



CLUSTAL O(1.2.3) multiple sequence alignment

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AALF018937 -----MLIVM
AALF003920 -----MLRCATNTNHR---I
AAEL017277 MFRSTRRRFTNWI SNKTKLKPDTDVFFLLDYFLVLSGVQLLTKNGYLRTAWNRYRTLGV
AALF003919 MFCSIKTRFTEWWKHLTKLKPGRDSFFLLDYFLVLAGIHLLTRNGYLRTVWNFYRALLFI
AALF018936 -----

AALF018937 QVILITRKIWSIFQTEDNFQLISNSLHMCVGFSIIFTRIFFIVRSFKQ-----
AALF003920 GTVIDDRHEARALTRAD-----GTAATSSERVS AVRSNRESSERRRAVAI
AAEL017277 HVLLMSRKIWSVFQTEDNFQLIANMMLCVGCLIFARCIFIVRSSEQ-----
AALF003919 HVVLMTRKVMEIFQTEDNFQLIANMMIMCVGCFIIFARCVFIVTSFKQ-----
AALF018936 -----

AALF018937 ---VNGV-RCFVNQRKFRADDPAAFAIRQRTYANTINITIAMILNCFVQTVIVLFTDLAN
AALF003920 IIIIDTRRAPVNVMRKFRADDPAAFAIRQRTYANTINITIAMILNCFVQTVIVLFTDLAN
AAEL017277 ---IKIV-RRFVNERKFKADDSFAMTVRQNTYNNNTIIVTVVMILNCFVQSGMILFTELGE
AALF003919 ---VNSI-RNLVNRREFQANDPTAMAIRQSAFNNAIFVTLFMAMNSLTQTFMVLFIDLK
AALF018936 -----

AALF018937 SESLQLPFYHRRTD-----
AALF003920 SESLQLPFYLTGVSSLENNLLEKIHSGMFSVYVYFASTNFLAVFLPLSTLKAEMEVGDA
AAEL017277 AESLLLPFYLEGLSSSENRIQKLYSGMFSVYASYASTNFLAVYLPMSLTKVELKVVDVA
AALF003919 TESLLLPFDLVGLSSSENFILQRIYSGMFSIYVFLASTNFLAVYLPALTALKAE MRIVVYS
AALF018936 -----

AALF018937 -----
AALF003920 FDKIMDHVDVRMAALELNEIDEIREEQFWKILQEELTQCFIAHTAVLDKVKDLKCLTDPT
AAEL017277 FEKIVHRVDERTVGKMQPLEDLNEAVFWEILRDELTOCIRAHGAVLARVKALKCLTDPT
AALF003919 YSKI TNQVEDRMSGLGHDAVDDSN EAHFWEILQDELTOCVRAAHA AVLDKVGEFKKLSDPT
AALF018936 -----MSGLGHKAVDDSN EAHFWEILQDELTOCVRAAHA AVLDKVGEFKKLSDPT

AALF018937 -----VTVVIQKLGVMALVLFSPQFDSFNTLSLEYSFRYTL ECYCFYVVSFRFNEEHNGI
AALF003920 FLMLYMTMLF IAVGVMAVLFSPQFDSFNTLSLEYSFRYTL ECYCFYVVSFRFNEEHNGI
AAEL017277 FLLLYMTMLF I AIGVIAVLF TPKFDSFNTISLEYTFRYTMEWYVLCYLVSNFNEEHNDI
AALF003919 FLLLYMTMLYAAIGVIAVLF TPKLNTFNTISLEYSMRYM LECFVFCHVVSNFNEQHNNI
AALF018936 FLLLYMTMLYAAIGVIAVLF TPKLNTFNTISLEYSMRYM LECFVFCHVVSNFNEQHNNI
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AALF018937 VNKLSQFHWGVDLRYSKRFAREYKRVSMVLMIMQSQKSLNFCGGFLFELTMGSFTSII
AALF003920 VNKLSHFHWGVDLRYSKRFAREYKRVSMVLMIMQSQKSLNFCGGFLFELTMGSFTSII
AAEL017277 AKKLSQFHWGVDLRYSKRFARDYKQIRSMVLMVIMQSQKSLNFCGGFLFELTMGSFTAVI
AALF003919 VNKLSQFHWGVDLRYSKRFSREYKQIRSMVLMIMQSQKSLNFCGGFLFELTMGSFTTIV
AALF018936 VNKLSQFHWGVDLRYSKRFSREYKQIRSMVLMIMQSQKSLNFCGGFLFELTMGSFTTIV
      .;***:*****:~::~*:~::~*:~::~*:~::~*:~::~*:~::~*:~::~*:~::~*

AALF018937 NKTYTLTTYFWNIKQRT
AALF003920 NKTYTLTTYFWNIKQRT
AAEL017277 NKTYTLTTYFWNIKQRG
AALF003919 NKTYTLTMYFWNIKKRE
AALF018936 NKTYTLTMYFWNIKKRE
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Figure S7. Alignment and phylogenetic tree of OR61. Upper panel: section of Gene Tree Image from VectorBase (VBGT00190000009797) extracted by Comparative Tool. Lower panel: sequences alignment of *Ae. albopictus* and *Ae. aegypti* orthologs using Clustal Omega.