PSI blast Iteration 9 for member of a conserved secreted protein of insects

gi|208657775|gb|ACI30184.1| hypothetical c

Query ID
    gi|208657775|gb|ACI30184.1| hypothetical conserved secreted protein [Anopheles darlingi]
Molecule type
    amino acid
Query Length
    126
Database Name
    nr
Description
    All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects See details
Program
    BLASTP 2.2.22+ Citation

Blast search databases information

Database Description Posted Date

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - composition-based statistics starting in round 2

Alejandro A. Schäffer, L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

- No new sequences were found above the 0.001 threshold

```
Sequences with    pattern at position  and  E-value BETTER than threshold

                                                                   Score    E
Sequences producing significant alignments:                       (Bits)  Value

● ☑  ref|XP_001866470.1|  conserved hypothetical protein [Culex qui...  134   2e-30 G
● ☑  gb|AAY85037.1|  IP05651p [Drosophila melanogaster]                 127   4e-28
● ☑  ref|XP_001660923.1|  hypothetical protein AaeL_AAEL010558 [Aed...  123   5e-27 UG
● ☑  ref|XP_001866469.1|  conserved hypothetical protein [Culex qui...  122   1e-26 UG
● ☑  gb|ACU30989.1|  secreted protein member of chemokine-like  fac...  121   2e-26
● ☑  gb|ACI30203.1|  hypothetical conserved protein [Anopheles darl...  121   2e-26
● ☑  ref|XP_309156.3|  AGAP000964-PA [Anopheles gambiae str. PEST] ...  121   2e-26 UG
● ☑  gb|ACI30184.1|  hypothetical conserved secreted protein [Anoph...  121   3e-26
● ☑  ref|XP_002040111.1|  GM16029 [Drosophila sechellia] >gb|EDW569...  120   4e-26 G
● ☑  ref|NP_726341.1|  CG30184 [Drosophila melanogaster] >gb|AAM682...  120   5e-26 UG
● ☑  ref|XP_002082812.1|  GD11778 [Drosophila simulans] >gb|EDX0839...  119   9e-26 G
● ☑  ref|XP_001978654.1|  GG17559 [Drosophila erecta] >gb|EDV47581....  117   5e-25 G
● ☑  ref|XP_002055767.1|  GJ19540 [Drosophila virilis] >gb|EDW65968...  116   6e-25 G
● ☑  ref|XP_001354423.1|  GA13737 [Drosophila pseudoobscura pseudoo...  116   6e-25 G
● ☑  ref|NP_608423.1|  CG15449 [Drosophila melanogaster] >ref|XP_00...  116   6e-25 UG
● ☑  ref|XP_002092643.1|  GE14306 [Drosophila yakuba] >gb|EDW92355....  116   8e-25 G
● ☑  ref|XP_002071641.1|  GK10090 [Drosophila willistoni] >gb|EDW82...  116   9e-25 G
● ☑  ref|XP_001991178.1|  GH12523 [Drosophila grimshawi] >gb|EDV998...  116   1e-24 G
● ☑  ref|XP_002010101.1|  GI14877 [Drosophila mojavensis] >gb|EDW07...  116   1e-24 G
● ☑  ref|XP_001660924.1|  hypothetical protein AaeL_AAEL010564 [Aed...  114   3e-24 UG
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● ☑	ref|XP_975314.1|	PREDICTED: similar to CG15449 CG15449-PA [Tr...	114	4e-24	UG
● ☑	ref|XP_001976431.1|	GG22868 [Drosophila erecta] >gb|EDV56831....	114	4e-24	G
● ☑	ref|XP_309155.3|	AGAP000963-PA [Anopheles gambiae str. PEST] ...	113	5e-24	UG
● ☑	ref|NP_001091800.1|	hypothetical protein LOC778505 [Bombyx mo...	110	5e-23	UG
● ☑	ref|XP_001361089.1|	GA15708 [Drosophila pseudoobscura pseudoo...	106	6e-22	G
● ☑	ref|XP_001966751.1|	GF19114 [Drosophila ananassae] >gb|EDV337...	106	7e-22	G
● ☑	ref|XP_002018237.1|	GL16872 [Drosophila persimilis] >gb|EDW36...	105	2e-21	G
● ☑	ref|XP_002055067.1|	GJ19171 [Drosophila virilis] >gb|EDW65268...	104	2e-21	G
● ☑	ref|XP_002039595.1|	GM22643 [Drosophila sechellia] >gb|EDW563...	104	4e-21	G
● ☑	ref|NP_572518.1|	CG7267 [Drosophila melanogaster] >ref|XP_002...	103	5e-21	UG
● ☑	ref|XP_001606621.1|	PREDICTED: hypothetical protein [Nasonia ...	102	1e-20	UG
● ☑	gb|ACN69164.1|	hypothetical conserved secreted protein [Stomo...	101	2e-20	
● ☑	ref|XP_001959837.1|	GF13066 [Drosophila ananassae] >gb|EDV366...	100	6e-20	G
● ☑	ref|XP_001661199.1|	hypothetical protein AaeL_AAEL010956 [Aed...	98.7	2e-19	UG
● ☑	ref|XP_001845632.1|	conserved hypothetical protein [Culex qui...	97.5	4e-19	UG
● ☑	ref|XP_002423901.1|	conserved hypothetical protein [Pediculus...	95.6	1e-18	G
● ☑	ref|XP_001119879.1|	PREDICTED: similar to CG15449-PA [Apis me...	93.3	8e-18	UG
● ☑	ref|XP_001655679.1|	hypothetical protein AaeL_AAEL002578 [Aed...	92.1	1e-17	UG
● ☑	ref|XP_001995529.1|	GH17713 [Drosophila grimshawi] >gb|EDV951...	92.1	2e-17	G
● ☑	ref|XP_002009616.1|	GI15456 [Drosophila mojavensis] >gb|EDW06...	91.8	2e-17	G
● ☑	ref|XP_001949085.1|	PREDICTED: similar to conserved hypotheti...	91.4	3e-17	UG
● ☑	dbj|BAH71208.1|	ACYPI008397 [Acyrthosiphon pisum]	90.6	4e-17	
● ☑	ref|XP_002047342.1|	GJ11981 [Drosophila virilis] >gb|EDW69684...	90.6	4e-17	G
● ☑	gb|ABV44719.1|	ryanodine receptor-like protein [Phlebotomus p...	90.2	6e-17	
● ☑	ref|XP_001984136.1|	GH16269 [Drosophila grimshawi] >gb|EDV964...	90.2	7e-17	G
● ☑	ref|XP_002005498.1|	GI20498 [Drosophila mojavensis] >gb|EDW09...	89.8	8e-17	G
● ☑	ref|XP_311473.3|	AGAP010471-PA [Anopheles gambiae str. PEST] ...	87.9	3e-16	UG
● ☑	ref|XP_002008949.1|	GI13768 [Drosophila mojavensis] >gb|EDW19...	87.5	4e-16	G
● ☑	ref|XP_002050796.1|	GJ22349 [Drosophila virilis] >gb|EDW61989...	87.5	4e-16	G
● ☑	ref|XP_002009617.1|	GI15457 [Drosophila mojavensis] >gb|EDW06...	87.5	4e-16	G
● ☑	ref|XP_001973440.1|	GG16083 [Drosophila erecta] >gb|EDV52466....	87.5	4e-16	G
● ☑	ref|XP_002009021.1|	GI11493 [Drosophila mojavensis] >gb|EDW19...	87.5	4e-16	G
● ☑	ref|XP_001956640.1|	GF25311 [Drosophila ananassae] >gb|EDV394...	87.1	5e-16	G
● ☑	ref|XP_002048071.1|	GJ13758 [Drosophila virilis] >gb|EDW70413...	87.1	5e-16	G
● ☑	ref|NP_649184.1|	CG6981, isoform A [Drosophila melanogaster] ...	87.1	5e-16	UG
● ☑	ref|XP_001984238.1|	GH15117 [Drosophila grimshawi] >gb|EDV965...	87.1	5e-16	G
● ☑	ref|XP_002061902.1|	GK16939 [Drosophila willistoni] >gb|EDW72...	87.1	5e-16	G
● ☑	ref|XP_002086307.1|	GE23065 [Drosophila yakuba] >gb|EDW99708....	87.1	6e-16	G
● ☑	ref|XP_002040612.1|	GM22258 [Drosophila sechellia] >gb|EDW441...	87.1	6e-16	G
● ☑	emb|CBE66942.1|	CG6981-PA [Drosophila ananassae] >emb|CBE6694...	86.8	6e-16	
● ☑	ref|XP_001353299.1|	GA20002 [Drosophila pseudoobscura pseudoo...	86.8	7e-16	G

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    ● ☑  ref|XP_976275.1|   PREDICTED: similar to conserved hypothetical...   86.8   7e-16 U G
    ● ☑  ref|XP_002047884.1|  GJ13688 [Drosophila virilis] >gb|EDW70226...   86.4   8e-16   G
    ● ☑  ref|XP_002074415.1|  GK10529 [Drosophila willistoni] >gb|EDW85...   86.0   1e-15   G
    ● ☑  emb|CBE67045.1|  CG6981-PA [Drosophila atripex]                      86.0   1e-15
    ● ☑  ref|XP_001948670.1|  PREDICTED: similar to CG13566 CG13566-PA,...   86.0   1e-15   G
    ● ☑  ref|XP_002030493.1|  GM25471 [Drosophila sechellia] >gb|EDW414...   86.0   1e-15   G
    ● ☑  ref|XP_002084862.1|  GD14494 [Drosophila simulans] >gb|EDX1044...   85.6   1e-15   G
    ● ☑  ref|XP_002074859.1|  GK19222 [Drosophila willistoni] >gb|EDW85...   85.6   2e-15   G
    ● ☑  ref|XP_002043968.1|  GM13685 [Drosophila sechellia] >gb|EDW512...   85.6   2e-15   G
    ● ☑  ref|XP_001354994.2|  GA20224 [Drosophila pseudoobscura pseudoo...   85.2   2e-15   G
    ● ☑  ref|XP_001984986.1|  GH14752 [Drosophila grimshawi] >gb|EDV973...   85.2   2e-15   G
    ● ☑  ref|XP_002075211.1|  GK16752 [Drosophila willistoni] >gb|EDW86...   84.8   2e-15   G
    ● ☑  ref|XP_002022417.1|  GL13023 [Drosophila persimilis] >gb|EDW26...   84.8   2e-15   G
    ● ☑  ref|XP_001986174.1|  GH21210 [Drosophila grimshawi] >gb|EDW010...   84.8   2e-15   G
    ● ☑  ref|XP_001972737.1|  GG15688 [Drosophila erecta] >gb|EDV51763....   84.4   3e-15   G
    ● ☑  ref|XP_001956408.1|  GF24609 [Drosophila ananassae] >gb|EDV392...   84.4   3e-15   G
    ● ☑  ref|XP_001843280.1|  conserved hypothetical protein [Culex qui...   84.1   4e-15 U G
    ● ☑  ref|XP_002094795.1|  GE22019 [Drosophila yakuba] >gb|EDW94507....   84.1   5e-15   G
    ● ☑  ref|XP_002027022.1|  GL21019 [Drosophila persimilis] >gb|EDW34...   83.7   5e-15   G
    ● ☑  ref|XP_002007920.1|  GI13205 [Drosophila mojavensis] >gb|EDW18...   83.7   6e-15   G
    ● ☑  ref|NP_729982.1|   CG9628, isoform B [Drosophila melanogaster] ...   83.7   6e-15 U G
    ● ☑  ref|NP_648710.1|   CG9628, isoform A [Drosophila melanogaster] ...   82.9   1e-14   G
    ● ☑  gb|EFA08060.1|   hypothetical protein TcasGA2_TC005656 [Triboli...   82.9   1e-14
    ● ☑  ref|XP_001353700.2|  GA21923 [Drosophila pseudoobscura pseudoo...   82.1   2e-14   G
    ● ☑  ref|NP_001156315.1|  hypothetical protein LOC100169413 [Acyrth...   82.1   2e-14 U G
    ● ☑  ref|XP_001977381.1|  GG19007 [Drosophila erecta] >gb|EDV46308....   81.0   3e-14   G
    ● ☑  ref|XP_002101085.1|  GE17420 [Drosophila yakuba] >gb|EDX02193....   81.0   4e-14   G
    ● ☑  ref|XP_966339.1|   PREDICTED: similar to ryanodine receptor-lik...   80.6   5e-14 U G
    ● ☑  ref|XP_002430041.1|  conserved hypothetical protein [Pediculus...   78.7   2e-13   G
    ● ☑  ref|XP_001357214.2|  GA12689 [Drosophila pseudoobscura pseudoo...   77.9   3e-13   G
    ● ☑  gb|ACN94686.1|   GA12689 [Drosophila miranda]                        77.9   3e-13
    ● ☑  ref|XP_002014263.1|  GL19107 [Drosophila persimilis] >gb|EDW28...   77.9   3e-13   G
    ● ☑  ref|XP_002427111.1|  conserved hypothetical protein [Pediculus...   72.9   1e-11   G
    ● ☑  ref|XP_002427110.1|  conserved hypothetical protein [Pediculus...   69.0   1e-10   G
NEW   ☑  ref|XP_002038007.1|  GM17988 [Drosophila sechellia] >gb|EDW544...   62.9   1e-08   G
NEW   ☑  ref|XP_001968858.1|  GG24274 [Drosophila erecta] >gb|EDV57917....   61.3   3e-08   G
NEW   ☑  ref|XP_002089166.1|  GE18971 [Drosophila yakuba] >gb|EDW88878....   61.3   3e-08   G
NEW   ☑  ref|NP_608969.1|   CG14000 [Drosophila melanogaster] >gb|AAM110...   61.3   3e-08 U G
    ● ☑  gb|EFA08059.1|   hypothetical protein TcasGA2_TC005655 [Triboli...   60.2   7e-08
NEW   ☑  ref|XP_001962403.1|  GF15443 [Drosophila ananassae] >gb|EDV316...   56.7   9e-07   G
    ● ☑  ref|NP_572519.1|   CG15366 [Drosophila melanogaster] >gb|AAF464...   54.0   5e-06 U G
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 ● ☑   ref|XP_002429371.1|  Cylicin-1, putative [Pediculus humanus co...  53.6    7e-06 G


Sequences with E-value WORSE than threshold

   ☐   ref|NP_611858.1|  CG13566 [Drosophila melanogaster] >gb|AAF471...  42.1    0.017 UG
   ☐   ref|XP_002040187.1|  GM15486 [Drosophila sechellia] >gb|EDW570...  41.7    0.024 G
   ☐   ref|XP_001902958.1|  hypothetical protein Bm1_57500 [Brugia ma...  41.3    0.031 G
   ☐   ref|XP_001688606.1|  AGAP004947-PA [Anopheles gambiae str. PES...  40.9    0.043 G
   ☐   ref|XP_001976508.1|  GG19973 [Drosophila erecta] >gb|EDV56908....  40.5    0.051 G
   ☐   ref|XP_002092725.1|  GE11506 [Drosophila yakuba] >gb|EDW92437....  40.1    0.080 G
   ☐   ref|YP_003122623.1|  hypothetical protein Cpin_2944 [Chitinoph...  39.4    0.13  G
   ☐   ref|XP_001959449.1|  GF12048 [Drosophila ananassae] >gb|EDV362...  38.2    0.31  G
   ☐   ref|XP_002049979.1|  GJ20448 [Drosophila virilis] >gb|EDW61172...  37.4    0.53  G
   ☐   ref|XP_002019797.1|  GL12591 [Drosophila persimilis] >gb|EDW38...  37.1    0.61  G
   ☐   ref|XP_002063776.1|  GK19098 [Drosophila willistoni] >gb|EDW74...  37.1    0.68  G
   ☐   ref|XP_001359954.2|  GA12902 [Drosophila pseudoobscura pseudoo...  36.7    0.78  G
```

