```
Drome-MTS       MEDKATTKDLDQWIEQLNECNQLTETQVRTLCDKAKEILSKESNVQEVKCPVTVCGDVHG
Tal-MTS         MEEKTQIKELDQWIEQLMECKQLGENQVKTLCEKAKEVLAKESNVQEVKSPVTVCGDVHG
Pedhu-PP-V      MEEKTSLKELDQWIEQLNECKQLTESQVKTLCDKAKEILAKESNVQEVKCPVTVCGDVHG
Nasvi-PPIIA     MEEKASLKELDQWIEQLNDCKQLTESQVKTLCDKAKEILAKESNVQEVKSPVTVCGDVHG
                **:*:  *:******** :*:** *.**:***:****:*:*********.**********

Drome-MTS       QFHDLMELFRIGGKSPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRERITILRGNHES
Tal-MTS         QFHDLMELFKIGGRSPDTNYLFMGDYVDRGYYSVETVTLLVTLKVRFRERITILRGNHES
Pedhu-PP-V      QFHDLMELFRIGGKSPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRERITILRGNHES
Nasvi-PPIIA     QFHDLMELFRIGGKSPDTNYLFMGDYVDRGYYSVETVTLLVALKVRYRERITILRGNHES
                *********:***:***************************:****:*************

Drome-MTS       RQITQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALVDGQIFCLHGGLSPSIDSLDHI
Tal-MTS         RQITQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALVDNQIFCLHGGLSPSIDTLDHI
Pedhu-PP-V      RQITQVYGFYDECLRKYGNANVWKFFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHI
Nasvi-PPIIA     RQITQVYGFYDECLRKYGNANVWKFFTDLFDYLPLTALVDGQIFCLHGGLSPSIDTLDHI
                ************************:***************.**************:****

Drome-MTS       RALDRLQEVPHEGPMCDLLWSDPDDRGGWGISPRGAGYTFGQDISETFNNTNGLTLVSRA
Tal-MTS         RALDRLQEVPHEGPMCDLLWSDPDDRGGWGISPRGAGYTFGQDISETFNHSNGLTLVSRA
Pedhu-PP-V      RALDRLQEVPHEGPMCDLLWSDPDDRGGWGISPRGAGYTFGQDISETFNHSNGLTLVSRA
Nasvi-PPIIA     RALDRLQEVPHEGPMCDLLWSDPDDRGGWGISPRGAGYTFGQDISETFNHSNGLTLVSRA
                *************************************************::*********

Drome-MTS       HQLVMEGYNWCHDRNVVTIFSAPNYCYRCGNQAALMELDDSLKFSFLQFDPAPRRGEPHV
Tal-MTS         HQLVMEGYNWCHERNVVTIFSAPNYCYRCGNQAAIMELDDSLKYSFLQFDPAPRRGEPHV
Pedhu-PP-V      HQLVMEGYNWCHDRNVVTIFSAPNYCYRCGNQAAIMELDDALKYSFLQFDPAPRRGEPHV
Nasvi-PPIIA     HQLVMEGYNWCHDRNVVTIFSAPNYCYRCGNQAAIMELDDALKYSFLQFDPAPRRGEPHV
                ************:*********************:*****:**:****************

Drome-MTS       TRRTPDYFL
Tal-MTS         TRRTPDYFL
Pedhu-PP-V      TRRTPDYFL
Nasvi-PPIIA     TRRTPDYFL
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Figure S11. Putative *Talitrus saltator* MICROTUBULE STAR (MTS) protein

Alignment of *Drosophila melanogaster* MTS (Drome-MTS; Accession no. AAF52567) with the *T. saltator* MTS (Tal-MTS) deduced from the Trinity *de novo* transcriptome assembly, together with the top two tblastn species homologue sequences *Pediculus humanus corporis* PP-V (Pedhu-PP-V; Accession No. XM_002426681) and *Nasonia vitripennis* PPIIA (Nasvi-PPIIA; Accession No. XM_001602456). '*' indicates identical amino acid residues in the two proteins, '.' and ':' indicate similar amino acid residues between the two proteins. In this figure SMART identified protein phosphatase 2Ac catalytic domains of the serine/threonine phosphatase family are highlighted in green.