SI Appendix 2

Bioinformatics searches of five Acps (Acp95EF, Acp53Ea, Msopa, Mst57Da and Andropin) from *D. melanogaster* against the *An. gambiae* Ensembl database. Searches were performed in the Matlab programming environment (Matlab version 7.0.4) with the support of the Bioinformatics Toolbox using the Smith-Waterman (1) and the Needleman-Wunsch (2) approaches for local and global alignment, respectively. The best three *An. gambiae* candidate homologues are shown, as well as the reverse analysis for each *Anopheles* candidate against the *D. melanogaster* genome. In those cases where the reverse analysis matches the forward search, only the best candidate is provided. Blosum 62 was used as scoring matrix, and gap penalty was set to 10 unless specified otherwise. When two or more candidate *Anopheles* genes are very similar or represent alleles of the same gene, their alignments are provided.

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ACP95EF

scoring matrix:
blosum62

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best alignment n: 1
names: acp95EF  - AGAP009361
identities: 14/54 (25%), positives: 32/54 (59%)
score: 1.450000e+001
MASVK-LFFIAILVVALSLNTSAAVLNPSSTAKPRFETKDRKLSAGALQ-SLAG
|| :| ||:||::|: |::: | :  :   | :|    :: : :| |::    :
MAMMKQLFYIALVVLILAVSCSMVDADTFLTKRPPGILRSVREAAEAMNYPKHS

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best alignment n: 2
names: acp95EF  - AGAP009357

identities: 12/57 (21%), positives: 31/57 (54%)
score: 3
MA-SVKLFFIAILVVALSLNTSAAVLNPSSTAKPR---FETKDRK-LSAGALQSLAG
|   |::|::|:|::   ::::  ::||::|:  |   |   |:  :  |:
MKFFVQVFLFALLALLGLVSAGKMAINPATTTTARPIFFPCFDEDGIFIGCTPH--P

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best alignment n: 3
names: acp95EF  - AGAP009355

identities: 12/57 (21%), positives: 31/57 (54%)
score: 3
MA-SVKLFFIAILVVALSLNTSAAVLNPSSTAKPR---FETKDRK-LSAGALQSLAG
|   |::|::|:|::   ::::  ::||::|:  |   |   |:  :  |:
MKFFVQVFLFALLALLGLVSAGKMAINPATTTTARPIFFPCFDEDGIFIGCTPH--P
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REVERSE SEARCH

scoring matrix:
blosum62 gap open 7
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best alignment n: 1
names: AGAP009361 - Acp95EF-PA type=protein; loc=3R:20054714..20054931; name=Acp95EF-PA;
dbxref=FlyBase:FBpp0083946,GB_protein:AAF56263.2,FlyBase_Annotation_IDs:CG17924-
PA,FlyBase:FBgn0002863; MD5=8e33212bf0750fe74cb869e9ea74e23e; parent=FBtr0084561; release=r4.3;
species=Dmel; length=52;
identities: 14/54 (25%), positives: 32/54 (59%)
score: 1.750000e+001
MAMMKQLFYIALVVLILAVSCSMVDADTFLTKRPPGILRSVREAAEAMNYPKHS
|| :| ||:||::|: |::: | :  :   | :|    :: : :| |::    :
MASVK-LFFIAILVVALSLNTSAAVLNPSSTAKPRFETKDRKLSAGALQ-SLAG

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best alignment n: 1
names: AGAP009357 - Dro-PA type=protein; loc=2R:10260853..10261044; name=Dro-PA;
dbxref=FlyBase:FBpp0086566,GB_protein:AAF58216.1,FlyBase_Annotation_IDs:CG10816-
PA,FlyBase:FBgn0010388; MD5=1ef7557d7cd0ac3cb9d691e361196bbc; parent=FBtr0087436; release=r4.3;
species=Dmel; length=64;
identities: 17/64 (26%), positives: 29/64 (45%)
score: 1.150000e+001
MKFFVQVFLFALLALLGLVSAGK-MAINPATTTTARPIFF---PCFDEDGIF-IGCTPHP----
||| :  :|:| :  :|::: ||    :|  |:  |||         || :   :  | |
MKFTIVFLLLACVFAMGVATPGKPRPYSPRPTSHPRPIRVRREALAIEDHLTQAAIRPPPILPA