Alignments

```
>☐ ref|XP_001866470.1| G conserved hypothetical protein [Culex quinquefasciatus]
 gb|EDS43424.1| G conserved hypothetical protein [Culex quinquefasciatus]
Length=185

 GENE ID: 6049759 CpipJ_CPIJ016150 | hypothetical protein
[Culex quinquefasciatus]

 Score =  134 bits (339),  Expect = 2e-30, Method: Composition-based stats.
 Identities = 63/121 (52%), Positives = 88/121 (72%), Gaps = 0/121 (0%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNK  65
            +SI+KFLEL L I C VLHY S  + D  T  L+ GTF GY VIL  +  GYL+   +++
Sbjct  63   MSIIKFLELCLTIACTVLHYYSFDDGDLVTGFLSTGTFCGYIVILTTVMVGYLMKAHVHR  122

Query  66   KLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            +L+LF+SL+GCA+F+ SGV I++ WE+A+ T T+ +AITK S+A+ NGV+F  D IFTFR
Sbjct  123  RLNLFYSLLGCALFLTSGVFIIEAWEHAFRTRTRDLAITKGSIAIINGVIFLMDTIFTFR  182

Query  126  D  126
            +
Sbjct  183  E  183


>☐ gb|AAY85037.1|  IP05651p [Drosophila melanogaster]
Length=172

 Score =  127 bits (320),  Expect = 4e-28, Method: Composition-based stats.
 Identities = 63/123 (51%), Positives = 94/123 (76%), Gaps = 0/123 (0%)

Query  4    SRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
             RL++VKFLEL  A+ C+VLH+ S  +RD  T  L  GTF GY +++I +FAG L+  P+
Sbjct  49   GRLNVVKFLELGFAVACLVLHFYSFNDRDIMTSFLATGTFTGYIIVIGVFAGVLMRAPI  108

Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFT  123
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            +K++D+FFS++GC +F+ASGV I++ WE ++ T T+ +A+ K+SL++ NGVLF FDA+FT
Sbjct  109  HKRIDIFFSVLGCTLFVASGVFIIEAWEFSFRTRTRDLALIKASLSIVNGVLFGFDAVFT  168

Query  124  FRD  126
            FRD
Sbjct  169  FRD  171


>☐ ref|XP_001660923.1| UG hypothetical protein AaeL_AAEL010558 [Aedes aegypti]
 gb|EAT37454.1| G conserved hypothetical protein [Aedes aegypti]
Length=126

 GENE ID: 5573532 AaeL_AAEL010558 | hypothetical protein [Aedes aegypti]
(10 or fewer PubMed links)

 Score =  123 bits (310),  Expect = 5e-27, Method: Composition-based stats.
 Identities = 90/126 (71%), Positives = 112/126 (88%), Gaps = 0/126 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MAVSRLS++KFLELAL I+CVVLHYKSLGE D+ T LL AGTFVGYS+ILI LFAG+LLG
Sbjct  1    MAVSRLSMLKFLELALTISCVVLHYKSLGETDEMTVLLVAGTFVGYSIILIGLFAGHLLG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120
            NP+NKK+DLFFSL+GCAMFIASGVL+L+ WE+ + T+ +++AI+K +LA+ NG +FF D+
Sbjct  61   NPINKKIDLFFSLLGCAMFIASGVLVLQAWESGFKTERRRLAISKGALAIINGAVFFIDS  120

Query  121  IFTFRD  126
            IFTFRD
Sbjct  121  IFTFRD  126


>☐ ref|XP_001866469.1| UG conserved hypothetical protein [Culex quinquefasciatus]
 gb|EDS43423.1| G conserved hypothetical protein [Culex quinquefasciatus]
Length=126

 GENE ID: 6049758 CpipJ_CPIJ016149 | hypothetical protein
[Culex quinquefasciatus]

 Score =  122 bits (307),  Expect = 1e-26, Method: Composition-based stats.
 Identities = 91/126 (72%), Positives = 112/126 (88%), Gaps = 0/126 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MAVSRLS+VKFLELA+ I+C VLHYKSLGE D+ T +L AGTFVG+SVILI LFAGYL+G
Sbjct  1    MAVSRLSLVKFLELAVTISCAVLHYKSLGESDELTIMLVAGTFVGFSVILIGLFAGYLMG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120
             P+NKK+D+FFSLIGCAMFIASGVL+L+ WE+ + T+ +++AI+K SLA+ NGVLFFFDA
Sbjct  61   TPINKKIDIFFSLIGCAMFIASGVLVLQAWESGFKTERRRLAISKGSLAIVNGVLFFFDA  120

Query  121  IFTFRD  126
            +FTFRD
Sbjct  121  VFTFRD  126


>☐ gb|ACU30989.1|  secreted protein member of chemokine-like  factor super family
[Ochlerotatus triseriatus]
Length=126

 Score =  121 bits (305),  Expect = 2e-26, Method: Composition-based stats.
 Identities = 93/125 (74%), Positives = 112/125 (89%), Gaps = 0/125 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MAVSRLSIVKFLELAL I+CV LHYKS+GE D+ T LL AGTFVGY++IL+ LFAGYLLG
Sbjct  1    MAVSRLSIVKFLELALTISCVALHYKSMGEADEMTRLLVAGTFVGYTIILVGLFAGYLLG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120
             P++KK+DLFFSL+GCAMFIASGVLIL+EWE+ + TD +K+AI+K +LAV NGVLFFFD+
Sbjct  61   EPISKKIDLFFSLLGCAMFIASGVLILQEWESGFKTDRRKMAISKGALAVINGVLFFFDS  120

Query  121  IFTFR  125
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            +FTFR
Sbjct  121  VFTFR  125


>☐ gb|ACI30203.1|  hypothetical conserved protein [Anopheles darlingi]
Length=126

 Score =  121 bits (305),  Expect = 2e-26, Method: Composition-based stats.
 Identities = 122/126 (96%), Positives = 124/126 (98%), Gaps = 0/126 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTT+LLTAGTFVGYSVILIALFAGYLLG
Sbjct  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTKLLTAGTFVGYSVILIALFAGYLLG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120
            NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTD+KKIAITK SLAVTNGVLFFFDA
Sbjct  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDSKKIAITKGSLAVTNGVLFFFDA  120

Query  121  IFTFRD  126
            IFT RD
Sbjct  121  IFTLRD  126


>☐ ref|XP_309156.3| UG AGAP000964-PA [Anopheles gambiae str. PEST]
 gb|EAA04904.3| G AGAP000964-PA [Anopheles gambiae str. PEST]
Length=129

 GENE ID: 1270459 AgaP_AGAP000964 | AGAP000964-PA [Anopheles gambiae str. PEST]
(10 or fewer PubMed links)

 Score =  121 bits (305),  Expect = 2e-26, Method: Composition-based stats.
 Identities = 114/126 (90%), Positives = 121/126 (96%), Gaps = 0/126 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MAVSRLSIVKFLELALAITCV+LHYKSLGERDD T+LL+AGTFVGYSVILIALFAGY+L
Sbjct  4    MAVSRLSIVKFLELALAITCVILHYKSLGERDDITKLLSAGTFVGYSVILIALFAGYMLS  63

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120
            NP+NKKLDLFFSLIGCAMFIASGVLILKEWENAW+TDTKKI I+K SLAVTNGVLFFFDA
Sbjct  64   NPINKKLDLFFSLIGCAMFIASGVLILKEWENAWNTDTKKIGISKGSLAVTNGVLFFFDA  123

Query  121  IFTFRD  126
            IFT RD
Sbjct  124  IFTLRD  129


>☐ gb|ACI30184.1|  hypothetical conserved secreted protein [Anopheles darlingi]
Length=126

 Score =  121 bits (303),  Expect = 3e-26, Method: Composition-based stats.
 Identities = 126/126 (100%), Positives = 126/126 (100%), Gaps = 0/126 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG
Sbjct  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120
            NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA
Sbjct  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120

Query  121  IFTFRD  126
            IFTFRD
Sbjct  121  IFTFRD  126


>☐ ref|XP_002040111.1| G GM16029 [Drosophila sechellia]
 gb|EDW56976.1| G GM16029 [Drosophila sechellia]
Length=223
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 GENE ID: 6615740 Dsec\GM16029 | GM16029 gene product from transcript GM16029-RA
[Drosophila sechellia] (10 or fewer PubMed links)

 Score =  120 bits (302),  Expect = 4e-26, Method: Composition-based stats.
 Identities = 22/124 (17%), Positives = 42/124 (33%), Gaps = 5/124 (4%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K +EL L++ C ++H+    E       L  GT+ G  +I      G      P
Sbjct  10   WFLFKMMELLLSLGCCLVHWTCFMEEGVPHIFLLCGTYGGSVIICFISLIGAFYAERPKM  69

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAIT----KSSLAVTNGVLFFFDA  120
            K   LF  ++G    +     +       + T+            + +A+  G ++
Sbjct  70   KHEALFGGILGGLHMVTVYANMYVATLEEFRTERWPSFYACCRDNAIVALYAGAIYLMHC  129

Query  121  IFTF  124
             F
Sbjct  130  TFAL  133


>☐ ref|NP_726341.1| UG CG30184 [Drosophila melanogaster]
 gb|AAM68254.1| G CG30184 [Drosophila melanogaster]
 gb|AAY54811.1| G IP08069p [Drosophila melanogaster]
Length=223

 GENE ID: 246506 CG30184 | CG30184 gene product from transcript CG30184-RA
[Drosophila melanogaster] (10 or fewer PubMed links)

 Score =  120 bits (301),  Expect = 5e-26, Method: Composition-based stats.
 Identities = 22/124 (17%), Positives = 42/124 (33%), Gaps = 5/124 (4%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K +EL L++ C ++H+    E       L  GT+ G  +I      G      P
Sbjct  10   WFLFKMMELLLSLGCCLVHWTCFMEEGVPHIFLLCGTYGGSVIICFISLIGAFYAERPTM  69

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAIT----KSSLAVTNGVLFFFDA  120
            K   LF  ++G    +     +       + T+            + +A+  G ++
Sbjct  70   KHEALFGGILGGLHMVTVYANMYVATLEEFRTERWPSFYACCRDNAIVALYAGAIYLMHC  129

Query  121  IFTF  124
             F
Sbjct  130  TFAL  133


>☐ ref|XP_002082812.1| G GD11778 [Drosophila simulans]
 gb|EDX08397.1| G GD11778 [Drosophila simulans]
Length=223

 GENE ID: 6735902 Dsim\GD11778 | GD11778 gene product from transcript GD11778-RA
[Drosophila simulans] (10 or fewer PubMed links)

 Score =  119 bits (299),  Expect = 9e-26, Method: Composition-based stats.
 Identities = 22/124 (17%), Positives = 42/124 (33%), Gaps = 5/124 (4%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K +EL L++ C ++H+    E       L  GT+ G  +I      G      P
Sbjct  10   WFLFKMMELLLSLGCCLVHWTCFMEEGVPHIFLLCGTYGGSVIICFISLIGAFYAERPTM  69

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAIT----KSSLAVTNGVLFFFDA  120
            K   LF  ++G    +     +       + T+            + +A+  G ++
Sbjct  70   KHEALFGGILGGLHMVTVYANMYVATLEEFRTERWPSFYACCRDNAIVALYAGAIYLMHC  129

Query  121  IFTF  124
             F
Sbjct  130  TFAL  133


>☐ ref|XP_001978654.1| G GG17559 [Drosophila erecta]
 gb|EDV47581.1| G GG17559 [Drosophila erecta]
Length=131
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 GENE ID: 6549873 Dere\GG17559 | GG17559 gene product from transcript GG17559-RA
[Drosophila erecta] (10 or fewer PubMed links)

 Score =  117 bits (293),  Expect = 5e-25, Method: Composition-based stats.
 Identities = 64/123 (52%), Positives = 94/123 (76%), Gaps = 0/123 (0%)

Query  4    SRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
             RL++VKFLEL  AI C+VLH+ S  +RD  T  L  GTF GY +++I +FAG L+  P+
Sbjct  8    GRLNVVKFLELGFAIACLVLHFYSFNDRDIMTSFLATGTFTGYIIVVIGVFAGVLMRAPI  67

Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFT  123
            +K++D+FFS++GC +F+ASGV I++ WE ++ T T+ +A+ K+SL++ NGVLF FDA+FT
Sbjct  68   HKRIDIFFSVLGCTLFVASGVFIIEAWEFSFRTRTRDLALIKASLSIVNGVLFGFDAVFT  127

Query  124  FRD  126
            FRD
Sbjct  128  FRD  130


>☐ ref|XP_002055767.1| G GJ19540 [Drosophila virilis]
 gb|EDW65968.1| G GJ19540 [Drosophila virilis]
Length=131

 GENE ID: 6632158 Dvir\GJ19540 | GJ19540 gene product from transcript GJ19540-RA
[Drosophila virilis] (10 or fewer PubMed links)

 Score =  116 bits (292),  Expect = 6e-25, Method: Composition-based stats.
 Identities = 65/122 (53%), Positives = 96/122 (78%), Gaps = 0/122 (0%)

Query  5    RLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLN  64
            RL++VKFLELA +I C+VLH+ S  +RD  T  +  GTF GY +++I +FAG L+  P++
Sbjct  9    RLNVVKFLELAFSIACLVLHFYSFNDRDIMTSFMATGTFTGYIIVVIGVFAGVLMRAPIH  68

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFTF  124
            K++D+FFS++GCA+F+ASGV I++ WE ++ T T+ +A+ K+SL++ NGVLF FDAIFTF
Sbjct  69   KRIDIFFSVLGCALFVASGVFIIEAWEFSFRTRTRDLALIKASLSIVNGVLFGFDAIFTF  128

Query  125  RD  126
            RD
Sbjct  129  RD  130


>☐ ref|XP_001354423.1| G GA13737 [Drosophila pseudoobscura pseudoobscura]
 ref|XP_002023021.1| G GL16585 [Drosophila persimilis]
 gb|EAL31476.1| G GA13737 [Drosophila pseudoobscura pseudoobscura]
 gb|EDW27126.1| G GL16585 [Drosophila persimilis]
Length=131

 GENE ID: 4814357 Dpse\GA13737 | GA13737 gene product from transcript GA13737-RA
[Drosophila pseudoobscura pseudoobscura] (10 or fewer PubMed links)

 Score =  116 bits (292),  Expect = 6e-25, Method: Composition-based stats.
 Identities = 65/123 (52%), Positives = 95/123 (77%), Gaps = 0/123 (0%)

Query  4    SRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
             RL++VKFLEL  A+ C+VLH+ S  +RD  T  L  GTF GY +++I +FAG L+  P+
Sbjct  8    GRLNVVKFLELGFAVACLVLHFYSFNDRDIMTSFLATGTFTGYIIVVIGVFAGVLMRAPI  67

Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFT  123
            +K++D+FFS++GCA+F+ASGV I++ WE ++ T T+ +A+ K+SL++ NGVLF FDAIFT
Sbjct  68   HKRIDIFFSVMGCALFVASGVFIIEAWEFSFRTRTRDLALIKASLSIVNGVLFGFDAIFT  127

Query  124  FRD  126
            FRD
Sbjct  128  FRD  130


>☐ ref|NP_608423.1| UG CG15449 [Drosophila melanogaster]
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 ref|XP_001967078.1|  GF21858 [Drosophila ananassae]
 ref|XP_002101950.1|  GE15320 [Drosophila yakuba]
 6 more sequence titles

ref|XP_002107515.1|  GD15513 [Drosophila simulans]
 gb|AAF50865.1|  CG15449 [Drosophila melanogaster]
 gb|EDV38397.1|  GF21858 [Drosophila ananassae]
 gb|EDX03058.1|  GE15320 [Drosophila yakuba]
 gb|EDX18500.1|  GD15513 [Drosophila simulans]
 gb|ACL88209.1|  CG15449-PA [synthetic construct]
Length=131

 GENE ID: 33079 CG15449 | CG15449 gene product from transcript CG15449-RA
[Drosophila melanogaster] (10 or fewer PubMed links)

 Score =  116 bits (292),  Expect = 6e-25, Method: Composition-based stats.
 Identities = 63/123 (51%), Positives = 94/123 (76%), Gaps = 0/123 (0%)

Query  4    SRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
             RL++VKFLEL  A+ C+VLH+ S  +RD  T  L  GTF GY +++I +FAG L+  P+
Sbjct  8    GRLNVVKFLELGFAVACLVLHFYSFNDRDIMTSFLATGTFTGYIIVVIGVFAGVLMRAPI  67

Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFT  123
            +K++D+FFS++GC +F+ASGV I++ WE ++ T T+ +A+ K+SL++ NGVLF FDA+FT
Sbjct  68   HKRIDIFFSVLGCTLFVASGVFIIEAWEFSFRTRTRDLALIKASLSIVNGVLFGFDAVFT  127

Query  124  FRD  126
            FRD
Sbjct  128  FRD  130


>☐ ref|XP_002092643.1|  GE14306 [Drosophila yakuba]
 gb|EDW92355.1|  GE14306 [Drosophila yakuba]
Length=223

 GENE ID: 6531856 Dyak\GE14306 | GE14306 gene product from transcript GE14306-RA
[Drosophila yakuba] (10 or fewer PubMed links)

 Score =  116 bits (291),  Expect = 8e-25, Method: Composition-based stats.
 Identities = 23/124 (18%), Positives = 42/124 (33%), Gaps = 5/124 (4%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K LEL L++ C ++H+    + D     L  GT+ G  +I      G      P
Sbjct  10   WFLFKMLELLLSLGCCLVHWSCCKKEDIPHIFLLCGTYGGSVIICFMSLIGAFYAERPTM  69

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAIT----KSSLAVTNGVLFFFDA  120
            K   LF  ++G    +     +       + T              + +A+  G ++
Sbjct  70   KHEALFGGILGVLHMVTVYANMYVATLEEFRTKRWPSFYACCRNNAIVALYAGAIYLLHC  129

Query  121  IFTF  124
             F
Sbjct  130  TFAL  133


>☐ ref|XP_002071641.1|  GK10090 [Drosophila willistoni]
 gb|EDW82627.1|  GK10090 [Drosophila willistoni]
Length=131

 GENE ID: 6648426 Dwil\GK10090 | GK10090 gene product from transcript GK10090-RA
[Drosophila willistoni] (10 or fewer PubMed links)

 Score =  116 bits (291),  Expect = 9e-25, Method: Composition-based stats.
 Identities = 65/123 (52%), Positives = 95/123 (77%), Gaps = 0/123 (0%)

Query  4    SRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
             RL++VKFLELA A  C++LH+ S  +RD  T  L  GTF GY ++++ +FAG L+  P+
Sbjct  8    GRLNLVKFLELAFATACLILHFYSFNDRDIMTAFLATGTFTGYIIVVLGVFAGVLMRAPI  67
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Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFT  123
            +K++D+FFS++GCA+F+ASGV I++ WE ++ T T+ +A+ K+SLA+ NGVLF FDAIFT
Sbjct  68   HKRIDIFFSVLGCALFVASGVFIIEAWEFSFRTRTRDLALIKASLAIVNGVLFGFDAIFT  127

Query  124  FRD  126
            FRD
Sbjct  128  FRD  130


>☐ ref|XP_001991178.1| G GH12523 [Drosophila grimshawi]
 gb|EDV99802.1| G GH12523 [Drosophila grimshawi]
Length=131

 GENE ID: 6564547 Dgri\GH12523 | GH12523 gene product from transcript GH12523-RA
[Drosophila grimshawi] (10 or fewer PubMed links)

 Score =  116 bits (290),  Expect = 1e-24, Method: Composition-based stats.
 Identities = 64/123 (52%), Positives = 96/123 (78%), Gaps = 0/123 (0%)

Query  4    SRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
             RL++VKFLELA ++ C+VLH+ S  +RD  T  +  GTF GY +++I +FAG L+  P+
Sbjct  8    GRLNVVKFLELAFSVACLVLHFYSFNDRDILTSFMATGTFTGYIIVVIGVFAGVLMRAPI  67

Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFT  123
            +K++D+FFS++GCA+F+ASGV I++ WE ++ T T+ +A+ K+SL++ NGVLF FDAIFT
Sbjct  68   HKRIDIFFSVLGCALFVASGVFIIEAWEFSFRTRTRDLALIKASLSIVNGVLFGFDAIFT  127

Query  124  FRD  126
            FRD
Sbjct  128  FRD  130


>☐ ref|XP_002010101.1| G GI14877 [Drosophila mojavensis]
