

**Supplementary File S1.** Multiple sequence alignment of Q0IFK9 homologs in other mosquito species. Multiple sequence alignment using Clustal Omega method was conducted in Geneious Prime v.2020.1.2.

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Q0IFK9_Ae._aegypti
KXJ69968_Ae._albopictus
XP_019549434_Ae._albopictus
XP_563491_A._gambiae
XP_001845014_C._quinquefasciatus
XP_001845020_C._quinquefasciatus
XP_312269_A._gambiae
XP_001662345_Ae._aegypti
XP_019563176_Ae._albopictus
KFB46015_A._sinensis
KFB46017_A._sinensis
ETN59818_A._darlingi
XP_003436203_A._gambiae

MSETEKKAE-QS-----TGGETETDGPKPDAEHQRKINVANLPWDVTEQQLRDLFSG
MTETDKKAE-QS-----TG-A-ETEGPKPDAEHQRKINVANLPWDVTEQQLRDLFSG
MSQVEKKTE-QS-----TG-EHETDTSKGNSEYQRRINVANLPWDVTEQQLRNLFSD
MTDAEKTAPETTAETKETTAKAENDGTEGQDVQKDNEHQRTINVGNLPKDITEQQLRDHFAG
MSDATKPVEKTQ-----DGTENEGDAPKTDNEHQRTINVGNLPSPDITEQQLRDHFSG
-----MCDNGKKLVGNLPPVDVTEKELRDHFKE
-----MADNPSRMKADNKKKLVGNLPPADITEEELRELFAD
-----MATAENTVNKAADNGKKLVGNLPPVDVTEDELREHFKD
-----MASAENTVNKAADNGKKLVGNLPPNDVTEDELREHFKD
-----MAENPSTMKADNKKKLVGNLPPADITEEELREHFKD
MTETEKNNVTTKTEADES--MNVDKEGNDVQKDNEHQRTINVGNLPKDITEQQLRDHFAG
-----MAENPSTMKADNKKKLVGNLPPNDVTEEELREHFKD
MTDAEKTAPETTAETKETTAKAENDGTEGQDVQKDNEHQRTINVGNLPKDITEQQLRDHFAG
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KFB46015_A._sinensis
KFB46017_A._sinensis
ETN59818_A._darlingi
XP_003436203_A._gambiae