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AGAP009355 and AGAP009357
are identical in Ensembl

identities: 55/55 (100%), positives: 55/55 (100%)
score: 1.455000e+002
MKFFVQVFLFALLALLGLVSAGKMAINPATTTTARPIFFPCFDEDGIFIGCTPHP
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
MKFFVQVFLFALLALLGLVSAGKMAINPATTTTARPIFFPCFDEDGIFIGCTPHP

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ACP53EA

scoring matrix:
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blosum62

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best alignment n: 1
names: acp53  - AGAP012706
identities: 28/125 (22%), positives: 64/125 (51%)
score: 1.950000e+001
MKLIKVTLVFSLLALVFVAQ----TEAQNPIWENWLACNRIGTKALASLLRETIPTVRNLLNCIDFNPPTDIGNSYLSKLKLYYELVKRG-ALDKTQCLIVPLKESVRLLRPYVKSLETNKCLGE
||   | ::|:|:|:: : |     : | |: |  :  | : :: | ::|:: :  | ::||                     :| ::||  :|: :  :  | : ::|| |::|:|  |: :|:
MK--TVIVLFALVAVATAMQPFYHPQEQFPMVE-IMPINTLDNRQLPKILESLVGLVDGFLNV--------------------FEATRRGDPVDREN--MRQLLQLLQLLPPFAKTL--NEQFGQ

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best alignment n: 2
names: acp53  - AGAP009370

identities: 28/125 (22%), positives: 64/125 (51%)
score: 19
MKLIKVTLVFSLLALVFVAQ----TEAQNPIWENWLACNRIGTKALASLLRETIPTVRNLLNCIDFNPPTDIGNSYLSKLKLYYELVKRG-ALDKTQCLIVPLKESVRLLRPYVKSLETNKCLGE
||   | ::|:|:|:: : |     : | |: |  :  | : :: | ::|:: :  | ::||                     :| ::||  :|: :  :  | : ::|| |::|:|  |: :|:
MK--TVIVLFALVAVATAMQPFYHPQDQFPMVE-IMPINTLDNRQLPKILESLVGLVDGFLNV--------------------FEATRRGDPVDREN--MRQLLQLLQLLPPFAKTL--NEQFGQ

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best alignment n: 3
names: acp53  - AGAP009369

identities: 25/127 (19%), positives: 59/127 (46%)
score: 5.000000e-001
MKLIKVTLVFSLLALVFVAQ----TEAQNPIWENWLACNRIGTKALASLLRETIPTVRNLLNCIDFNPPTDIGNSYLSKLKLYYELVKRG-ALDKTQCLIVPLKESVRLLRPYVKSLETNKCLGE--
||   | ::|:|:|:: : |     : | |: |  :  | : :: | ::|:: :  | ::||                     :| ::||  :|: :  :  |:  : ||   | ::   : :|:
MK--TVIVLFALVAVATAMQPFYHPQEQFPMVE-IMPINTLDNRQLPKILESLVGLVDGFLNV--------------------FEATRRGDPVDREN--MRQLSFLLTLLPSIVDTVY--RIFGQPT

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REVERSE SEARCH

scoring matrix:
blosum62
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best alignment n: 1
names: AGAP012706- Acp53Ea-PA type=protein; loc=2R:complement(12264722..12265146); name=Acp53Ea-
PA; dbxref=FlyBase:FBpp0086228,GB_protein:AAF57959.1,FlyBase_Annotation_IDs:CG8622-
PA,FlyBase:FBgn0015584; MD5=af81747df948935ac444b7809ec13a15; parent=FBtr0087080; release=r4.3;
species=Dmel; length=120;
identities: 28/125 (22%), positives: 64/125 (51%)
score: 1.950000e+001
MK--TVIVLFALVAVATAMQPFYHPQEQFPMVE-IMPINTLDNRQLPKILESLVGLVDGFLNV--------------------FEATRRGDPVDREN--MRQLLQLLQLLPPFAKTL--NEQFGQ
||   | ::|:|:|:: : |     : | |: |  :  | : :: | ::|:: :  | ::||                     :| ::||  :|: :  :  | : ::|| |::|:|  |: :|:
MKLIKVTLVFSLLALVFVAQ----TEAQNPIWENWLACNRIGTKALASLLRETIPTVRNLLNCIDFNPPTDIGNSYLSKLKLYYELVKRG-ALDKTQCLIVPLKESVRLLRPYVKSLETNKCLGE