 gb|EDW07418.1| G GI14877 [Drosophila mojavensis]
Length=131

 GENE ID: 6584446 Dmoj\GI14877 | GI14877 gene product from transcript GI14877-RA
[Drosophila mojavensis] (10 or fewer PubMed links)

 Score =  116 bits (290),  Expect = 1e-24, Method: Composition-based stats.
 Identities = 63/123 (51%), Positives = 96/123 (78%), Gaps = 0/123 (0%)

Query  4    SRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
             RL++VKFLELA ++ C+VLH+ S  +RD  T  +  GTF GY +++I +FAG L+  P+
Sbjct  8    GRLNVVKFLELAFSVACLVLHFYSFNDRDIMTSFMATGTFTGYIIVVIGVFAGVLMRAPI  67

Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFT  123
            +K++D+FFS++GCA+F+ASG+ I++ WE ++ T T+ +A+ K+SL++ NGVLF FDAIFT
Sbjct  68   HKRIDIFFSVLGCALFVASGIFIIEAWEFSFRTRTRDLALIKASLSIVNGVLFGFDAIFT  127

Query  124  FRD  126
            FRD
Sbjct  128  FRD  130


>☐ ref|XP_001660924.1| UG hypothetical protein AaeL_AAEL010564 [Aedes aegypti]
 gb|EAT37455.1| G conserved hypothetical protein [Aedes aegypti]
Length=131

 GENE ID: 5573526 AaeL_AAEL010564 | hypothetical protein [Aedes aegypti]
(10 or fewer PubMed links)

 Score =  114 bits (287),  Expect = 3e-24, Method: Composition-based stats.
 Identities = 62/121 (51%), Positives = 88/121 (72%), Gaps = 0/121 (0%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNK  65
            LSI+KFLEL LA+ C VLHY S  + D  T  L  GTF GY VIL  +  GYL+   +++
Sbjct  9    LSIIKFLELCLAVACTVLHYYSFDDGDLVTGFLATGTFCGYIVILTTVMVGYLMKAHIHR  68

Query  66   KLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
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            +L+LF+SL+GCA+F+ +G+ I++ WE+A+ T T+ +AITK S+A+ NGV+F  D IFTFR
Sbjct  69   RLNLFYSLLGCALFLTAGIFIIEAWEHAFRTRTRDLAITKGSIAIINGVIFLMDTIFTFR  128

Query  126  D  126
            +
Sbjct  129  E  129


>☐ ref|XP_975314.1| PREDICTED: similar to CG15449 CG15449-PA [Tribolium castaneum]
 gb|EFA08752.1| hypothetical protein TcasGA2_TC006429 [Tribolium castaneum]
Length=128

 GENE ID: 664209 TcasGA2_TC006429 | similar to CG15449 CG15449-PA
[Tribolium castaneum] (10 or fewer PubMed links)

 Score =  114 bits (285),  Expect = 4e-24, Method: Composition-based stats.
 Identities = 56/125 (44%), Positives = 87/125 (69%), Gaps = 0/125 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MAVSRLSI+KFLELA+A+TC+ LHYKS    D  T  L+   F G+ +IL+   FAG+L+
Sbjct  1    MAVSRLSIIKFLELAIAVTCIGLHYKSEVPGDFNTNTLSVAAFGGFVIILVGGFAGHLMS  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120
             P+N+++D+FF L+GCA FIA+G + ++ +++    + +   + K+SLA+  G LF  D+
Sbjct  61   TPINRRIDIFFCLVGCATFIAAGAMNIEYFKDVRKGEYRDYGLAKASLAIIGGALFLVDS  120

Query  121  IFTFR  125
            + T+R
Sbjct  121  LLTWR  125


>☐ ref|XP_001976431.1| GG22868 [Drosophila erecta]
 gb|EDV56831.1| GG22868 [Drosophila erecta]
Length=223

 GENE ID: 6547887 Dere\GG22868 | GG22868 gene product from transcript GG22868-RA
[Drosophila erecta] (10 or fewer PubMed links)

 Score =  114 bits (285),  Expect = 4e-24, Method: Composition-based stats.
 Identities = 23/124 (18%), Positives = 43/124 (34%), Gaps = 5/124 (4%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K +EL L++ C ++H+    +       L  GT+ G  +I I    G      P
Sbjct  10   WFLFKMMELLLSLGCCLVHWSCCKKEGIPHIFLLCGTYGGSVIICIMSLIGAFYAERPTM  69

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAIT----KSSLAVTNGVLFFFDA  120
            K   LF  ++G    I     +       + T+            + +A+  G ++
Sbjct  70   KHEALFGGILGSLHMITVYANMYVATLEEFRTERWPSFYACCRDNAIVALYAGAIYLLHC  129

Query  121  IFTF  124
             F
Sbjct  130  TFAL  133


>☐ ref|XP_309155.3| AGAP000963-PA [Anopheles gambiae str. PEST]
 gb|EAA04905.4| AGAP000963-PA [Anopheles gambiae str. PEST]
Length=131

 GENE ID: 1270458 AgaP_AGAP000963 | AGAP000963-PA [Anopheles gambiae str. PEST]
(10 or fewer PubMed links)

 Score =  113 bits (284),  Expect = 5e-24, Method: Composition-based stats.
 Identities = 64/121 (52%), Positives = 87/121 (71%), Gaps = 0/121 (0%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNK  65
            LSI+KFLEL+LA+TC  LHY S  + D  T  L  GTF G+ VIL  + AGYL+   L++
Sbjct  9    LSIIKFLELSLAVTCTTLHYYSFNDGDLVTGFLATGTFCGFIVILFTVMAGYLMKAHLHR  68

Query  66   KLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            +L +F+SL+GC  F+ SGV I++ WE+A+ T T+ +AITK S+AV NGV+F  D IFTFR
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Sbjct  69   RLSIFYSLLGCVCFLTSGVFIIEAWEHAFRTRTRDLAITKGSIAVINGVIFLMDTIFTFR  128

Query  126  D  126
            +
Sbjct  129  E  129


>☐ ref|NP_001091800.1| UG hypothetical protein LOC778505 [Bombyx mori]
 gb|ABJ97187.1| G hypothetical protein [Bombyx mori]
Length=126

 GENE ID: 778505 LOC778505 | hypothetical protein LOC778505 [Bombyx mori]

 Score =  110 bits (275),  Expect = 5e-23, Method: Composition-based stats.
 Identities = 56/125 (44%), Positives = 83/125 (66%), Gaps = 1/125 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MA+SRLSI+KFLELAL  +CV LHY S    D    +L  GTFVGY +I     AGY++
Sbjct  1    MAISRLSIIKFLELALTCSCVALHYHSY-NADADIGMLVTGTFVGYLIIFAGAAAGYIMQ  59

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDA  120
             P +K++D+F+SL+G A+F+ASG +I+  +++   ++ K   + K+SLA+ NG +   DA
Sbjct  60   TPSHKRIDIFYSLVGVALFVASGAIIIDRFQHYGKSEIKDKNLAKASLAIINGAILLVDA  119

Query  121  IFTFR  125
            + T R
Sbjct  120  VLTQR  124


>☐ ref|XP_001361089.1| G GA15708 [Drosophila pseudoobscura pseudoobscura]
 gb|EAL25665.1| G GA15708 [Drosophila pseudoobscura pseudoobscura]
Length=226

 GENE ID: 4804546 Dpse\GA15708 | GA15708 gene product from transcript GA15708-RA
[Drosophila pseudoobscura pseudoobscura] (10 or fewer PubMed links)

 Score =  106 bits (266),  Expect = 6e-22, Method: Composition-based stats.
 Identities = 21/130 (16%), Positives = 40/130 (30%), Gaps = 11/130 (8%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K LEL L+  C  +H++   +       L   T+ G S+I +    G      P
Sbjct  8    WLLFKVLELVLSFCCCYIHWRCFQDEGIPHIFLLCATYGGSSIICLLAIIGMFYAEKPTM  67

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAIT----------KSSLAVTNGV  114
            +    F  L G    +   V +            K                +++A+
Sbjct  68   QLESAFSGLFGTLHLVTIFVHMYLALHGNKLVYLKSQGANWHGYYICCRDNATVALYATA  127

Query  115  LFFFDAIFTF  124
            +++    F
Sbjct  128  VYYLHCTFAL  137


>☐ ref|XP_001966751.1| G GF19114 [Drosophila ananassae]
 gb|EDV33796.1| G GF19114 [Drosophila ananassae]
Length=125

 GENE ID: 6501877 Dana\GF19114 | GF19114 gene product from transcript GF19114-RA
[Drosophila ananassae] (10 or fewer PubMed links)

 Score =  106 bits (266),  Expect = 7e-22, Method: Composition-based stats.
 Identities = 42/126 (33%), Positives = 71/126 (56%), Gaps = 3/126 (2%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K +ELA++I C+V++            L+  GT  G+++I   L  G+++
Sbjct  1    MEFNNRLLLKIIELAISIACIVMYEVDGALSSRP--LIVCGTIGGFTIICGVLLIGHVIN  58

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENA-WSTDTKKIAITKSSLAVTNGVLFFFD  119
            + + K+L+   SLIGC +F+ASG L++ EW +A   TD K+ AI   SL + NG +F  D
Sbjct  59   SLVEKRLNALISLIGCVLFVASGALVIDEWHDARLQTDRKRNAIAAGSLMIINGAVFLLD  118
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Query  120  AIFTFR  125
             +   R
Sbjct  119  TLSICR  124


>☐ ref|XP_002018237.1| G GL16872 [Drosophila persimilis]
 gb|EDW36076.1| G GL16872 [Drosophila persimilis]
Length=226

 GENE ID: 6592425 Dper\GL16872 | GL16872 gene product from transcript GL16872-RA
[Drosophila persimilis] (10 or fewer PubMed links)

 Score =  105 bits (262),  Expect = 2e-21, Method: Composition-based stats.
 Identities = 21/130 (16%), Positives = 40/130 (30%), Gaps = 11/130 (8%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K LEL L+  C  +H++   +       L   T+ G S+I +    G      P
Sbjct  8    WLLFKVLELVLSFCCCYIHWRCFQDEGIPHIFLLCATYGGSSIICLLAIIGMFYAEKPTM  67

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAIT----------KSSLAVTNGV  114
            +    F  L G    +   V +            K                +++A+
Sbjct  68   QLESAFSGLFGTLHLVTIFVHMYLALHGNKLLYLKSQGANWHGYYICCRDNATVALYATA  127

Query  115  LFFFDAIFTF  124
            +++    F
Sbjct  128  VYYLHCAFAL  137


>☐ ref|XP_002055067.1| G GJ19171 [Drosophila virilis]
 gb|EDW65268.1| G GJ19171 [Drosophila virilis]
Length=126

 GENE ID: 6631609 Dvir\GJ19171 | GJ19171 gene product from transcript GJ19171-RA
[Drosophila virilis] (10 or fewer PubMed links)

 Score =  104 bits (261),  Expect = 2e-21, Method: Composition-based stats.
 Identities = 41/127 (32%), Positives = 69/127 (54%), Gaps = 4/127 (3%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K +EL +AI CVVL+            L+  GT  G+++I   L  G+++
Sbjct  1    MEFNNRLLLKIIELGIAIACVVLYEVVGDLSKRP--LIVCGTIGGFTIICAVLLIGHVIN  58

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWEN--AWSTDTKKIAITKSSLAVTNGVLFFF  118
            + + K+L+   SL+GC +F+ASG L++ EW +   +  D K+ AI   SL + NG +F
Sbjct  59   SVVEKRLNALISLLGCILFVASGALVIDEWHDIYDFLKDRKRNAIAAGSLMIINGAVFLL  118

Query  119  DAIFTFR  125
            D +   R
Sbjct  119  DTLSICR  125


>☐ ref|XP_002039595.1| G GM22643 [Drosophila sechellia]
 gb|EDW56337.1| G GM22643 [Drosophila sechellia]
Length=121

 GENE ID: 6615179 Dsec\GM22643 | GM22643 gene product from transcript GM22643-RA
[Drosophila sechellia] (10 or fewer PubMed links)

 Score =  104 bits (259),  Expect = 4e-21, Method: Composition-based stats.
 Identities = 55/111 (49%), Positives = 84/111 (75%), Gaps = 0/111 (0%)

Query  16   LAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIG  75
             A+ C+VLH+ S  +RD  T  L  GTF GY +++I +FAG L+  P++K++D+FFS++G
Sbjct  10   FAVACLVLHFYSFNDRDIMTSFLATGTFTGYIIVVIGVFAGVLMRAPIHKRIDIFFSVLG  69

Query  76   CAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFRD  126
            C +F+ASGV I++ WE ++ T T+ +A+ K+SL++ NGVLF FDA+FTFRD
Sbjct  70   CTLFVASGVFIIEAWEFSFRTRTRDLALIKASLSIVNGVLFGFDAVFTFRD  120
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>☐ ref|NP_572518.1| UG CG7267 [Drosophila melanogaster]
 ref|XP_002106511.1| UG GD16087 [Drosophila simulans]
 gb|AAF46435.2| G CG7267 [Drosophila melanogaster]
 gb|EDX17464.1| G GD16087 [Drosophila simulans]
 gb|ACP28219.1| G GM12243p [Drosophila melanogaster]
Length=125

 GENE ID: 31831 CG7267 | CG7267 gene product from transcript CG7267-RB
[Drosophila melanogaster] (Over 10 PubMed links)

 Score =  103 bits (258),  Expect = 5e-21, Method: Composition-based stats.
 Identities = 46/126 (36%), Positives = 71/126 (56%), Gaps = 3/126 (2%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K +ELA+AI C+VL+            ++ AGT  GY+VI   L  G++L
Sbjct  1    MEFNNRLLLKIIELAIAIACIVLYETVGNLS--LHPVIVAGTVGGYTVICGVLLIGHVLN  58

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENA-WSTDTKKIAITKSSLAVTNGVLFFFD  119
            + + K+L+  FSLIGC +F+ASG L++ EW     +TD K+ AI   SL + N  +F  D
Sbjct  59   SLVEKRLNALFSLIGCLLFVASGALVIDEWHGGLLNTDRKRQAIGAGSLMIINAAVFLLD  118

Query  120  AIFTFR  125
             +   R
Sbjct  119  TLCICR  124


>☐ ref|XP_001606621.1| UG PREDICTED: hypothetical protein [Nasonia vitripennis]
Length=562

 GENE ID: 100123014 LOC100123014 | hypothetical protein LOC100123014
[Nasonia vitripennis]

 Score =  102 bits (254),  Expect = 1e-20, Method: Composition-based stats.
 Identities = 49/113 (43%), Positives = 75/113 (66%), Gaps = 3/113 (2%)

Query  13   ELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFS  72
            E  LA   + LHY S  +      +LT GT+ GY +IL+ LFAG ++G P+N+++DLFFS
Sbjct  450  EQLLACILIGLHYHS--QTYGHEMMLTTGTYCGYVIILVGLFAGGVMGTPVNRRVDLFFS  507

Query  73   LIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            L+GCA+FIASG +++       S ++    + K+S+++  GVLFF DA+FTF+
Sbjct  508  LVGCALFIASGAVVIDN-HQHESGESFNKHMAKASISIIEGVLFFVDAVFTFK  559


>☐ gb|ACN69164.1|  hypothetical conserved secreted protein [Stomoxys calcitrans]
Length=127

 Score =  101 bits (253),  Expect = 2e-20, Method: Composition-based stats.
 Identities = 41/128 (32%), Positives = 70/128 (54%), Gaps = 5/128 (3%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K LEL +AI C+VL   S    +    L+  GT  G++VI   +  G+++
Sbjct  1    MQFNNRVLLKILELVIAIVCIVLWETSGNFSN--NALIVCGTMGGFAVICGVILIGHVIN  58

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENA---WSTDTKKIAITKSSLAVTNGVLFF  117
            +   K+++  FS+IGC +F+ SG LI+ +W +       ++K+ A+   SL + NG +F
Sbjct  59   SVXEKRINGLFSIIGCVLFVISGALIIDQWHDRSDLLFKESKRNALAAGSLMIINGAVFL  118

Query  118  FDAIFTFR  125
             D I  FR
Sbjct  119  MDTISIFR  126


>☐ ref|XP_001959837.1| G GF13066 [Drosophila ananassae]
 gb|EDV36659.1| G GF13066 [Drosophila ananassae]
Length=228

 GENE ID: 6495909 Dana\GF13066 | GF13066 gene product from transcript GF13066-RA
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[Drosophila ananassae] (10 or fewer PubMed links)

 Score =  100 bits (249),  Expect = 6e-20, Method: Composition-based stats.
 Identities = 22/124 (17%), Positives = 39/124 (31%), Gaps = 5/124 (4%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
               +K  E  L+  C  +HY            L  GT+ G S++      G      P
Sbjct  11   WLFLKLTEFLLSGGCCYMHYYCFMTEKIPHMFLLCGTYGGSSIMCFLAVIGVFYAEKPAM  70

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK----KIAITKSSLAVTNGVLFFFDA  120
            K    F +++G    +     +     N +         +     S +A+    +FF
Sbjct  71   KYEAAFSAILGSMFLLTVFAQMHMATMNNFKQKHWAGFYECCRDNSLIALYAAAIFFIHC  130

Query  121  IFTF  124
             F+
Sbjct  131  SFSL  134


>☐ ref|XP_001661199.1| UG hypothetical protein AaeL_AAEL010956 [Aedes aegypti]
 gb|EAT37006.1| G conserved hypothetical protein [Aedes aegypti]
Length=172

 GENE ID: 5574129 AaeL_AAEL010956 | hypothetical protein [Aedes aegypti]
(10 or fewer PubMed links)

 Score = 98.7 bits (245),  Expect = 2e-19, Method: Composition-based stats.
 Identities = 31/131 (23%), Positives = 51/131 (38%), Gaps = 13/131 (9%)

Query  8    IVKFLELALAITCVVLHYKSLGER------DDTTELLTAGTFVGYSVILIALFAGYLLGN  61
            + K LELA+AI C+ L                 T  L   TFV + +  +     G ++
Sbjct  34   VFKLLELAVAIICIGLIDDPANNSRLRPFATTRTIALAYSTFVPFLMFSVIYLFGKVIRE  93

Query  62   PLNKKLDLFFSLIGCAMFIASGVLILKEWENAW-------STDTKKIAITKSSLAVTNGV  114
             +  KL    +L    +++A+ + IL +W           +T          S+AV   +
Sbjct  94   NIPWKLQSLLNLTAFILYLATAICILHDWSETKNRNYWPPNTQRMDFLCGAGSVAVVGAL  153

Query  115  LFFFDAIFTFR  125
            L+  D I T R
Sbjct  154  LYLLDLIVTTR  164


>☐ ref|XP_001845632.1| UG conserved hypothetical protein [Culex quinquefasciatus]
 gb|EDS40988.1| G conserved hypothetical protein [Culex quinquefasciatus]
Length=149

 GENE ID: 6035445 CpipJ_CPIJ003950 | hypothetical protein
[Culex quinquefasciatus]

 Score = 97.5 bits (242),  Expect = 4e-19, Method: Composition-based stats.
 Identities = 31/138 (22%), Positives = 52/138 (37%), Gaps = 19/138 (13%)

Query  6    LSIVKFLELALAITC----------VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFA  55
            ++I+K L L + I            V   +    E+    E++ +G FVGY +
Sbjct  1    MAILKALNLVILIIYRTGYGGDFLGVGGTWNLNEEKSPDAEIVASGVFVGYFIYTSVQLI  60

Query  56   GYLLGNPLNKKL--DLFFSLIGCAMFIASGVLILKEWENAWS-------TDTKKIAITKS  106
             +  G    K+   D   +++G  M+IA G   L  W            T  +   +
Sbjct  61   TFCFGTTKLKRELSDTIMNVVGTFMWIAVGGTALHYWHGFQPEYDFQQITSERTAGLAMG  120

Query  107  SLAVTNGVLFFFDAIFTF  124
            SL V  G L+  D++  F
Sbjct  121  SLCVVTGALYLADSVLAF  138


>☐ ref|XP_002423901.1| G conserved hypothetical protein [Pediculus humanus corporis]
 gb|EEB11163.1| G conserved hypothetical protein [Pediculus humanus corporis]
Length=143

 GENE ID: 8238019 Phum_PHUM094210 | hypothetical protein
[Pediculus humanus corporis]
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 Score = 95.6 bits (237),  Expect = 1e-18, Method: Composition-based stats.
 Identities = 46/112 (41%), Positives = 69/112 (61%), Gaps = 1/112 (0%)

Query  15   ALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLI  74
             L ITCV LHY S    D    +++ GTF G+ +ILI ++AGYL   P++K++D F+S+
Sbjct  7    LLTITCVGLHYHSFEANDKYGLIVSTGTFCGFLIILIGVYAGYLFSMPISKRIDAFYSIC  66

