Gaps	Frame
214 bits(544) 2	e-61() Compositional matrix adjust.	130/158(82%)	138/158(87%)	10/158(6%)	+1
Features:						
Query	532	DRPANRGRYGSFNNDDRPFERNQDRDF DRPANRGRYG+FNNDDR FERNODRDF				
Sbjct	211	DRPANRGRYGNFNNDDR-FERNQDRDF				
Query	712	NQQSERPsggmtglgggs NOOSERP G +G GGS	ggsgglgvggg GG GG GGG	ssmgAIDDNER	PRLQLKPRTI	A 864
Sbjct	270	NÕÕSERPSGGLGGGGGGLGGS				
Query	865	APINAVAETKOSASIFGNAKPREEKLK APINAVAETKOSASIFGNAKPREEKLK				
Sbjct	330	APINAVAETKÕSASIFGNAKPREEKLK				

Range 2: 1 to 111

Score	Expect	Method	Identities	Positives	Gaps	Frame	
207 bits(5	528) 4e-59()	Compositional matrix adjust.	99/111(89%)	104/111(93%)	0/111(0%)	+1	
Features:							
Query '		GGYEHARSGFGGDRASKOLPTEP GGYEHAR GFGG+R K LPTEP					

Sbjct 1 MAGRGGYEHARGGFGGERQMKVLPTEPPFLAFVGNLPQGLVQGDVMKIFQDFEVKNVRLV 60

Query 187 KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN 339
KDRETD FKGFCYVEFETL+NLERALE DGRIKLDDLSAPLRIDIADR+KN
Sbjct 61 KDRETDMFKGFCYVEFETLENLERALEFDGRIKLDDLSAPLRIDIADRKKN 111

uncharacterized protein Dpse_GA18178, isoform C [Drosophila pseudoobscura pseudoobscura] Sequence ID: **ref|XP_015041558.1**| Length: 402 Number of Matches: 2

▶ See 1 more title(s) Range 1: 245 to 401

Score		Expect Method	Identities	Positives	Gaps	Frame
214 bits	(545)	3e-61() Compositional matrix adjust.	130/158(82%)	138/158(87%)	10/158(6%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD DRPANRGRYG+FNNDDR FERNQDRD				
Sbjct	245	DRPANRGRYGNFNNDDR-FERNQDRD				
Query	712	NQQSERPsggmtglggg NOOSERP G +G GG	sggsgglgvggg SG GG G GG	ssmgAIDDNER	PRLQLKPRTI	A 864
Sbjct	304	NÕÕSERPSGGLGGGGGGLGGSGGLGG				
Query	865	APINAVAETKOSASIFGNAKPREEKL APINAVAETKOSASIFGNAKPREEKL				
Sbjct	364	APINAVAETKÕSASIFGNAKPREEKL				

Range 2: 47 to 145

Score		Expect	Method	Identities	Positives	Gaps	Frame
184 bits	(467)	5e-50()	Compositional matrix adjust.	88/99(89%)	93/99(93%)	0/99(0%)	+1
Features	s:						
Query	43	GFGGDF GFGG+F	RASKQLPTEPPFIAFVGNLPQGLVQ R K LPTEPPF+AFVGNLPQGLVQ				
Sbjct	47		ROMKVLPTEPPFLAFVGNLPOGLV				
Query	223		TLDNLERALECDGRIKLDDLSAPLI TL+NLERALE DGRIKLDDLSAPLI		339		
Sbjct	107		TLENLERALEFDGRIKLDDLSAPLI		145		

GH24789 [Drosophila grimshawi]

Sequence ID: ref|XP_001992509.1| Length: 145 Number of Matches: 1

▶ See 1 more title(s) Range 1: 14 to 145

Identities	Positives	Gaps	Frame
115/151(76%)	123/151(81%)	23/151(15%)	+1
NGDN 981			
NGDN 145			
	EGSYGNQSRDO EGSYGNQSRDO EGSYGNQSRDO EGSYGNQSRDO AID: AID: AID: AID: AID: AID: AID: AID:	15/151(76%) 123/151(81%) EGSYGNQSRDGDRYNNFNRHRI EGSYGNQSRDGDRYNNFSRHRI EGSYGNQSRDGDRYNNFSRHRI gggssmgAIDDNERPRLQLKPF AIDD ERPRLQLKPFAIDDTERPRLQLKPF	15/151(76%) 123/151(81%) 23/151(15%) EGSYGNQSRDGDRYNNFNRHRDRERTHYNPNQ EGSYGNQSRDGDRYNNF+RHRDRERTHYNPNQ EGSYGNQSRDGDRYNNFSRHRDRERTHYNPNQ gggssmgAIDDNERPRLQLKPRTIAAPINAVA AIDD ERPRLQLKPRTIAAPINAVA AIDD ERPRLQLKPRTIAAPINAVAAIDDTERPRLQLKPRTIAAPINAVA

GL20267 [Drosophila persimilis]

Sequence ID: ref|XP_002023289.1| Length: 300 Number of Matches: 2

▶ See 1 more title(s) kange 1: 1 to 111

Score		Expect	Method	Identities	Positives	Gaps	Frar	me
207 bit	s(527)	9e-60()	Compositional matrix adjust.	99/111(89%)	104/111(93%)	0/111(0%)	+1	
Feature	es:							
Query	7		GYEHARSGFGGDRASKQLPTEPP					186
Sbjct	1		GYEHAR GFGG+R K LPTEPP GYEHARGGFGGERQMKVLPTEPP					60
Query	187	KDRET	DQFKGFCYVEFETLDNLERALEC	DGRIKLDDLS	APLRIDIADRRK	IN 339		

Range 2: 129 to 285

Score		Expect Method	Identities	Positives	Gaps	Frame
206 bits	(524)	3e-59() Compositional matrix adjust.	126/158(80%)	134/158(84%)	10/158(6%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD DRPANRGRYG+FNNDDR FERNODRD				
Sbjct	129	DRPANRGRYGNFNNDDR-FERNQDRD				
Query	712	NQQSERPsggmtglggg NOOSERP G +G GG	sggsgglgvggg SG GG G GGG			
Sbjct	188	NÕÕSERPSGGLGGGGGGLGGSGGLGG				
Query	865	APINAVAETKOSASIFGNAKPREEKLI APINAVAE+KOSAS FGNAKPREEKLI				
Sbjct	248	APINAVAESKQSASFFGNAKPREEKL	~			

PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Bactrocera dorsalis]

Sequence ID: ref|XP_011213861.1| Length: 294 Number of Matches: 2

Range 1: 1 to 109

Score		Expect	Method	Identities	Positives	Gaps	Frame	
202 bits	(515)	4e-58()	Compositional matrix adjust.	100/111(90%)	104/111(93%)	2/111(1%)	+1	
Features	s:							
Query	7		GGYEHARSGFGGDRASKOLPTEPI					
Sbjct	1		GG++HAR+ GDR KQLPTEPI GGFDHARNYGDRPGKQLPTEPI	PFIA+VGNLPQG PFIAYVGNLPQG				
Query	187		PDOFKGFCYVEFETLDNLERALEC					
Sbjct	59		PDQFKGFCYVEFETLDNLERALEC PDQFKGFCYVEFETLDNLERALEC					

Range 2: 160 to 286

Score		Expect Method	Identities	Positives	Gaps	Frame
146 bits	(369) (6e-37() Compositional matrix adjust.	92/149(62%)	109/149(73%)	27/149(18%)	+1
Features	S :					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD DRPANRGRYG+FNNDDR FERN DR+				
Sbjct	160	DRPANRGRYGNFNNDDR-FERNHDRN				
Query	697	THYNPNQQSERPsggmtglgggsggs	gglgvgggssm		QLKPRTIAAPI LKPRTI API	
Sbjct	217	SNFNPSH-NDRPAPAAAPLG				
Query	877	AVAETKQSASIFGNAKPREEKLKELQ A+AETKQSA+IFGNAKPREEKLKELQ				
Sbjct	258	ALAETKOSAAIFGNAKPREEKLKELO				

PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Bactrocera cucurbitae]

Sequence ID: ref|XP_011187272.1| Length: 297 Number of Matches: 2

Range 1: 1 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame
202 bits	(515)	5e-58() Compositional matrix adjust.	99/111(89%)	104/111(93%)	2/111(1%)	+1
Features	S :					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEP MAGR G++HAR+ GDR KOLPTEP		GLVQGDVIKIFÇ GLVQGDVIKIFÇ		
Sbjct	1	MAGRAGFDHARNYGDRPGKQLPTEP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALE KDRETDQFKGFCYVEFETL+NLERALE				
Sbjct	59	KDRETDOFKGFCYVEFETLENLERALE				

Range 2: 161 to 286

Score	Expect	Method	Identities	Positives	Gaps	Frame
152 bits(383)	8e-39()	Compositional matrix adjust.	95/148(64%)	110/148(74%)	27/148(18%)	+1

Features:

DRPANRGRYGSFNNDDRPFERNQDRDRGQREGSYGNQSRDG--DRYNNFNRHR---DRER DRPANRGRYG+FNNDDR FERN DR+ QREGS+G QSRDG DRYNNF+R+R DRER DRPANRGRYGNFNNDDR-FERNHDRN--QREGSFGAQSRDGGNDRYNNFSRNRGERDRER Query 532 696 Sbjct 161 217 THYNPNQQSERPsggmtglgggsggsgglgvgggssmgAIDDNERPRLQLKPRTIAAPIN +++NP ++RP+ LG +IDD+ERPRL LKPRTI APIN SNFNPTH-NDRPAPAAAPLG-----SIDDSERPRLNLKPRTIQAPIN 876 Query 697 Sbjct 218 258 AVAETKQSASIFGNAKPREEKLKELQQN 960 A+AETKQSA+IFGNAKPREEKLKELQQN ALAETKQSAAIFGNAKPREEKLKELQQN 286 Query 877 Sbjct 259

PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Bactrocera dorsalis]

Sequence ID: ref|XP_011213860.1| Length: 327 Number of Matches: 2

Range 1: 1 to 109

Score		Expect	Method	Identities	Positives	Gaps	Frame
203 bits	(516)	7e-58()	Compositional matrix adjust.	100/111(90%)	104/111(93%)	2/111(1%)	+1
Features	s:						
Query	7		GGYEHARSGFGGDRASKQLPTEPI GG++HAR+ GDR KOLPTEPI	PFIAFVGNLPQG PFIA+VGNLPQG			
Sbjct	1		GGFDHARNYGDRPGKÕLPTEPI				
Query	187		rdofkgfcyvefetldnleraleo rdofkgfcyvefetldnleraleo				
Sbjct	59		rdofkgfcyvefetldnleraleo				

Range 2: 193 to 319

Score

Expect Method

		Lanca and the same	
146 bits	(368) 2	2e-36() Compositional matrix adjust. 92/149(62%) 109/149(73%) 27/149(18%) +1	
Features	s:		
Query	532	DRPANRGRYGSFNNDDRPFERNQDRDRGQREGSYGNQSRDGDRYNNFNRHRDRER DRPANRGRYG+FNNDDR FERN DR+ REGS+G OSRDG DRYNNF+R+R DRER	696
Sbjct	193		249
Query	697	THYNPNQQSERPsggmtglgggsggsgglgvgggssmgAIDDNERPRLQLKPRTIAAPIN +++NP+ ++RP+ LG +IDD+ERPRL LKPRTI APIN	876
Sbjct	250		290
Query	877	AVAETKQSASIFGNAKPREEKLKELQQNV 963 A+AETKOSA+IFGNAKPREEKLKELO +	
Sbjct	291	ALAETKOSA IFGNAKPREEKLKELONDT 319	

Identities

Positives

Gaps

Frame

PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Bactrocera cucurbitae]

Sequence ID: ref|XP_011187268.1| Length: 328 Number of Matches: 2

Range 1: 1 to 109

Score		Expect	Method	Identities	Positives	Gaps	Frame
202 bits	(515)	9e-58()	Compositional matrix adjust.	99/111(89%)	104/111(93%)	2/111(1%)	+1
Features	s:						
Query	7		GYEHARSGFGGDRASKQLPTEPP G++HAR+ GDR KOLPTEPP		GLVQGDVIKIFQ GLVQGDVIKIFQ		
Sbjct	1		AGFDHARNYGDRPGKQLPTEPP				
Query	187		DOFKGFCYVEFETLDNLERALEC				
Sbjct	59		DOFKGFCYVEFETL+NLERALEC DOFKGFCYVEFETLENLERALEC				

Range 2: 192 to 317

Score		Expect Method	Identities	Positives	Gaps	Frame
151 bits(381)	3e-38() Compositional matrix adjust.	95/148(64%)	110/148(74%)	27/148(18%)	+1
Features	:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRDF DRPANRGRYG+FNNDDR FERN DR+		SRDGDRYNN SRDG DRYNN		
Sbjct	192	DRPANRGRYGNFNNDDR-FERNHDRN-				
Query	697	THYNPNQQSERPsggmtglgggsggsg	glgvgggssm		QLKPRTIAAPI LKPRTI API	
Sbjct	249	SNFNPTH-NDRPAPAAAPLG				
Query	877	AVAETKQSASIFGNAKPREEKLKELQQ A+AETKOSA+IFGNAKPREEKLKELOO				
Sbjct	290	ALAETKOSAAIFGNAKPREEKLKELQQ				

PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Bactrocera oleae]

Sequence ID: ref|XP_014090168.1| Length: 294 Number of Matches: 2

Range 1: 1 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame
201 bits	(511)	2e-57() Compositional matrix adjust.	99/111(89%)	104/111(93%)	2/111(1%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPI MA RGG++HAR+ GDR KOLPTEPI		GLVQGDVIKIFÇ GLVQGDVIKIFÇ		
Sbjct	1	MAVRGGFDHARNYGDRPGKQLPTEPI				
Query	187	KDRETDQFKGFCYVEFETLDNLERALE(
Sbjct	59	KDRETDQFKGFCYVEFETL+NLERALEC KDRETDQFKGFCYVEFETLENLERALEC				

Range 2: 160 to 291

Score		Expect Method	Identities	Positives	Gaps	Frame
145 bits	(365) 2	2e-36() Compositional matrix adjust.	92/154(60%)	109/154(70%)	27/154(17%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD				
Sbjct	160	DRPANRGRYG+FNNDDR FERN DR+ DRPANRGRYGNFNNDDR-FERNHDRN				
Query	697	THYNPNQQSERPsggmtglgggsggs	gglgvgggssm	ngAIDDNERPRL	QLKPRTIAAPI LKPRTI API	N 876
Sbjct	217	SNFNPSH-NDRPAPAAAPLG				
Query	877	AVAETKQSASIFGNAKPREEKLKELQ A+AETKOSA+IFGNAKPREEK KELO	~	78		
Sbjct	258	ALAETKOSATIFGNAKPREEKFKELQ		91		

PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Bactrocera oleae]

Sequence ID: ref|XP_014090165.1| Length: 327 Number of Matches: 2

▶ See 2 more title(s) Range 1: 1 to 109

Scor	e	Expect	Method	Identities	Positives	Gaps	Frame	<u>e</u>
201 l	oits(512)	3e-57()	Compositional matrix adjust.	99/111(89%)	104/111(93%)	2/111(1%)	+1	
Feat	ures:							
Quer	y 7		GYEHARSGFGGDRASKQLPTEPP GG++HAR+ GDR KOLPTEPP		GLVQGDVIKIFÇ GLVQGDVIKIFÇ			86
Sbjc	t 1		GGFDHARNYGDRPGKQLPTEPP	~	~ -	•		8
Quer	y 187		DOFKGFCYVEFETLDNLERALECTOFKGFCYVEFETL+NLERALEC					
Sbjc	t 59		DOFKGFCYVEFETLENLERALEC					

Range 2: 193 to 324

Score		Expect Method	Identities	Positives	Gaps	Frame
144 bits	(364) 8	8e-36() Compositional matrix adjust.	92/154(60%)	109/154(70%)	27/154(17%)	+1
Features	S :					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD DRPANRGRYG+FNNDDR FERN DR+		SRDGDRYNN SRDG DRYNN		
Sbjct	193	DRPANRGRYGNFNNDDR-FERNHDRN				
Query	697	THYNPNQQSERPsggmtglgggsggs +++NP+ ++RP+ LG	gglgvgggssm		QLKPRTIAAPI LKPRTI API	
Sbjct	250	SNFNPSH-NDRPAPAAAPLG				
Query	877	AVAETKQSASIFGNAKPREEKLKELQ A+AETKQSA+IFGNAKPREEK KELQ		78		
Sbjct	291	ALAETKOSAAIFGNAKPREEKFKELO		24		

PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Ceratitis capitata]

Sequence ID: ref|XP_012157029.1| Length: 291 Number of Matches: 2

Range 1: 1 to 109

Score	Expect	Method	Identities	Positives	Gaps	Frame
199 bits(507)	7e-57()	Compositional matrix adjust.	98/111(88%)	104/111(93%)	2/111(1%)	+1
Features:						

Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLV MAGRG ++HAR+ GDR KQLPTEPPFIA+VGNLPQGLVQGDVIKIFQDFEVK VRLV	186
Sbjct	1	MAGRGVFDHARNFGDRPGKQLPTEPPFIAYVGNLPQGLVQGDVIKIFQDFEVKNVRLV	58
Query	187	KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN 339 KDRETDQFKGFCYVEFETL+NLE+ALECDGRIKLDDLSAPLRIDIADRRKN	
Sbict	59	KDRETDÖFKGFCYVEFETLENLEKALECDGRIKLDDLSAPLRIDIADRRKN 109	

Range 2: 159 to 280

Score	-	Expect Method	Identities	Positives	Gaps	Frame
146 bits(368) 9	e-37() Compositional matrix adjust.	92/144(64%)	104/144(72%)	27/144(18%)	+1
Features	:					
Query	538	PANRGRYGSFNNDDRPFERNQDRDRG PANRGRYG+FNNDDR FERN DR+				
Sbjct	159	PANRGRYGNFNNDDR-FERNHDRN	~			
Query	703	YNPNQQSERPsggmtglgggsggsgg +NPN ++RP+ LG		IDDNERPRLQLI		
Sbjct	216	FNPNH-NDRPAPAPAPLG				
Query	883	AETKQSASIFGNAKPREEKLKELQ AETKOSA+IFGNAKPREEK KE O	954			
Sbjct	257		280			

PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Ceratitis capitata]

Sequence ID: **ref|XP_012157028.1|** Length: 322 Number of Matches: 2 Range 1: 1 to 109

Score		Expect Method	Method Identities		Gaps	Frame	
200 bits((508)	1e-56() Compositional m	atrix adjust. 98/111(88%)	104/111(93%)	2/111(1%)	+1	
Features	3 :						
Query	7	MAGRGGYEHARSGFGGDR MAGRG ++HAR+ GDR	ASKQLPTEPPFIAFVGNLPQ KOLPTEPPFIA+VGNLPQ				
Sbjct	1		PGKQLPTEPPFIAYVGNLPQ				
Query	187		LDNLERALECDGRIKLDDLS L+NLE+ALECDGRIKLDDLS				
Sbjct	59	~	LENLEKALECDGRIKLDDLS.				

Range 2: 188 to 311

Score		Expect Method	Identities	Positives	Gaps	Frame
149 bits	(375)	2e-37() Compositional matrix adjust.	94/146(64%)	106/146(72%)	27/146(18%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD DRPANRGRYG+FNNDDR FERN DR+				
Sbjct	188	DRPANRGRYGNFNNDDR-FERNHDRN				
Query	697	THYNPNQQSERPsggmtglgggsggs H+NPN ++RP+ LG	gglgvgggssm		QLKPRTIAAPI LKPRTI API	
Sbjct	245	PHFNPNH-NDRPAPAPAPLG				
Query	877	AVAETKQSASIFGNAKPREEKLKELQ A+AETKQSA+IFGNAKPREEK KE Q				
Sbjct	286	ALAETKOSATIFGNAKPREEKFKEFQ				

Rbp2 [Drosophila busckii]

Sequence ID: gb|ALC49657.1| Length: 311 Number of Matches: 2

Range 1: 182 to 311

Score		Expect Method	Identities	Positives	Gaps	Frame		
195 bits	(495)	6e-55() Compositional matrix adjust.	110/151(73%)	118/151(78%)	22/151(14%)	+1		
Features:								
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD DRPANRGRYG+FNNDDR F+RNO+RD						
Sbjct	182	DRPANRGRYGNFNNDDR-FDRNQERD						
Query	709	PNQQSERPsggmtglgggsggsgglg PNO +ERP	vgggssmgAID	DNERPRLQLKPI D ERPRLQLKPI	RTIAAPINAVA	E 888		
Sbjct	241	PNQHNERP						
Query	889	TKQSASIFGNAKPREEKLKELQQNVN TKQSASIFGNAKPREEK+KE + N	HNGDN 981 NGDN					
Sbjct	281	TKQSASIFGNAKPREEKIKEPEPNEE						

Score		Expect	Method	Identities	Positives	Gaps	Frame
182 bits	(463)	3e-50()	Compositional matrix adjust.	86/89(97%)	88/89(98%)	0/89(0%)	+1
Features	s:						
Query	73		PFIAFVGNLPQGLVQGDVIKIFQDE PFIA+VGNLPQGLVQGDVIKIFQDE				
Sbjct	1		PFIAYVGNLPQGLVQGDVIKIFQDE				
Query	253		CDGRIKLDDLSAPLRIDIADRRKN CDGRIKLDDLSAPLRIDIADRRKN	339			
Sbjct	61		CDGRIKLDDLSAFLRIDIADRRKN	89			

hypothetical protein FF38_09267, partial [Lucilia cuprina]

Sequence ID: gb|KNC26965.1| Length: 279 Number of Matches: 2

Range 1: 1 to 109

Score		Expect Method		Identities	Positives	Gaps	Frame	
192 bits	(488)	3e-54()	Compositional matrix adjust.	92/111(83%)	102/111(91%)	2/111(1%)	+1	
Features	s:							
Query	7		GYEHARSGFGGDRASKQLPTEPF GG+EH R+ GDR KOLP+EPF		GLVQGDVIKIFQ GLVQGDV+KIF			
Sbjct	1		GGFEHPRNYGDRGGKQLPSEPF					
Query	187		DOFKGFCYVEFETLDNLERALEC DOFKGFCYVEFETLDNLERALE					
Sbjct	59		DQFKGFCYVEFETLDNLERALEF					

Range 2: 192 to 242

Score		Expect	Method	Identities	Positives	Gaps	Frame
61.2 bits	(147)	5e-07()	Compositional matrix adjust.	35/52(67%)	41/52(78%)	4/52(7%)	+1
Features	:						
Query	532		RGRYGSFNNDDRPFERNQDRDRGQF RGRYG+FNNDDR +RN DR F	REGSYGNOSRD REGS+G OSRD			
Sbjct	192		RGRYGNFNNDDRYNDRNH-HDRNHF				

PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Bactrocera cucurbitae]

Sequence ID: ref|XP_011187271.1| Length: 320 Number of Matches: 2

Range 1: 6 to 101

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
190 bits(482)	5e-53()	Compositional matrix adjust.	91/96(95%)	93/96(96%)	0/96(0%)	+1	
Features	:							
Query	52		KQLPTEPPFIAFVGNLPQGLVQGDV KOLPTEPPFIA+VGNLPOGLVOGDV					231
Sbjct	6		(QLPTEPPFIAYVGNLPQGLVQGDV					65
Query	232		NLERALECDGRIKLDDLSAPLRIDI NLERALECDGRIKLDDLSAPLRIDI		39			
Sbjct	66		NLERALECDGRIKLDDLSAPLRIDI NLERALECDGRIKLDDLSAPLRIDI		01			

Range 2: 184 to 309

Score		Expect Method	Identities	Positives	Gaps	Frame
151 bits	(382)	2e-38() Compositional matrix adjust.	95/148(64%)	110/148(74%)	27/148(18%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRDI DRPANRGRYG+FNNDDR FERN DR+		SRDGDRYNN SRDG DRYNN		
Sbjct	184	DRPANRGRYGNFNNDDR-FERNHDRN				
Query	697	THYNPNQQSERPsggmtglgggsggs	gglgvgggssm		QLKPRTIAAPI LKPRTI API	
Sbjct	241	SNFNPTH-NDRPAPAAAPLG				
Query	877	AVAETKQSASIFGNAKPREEKLKELQ A+AETKOSA+IFGNAKPREEKLKELQ				
Sbjct	282	ALAETKÕSAAIFGNAKPREEKLKELÕ				

Sequence ID: ref|XP_001648291.1| Length: 314 Number of Matches: 2

▶ See 1 more title(s) Range 1: 3 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame
155 bits	(391)	7e-40() Compositional matrix adjust.	74/111(67%)	94/111(84%)	2/111(1%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGG+++ R +GG+RA + LPTEPP				
Sbjct	3	MAGRGGHDNNRYGGERARRPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KD+ETD FKGFCYVEF TLD L++AL+		APLRIDIADRRI		
Sbjct	61	KDKETDVFKGFCYVEFGTLDELKQALDL				

Range 2: 245 to 285

Score		Expect	Method	Identities	Positives	Gaps	Frame
67.0 bits	s(162)	6e-09()	Compositional matrix adjust.	29/41(71%)	37/41(90%)	0/41(0%)	+1
Features	s:						
Query	820	20 DNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL D RP+L LKPRT+A P+NA+AETKQ+A+IFGNA+PREEK+					
Sbjct	245		LNLKPRTVATPLNALAETKQAAA:				

AAEL004010-PB, partial [Aedes aegypti]

Sequence ID: ref|XP_001648292.1| Length: 313 Number of Matches: 2

▶ See 1 more title(s) kange 1: 3 to 111

Score			Expect	Method	Identities	Positives	Gaps	Fra	me
	155 bits(3	391)	7e-40()	Compositional matrix adjust.	74/111(67%)	94/111(84%)	2/111(1%)	+1	
	Features	:							
	Query	7		GYEHARSGFGGDRASKQLPTEPPI G+++ R +GG+RA + LPTEPP+					186
	Sbjct	3		GHDNNRYGGERARRPLPTEPPY					60
	Query	187		DQFKGFCYVEFETLDNLERALECI D FKGFCYVEF TLD L++AL+ I					
	Sbjct	61		DVFKGFCYVEFGTLDELKQALDLI					