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ALIGNMENT BETWEEN:
AGAP012706
AGAP009370
AGAP009369


best alignment n: 1
names: AGAP012706 - AGAP009370
 (alleles of the same gene)
identities: 97/98 (98%), positives: 98/98 (100%)
score: 2.465000e+002
MKTVIVLFALVAVATAMQPFYHPQEQFPMVEIMPINTLDNRQLPKILESLVGLVDGFLNVFEATRRGDPVDRENMRQLLQLLQLLPPFAKTLNEQFGQ
||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MKTVIVLFALVAVATAMQPFYHPQDQFPMVEIMPINTLDNRQLPKILESLVGLVDGFLNVFEATRRGDPVDRENMRQLLQLLQLLPPFAKTLNEQFGQ

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best alignment n: 2
names: AGAP012706- AGAP009369

identities: 87/100 (87%), positives: 91/100 (91%)
score: 2.085000e+002
MKTVIVLFALVAVATAMQPFYHPQEQFPMVEIMPINTLDNRQLPKILESLVGLVDGFLNVFEATRRGDPVDRENMRQLLQLLQLLPPFAKTLNEQFGQ--
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  || ||| :: |: : |||
MKTVIVLFALVAVATAMQPFYHPQEQFPMVEIMPINTLDNRQLPKILESLVGLVDGFLNVFEATRRGDPVDRENMRQLSFLLTLLPSIVDTVYRIFGQPT

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MSOPA

scoring matrix:
blosum62

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best alignment n: 1
names: CG14560(MsOPA)  - AGAP009353

identities: 18/86 (20%), positives: 46/86 (53%)
score: 9.500000e+000
M-NFIQIAVLFVLVAVALARPQEDPANLPAPEAA--AAPPAAAAAPPAAAAAPPAPPAPPAAAPQAAPAGGSGRKKNVNHNVITIG
| |::::|:| ::: ::||  | : :::| |     :    |: :  |: :: |:  :|    ||::       : ||: :|:
MSNIVKLALLTLIALIGLAVGQLSEGSVPKPTFPDYVIYVEACETYGAGKCGHPTSDVPTEPMPQSSQQ----IETNVQ-SVLQNF

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best alignment n: 2
names: CG14560(MsOPA)  - AGAP012680
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identities: 18/86 (20%), positives: 45/86 (52%)
score: 9
M-NFIQIAVLFVLVAVALARPQEDPANLPAPEAA--AAPPAAAAAPPAAAAAPPAPPAPPAAAPQAAPAGGSGRKKNVNHNVITIG
| |::::|:| ::: ::||  | : :::| |     :    |: :  |: :: |:   |    ||::       : ||: :|:
MSNIVKLALLTLIALIGLAVGQLSEGSVPKPTFPDYVIYVEACETYGAGKCGHPTSDEPTEPMPQSSQQ----IETNVQ-SVLQNF

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best alignment n: 3
names: CG14560(MsOPA)  - AGAP009356
identities: 15/83 (18%), positives: 37/83 (44%)
score: 3
MNFIQIAVLFVLVAVALARPQEDPANLPAPEAAAAPPAAAAAPPAAAAAPPAPPAPPAAAPQAAPAGGSGRKKNVNHNVITIG
|:|:  ::||:::|: |:: : :|::           : :    : ::| |    | |   | :       |:| |     :
MKFLATTILFAFIAL-LGQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRPLADIKQET-------KQNKN----LMR