Query  75   GCAMFIASGVLILKEW-ENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            GCA+F+ASG L +  +    +  +   I + K SLAV NG++F  DAI   +
Sbjct  67   GCALFVASGALSIDHFQHKKYDKELSDIGLAKGSLAVINGLVFLVDAIVNRK  118


>☐ ref|XP_001119879.1| UG PREDICTED: similar to CG15449-PA [Apis mellifera]
Length=128

 GENE ID: 724580 LOC724580 | similar to CG15449-PA [Apis mellifera]
(10 or fewer PubMed links)

 Score = 93.3 bits (231),  Expect = 8e-18, Method: Composition-based stats.
 Identities = 48/126 (38%), Positives = 76/126 (60%), Gaps = 1/126 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M +++ +I K +EL +    + LHY S  +    +  LT GTF GY +IL+ +  G +LG
Sbjct  1    MGMNKATIFKVVELIIVCVLIGLHYHSFSDSSLMSAFLTMGTFGGYLIILVGMCLGIILG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENA-WSTDTKKIAITKSSLAVTNGVLFFFD  119
              ++ +LDLFFS++GC +FI +G LIL  + NA +  + +   I K  +++  GVLF  D
Sbjct  61   ATIDHRLDLFFSIVGCILFIIAGALILDHFINAVYRGNFRNTGIAKGLISIVQGVLFLID  120

Query  120  AIFTFR  125
            A+F FR
Sbjct  121  AVFAFR  126


>☐ ref|XP_001655679.1| UG hypothetical protein AaeL_AAEL002578 [Aedes aegypti]
 gb|EAT46164.1| G conserved hypothetical protein [Aedes aegypti]
Length=146

 GENE ID: 5575305 AaeL_AAEL002578 | hypothetical protein [Aedes aegypti]
(10 or fewer PubMed links)

 Score = 92.1 bits (228),  Expect = 1e-17, Method: Composition-based stats.
 Identities = 25/113 (22%), Positives = 43/113 (38%), Gaps = 9/113 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL--DLFFSLIGCAM  78
            V   +    E+    E++ +G FVGY +        +  G    K+   D   +++G  M
Sbjct  23   VGGTWNLNEEKSPDAEIVASGVFVGYFIYTSVQLITFCFGTTKLKRELSDTIMNVVGTFM  82

Query  79   FIASGVLILKEWENA-------WSTDTKKIAITKSSLAVTNGVLFFFDAIFTF  124
            ++A G   L  W            T  +   +   SL V  G L+  D++  F
Sbjct  83   WVAVGGTALHYWHGYLAEHDFQHITSERTAGLALGSLCVVTGALYLADSVLAF  135


>☐ ref|XP_001995529.1| G GH17713 [Drosophila grimshawi]
 gb|EDV95181.1| G GH17713 [Drosophila grimshawi]
Length=235

 GENE ID: 6569554 Dgri\GH17713 | GH17713 gene product from transcript GH17713-RA
[Drosophila grimshawi] (10 or fewer PubMed links)

 Score = 92.1 bits (228),  Expect = 2e-17, Method: Composition-based stats.
 Identities = 34/123 (27%), Positives = 59/123 (47%), Gaps = 1/123 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K LEL    + ++L          +  +L  GT  GY +I  AL  G+LLG
Sbjct  1    MEFNNRLLLKILELIFTASIIILIETVADLSYSSQAMLVCGTLTGYLIICSALSVGHLLG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDT-KKIAITKSSLAVTNGVLFFFD  119
              ++K++D+  S+ GC +F+++G +IL  W   +     K   +    LA+   V+F  D
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Sbjct  61   ANVDKRIDIIISVSGCVLFVSTGAIILSRWSGCYEAARDKNTMLASGVLAIVAAVIFIAD  120

Query  120  AIF  122

Sbjct  121  TFV  123


 Score = 86.8 bits (214),  Expect = 7e-16, Method: Composition-based stats.
 Identities = 38/112 (33%), Positives = 62/112 (55%), Gaps = 4/112 (3%)

Query  16   LAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIG  75
            +AI C+VL+            L+  GT  G+++I   L  G++LG+ + K+L+   SL+G
Sbjct  125  IAIACIVLYEVVGDLSKRP--LIVCGTIGGFTIICAVLLVGHVLGSVVEKRLNALISLLG  182

Query  76   CAMFIASGVLILKEWEN--AWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            C +F+ASG L++ EW +   +  D K+ AI   SL + NG +F  D +    R
Sbjct  183  CILFVASGALVIDEWHDMYEFLKDRKRNAIAAGSLMIINGAVFLLDTLSICR  234


>☐ ref|XP_002009616.1| G GI15456 [Drosophila mojavensis]
 gb|EDW06933.1| G GI15456 [Drosophila mojavensis]
Length=128

 GENE ID: 6583956 Dmoj\GI15456 | GI15456 gene product from transcript GI15456-RA
[Drosophila mojavensis] (10 or fewer PubMed links)

 Score = 91.8 bits (227),  Expect = 2e-17, Method: Composition-based stats.
 Identities = 33/125 (26%), Positives = 58/125 (46%), Gaps = 1/125 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K +EL    + ++L          +  +L  GT  GY +I  AL  G+LLG
Sbjct  1    MEFNNRLLLKIIELIFTASIIILIESVTDHSYSSQAMLVCGTLTGYLIICSALSIGHLLG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWS-TDTKKIAITKSSLAVTNGVLFFFD  119
              L+K++D+ F++ GC +F+++G +I   W +    T  K   +    L+      F  D
Sbjct  61   AKLDKRIDILFTVSGCVLFVSTGAIIFDRWMHRVELTRNKNTILASGVLSFATAAFFIVD  120

Query  120  AIFTF  124
                F
Sbjct  121  TFVIF  125


>☐ ref|XP_001949085.1| UG PREDICTED: similar to conserved hypothetical protein [Acyrthosiphon
pisum]
Length=128

 GENE ID: 100167617 LOC100167617 | similar to conserved hypothetical protein
[Acyrthosiphon pisum]

 Score = 91.4 bits (226),  Expect = 3e-17, Method: Composition-based stats.
 Identities = 55/126 (43%), Positives = 82/126 (65%), Gaps = 1/126 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MA+++++++KFLELAL I   VLHY S    D T+ ++T GT+VGY +IL  +F G   G
Sbjct  1    MAITKITMIKFLELALTIIIFVLHYNSFPGGDTTSIMITTGTYVGYVIILAGIFIGLFTG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWEN-AWSTDTKKIAITKSSLAVTNGVLFFFD  119
             P++ +LD+FF LIG A+FI SGV+    +   A  +      +TK+ L++ NGV+F  D
Sbjct  61   TPISSRLDMFFVLIGAALFITSGVMSYNYYNGFALKSSYVNTGLTKAWLSILNGVVFVVD  120

Query  120  AIFTFR  125
            A FT+R
Sbjct  121  AAFTYR  126


>☐ dbj|BAH71208.1|  ACYPI008397 [Acyrthosiphon pisum]
Length=128

 Score = 90.6 bits (224),  Expect = 4e-17, Method: Composition-based stats.
 Identities = 54/126 (42%), Positives = 81/126 (64%), Gaps = 1/126 (0%)
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Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            MA+++++++KFLELAL I   VLHY      D T+ ++T GT+VGY +IL  +F G   G
Sbjct  1    MAITKITMIKFLELALTIIIFVLHYNRFPGGDTTSIMITTGTYVGYVIILAGIFIGLFTG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWEN-AWSTDTKKIAITKSSLAVTNGVLFFFD  119
             P++ +LD+FF LIG A+FI SGV+    +   A  +      +TK+ L++ NGV+F  D
Sbjct  61   TPISSRLDMFFVLIGAALFITSGVMSYNYYNGFALKSSYVNTGLTKAWLSILNGVVFVVD  120

Query  120  AIFTFR  125
            A FT+R
Sbjct  121  AAFTYR  126


>☐ ref|XP_002047342.1| G GJ11981 [Drosophila virilis]
 gb|EDW69684.1| G GJ11981 [Drosophila virilis]
Length=287

 GENE ID: 6623648 Dvir\GJ11981 | GJ11981 gene product from transcript GJ11981-RA
[Drosophila virilis] (10 or fewer PubMed links)

 Score = 90.6 bits (224),  Expect = 4e-17, Method: Composition-based stats.
 Identities = 21/132 (15%), Positives = 45/132 (34%), Gaps = 13/132 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGE--RDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
              + + LE+     C+ +H  +           L+  GTF+GY ++    +   + G
Sbjct  5    WLLFRALEMIFESICMAIHMVASLHFAEPMPHCLIFCGTFIGYLLLAFIRWVRLISGQRT  64

Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAW------STDTKKIAI-----TKSSLAVTN  112
                 +F SL G  +     +L +   EN +        +            +S + +
Sbjct  65   LLHPAMFISLSGMLLHFICALLSMNYAENDFHLKYMGPQEELDHVFFGFCKQQSVVCIVT  124

Query  113  GVLFFFDAIFTF  124
            G ++   +I
Sbjct  125  GAIYLMQSILLL  136


>☐ gb|ABV44719.1|  ryanodine receptor-like protein [Phlebotomus papatasi]
Length=157

 Score = 90.2 bits (223),  Expect = 6e-17, Method: Composition-based stats.
 Identities = 25/141 (17%), Positives = 50/141 (35%), Gaps = 23/141 (16%)

Query  7    SIVKFLELALAITC--------------VVLHYKSLGERDDTTELLTAGTFVGYSVILIA  52
              +K  +L L I                V   +    E+    E++ +G  VG+ +
Sbjct  10   VFLKVFKLVLNIVILILYRTGYGGDFLGVGGTWNLNEEKSPDAEIVASGVIVGFMIYTSV  69

Query  53   LFAGYLLGNPLNKKL--DLFFSLIGCAMFIASGVLILKEWENAWS-------TDTKKIAI  103
                Y  G   +K+   D   +++G  M++A G   L  W               +++ +
Sbjct  70   QLITYAFGTTAHKRELSDTIMNVVGTFMWVAVGGTALHYWHGYMPDHDFLHVATERQVGL  129

Query  104  TKSSLAVTNGVLFFFDAIFTF  124
               +L + +G L+  D +  F
Sbjct  130  AMGALCIISGALYLVDTVLAF  150


>☐ ref|XP_001984136.1| G GH16269 [Drosophila grimshawi]
 gb|EDV96484.1| G GH16269 [Drosophila grimshawi]
Length=275

 GENE ID: 6557491 Dgri\GH16269 | GH16269 gene product from transcript GH16269-RA
[Drosophila grimshawi] (10 or fewer PubMed links)

 Score = 90.2 bits (223),  Expect = 7e-17, Method: Composition-based stats.
 Identities = 19/132 (14%), Positives = 43/132 (32%), Gaps = 13/132 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGE--RDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
              + K L++ L + C+ +H              L+  GTF  + ++ +      + G
Sbjct  5    WLLFKVLQVVLDLICISIHITGSLHFAEPLPHNLIFCGTFSSFFLLSVIRCIRLIGGQRT  64
```

```
Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAW------STDTKKIA----ITKSSL-AVTN  112
                +L  ++    +      + ++  E  +        +    A      K SL  +
Sbjct  65   VLHPELIIAVCSMLLHFICAWVSMQYAEGDFHLQFMGPREELDHAYFGYCKKQSLACIVT  124

Query  113  GVLFFFDAIFTF  124
            G ++   AI
Sbjct  125  GAVYLLQAILVL  136


>☐ ref|XP_002005498.1| G GI20498 [Drosophila mojavensis]
 gb|EDW09433.1| G GI20498 [Drosophila mojavensis]
Length=209

 GENE ID: 6579616 Dmoj\GI20498 | GI20498 gene product from transcript GI20498-RA
[Drosophila mojavensis] (10 or fewer PubMed links)

 Score = 89.8 bits (222),  Expect = 8e-17, Method: Composition-based stats.
 Identities = 20/130 (15%), Positives = 42/130 (32%), Gaps = 11/130 (8%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNK  65
             ++ K LE+ L+  C   H     E       +   T+    ++ +A   G L    +
Sbjct  10   WALFKILEIFLSSACCYRHLFCYLEHQIPNVFILCATYASGVLLGVAGLVGSLFYERVAH  69

Query  66   KLDLFFS-LIGCAMFIASGVLILKEWENAWSTDTKKIAITK----------SSLAVTNGV  114
            +++   S  +G    I   V +     N   +  ++    K          ++ A
Sbjct  70   RVEALMSGTMGTLNMITVYVHMYLLEHNQLMSFLREQEQEKYAFLICCKSNATWAWFAVG  129

Query  115  LFFFDAIFTF  124
            L++    F
Sbjct  130  LYYLHCSFAL  139


>☐ ref|XP_311473.3| UG AGAP010471-PA [Anopheles gambiae str. PEST]
 gb|EAA07189.3| G AGAP010471-PA [Anopheles gambiae str. PEST]
Length=157

 GENE ID: 1272566 AgaP_AGAP010471 | AGAP010471-PA [Anopheles gambiae str. PEST]
(10 or fewer PubMed links)

 Score = 87.9 bits (217),  Expect = 3e-16, Method: Composition-based stats.
 Identities = 23/113 (20%), Positives = 45/113 (39%), Gaps = 9/113 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL--DLFFSLIGCAM  78
            +   +    E+    E++ +G FVG+ +        +  G   +K    D   +++G  M
Sbjct  38   IGGTWNLNEEKSPDAEIVASGVFVGFIIYTGVQLLTFGFGTTKHKYELSDTIMNVVGTFM  97

Query  79   FIASGVLILKEWENAWS-------TDTKKIAITKSSLAVTNGVLFFFDAIFTF  124
            ++A G   L  W    +       T  +   +   +L V NG L+  D++  F
Sbjct  98   WVAVGGTALHYWHGYLAEHDFENITSERTAGLALGALCVINGALYLADSVLAF  150


>☐ ref|XP_002008949.1| G GI13768 [Drosophila mojavensis]
 gb|EDW19425.1| G GI13768 [Drosophila mojavensis]
Length=162

 GENE ID: 6583276 Dmoj\GI13768 | GI13768 gene product from transcript GI13768-RA
[Drosophila mojavensis] (10 or fewer PubMed links)

 Score = 87.5 bits (216),  Expect = 4e-16, Method: Composition-based stats.
 Identities = 24/113 (21%), Positives = 45/113 (39%), Gaps = 9/113 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL--DLFFSLIGCAM  78
            +   +    E+    E++ +G  VG+ +        Y  G   +K    D   +++G  M
Sbjct  38   IGGTWNLNEEKSADAEIVASGVMVGFLIYTGCHTIAYFFGTTKHKGELCDTIMNVVGTFM  97

Query  79   FIASGVLILKEWENAWSTD-------TKKIAITKSSLAVTNGVLFFFDAIFTF  124
            +IA G + L  W+   S +        +++ I   SL V  G L+  D +
Sbjct  98   WIAVGGVALHYWKGYMSDEGFLYVNSERQVGIAMGSLCVIEGALYLLDTVLAC  150
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>☐ ref|XP_002050796.1| G GJ22349 [Drosophila virilis]
 gb|EDW61989.1| G GJ22349 [Drosophila virilis]
Length=219

 GENE ID: 6626080 Dvir\GJ22349 | GJ22349 gene product from transcript GJ22349-RA
[Drosophila virilis] (10 or fewer PubMed links)

 Score = 87.5 bits (216),  Expect = 4e-16, Method: Composition-based stats.
 Identities = 19/130 (14%), Positives = 35/130 (26%), Gaps = 12/130 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K  EL ++     +H   L +       L   TF   S+I I    G    +
Sbjct  10   WVLFKIFELLISSISGYVHLNGLNDG-IPHIFLPCATFGSGSIIGILSLVGTFFADQLTM  68

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITK----------SSLAVTNGV  114
                L    +G          +     N      K +   K          + L++
Sbjct  69   WFEALTSGTLGTLYLANVYAHMYLVQHNKMLPFLKDLEEEKDGYIICCKRNAILSLYAVA  128

Query  115  LFFFDAIFTF  124
            +++    F
Sbjct  129  IYYLHCTFAL  138


>☐ ref|XP_002009617.1| G GI15457 [Drosophila mojavensis]
 gb|EDW06934.1| G GI15457 [Drosophila mojavensis]
Length=119

 GENE ID: 6583957 Dmoj\GI15457 | GI15457 gene product from transcript GI15457-RA
[Drosophila mojavensis] (10 or fewer PubMed links)

 Score = 87.5 bits (216),  Expect = 4e-16, Method: Composition-based stats.
 Identities = 39/112 (34%), Positives = 62/112 (55%), Gaps = 4/112 (3%)

Query  16   LAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIG  75
            +AI CVVL+            L+  GT VGY++I   L  G+ + + + K+L+   SL+G
Sbjct  9    IAIACVVLYEVVGDLSKRP--LIVCGTIVGYTIICAVLLIGHFINSVVEKRLNALLSLLG  66

Query  76   CAMFIASGVLILKEWENAWS--TDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            C +F+ASG L++ EW +A+    D K+ A+   SL + NG +F  D +   R
Sbjct  67   CILFVASGALVIDEWHDAYDFLKDRKRNALAAGSLMIINGAVFLLDMLSICR  118


>☐ ref|XP_001973440.1| G GG16083 [Drosophila erecta]
 gb|EDV52466.1| G GG16083 [Drosophila erecta]
Length=162

 GENE ID: 6545790 Dere\GG16083 | GG16083 gene product from transcript GG16083-RA
[Drosophila erecta] (10 or fewer PubMed links)

 Score = 87.5 bits (216),  Expect = 4e-16, Method: Composition-based stats.
 Identities = 27/141 (19%), Positives = 53/141 (37%), Gaps = 23/141 (16%)

Query  7    SIVKFLELALAITC--------------VVLHYKSLGERDDTTELLTAGTFVGYSVILIA  52
              +K L+L + +                +   +    E+    E++ +G  VG+ +
Sbjct  10   IFIKALKLIINLVILFLYRWGDGGEFLGIGGTWNLNEEKSADAEIVASGVMVGFLIYTGC  69

Query  53   LFAGYLLGNPLNKKL--DLFFSLIGCAMFIASGVLILKEWENAWSTD-------TKKIAI  103
                +  G   +K    D   +++GC M+IA G + L  W+   S +        +++ I
Sbjct  70   HTIAFAFGTTKHKGELCDTIMNVVGCIMWIAVGGVALHYWKGYMSDEGFVYVNAERQVGI  129

Query  104  TKSSLAVTNGVLFFFDAIFTF  124
               SL V  G L+  D +
Sbjct  130  AMGSLCVIEGALYLLDTVLAC  150


>☐ ref|XP_002009021.1| G GI11493 [Drosophila mojavensis]
 gb|EDW19497.1| G GI11493 [Drosophila mojavensis]
Length=175
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 GENE ID: 6583351 Dmoj\GI11493 | GI11493 gene product from transcript GI11493-RA
[Drosophila mojavensis] (10 or fewer PubMed links)

 Score = 87.5 bits (216),  Expect = 4e-16, Method: Composition-based stats.
 Identities = 26/133 (19%), Positives = 51/133 (38%), Gaps = 13/133 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLL  59
            L  +K +EL L I C+ L  +                 L   TF   ++         L
Sbjct  35   LITIKVVELCLLICCLGLIDEPATNSHLRVFITPRVMALCYVTFGALTIYTAIYLIMALF  94

Query  60   GNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTN  112
            G+    +    +SL G  ++IA   L+ ++W N    +          + +  +S+++
Sbjct  95   GDLTPWRTATLWSLAGFILYIAVTALLFRDWSNTKDRNYWHPNMHRLDLVMASASISLVT  154

Query  113  GVLFFFDAIFTFR  125
            G+++  D + T R
Sbjct  155  GLIYLLDVLLTIR  167


>☐ ref|XP_001956640.1| G GF25311 [Drosophila ananassae]
 gb|EDV39446.1| G GF25311 [Drosophila ananassae]
Length=162

 GENE ID: 6507934 Dana\GF25311 | GF25311 gene product from transcript GF25311-RA
[Drosophila ananassae] (10 or fewer PubMed links)

 Score = 87.1 bits (215),  Expect = 5e-16, Method: Composition-based stats.
 Identities = 27/141 (19%), Positives = 52/141 (36%), Gaps = 23/141 (16%)

Query  7    SIVKFLELALAITCV--------------VLHYKSLGERDDTTELLTAGTFVGYSVILIA  52
              +K L+L + +  +                 +    E+    E++ +G  VG+ +
Sbjct  10   IFIKALKLIINLVIIFLYRWGDGGEFLGIGGTWNLNEEKSADAEIVASGVMVGFLIYTGC  69

Query  53   LFAGYLLGNPLNKKL--DLFFSLIGCAMFIASGVLILKEWENAWSTD-------TKKIAI  103
                Y  G   +K    D   +++G  M+IA G + L  W+   S +        +++ I
Sbjct  70   HTIAYAFGTTKHKGELCDTIMNVVGTIMWIAVGGVALHYWKGYMSDEGFLYVNSERQVGI  129

Query  104  TKSSLAVTNGVLFFFDAIFTF  124
               SL V  G L+  D +
Sbjct  130  AMGSLCVIEGALYLLDTVLAC  150


>☐ ref|XP_002048071.1| G GJ13758 [Drosophila virilis]
 gb|EDW70413.1| G GJ13758 [Drosophila virilis]
Length=162