HEVEKVEIYHYRKYTLALVLFKDKDTAAAAAELAEKENS MFRDRRLRMHMEFTSIRHIKREV
HEVEKVEIYHYRKYTLALVLFKDKDTAAAAALADKENAMFRDRRLRMHMEFTTIRHIKREV
HEVEKVDIYHYRRYTVAAVLFKNKETKAAALAGKENFMFGDRRLRMYSELTYIRYIKREL
HEVERVEIYHYLRNTLALLVFKEKAAQKACEEKDGSMLNDRRLRIHIEYITIRYTKKDV
YEIERVDIYHYRKYTLALLLFKEKDAAAKAVEEKEHSTLRGRRIRVHLEYMTIRHIKREV
FTVENVEIFHYLKYTLALLLFKDKDTATKALKAKEGTLFRNRRLRMHIEYIAIWNIKKNV
HPVESVEIFHYKQYTLALLLFKDKETATKALKEKENS VFGRRLRMHLEFIVICHMKKDV
FTVENVEIFHYLKYTLALLLFKDKDTATKALKEKEGSMFRNRRLRMHIEYIAIWNIKKNV
FTVENVEIFHYLKYTLALLLFKDKDTATKALKEKEGSMFRNRRLRMHIEYIAIWNIKKNV
HPVESVEIFHYKQYTLALLLFKDKETATKALKEHDNSVFRGRRLRMHLEYIVICHMKKDV
HEVERVEIYHYRNTLALLLFKDKVAAQKAIDEKDGKMMGDRRLRIHLEYITIRYTKKDV
HPVESVEIFHYKQYTLALLLFKDKETATKALKEKENS VFGRRLRMHLEYIVICHMKKDA
HEVERVEIYHYLRNTLALLVFKEKAAQKACEEKDGSMLNDRRLRIHIEYITIRYTKKDV
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IVTVVEDENMTTEEQLWDKVKAAAGVEPTSVLIFYPLGYVTLEKECDKAPILEKLKAAGFNA
VTVVIEDENMTTEEQLWDKVKAAAGVEPTSVLIFYPLGYVTLEKECDKPALLEKLKTAGFNV
VVTAIEDENMTTEEQLWDKVKAAAGVEPTSVLIFYPLGYVTLEKCDKPAVLEKLKAAGFNA
IVAVLDD-DMTEEKLYDRVKE-HCEVTQVFI FHPLGYVHLGKDVDKAAVLEKLNAGGLKA
IVTVLDDNTTEDQLWDKIKAAAGVEPTSVLVFYPLGYVLDKADKPALEKLTAAGFNA
FVYVVD-NTTEEDVYDKFKT-ITEVTGVLVFHPLAYVSCNTQEQQKEAAIKELNAEETTV
FVHVVDNENVTEEDVYEKFKD-LAKVQSVVLFHPLAYVTCTSPEDKEEAMKKIVEAGINV
FVTVVDD-NTTEEEVYDKYKD-VTEITGVLVFHPLAYVSCNTQEQQKEAAIKELNSEEVKV
FVTVVDD-NTTEEQVYDKYKD-VTEITGVLVFHPLAYVSCNTQEQQKETAMKELNSEETV
FVYVVDNENVTEEDVYEKFKD-LAKLQSVVLFHPLAYVTCTSPEDKEEAMKKIAEAGINV
IVTVVDD-DMTEEKLYDRVKE-HCEVTQVFI FHPLGYVHLGKADKTVVLEKLNAGGLKA
FVYVVDNENVTEEDVYEKFKD-LAKVQSVVLFHPLAYVTCTSPEDKEEATKKIAEAGINV
IVAVLDD-DMTEEKLYDRVKE-HCEVTQVFI FHPLGYVHLGKDVDKAAVLEKLNAGGLKA
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HDLNQRDQNHLDIWRRAAKLFFRNRRNVQLLNIPNKWIEDKEEMKKQCAEGGTITEAVSN
HDVNQRDQNHLDIWRRAAKLFFRNRRNVQLLNIPNKWIEDKEEMKKQCAEGGTITEAVSN
HDVNQRDQNHLDIWRREATLFFRNRRNVQLLNIPSKWIEDKEEMKKQCAEGGTITEAVTS
YDVNGRDQNHLDIWRRAAKLFFRNRRNVQLLNIPQKWVENTEELKKACSEAGTITEAIAN
HDVNQRDQNHLDIWRRAAKLFFRNRRNVQLLNIPTKWIEDKEEMKKQCAEGGVITEAVSN
YDLTGHDQNHHDIIWRRAAKLFFRNMRNVSLINLPESWVSNQEELKKAVEGTGTLTEVKVI
YDCNGHDQNHHDIVLRAAKLFFRNLRNVQMYNIPESWISSQDELKKAVESSGTVTEVRVT
YDVTGHDQNHHDIIWRRAAKLFFRNMRNVSLINLPESWVSNQEELKKAVAHTGTTTEVKVI
YDVTGHDQNHHDIIWRRAAKLFFRNMRNVSLINLPESWVSNQEELKKAVAHTGTTTEVKVI
YECGHGDQNHHDIVLRAAKLFFRNLRNVQMYNIPENWVNSQDELKKAVESSGTVTEVRVT
YDVNGRDQNHLDIWRRAAKLFFRNRRNVQLLNVQKWVENTDELKKACSEAGTITEAVAN
YECNGRDQNHLDIVMRAAKLFFRNLRNVQMYNIPESWVNSQDELKKAVESSGTVTEVRVT
YDVNGRDQNHLDIWRRAAKLFFRNRRNVQLLNIPQKWVENTEELKKACSEAGTITEAIAN
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XP_001845020_C._quinquefasciatus

NVTQNPQMASNYARIFYETEEQAVKAAKALNGRVVDGKRIHALHLSALMPNYKTSVYVT
NVTQNPVVASNYARIFYETEEQAAKAAKALNGRVVEGKRIHALHLSALMPNYKTSVYVT
NAAQNPSVIPNYARIFYETEEQAAKAAKALNGRVVEGKRIHALYPGIVLMPNYKTSVYVT
NVSQGS--SNYYARIFYETEEQAAKAAELLNGKVFEGKRIHALHLSALLPNYKTSVYVA
NVNQS---SSNYARVIFYETEEQAKAAASLNGRIVEGKRIHALHLSALIPNYKTSVYVT
NNSHGS----VAQLFYEDEDTARNASQTLNQVFEKGKRIHALHVTAALIPDYTSSVYLT

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XP\_312269\_A.\_gambiae  
XP\_001662345\_Ae.\_aegypti  
XP\_019563176\_Ae.\_albopictus  
KFB46015\_A.\_sinensis  
KFB46017\_A.\_sinensis  
ETN59818\_A.\_darlingi  
XP\_003436203\_A.\_gambiae