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REVERSE SEARCH

scoring matrix:
blosum62 gap 7

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best alignment n: 1 salivary gland peptide
names: AGAP009353  - Sgs7-PA type=protein; loc=3L:11483843..11484130; name=Sgs7-PA;
dbxref=FlyBase:FBpp0075826,GB_protein:AAF50058.1,FlyBase_Annotation_IDs:CG18087-
PA,FlyBase:FBgn0003377; MD5=951024acfa2109cee92ce0086e5f0056; parent=FBtr0076095; release=r4.3;
species=Dmel; length=74;
identities: 22/93 (23%), positives: 39/93 (41%)
score: 1.850000e+001
MSNIVKLALLTLIALIGLAVGQLSEGSVPKPTFPDYVIYVEACETYGAGKCGHPTSDVPTEPMPQSSQQIETNVQSVLQNF------------
|    ||  :|:|| | | :|           | | ::   |||   :| |    :  | :|  |  ||: :::::: |::
M----KLIAVTIIACI-LLIG-----------FSDLALG-GACECQPCGPGGKACTGCPEKP--QLCQQLISDIRNLQQKIRKCVCGEPQWMI

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best alignment n: 2
names: AGAP009353 - msopa-PA type=protein; loc=3L:22016674..22016922; name=msopa-PA;
dbxref=FlyBase:FBpp0078135,GB_protein:AAF51808.1,FlyBase_Annotation_IDs:CG14560-
PA,FlyBase:FBgn0004414; MD5=f5980bcb5e8ddbfb26233fb156253468; parent=FBtr0078482; release=r4.3;
species=Dmel; length=83;
identities: 20/93 (21%), positives: 49/93 (52%)
score: 1.650000e+001
MSNIVKLALLTLIALIGLAVGQLSEGSVPKPTFPDYVIYVEACETYGAGKCGHPTSDV--PTEPMPQSSQ-QI--------ETNVQ-SVLQNF
| |::::|:| ::: ::||  | : :::| |         ||: :  |: :: |:: :  |: | | ::  |         : ||: :|:
M-NFIQIAVLFVLVAVALARPQEDPANLPAP---------EAAAAPPAAAAAPPAAAAAPPAPPAPPAAAPQAAPAGGSGRKKNVNHNVITIG

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scoring matrix:
blosum62 gap 10

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best alignment n: 1
names: AGAP009353   - msopa-PA type=protein; loc=3L:22016674..22016922; name=msopa-PA;
dbxref=FlyBase:FBpp0078135,GB_protein:AAF51808.1,FlyBase_Annotation_IDs:CG14560-
PA,FlyBase:FBgn0004414; MD5=f5980bcb5e8ddbfb26233fb156253468; parent=FBtr0078482; release=r4.3;
species=Dmel; length=83;
identities: 18/86 (20%), positives: 46/86 (53%)
score: 9.500000e+000
MSNIVKLALLTLIALIGLAVGQLSEGSVPKPTFPDYVIYVEACETYGAGKCGHPTSDVPTEPMPQSSQQ----IETNVQ-SVLQNF
| |::::|:| ::: ::||  | : :::| |     :    |: :  |: :: |:  :|    ||::       : ||: :|:
M-NFIQIAVLFVLVAVALARPQEDPANLPAPEAA--AAPPAAAAAPPAAAAAPPAPPAPPAAAPQAAPAGGSGRKKNVNHNVITIG

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best alignment n: 2
names: AGAP009353 - Sgs7-PA type=protein; loc=3L:11483843..11484130; name=Sgs7-PA;
dbxref=FlyBase:FBpp0075826,GB_protein:AAF50058.1,FlyBase_Annotation_IDs:CG18087-
PA,FlyBase:FBgn0003377; MD5=951024acfa2109cee92ce0086e5f0056; parent=FBtr0076095; release=r4.3;
species=Dmel; length=74;
identities: 22/93 (23%), positives: 39/93 (41%)
score: 9.500000e+000
MSNIVKLALLTLIALIGLAVGQLSEGSVPKPTFPDYVIYVEACETYGAGKCGHPTSDVPTEPMPQSSQQIETNVQSVLQNF-------
|    ||  :|:|| | | :|           | | ::   |||   :|  |   :  | :|  |  ||: :::::: |::
M----KLIAVTIIACI-LLIG-----------FSDLALG-GACECQPCGPGGKACTGCPEKP--QLCQQLISDIRNLQQKIRKCVCGEPQWMI

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AGAP009353 and AGAP012680 are alleles

