```
Drome-SIR2       ------MMENYEEIRLGHIR--SKDLGNQVPDTTQFY--PPTKFDFGAEILASTSTEAEA
Tal-SIRT1        --EGLRVMDSTVPAKRLRLDYSGEMLANEQKESFQYYIRTPDMLSTGG-RVSSTSSTSSV
Micde-SIRT1      MASGSELPEYSSSVKRRKIE------------GQVYRVSEPLDLDFSESKQPRQSSSSDL
Fopar-SIR2       MASGSELPEYSSQVKRRKIE------------SKVYGVSVHFNIDFPEVKVNRDTQNIDI
                       : :     .  .:                :       :.         :   .

Drome-SIR2       EAEATATTTEPATSEL------------------------AGKANGEIKTKTLAAREEQE
Tal-SIRT1        AMEGGSLTCDSGFNELTPPRLLEEEPQSQLSSVSGSLSSHSPQPHGIKRSHASCIDEDDE
Micde-SIRT1      E---EPLSGDSGFTEL------------------------S---DGSKSMSTTP------
Fopar-SIR2       E---EPLGGDSGFTDM------------------------S---DGAKSMSNTP------
                      .   :.. .::                        :    *

Drome-SIR2       IGA------------------NLEHKTKNPT-----KSMGEDEDDEEEEEEDDEEEE---
Tal-SIRT1        ETAPPARRSPVASLSLGAQRSSMSHCSNSPSPSHHFHNHHSSLDGGDPDDANDGDDN--S
Micde-SIRT1      ---------------------DLMHLSSTPS-----RTDSTSDDTGCPLDTADEKDEVSS
Fopar-SIR2       ---------------------ESTNLSSTPS-----RTDSTSDDTGCPLDTADEKDEVSS
                                      .  : :..*:     ..   . *     :  * .::

Drome-SIR2       -EDDEEGITGTSNEDEDSSSNCSSSVEPDWK---LRWLQREFYTGRVPRQVIASIMPHFA
Tal-SIRT1        VSSDDSRVSRLSNGDDDAAGGEGSDCGEEGTPEPAHWVQQQMRRGQNPRAVLSRVLGADP
Micde-SIRT1      TVSNLSDLSGLSELSEDS--------GHLWR-NASSWVQKQMITGANPRELLQHLL-MDP
Fopar-SIR2       TVSNLSDLSGLSELSEET--------GQLWR-SASAWVQKQMQTGTDPRDLLQHLL-MDP
                   .: . ::  *: .:::                  *:*.::  *  ** ::  ::   .

Drome-SIR2       TGLAGDTDDSVLWDYLAHLLNEPKRRNKLASVNTFDDVISLVKKSQKIIVLTGAGVSVSC
Tal-SIRT1        SDIPEHVSDEMIWRLLLNVLTDGPRRERLRHLNTLDDAVRLMRTSRRIIVLTGAGVSVSC
Micde-SIRT1      TQIPEQVDDITLWKLVLNIMSDPPRRHKLEHINTLADVVRLIKNSKKIIVLTGAGVSVSC
Fopar-SIR2       TQIPEQVDDITLWKLVLNIMSDPPRRQKLSYVNTLNDVVRLIKDSKKIIILTGAGVSVSC
                 : :.  ..*  :*  : :::.:  ** .*  :**: *.: *:. *..**:**********

Drome-SIR2       GIPDFRSTNGIYARLAHDFPDLPDPQAMFDINYFKRDPRPFYKFAREIYPGEFQPSPCHR
Tal-SIRT1        GIPDFRSRDGIYARLAVDFPNLPDPQAMFDINFFKRDPRPFFKFAREIYPGQFTPSLCHR
Micde-SIRT1      GIPDFRSRDGIYSRLAQDFPDLPDPQAMFDINYFGQDPRPFFKFAREIYPGQFKPSPCHR
Fopar-SIR2       GIPDFRSRDGIYSRLAQDFPNLPDPQAMFDINFFAQDPRPFFKFAREIYPGLFKPSPCHR
                 ******* :***:*** ***:***********:* .*****:********* * ** ***

Drome-SIR2       FIKMLETKGKLLRNYTQNIDTLERVAGIQRVIECHGSFSTASCTKCRFKCNADALRADIF