 GENE ID: 6624462 Dvir\GJ13758 | GJ13758 gene product from transcript GJ13758-RA
[Drosophila virilis] (10 or fewer PubMed links)

 Score = 87.1 bits (215),  Expect = 5e-16, Method: Composition-based stats.
 Identities = 25/113 (22%), Positives = 46/113 (40%), Gaps = 9/113 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL--DLFFSLIGCAM  78
            +   +    E+    E++ +G  VG+ +        YL G   +K    D   +++G  M
Sbjct  38   IGGTWNLNEEKSADAEIVASGVMVGFFIYTACHTIAYLFGTTKHKGELCDTIMNVVGTFM  97

Query  79   FIASGVLILKEWENAWSTD-------TKKIAITKSSLAVTNGVLFFFDAIFTF  124
            +IA G + L  W+   S +        +++ I   SL V  G L+  D +
Sbjct  98   WIAVGGVALHYWKGYMSDEGFLYVNSERQVGIAMGSLCVIEGALYLLDTVLAC  150


>☐ ref|NP_649184.1| UG CG6981, isoform A [Drosophila melanogaster]
 ref|NP_730487.1| G CG6981, isoform B [Drosophila melanogaster]
 ref|XP_002095512.1| G GE19647 [Drosophila yakuba]
 32 more sequence titles

ref|XP_002085601.1| UG GD14857 [Drosophila simulans]
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 gb|AAF49062.1|  CG6981, isoform A [Drosophila melanogaster]
 gb|AAG22313.1|  CG6981, isoform B [Drosophila melanogaster]
 gb|AAK93461.1|  LP03829p [Drosophila melanogaster]
 emb|CAL26659.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26660.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26661.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26662.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26663.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26664.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26665.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26666.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26667.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26668.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26669.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26670.1|  CG6981 [Drosophila melanogaster]
 emb|CAL26671.1|  CG6981 [Drosophila simulans]
 gb|EDW95224.1|  GE19647 [Drosophila yakuba]
 gb|EDX11186.1|  GD14857 [Drosophila simulans]
 gb|ACL90605.1|  CG6981-PA [synthetic construct]
 emb|CAR93744.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93745.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93746.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93747.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93748.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93749.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93750.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93751.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93752.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93753.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93754.1|  CG6981-PA [Drosophila melanogaster]
 emb|CAR93755.1|  CG6981-PA [Drosophila melanogaster]
Length=162

 GENE ID: 40207 CG6981 | CG6981 gene product from transcript CG6981-RB
[Drosophila melanogaster] (Over 10 PubMed links)

 Score = 87.1 bits (215),  Expect = 5e-16, Method: Composition-based stats.
 Identities = 27/141 (19%), Positives = 53/141 (37%), Gaps = 23/141 (16%)

Query  7    SIVKFLELALAITCV--------------VLHYKSLGERDDTTELLTAGTFVGYSVILIA  52
              +K L+L + +  +                 +    E+    E++ +G  VG+ +
Sbjct  10   IFIKALKLIINLVIIFLYRWGDGGEFLGIGGTWNLNEEKSADAEIVASGVMVGFLIYTGC  69

Query  53   LFAGYLLGNPLNKKL--DLFFSLIGCAMFIASGVLILKEWENAWSTD-------TKKIAI  103
                +  G   +K    D   +++GC M+IA G + L  W+   S +        +++ I
Sbjct  70   HTIAFAFGTTKHKGELCDTIMNVVGCIMWIAVGGVALHYWKGYMSDEGFLYVNSERQVGI  129

Query  104  TKSSLAVTNGVLFFFDAIFTF  124
               SL V  G L+  D +
Sbjct  130  AMGSLCVIEGALYLLDTVLAC  150


>☐ ref|XP_001984238.1|  GH15117 [Drosophila grimshawi]
 gb|EDV96586.1|  GH15117 [Drosophila grimshawi]
Length=162

 GENE ID: 6556525 Dgri\GH15117 | GH15117 gene product from transcript GH15117-RA
[Drosophila grimshawi] (10 or fewer PubMed links)
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 Score = 87.1 bits (215),  Expect = 5e-16, Method: Composition-based stats.
 Identities = 25/113 (22%), Positives = 46/113 (40%), Gaps = 9/113 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL--DLFFSLIGCAM  78
            +   +    E+    E++ +G  VG+ +        YL G   +K    D   +++G  M
Sbjct  38   IGGTWNLNEEKSADAEIVASGVMVGFLIYTGCHTIAYLFGTTKHKGELCDTIMNVVGTIM  97

Query  79   FIASGVLILKEWENAWSTD-------TKKIAITKSSLAVTNGVLFFFDAIFTF  124
            +IA G + L  W+   S +        +++ I   SL V  G L+  D +
Sbjct  98   WIAVGGVALHYWKGYMSDEGFLYVNSERQVGIAMGSLCVIEGALYLLDTVLAC  150


>☐ ref|XP_002061902.1| G GK16939 [Drosophila willistoni]
 gb|EDW72888.1| G GK16939 [Drosophila willistoni]
Length=162

 GENE ID: 6639374 Dwil\GK16939 | GK16939 gene product from transcript GK16939-RA
[Drosophila willistoni] (10 or fewer PubMed links)

 Score = 87.1 bits (215),  Expect = 5e-16, Method: Composition-based stats.
 Identities = 26/141 (18%), Positives = 52/141 (36%), Gaps = 23/141 (16%)

Query  7    SIVKFLELALAITCV--------------VLHYKSLGERDDTTELLTAGTFVGYSVILIA  52
              +K L+L + +  +                 +    E+    E++ +G  VG+ +
Sbjct  10   IFIKALKLVINLVIIFLYRWGDGGEFLGIGGTWNLNEEKSADAEIVASGVMVGFLIYTGC  69

Query  53   LFAGYLLGNPLNKKL--DLFFSLIGCAMFIASGVLILKEWENAWSTD-------TKKIAI  103
                Y  G   +K    D   +++G  M++A G + L  W+   S +        +++ I
Sbjct  70   HTIAYAFGTTKHKGELCDTIMNVVGVFMWVAVGGVALHYWKGYMSDEGFLYVNSERQVGI  129

Query  104  TKSSLAVTNGVLFFFDAIFTF  124
               SL V  G L+  D +
Sbjct  130  AMGSLCVIEGALYLLDTVLAC  150


>☐ ref|XP_002086307.1| G GE23065 [Drosophila yakuba]
 gb|EDW99708.1| G GE23065 [Drosophila yakuba]
Length=162

 GENE ID: 6539416 Dyak\GE23065 | GE23065 gene product from transcript GE23065-RA
[Drosophila yakuba] (10 or fewer PubMed links)

 Score = 87.1 bits (215),  Expect = 6e-16, Method: Composition-based stats.
 Identities = 27/141 (19%), Positives = 53/141 (37%), Gaps = 23/141 (16%)

Query  7    SIVKFLELALAITCV--------------VLHYKSLGERDDTTELLTAGTFVGYSVILIA  52
              +K L+L + +  +                 +    E+    E++ +G  VG+ +
Sbjct  10   IFIKALKLIINLVIIFLYRWGDGGEFLGIGGTWNLNEEKSADAEIVASGVMVGFFIYTGC  69

Query  53   LFAGYLLGNPLNKKL--DLFFSLIGCAMFIASGVLILKEWENAWSTD-------TKKIAI  103
                +  G   +K    D   +++GC M+IA G + L  W+   S +        +++ I
Sbjct  70   HTIAFAFGTTKHKGELCDTIMNVVGCIMWIAVGGVALHYWKGYMSDEGFLYVNSERQVGI  129

Query  104  TKSSLAVTNGVLFFFDAIFTF  124
               SL V  G L+  D +
Sbjct  130  AMGSLCVIEGALYLLDTVLAC  150


>☐ ref|XP_002040612.1| G GM22258 [Drosophila sechellia]
 gb|EDW44165.1| G GM22258 [Drosophila sechellia]
Length=162

 GENE ID: 6616248 Dsec\GM22258 | GM22258 gene product from transcript GM22258-RA
[Drosophila sechellia] (10 or fewer PubMed links)

 Score = 87.1 bits (215),  Expect = 6e-16, Method: Composition-based stats.
 Identities = 23/113 (20%), Positives = 46/113 (40%), Gaps = 9/113 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL--DLFFSLIGCAM  78
            +   +    E+    E++ +G  VG+ +        +  G   +K    D   +++GC M
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Sbjct  38   IGGTWNLNEEKSADAEIVASGVMVGFLIYTGCHTIAFAFGTTKHKGELCDTIMNVVGCIM  97

Query  79   FIASGVLILKEWENAWSTD-------TKKIAITKSSLAVTNGVLFFFDAIFTF  124
            +IA G + L  W+   + +        +++ I   SL V  G L+  D +
Sbjct  98   WIAVGGVALHYWKGYMADEGFLYVNSERQVGIAMGSLCVIEGALYLLDTVLAC  150


>☐ emb|CBE66942.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66943.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66944.1|  CG6981-PA [Drosophila ananassae]
 9 more sequence titles

emb|CBE66945.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66946.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66947.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66948.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66949.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66950.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66951.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66952.1|  CG6981-PA [Drosophila ananassae]
 emb|CBE66953.1|  CG6981-PA [Drosophila ananassae]
Length=164

 Score = 86.8 bits (214),  Expect = 6e-16, Method: Composition-based stats.
 Identities = 25/112 (22%), Positives = 46/112 (41%), Gaps = 8/112 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL-DLFFSLIGCAMF  79
            +   +    E+    E++ +G  VG+ +        Y  G   +K L D   +++G  M+
Sbjct  41   IGGTWNLNEEKSADAEIVASGVMVGFLIYTGCHTIAYAFGTTKHKGLCDTIMNVVGTIMW  100

Query  80   IASGVLILKEWENAWSTD-------TKKIAITKSSLAVTNGVLFFFDAIFTF  124
            IA G + L  W+   S +        +++ I   SL V  G L+  D +
Sbjct  101  IAVGGVALHYWKGYMSDEGFLYVNSERQVGIAMGSLCVIEGALYLLDTVLAC  152


>☐ ref|XP_001353299.1| G GA20002 [Drosophila pseudoobscura pseudoobscura]
 ref|XP_002021019.1| G GL25117 [Drosophila persimilis]
 gb|EAL30802.1| G GA20002 [Drosophila pseudoobscura pseudoobscura]
 gb|EDW40175.1| G GL25117 [Drosophila persimilis]
Length=162

 GENE ID: 4813568 Dpse\GA20002 | GA20002 gene product from transcript GA20002-RA
[Drosophila pseudoobscura pseudoobscura] (10 or fewer PubMed links)

 Score = 86.8 bits (214),  Expect = 7e-16, Method: Composition-based stats.
 Identities = 28/141 (19%), Positives = 53/141 (37%), Gaps = 23/141 (16%)

Query  7    SIVKFLELALAITCV--------------VLHYKSLGERDDTTELLTAGTFVGYSVILIA  52
              +K L+L + +  +                 +    E+    E++ +G  VG+ +
Sbjct  10   IFIKALKLIINLVIIFLYRWGDGGEFLGIGGTWNLNEEKSADAEIVGSGVMVGFLIYTGC  69

Query  53   LFAGYLLGNPLNKKL--DLFFSLIGCAMFIASGVLILKEWENAWSTD-------TKKIAI  103
                Y  G   +K    D   +++GC M+IA G + L  W+   S +        +++ I
Sbjct  70   HTIAYAFGTTKHKGELCDTIMNVVGCIMWIAVGGVALHYWKGYMSDEGFLYVNSERQVGI  129

Query  104  TKSSLAVTNGVLFFFDAIFTF  124
               SL V  G L+  D +
Sbjct  130  AMGSLCVIEGALYLLDTVLAC  150


>☐ ref|XP_976275.1| UG PREDICTED: similar to conserved hypothetical protein [Tribolium
castaneum]
 gb|EFA08062.1| G hypothetical protein TcasGA2_TC005658 [Tribolium castaneum]
Length=325

 GENE ID: 658222 TcasGA2_TC005658 | hypothetical protein LOC658222
[Tribolium castaneum] (10 or fewer PubMed links)

 Score = 86.8 bits (214),  Expect = 7e-16, Method: Composition-based stats.
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 Identities = 37/146 (25%), Positives = 56/146 (38%), Gaps = 27/146 (18%)

Query  1    MAVS--RLSIVKFLELALAITCVVLHYKSLGER----------------------DDTTE  36
            MA++  R +I+K LE+A  I C+     +  E                       D+
Sbjct  1    MAINFDRWTILKLLEVASTIACLAFKRVTDDEASRLFLYLQKLSREWRILNNVTWDNVGA  60

Query  37   LLTAGTFVGYSVILIALFAGYLLGN-PLNKKLDLFFSL-IGCAMFIASGVLILKEWENAW  94
             +   T+ GY +I   ALF G L G  P  K++  F  L +G  +FI  G L      ++
Sbjct  61   AVADTTYGGYLIITTALFIGRLTGELPTQKRITEFVLLGVGTLLFIILGSLEFAA-LDSV  119

Query  95   STDTKKIAITKSSLAVTNGVLFFFDA  120
              D    A    +L +    LF  D
Sbjct  120  PEDLVDNAAVIGTLTLVTAALFLLDM  145


>☐ ref|XP_002047884.1|  GJ13688 [Drosophila virilis]
 gb|EDW70226.1|  GJ13688 [Drosophila virilis]
Length=175

 GENE ID: 6624117 Dvir\GJ13688 | GJ13688 gene product from transcript GJ13688-RA
[Drosophila virilis] (10 or fewer PubMed links)

 Score = 86.4 bits (213),  Expect = 8e-16, Method: Composition-based stats.
 Identities = 24/133 (18%), Positives = 50/133 (37%), Gaps = 13/133 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLL  59
            L  +K +EL L I C+ L  +                 L   TF   ++         L
Sbjct  35   LISIKVVELCLLICCLGLIDEPATNSHLRIFITPRVMALCYVTFGALAIYTAIYLIMALF  94

Query  60   GNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTN  112
            G+    +    +SL+G  +F+A   L+ ++W      +          + +  +S+++
Sbjct  95   GDLTPWRTATLWSLVGFVLFVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASISLVT  154

Query  113  GVLFFFDAIFTFR  125
             +++  D + T R
Sbjct  155  ALVYLLDVLLTIR  167


>☐ ref|XP_002074415.1|  GK10529 [Drosophila willistoni]
 gb|EDW85401.1|  GK10529 [Drosophila willistoni]
Length=175

 GENE ID: 6651960 Dwil\GK10529 | GK10529 gene product from transcript GK10529-RA
[Drosophila willistoni] (10 or fewer PubMed links)

 Score = 86.0 bits (212),  Expect = 1e-15, Method: Composition-based stats.
 Identities = 24/133 (18%), Positives = 52/133 (39%), Gaps = 13/133 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLL  59
            L  VK +EL L I C+ L  +                 L+  TF   ++         L
Sbjct  35   LICVKVVELCLLICCLGLIDEPATNSHLRVFITPRVMALSYVTFGALTIYTAIYLIMALF  94

Query  60   GNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTN  112
            G+    +  + ++L+G  ++IA   L+ ++W      +          + +  +S+++
Sbjct  95   GDLPPWRTSVLWALVGFVLYIAVTALLFRDWATTKDRNYWHPNMHRLDLVMASASISLVT  154

Query  113  GVLFFFDAIFTFR  125
             +++  D + T R
Sbjct  155  ALVYLLDVLLTIR  167


>☐ emb|CBE67045.1|  CG6981-PA [Drosophila atripex]
Length=164

 Score = 86.0 bits (212),  Expect = 1e-15, Method: Composition-based stats.
 Identities = 24/112 (21%), Positives = 46/112 (41%), Gaps = 8/112 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL-DLFFSLIGCAMF  79
            +   +    E+    E++ +G  VG+ +        +  G   +K L D   +++G  M+
Sbjct  41   IGGTWNLNEEKSADAEIVASGVMVGFLIYTGCHTIAFAFGTTKHKGLCDTIMNVVGTIMW  100
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Query  80   IASGVLILKEWENAWSTD-------TKKIAITKSSLAVTNGVLFFFDAIFTF  124
            IA G + L  W+   S +        +++ I   SL V  G L+  D +
Sbjct  101  IAVGGVALHYWKGYMSDEGFLYVNSERQVGIAMGSLCVIEGALYLLDTVLAC  152


>☐ ref|XP_001948670.1| G PREDICTED: similar to CG13566 CG13566-PA, partial [Acyrthosiphon
pisum]
Length=439

 GENE ID: 100168034 LOC100168034 | similar to CG13566 CG13566-PA
[Acyrthosiphon pisum]

 Score = 86.0 bits (212),  Expect = 1e-15, Method: Composition-based stats.
 Identities = 32/104 (30%), Positives = 52/104 (50%), Gaps = 4/104 (3%)

Query  25   YKSLGE--RDDTTELLTAGTFVGYSVILIALFAGYLLGNPLN-KKLDLFFSLIGCAMFIA  81
            +  L    R+    L    TF GY +I +AL+  YL+G   N KK + F  +IG A+FIA
Sbjct  31   WPLLNNITRNGAGSLFADVTFGGYIIICVALYIAYLMGELKNSKKTESFLLVIGAALFIA  90

Query  82   SGVLILKEWENAWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
             G L+L    ++   +    A+   +L++  G++F  D   + R
Sbjct  91   VGCLVLTA-VDSVPGNLIVNALVLGTLSIVTGMVFVLDTCLSNR  133


>☐ ref|XP_002030493.1| G GM25471 [Drosophila sechellia]
 gb|EDW41479.1| G GM25471 [Drosophila sechellia]
Length=175

 GENE ID: 6605675 Dsec\GM25471 | GM25471 gene product from transcript GM25471-RA
[Drosophila sechellia] (10 or fewer PubMed links)

 Score = 86.0 bits (212),  Expect = 1e-15, Method: Composition-based stats.
 Identities = 24/132 (18%), Positives = 49/132 (37%), Gaps = 13/132 (9%)

Query  7    SIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLLG  60
              +K +EL L I C+ L  +                 L   TF   ++         L G
Sbjct  36   ICIKIVELCLLICCLGLIDEPATNSHLRVFITPRVASLCYVTFGALTIYTAIYLIMALFG  95

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTNG  113
            +    +    ++L+G  +F+A   L+ ++W      +          + +  +S+A+
Sbjct  96   DLTPWRTATLWNLVGFVLFVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASIALVTS  155

Query  114  VLFFFDAIFTFR  125
            ++F  D + T R
Sbjct  156  LVFLLDILITLR  167


>☐ ref|XP_002084862.1| G GD14494 [Drosophila simulans]
 gb|EDX10447.1| G GD14494 [Drosophila simulans]
Length=175

 GENE ID: 6738047 Dsim\GD14494 | GD14494 gene product from transcript GD14494-RA
[Drosophila simulans] (10 or fewer PubMed links)

 Score = 85.6 bits (211),  Expect = 1e-15, Method: Composition-based stats.
 Identities = 24/132 (18%), Positives = 49/132 (37%), Gaps = 13/132 (9%)

Query  7    SIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLLG  60
              +K +EL L I C+ L  +                 L   TF   ++         L G
Sbjct  36   ICIKIVELCLLICCLGLIDEPATNSHLRVFITPRVASLCYVTFGALTIYTAIYLIMALFG  95

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTNG  113
            +    +    ++L+G  +F+A   L+ ++W      +          + +  +S+A+
Sbjct  96   DLTPWRTATLWNLVGFVLFVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASIALVTS  155

Query  114  VLFFFDAIFTFR  125
            ++F  D + T R
Sbjct  156  LVFLLDILITLR  167
```