TGNFGP-----AAQVFYETADEAKAAAEKLNQQLFEGKRVHAHHVIATMIPNFKTSVYVE  
NNSHGA-----VAQLFYENEETARKAALELNQKIFDGKRIHALHVTAALIPNYETSVYLT  
NNSHGA-----VAQLFYENEETAKKAALELNQKIFDGKRIHALHVTAALIPNYETSVYLT  
TGNFGP-----AAQVFYESAEEAKAAADKLNQQIFEGKRIHAHHVIATMIPNYKTSVYVE  
NVNQAA--SNYYARIFFETEEQAAKAAELLNGKVFEGKRIHALHLSSALLPNYKTSVYAS  
TGNFGP-----AAQVFYETADEAKAAADKLNQQLFEGRRIHAAHHVIATMIPNYRTSVYIE  
NVSQGS--SNYYARIFFETEEQAAKAAELLNGKVFEGKRIHALHLSSALLPNYKTSVYVA  
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ETN59818\_A.\_darlingi  
XP\_003436203\_A.\_gambiae

SLDKGVTEEQVYDHFQFGEIEFTNRRNCGD-AAIICYKNAASAEKALACTTFPAPTEEN  
ALDRGVTEEQVYDHFQFGEIEFTNRRNCGD-AAIICFKNAASAEKALACTTFPAPTEEN  
SLSKGVTEEQVYDYFFKQFGEIEFTSRNRCGD-AAIICFKNAASVDKALACTTFPAPTEEN  
PLERTVTEEEVYEHFKQFGDIDFVNRRNCGE-NAIVCYKTSEAAEKALACTTFPAPTEAN  
SLEKTVTEENVYDHFQFGEIEFVNRRNCND-AAIVCFKSADSVEKAICTKLPAPTEAD  
GLEKPISEETIYSHFEQFGEIEFVSRRCADDEHAICFKNSSAVEAALECKTLPVPKPD  
SLDKTITEEMLYAHFEQYGEIDFVNRRKFGDEHGMVCFKEASSVDRALECTTLPVTKEG  
SLEKATSEETIYDHFQFGEIEFVSRRCADDEHAVICFKNASAVEKALECKTLPITKPLS  
SLEKATSEETIYDHFQFGEIEFVSRRCADDEHAVICFKDASAVEKALECKTLPVPKADS  
SLDKSVTEEILYDHFQYGEIDFVNRRKFGDEHGLVCFKEASSVERALECTALPMPKKED  
PLEKTVTEEDVYDYFFKQFGEIDFVNRRNCVD-NAIVCFKSEDAVEKALACTTFPAPTEAN  
QLDKSITEEQLYDHFQYGEIEFVNRRKFGDEHGLVCFKEASSVEKALLCTALPLPKKEV  
PLERTVTEEEVYEHFKQFGDIDFVNRRNCGE-NAIVCYKTSEAAEKALACTTFPAPTEAN  
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KFB46015\_A.\_sinensis  
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XP\_003436203\_A.\_gambiae

