SUPPLEMENTARY ONLINE DATA
Chaperone ligand-discrimination by the TPR-domain protein Tah1

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                 TPR1-H1a          TPR1-H1b             TPR1-H2a
                 -------------    -------------        -------------    ----
Hop    -MEQVNELKEKGNKALSVGNIDDALQCYSEAIKLDPH-NHVLYSNRSAAYAKKGDYQKAY  58
Sti1   MSLTADEYKQQGNAAFTAKDYDKAIELFTKAIEVSETPNHVLYSNRSACYTSLKKFSDAL  60
Tah1   -----------------------------------------------------------

           TPR1-H2b         TPR1-H3a            TPR1-H3b           TPR1-Hc
           ---------       -------------       ----------------    ------------
Hop    EDGCKTVDLKPDWGKGYSRKAAALEFLNRFEEAKRTYEEGLKHEANNPQLKEGLQNMEAR  118
Sti1   NDANECVKINPSWSKGYNRLGAAHLGLGDLDEAESNYKKALELDASNKAAKEGLDQVHRT  120
Tah1   -----------------------------------------------------------

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Hop    LAERK------FMNPFNMPNLYQKLESDPRTRTLLSDPTYRELIEQLRNKPSDLGTKLQ-  171
Sti1   QQARQAQPDLGLTQLFADPNLIENLKKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT  180
Tah1   -----------------------------------------------------------

Hop    DPRIMTTLSVLLGVDLGSMDEEEEIATPPPP--------------------------PP  204
Sti1   DPRLMTIMATLMGVDLNMDDINQSNSMPKEPETSKSTEQKKDAEPQSDSTTSKENSSKAP  240
Tah1   -----------------------------------------------------------

                     TPR2a-H1a          TPR2a-H1b
                     -------------      -------------    ----
Hop    PKKETK-PEPMEEDLPENKKQALKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYIT  263
Sti1   QKEESKESEPMEVDEDDSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELH-KDITYLN  299
Tah1   -----------------------------------------------------------

    TPR2a-H2a        TPR2a-H2b             TPR2a-H3a           TPR2a-H3b
    ---------       -------------         -------------       --------
Hop    NQAAVYFEKGDYNKCRELCEKAIEVGRENREDYRQIAKAYARIGNSYFKEEKYKDAIHFY  323
Sti1   NRAAAEYEKGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGDLKKTIEYY  359
Tah1   -----------------------------------------------------------

                   TPR2a-Hc              TPR2b-H1a          TPR2b-H1b
                   -------------        -------------       --------
Hop    NKSLAEHRTPDVLKKCQQAEKILKEQERLAYINPDLALEEKNKGNECFQKGDYPQAMKHY  383
Sti1   QKSLTEHRTADILTKLRNAEKELKKAEEAEAYVNPEKAEEARLEGKEYFTKSDWPNAVKAY  419
Tah1   -------------------------------MSQFEKQKEQGNSLFKQGLYREAVHCY  27
                                       .  : :*:. * :. : :*:. *

               TPR2b-H2a          TPR2b-H2b            TPR2b-H3a
               -------------      -------------        -------------
Hop    TEAIKRNPKDAKLYSNRAACYTKLLEFQLALKDCEECIQLEPTFIKGYTRKAAALEAMKD  443
Sti1   TEMIKRAPEDARGYSNRAAALAKLMSFPEAIADCNKAIEKDPNFVRAYIRKATAQIAVKE  479
Tah1   DQLITAQPQNPVGYSNKAMALIKLGEYTQAIQMCQQGLRYTSTAEHVAIR-SKLQYRLEL  86
        : *.  *::.   ***:*  .  ** .: *: *::: :.  .. .   * :    ::

        TPR2b-H3b              TPR2b-Hc
        ---------------      -------------
Hop    YTKAMDVYQKALDLD------SSCKEAADGYQRCMMAQYN---RHDSPEDVKRRAMADPE  494
Sti1   YASALETLDAARTKDAEVNNGSSAREIDQLYYKASQQRFQPGTSNETPEETYQRAMKDPE  539
Tah1   AQGAVGSVQIPVVEV--------DELPEGYDRS------------------------  111
        *:   :  .           *  : * :.

Hop    VQQIMSDPAMRLILEQMQKDPQALSEHLKNPVIAQKIQKLMDVGLIAIR-  543
Sti1   VAAIMQDPVMQSILQQAQQNPAALQEHMKNPEVFKKIQTLIAAGIIRTGR  589
Tah1   -------------------------------------------------
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Figure S1   See Figure legend on next page.

Figure S1   Amino-acid-sequence alignment of TPR-domain proteins, Hop, Sti1 and Tah1

The sequences were obtained from GenBank®. The accession numbers were: human Hop, NM_006819; *Saccharomyces cerevisiae* Sti1, Z74935; and Tah1, NC_001135. The sequence alignment was generated using Clustal W [1]. TPR1, 2a and 2b represent the TPR motifs. H1a–c, H2a–c and H3a–c represent the TPR domain helices. Residues shown in red are part of the TPR consensus as they are residues that are involved in packing interactions between α-helices of neighbouring TPR motifs. Residues in green are part of the carboxylate clamp and other electrostatic interactions with the EEVD peptide, whereas those in cyan are involved in van der Waals contacts. Residues that are conserved between all three proteins are indicated '*', ':', or '.'.

REFERENCES

1   Thompson, J. D., Higgins, D. G. and Gibson, T. J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res. **22**, 4673–4680