Range 2: 244 to 284

Score		Expect	Method	Identities	Positives	Gaps	Frame
67.0 bits	s(162)	7e-09()	Compositional matrix adjust.	29/41(71%)	37/41(90%)	0/41(0%)	+1
Features	s:						
Query	820		RLQLKPRTIAAPINAVAETKQSASI L LKPRT+A P+NA+AETKQ+A+I				
Sbjct	244		LNLKPRTVATPLNALAETKQAAA:				

AAEL004010-PC, partial [Aedes aegypti]

Sequence ID: ref|XP_001648293.1| Length: 335 Number of Matches: 2

▶ See 1 more title(s) Range 1: 3 to 111

Score		Expect	Method	Identities	Positives	Gaps	Frame	
155 bits	(392)	8e-40()	Compositional matrix adjust.	74/111(67%)	94/111(84%)	2/111(1%)	+1	
Features	S :							
Query	7		GYEHARSGFGGDRASKQLPTEPPE G+++ R +GG+RA + LPTEPP+					
Sbjct	3		GHDNNRYGGERARRPLPTEPPY					
Query	187		DQFKGFCYVEFETLDNLERALECI D FKGFCYVEF TLD L++AL+ I					
Sbjct	61		D FRGFCIVEF ILD LTTALT I DVFKGFCYVEFGTLDELKQALDLI					

Range 2: 266 to 306

67.4 bits(163) 7e-09() Compositional matrix adjust. 29/41(71%) 37/41(90%) 0/41(0%) +1

Features:

Query 820 DNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL 942 D RP+L LKPRT+A P+NA+AETKQ+A+IFGNA+PREEK+ Sbjct 266 DAGRPKLNLKPRTVATPLNALAETKQAAAIFGNARPREEKI 306

AAEL004010-PD, partial [Aedes aegypti]

Sequence ID: ref|XP_001648290.1| Length: 334 Number of Matches: 2

See 1 more title(s)

Range 1: 3 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame	
155 bits	(392)	8e-40() Compositional matrix adjust.	74/111(67%)	94/111(84%)	2/111(1%)	+1	
Features	s:						
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP					
Sbjct	3	MAGRGG+++ R +GG+RA + LPTEPP MAGRGGHDNNRYGGERARRPLPTEPP					
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC					
Sbjct	61	KD+ETD FKGFCYVEF TLD L++AL+ KDKETDVFKGFCYVEFGTLDELKQALDL		LRIDIA+++I ALRIDIAEQKI			

Range 2: 265 to 305

Score		Expect	Method	Identities	Positives	Gaps	Frame
67.4 bits	s(163)	6e-09()	Compositional matrix adjust.	29/41(71%)	37/41(90%)	0/41(0%)	+1
Feature	s:						
Query	Query 820 DNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL 942 D RP+L LKPRT+A P+NA+AETKO+A+IFGNA+PREEK+						
Sbjct	265		L LKEKITA ETNATAEIKOTAT LNLKPRTVATPLNALAETKQAAA				

uncharacterized protein Dere_GG11771 [Drosophila erecta]

Sequence ID: ref|XP_001981160.1| Length: 495 Number of Matches: 2

▶ See 1 more title(s) kange 1: 62 to 150

Score		Expect	Method	Identities	Positives	Gaps	Frame
157 bits	(396)	3e-39()	Compositional matrix adjust.	70/89(79%)	81/89(91%)	0/89(0%)	+1
Features	s:						
Query	70		PPFIAFVGNLPQGLVQGDVIKIFQI PPFIA+VGNLP+GLVQGDV+KIF I				
Sbjct	62	~	PPFIAYVGNLPKGLVQGDV*KIFSI				
Query	250		ECDGRIKLDDLSAPLRIDIADRRK	336			
Sbjct	122		C+GRIKLD+ SAPLRIDIAD R+ SCNGRIKLDNFSAPLRIDIADHRR	150			

Range 2: 405 to 447

Score	Ex	pect	Method	Identities	Positives	Gaps	Frame
63.9 bits(1	54) 1e-	-07()	Compositional matrix adjust.	27/43(63%)	37/43(86%)	0/43(0%)	+1
Features:							
Query 8		AIDDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEK 939 +DD++RP+L LKPRT+ APIN++AETKO+A IFG AKPR++					
Sbjct 4		VLDDDDRPKLVLKPRTVTAPINSLAETKQAALIFGKAKPRDDS 447					

uncharacterized protein Dyak_GE10899, isoform B [Drosophila yakuba] Sequence ID: ref|XP_015049122.1| Length: 505 Number of Matches: 2

▶ See 1 more title(s) Range 1: 74 to 162

Score	Expect	Method	Identities	Positives	Gaps	Frame
156 bits(394)	6e-39()	Compositional matrix adjust.	70/89(79%)	81/89(91%)	0/89(0%)	+1
Features:						

Features:

Query	70	QLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLVK Q+PTEPPFIA+VGNLP+GLVQGDV+KIF DFEVK VRL+K	249
Sbjct	74		133
Query	250	LERALECDGRIKLDDLSAPLRIDIADRRK 336 L+RAL C+GRIKLD+ SAPLRIDIAD R+	
Sbjct	134	LKRALSCNGRIKLDNFSAPLRIDIADHRR 162	

Range 2: 359 to 464

Score		Expect	Method	Identities	Positives	Gaps	Frame
63.9 bits	s(154)	1e-07()	Compositional matrix adjust.	47/107(44%)	59/107(55%)	15/107(14%)	+1
Features	S :						
Query	661	YNNF- Y NF	-NRHRDRERTHYNPNQQSER NR+RDR R HYNPN	F	esggmtglggg	sggsgglgvgg GS G G	798
Sbjct	359	,-	QNRNRDR-RGHYNPNNAGNSGS	YNGNGNGNFGA	•	00 0	SS 417
Query	799		IDDNERPRLQLKPRTIAAPINA			939	
Sbjct	418		+DD++RP+L LKPRT+ APIN+ LDDDDRPKLVLKPRTVTAPINS			464	

uncharacterized protein Dyak_GE10899, isoform A [Drosophila yakuba] Sequence ID: **ref|XP_002099432.1|** Length: 502 Number of Matches: 2

▶ See 1 more title(s) Range 1: 74 to 162

Score		Expect	Method	Identities	Positives	Gaps	Fran	me
156 bits	(394)	6e-39()	Compositional matrix adjust.	70/89(79%)	81/89(91%)	0/89(0%)	+1	
Features	s:							
Query	70		PPFIAFVGNLPQGLVQGDVIKIFQI PPFIA+VGNLP+GLVQGDV+KIF I					249
Sbjct	74		PPFIAYVGNLPKGLVQGDV#KIFSI					133
Query	250		ECDGRIKLDDLSAPLRIDIADRRK C+GRIKLD+ SAPLRIDIAD R+	336				
Sbjct	134		SCNGRIKLDNFSAPLRIDIADHRR	162				

Range 2: 356 to 461

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
63.9 bits(154)	1e-07()	Compositional matrix adjust.	47/107(44%)	59/107(55%)	15/107(14%)	+1	
Features:								
Query	661	YNNF- Y NF	-NRHRDRERTHYNPNQQSER	P	sggmtglggg: G		g	798
Sbjct	356		QNRNRDR-RGHYNPNNAGNSGS	YNGNGNGNFGA	•	00 0	S	414
Query	799		IDDNERPRLQLKPRTIAAPINAV +DD++RP+L LKPRT+ APIN+-			939		
Sbjct	415		LDDDDRPKLVLKPRTVTAPINSI	~		461		

uncharacterized protein Dwil_GK14152 [Drosophila willistoni]

Sequence ID: ref|XP_002073502.2| Length: 458 Number of Matches: 2

▶ See 1 more title(s) Range 1: 71 to 160

Score		Expect	Method	Identities	Positives	Gaps	Fran	me
155 bits	(392)	8e-39()	Compositional matrix adjust.	69/90(77%)	82/90(91%)	0/90(0%)	+1	
Features	s:							
Query	67		EPPFIAFVGNLPQGLVQGDVIKIF(+PPFIA+VGNLP+GLVQGDV+KIF					246
Sbjct	71		DPPFIAYVGNLPKGLVQGDVKIF:					130
Query	247	-	LECDGRIKLDDLSAPLRIDIADRRI L C+GRIKLD+ SAPLRIDIAD R-					
Sbjct	131		LSCNGRIKLDNYSAPLRIDIADHRI					

Range 2: 391 to 431

Score	Expect	Method	Identities	Positives	Gaps	Frame
64.3 bits(155)	9e-08()	Compositional matrix adjust.	28/41(68%)	37/41(90%)	0/41(0%)	+1
Features:						

Query 817 DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEK 939 DD++RP+L LKPRT+ PINA+A+TKQ+ASIFG AKPR+E+ Sbjct 391 DDDDRPKLVLKPRTVTDPINALADTKQAASIFGKAKPRDER 431

uncharacterized protein Dpse_GA12257 [Drosophila pseudoobscura pseudoobscura]

Sequence ID: ref|XP_001357599.3| Length: 471 Number of Matches: 2

See 1 more title(s)

Range 1: 98 to 190

Score		Expect	Method	Identities	Positives	Gaps	Frame	i
155 bits	(391)	1e-38()	Compositional matrix adjust.	69/93(74%)	83/93(89%)	0/93(0%)	+1	
Features	s:							
Query	61		PTEPPFIAFVGNLPQGLVQGDVIKI					
Sbjct	98		PTEPPF A+VGNLPQGLVQGDV+KI PTEPPFSAYVGNLPQGLVQGDVMKI					
Query	241		RALECDGRIKLDDLSAPLRIDIADI RA+ C+GRIKLD+ SAPLRIDIAD					
Sbjct	158		RAIACNGRIKLDY SAFLKIDIAD RAIACNGRIKLDNFSAPLRIDIADI					

Range 2: 371 to 454

Score		Expect Method	Identities	Positives	Gaps	Frame
60.8 bits	s(146)	1e-06() Compositional matrix adjust.	45/96(47%)	55/96(57%)	14/96(14%)	+1
Features	s:					
Query	661	YNNFNRHRDRERTHYNPNQQSERPSQ Y NF NR+RDR R HYNPN	ggmtglgggsg	gsgglgvggg: G	ssmgAIDDNE	
Sbjct	371	YTNFVQNRNRDR-RGHYNPN	0 0 00	•		
Query	835	RLQLKPRTIAAPINAVAETKQSASIFG +L LKPRT+ PINA+A T+O++ IFG		942		
Sbjct	419	KLLLKPRTVTDPINALANTEQASKIFGE		454		

GL13513 [Drosophila persimilis]

Sequence ID: ref|XP_002020435.1| Length: 471 Number of Matches: 2

▶ See 1 more title(s) kange 1: 98 to 189

Score		Expect	Method	Identities	Positives	Gaps	Fran	ne
154 bits	(390)	1e-38()	Compositional matrix adjust.	69/92(75%)	82/92(89%)	0/92(0%)	+1	
Features	s:							
Query	61		PTEPPFIAFVGNLPQGLVQGDVIK PTEPPF A+VGNLPQGLVQGDV+K					240
Sbjct	98		PTEPPFSAYVGNLPQGLVQGDVMK					157
Query	241		RALECDGRIKLDDLSAPLRIDIADI RA+ C+GRIKLD+ SAPLRIDIAD					
Sbjct	158		RAIACNGRIKLDNFSAPLRIDIAD					

Range 2: 371 to 454

Score		Expect Method	Identities	Positives	Gaps	Frame
60.5 bits	s(145)	1e-06() Compositional matrix adjust.	45/96(47%)	55/96(57%)	14/96(14%)	+1
Feature	s:					
Query	661	YNNFNRHRDRERTHYNPNQQSERPsg				
Sbjct	371	Y NF NR+RDR R HYNPN YTNFVQNRNRDR-RGHYNPN	G G GS GGGNGSL	G RGNSPGSTSVI	S IDD+ 1 RSANRIDDDN1	
Query	835	RLQLKPRTIAAPINAVAETKQSASIFGN		942		
Sbjct	419	+L LKPRT+ PINA+A T+Q++ IFG KLLLKPRTVTDPINALANTEQASKIFGK		454		

CG1340, isoform A [Drosophila melanogaster]

Sequence ID: ref|NP_651820.1| Length: 459 Number of Matches: 2

See 5 more title(s)

Range 1: 57 to 144

Score Expect Method Identities Positives Gaps Frame

153 bits	(386)	5e-38() Compositional matrix adjust. 68/88(77%) 79/88(89%) 0/88(0%) +1	
Features	s:		
Query	73	LPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLVKDRETDQFKGFCYVEFETLDNL 252 +PTEPPFIA+VGNLP+GLVQGDV+KIF DFEVK VRL+KDRETD+FKG+ YVEFETL L	2
Sbjct	57	VPTEPPFIAYVGNLPKGLVQGDVMKIFSDFEVKNVRLIKDRETDEFKGYGYVEFETLAQL 116	5
Query	253	ERALECDGRIKLDDLSAPLRIDIADRRK 336 + AL C+GRIKLD+ SAPLRIDIAD R+	
Sbjct	117	KSALNCNGRIKLDNFSAPLRIDIADHRR 144	

Range 2: 388 to 428

Score		Expect	Method	Identities	Positives	Gaps	Frame
62.0 bits	s(149)	4e-07()	Compositional matrix adjust.	27/41(66%)	36/41(87%)	0/41(0%)	+1
Features	s:						
Query	817		PRLQLKPRTIAAPINAVAETKQSAS P+L LKPRT+ APIN++AETKQ+A				
Sbjct	388		KLVLKPRTVTAPINSLAETKQAAI				

uncharacterized protein Dana_GF22920 [Drosophila ananassae]