K-----DATKEVVVKYDGPLVLRPVALKRKL  
K-----DATKEVAVKKYDGPLVLRPVALKRKL  
K-----DATKEVVVKYDGPLVLRPFTFKRKL  
K-----EATKTVTVLRDGPLVLRATSVKRKA  
K-----DATTEITVKKYDGPLLLRSLAMKRKL  
EE-----TEDKTIGVKYNGPLIIDLKPSHVKK  
EE-----TTTEDKTIVVKRYDGPLVLDIKLPAMKK  
DV-----TEERAITVKRYNGPLIIDLKPSHVKK  
DK-----TEDRAITVKYNGPLIIDLKPSHVKK  
E-----TANVEKTIVVKRYDGPLVLDIKLPPIKK  
K-----EATKTITVKRYDGPLVLRAGVKKRQ  
GSEEEAAPAATTTDGTASATAAATTSAAAVTPTETETKTIVVKRYDGPLVLDIKLPQKK  
K-----EATKTVTVLRDGPLVLRATSVKRKA  
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Q0IFK9\_Ae.\_aegypti  
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KAGEEE-----KDQAEKTKEQQSVLGKCLKAYHPIFVGNVPLNCPPLELKH  
KPGEEE-----KDQAEKTKEQQSVLNKCLKAYHPIYVGNVPLNCPPLELKH  
ESTEGE-----KVKTEKTKEQRSVLHKLKAYHPIYVGNVPLNCPPLELKH  
ASGTAKGAAGEGKTRESRP--AGGSDREKSHKDILQKLQAFYPVYVSNIPFSCPAHVIRE  
KTNEDGTP-----ADPEEKTKEADVLKKLQAYHPVFGVGNVPLNCPPLELKH  
--LLED-----GEESKMRPPLPLAKLWPIYVSNLPHYADKRDMD  
GASSEE-----GEEQKQRPPQPPLAKLWPIYVANLPYKADKREIKQ  
--LLED-----GEESKMRPPLPLAKLWPIYVSNLPHYADKRDIRD  
--LLED-----GEESKMRPPLPLAKLWPIYVSNLPHYADKRDIRD  
NSTGEE-----GEEQKQRPPQPPLAKLWPIYVANLPYKADKREIKQ  
AATTK-RTAPDGKTRERTIGAAGAERTHDKDILQKLQAFWPVYVSNVPYSCPSHVIRD  
GATSEE-----PEEQKQRPPAPLAKLWPIYVANLPYKADKREIKK  
ASGTAKGAAGEGKTRESRP--AGGSDREKSHKDILQKLQAFYPVYVSNIPFSCPAHVIRE  
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YFA-QHGPIKFMFSPQI-LAYRNSAPHPVKTFIIYYMNRPSQQNAVRFDDHKFFGGHRLH  
YFA-QHGPIKFMFSPQI-LSYRNSAPHPVKTFIIYYMNRVSQQNAVRFDDHKFFGGHRLH  
YFA-QHGPIKFMFSPQI-FSYRNSAPHPVKTFIVYYMNRPSQQNAVRFDDHKFFGGHRLH  
FFSGAGGEVKFIFSPQHYHPYRLSSPQPVKTAMVYVYTRSDMLNAIKQLDKMLNNQHLH  
YFA-QHGPIKFMFSPQI-VTYQTSAPHPVKTFIIYYNFRPSALNACKFLDHKFFGGHRLH  
YFSSVGGHIKFI FSPNI-PAYKTSQTSMVMAALIYYARREQATDAIKAFNGKHFFQNRCLH  
YFSSYGGHIKFI FSPNI-PSYKQSQTSMVMAALIYFARREQANEAIKAFNGKHFFQSKCLH  
YFSSVGGHIKFI FSPNI-PAYKTSQTSMVMAALIYYARREQATDAIKAFNGKHFFQNRCLH  
YFSSVGGHIKFI FSPNI-PAYKTSQTSMVMAALIYYARREQATDAIKAFNGKHFFQNRCLH  
YFSSYGGHIKFI FSPNI-PSYKQSQTSMVMAALIYFARREQANEAIKAFNGKHFFQSKCLH  
LFSSQGGEVKFLFSPQYLYTLRLSAPQPVKTVMYYTRNDMYNALKHFDKALLGHHLN  
YFSSFGGHIKFI FSPNI-PSYKQSQTSMVMAALIYFARREQANEAIKAFNGKHFFQSKCLH  
FFSGAGGEVKFIFSPQHYHPYRLSSPQPVKTAMVYVYTRSDMLNAIKQLDKMLNNQHLH  
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VLPLRGTDQNMDVKKTIKMTKIP-FMSEDALFKKIKPFVGKINRIVKKSRLIAYIELEDSA  
VLPLRGTDQNMDVKKTIKMTKIP-FMSEDALFKKIKPFVGKINRIVKKARLAAYIELEDTA  
VLPLRGAQCMQDVKKTIKMTQLP-SMSEDALFKKIKPFVGKINRIVKKVRFEAFIELEDTA  
VLPGRGDCNFSQQKTVKLSKITESLSEDAIFRKMMP-LGKVVRLTKKNSLAFVEFADAA  
VLPLRGELNFDVKKTVKITKIP-YLSEDALFKKVPYVGKINRIVKKTRVAAYIELNDLA  
VFPGRKDTYFNPETSVRLVRLTIGVSEKLFKEKFRK-FGFIECVVKRNRNTALIEFRDKE  
VFPGRKDTYFDVEKSIKVVRNLAVTEEKLFEKFRK-FGFIECVVKDRRTTAYIEFRDKE  
VFPGRKDTYFNPETSVRLVRLTIGVTEEKLFEKFRK-FGFIECVVKRNRNTALIEFRDKE  
VFPGRKDTYFNPETSVRLVRLTIGVTEEKLFEKFRK-FGFIECVVKRNRNTALIEFRDKE  
VFPGRKDTYFDTEKSIKVVRNLAVTEEKLFEKFRK-FGFIECVVKDRRTTAFIEFRDKE  
VIPGRGESNFEQNTVRLSRINESLSEDAIFRKMCP-LGKIVRLTKKSRSLAFVEFADAA  
VFPGRKDTYFDTEKSIKVIRLNIAVTEEKLFEKFRK-FGFIECVVKDRRTTAYIEFRDKE  
VLPGRGDCNFSQQKTVKLSKITESLSEDAIFRKMMP-LGKVVRLTKKNSLAFVEFADAA  
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DVEKMMNVETPDHPLPKGKMEQLKTPISARLYNEDDVRVLNGIAKIVAKNPMDLKKNIQ-  
DVKMMNTETADHPLPKGKMEQLKTPISTRVYNEDDVRVLNGIAKIVAKNPMDLKKTPLP  
DVVKLMKTETPNHPLPKSKMEQLTTPISVRLYDEDDVRILNGIAKIVEKNPMDLKKTVLP  
DVEKVLKMKPDELTINC-VYSKITKDVSRRLYNESDPRILGTIVRLLRNPKMLNKTGA  
VDVKFMDVDAADHPLNKAKEPI SANTSVRLYDENDTRVLRGIAKIIAKNPMDLKKVAPG  
VCDKVLQLPDGEKPVRC-GIEPLTTKVNKIKFENDEKISLAMQEI IDKNPAVLENVQSN  
IAEKVLKLDEKQRPVRC-NVEAVTGKINKKIKFENDEKISLAMQEI IDKNPAVLENVSSD  
VCDKVLQLPDSEKPVRC-GIEPLTTKVNKIKFENDEKISLAMQEI IDKNPAVLENVQST  
VCDKVLQLSDSEKPVRC-GIEPLTTKVNKIKFENDEKISLAMQDI IDKNPAVLENVQST  
IAEKVLKLDEKQRPVRC-NVEPVTGKINKKIKFENDEKISLAMQEI IDKNPAVLENVSSD  
DVEKILKMKQEELPINC-VYSKITKDVNRRLYNESDPRIVGTIVRLMRNPKMLTKTTGA  
IAEKVLKLDEKQRPVRC-LVEPVTGKINKKIKFENDEKISLAMQEI IDKNPAVLENVSSD  
DVEKVLKMKPDELTINC-VYSKITKDVSRRLYNESDPRILGTIVRLLRNPKMLNKTGA  
\*.: . : : . : . : \*