Tal-SIRT1        FIRSMENHNKLLRNYTQNIDTLEQVAGINNVIQCHGSFASATCQRCGFKVSAGAIKDDIF
Micde-SIRT1      FIKMLDKKNKLLRNYSQNIDTLEQVAGIENVIECHGSFATASCTKCKYQVTAEDIREDIF
Fopar-SIR2       FIKMLEKHKKLLRNYSQNIDTLEQVAGIENVIECHGSFATASCTKCKFQVTAEDIRTDIF
                 **. ::.: ******:*******.****:.**:*****::*:* .* :: .*  :. ***

Drome-SIR2       AQRIPVCPQCQPNKEQ--------------------------------------------
Tal-SIRT1        QQRIPMCPHCTPPTTPLPCYGPRDSFYGHHHGGDTPTPPLQSSASLQASPARNESTSPQP
Micde-SIRT1      AQRIPLCPKCYTNSLP--------------------------------------------
Fopar-SIR2       SQRIPLCPKCSTNSLP--------------------------------------------
                  ****:**:* . .

Drome-SIR2       ----------------------------------SVDASVAVTEEELRQLV-ENGIMKPD
Tal-SIRT1        GAAGSESPQQATGASHNLNLADSPAHNDDDSNLETFNLATLCARSDSSNLMQSQPIMKPD
Micde-SIRT1      ------------------------------------SLSSTNTNDNYANFV-SQGIMKPD
Fopar-SIR2       ------------------------------------SLATTNTSQNYTDLV-SLGIMKPD
                                                     . :   : .:  ::: .  *****

Drome-SIR2       IVFFGEGLPDEYHTVMATDKDVCDLLIVIGSSLKVRPVAHIPSSIPATVPQILINREQLH
Tal-SIRT1        IVFFGEGLPDEFHDSISEDQNQCDLLIVIGSSLKVRPVAHIPNSIPPHVPQILINREPLD
Micde-SIRT1      IVFFGEGLPDAFHDAIANDKDECDLLIVIGSSLKVRPVALIPSSIPSYVPQILINRESLP
Fopar-SIR2       IVFFGEGLPDAFHDSIAKDKDECDLLIVIGSSLKVRPVALIPSSIPSHIPQILINRESLP
                 ********** :*  :: *:: ***************** **.***. :******** *

Drome-SIR2       HLKFDVELLGDSDVIINQICHRLSDNDDCWRQLCCDESVLTESKELMPPEHSNHHLHHHL
Tal-SIRT1        HLTFDIELLGDCDVIVNELCHRLGPS---WTNVCNSHVRLSEIRDL-PPKPETP------
Micde-SIRT1      HLKFDIELLGDGDIIINQLCHLIGEE---FSEICWKKDILEETPHLLPPRFITD------
Fopar-SIR2       HLKFDVELLGDGDIIINQLCHLMGEE---FLQLCWSEKLLEETPHLLPPRFEDS------
                 **.**:***** *:*:*::** :. .   : ::* .   * *   * **
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Drome-SIR2       LHHRHCSSESERQSQLDTDTQSIKSNSSADYILGSAGTCSDSGFESSTFSCGKRSTAAEA
Tal-SIRT1        ------SSSPASARLVAGDGDASVAGSGVAPVAAV--------ADAPHPKDEDDIEALRA
Micde-SIRT1      ---------DSWERSQDSTINQELSQDSTEVVLKT--------YHHNVSTESQDSLMINS
Fopar-SIR2       -----------WERSTTS------TQDSTEVILKQ----------HNLFNESQDSLSINS
                                         : ...  :                 .  .      :

Drome-SIR2       AAIERIKTDILVELNETTAL--SCDRLGLEGPQTTVESYRHLSIDSSKDSGIEQCDNEAT
Tal-SIRT1        CWAPKIRESVAARLPENCYLYNGGHRYVFKGAEVFYDPDDVEGDDDSQNQEDDDDDDDED