Sequence ID: ref|XP_001964679.2| Length: 540 Number of Matches: 2

▶ See 1 more title(s) Range 1: 77 to 164

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
154 bits(3	388)	5e-38()	Compositional matrix adjust.	69/88(78%)	80/88(90%)	0/88(0%)	+1	
Features	:							
Query	73		PFIAFVGNLPQGLVQGDVIKIFQDE				ΝĻ	252
Sbjct	77		PFIA+VGNLP+GLVQGDV+KIF DE PFIAYVGNLPKGLVQGDVMKIFSDE				QL	136
Query	253		CDGRIKLDDLSAPLRIDIADRRK	336				
Sbjct	137		C+GRIKLD+ SAPLRIDIAD R+ CNGRIKLDNFSAPLRIDIADHRR	164				

Range 2: 441 to 481

Score		Expect	Method	Identities	Positives	Gaps	Frame
65.9 bits	s(159)	4e-08()	Compositional matrix adjust.	29/41(71%)	37/41(90%)	0/41(0%)	+1
Features	s:						
Query	814		PRLQLKPRTIAAPINAVAETKQS P+L LKPRT+ APINA+AETKO+				
Sbjct	441		RPKLVLKPRTVTAPINALAETKQA				

PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Stomoxys calcitrans]

Sequence ID: ref|XP_013105640.1| Length: 297 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
149 bits	(375)	1e-37() Compositional matrix adjust.	78/113(69%)	90/113(79%)	7/113(6%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGG+E++RS +GG KÖLPTEPP	FIAFVGNLPQC +IA+VGNLPQ			
Sbjct	1		YIAYVGNLPQ			
Query	181	LVKDRETDQFKGFCYVEFETLDNLERAL LV DR TD FKGFCYVEF++L+ LE L		SAPLRIDIADI APLRIDIA+1		
Sbjct	56	LVNDRVTDVFKGFCYVEFDSLETLEDVL				

Range 2: 169 to 288

Score		Expect	Method	Identities	Positives	Gaps	Frame
128 bits	(322)	3e-30()	Compositional matrix adjust.	81/144(56%)	96/144(66%)	31/144(21%)	+1
Feature	s:						
Query	538		GRYGSFNNDDRPFERNQDRDRGQ	~			R 696
Sbjct	169		GRYG+FNNDDR +RN +DR Q GRYGNFNNDDRYNDRNH-QDRNQ	REGSYG SRI REGSYGGNSRI			E 227
Query	697	THYNI	PNQQSERPsggmtglgggsggsg	glgvgggssm	JAIDDNERPRL	QLKPRTIAAPI	N 876

HYN ++RPS +IDD+ERPRLQLKPRT+AAPIN 26

Sbjct 228 RHYN---NDRPSSVAPLG-----SIDDSERPRLQLKPRTVAAPIN 26

Query 877 AVAETKQSASIFGNAKPREEKLKE 948
+AETKQ+A+IFGNAKPREEKLK+
Sbjct 265 GLAETKQAAAIFGNAKPREEKLKD 288

PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Stomoxys calcitrans]

Sequence ID: ref[XP_013105638.1] Length: 323 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
149 bits	(376)	1e-37() Compositional matrix adjust.	78/113(69%)	90/113(79%)	7/113(6%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPF MAGRGG+E++RS +GG KOLPTEPF	FIAFVGNLPQG +IA+VGNLPQ			
Sbjct	1	MAGRGGFENSRS-YGGKQLPTEPF				
Query	181	LVKDRETDQFKGFCYVEFETLDNLERAL LV DR TD FKGFCYVEF++L+ LE I		SAPLRIDIADI APLRIDIA+1		
Sbjct	56	LVNDRVTDVFKGFCYVEFDSLETLEDVL				

Range 2: 193 to 314

Score		Expect	Method	Identities	Positives	Gaps	Frame
132 bits	(331)	3e-31()	Compositional matrix adjust.	83/146(57%)	98/146(67%)	31/146(21%)	+1
Features	s:						
Query	532		NRGRYGSFNNDDRPFERNODRDR				
Sbjct	193		RGRYG+FNNDDR +RN +DR ARGRYGNFNNDDRYNDRNH-QDR		SRDG DRYNN SRDGGNDRYNN		R R 251
Query	691		YNPNQQSERPsggmtglgggsgg YN ++RPS	sgglgvgggss	smgAIDDNERP	RLQLKPRTIAA RLQLKPRT+AA	P 870
Sbjct	252		YNNDRPSSVAPLG				
Query	871		AETKQSASIFGNAKPREEKLKE AETKO+A+IFGNAKPREEKLK+	948			
Sbjct	289		AETKQAAAIFGNAKPREEKLKD	314			

GD21542 [Drosophila simulans]

Sequence ID: ref|XP_002105546.1| Length: 472 Number of Matches: 2

▶ See 3 more title(s) Range 1: 53 to 140

Score		Expect	Method	Identities	Positives	Gaps	Frame
151 bits	(382)	2e-37()	Compositional matrix adjust.	68/88(77%)	79/88(89%)	0/88(0%)	+1
Features	s:						
Query	73		PFIAFVGNLPQGLVQGDVIKIFQD				NL 252
Sbjct	53		PFIA+VGNLP+GLVQGDV+KIF D PFIAYVGNLPKGLVQGDVMKIFSD				QL 112
Query	253		CDGRIKLDDLSAPLRIDIADRRK C+GRIKLD+ SAPLRIDIAD R+	336			
Sbjct	113		CNGRIKLDNFSAPLRIDIADHRR	140			

Range 2: 324 to 435

Score		Expect Method	Identities	Positives	Gaps	Frame
65.1 bits	s(157)	5e-08() Compositional matrix adjust.	46/113(41%)	60/113(53%)	15/113(13%)	+1
Features	S :					
Query	661	YNNFNRHRDRERTHYNPNQQSERPS	ggmtglgg	gs	ggsgglgvggg	s 801
Sbjct	324	Y NF NR+RDR R HYNPN YTNFVQNRNRDR-RGHYNPNNSGSSGG	YNNHGNSSFGG	SDNNRPVHGAS:	ESASCGTGPSS	SS 382
Query	802	smgAI-DDNERPRLQLKPRTIAAPINA + A+ DD++RP+L LKPRT+ APIN+			KELQQ 957	
Sbjct	383	TQFAVRDDDDRPKLVLKPRTVTAPINS			TPVSS 435	

GM12901 [Drosophila sechellia]

Sequence ID: ref|XP_002037394.1| Length: 502 Number of Matches: 2

▶ See 1 more title(s)

Range 1: 82 to 169

Score		Expect	Method	Identities	Positives	Gaps	Frame
150 bits	(380)	5e-37()	Compositional matrix adjust.	68/88(77%)	79/88(89%)	0/88(0%)	+1
Features	s:						
Query	73		PFIAFVGNLPQGLVQGDVIKIFQDE PFIA+VGNLP+GLVQGDV+KIF DE				_
Sbjct	82		PFIAYVGNLPKGLVQGDV#KIFSDE				QL 141
Query	253		CDGRIKLDDLSAPLRIDIADRRK C+GRIKLD+ SAPLRIDIAD R+	336			
Sbjct	142		CNGRIKLDH SAPLRIDIAD RH	169			

Range 2: 419 to 459

Score		Expect Method	Identities	Positives	Gaps	Frame
64.7 bits	s(156)	8e-08() Compositional matrix adjust.	28/41(68%)	37/41(90%)	0/41(0%)	+1
Features	S :					
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQSA DD++RP+L LKPRT+ APIN++AETKQ+A				
Sbjct	419	DDDDRPKLVLKPRTVTAPINSLAETKÕAA				

CG1340 [Drosophila busckii]

Sequence ID: gb|ALC47603.1| Length: 439 Number of Matches: 2

Range 1: 37 to 126

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
149 bits	(376)	9e-37()	Compositional matrix adjust.	66/90(73%)	82/90(91%)	0/90(0%)	+1	
Features	s:							
Query	67	~	EPPFIAFVGNLPQGLVQGDVIKIF(~	~			246
Sbjct	37		+PP+IAFVGNLP+GLVQGDV+KIF DPPYIAFVGNLPKGLVQGDVMKIFI					96
Query	247		LECDGRIKLDDLSAPLRIDIADRRI					
Sbjct	97	L+RAI QLKRAI	L +GRIKLD+LSAPLRIDIAD R- LSRNGRIKLDNLSAPLRIDIADHRI					

Range 2: 323 to 407

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
72.0 bits	(175)	3e-10()	Compositional matrix adjust.	46/99(46%)	54/99(54%)	16/99(16%)	+1	
Features	s:							
Query	643	SRDGDI S D	RYNNFNRHRDRERTHYNPNQQS Y NF NR RDR R HYNPN++	SERPsggmtg]	Lgggsggsgg]	Lgvgggssmg	ΑI	816
Sbjct	323	~ ~	HYANFGQNRTRDR-RGHYNPNERG	}	GHAARS	SEQSSRVIAS	$^{ m L}$	368
Query	817		PRLQLKPRTIAAPINAVAETKQSA P++ LKPRTI PINA+AETKQ+A					
Sbjct	369		PKIVLKPRTINEPINALAETKQAA					

uncharacterized protein Dvir_GJ24240 [Drosophila virilis]

Sequence ID: ref|XP_002054082.2| Length: 411 Number of Matches: 2

▶ See 1 more title(s) Range 1: 41 to 129

Score		Expect	Method		Identities	Positives	Gaps	Fram	е
148 bits	(374)	1e-36()	Compositional ma	atrix adjust.	67/89(75%)	81/89(91%)	0/89(0%)	+1	
Features	S :								
Query	70		PPFIAFVGNLPQGI PP+IAFVGNLP+GI						249
Sbjct	41		PPYIAFVGNLPKGI	~					100
Query	250	LERALI	ECDGRIKLDDLSAF +GRIKLD+LSAF		336				
Sbjct	101		SRNGRIKLDNLSAF		129				

Range 2: 296 to 379

Score	Expect Method	Identities	Positives	Gaps	Frame

70.1 bits(170) 1e-09() Compositional matrix adjust. 45/101(45%) 60/101(59%) 19/101(18%) +1

Features:

Query	643	SRDGDRYNNFNRHRDRERTHYNPNQQSERPsggmtglggg S D Y+NF NR RDR R HYNPN++ +	sggsgglgvgggssmgAI	816
		SNDNGHYSNFGQNRTRDR-RGHYNPNERYNQ		
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEK DD++RP++ L+PRT+ PINA+AETKQ+ASIFGNAKPR+ +	939	
Sbjct	339	DDDDRPKIVLQPRTVTEPINALAETKQAASIFGNAKPRKSQ	379	

GH14211 [Drosophila grimshawi]

Sequence ID: ref|XP_001995925.1| Length: 410 Number of Matches: 2

▶ See 1 more title(s) Range 1: 56 to 143

Score		Expect	Method	Identities	Positives	Gaps	Frame
148 bits	(373)	2e-36()	Compositional matrix adjust.	68/88(77%)	80/88(90%)	0/88(0%)	+1
Features	s:						
Query	73		PFIAFVGNLPQGLVQGDVIKIFQD PFIAFVGNLP+GLVQGDV+KIF+D				
Sbjct	56		PFIAFVGNLPKGLVQGDVMKIFED:				
Query	253	ERALE(CDGRIKLDDLSAPLRIDIADRRK	336			
Sbjct	116		+GRIKLD+LSAPLRIDIAD R+ RNGRIKLDNLSAPLRIDIADHRR	143			

Range 2: 308 to 395

Score		Expect	Method	Identities	Positives	Gaps	Frame)
66.2 bits	s(160)	2e-08()	Compositional matrix adjust.	44/108(41%)	56/108(51%)	22/108(20%)	+1	
Features	S :							
Query	643	SRDGD S D	RYNNFNRHRDRERTHYNPNQ Y+NF NR RDR R HYNPN	QSERPsggmtg	glgggsggsgg	lgvgggssmgA +S +		.6
Sbjct	308	2 2	GHYSNFGQNRTRDRRR-HYNPND		IY		-	· 7
Query	817		RPRLQLKPRTIAAPINAVAETKQ		~~	960		
Sbjct	348		RP++ L+PR++ PINA+AETKQ RPKIVLQPRSVTEPINALAETKQ		~ -	395		

splicing factor [Anopheles darlingi]

Sequence ID: **gb|ETN59545.1**| Length: 351 Number of Matches: 2 Range 1: 1 to 107

Score		Expect Method	Identities	Positives	Gaps	Frame
145 bits	(367)	4e-36() Compositional matrix adjust.	67/111(60%)	88/111(79%)	4/111(3%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP				
Sbjct	1	MAGRG ++ +GGDR K LPTEPP MAGRGSHDRYGGDRPRKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KD++TD FKGFCYVEFET+++L+ LE		PLRIDIADRRI		
Sbjct	57	KDKDTDMFKGFCYVEFETVEDLQDVLEL				