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KFB46015\_A.\_sinensis  
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XP\_003436203\_A.\_gambiae

-PP-----NKRPRMEFGGPGFNQGGP-----GFVPNN-----  
-PP-----NKRPRMDFGGPGFDQGGP-----GFNP-----  
--L-----NKRPRMDFGGPGFNQGGP-----GFNP-----  
GPLMGGN--TAVGGGPGGFGGKRPMPNGPPGGKLFLLIDLLVCFTLHRLYFPVHFHNVE  
-QL-----NKRPRLN-GPGTFNQGPV-----GFNPSN-----  
RF--SGP-----PPLKRGFRNGPDPNFGNLGNR-----NDFNSMN-----  
RS--SGP-----PPLKRSRFSGPA-NFGMQGPR-----NQFN-PN-----  
RF--SGP-----PPLKRGFRNGPDPNFGG--NR-----GD--FN-----  
RF--SGP-----PPLKRGFRNGPDPNFG--NR-----GD--FN-----  
RS--SGP-----PPLKRSRFSGPS-NFGMQGPR-----SQFN-PN-----  
GPLMSRGPMNVGGGPGRFAGGKRPRMSGPPGFGNP-PP-----FNPNNGGNLN  
RS--SGP-----PPLKRGFRSGPA-NFGMQGPR-----NQFN-AN-----  
GPLMGGN--TAVGGGPGGFGGKRPMPNGPPGGFGNVPP-----FNPNAGG-----  
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KFB46017\_A.\_sinensis  
ETN59818\_A.\_darlingi  
XP\_003436203\_A.\_gambiae

-----NMNPNAIQDLLRLAFMSGKNVGESLASNQS-----  
-----NMNPNAIQDLLRLAFMSGKNVGENLASNQS-----  
-----NMNPNAIQDLLRLAFLSGKNVGESLASNQS-----  
MHFCLLNSSTHSAFARNSSISRYKFAYFLLLFHHSNFH-----  
-----NMNPNQAIQDLLRLAFMSGKNVGESLATGGQ-----  
-----SNNDFSNPQVIQDLLRLAFISGKNLGEGLASGNN-----  
-----NGGDFSNPQVIQDLLRLAFISGKNLGEGLAISGN-----  
-----NGNDFSNPQVIQDLLRLAFISGKNLGEGLIASGNN-----  
-----NGNDFSNPQVIQDLLRLAFISGKNLGEGLIASGNN-----  
-----AGNDFSNPQVLQDLLRLAFISGKNLGEGLANGGQ-----  
-----NNQAIQDLLRLAFMSGKNVGETLAAGGG--SGNQGPNRG  
-----SATDFSNPQVIQDLLRLAFISGKNLGEGLAISGN-----  
-----NNLNNQA----IQDLLRLAFMSGKNVGESLAAGGGNVGGNQGPNRG  
: : \* \* \* \* . :

