

A

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TvTUBα1 -MREVISIHVGQAGVQIGNGCWELYCLEHGIQPDGQLPSDKTIGVEDDAFNTFFSETGAG 59
TvTUBβ2 MVR EIVHIQAGQCGNQIGAK FWEVISDEHGIDPTGSYHGSDQL--ER INVYYNEATGG 58
      :*: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*: :*

TvTUBα1 KHVPR AVFVDLEPTVVDEVRTGTYRQLFHPEQLISGKEDAANNYARGHYTVGKEIIDLTL 119
TvTUBβ2 KYVPR AILVDLEPGTMDSVRAGQFGQLFRPDNFVFGQSGAGNNWAKGYYTEGQELCESIL 118
      *:*****:***** :*:***** :*:***** :*:***** :*:***** :*:***** :*

      2.728
TvTUBα1 DRIRKLADQCTGLQGFLIFHSEGGGTGAGFGSLLLERLSVDYGKKSKEFTVYPSPQVST 179
TvTUBβ2 DVIRKEAESDCDCLQGFLVHSIGGGTGAGLGTLLLNKLREEYPDRILSTYSIVPSPKVSD 178
      * *** :*. * **** :*. :*****:*****:***** :* .. : : : :*:**

TvTUBα1 AIVEPYNSILATHSMIDHSDCAFMVDNEALYDLCRRALDIERPTYTNLNLIGQVVSSLT 239
TvTUBβ2 TVVEPYNCTLSVHQLVESADEVFCIDNEALYDICFRTLKLTPTYGDLNHLVSMVMSGTT 238
      :*:*****. :*. :*: :* :*****:***** :*: :* :*: :*: :* :*

TvTUBα1 ASLRFDGALNVDFTEFQTNLVPIARIHFPICSYAPVISAEKAYHEQLSVAEITNSLFEP 299
TvTUBβ2 CALR FPGQLNSDLRK LAVNLVPFPR LHFFIVGFAPLTSRGSQQYRALTVPELTSQLFDNK 298
      :*.*** * ** * : : : :*****:***** * : : : :* :* :* :* :* :*

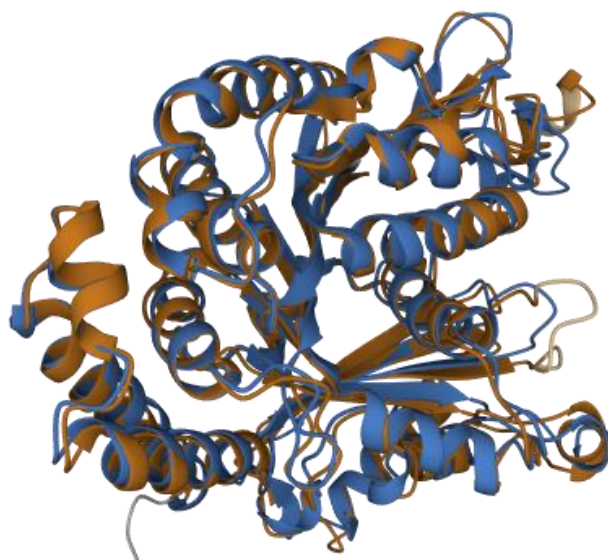
      1.2380
TvTUBα1 NMMVK CDPRHGK YMACTLLYRGDVPVK DVSAAVATIKTKR TIQFVDWCPTGFKMGINYQP 359
TvTUBβ2 NMMAA CDPRRGVYLTASAHFRGRMSSK EVDEQMLNIQARNTSYFVEWIPSNVKSACDIP 358
      ***. ***** :*: : :* : :* : :* :* :* :* :* :* :* :* :*

TvTUBα1 PTVVPGGDLAKVQR AVCMLANTTAIAEAWSRLDHKFDLMYAKRAVHWYVGEEMEEAEFP 419
TvTUBβ2 PRGL-----KMAATFIGNTTAFRELFTRVDSQFQKMYARRAFIHWYVNEGLETVFEFD 410
      * : : * : :*:***** :* :*: :* :* :* :* :* :* :* :* :*

TvTUBα1 EARED LALLEKDYDEVAAESVEGG--DEEEDGGEM-- 452
TvTUBβ2 EARSNM TDLIQEYEMYETAGVEEQGEGEDEEGEAAA 447
      ***. :*: :* :* : :* :* :* :* :*

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B



Supplementary Figure S11. Alignment and modeling of TvTUBα1 and TvTUBβ2 identified by LC-ESI-MS. **A)** Peptides identified of the TvTUBα1 are shaded in brown and for TvTUBβ2 are shaded in blue. The aa box are putative antigen regions common among the two proteins. The top number

indicates the overall prediction for the antigen (threshold for this model is 0.5, VaxiJen v2.0). **B)** Comparison of 3D structure of the TvTUB α 1 (brown) and TvTUB β 2 (blue). The overlapping of TvTUB α 1 against TvTUB β 2 structures was made in PDB Pairwise Structure Alignment (<https://www.rcsb.org/alignment>). TM-score: 0.95, SI%: 43 and SS%: 62. **TM-score**, template modeling score. It is a measure of topological similarity between the template and 3D model structures. The TM-score ranges between 0 and 1, where 1 indicates a perfect match and 0 is no match between the two structures. **SI%** (sequence identity percentage) is the percent of paired residues in the alignment that are identical in sequence. **SS%** (sequence similarity percentage) is the percent of paired residues in the alignment that are similar in sequence (Xu and Zhang, 2010).
* Represents identical nucleotides.