ALIGNMENT BETWEEN
AGAP009353
AGAP012680

best alignment n: 1
names: AGAP009353 - AGAP012680

identities: 80/81 (98%), positives: 80/81 (98%)
score: 205
MSNIVKLALLTLIALIGLAVGQLSEGSVPKPTFPDYVIYVEACETYGAGKCGHPTSDVPTEPMPQSSQQIETNVQSVLQNF
||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
MSNIVKLALLTLIALIGLAVGQLSEGSVPKPTFPDYVIYVEACETYGAGKCGHPTSDEPTEPMPQSSQQIETNVQSVLQNF

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MST57DA
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scoring matrix:
blosum62
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best alignment n: 1
names: Mst57Da  - AGAP009359

identities: 21/83 (25%), positives: 37/83 (44%)
score: 9.500000e+000
MKFLALFVTLLVVLALVSAQKSQNTNHNVIVIGAKKPGAAPAAAAAAAPAAPPAAAPAAAPAAPEAGLADAPAES--------
||||| :: |:: :||: :| | : ::| | :  |   :      : : | ||:  |          |||   |:
MKFLATII-LFAFIALI-GQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRP----------LADIKQETKENKNLMR

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best alignment n: 2
names: Mst57Da  - AGAP009354

identities: 21/83 (25%), positives: 37/83 (44%)
score: 9.500000e+000
MKFLALFVTLLVVLALVSAQKSQNTNHNVIVIGAKKPGAAPAAAAAAAPAAPPAAAPAAAPAAPEAGLADAPAES--------
||||| :: |:: :||: :| | : ::| | :  |   :      : : | ||:  |          |||   |:
MKFLATII-LFAFIALI-GQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRP----------LADIKQETKENKDLMR

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best alignment n: 3
names: Mst57Da  - AGAP009357

identities: 19/78 (24%), positives: 33/78 (42%)
score: 9
MKFL--ALFVTLLVVLALVSAQKSQNTNHNVIVIGAKKPGAAPAAAAAAAPAAPPAAAPAAAPAAPEAGL-ADAPAES
|||:  ::: :||::|:|||| |                        |  ||:  :| |   |:  | |:   :  :
MKFFVQVFLFALLALLGLVSAGKM-----------------------AINPATTTTARPIFFPCFDEDGIFIGCTPHP

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REVERSE SEARCH

scoring matrix:
blosum62
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best alignment n: 1
names: AGAP009354  - CG13159-PA type=protein; loc=2R:7891276..7891503; name=CG13159-PA;
dbxref=FlyBase:FBpp0087023,GB_protein:AAF58525.1,FlyBase_Annotation_IDs:CG13159-
PA,FlyBase:FBgn0033721; MD5=d9cf6cc78390454d1e68f859559f416e; parent=FBtr0087912; release=r4.3;
species=Dmel; length=76;
identities: 18/83 (21%), positives: 39/83 (46%)
score: 1.150000e+001
MKFLATIIILFAFIALIGQGS-------AEPSRNDISVYEKLCQ----TFGLEKDCWTTANPPTKRPLADIKQETKENKDLMR
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|||:|::: |: :  |:::|        : ||    ::|         |:    |  ||:: | |: | ::  : |::
MKFFAVLVCFSAVLAIAMASTATTTSTPTTPSSPTTTTYTYTTTPTYPTYTYTTD--TTTTKPIKQQLLSLLFNKKSG-----

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best alignment n: 2
names: AGAP009354 - Mst57Da-PA type=protein; loc=3R:complement(21657374..21657598); name=Mst57Da-
PA; dbxref=FlyBase:FBpp0084288,GB_protein:AAF56515.1,FlyBase_Annotation_IDs:CG9074-
PA,FlyBase:FBgn0011668; MD5=a98e98631d6e55d45d1b6b62ed7f856c; parent=FBtr0084914; release=r4.3;
species=Dmel; length=75;
identities: 21/83 (25%), positives: 37/83 (44%)
score: 9.500000e+000
MKFLATII-LFAFIALI-GQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRP----------LADIKQETKENKDLMR
||||| :: |:: :||: :| | : ::| | :  |   :      : : | ||:  |          |||   |:
MKFLALFVTLLVVLALVSAQKSQNTNHNVIVIGAKKPGAAPAAAAAAAPAAPPAAAPAAAPAAPEAGLADAPAES--------

