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CLUSTAL O(1.2.0) multiple sequence alignment

Bactrocera MHSRKTLLGTLLWIG-FLLNFIWAQKELRRDETYPPPELLKELQPVHDSCVAKTGVTEEA 59
Anopheles  -----MKLVTFVFAALLCCSMTLGDTTPRRDAEYPPPELLEALKPLHDICLGKTGVTEEA 55
Culex      MAARCAKTLVLFSAVLGIAVVVLADVTPRRDAEYPPPELLEALKPLHDICAKKTGVTDEA 60
Aedes      ------MNGSVVFVLSALVSLSVGDVTPRRDAEYPPPEFLEAMKPLREICIKKTGVTEEA 54
                    ..        .  .:   ***  *****:*: ::*::: *  *****:**

Bactrocera IKEFSDGDVHEDELLKCYMYCVFEETDVLHEDGEVHLEKILDKXPESMHVIALHMGKKCL 119
Anopheles  IKKFSDEEIHEDEKLKCYMNCLFHEAKVVDDNGDVHLEKLHDSLPSSMHDIAMHMGKRCL 115
Culex      IIEFSDGKIHEDEKLKCYMNCLFHEAKVVDDNGDVHLEKLHDSLPNSMHDIAMHMGKRCL 120
Aedes      IIEFSDGKVHEDENLKCYMNCLFHEAKVVDDTGHVHLEKLHDALPDSMHDIALHMGKRCL 114
           * :*** .:**** ***** *:*.*:.*:.: *.*****: *  *.*** **:****:**

Bactrocera YPKGDNKCERAFWLHRCWKEADPKHYFLI 148
Anopheles  YPEGETLCDKAFWLHKCWKQSDPKHYFLV 144
Culex      YPEGENLCEKAFWLHKCWKQADPKHYFLV 149
Aedes      YPEGENLCEKAFWLHKCWKESDPKHYFL- 142
           **:*:. *::*****:***::*******
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