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>☐ ref|XP_002074859.1|  GK19222 [Drosophila willistoni]
 gb|EDW85845.1|  GK19222 [Drosophila willistoni]
Length=211

 GENE ID: 6652138 Dwil\GK19222 | GK19222 gene product from transcript GK19222-RA
[Drosophila willistoni] (10 or fewer PubMed links)

 Score = 85.6 bits (211),  Expect = 2e-15, Method: Composition-based stats.
 Identities = 16/96 (16%), Positives = 27/96 (28%), Gaps = 1/96 (1%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGN-PLN  64
              + K LEL L+     +H +           L   T+ G ++I      G      P
Sbjct  10   WLLFKVLELVLSGVGCYVHIRCFQSEGTPHIFLLCATYGGSAIICALSIIGMFYAEKPTM  69

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKK  100
            K       L+G    +     +     +      K
Sbjct  70   KLEAAISGLLGTLHMLTVYANMYLAEHDIELMFLKN  105


>☐ ref|XP_002043968.1|  GM13685 [Drosophila sechellia]
 gb|EDW51256.1|  GM13685 [Drosophila sechellia]
Length=247

 GENE ID: 6619754 Dsec\GM13685 | GM13685 gene product from transcript GM13685-RA
[Drosophila sechellia] (10 or fewer PubMed links)

 Score = 85.6 bits (211),  Expect = 2e-15, Method: Composition-based stats.
 Identities = 36/92 (39%), Positives = 54/92 (58%), Gaps = 1/92 (1%)

Query  35   TELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENA-  93
              ++ AGT  GY+VI   L  G++L + + K+L+  FSLIGC +F+ASG L++ EW
Sbjct  155  HPVIVAGTVGGYTVICGVLLIGHVLNSLVEKRLNALFSLIGCLLFVASGALVIDEWHGGL  214

Query  94   WSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
             +TD K+ AI   SL + N  +F  D +   R
Sbjct  215  LNTDRKRQAIGAGSLMIINAAVFLLDTLCICR  246


 Score = 71.0 bits (173),  Expect = 3e-11, Method: Composition-based stats.
 Identities = 31/133 (23%), Positives = 60/133 (45%), Gaps = 20/133 (15%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIAL-------  53
            M  +    ++K +EL    +T ++L             LL  GT +GY +    +
Sbjct  1    MEFNNRLLLKIIELVFIVTSIILIESISDLTFIRQALLVHGTLMGYLITCFVIATGKSQD  60

Query  54   ------------FAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENA-WSTDTKK  100
                        F+G++ G  ++K+LD+ FS+ G  +F A+G +IL +W     S + ++
Sbjct  61   ASNLAPVYEMDMFSGHVSGTVVDKRLDILFSIGGFFLFGAAGTIILAQWLGYCKSQEERE  120

Query  101  IAITKSSLAVTNG  113
            + +    L++ NG
Sbjct  121  VLLASGILSLANG  133


>☐ ref|XP_001354994.2|  GA20224 [Drosophila pseudoobscura pseudoobscura]
 gb|EAL32050.2|  GA20224 [Drosophila pseudoobscura pseudoobscura]
Length=228

 GENE ID: 4815142 Dpse\GA20224 | GA20224 gene product from transcript GA20224-RA
[Drosophila pseudoobscura pseudoobscura] (10 or fewer PubMed links)

 Score = 85.2 bits (210),  Expect = 2e-15, Method: Composition-based stats.
 Identities = 33/90 (36%), Positives = 53/90 (58%), Gaps = 1/90 (1%)

Query  37   LLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWST  96
            L+  GT  G+++I   L  G+++ + + K+L+   SLIGC +F+ASG L++ EW +A
Sbjct  138  LIVCGTIGGFTIICGVLLIGHVINSLVEKRLNALISLIGCILFVASGALVIDEWHDAVLQ  197

Query  97   -DTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
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             D K+ AI   SL + NG +F  D +   R
Sbjct  198  KDRKRNAIAAGSLMIINGAVFLLDTLSICR  227


 Score = 82.9 bits (204),  Expect = 1e-14, Method: Composition-based stats.
 Identities = 32/114 (28%), Positives = 59/114 (51%), Gaps = 1/114 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K +EL    T ++L       R  +  +L  GT  GY++I   L  G+L+G
Sbjct  1    MEFNNRLLLKIIELTFIATSIILIESVADHRYSSQAMLVCGTLTGYAIICATLGIGHLVG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDT-KKIAITKSSLAVTNG  113
              ++K++D+ FS+    +FIASG +IL  W + +  ++ K   +  +   + NG
Sbjct  61   ANIDKRIDVLFSVAAVILFIASGAVILDRWLDVYEVESDKNSVLAAAIFCLANG  114


>☐ ref|XP_001984986.1| GH14752 [Drosophila grimshawi]
 gb|EDV97334.1| GH14752 [Drosophila grimshawi]
Length=175

 GENE ID: 6556977 Dgri\GH14752 | GH14752 gene product from transcript GH14752-RA
[Drosophila grimshawi] (10 or fewer PubMed links)

 Score = 85.2 bits (210),  Expect = 2e-15, Method: Composition-based stats.
 Identities = 23/133 (17%), Positives = 50/133 (37%), Gaps = 13/133 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLL  59
            L  +K +EL L I C+ L  +                 L   TF   ++         L
Sbjct  35   LITIKVVELCLLICCLGLIDEPATNSQLRVFITPRVMALCYVTFGALAIYTAIYLIMALF  94

Query  60   GNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTN  112
            G+    +    +SL+G  +++A   L+ ++W      +          + +  +S+++
Sbjct  95   GDLSPWRTATLWSLVGFVLYVAVTALLFQDWSTTKDRNYWHPNMHRLDLVMASASISLVT  154

Query  113  GVLFFFDAIFTFR  125
             +++  D + T R
Sbjct  155  ALVYLLDVLLTIR  167


>☐ ref|XP_002075211.1| GK16752 [Drosophila willistoni]
 gb|EDW86197.1| GK16752 [Drosophila willistoni]
Length=206

 GENE ID: 6652874 Dwil\GK16752 | GK16752 gene product from transcript GK16752-RA
[Drosophila willistoni] (10 or fewer PubMed links)

 Score = 84.8 bits (209),  Expect = 2e-15, Method: Composition-based stats.
 Identities = 38/112 (33%), Positives = 62/112 (55%), Gaps = 3/112 (2%)

Query  15   ALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLI  74
            A+AI C+V++            L+  GT  G+++I   L  G+++ + + K+L+   SLI
Sbjct  96   AIAIACIVMYEVDGALSSRP--LIVCGTIGGFAIICGVLLIGHVINSLVEKRLNALISLI  153

Query  75   GCAMFIASGVLILKEWENAWST-DTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            GC +F+ASG L++ EW +A    D K+ AI   SL + NG +F  D +   R
Sbjct  154  GCILFVASGALVIDEWHDALLQKDRKRNAIAAGSLMIINGAVFLLDTLSICR  205


 Score = 77.1 bits (189),  Expect = 5e-13, Method: Composition-based stats.
 Identities = 29/96 (30%), Positives = 55/96 (57%), Gaps = 0/96 (0%)

Query  1   MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
           M  +   ++K +ELA  +T ++L          +  +L  GT  GY++I   L  G+LLG
Sbjct  1   MEFNNRLLLKIIELAFTMTSIILIESVADHSYSSQAMLICGTLTGYTIICATLALGHLLG  60

Query  61  NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWST  96
             +++++D+ F++ GC +FI+SG +IL  W  +++
Sbjct  61  AKVDRRIDILFAVAGCILFISSGAIILDRWLGSFTA  96
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>☐ ref|XP_002022417.1| G GL13023 [Drosophila persimilis]
 gb|EDW26452.1| G GL13023 [Drosophila persimilis]
Length=228

 GENE ID: 6597409 Dper\GL13023 | GL13023 gene product from transcript GL13023-RA
[Drosophila persimilis] (10 or fewer PubMed links)

 Score = 84.8 bits (209),  Expect = 2e-15, Method: Composition-based stats.
 Identities = 33/90 (36%), Positives = 53/90 (58%), Gaps = 1/90 (1%)

Query  37   LLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWST  96
            L+  GT  G+++I   L  G+++ + + K+L+   SLIGC +F+ASG L++ EW +A
Sbjct  138  LIVCGTIGGFTIICGVLLIGHVINSLVEKRLNALISLIGCILFVASGALVIDEWHDAVLQ  197

Query  97   -DTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
             D K+ AI   SL + NG +F  D +   R
Sbjct  198  KDRKRNAIAAGSLMIINGAVFLLDTLSICR  227


 Score = 82.1 bits (202),  Expect = 2e-14, Method: Composition-based stats.
 Identities = 32/114 (28%), Positives = 59/114 (51%), Gaps = 1/114 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K +EL    T ++L       R  +  +L  GT  GY++I   L  G+L+G
Sbjct  1    MEFNNRLLLKIIELTFIATSIILIESVADHRYSSQAMLVCGTLTGYAIICATLGIGHLVG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDT-KKIAITKSSLAVTNG  113
              ++K++D+ FS+    +FIASG +IL  W + +  ++ K   +  +   + NG
Sbjct  61   ANIDKRIDVLFSVAAVILFIASGAVILDRWLDVYEIESDKNSVLAAAIFCLANG  114
```

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>☐ ref|XP_001986174.1| G GH21210 [Drosophila grimshawi]
 gb|EDW01041.1| G GH21210 [Drosophila grimshawi]
Length=195

 GENE ID: 6559580 Dgri\GH21210 | GH21210 gene product from transcript GH21210-RA
[Drosophila grimshawi] (10 or fewer PubMed links)

 Score = 84.8 bits (209),  Expect = 2e-15, Method: Composition-based stats.
 Identities = 14/130 (10%), Positives = 36/130 (27%), Gaps = 11/130 (8%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFV-GYSVILIALFAGYLLGNPLN  64
              + K LE  L+  C  +H K           +   T+  G  + ++ +   +
Sbjct  10   WLLFKLLETILSSICCYVHIKCFESDGVPDIFILCATYGSGCVIGILGILCSFFTLKLNL  69

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKI----------AITKSSLAVTNGV  114
                +   ++G          +     +      K              T ++L++
Sbjct  70   TTEAITSGVLGSLHLFTVYAHMYLAEHDKLLAFFKDHEKDSYGFLCCCQTNATLSLYAVA  129

Query  115  LFFFDAIFTF  124
            +++    F
Sbjct  130  VYYLHCNFAL  139
```

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>☐ ref|XP_001972737.1| G GG15688 [Drosophila erecta]
 gb|EDV51763.1| G GG15688 [Drosophila erecta]
Length=175

 GENE ID: 6545924 Dere\GG15688 | GG15688 gene product from transcript GG15688-RA
[Drosophila erecta] (10 or fewer PubMed links)

 Score = 84.4 bits (208),  Expect = 3e-15, Method: Composition-based stats.
 Identities = 23/132 (17%), Positives = 49/132 (37%), Gaps = 13/132 (9%)

Query  7    SIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLLG  60
              +K +EL L I C+ L  +                 L   TF   ++         L G
Sbjct  36   ICIKIVELCLLICCLGLIDEPATNSHLRVFITPRVASLCYVTFGALTIYTAIYLIMALFG  95