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best alignment n: 1
names: AGAP009359- CG17278-PA type=protein; loc=3R:complement(16846995..16848420); name=CG17278-
PA; dbxref=FlyBase:FBpp0083449,GB_protein:AAF55833.2,FlyBase_Annotation_IDs:CG17278-
PA,FlyBase:FBgn0046763; MD5=fbc5a4cc67eeb73bc512520ce217b7ab; parent=FBtr0084047; release=r4.3;
species=Dmel; length=80;
identities: 23/84 (27%), positives: 45/84 (53%)
score: 19
MKFLATIIILFAFIAL-IGQ--GSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTK--RPLADIKQET-KENKNLMR------
||: |::: :|::|| : |  |  :|| :   | |  |:|   :: | :  :  ||  | |: :| |:  :| |:::
MKLSAVLLAIALLALSLVQCLGLPDPSTK--CVME--CDTQEYRSICAADDKGSTKTYRNLCVMKTENCLQNANFQKISDKECP

best alignment n: 1
names: cg17278  - AGAP11482
identities: 26/88 (29%), positives: 45/88 (51%)
score: 2.350000e+001
MK-LSAV-LLAIALLALSLVQCLGLPDPSTKCVMECDTQEYRSICAADDKGSTKTYRNLCVMKTENCLQNANFQK------ISDKECP
|: || : |:::::||| |    |       |   |  ::|| :|::|     ||| | ||:   :|  |:|: :      : | :|
MRFLSYINLMVLGVLALVLSASAG------PC--GC-PRSYRPVCGTD----LKTYSNQCVL---DCRINSNYGRKFGLKLLRDGHC-

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best alignment n: 2
names: AGAP009359- CG13159-PA type=protein; loc=2R:7891276..7891503; name=CG13159-PA;
dbxref=FlyBase:FBpp0087023,GB_protein:AAF58525.1,FlyBase_Annotation_IDs:CG13159-
PA,FlyBase:FBgn0033721; MD5=d9cf6cc78390454d1e68f859559f416e; parent=FBtr0087912; release=r4.3;
species=Dmel; length=76;
identities: 18/83 (21%), positives: 39/83 (46%)
score: 1.750000e+001
MKFLATIIILFAFIALIGQGS--------AEPSRNDISVYEKLCQ----TFGLEKDCWTTANPPTKRPLADIKQETKENKNLMR
|||:|::: |: :  |:::|        : ||    ::|         |:    |  ||:: | |: | ::  : |::
MKFFAVLVCFSAVLAIAMASTATTTSTPTTPSSPTTTTYTYTTTPTYPTYTYTTD--TTTTKPIKQQLLSLLFNKKSG-----
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best alignment n: 3
names: AGAP009359  - CG15212-PA type=protein; loc=3L:5105551..5105877; name=CG15212-PA;
dbxref=FlyBase:FBpp0076866,GB_protein:AAF50794.1,FlyBase_Annotation_IDs:CG15212-
PA,FlyBase:FBgn0040842; MD5=ba85ec81cfac93e50cdbb1382554ca94; parent=FBtr0077163; release=r4.3;
species=Dmel; length=63;
identities: 23/77 (29%), positives: 41/77 (53%)
score: 1.550000e+001
MKFLA-TII--LFAFIALIGQGSAEPSRNDI---SVYEKLCQTFGLEKDCWTTANPPTKRPLADIKQETKENKNLMR
||:|| ||:  |:| ||||   || |  :::   ::|:    :|    |   : :|   : :  :|:  | :| |:
MKYLALTIFVCLMA-IALI---SAVPVDESLIGDNIYQP---AFD---D---VQRPQDPQAIFKLKKLLKLKK-LLG

best alignment n: 1
names: CG15212  - AGAP012528
identities: 30/65 (46%), positives: 50/65 (76%)
score: 61
MKYLALTIFVCLMAIALISAVPV--DESLIGDNIYQPAFDDVQRPQDPQAIFKLKKLLKLKKLLG
::  ::|:||  :|:||:||:|:  |||::| ::|:   |: : ||||||::||||| ||  :||
LSLQSFTLFV--LAVALVSALPAVNDESILGGDVYEAEVDSFN-PQDPQAFLKLKKLKKLL-FLG