Range 2: 272 to 313

Score		Expect Method	Identities	Positives	Gaps	Frame
69.3 bits	s(168)	1e-09() Compositional matrix adjust.	30/42(71%)	39/42(92%)	0/42(0%)	+1
Features	s:					
Query	826	ERPRLQLKPRTIAAPINAVAETKQSASIF ERPRL+L PR++ AP+NA+AETKO+A+IF				
Sbjct	272	ERPRLKLAPRSVNAPLNALAETKQAAAII				

AGAP003219-PB [Anopheles gambiae str. PEST]

Sequence ID: ref|XP_003436420.1| Length: 384 Number of Matches: 2

See 1 more title(s)

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
146 bits	(368)	6e-36() Compositional matrix adjust.	68/111(61%)	90/111(81%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRG +++ R G DRA K LPTEPP				
Sbjct	1	MAGRGTHDNNRYGDRARKPLPTEPP				
Query	187	KDRETDOFKGFCYVEFETLDNLERALEC				
Sbjct	58	KD+ETD FKGFCYVEF+TL++LE+ L+ 1 KDKETDVFKGFCYVEFDTLEDLEKVLOL			·-·	

Range 2: 303 to 341

Score		Expect Method	Identities	Positives	Gaps	Frame
67.4 bits	s(163)	8e-09() Compositional ma	trix adjust. 30/39(77%)	36/39(92%)	0/39(0%)	+1
Features	S :					
Query	826	ERPRLQLKPRTIAAPINAVA ERPRL+L PR+ AP+NA+A	ETKQSASIFGNAKPREEKL ETKQSA+IFGNA+PREEKL	942		
Sbjct	303	ERPRLKLAPRSTNAPLNALA		341		

splicing factor [Culex quinquefasciatus]

Sequence ID: ref|XP_001848859.1| Length: 330 Number of Matches: 2

▶ See 1 more title(s) Range 1: 3 to 100

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
145 bits	(365)	6e-36()	Compositional matrix adjust.	66/98(67%)	84/98(85%)	0/98(0%)	+1	
Features	s:							
Query	46		ASKQLPTEPPFIAFVGNLPQGLVQ A + LPTEPP+IA+VGNLPQG+VQ					225
Sbjct	3		ARRPLPTEPPYIAYVGNLPQGVVQ0					62
Query	226		LDNLERALECDGRIKLDDLSAPLR LD L+ AL+ DG I L+D +A LR		339			
Sbjct	63		LDELKEALDLDGLIVLNDSTAALR		100			

Range 2: 172 to 301

Score		Expect Method	Identities	Positives	Gaps	Frame
72.8 bits	s(177)	9e-11() Compositional matrix adjust.	57/143(40%)	68/143(47%)	19/143(13%)	+1
Features	S :					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRDR DR NRGRYG+FN + R RD	GQREGSYGNQ- R+G GN	SRDG-D		E 693
Sbjct	172	DRGPNRGRYGNFNEEGREGGGRDD				G 228
Query	694	RTHYNPNQQSERPsggmtglgggsggs	gglgvgggssm		LQLKPRTIAAP L LKPRT+AAP	
Sbjct	229	GAGAGRRDNRDNDRRKD	QPQHSAAPGLS			
Query	874	NAVAETKQSASIFGNAKPREEKL 94 NA+AETKQ+A+IFG AKPREEK+	2			
Sbjct	279	NALAETKQAAAIFGAAKPREEKV 30	1			

AGAP003219-PA [Anopheles gambiae str. PEST]

Sequence ID: ref|XP_312928.5| Length: 349 Number of Matches: 2

▶ See 1 more title(s) Kange 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
145 bits	(365)	7e-36() Compositional matrix adjust.	68/111(61%)	90/111(81%)	3/111(2%)	+1
Features	S:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPPI MAGRG +++ R G DRA K LPTEPP-				
Sbjct	1	MAGRGTHDNNRYGDRARKPLPTEPPY				
Query	187	KDRETDQFKGFCYVEFETLDNLERALECI KD+ETD FKGFCYVEF+TL++LE+ L+ I				
Sbjct	58	KDKETDVFKGFCYVEFDTLEDLEKVLQLI				

Score		Expect	Method	Identities	Positives	Gaps	Frame
66.6 bits	s(161)	1e-08()	Compositional matrix adjust.	30/39(77%)	36/39(92%)	0/39(0%)	+1
Features	s:						
Query	826		LKPRTIAAPINAVAETKQSASIF		942		
Sbjct	268		L PR+ AP+NA+AETKQSA+IF(LAPRSTNAPLNALAETKQSAAIF(306		

PREDICTED: eukaryotic translation initiation factor 4H isoform X3 [Musca domestica]

Sequence ID: **ref|XP_005190146.1|** Length: 274 Number of Matches: 2 Range 1: 149 to 269

Score		Expect Method	Identities	Positives	Gaps	Frame
143 bits	(360)	8e-36() Compositional matrix adjust.	86/144(60%)	104/144(72%)	25/144(17%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD DRPA RGRYG+FNNDDR +RNODR+		SRDGDRYNNFN: SRDGDRYNNF+:		
Sbjct	149	DRPAARGRYGNFNNDDRYNDRNQDRN				
Query	706	NPNQQSERPsggmtglgggsggsggl N O++RP LG	gvgggssmgAI +T	DDNERPRLQLK: DD+ERPRLQL+:	PRTIAAPINAV PRT+ APIN +	A 885
Sbjct	207	NQNDRPPSAAAPLG				
Query	886	ETKQSASIFGNAKPREEKLKELQQ ETKQ+A+IFGNAKPREEKLKE ++	957			
Sbjct	246		269			

Range 2: 5 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame
129 bits	(325)	8e-31() Compositional matrix adjust.	65/110(59%)	80/110(72%)	7/110(6%)	+1
Feature	s:					
Query	16	RGGYEHARSGFGGDRASKQLPTEPPFIA RGG++ R + +KOLPTEPP+ A			FEVKYVRLV ++VK VRLV	
Sbjct	5	RGGFDQPRNYGNKQLPTEPPYTA			· · · - · · - · - · - · - · - · - · - ·	•
Query	190	DRETDOFKGFCYVEFETLDNLERALECD		PLRIDIADRRKN PLRIDIA+ ++N		
Sbjct	60	DR TD FKGFCYVEFE L+ LE L D DRVTDVFKGFCYVEFENLETLEEVLRLD				

PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Musca domestica]

Sequence ID: **ref|XP_005190145.1**| Length: 292 Number of Matches: 2 Range 1: 167 to 287

Score	l	Expect Method	Identities	Positives	Gaps	Frame
143 bits(3	60) 1	le-35() Compositional matrix adjust.	86/144(60%)	104/144(72%)	25/144(17%)	+1
Features:						
Query 5	32	DRPANRGRYGSFNNDDRPFERNQDRD DRPA RGRYG+FNNDDR +RNODR+		SRDGDRYNNFNI SRDGDRYNNF+I		
Sbjct 1	67	DRPAARGRYGNFNNDDRYNDRNQDRN				
Query 7	06	NPNQQSERPsggmtglgggsggsggl		DDNERPRLQLKI DD+ERPRLOL+		
Sbjct 2	25			DDSERPRLQLQ:		
Query 8	886	ETKQSASIFGNAKPREEKLKELQQ ETKQ+A+IFGNAKPREEKLKE ++	957			
Sbjct 2	64		287			

Range 2: 5 to 109

Score		Expect Method	Identities	Positives	Gaps	Frai	me
129 bits(3	325)	1e-30() Compositional matrix adjust.	65/110(59%)	80/110(72%)	7/110(6%)	+1	
Features	:						
Query	16	RGGYEHARSGFGGDRASKQLPTEPPFIAF RGG++ R + +KOLPTEPP+ A+			FEVKYVRLV ++VK VRLV		189
Sbjct	5	RGGFDQPRNYGNKQLPTEPPYTAY					
Query	190	DRETDOFKGFCYVEFETLDNLERALECDG		LRIDIADRRKN LRIDIA+ ++N			
Sbjct	60	DRVTDVFKGFCYVEFENLETLEEVLRLDG			•		

PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Musca domestica]

Sequence ID: ref|XP_011295194.1| Length: 318 Number of Matches: 2

Range 1: 193 to 313

Score Expect Method Identities Positives Gaps Fra	me
143 bits(360) 2e-35() Compositional matrix adjust. 86/144(60%) 104/144(72%) 25/144(17%) +1	
Features:	
Query 532 DRPANRGRYGSFNNDDRPFERNQDRDRGQREGSYGNQSRDGDRYNNFNRHRDRERTHY DRPA RGRYG+FNNDDR +RNQDR+ REGS+G QSRDGDRYNNF+R+R DRER H+	705
Sbjct 193 DRPAARGRYGNFNNDDRYNDRNQDRNHREGSFGGQSRDGDRYNNFSRNRGGDRERGHF	250
Query 706 NPNQQSERPsggmtglgggsggsgglgvgggssmgAIDDNERPRLQLKPRTIAAPINAVA N Q++RP LG +IDD+ERPRLQL+PRT+ APIN +A	885
Sbjct 251 NQNDRPPSAAAPLGSIDDSERPRLQLQPRTVDAPINGLA	289
Query 886 ETKQSASIFGNAKPREEKLKELQQ 957 ETKQ+A+IFGNAKPREEKLKE ++	
Sbjct 290 ETKQAAAIFGNAKPREEKLKEARE 313	

Range 2: 5 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame		
130 bits	(326)	1e-30() Compositional matrix adjust.	65/110(59%)	80/110(72%)	7/110(6%)	+1		
Features	Features:							
Query	16	RGGYEHARSGFGGDRASKQLPTEPPFIA						
Sbjct	5	RGG++ R + +KQLPTEPP+ A RGGFDQPRNYGNKQLPTEPPYTA			++VK VRLV GYKVKSVRLV	•		
Query	190	DRETDQFKGFCYVEFETLDNLERALECD						
Sbjct	60	DR TD FKGFCYVEFE L+ LE L D DRVTDVFKGFCYVEFENLETLEEVLRLD	U = 122 =	LRIDIA+ ++N LRIDIAESKRI	•			

AGAP003219-PA-like protein [Anopheles sinensis]

Sequence ID: **gb|KFB53209.1|** Length: 125 Number of Matches: 1 Range 1: 11 to 108

Score		Expect	Method	Identities	Positives	Gaps	Frai	me
137 bits	(346)	2e-35()	Compositional matrix adjust.	62/98(63%)	82/98(83%)	0/98(0%)	+1	
Features	Features:							
Query	46		ASKQLPTEPPFIAFVGNLPQGLVQO A K LPTEPP++A+VGNLP G+VOO					225
Sbjct	11		ARKPLPTEPPYLAYVGNLPHGIVÕO					70
Query	226		LDNLERALECDGRIKLDDLSAPLRI L +LE+ L+ DG I L++ PLRI	IDIADRRKN ID+A+++KN	339			
Sbjct	71		LHDLEKVLQLDGMIVLNERPEPLR		108			

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Cerapachys biroi]

Sequence ID: **ref|XP_011343457.1|** Length: 269 Number of Matches: 2 Range 1: 1 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame
140 bits	(353)	7e-35() Compositional matrix adjust.	66/111(59%)	86/111(77%)	2/111(1%)	+1
Features:						
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY+ +R GG R+ K LPTEPP				
Sbjct	1	MAGRGGYDDSRDYSGGHRSRKPLPTEPP				
Query	187	KDRETDOFKGFCYVEFETLDNLERALEC				
Sbjct	61	KDR+TD+FKGFCYVEFE L +LE ALE KDRDTDKFKGFCYVEFEDLADLEAALEM		++ID+A+ ++ LIKIDVAEGKE		

Range 2: 225 to 266

Score		Expect Method	Identities	Positives	Gaps	Frame
57.4 bits	s(137)	8e-06() Compositional matrix adjus	st. 24/42(57%)	34/42(80%)	0/42(0%)	+1
Features:						
Query 817 DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL D R RL+LKPRT+ P+N++AE+ +++SI+G AKPREEKL						
Sbjct	225	DTTGRKRLELKPRTVKEPVNSMAESS				

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Cerapachys biroi]

Sequence ID: ref|XP_011343458.1| Length: 263 Number of Matches: 2

Range 1: 1 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame
140 bits	(352)	9e-35() Compositional matrix adjust.	66/111(59%)	86/111(77%)	2/111(1%)	+1
Features	S :					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPF MAGRGGY+ +R GG R+ K LPTEPF				
Sbjct	1	MAGRGGYDDSRDYSGGHRSRKPLPTEPF				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDR+TD+FKGFCYVEFE L +LE ALE		PLRIDIADRRI ++ TD+A+ ++		
Sbjct	61	KDRDTDKFKGFCYVEFEDLADLEAALEM				

Range 2: 219 to 260

Score)	Expect	Method	Identities	Positives	Gaps	Frame
57.4 b	oits(137)	8e-06()	Compositional matrix adjust.	24/42(57%)	34/42(80%)	0/42(0%)	+1
Featu	Features:						
Query	Query 817 DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL D R RL+LKPRT+ P+N++AE+ +++SI+G AKPREEKL						
Sbjct	219		RLELKPRTVKEPVNSMAESSKTS				

PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Linepithema humile]