Q0IFK9\_Ae.\_aegypti  
KXJ69968\_Ae.\_albopictus  
XP\_019549434\_Ae.\_albopictus  
XP\_563491\_A.\_gambiae  
XP\_001845014\_C.\_quinquefasciatus  
XP\_001845020\_C.\_quinquefasciatus  
XP\_312269\_A.\_gambiae

-----SF--GPDPPVANSNN-----FGDGGFGNRNR-----NNQ--GGNQGNFRGQGRM  
-----SF--GPDPPVANSNN-----FGDGGFGNRNR-----NNQ--GGNQGNFRGQGRM  
-----SF--GSDSSIANSTN-----FGDGSFGNRNR-----NSQ--GGNQGNIRGQGKM  
-----SFN-APDPPLANSNN-----FGDGGFRGNNNRGGN--NQM--GGGQSNFRPNNRN  
---NPFNNSSDSPLSSLNLANG-----FSGRNFGGGSNNNGFEQ-----  
---SNPFN-SGDPPLPNLN-L-T-----N-GFGG-GNQRNSF--NNSNNGNFGGS---

XP\_001662345\_Ae.\_aegypti  
XP\_019563176\_Ae.\_albopictus  
KFB46015\_A.\_sinensis  
KFB46017\_A.\_sinensis  
ETN59818\_A.\_darlingi  
XP\_003436203\_A.\_gambiae

Q0IFK9\_Ae.\_aegypti  
KXJ69968\_Ae.\_albopictus  
XP\_019549434\_Ae.\_albopictus  
XP\_563491\_A.\_gambiae  
XP\_001845014\_C.\_quinquefasciatus  
XP\_001845020\_C.\_quinquefasciatus  
XP\_312269\_A.\_gambiae  
XP\_001662345\_Ae.\_aegypti  
XP\_019563176\_Ae.\_albopictus  
KFB46015\_A.\_sinensis  
KFB46017\_A.\_sinensis  
ETN59818\_A.\_darlingi  
XP\_003436203\_A.\_gambiae

Q0IFK9\_Ae.\_aegypti  
KXJ69968\_Ae.\_albopictus  
XP\_019549434\_Ae.\_albopictus  
XP\_563491\_A.\_gambiae  
XP\_001845014\_C.\_quinquefasciatus  
XP\_001845020\_C.\_quinquefasciatus  
XP\_312269\_A.\_gambiae  
XP\_001662345\_Ae.\_aegypti  
XP\_019563176\_Ae.\_albopictus  
KFB46015\_A.\_sinensis  
KFB46017\_A.\_sinensis  
ETN59818\_A.\_darlingi  
XP\_003436203\_A.\_gambiae

Q0IFK9\_Ae.\_aegypti  
KXJ69968\_Ae.\_albopictus  
XP\_019549434\_Ae.\_albopictus  
XP\_563491\_A.\_gambiae  
XP\_001845014\_C.\_quinquefasciatus  
XP\_001845020\_C.\_quinquefasciatus  
XP\_312269\_A.\_gambiae  
XP\_001662345\_Ae.\_aegypti  
XP\_019563176\_Ae.\_albopictus  
KFB46015\_A.\_sinensis  
KFB46017\_A.\_sinensis  
ETN59818\_A.\_darlingi  
XP\_003436203\_A.\_gambiae

Q0IFK9\_Ae.\_aegypti  
KXJ69968\_Ae.\_albopictus  
XP\_019549434\_Ae.\_albopictus  
XP\_563491\_A.\_gambiae  
XP\_001845014\_C.\_quinquefasciatus  
XP\_001845020\_C.\_quinquefasciatus  
XP\_312269\_A.\_gambiae  
XP\_001662345\_Ae.\_aegypti  
XP\_019563176\_Ae.\_albopictus  
KFB46015\_A.\_sinensis  
KFB46017\_A.\_sinensis  
ETN59818\_A.\_darlingi  
XP\_003436203\_A.\_gambiae

---NPFN-SSDSPLSGLNLSNG-----FSGRNFSGGSNNFSGNNAGNRNNFSGN---  
---NPFN-SSDSPLSGLNLSNG-----FSGRSFSGGSNSFGNNPGNRGNFSGN---  
-HGNNPFT-GGDPPLPSLNNL-G-----N-GFGGGGGQRRNF-NNSNNGNFSGS---  
GGGGSFN-NADPPI SNQGGGNNAFGGGDGGFGAGGGGGGGGRNMNRNQN-NFRGGNRN  
---SNPFN-SGDPPLANLNNG-----F-GGSGGGNRRNF-NNSNSGNFSGN---  
GGGGGSFN-NADPPI SNQGGGNNAFGGGDGGFGAGGGGGGGGRNMNRNQNMMNFRGGNRN