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best alignment n: 4
names: AGAP009359 - CG7377-PA type=protein; loc=3L:11563642..11563923; name=CG7377-PA;
dbxref=FlyBase:FBpp0075831,GB_protein:AAS65027.1,FlyBase_Annotation_IDs:CG7377-
PA,FlyBase:FBgn0036176; MD5=7f45a467479be516afd30b0a153a6565; parent=FBtr0076100; release=r4.3;
species=Dmel; length=94;
identities: 19/94 (20%), positives: 50/94 (53%)
score: 1.550000e+001
MKFLATIILFA----FIALIGQGSAEPSRNDISVYEKLCQ------TFGLEKDCWTT--ANPPT--KRPLADIKQET---KENKNLMR------
||: ::::|:|    |:: :::||:  : :| ::    ::      | : ::|  ||  |:| :  |: :   |:::   |: |:: |
MKYSCVLLLLATVACFLVSLSSGSTTTTSTDATTTTTTASSSDTTTTTASSSDTTTTTTASPSSSKKKHVIHYKRKVHRPKKVKTIRRKKNRSG

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best alignment n: 5
names: AGAP009359 - Mst57Da-PA type=protein; loc=3R:complement(21657374..21657598); name=Mst57Da-
PA; dbxref=FlyBase:FBpp0084288,GB_protein:AAF56515.1,FlyBase_Annotation_IDs:CG9074-
PA,FlyBase:FBgn0011668; MD5=a98e98631d6e55d45d1b6b62ed7f856c; parent=FBtr0084914; release=r4.3;
species=Dmel; length=75;
identities: 21/83 (25%), positives: 37/83 (44%)
score: 1.550000e+001
MKFLATII-LFAFIALI-GQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRP----------LADIKQETKENKNLMR
||||| :: |:: :||: :| | : ::| | :  |   :      : : | ||:  |          |||   |:
MKFLALFVTLLVVLALVSAQKSQNTNHNVIVIGAKKPGAAPAAAAAAAPAAPPAAAPAAAPAAPEAGLADAPAES--------

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best alignment n: 1
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names: AGAP009357 - Dro-PA type=protein; loc=2R:10260853..10261044; name=Dro-PA;
dbxref=FlyBase:FBpp0086566,GB_protein:AAF58216.1,FlyBase_Annotation_IDs:CG10816-
PA,FlyBase:FBgn0010388; MD5=1ef7557d7cd0ac3cb9d691e361196bbc; parent=FBtr0087436; release=r4.3;
species=Dmel; length=64;
identities: 17/64 (26%), positives: 29/64 (45%)
score: 1.150000e+001
MKFFVQVFLFALLALLGLVSAGK-MAINPATTTTARPIFF---PCFDEDGIF-IGCTPHP----
||| :  :|:| :  :|::: ||    :|  |:  |||         || :   :  | |
MKFTIVFLLLACVFAMGVATPGKPRPYSPRPTSHPRPIRVRREALAIEDHLTQAAIRPPPILPA

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best alignment n: 2
names: AGAP009357  - IM2-PA type=protein; loc=2R:13901536..13901732; name=IM2-PA;
dbxref=FlyBase:FBpp0085845,GB_protein:AAF57708.1,FlyBase_Annotation_IDs:CG18106-
PA,FlyBase:FBgn0025583; MD5=52f1d1d95585980583244870c8b71b44; parent=FBtr0086664; release=r4.3;
species=Dmel; length=45;
identities: 19/63 (30%), positives: 27/63 (42%)
score: 1.150000e+001
MKFF--VQVFLFALLALLGLV----SAGKMAINPATTTTARPIFFPCFDEDGIFIGCTPH--P
||||  | ||:|:|||| : |    : |:::||                  |    |: |
MKFFSVVTVFVFGLLALANAVPLSPDPGNVVIN------------------GDCKYCNVHGGK