Sequence ID: ref|XP_012221230.1| Length: 276 Number of Matches: 2

Range 1: 1 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame
138 bits	(348)	4e-34() Compositional matrix adjust.	65/111(59%)	85/111(76%)	2/111(1%)	+1
Features:						
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY+ +R G R+ K LPTEPP				
Sbjct	1	MAGRGGYDDSRDYSSGHRSRKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDR+TD+FKGFCYVEFE L +LE ALE		PLRIDIADRRI ++TD+A+		
Sbjct	61	KDRDTDKFKGFCYVEFEELADLEAALEM				

Range 2: 230 to 276

Score		Expect Method	Identities	Positives	Gaps	Frame
60.8 bits	s(146)	6e-07() Compositional matrix adjust.	26/47(55%)	38/47(80%)	0/47(0%)	+1
Features						
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQ	~~~	57		
Sbjct	230	D + R RL+LKPRT+ P+NA+AE+ +++SI+G AKPREEKLK + + DTSGRKRLELKPRTVKEPVNAMAESSKTSSIYGGAKPREEKLKMMDK			76	

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Apis mellifera]

Sequence ID: ref|XP_006566940.1| Length: 263 Number of Matches: 2

▶ See 2 more title(s) Range 1: 1 to 110

Score		Expect Method	Identities	Positives	Gaps	Frame
137 bits	(346)	6e-34() Compositional matrix adjust.	68/112(61%)	87/112(77%)	3/112(2%)	+1
Features:						
Query	7	MAGRGGYEHARSGFGGDRAS-KQLPTEF MAGRGGYE +R GG R+ K LPTEF				
Sbjct	1	MAGRGGYEDSRDYGGGYRSGRKPLPTEP				
Query	184	VKDRETDQFKGFCYVEFETLDNLERALE				
Sbjct	61	VKD+ETD+FKGFCYVEFE L +LE ALE VKDKETDRFKGFCYVEFEDLADLEAALE				

Range 2: 157 to 258

Score	Expect Method	Identities	Positives	Gaps	Frame
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56.6 bits(135) 1e-05() Compositional matrix adjust. 46/137(34%) 60/137(43%) 35/137(25%) +1 Features: DRPANRGRYGSFNNDDRPFERNQDRDRGQREGSYGNQSRDGDRYNNFNRHRDRERTHYNP D +NRG Y FN+D R R+ R SYGN R + +R+ H P DMRSNRGNYSQFNDDTGGGSREWSRNASSR--SYGN-----RPASRGTGTERKPFHDEP Query 532 711 Sbjct 157 208 NQQSERPsggmtglgggsggglgvgggssmgAIDDNERPRLQLKPRTIAAPINAVAET
+ P+ D R RL L PRTI PINA+AE+
FHKDPPPA-----DTTGRKRLVLAPRTIQDPINAIAES 891 Query 712

241

892 KQSASIFGNAKPREEKL 942 Query +S+SI+G AKPREEK+ Sbjct 242 SKSSSIYGGAKPREEKI

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Apis mellifera]

Sequence ID: ref|XP_392894.1| Length: 274 Number of Matches: 2

▶ See 2 more title(s)

209

Range 1: 1 to 110

Sbjct

Score		Expect Method	Identities	Positives	Gaps	Frame
137 bits	(346)	8e-34() Compositional matrix adjust.	68/112(61%)	87/112(77%)	3/112(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRAS-KQLPTEP MAGRGGYE +R GG R+ K LPTEP				
Sbjct	1	MAGRGGYEDSRDYGGGYRSGRKPLPTEP				
Query	184	VKDRETDQFKGFCYVEFETLDNLERALE VKD+ETD+FKGFCYVEFE L +LE ALE		SAPLRIDIADRI + ++ID+A+ -		
Sbjct	61	VKDKETDRFKGFCYVEFEDLADLEAALE			· · -•	

Range 2: 168 to 269

Score		Expect Method	Identities	Positives	Gaps	Frame
57.0 bits	s(136)	1e-05() Compositional matrix adjust.	46/137(34%)	59/137(43%)	35/137(25%)	+1
Features	s:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRD D +NRG Y FN+D R R+		SRDGDRYNNFN R +	RHRDRERTHYN +R+ H	_
Sbjct	168	D THRG I FNTD R RT DMRSNRGNYSQFNDDTGGGSREWSRN				_
Query	712	NQQSERPsggmtglgggsggsgglgv	gggssmgAIDD1 D	NERPRLQLKPR R RL L PR		
Sbjct	220	FHKDPPP	_			
Query	892	KQSASIFGNAKPREEKL 942 +S+SI+G AKPREEK+				
Sbjct	253	SKSSSIYGGAKPREEKI 269				

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Dinoponera quadriceps]

Sequence ID: ref|XP_014470233.1| Length: 276 Number of Matches: 2

▶ See 2 more title(s) Range 1: 1 to 110

Score		Expect	Method	Identities	Positives	Gaps	Frame
136 bits	(343)	2e-33()	Compositional matrix adjust.	66/112(59%)	87/112(77%)	3/112(2%)	+1
Features	s:						
Query	7		GYEHARS-GFGGDRASKQLPTEP GY+ +R GG R+ K LPTEP				
Sbjct	1		GYDDSRDYSSGGYRSRKPLPTEP:				
Query	184		TDQFKGFCYVEFETLDNLERALETD+FKGFCYVEFE L +LE ALE		APLRIDIADRE		
Sbjct	61		TDKFKGFCYVEFEDLADLEAALE			· · • •	

Range 2: 230 to 276

Score		Expect	Method	Identities	Positives	Gaps	Frame
60.5 bits	s(145)	7e-07()	Compositional matrix adjust.	27/47(57%)	37/47(78%)	0/47(0%)	+1
Features	S :						
Query	817		DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKLKELQQ 9 D R RL+LKPRTI P+NA+AE+ +++SI+G AKPREEKLK + +				
Sbjct	230		RLELKPRTIKDPVNALAESTKNSS			76	

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Wasmannia auropunctata]

Sequence ID: ref|XP_011697818.1| Length: 273 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
136 bits	(342)	3e-33() Compositional matrix adjust.	64/111(58%)	87/111(78%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY+ +R + R+ K LPTEPP				
Sbjct	1	MAGRGGYDDSRD-YPTHRSRKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDR+TD+FKGFCYVEFE L +LE+ALE		PLRIDIADRRI ++ TD+A+ ++		
Sbjct	60	KDRDTDKFKGFCYVEFEDLSDLEKALEM				

Range 2: 229 to 272

Score		Expect Method	Identities	Positives	Gaps	Frame
60.1 bits(144)		1e-06() Compositional matrix adjust.	25/44(57%)	36/44(81%)	0/44(0%)	+1
Feature	s:					
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQS D R RL+LKPRT+ P+NA+AE+ ++				
Sbjct	229	DTTGRKRLELKPRTVKEPVNAIAESSKT				

PREDICTED: eukaryotic translation initiation factor 4H-like [Bombus impatiens]

Sequence ID: ref|XP_012247500.1| Length: 267 Number of Matches: 2

Range 1: 1 to 110

Score		Expect	Method	Identities	Positives	Gaps	Frame
136 bits	(342)	3e-33()	Compositional matrix adjust.	68/112(61%)	86/112(76%)	3/112(2%)	+1
Features	S :						
Query	7	MAGRG MAGRG	GYEHARSGFGGDRAS-KQLPTEP: GYE R GG R+ K LPTEP:				
Sbjct	1		GYEDLRDYGGGYRSGRKPLPTEP:				
Query	184		TDQFKGFCYVEFETLDNLERALEGE TD+FKGFCYVEFE L +LE ALE		APLRIDIADRE		
Sbjct	61		TDRFKGFCYVEFEELADLEAALE			· - •	

Range 2: 221 to 262

Score		Expect	Method	Identities	Positives	Gaps	Frame
55.8 bits	s(133)	3e-05()	Compositional matrix adjust.	26/42(62%)	33/42(78%)	0/42(0%)	+1
Features:							
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKL 942 D + R RL L PRTI PINA+AE+ +S+SI+G AKPREEK+					
Sbjct	221		RLVLAPRTIQDPINAIAESSKSS				

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Dinoponera quadriceps]

Sequence ID: **ref|XP_014470237.1**| Length: 269 Number of Matches: 2 Range 1: 1 to 110

Score		Expect Method	Identities	Positives	Gaps	Frame
136 bits	(342)	3e-33() Compositional matrix adjust.	66/112(59%)	87/112(77%)	3/112(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARS-GFGGDRASKQLPTE MAGRGGY+ +R GG R+ K LPTE				
Sbjct	1	MAGRGGYDDSRDYSSGGYRSRKPLPTE				
Query	184	VKDRETDQFKGFCYVEFETLDNLERALI VKDR+TD+FKGFCYVEFE L +LE ALI		SAPLRIDIADRI + ++TD+A+ ·		
Sbjct	61	VKDRDTDKFKGFCYVEFEDLADLEAALI			· ·	

Range 2: 223 to 269

Score	Expect Method	Identities	Positives	Gaps	Frame
60.5 bits(145)	7e-07() Compositional matrix adju	st. 27/47(57%)	37/47(78%)	0/47(0%)	+1

Features:

Ouerv	817	DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKLKELQQ	957
guori	0 _ /	D R RL+LKPRTI P+NA+AE+ +++SI+G AKPREEKLK + +	, ,
Shict	223	DTTGRKRIELKPRTIKDPVNALAESTKNSSIYGGAKPREEKLKMMDK	269

PREDICTED: eukaryotic translation initiation factor 4H-like [Bombus terrestris]

Sequence ID: ref|XP_012170299.1| Length: 267 Number of Matches: 2

Range 1: 1 to 110

Score		Expect Method	Identities	Positives	Gaps	Frame
136 bits	(342)	3e-33() Compositional matrix adjust.	68/112(61%)	86/112(76%)	3/112(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRAS-KQLPTEF				
Sbjct	1	MAGRGGYE R GG R+ K LPTER MAGRGGYEDLRDYGGGYRSGRKPLPTER				_
Query	184	VKDRETDQFKGFCYVEFETLDNLERALE VKD+ETD+FKGFCYVEFE L +LE ALE				
Sbjct	61	VKDKETDRFKGFCYVEFEELADLEAALE				

Range 2: 221 to 262

Score	Expect Method	Identities	Positives	Gaps	Frame
55.5 bits(132)	3e-05() Compositional matrix adjust.	26/42(62%)	33/42(78%)	0/42(0%)	+1
Features:					
Query 817	DDNERPRLQLKPRTIAAPINAVAETKQSAS D + R RL L PRTI PINA+AE+ +S+S				
Sbjct 221	DTSGRKRLILAPRTIQDPINAIAESSKSS				

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Wasmannia auropunctata]

Sequence ID: ref|XP_011697819.1| Length: 267 Number of Matches: 2

Range 1: 1 to 108

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
135 bits(341)	3e-33()	Compositional matrix adjust.	64/111(58%)	87/111(78%)	3/111(2%)	+1	
Features	:							
Query	7		GYEHARSGFGGDRASKQLPTEPPI GY+ +R + R+ K LPTEPP+					186
Sbjct	1		GYDDSRD-YPTHRSRKPLPTEPPY					59
Query	187		DQFKGFCYVEFETLDNLERALECI D+FKGFCYVEFE L +LE+ALE I		PLRIDIADRRI ++TD+A+ ++			
Sbjct	60		DKFKGFCYVEFEDLSDLEKALEMI					

Range 2: 223 to 266

Score		Expect	Method	Identities	Positives	Gaps	Frame
60.1 bits	s(144)	1e-06()	Compositional matrix adjust.	25/44(57%)	36/44(81%)	0/44(0%)	+1
Feature	s:						
Query	817		PRLQLKPRTIAAPINAVAETKQSAS RL+LKPRT+ P+NA+AE+ +++5				
Sbjct	223		RLELKPRTVKEPVNAIAESSKTS				

eukaryotic translation initiation factor 4H [Chironomus tentans]

Sequence ID: emb|CAD55310.1| Length: 316 Number of Matches: 2

Range 1: 6 to 100

Score	Expect	Method	Identities	Positives	Gaps	Frame
137 bits(34	4) 3e-33()	Compositional matrix adjust.	64/95(67%)	78/95(82%)	0/95(0%)	+1
Features:						
Query 5	DRASK	QLPTEPPFIAFVGNLPQGLVQGDV C PT+PPFIAFVGNLPQG+VQGDV		VRLVKDRETD VRLVKD+ETD		
Sbjct 6		X FITTETTAFVGNLFQGTVQGDV XPFPTDPPFIAFVGNLPQGVVQGDV				
Query 2		ILERALECDGRIKLDDLSAPLRIDI -LE A+ DGRI LD+ PLRID+)		
Sbjct 6	· - · ·	DLEEAVNLDGRIVLDNNPQPLRIDV)		

Score		Expect	Method	Identities	Positives	Gaps	Frame
57.4 bits	s(137)	1e-05()	Compositional matrix adjust.	25/40(63%)	34/40(85%)	0/40(0%)	+1
Features	s:						
Query	829	RPRLQLI RP+L+L	KPRTIAAPINAVAETKQSASIFGN PRT+ P+N +AETKQ+A+IFG				
Sbjct	269		APRTVKEPVNGLAETKQAAAIFGI				

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Megachile rotundata]