Micde-SIRT1      NTTPKRLENTDICISP----FHAGH---MEATEESFA-----LLGESPKRPLGDSSLESS
Fopar-SIR2       NTTPKHLGSTEICISP----FDAGH---MEGNDGF-------SLLESPKRPLDESSVESS
                     .   .    :        .     ::. :            .* .    : . :

Drome-SIR2       PSYV-----------R----PSNLVQETKTVAPSLTPIPQ--QRGKRQTAAERLQPGTFY
Tal-SIRT1        GELVDNDDDSSPPLHE----ASNSLNPKLVSGDALSGIPSEKEFLPSFSLQNTKEPATGV
Micde-SIRT1      PKRINLEVRASPPSSSGSSGSSGSISRSLDDSQDINYTTS--RYNRVISVESTSENNGHI
Fopar-SIR2       PKRLN---------SR----SCGSTPRSSDDGERF-------RFTRVVSFESTPENNGQV
                  . :                ...    .   .  :             :  .  :

Drome-SIR2       SHTNNYSYVFPGAQVFWD-------------------NDYSDDDDEEEERSHNRHSDLFG
Tal-SIRT1        SPPHSLDDVVEAVQAVEEA----------DQLLYSSCDTITHSDCTR--RTLSCDSSASS
Micde-SIRT1      ---YNLEECHVVPRIIDDSTLKNSISTLDDLTQSNNSNTPVDVDSSNDSEELLDSDKSNG
Fopar-SIR2       ---FNLEECHVLPRILDQ-------------------DSGVKGEERRDERE---GEDKYG
                     . .      . . :                   :     :           ..  .

Drome-SIR2       NVGHNYKDDDE-----DACD-LNAVPLSPLLPPSLEAHIVTD---IVNGSNEPLPNSSPG
Tal-SIRT1        SSCHLSTAATV------TVEAPSVQEMDSLLSGSEQEEDCVDSD-WM-----TLHASLAD
Micde-SIRT1      KSRHISIDSAIDSGLGDSCNSVDSSDDKSTIEQGDSKRHNLQRHCWQPEVKESLASRLPE
Fopar-SIR2       KSRHASIDSAIDSGIGDSCNSVDSSEAKEI----EEKRQEIERR-WQGEIKESLANRLPE
                 .  *             : :  .    .       .     :          .*    .

Drome-SIR2       QKRTACIIEQQPTPAIETEIPPLKKRRPSEENKQQTQIERSEESPPPGQLAAV
Tal-SIRT1        TPSFSSDVAAPTLRPSEDCSRPESQPQFNEPSESAPKLNDKIESISRTSVAL-
Micde-SIRT1      NTYYQVSPGKYIFTGAEIYIEPDDYEQLSSSSSRSPSMSTMIRPATEYNTT--
Fopar-SIR2       GSYYQVSSGKYIFPGAEIYLEGDD---FGEPETRANEISSLTYTEDECRTT--
                                 *      .    .. .    .:.    .      :
```

Figure S21. Putative *Talitrus saltator* SIRT1 protein

Alignment of *Drosophila melanogaster* SIR2 (Drome-SIR2; Accession No. NP_477351) with the *T. saltator* (Tal-SIRT1) deduced from the Trinity *de novo* transcriptome assembly, together with the top two tblastn species homologue sequences *Microplitis demolitor* SIRT1 (Micde-SIRT1; Accession No. XM_008555996) and *Fopius arisanus* SIR2 (Fopar-SIR2; Accession No. XM_011303457). '*' indicates identical amino acid residues in the two proteins, '.' and ':' indicate similar amino acid residues between the two proteins. In this figure one SMART identified SIR2 domain is highlighted in yellow.