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best alignment n: 3
names: AGAP009357  - CG18107-PA type=protein; loc=2R:13899500..13899698; name=CG18107-PA;
dbxref=FlyBase:FBpp0085844,GB_protein:AAF57710.1,FlyBase_Annotation_IDs:CG18107-
PA,FlyBase:FBgn0034330; MD5=9da71d010318ba3b52ebe47169ec7ba3; parent=FBtr0086663; release=r4.3;
species=Dmel; length=45;
identities: 13/57 (22%), positives: 32/57 (56%)
score: 9
MKFFVQVFLFALLALLGLVSAGKMAINPATTTTARPIFFPCFDEDGIFIGCTPH--P
|:||: | :| :|:||:|::|  :: :|:::              :|  ::|: :
MRFFAIVTVF-VLGLLALANAIPLSPDPGNVII-----------NGDCVNCNVRGGK

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best alignment n: 4
names: AGAP009357  - Mst57Da-PA type=protein; loc=3R:complement(21657374..21657598); name=Mst57Da-
PA; dbxref=FlyBase:FBpp0084288,GB_protein:AAF56515.1,FlyBase_Annotation_IDs:CG9074-
PA,FlyBase:FBgn0011668; MD5=a98e98631d6e55d45d1b6b62ed7f856c; parent=FBtr0084914; release=r4.3;
species=Dmel; length=75;
identities: 19/78 (24%), positives: 33/78 (42%)
score: 9
MKFFVQVFLFALLALLGLVSAGKM-----------------------AINPATTTTARPIFFPCFDEDGIFIGCTPHP
|||:  ::: :||::|:|||| |                        |  ||:  :| |   |:  | |:   :  :
MKFL--ALFVTLLVVLALVSAQKSQNTNHNVIVIGAKKPGAAPAAAAAAAPAAPPAAAPAAAPAAPEAGL-ADAPAES

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best alignment n: 1
names: AGAP009359  - AGAP009354
identities: 70/71 (98%), positives: 71/71 (100%)
score: 1.825000e+002
MKFLATIILFAFIALIGQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRPLADIKQETKENKNLMR
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
MKFLATIILFAFIALIGQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRPLADIKQETKENKDLMR

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best alignment n: 2
names: AGAP009359 - AGAP009356
identities: 68/71 (95%), positives: 70/71 (98%)
score: 180
MKFLATIILFAFIALIGQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRPLADIKQETKENKNLMR
|||||| ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||:||||||
MKFLATTILFAFIALLGQGSAEPSRNDISVYEKLCQTFGLEKDCWTTANPPTKRPLADIKQETKQNKNLMR

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ANP-PA

scoring matrix:
blosum62

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best alignment n: 1
names: Anp   - AGAP009429

identities: 20/76 (26%), positives: 32/76 (42%)
score: 1.750000e+001
MKYFVVLVVLALILAISVGPSDA-------------------VFIDILDKVENAIHNAAQVGIGFAKPFEKLINPK
||: :||||   |||::: || |                   :  |:| :: : | : |  | : ||       |
MKFAIVLVVAFAILAFATTPSAANESKLKSATHLMDHLVKAPIVSDLLKSLADHIDHKAAEGAA-AKETTTPAPPA

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REVERSE SEARCH

best alignment n: 1
names: AGAP009429 - Anp-PA type=protein; loc=3R:26035707..26035939; name=Anp-PA;
dbxref=FlyBase:FBpp0084976,GB_protein:AAF57024.1,FlyBase_Annotation_IDs:CG1361-
PA,FlyBase:FBgn0000094; MD5=da1477d3322884499848ae1280af5c25; parent=FBtr0085611; release=r4.3;
species=Dmel; length=57;
identities: 20/76 (26%), positives: 32/76 (42%)
score: 1.750000e+001
MKFAIVLVVAFAILAFATTPSAANESKLKSATHLMDHLVKAPIVSDLLKSLADHIDHKAAEGAA-AKETTTPAPPA
||: :||||   |||::: || |                   :  |:| :: : | : |  | : ||       |
MKYFVVLVVLALILAISVGPSDA-------------------VFIDILDKVENAIHNAAQVGIGFAKPFEKLINPK
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1. Smith, T. F. & Waterman, M. S. (1981) *J Mol Biol* **147**, 195-7.
2. Needleman, S. B. & Wunsch, C. D. (1970) *J Mol Biol* **48**, 443-53.