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTNG  113
            +    +    ++L+G  +F+A   L+ ++W      +          + +  +S+++
```

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Sbjct  96   DMTPWRTTTLWNLVGFVLFVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASISLVTS  155

Query  114  VLFFFDAIFTFR  125
            ++F  D + T R
Sbjct  156  LVFLLDILITLR  167


>☐ ref|XP_001956408.1| G GF24609 [Drosophila ananassae]
 gb|EDV39214.1| G GF24609 [Drosophila ananassae]
Length=175

 GENE ID: 6507240 Dana\GF24609 | GF24609 gene product from transcript GF24609-RA
[Drosophila ananassae] (10 or fewer PubMed links)

 Score = 84.4 bits (208),  Expect = 3e-15, Method: Composition-based stats.
 Identities = 24/133 (18%), Positives = 50/133 (37%), Gaps = 13/133 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLL  59
            L  +K +EL L I C+ L  +                 L   TF   ++         L
Sbjct  35   LICIKVVELCLLICCLGLIDEPATNSHLRVFITPRVMALCYVTFGALAIYTAIYLIMALF  94

Query  60   GNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTN  112
            G+    +    ++L+G  +F+A   L+ ++W      +          + +  +S+++
Sbjct  95   GDMTPWRTATLWALVGFCLFVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASISLVT  154

Query  113  GVLFFFDAIFTFR  125
             ++F  D + T R
Sbjct  155  SLVFLLDILITIR  167


>☐ ref|XP_001843280.1| UG conserved hypothetical protein [Culex quinquefasciatus]
 gb|EDS31782.1| G conserved hypothetical protein [Culex quinquefasciatus]
Length=148

 GENE ID: 6032733 CpipJ_CPIJ001382 | hypothetical protein
[Culex quinquefasciatus]

 Score = 84.1 bits (207),  Expect = 4e-15, Method: Composition-based stats.
 Identities = 28/134 (20%), Positives = 48/134 (35%), Gaps = 13/134 (9%)

Query  5    RLSIVKFLELALAITCVVLHYKSLGER------DDTTELLTAGTFVGYSVILIALFAGYL  58
             L+    L  A+AI C+ L                 T  L   TFV + +  +    G +
Sbjct  7    NLAFYYALGNAVAIICIGLIDDPANNSRFRVFLATRTASLAYSTFVPFLIFSVIYLFGKV  66

Query  59   LGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAW-------STDTKKIAITKSSLAVT  111
            +   +  KL    +L    +++AS   IL +W           +T          ++AV
Sbjct  67   IRENIPWKLQSLLNLTAFILYLASAACILNDWSETKTRNYWPPNTQRMDYMCGAGAVAVI  126

Query  112  NGVLFFFDAIFTFR  125
              +++  D I T R
Sbjct  127  GALIYLLDLIVTVR  140


>☐ ref|XP_002094795.1| G GE22019 [Drosophila yakuba]
 gb|EDW94507.1| G GE22019 [Drosophila yakuba]
Length=175

 GENE ID: 6534109 Dyak\GE22019 | GE22019 gene product from transcript GE22019-RA
[Drosophila yakuba] (10 or fewer PubMed links)

 Score = 84.1 bits (207),  Expect = 5e-15, Method: Composition-based stats.
 Identities = 22/132 (16%), Positives = 48/132 (36%), Gaps = 13/132 (9%)

Query  7    SIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLLG  60
              +K +EL L I C+ L  +                 L   TF   ++         L G
Sbjct  36   ICIKIVELCLLICCLGLIDEPATNSHLRVFITPRVASLCYVTFGALTIYTAIYLIMALFG  95

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTNG  113
            +    +    ++L+   +F+A   L+ ++W      +          + +  +S+A+
Sbjct  96   DLTPWRTATLWNLVAFVLFVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASIALVTS  155
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Query  114  VLFFFDAIFTFR  125
            +++  D + T R
Sbjct  156  LVYLLDILITLR  167


>☐ ref|XP_002027022.1| G GL21019 [Drosophila persimilis]
 gb|EDW34837.1| G GL21019 [Drosophila persimilis]
Length=175

 GENE ID: 6601975 Dper\GL21019 | GL21019 gene product from transcript GL21019-RA
[Drosophila persimilis] (10 or fewer PubMed links)

 Score = 83.7 bits (206),  Expect = 5e-15, Method: Composition-based stats.
 Identities = 23/133 (17%), Positives = 50/133 (37%), Gaps = 13/133 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLL  59
            L  +K +EL L I C+ L  +                 L   TF   ++         L+
Sbjct  35   LICIKVVELCLLICCLGLIDEPATNSHLRVFITPRVIALCYVTFGALTIYTAIYLIMALV  94

Query  60   GNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTN  112
            G+    +    +SL+   +++A   L+ ++W      +          + +  +S+A+
Sbjct  95   GDLTPWRTATLWSLVAFCLYVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASIALVT  154

Query  113  GVLFFFDAIFTFR  125
             +++  D + T R
Sbjct  155  SLVYLLDILLTIR  167


>☐ ref|XP_002007920.1| G GI13205 [Drosophila mojavensis]
 gb|EDW18396.1| G GI13205 [Drosophila mojavensis]
Length=232

 GENE ID: 6582216 Dmoj\GI13205 | GI13205 gene product from transcript GI13205-RA
[Drosophila mojavensis] (10 or fewer PubMed links)

 Score = 83.7 bits (206),  Expect = 6e-15, Method: Composition-based stats.
 Identities = 20/131 (15%), Positives = 47/131 (35%), Gaps = 12/131 (9%)

Query  6    LSIVKFLELALAITCVVLH-YKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLN  64
                K LE+     C  +H   +L E   +  +   GTFVG+ ++     A  ++G
Sbjct  5    WLFFKLLEILAGSACTYVHRMGTLQEEPISHNMFFCGTFVGFVLLAAIHCARLVMGLRTL  64

Query  65   KKLDLFFSLIGCAMFIASGVLIL-KEWENAWSTDTKKIAITK----------SSLAVTNG  113
             +  LF S++G  M +   ++ +    ++        +              S +++
Sbjct  65   LRPLLFISVLGFCMHVLCALVSMGFAEKDFHLQFMSDVGENSHNYFRECRLQSIISMVTA  124

Query  114  VLFFFDAIFTF  124
             ++  + +
Sbjct  125  GIYLIEGVLVL  135


>☐ ref|NP_729982.1| UG CG9628, isoform B [Drosophila melanogaster]
 ref|NP_001163442.1| G CG9628, isoform C [Drosophila melanogaster]
 gb|AAF49725.2| G CG9628, isoform B [Drosophila melanogaster]
 gb|AAN71160.1| G GH08457p [Drosophila melanogaster]
 gb|ACL92658.1|  CG9628-PA [synthetic construct]
 gb|ACZ94713.1| G CG9628, isoform C [Drosophila melanogaster]
Length=175

 GENE ID: 39593 CG9628 | CG9628 gene product from transcript CG9628-RA
[Drosophila melanogaster] (10 or fewer PubMed links)

 Score = 83.7 bits (206),  Expect = 6e-15, Method: Composition-based stats.
 Identities = 23/132 (17%), Positives = 48/132 (36%), Gaps = 13/132 (9%)

Query  7    SIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLLG  60
              +K +EL L I C+ L  +                 L   TF   ++         L G
```

```
Sbjct  36   ICIKIVELCLLICCLGLIDEPATNSHLRVFITPRVASLCYVTFGALTIYTAIYLIMALFG  95

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTNG  113
            +    +    ++L+   +F+A   L+ ++W      +          + +  +S+A+
Sbjct  96   DLTPWRTATLWNLVAFVLFVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASIALVTS  155

Query  114  VLFFFDAIFTFR  125
            ++F  D + T R
Sbjct  156  LVFLLDILITLR  167


>☐ ref|NP_648710.1| G CG9628, isoform A [Drosophila melanogaster]
 gb|AAF49726.1| G CG9628, isoform A [Drosophila melanogaster]
 gb|AAL28716.1| G LD13706p [Drosophila melanogaster]
 gb|ACL83885.1|  CG9628-PA [synthetic construct]
 gb|ACL89005.1|  CG9628-PA [synthetic construct]
Length=162

 GENE ID: 39593 CG9628 | CG9628 gene product from transcript CG9628-RA
[Drosophila melanogaster] (10 or fewer PubMed links)

 Score = 82.9 bits (204),  Expect = 1e-14, Method: Composition-based stats.
 Identities = 23/132 (17%), Positives = 48/132 (36%), Gaps = 13/132 (9%)

Query  7    SIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLLG  60
              +K +EL L I C+ L  +                 L   TF   ++          L G
Sbjct  23   ICIKIVELCLLICCLGLIDEPATNSHLRVFITPRVASLCYVTFGALTIYTAIYLIMALFG  82

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTNG  113
            +    +    ++L+   +F+A   L+ ++W      +          + +  +S+A+
Sbjct  83   DLTPWRTATLWNLVAFVLFVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASIALVTS  142

Query  114  VLFFFDAIFTFR  125
            ++F  D + T R
Sbjct  143  LVFLLDILITLR  154


>☐ gb|EFA08060.1|  hypothetical protein TcasGA2_TC005656 [Tribolium castaneum]
Length=1071

 Score = 82.9 bits (204),  Expect = 1e-14, Method: Composition-based stats.
 Identities = 19/120 (15%), Positives = 39/120 (32%), Gaps = 11/120 (9%)

Query  9    VKFLELALAITCVVL---HYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNK  65
            V+ +E  L + C+ L       + +     ++L   T   + +I +          P+
Sbjct  22   VRVVEAVLCLVCIALAAAIDVKIHDMHIAFKILLTFTAAAFVIITVYDVIATSYARPIYW  81

Query  66   KLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIAITKSSLA-VTNGVLFFFDAIFTF  124
                 F++ G   F     LI+        T    + +    +A     ++F  D I
Sbjct  82   NAWTLFTITGALFFFLGVGLIIA-------TGFGHVLLILGVVAYAVTAIIFLLDTILIL  134


>☐ ref|XP_001353700.2| G GA21923 [Drosophila pseudoobscura pseudoobscura]
 gb|EAL29433.2|  GA21923 [Drosophila pseudoobscura pseudoobscura]
Length=175

 GENE ID: 4813692 Dpse\GA21923 | GA21923 gene product from transcript GA21923-RA
[Drosophila pseudoobscura pseudoobscura] (10 or fewer PubMed links)

 Score = 82.1 bits (202),  Expect = 2e-14, Method: Composition-based stats.
 Identities = 22/133 (16%), Positives = 50/133 (37%), Gaps = 13/133 (9%)

Query  6    LSIVKFLELALAITCVVLHYKSLGERD------DTTELLTAGTFVGYSVILIALFAGYLL  59
            L  +K +EL L I C+ L  +                 L   TF   ++          L+
Sbjct  35   LICIKVVELCLLICCLGLIDEPATNSHLRVFITPRVIALCYVTFGALTIYTAIYLIMALV  94

Query  60   GNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTK-------KIAITKSSLAVTN  112
            G+    +    +SL+   +++A   L+ ++W      +          + +  +S+A+
Sbjct  95   GDLTPWRTATLWSLVAFCLYVAVTALLFRDWSTTKDRNYWHPNMHRLDLVMASASIALVT  154
```

```
Query  113  GVLFFFDAIFTFR  125
             +++  + + T R
Sbjct  155  SLVYLLEILLTIR  167


>☐ ref|NP_001156315.1| UG hypothetical protein LOC100169413 [Acyrthosiphon pisum]
 dbj|BAH71620.1| G ACYPI010034 [Acyrthosiphon pisum]
Length=160

 GENE ID: 100169413 Acypi010034 | similar to ryanodine receptor-like protein
[Acyrthosiphon pisum]

 Score = 82.1 bits (202),  Expect = 2e-14, Method: Composition-based stats.
 Identities = 29/113 (25%), Positives = 51/113 (45%), Gaps = 9/113 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKL--DLFFSLIGCAM  78
            V   +    E++   E++ +G FVG+ +  + +   Y  G+   KK   D+  + +G  M
Sbjct  38   VGGTWNLNEEKNPDAEIVASGVFVGFFIYTVVILISYGFGSNHQKKTLVDIIMNFVGMFM  97

Query  79   FIASGVLILKEWENAWS-------TDTKKIAITKSSLAVTNGVLFFFDAIFTF  124
            FIA G + L  W    +       T  + I IT   L V +G ++  D + +F
Sbjct  98   FIAVGGIALHYWIGYQNENKYISVTSERAIGITVGVLCVISGAIYLVDTVLSF  150


>☐ ref|XP_001977381.1| G GG19007 [Drosophila erecta]
 gb|EDV46308.1| G GG19007 [Drosophila erecta]
Length=228

 GENE ID: 6549905 Dere\GG19007 | GG19007 gene product from transcript GG19007-RA
[Drosophila erecta] (10 or fewer PubMed links)

 Score = 81.0 bits (199),  Expect = 3e-14, Method: Composition-based stats.
 Identities = 35/92 (38%), Positives = 54/92 (58%), Gaps = 1/92 (1%)

Query  35   TELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENA-  93
              ++ AGT  GY+VI   L  G+++ + + K+L+  FSLIGC +F+ASG L++ EW
Sbjct  136  HPVIVAGTVGGYTVICGVLLVGHVVNSLVEKRLNALFSLIGCLLFVASGALVIDEWHGGL  195

Query  94   WSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
             +TD K+ AI   SL + N  +F  D +   R
Sbjct  196  LNTDRKRQAIGAGSLMIINAAVFLLDTLCICR  227


 Score = 75.6 bits (185),  Expect = 2e-12, Method: Composition-based stats.
 Identities = 31/114 (27%), Positives = 58/114 (50%), Gaps = 1/114 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K +EL   +T ++L             +L  GT VGY +    +  G+L G
Sbjct  1    MEFNNRLLLKIIELVFIMTSIILIESVSELAFIRQAMLVHGTLVGYLITCSVIATGHLGG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWE-NAWSTDTKKIAITKSSLAVTNG  113
              ++K+LD+ FS+ G  +F A+G +IL +W  +  S +  ++ +    L++ NG
Sbjct  61   IVVDKRLDIIFSIGGFILFGATGTIILAQWLAHCKSQEEWEMLLVSGILSLANG  114


>☐ ref|XP_002101085.1| G GE17420 [Drosophila yakuba]
 gb|EDX02193.1| G GE17420 [Drosophila yakuba]
Length=230

 GENE ID: 6525248 Dyak\GE17420 | GE17420 gene product from transcript GE17420-RA
[Drosophila yakuba] (10 or fewer PubMed links)

 Score = 81.0 bits (199),  Expect = 4e-14, Method: Composition-based stats.
 Identities = 34/95 (35%), Positives = 55/95 (57%), Gaps = 3/95 (3%)

Query  34   TTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENA  93
            +  ++ AGT  GY+VI   L  G+++ + + K+L+  FSLIGC +F+ASG +++ EW
Sbjct  135  SHAVIVAGTIGGYTVICGVLLVGHVINSLVEKRLNALFSLIGCLLFVASGAMVIDEWHGG  194

Query  94   WS---TDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
```

```
             +   TD K+ AI   SL + N  +F  D +   R
Sbjct  195  VNIITTDRKRQAIGAGSLMIINAAVFLLDTLCICR  229


 Score = 76.0 bits (186),  Expect = 1e-12, Method: Composition-based stats.
 Identities = 29/114 (25%), Positives = 55/114 (48%), Gaps = 1/114 (0%)

Query  1    MAVSRLSIVKFLELALAITCVVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLG  60
            M  +   ++K +EL   +  + L             LL  GT +GY +    +  G+++G
Sbjct  1    MEFNNRLLLKIIELVFIVASITLIEGIADLTFIRQALLVHGTLIGYLITCFVIATGHVVG  60

Query  61   NPLNKKLDLFFSLIGCAMFIASGVLILKEWENA-WSTDTKKIAITKSSLAVTNG  113
              ++K+LD+ FS+ G  +F A+G +IL +W     S   + + +    L++ NG
Sbjct  61   TAVDKQLDILFSIGGFILFGATGTIILAQWLEYCKSQVERDVVLASGILSLANG  114


>☐ ref|XP_966339.1| UG PREDICTED: similar to ryanodine receptor-like protein [Tribolium
castaneum]
 gb|EFA08057.1| G hypothetical protein TcasGA2_TC005653 [Tribolium castaneum]
Length=158

 GENE ID: 657157 TcasGA2_TC005653 | similar to ryanodine receptor-like protein
[Tribolium castaneum] (10 or fewer PubMed links)

 Score = 80.6 bits (198),  Expect = 5e-14, Method: Composition-based stats.
 Identities = 19/113 (16%), Positives = 43/113 (38%), Gaps = 9/113 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKK--LDLFFSLIGCAM  78
            V   +    E++   E++ +G FVGY +               +K    D+  ++IG  +
Sbjct  38   VGGTWNLNEEKNPDAEIVASGIFVGYFIYTCVSIISLCFATADHKNTFTDILMNIIGVFL  97

Query  79   FIASGVLILKEWENAWS-------TDTKKIAITKSSLAVTNGVLFFFDAIFTF  124
            ++A G   +  W               +++ +   +L + NG  +  D + +
Sbjct  98   WVAIGATAIHYWSGYLLEHKYQTTASEREVGLAMGALCILNGAAYLIDTVLSV  150


>☐ ref|XP_002430041.1| G conserved hypothetical protein [Pediculus humanus corporis]
 gb|EEB17303.1| G conserved hypothetical protein [Pediculus humanus corporis]
Length=143

 GENE ID: 8238407 Phum_PHUM460340 | hypothetical protein
[Pediculus humanus corporis]

 Score = 78.7 bits (193),  Expect = 2e-13, Method: Composition-based stats.
 Identities = 30/132 (22%), Positives = 53/132 (40%), Gaps = 14/132 (10%)

Query  8    IVKFLELALAITCVVLHYKSLGER----DDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
            I+K +EL LAI  V L    +       +     +   ++  Y +I   L   ++ G  +
Sbjct  10   ILKLIELCLAIIAVGLIVDPINNGVLSFNHNHSGIVYVSWPSYIIINTILLISFVAGERI  69

Query  64   NKKLDLFFSLIGCAMFIASGVLILKEWENAWSTD----------TKKIAITKSSLAVTNG  113
             K   + FS IG  +F+A+  + L+ W    S +              +I    LA+
Sbjct  70   PKITQVLFSFIGGCLFVAAAAVSLENWRKHHSGEINLLKMNVQQYSDQSIASGILALFCA  129

Query  114  VLFFFDAIFTFR  125
            + FF D + T +
Sbjct  130  LTFFIDTVITLK  141


>☐ ref|XP_001357214.2| G GA12689 [Drosophila pseudoobscura pseudoobscura]
 gb|EAL34283.2|  GA12689 [Drosophila pseudoobscura pseudoobscura]
Length=461

 GENE ID: 4818054 Dpse\GA12689 | GA12689 gene product from transcript GA12689-RA
[Drosophila pseudoobscura pseudoobscura] (10 or fewer PubMed links)

 Score = 77.9 bits (191),  Expect = 3e-13, Method: Composition-based stats.
 Identities = 19/137 (13%), Positives = 40/137 (29%), Gaps = 22/137 (16%)

Query  6    LSIVKFLELALAITCVVLHYKSLG--ERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
```

```
                K +E+ L   C+  H +            +L   TF  Y+++        LL
Sbjct  5    WVFFKLIEVFLGSICMGFHVEGSMYWPEPIPHIILYCATFGSYTLLAALGAFRLLLKKSS  64

Query  64   NKKLDLFFSLIGCAMFIASGVLILK----------------EWENAWSTDTKKIAITKSS  107
                +L  +     +    G+L+++                  E+      K+ +I
Sbjct  65   ILSSELLLAASAMGLHYFCGLLVMRSARQDKHLSAMNSTWQYLEHPHFARCKRQSIG---  121

Query  108  LAVTNGVLFFFDAIFTF  124
             A+  G ++
Sbjct  122  -ALITGTMYLMHMFLLL  137
```

> ☐ gb|ACN94686.1| GA12689 [Drosophila miranda]
Length=462

```
 Score = 77.9 bits (191),  Expect = 3e-13, Method: Composition-based stats.
 Identities = 19/137 (13%), Positives = 40/137 (29%), Gaps = 22/137 (16%)

Query  6    LSIVKFLELALAITCVVLHYKSLG--ERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
                K +E+ L   C+  H +            +L   TF  Y+++        LL
Sbjct  5    WVFFKLIEVFLGSICMGFHVEGSMYWPEPIPHIILYCATFGSYTLLAALGAFRLLLKKSS  64

Query  64   NKKLDLFFSLIGCAMFIASGVLILK----------------EWENAWSTDTKKIAITKSS  107
                +L  +     +    G+L+++                  E+      K+ +I
Sbjct  65   ILSSELLLAASAMGLHYFCGLLVMRSAMQDKHLSAMNSTWQYLEHPHFARCKRQSIG---  121

Query  108  LAVTNGVLFFFDAIFTF  124
             A+  G ++
Sbjct  122  -ALITGTMYLMHMFLLL  137
```

> ☐ ref|XP_002014263.1| GL19107 [Drosophila persimilis]
 gb|EDW28259.1| GL19107 [Drosophila persimilis]
Length=378

 GENE ID: 6588831 Dper\GL19107 | GL19107 gene product from transcript GL19107-RA
[Drosophila persimilis] (10 or fewer PubMed links)

```
 Score = 77.9 bits (191),  Expect = 3e-13, Method: Composition-based stats.
 Identities = 19/137 (13%), Positives = 41/137 (29%), Gaps = 22/137 (16%)

Query  6    LSIVKFLELALAITCVVLHYKSLG--ERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
                K +E+ L   C+  H +            +L   TF  Y+++        LL
Sbjct  5    WVFFKLIEVFLGSICMGFHVEGSMYWPEPIPHIILYCATFGSYTLLAALGAFRLLLKKSS  64

Query  64   NKKLDLFFSLIGCAMFIASGVLILK----------------EWENAWSTDTKKIAITKSS  107
                +L  +     +  + G+L+++                  E+      K+ +I
Sbjct  65   ILSSELLLAASAMGLHYSCGLLVMRSARQDKHLSAMNSTWQYLEHPHFARCKRQSIG---  121

Query  108  LAVTNGVLFFFDAIFTF  124
             A+  G ++
Sbjct  122  -ALITGTMYLMHMFLLL  137
```

> ☐ ref|XP_002427111.1| conserved hypothetical protein [Pediculus humanus corporis]
 gb|EEB14373.1| conserved hypothetical protein [Pediculus humanus corporis]
Length=155