NMNQNQNRGN--ANN--FGGNTNAGGNNFQASPGNQ-N-RGGQNMNRGNQQ-NQNRAG--  
N--QNQNRGN--AGN--FGGNNNAGGNNFQGSFGNQ-N-RGGQNMNRGNQQ-NQNR-G--  
N--QN-----SGGNNNAGGNNFQGSFGNQ-N-RGGQNMNRVNNQQ-NQNR-S--  
-----  
NMNNQNNQNR--N-----NNFNAGGNNFQGAQAN-RGNQGNANNRNPSQNRVQGG  
-----  
-----SNNASGNMGGGNR-NNM--GGGVNRNFG-QNVGGGGGA  
-----PNNPGQRNFGGQ-----Q-RNPNNPGNAFSGGNP-  
-----LNNPGQRNFGGQ-----QQQNRNPNPGNAFSGGSNQ  
-----SNNAGGNMGGN-R-NNM--GGGVNRNFG-QNVGGGGGG  
NANNVGGNRGLGGGGLGNSNNNAGGNNNFGNNQNG-VGGGGGPRSGGALGG-GNSG  
-----SNNSGGGNMGNRGGNMGGSGGLNRNFGGQNLGGGGNG  
NQNNVGGNRGLG-----NNSNNNAGGNNNFGNQ-QS-GGSGGPRGGGALGG-GGGN

----GNMNQ-----GNNMNQAGGGNVN--RPQQNKPMNMNT-----  
----GNMNQ-----GNNMNQS-GGNVN--RPQQNKPMNMNT-----  
----GNMT-----SNMNQS-GGNFN--RPQQNKPMNMKT-----  
-----  
GQGQGGVQQNRNVTQQ-----QQNKPNVQGGGNL--LG-QNRPNQNGG-----  
-----  
MGSGGYGRVNMGG--G-----FGGKRFNGGSQQTNRMQ-----  
NKFGSSN-----NQQQNRNLN-----  
NKFGGGS-----NNQQNRNQ-----  
GNMGGGYRNNLGG--N-----FGGKRFNG-SQQSNRMQ-----  
G-GGGMMNRNNPNMNRNN--NQNMNRKAGGNVN--VQQQTPMVGGGIGGN----  
GGIGGGYRSNLGG--N-----FGGKRFNG-SQQTNRMQ-----  
NNSGGMMNRNM-NMNRNNSNNMNMNRKRTGGNN--LPQQNAALPAGGVAAVGGG

-----GN-----QNQRNNQVGGGGMNRNQNQNNR  
-----GN-----QNQRNNQVGGG-NMNRNQ---N  
-----GN-----Q--NRNNQVGGF-NMNRNQ---N  
-----  
-----GN-----NVNVRNNSQ---TRNQNGNRNN  
-----  
-----NNRQ-----GG-----GNQ--NRRF-----  
-----QNR-----PERNM--NRRF-----  
-----QNRQ-----GGNM--NRRF-----  
-----NNRQ-----GG--GGGGGGGNQ--NRRF-----  
---NKGGLRGNN-QGLGVGGMGTVGGGGGGNNMNRNNSNNLGGGGMGGNRNNR  
-----NNRQ-----GG--GGGG-GGNNQ--NRRF-----  
NMNKGGMGRNNQGMG-----GGSGMGSGGGGNMNRNNSNMGGSGMGGNRNNR

NNF-DNDNSFG---GG-NNFGNRNNNFSNDSFGSND---NNFGGNNS---GSNNFSNDN  
RNF-DNDNSFG---GG-NNFGNRNNNFSNDSFGNDD---NNFGNN---SSNNFSNDN  
SSF-DNDNSFG---GG-NNFGNRNRSNNFSNDSFGIDD---NNFDNN---GSNNFSNDN  
-----  
NNFASDDNSFGSGGGG-GNYNARSNNNFSNNDFSND-----SFGNSND---GGNSFGNQ  
-----  
-----  
-----  
-----  
NNY-NNDSNS-----SFGGSDSSISSPEYAMITE-----  
-----  
NNF-NDTSSFGVGGGNSNSFGGNNNFSNDFGGGRNNDNSYSNDFGGGRNDSYSSDS

NFGGN-----NRGNNF'GGNKRQNDNFNNSFGSGNN-----SGGNNRFNNDGNNFNSNF  
 -FGG-----NTNRNF'GGNKRQNDNFN-SFGSGNNS--GSSGGNNRFNNDGNNFSSNF  
 -YGG-----NTSRNF'GGNMRQNDNFN-SFGSGNNS--GSTGGNNRFINDGNNYKSSF  
 -----  
 NFNNRQ---NQSDSFGG-----NSFGGGNNRFQNDNNGGNSF'GNNGGNFNN--  
 -----  
 -----  
 -----  
 -----  
 -----  
 -----  
 -----  
 NFGGNSGGGGGRN'F'GGNRNN-----DSYGSNRNDNFGSGGGSSNFGG-GN-----