Sequence ID: ref|XP_012144422.1| Length: 274 Number of Matches: 2

Range 1: 1 to 110

Score		Expect	Method	Identities	Positives	Gaps	Fram	ıe
135 bits(341) 4	4e-33()	Compositional matrix adjust.	66/112(59%)	87/112(77%)	3/112(2%)	+1	
Features	:							
Query	7		GYEHARSGFGGDRAS-KQLPTEP					183
Sbjct	1		GYE +R GG R+ K LPTEP: GYEDSRDYGGGHRSGRKPLPTEP:					50
Query	184		TDQFKGFCYVEFETLDNLERALEGTD+FKGFCYVEFE L +LE AL+		APLRIDIADRF			
Sbjct	61		TDKFKGFCYVEFEDLADLEMALD			· - ·		

Range 2: 226 to 269

Score		Expect	Method	Identities	Positives	Gaps	Frame
60.5 bits	(145)	7e-07()	Compositional matrix adjust.	29/44(66%)	35/44(79%)	0/44(0%)	+1
Features	3 :						
Query	811		RPRLQLKPRTIAAPINAVAETKQS R RL L PRTI APINA+AE+ +S				
Sbjct	226		RKRLVLAPRTIQAPINAMAESSKS				

PREDICTED: eukaryotic translation initiation factor 4H-like [Monomorium pharaonis]

Sequence ID: ref|XP_012532397.1| Length: 267 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Fram	<u>e</u>
135 bits(339)	6e-33() Compositional matrix adjust.	64/111(58%)	85/111(76%)	3/111(2%)	+1	
Features	:						
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPPI MAGRGGY+ +R + R+ K LPTEPP-	~	~	•		86
Sbjct	1	MAGRGGYDDSRD-YSSHRSRKPLPTEPPY					9
Query	187	KDRETDQFKGFCYVEFETLDNLERALECI KDR+TD+FKGFCYVEFE L +LE ALE I		PLRIDIADRRK ++ID+A+ ++			
Sbjct	60	KDRDTDKFKGFCYVEFEDLADLEAALEMI					

Range 2: 222 to 264

Score		Expect	Method	Identities	Positives	Gaps	Frame
60.8 bits	(146)	5e-07()	Compositional matrix adjust.	26/43(60%)	35/43(81%)	0/43(0%)	+1
Features	S :						
Query	817		RLQLKPRTIAAPINAVAETKQSAS RL+LKPRT+ P+NA+AE+ +++5				
Sbjct	222		RLELKPRTVKEPVNAIAESSKTS				

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Harpegnathos saltator]

Sequence ID: ref|XP_011142296.1| Length: 271 Number of Matches: 2

Range 1: 1 to 109

Score	Expect	Method	Identities	Positives	Gaps	Frame	
134 bits(338)	1e-32()	Compositional matrix adjust.	63/111(57%)	85/111(76%)	2/111(1%)	+1	
Features:							
Query 7	MAGRG	GYEHARSGFGGDRASKQLPTEPP	FIAFVGNLPQG	LVQGDVIKIFÇ	QDFEVKYVRI	LV 18	6

Sbjct	1	MAGRGGY+ +R G R+ K LPT PP+ A+VGNLP G+VQGDV KIF+ VK +RLV MAGRGGYDDSRDYSSGHRSRKPLPTGPPYTAYVGNLPNGIVQGDVDKIFEKLNVKVIRLV	60
Query	187	KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN 339 KD++TD+FKGFCYVEFE L +LE ALE DG +++D + ++ID+A+ ++N	
Sbict	61	KDKDTDKFKGFCYVEFEDLADLEAALEMDGAVEVDKSLIKIDVAEIKRN 109	

Range 2: 225 to 271

Score		Expect	Method	Identities	Positives	Gaps	Frame
60.5 bits	s(145)	7e-07()	Compositional matrix adjust.	27/47(57%)	37/47(78%)	0/47(0%)	+1
Features	s:						
Query	817		RLQLKPRTIAAPINAVAETKQSAS RL+LKPRTI P+NA+AE+ +++5			57	
Sbjct	225		RLELKPRTIKDPVNALAESTKNS			71	

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Harpegnathos saltator]

Sequence ID: ref|XP_011142297.1| Length: 264 Number of Matches: 2

Range 1: 1 to 109

Score		Expect	Method	Identities	Positives	Gaps	Frame	
134 bits	(337)	1e-32()	Compositional matrix adjust.	63/111(57%)	85/111(76%)	2/111(1%)	+1	
Features	s:							
Query	7		GYEHARSGFGGDRASKQLPTEPP	~	~	•		
Sbjct	1		GY+ +R G R+ K LPT PP GYDDSRDYSSGHRSRKPLPTGPP					
Query	187		DOFKGFCYVEFETLDNLERALECT		PLRIDIADRRK ++ID+A+ ++			
Sbjct	61		DKFKGFCYVEFEDLADLEAALEM					

Range 2: 218 to 264

Score		Expect Method	Identities	Positives	Gaps	Frame
60.5 bits	s(145)	7e-07() Compositional matrix adjust.	27/47(57%)	37/47(78%)	0/47(0%)	+1
Feature	s:					
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKLKELQ D R RL+LKPRTI P+NA+AE+ +++SI+G AKPREEKLK +			57	
Sbjct	218	DTTGRKRLELKPRTIKDPVNALAESTKN			64	

PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Stomoxys calcitrans]

Sequence ID: **ref|XP_013105639.1|** Length: 313 Number of Matches: 2 Range 1: 4 to 98

Score		Expect	Method	Identities	Positives	Gaps	Fra	me
135 bits	(340)	1e-32()	Compositional matrix adjust.	67/95(71%)	75/95(78%)	2/95(2%)	+1	
Features	s:							
Query	61		PTEPPFIAFVGNLPQGLVQGDVIK PTEPP+IA+VGNLPQ LVQGDV+K		VRLVKDRETD VRLV DR TD	~		234
Sbjct	4		PTEPPYIAYVGNLPQRLVQGDVVK					63
Query	235	ETLDNI ++L+ I	LERALECDGRIKLDDLSAPLRIDIA LE L DG I +DD APLRIDIA)			
Sbjct	64	· ·	LEDVLRRDGLINVDDNGAPLRIDIA					

Range 2: 183 to 304

Score		Expect Method	Identities	Positives	Gaps	Frame
132 bits(332) 2	2e-31() Compositional matrix adjust.	83/146(57%)	98/146(67%)	31/146(21%)	+1
Features	:					
Query	532	DRPANRGRYGSFNNDDRPFERNQDRDR DRPA RGRYG+FNNDDR +RN +DR	~ ~	SRDGDRYNN SRDG DRYNN		OR 690 -R
Sbjct	183	DRPAARGRYGNFNNDDRYNDRNH-QDR				
Query	691	ERTHYNPNQQSERPsggmtglgggsgg HYN ++RPS	sgglgvgggss		RLQLKPRTIAA RLÕLKPRT+AA	
Sbjct	242	GERHYNNDRPSSVAPLG			~	
Query	871	INAVAETKQSASIFGNAKPREEKLKE IN +AETKO+A+IFGNAKPREEKLK+	948			
Sbjct	279	INGLAETKQAAAIFGNAKPREEKLKD	304			

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X5 [Nasonia vitripennis]

Sequence ID: ref|XP_008217447.1| Length: 290 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
134 bits	(337)	2e-32() Compositional matrix adjust.	64/111(58%)	88/111(79%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY+ R + G R+SK LPTEPP				
Sbjct	1	MAGRGGYDDLRD-YSGSRSSKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDRETD+FKGFCYVEFE L +L+ A++				
Sbjct	60	KDRETDRFKGFCYVEFEDLSDLKNAIKL				

Range 2: 239 to 284

Score		Expect Method	Identities	Positives	Gaps	Frame
53.9 bi	its(128)	1e-04() Compositional matrix adjust.	25/46(54%)	33/46(71%)	0/46(0%)	+1
Featur	es:					
Query	811	AIDDNERPRLQLKPRTIAAPINAVAETKQ A D R RL L PRT+ P+NA+AET			8	
Sbjct	239	APDTTGRKRLVLAPRTVQDPVNALAETAT			4	

PREDICTED: eukaryotic translation initiation factor 4H-like [Solenopsis invicta]

Sequence ID: ref|XP_011162080.1| Length: 268 Number of Matches: 2

Range 1: 1 to 108

Score		Expect	Method	Identities	Positives	Gaps	Frame
134 bits	(336)	2e-32()	Compositional matrix adjust.	64/111(58%)	85/111(76%)	3/111(2%)	+1
Features	s:						
Query	7		GYEHARSGFGGDRASKQLPTEPPI GY+ +R + R+ K LPTEPP-				
Sbjct	1		GYDDSRD-YPTHRSRKPLPTEPP				
Query	187		DQFKGFCYVEFETLDNLERALECI D+FKGFCYVEFE L +LE ALE I		PLRIDIADRRK ++ID+A+ ++		
Sbjct	60		DTFRGFCYVEFE L TLE ALE I DKFKGFCYVEFEDLTDLEAALEMI				

Range 2: 222 to 264

Score		Expect Method	Identities	Positives	Gaps	Frame
61.2 bits	s(147)	4e-07() Compositional matrix adjust.	27/43(63%)	35/43(81%)	0/43(0%)	+1
Features	s:					
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQSA D R RL+LKPRTI P+NA+AE+ ++-				
Sbjct	222	DTTGRKRLELKPRTIKEPVNAIAESSKT:				

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Vollenhovia emeryi]

Sequence ID: ref|XP_011866332.1| Length: 252 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
133 bits	(335)	2e-32() Compositional matrix adjust.	64/111(58%)	85/111(76%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY+ +R + R+ K LPTEPP				
Sbjct	1	MAGRGGYDDSRD-YSTHRSRKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDR+TD+FKGFCYVEFE L +LE ALE		PLRIDIADRRI ++ID+A+		
Sbjct	60	KDRDTDKFKGFCYVEFEDLADLEAALEM				

Range 2: 207 to 249

Score Expect Method	Identities	Positives	Gaps	Frame	_
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60.5 bits(145) 6e-07() Compositional matrix adjust. 26/43(60%) 35/43(81%) 0/43(0%) +1

Features:

Query 817 DDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKLK 945 D R RL+LKPRT+ P+NA+AE+ +++SI+G AKPREEKLK Sbjct 207 DTTGRKRLELKPRTVKEPVNAIAESSKTSSIYGGAKPREEKLK 249

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Vollenhovia emeryi]

Sequence ID: ref|XP_011866331.1| Length: 270 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
133 bits	(335)	3e-32() Compositional matrix adjust.	64/111(58%)	85/111(76%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY+ +R + R+ K LPTEPP				
Sbjct	1	MAGRGGYDDSRD-YSTHRSRKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDR+TD+FKGFCYVEFE L +LE ALE		PLRIDIADRRI ++ ID+A+ ++		
Sbjct	60	KDRDTDKFKGFCYVEFEDLADLEAALEM				

Range 2: 225 to 267

Score		Expect	Method	Identities	Positives	Gaps	Frame
60.1 bits	s(144)	9e-07()	Compositional matrix adjust.	26/43(60%)	35/43(81%)	0/43(0%)	+1
Feature	s:						
Query	817		PRLQLKPRTIAAPINAVAETKQSA RL+LKPRT+ P+NA+AE+ +++				
Sbjct	225		KLTLKPKIT PTNATAET TTT KRLELKPRTVKEPVNAIAESSKTS				

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Nasonia vitripennis]

Sequence ID: ref[XP_008217446.1] Length: 297 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
134 bits	(337)	3e-32() Compositional matrix adjust.	64/111(58%)	88/111(79%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY+ R + G R+SK LPTEPP				
Sbjct	1	MAGRGGYDDLRD-YSGSRSSKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDRETD+FKGFCYVEFE L +L+ A++				
Sbjct	60	KDRETDFFKGFCYVEFEDLSDLKNAIKL	_			

Range 2: 246 to 291

Score		Expect Method	Identities	Positives	Gaps	Frame
53.9 bit	s(128)	1e-04() Compositional matrix adjust.	25/46(54%)	33/46(71%)	0/46(0%)	+1
Feature	s:					
Query	811	AIDDNERPRLQLKPRTIAAPINAVAETKO A D R RL L PRT+ P+NA+AET			8	
Sbjct	246	APDTTGRKRLVLAPRTVQDPVNALAETA:			1	

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Acromyrmex echinatior]

Sequence ID: ref|XP_011058247.1| Length: 274 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
133 bits	(334)	3e-32() Compositional matrix adjust.	64/111(58%)	85/111(76%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY+ +R + R+ K LPTEPP				
Sbjct	1	MAGRGGYDDSRD-YPTHRSRKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDR+TD+FKGFCYVEFE L +LE ALE		PLRIDIADRRI ++ID+A+ +-		

Range 2: 227 to 269

Score		Expect	Method	Identities	Positives	Gaps	Frame
57.8 bits(138)		6e-06()	Compositional matrix adjust.	24/43(56%)	35/43(81%)	0/43(0%)	+1
Features	S :						
Query	817		RLQLKPRTIAAPINAVAETKQSAS RL+L+PRT+ P+N++AE+ +++S				
Sbjct	227		RLELQPRTVKEPVNSIAESSKTSS				

PREDICTED: eukaryotic translation initiation factor 4H-like [Atta cephalotes] Sequence ID: **ref|XP_012061221.1**| Length: 274 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
133 bits	(334)	4e-32() Compositional matrix adjust.	64/111(58%)	85/111(76%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP				
Sbjct	1	MAGRGGY+ +R + R+ K LPTEPP MAGRGGYDDSRD-YPTHRSRKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDR+TD+FKGFCYVEFE L +LE ALE		PLRIDIADRRI ++ID+A+		
Sbjct	60	KDRDTDKFKGFCYVEFEDLADLEAALEM			-·	