 GENE ID: 8229744 Phum_PHUM294820 | hypothetical protein
[Pediculus humanus corporis]

```
 Score = 72.9 bits (178),  Expect = 1e-11, Method: Composition-based stats.
 Identities = 28/113 (24%), Positives = 49/113 (43%), Gaps = 10/113 (8%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLL-GNPLNKKLDLFFSLIGCAMF  79
            V   +    E+    E++ +G FVGY V  +++   YLL G  +    D   +++G  M+
Sbjct  38   VGGTFNLNEEKAVDVEIMASGIFVGYLVYNLSVLITYLLTGERII--NDCIMNVLGLFMW  95

Query  80   IASGVLILKEWENA-------WSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            IA     L  W+N         + + +   +   SL V N  L   D+ F+ +
```

```
Sbjct  96   IAVAGTALHYWDNYAHQHQFDITGNERSSGLALGSLCVFNAFLHLADSAFSIK  148


>☐ ref|XP_002427110.1| conserved hypothetical protein [Pediculus humanus corporis]
 gb|EEB14372.1| conserved hypothetical protein [Pediculus humanus corporis]
Length=139

 GENE ID: 8229743 Phum_PHUM294810 | hypothetical protein
[Pediculus humanus corporis]

 Score = 69.0 bits (168),  Expect = 1e-10, Method: Composition-based stats.
 Identities = 23/103 (22%), Positives = 41/103 (39%), Gaps = 8/103 (7%)

Query  21   VVLHYKSLGERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFI  80
            V   +    E++   E+L +G FVGY +  I+    Y + +  +   D   +LIG  ++
Sbjct  38   VGAVWNFNEEKNVDVEILASGVFVGYLLYNISALITYCISSEKSAN-DCLMNLIGIFLWT  96

Query  81   ASGVLILKEWE-------NAWSTDTKKIAITKSSLAVTNGVLF  116
                  L  W        N + +  K + +   SL+V N
Sbjct  97   GVAGTALHYWPGFQNEHGNEYKSTEKDVGMAVGSLSVLNAAAH  139


>☐ ref|XP_002038007.1| GM17988 [Drosophila sechellia]
 gb|EDW54425.1| GM17988 [Drosophila sechellia]
Length=376

 GENE ID: 6613539 Dsec\GM17988 | GM17988 gene product from transcript GM17988-RA
[Drosophila sechellia] (10 or fewer PubMed links)

 Score = 62.9 bits (152),  Expect = 1e-08, Method: Composition-based stats.
 Identities = 21/137 (15%), Positives = 39/137 (28%), Gaps = 22/137 (16%)

Query  6    LSIVKFLELALAITCVVLHYKSLG--ERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
                K +E+ L   C+  H +            +L   TF  ++ +        +L
Sbjct  5    WVFFKLIEVLLGSVCMFFHIRGSSYWPERTPHMILYCATFSSFTALAALGAFRLVLARST  64

Query  64   NKKLDLFFSLIGCAMFIASGVLI----------------LKEWENAWSTDTKKIAITKSS  107
                 L  +L         GVLI                ++  E+      K+ +I
Sbjct  65   VLSSQLLLTLSAVLSHYICGVLIMRTAMLDPHLPFINSTIEYLEHPHFAHCKRQSIA---  121

Query  108  LAVTNGVLFFFDAIFTF  124
             A+  G ++       F
Sbjct  122  -ALVTGTMYLMHMFHVF  137


>☐ ref|XP_001968858.1| GG24274 [Drosophila erecta]
 gb|EDV57917.1| GG24274 [Drosophila erecta]
Length=397

 GENE ID: 6542937 Dere\GG24274 | GG24274 gene product from transcript GG24274-RA
[Drosophila erecta] (10 or fewer PubMed links)

 Score = 61.3 bits (148),  Expect = 3e-08, Method: Composition-based stats.
 Identities = 21/137 (15%), Positives = 40/137 (29%), Gaps = 22/137 (16%)

Query  6    LSIVKFLELALAITCVVLHYKSLG--ERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
                K +E+ L   C+  H +            +L   TF  ++ +        +L
Sbjct  5    WVFFKLIEVVLGSLCMFFHIRGSSYWPERTPHVILYCATFSSFTALAALGAFRLILARSS  64

Query  64   NKKLDLFFSLIGCAMFIASGVLI----------------LKEWENAWSTDTKKIAITKSS  107
                 L  +L       + GVLI                ++  E+      K+ +I
Sbjct  65   VLSSQLLLTLSAVLAHYSCGVLIMRTAMLDPHLASINSTIEYLEHPHFAHCKQKSIA---  121

Query  108  LAVTNGVLFFFDAIFTF  124
             A+  G ++       F
Sbjct  122  -ALITGTMYLMHMFHVF  137


>☐ ref|XP_002089166.1| GE18971 [Drosophila yakuba]
```

```
 gb|EDW88878.1| G GE18971 [Drosophila yakuba]
Length=397

 GENE ID: 6528099 Dyak\GE18971 | GE18971 gene product from transcript GE18971-RA
[Drosophila yakuba] (10 or fewer PubMed links)

 Score = 61.3 bits (148),  Expect = 3e-08, Method: Composition-based stats.
 Identities = 21/137 (15%), Positives = 39/137 (28%), Gaps = 22/137 (16%)

Query  6    LSIVKFLELALAITCVVLHYKSLG--ERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
                K +E+ L   C+  H +            +L   TF  ++ +        +L
Sbjct  5    WVFFKLIEVVLGSACMFFHIRGSSYWPERTPHVILYCATFSSFTALAALGAFRLMLARSS  64

Query  64   NKKLDLFFSLIGCAMFIASGVLI----------------LKEWENAWSTDTKKIAITKSS  107
                 L  +L         GVLI                ++  E+      K+ +I
Sbjct  65   VLSSQLLLTLSAVLSHYFCGVLIMRTAMEDPHLASINSTIEYLEHPHFAYCKQKSIA---  121

Query  108  LAVTNGVLFFFDAIFTF  124
             A+  G ++       F
Sbjct  122  -ALITGTMYLMHMFHVF  137


>☐ ref|NP_608969.1| UG CG14000 [Drosophila melanogaster]
 gb|AAM11016.1| G AT26438p [Drosophila melanogaster]
 gb|AAF52301.2| G CG14000 [Drosophila melanogaster]
 gb|ACL87403.1|  CG14000-PA [synthetic construct]
 gb|ACL92014.1|  CG14000-PA [synthetic construct]
Length=398

 GENE ID: 33820 CG14000 | CG14000 gene product from transcript CG14000-RA
[Drosophila melanogaster] (10 or fewer PubMed links)

 Score = 61.3 bits (148),  Expect = 3e-08, Method: Composition-based stats.
 Identities = 22/137 (16%), Positives = 39/137 (28%), Gaps = 22/137 (16%)

Query  6    LSIVKFLELALAITCVVLHYKSLG--ERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
                K +E+ L   C+  H +            +L   TF  ++ +        LL
Sbjct  5    WVFFKLIEVLLGSVCMFFHIRGSSYWPERTPHVILYCATFSSFTALAALGAFRLLLARST  64

Query  64   NKKLDLFFSLIGCAMFIASGVLI----------------LKEWENAWSTDTKKIAITKSS  107
                 L  +L         GVLI                ++  E+      K+ +I
Sbjct  65   VLSSQLLLTLSAVLSHYFCGVLIMRTAMLDPHLAFINSTIEYLEHPHFAHCKQQSIA---  121

Query  108  LAVTNGVLFFFDAIFTF  124
             A+  G ++       F
Sbjct  122  -ALVTGTMYLMHMFHVF  137


>☐ gb|EFA08059.1|  hypothetical protein TcasGA2_TC005655 [Tribolium castaneum]
Length=265

 Score = 60.2 bits (145),  Expect = 7e-08, Method: Composition-based stats.
 Identities = 24/93 (25%), Positives = 39/93 (41%), Gaps = 5/93 (5%)

Query  10   KFLELALAITCVVLHYKSL-----GERDDTTELLTAGTFVGYSVILIALFAGYLLGNPLN  64
            K LEL L I C+   + +L     G  D     +    + GY +I + L   Y L   +
Sbjct  32   KILELLLCIICIGTVFDALKTMGIGNSDLHHIGIMYTAYTGYILITLTLLTSYYLEATIP  91

Query  65   KKLDLFFSLIGCAMFIASGVLILKEWENAWSTD  97
             K    FS+ G  +F+ +GVL++ +
Sbjct  92   YKTSALFSVCGAGLFLTTGVLLIVDRSAYMRRY  124


 Score = 51.3 bits (122),  Expect = 3e-05, Method: Composition-based stats.
 Identities = 26/122 (21%), Positives = 53/122 (43%), Gaps = 11/122 (9%)

Query  15   ALAITCVVLHYKSLGE-----RDDTTELLTAGTFVGYSVILIALFAGYLLGNPLNKKLDL  69
             + + C+   ++   E            +    + GY +I + L AG  +G+ +     +
Sbjct  139  LICVVCLGFIFEPANEIHLGGNYMHHTGVMYTAYTGYMLINVVLLAGRAIGDRIPYITII  198
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Query  70   FFSLIGCAMFIASGVLILKEWENAWSTDT--KKIAITKSSLAV----TNGVLFFFDAIFT  123
             F +IG A+F+ +GVL+L +           ++  +T  +++V     N  +F  +A FT
Sbjct  199  VFDVIGAALFLITGVLLLVDRIRLARDIFHPRQYLLTMMTVSVCFAFANCGVFLLEAFFT  258

Query  124  FR  125
             R
Sbjct  259  RR  260


>☐ ref|XP_001962403.1| G GF15443 [Drosophila ananassae]
 gb|EDV31624.1| G GF15443 [Drosophila ananassae]
Length=417

 GENE ID: 6498251 Dana\GF15443 | GF15443 gene product from transcript GF15443-RA
[Drosophila ananassae] (10 or fewer PubMed links)

 Score = 56.7 bits (136),  Expect = 9e-07, Method: Composition-based stats.
 Identities = 15/137 (10%), Positives = 42/137 (30%), Gaps = 22/137 (16%)

Query  6    LSIVKFLELALAITCVVLHYKSLG--ERDDTTELLTAGTFVGYSVILIALFAGYLLGNPL  63
                K +E+ L   C+ +H +      +  +  ++   TF+ ++ +        L+
Sbjct  5    WVFFKLIEVVLGALCMSIHMRGAILWPQYVSHVIIYCATFISFTALAALGAFRLLITQKC  64

Query  64   NKKLDLFFSLIGCAMFIASGVLILK----------------EWENAWSTDTKKIAITKSS  107
                 L  +L         G+ +++                  E+   +  K+ +I
Sbjct  65   VLSSQLLLTLGAVIAHYFCGLFVMRDIANINLLSAANNSNEYLEHPAFSICKQQSIA---  121

Query  108  LAVTNGVLFFFDAIFTF  124
             ++  G ++
Sbjct  122  -SLITGTMYLMHMFHVL  137


>☐ ref|NP_572519.1| UG CG15366 [Drosophila melanogaster]
 gb|AAF46436.1| G CG15366 [Drosophila melanogaster]
Length=117

 GENE ID: 31832 CG15366 | CG15366 gene product from transcript CG15366-RA
[Drosophila melanogaster] (10 or fewer PubMed links)

 Score = 54.0 bits (129),  Expect = 5e-06, Method: Composition-based stats.
 Identities = 25/103 (24%), Positives = 48/103 (46%), Gaps = 20/103 (19%)

Query  33   DTTELLTAGTFVGYSVILIAL-------------------FAGYLLGNPLNKKLDLFFSL  73
                LL  GT +GY +    +                   F+G++ G  ++K+LD+ FS+
Sbjct  4    IRHALLVHGTLIGYLITCFVIATGKTLKASNLATVYEVDMFSGHVSGTVVDKRLDILFSI  63

Query  74   IGCAMFIASGVLILKEWENA-WSTDTKKIAITKSSLAVTNGVL  115
             G  +F A+G +IL +W     S + +++ +    L++ NG +
Sbjct  64   GGFFLFGAAGTIILAQWLGYCKSQEERQLLLASGILSLANGAI  106


>☐ ref|XP_002429371.1| G Cylicin-1, putative [Pediculus humanus corporis]
 gb|EEB16633.1| G Cylicin-1, putative [Pediculus humanus corporis]
Length=781

 GENE ID: 8230225 Phum_PHUM430470 | Cylicin-1, putative
[Pediculus humanus corporis]

 Score = 53.6 bits (128),  Expect = 7e-06, Method: Composition-based stats.
 Identities = 23/93 (24%), Positives = 38/93 (40%), Gaps = 2/93 (2%)

Query  34   TTELLTAGTFVGYSVILIALFAGYLLGNPLN-KKLDLFFSLIGCAMFIASGVLILKEWEN  92
               +    T+  Y +I I L  G   G     +K++ FF ++G  +FIA+G L L   E
Sbjct  36   NGAIFADVTYGSYIIITIGLIIGQCSGELKRCRKMENFFLIVGAILFIATGSLELAALE-  94

Query  93   AWSTDTKKIAITKSSLAVTNGVLFFFDAIFTFR  125
            +        A      ++  G LF  D +   +
Sbjct  95   SVEERLVDNAAILGVFSLVAGFLFIIDLLTASK  127
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>☐ ref|NP_611858.1| UG CG13566 [Drosophila melanogaster]
 gb|AAF47117.1| G CG13566 [Drosophila melanogaster]
Length=207

 GENE ID: 37813 CG13566 | CG13566 gene product from transcript CG13566-RA
[Drosophila melanogaster] (10 or fewer PubMed links)

 Score = 42.1 bits (98),  Expect = 0.017, Method: Composition-based stats.
 Identities = 19/81 (23%), Positives = 27/81 (33%), Gaps = 0/81 (0%)

Query  42   TFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKI  101
            TFVGY+ I   L    ++    N        L    +F     L++       S D
Sbjct  69   TFVGYTFIAAVLLLTRIIEGTSNYGTCEIILLTCGVLFFTIEGLLIFFTVEQLSEDLLIF  128

Query  102  AITKSSLAVTNGVLFFFDAIF  122
            A    +L      LF  D +F
Sbjct  129  AYALGALCFICAALFALDLMF  149


>☐ ref|XP_002040187.1| G GM15486 [Drosophila sechellia]
 gb|EDW57052.1| G GM15486 [Drosophila sechellia]
Length=207

 GENE ID: 6615817 Dsec\GM15486 | GM15486 gene product from transcript GM15486-RA
[Drosophila sechellia] (10 or fewer PubMed links)

 Score = 41.7 bits (97),  Expect = 0.024, Method: Composition-based stats.
 Identities = 19/81 (23%), Positives = 27/81 (33%), Gaps = 0/81 (0%)

Query  42   TFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKI  101
            TFVGY+ I   L    ++    N        L    +F     L++       S D
Sbjct  69   TFVGYTFIAAVLLLTRIIEGTSNYGTCEVILLTCGVLFFTIEGLLIFFTVEQLSEDLLVF  128

Query  102  AITKSSLAVTNGVLFFFDAIF  122
            A    +L      LF  D +F
Sbjct  129  AYALGALCFVCAALFALDLMF  149


>☐ ref|XP_001902958.1| G hypothetical protein Bm1_57500 [Brugia malayi]
 gb|EDP28194.1| G hypothetical protein Bm1_57500 [Brugia malayi]
Length=360

 GENE ID: 6106382 Bm1_57500 | hypothetical protein [Brugia malayi]
(10 or fewer PubMed links)

 Score = 41.3 bits (96),  Expect = 0.031, Method: Composition-based stats.
 Identities = 27/145 (18%), Positives = 50/145 (34%), Gaps = 26/145 (17%)

Query  6    LSIVKFLELA-----LAITCVVLHYKSLGE---------RDDTTELLTAGTFVGYSVILI  51
               +K +EL      L    V      + E              + L       +S + +
Sbjct  211  RVAIKAIELVGAFLMLGAATVGFIISPVSELSLYAFVKMTHTEWQGLVLAVSGSFSALCL  270

Query  52   ALFAGYLLGNPLN--KKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKIA-------  102
             +  G   GN     ++ D   SL+G   ++  GV+    +      D+KKI
Sbjct  271  FMLFGSFFGNRYMLWRRFDYLISLVGSFGYLFVGVIE-AYYATCHPPDSKKIIGLVCHRL  329

Query  103  --ITKSSLAVTNGVLFFFDAIFTFR  125
              I  ++L   N +++  D + +FR
Sbjct  330  EWIIATALIFINVIVYIVDCVLSFR  354


>☐ ref|XP_001688606.1| G AGAP004947-PA [Anopheles gambiae str. PEST]
 gb|EDO63986.1| G AGAP004947-PA [Anopheles gambiae str. PEST]
Length=245

 GENE ID: 5667388 AgaP_AGAP004947 | AGAP004947-PA [Anopheles gambiae str. PEST]
(10 or fewer PubMed links)
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 Score = 40.9 bits (95),  Expect = 0.043, Method: Composition-based stats.
 Identities = 19/118 (16%), Positives = 33/118 (27%), Gaps = 14/118 (11%)

Query  17   AITCVVLHYKSLGE--RDDTTELLTAGTFVGYSVILIALFAGYLLG-NPLNKKLDLFFSL  73
             + C  LH +           E+L  G +  Y +I    F     G   LN  ++   S
Sbjct  62   CLICAGLHIQGFLHYPEPFPHEMLFCGLYASYFLISFYSFLFLYKGCCELNYTVEAIVSG  121

Query  74   IGCAMFIASG-VLILKEWENAWSTDTKK----------IAITKSSLAVTNGVLFFFDA  120
                +F+ S  V +    ++                      +S  A     +F
Sbjct  122  AAFLLFVVSAFVSMYHAEKDIHLQYLTDEEEWYHPFFVYCRLQSLGATITAQMFLVHC  179


>☐ ref|XP_001976508.1|  GG19973 [Drosophila erecta]
 gb|EDV56908.1|  GG19973 [Drosophila erecta]
Length=207

 GENE ID: 6548131 Dere\GG19973 | GG19973 gene product from transcript GG19973-RA
[Drosophila erecta] (10 or fewer PubMed links)

 Score = 40.5 bits (94),  Expect = 0.051, Method: Composition-based stats.
 Identities = 17/81 (20%), Positives = 27/81 (33%), Gaps = 0/81 (0%)

Query  42   TFVGYSVILIALFAGYLLGNPLNKKLDLFFSLIGCAMFIASGVLILKEWENAWSTDTKKI  101
            TFVG++ +   L    ++    N        L    +F     L++       S D
Sbjct  69   TFVGFTFVAAVLLLTRIIEGTSNYGTCEIILLTCGVLFFTIEGLLIFFTVEQLSEDLLVY  128

Query  102  AITKSSLAVTNGVLFFFDAIF  122
            A    +L      LF  D +F
Sbjct  129  AYALGALCFICAALFALDLMF  149
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