NNRRNQ-NRFDNDNDDNNFTGNG--GNNFG-----  
 NNRNNQNNRFDND-DNNFSGNTGGNKGGNF-----  
 NNRSNQNSFDNG-N----NFSGNKGGNF-----  
 -----RNNRFADNNDN-SDNVVG-NGGGFN-----

-----  
 -----  
 -----  
 -----  
 -----  
 -----  
 -----  
 -----  
 -----A FGNNSRFSNDNDGP FSGNSGGNAGGGNSSFGANNRGNSSS SRFSDDNI GGGGYGGG

[illegible]

SGGNFGGNNS-----GFNSGNAGGNKWNNNNSQQS-----NTGSRLAGSI---FSRR  
 RGGNFGGNNS-----GFNSGNAGGNKWNNNNSQQS-----NTGSRLAAPEGELFVGL  
 RSGNFGANNNS-----GFSPGNAGGNKWNNNNSQQS-----NTGSRLAGSI---FSRR  
 -----  
 FGGN---G-----NGGGGFNKWNNNNSNNSGQSNNNQNSGGRLAG---TIFSRR  
 -----  
 -----  
 -----  
 -----  
 -----  
 -----  
 YNNNFGGGNSNNSGGNNFRNNDNNGGWNSNNSGLG--GGRSNNNQDNIGRLAGSLFSRR

F-----  
 LLLIVNFLYRVLKPVVRNNRADTFDDERYYSITPTPALPVPATIQAVAPATAATSVITS  
 F-----  
 F-----  
 -----  
 -----  
 -----

XP_019563176_Ae._albopictus	-----
KFB46015_A._sinensis	-----
KFB46017_A._sinensis	-----
ETN59818_A._darlingi	-----
XP_003436203_A._gambiae	F-----

Q0IFK9_Ae._aegypti	-----
KXJ69968_Ae._albopictus	DNTFQSEYIPVPRDERYEFPGMMPRDTRMYETGLVSGSDNTISNPVPLYRDERHYYPVST
XP_019549434_Ae._albopictus	-----
XP_563491_A._gambiae	-----
XP_001845014_C._quinquefasciatus	-----
XP_001845020_C._quinquefasciatus	-----
XP_312269_A._gambiae	-----
XP_001662345_Ae._aegypti	-----
XP_019563176_Ae._albopictus	-----
KFB46015_A._sinensis	-----
KFB46017_A._sinensis	-----
ETN59818_A._darlingi	-----
XP_003436203_A._gambiae	-----

Q0IFK9_Ae._aegypti	-----
KXJ69968_Ae._albopictus	ITSSYILDNRQYEQSINSPPSMHDLRYQPTTHTITSGMLYNDRHYETANSLGSLSNLASA
XP_019549434_Ae._albopictus	-----
XP_563491_A._gambiae	-----
XP_001845014_C._quinquefasciatus	-----
XP_001845020_C._quinquefasciatus	-----
XP_312269_A._gambiae	-----
XP_001662345_Ae._aegypti	-----
XP_019563176_Ae._albopictus	-----
KFB46015_A._sinensis	-----
KFB46017_A._sinensis	-----
ETN59818_A._darlingi	-----
XP_003436203_A._gambiae	-----

Q0IFK9_Ae._aegypti	-----
KXJ69968_Ae._albopictus	NECHGVEMMMRQDAAAVAAAAVIEHGAAAEVAVWGRAEMERQDEIDRQYLVLLPREDKIEP
XP_019549434_Ae._albopictus	-----
XP_563491_A._gambiae	-----
XP_001845014_C._quinquefasciatus	-----
XP_001845020_C._quinquefasciatus	-----
XP_312269_A._gambiae	-----
XP_001662345_Ae._aegypti	-----
XP_019563176_Ae._albopictus	-----
KFB46015_A._sinensis	-----
KFB46017_A._sinensis	-----
ETN59818_A._darlingi	-----
XP_003436203_A._gambiae	-----

Q0IFK9_Ae._aegypti	----
KXJ69968_Ae._albopictus	QDEL
XP_019549434_Ae._albopictus	----
XP_563491_A._gambiae	----
XP_001845014_C._quinquefasciatus	----
XP_001845020_C._quinquefasciatus	----
XP_312269_A._gambiae	----
XP_001662345_Ae._aegypti	----
XP_019563176_Ae._albopictus	----
KFB46015_A._sinensis	----
KFB46017_A._sinensis	----
ETN59818_A._darlingi	----
XP_003436203_A._gambiae	----