Range 2: 227 to 269

Score		Expect Method		Identities	Positives	Gaps	Frame
57.8 bits	s(138)	6e-06() Composition	onal matrix adjust.	24/43(56%)	35/43(81%)	0/43(0%)	+1
Features	s:						
Query	817	DDNERPRLQLKPRT	IAAPINAVAETKQSA + P+N++AE+ +++				
Sbjct	227	DTTGRKRLELQPRT					

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Acromyrmex echinatior]

Sequence ID: ref|XP_011058248.1| Length: 268 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
132 bits	(333)	4e-32() Compositional matrix adjust.	64/111(58%)	85/111(76%)	3/111(2%)	+1
Features	S :					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPPI MAGRGGY+ +R + R+ K LPTEPP-				
Sbjct	1	MAGRGGYDDSRD-YPTHRSRKPLPTEPPY				
Query	187	KDRETDQFKGFCYVEFETLDNLERALECI KDR+TD+FKGFCYVEFE L +LE ALE I		PLRIDIADRRI ++ + + + + + + + + + + + + + + + + + +		
Sbjct	60	KDRDTDKFKGFCYVEFEDLADLEAALEMI				

Range 2: 221 to 263

Score		Expect Method	Identities	Positives	Gaps	Frame
57.8 bits	s(138)	6e-06() Compositional matrix adjust.	24/43(56%)	35/43(81%)	0/43(0%)	+1
Features	S :					
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQSA D R RL+L+PRT+ P+N++AE+ +++				
Sbjct	221	DTTGRKRLELQPRTVKEPVNSIAESSKTS				

PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Polistes dominula]

Sequence ID: ref|XP_015174166.1| Length: 259 Number of Matches: 2

Range 1: 1 to 109

Score	Expect	Method	identities	Positives	Gaps	Frame
132 bits(332)	6e-32()	Compositional matrix adjust.	65/111(59%)	82/111(73%)	2/111(1%)	+1

Features: MAGRGGYEHARSGFGGDRASKQLPTEPPFIAFVGNLPQGLVQGDVIKIFQDFEVKYVRLV MAGRGGY R R+ K LPTEPP+ AFVGNLP G+VQGDV KIF+ VK VRLV MAGRGGYVDPRDYGSSYRSRKPLPTEPPYTAFVGNLPNGIVQGDVDKIFKQLNVKGVRLV Query 7 186 Sbjct 1 60 KDRETDQFKGFCYVEFETLDNLERALECDGRIKLDDLSAPLRIDIADRRKN KDRETD+FKGFCYVEFE L +LE AL+ DG + ++ + ++ID+A+ ++N KDRETDRFKGFCYVEFEDLSDLEAALDLDGSVDVE--GSIIKIDVAEGKRN 339 Query 187

Range 2: 216 to 254

Sbjct 61

Score		Expect	Method	Identities	Positives	Gaps	Frame
56.2 bits	s(134)	1e-05()	Compositional matrix adjust.	25/39(64%)	32/39(82%)	0/39(0%)	+1
Features	s:						
Query	829	~	KPRTIAAPINAVAETKQSASIFG PR+I P+NA+AE+ +S+SI+G		945		
Sbjct	216		APRSIPDPVNAIAESSKSSSIYG		254		

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X2 [Ceratosolen solmsi marchali] Sequence ID: ref|XP_011494499.1| Length: 297 Number of Matches: 2

Range 1: 1 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame
132 bits	(333)	8e-32() Compositional matrix adjust.	63/111(57%)	85/111(76%)	2/111(1%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRG Y R GG R+SK LPTEPP				
Sbjct	1	MAGRGDYNDLRDYSGGSRSSKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDRETD+FKGFCYVEF+ L +L+ A++		APLRIDIADRRI		
Sbjct	61	KDRETDRFKGFCYVEFQDLSDLKNAIKL				

Range 2: 247 to 292

Score		Expect	Method	Identities	Positives	Gaps	Frame
50.1 bits	s(118)	0.002()	Compositional matrix adjust.	25/46(54%)	31/46(67%)	0/46(0%)	+1
Features	s:						
Query	811		RPRLQLKPRTIAAPINAVAETKQ R RL L PRTI P+N++AET	SASIFGNAKPR SI+G AKPR		. 8	
Sbjct	247		RKRLVLTPRTIQDPVNSLAETTI			2	

PREDICTED: eukaryotic translation initiation factor 4H isoform X1 [Polistes dominula]

Sequence ID: ref|XP_015174165.1| Length: 277 Number of Matches: 2

Range 1: 1 to 109

Score		Expect	Method	Identities	Positives	Gaps	Frame
132 bits	(332)	9e-32()	Compositional matrix adjust.	65/111(59%)	82/111(73%)	2/111(1%)	+1
Features	S :						
Query	7	MAGRG MAGRG	GYEHARSGFGGDRASKQLPTEPPI				
Sbjct	1		GY R R+ K LPTEPP- GYVDPRDYGSSYRSRKPLPTEPPY				
Query	187		DQFKGFCYVEFETLDNLERALECI D+FKGFCYVEFE L +LE AL+ I		PLRIDIADRRK ++ID+A+ ++		
Sbjct	61		DRFKGFCYVEFEDLSDLEAALDLI	_			

Range 2: 234 to 272

Score		Expect	Method	Identities	Positives	Gaps	Frame
56.6 bits	s(135)	1e-05()	Compositional matrix adjust.	25/39(64%)	32/39(82%)	0/39(0%)	+1
Features	S :						
Query	829		KPRTIAAPINAVAETKQSASIFGI PR+I P+NA+AE+ +S+SI+G		945		
Sbjct	234		APRSIPDPVNAIAESSKSSSIYG		272		

Score		Expect Method	Identities	Positives	Gaps	Frame
132 bits	(332)	9e-32() Compositional matrix adjust.	68/113(60%)	87/113(76%)	4/113(3%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTE MAGRGGYE +R +G G + K LPTE				
Sbjct	1	MAGRGGYEDSRDYTGGGHHGSRKPLPTE				
Query	181	LVKDRETDQFKGFCYVEFETLDNLERAL LVKDRETD FKGFCYVEFE L +LE AL				
Sbjct	61	LVKDRETDVFKGFCYVEFEELSDLESAL			· · · - ·	

Range 2: 241 to 278

Score		Expect	Method	Identities	Positives	Gaps	Frame
50.8 bits	s(120)	0.001()	Compositional matrix adjust.	22/38(58%)	30/38(78%)	0/38(0%)	+1
Features	s:						
Query	817		PRLQLKPRTIAAPINAVAETKQSAS RL LKPRT+ P+NA+AE+ +S+S		930		
Sbjct	241		RLVLKPRTVPDPVNAIAESSKSS		278		

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X3 [Pogonomyrmex barbatus]

Sequence ID: **ref|XP_011640375.1**| Length: 274 Number of Matches: 2 Range 1: 1 to 108

	Score		Expect	Method	Identities	Positives	Gaps	Fra	me
	132 bits(3	331)	1e-31()	Compositional matrix adjust.	63/111(57%)	84/111(75%)	3/111(2%)	+1	
	Features:								
(Query	7		GYEHARSGFGGDRASKQLPTEPPF Y+ +R + R+ K LPTEPP+					186
	Sbjct	1		AYDDSRD-YPTHRSRKPLPTEPPY					59
(Query	187		DQFKGFCYVEFETLDNLERALECI D+FKGFCYVEFE L +LE ALE I		PLRIDIADRRK ++TD+A+ ++			
	Sbjct	60		DKFKGFCYVEFEDLSDLEAALEMI					

Range 2: 228 to 274

Score		Expect	Method	Identities	Positives	Gaps	Frame
60.1 bits	(144)	9e-07()	Compositional matrix adjust.	26/47(55%)	37/47(78%)	0/47(0%)	+1
Features	s:						
Query	817		PRLQLKPRTIAAPINAVAETKQSAS RL+LKPRT+ P+N++AE+ +++5			57	
Sbjct	228		RLELKPRTVKEPVNSMAESSKTS	_		74	

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Ceratosolen solmsi marchali] Sequence ID: ref|XP_011494498.1| Length: 304 Number of Matches: 2

Range 1: 1 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame	
132 bits(3	333)	1e-31() Compositional matrix adjust.	63/111(57%)	85/111(76%)	2/111(1%)	+1	•
Features	:						
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRG Y R GG R+SK LPTEPP					5
Sbjct	1	MAGRGDYNDLRDYSGGSRSSKPLPTEPP					
Query	187	KDRETDQFKGFCYVEFETLDNLERALECT KDRETD+FKGFCYVEF+ L +L+ A++					
Sbjct	61	KDRETDRFKGFCYVEFQDLSDLKNAIKL					

Range 2: 254 to 299

Score	Expect	Method	Identities	Positives	Gaps	Frame
50.4 bits(119)	0.002()	Compositional matrix adjust.	25/46(54%)	31/46(67%)	0/46(0%)	+1
Features:						

Query 811 AIDDNERPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKLKE 948 A D R RL L PRTI P+N++AET SI+G AKPREEK+ + Sbjct 254 APDMKGRKRLVLTPRTIQDPVNSLAETTIRNSIYGGAKPREEKITD 299

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X1 [Athalia rosae]

Sequence ID: ref|XP_012251395.1| Length: 289 Number of Matches: 2

Range 1: 1 to 111

Score		Expect Method	Identities	Positives	Gaps	Frame
132 bits	(332)	1e-31() Compositional matrix adjust.	68/113(60%)	87/113(76%)	4/113(3%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTE MAGRGGYE +R +G G + K LPTE				
Sbjct	1	MAGRGGYEDSRDYTGGGHHGSRKPLPTE				
Query	181	LVKDRETDQFKGFCYVEFETLDNLERAI LVKDRETD FKGFCYVEFE L +LE AI				
Sbjct	61	LVKDRETDVFKGFCYVEFEELSDLESAI			· · - ·	

Range 2: 242 to 279

Score		Expect	Method	Identities	Positives	Gaps	Frame
50.8 bits	s(120)	0.001()	Compositional matrix adjust.	22/38(58%)	30/38(78%)	0/38(0%)	+1
Feature	s:						
Query	817		PRLQLKPRTIAAPINAVAETKQSAS RL LKPRT+ P+NA+AE+ +S+S		930		
Sbjct	242		RLVLKPRTVPDPVNAIAESSKSS		279		

PREDICTED: eukaryotic translation initiation factor 4H-like isoform X4 [Pogonomyrmex barbatus]

Sequence ID: ref|XP_011640376.1| Length: 268 Number of Matches: 2

Range 1: 1 to 108

Score		Expect Method	Identities	Positives	Gaps	Frame
131 bits	(330)	1e-31() Compositional matrix adjust.	63/111(57%)	84/111(75%)	3/111(2%)	+1
Features	s:					
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRG Y+ +R + R+ K LPTEPP				
Sbjct	1	MAGRGAYDDSRD-YPTHRSRKPLPTEPP				
Query	187	KDRETDQFKGFCYVEFETLDNLERALECI KDR+TD+FKGFCYVEFE L +LE ALE I		PLRIDIADRRI ++ID+A+		
Sbjct	60	KDRDTDKFKGFCYVEFEDLSDLEAALEM				

Range 2: 222 to 268

Score		Expect Method	Identities	Positives	Gaps	Frame
60.1 bits	s(144)	1e-06() Compositional matrix adjust.	26/47(55%)	37/47(78%)	0/47(0%)	+1
Features	S :					
Query	817	DDNERPRLQLKPRTIAAPINAVAETKQSA D R RL+LKPRT+ P+N++AE+ +++			57	
Sbjct	222	DTTGRKRLELKPRTVKEPVNSMAESSKTS			68	

PREDICTED: eukaryotic translation initiation factor 4H isoform X2 [Polistes canadensis]

Sequence ID: ref|XP_014611152.1| Length: 258 Number of Matches: 2

Range 1: 1 to 109

Score		Expect Method	Identities	Positives	Gaps	Frame		
130 bits	(328)	2e-31() Compositional matrix adjust.	65/111(59%)	82/111(73%)	2/111(1%)	+1		
Features:								
Query	7	MAGRGGYEHARSGFGGDRASKQLPTEPP MAGRGGY R R+ K LPTEPP						
Sbjct	1	MAGRGGY R R+ K LPTEPP MAGRGGYVDPRDYGVNYRSRKPLPTEPP						
Query	187	KDRETDQFKGFCYVEFETLDNLERALEC KDRETD+FKGFCYVEFE L +LE AL+						
Sbjct	61	KDRETDRFKGFCYVEFEDLSDLEAALDL						

Score		Expect Method	Identities	Positives	Gaps	Frame			
56.6 bits(135)		1e-05() Compositional matrix adjust.	25/39(64%)	32/39(82%)	0/39(0%)	+1			
Features:									
Query	829	RPRLQLKPRTIAAPINAVAETKQSASIFGNAKPREEKLK R RL L PR+I P+NA+AE+ +S+SI+G AKPREEKLK		945					
Sbjct	215	RKRLVLAPRSIPDPVNAIAESSKSSSIY		253					