Figure S1. Sequence Alignment of the YAP-binding domain of TEAD from various species. (Related to Figure 1)

The amino acid residues lining the central pocket are indicated and shown in red. Note the high degree of conservation of these residues among various species. The # sign indicates the location of two residues mutated in TEAD dm.

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                                #
TEAD2_HUMAN       RGLGTARLQLVEFSAFVEPPDAVDSYQRHLFVHISQHCPSPGAPPLESVDVRQIYDKFPE
TEAD4_HUMAN       RSVASSKLWMLEFSAFLEQQQDPDTYNKHLFVHIGQSSPSYSDPYLEAVDIRQIYDKFPE
TEAD2_BOVINE      RALGTARLQLVEFSAFVEPPDATDSYQRHLFVHISQHCPSPGAPPLESVDVRQIYDKFPE
TEAD2_MOUSE       RALGTARLQLIEFSAFVEPPDAVDSFQRHLFVHISQQCPSPGAPPLESVDVRQIYDKFPE
TEAD1_DANRE       RSIGTSKLRLVEFSAFLEHQRDPDLYNKHLFVHIGQTNYSYSDALLETVDIRQIYDKFPE
Sd_DROME          RAIATHKFRLLEFTAFMEIQRD-EIYHRHLFVQLGGK-PSFSDPLLETVDIRQIFDKFPE
                              * *                *

TEAD2_HUMAN       KKGGLRELYDRGPPHAFFLVKFWADLNWGPSGEEAGAGGSISSGGFYGVSSQYESLEHMT
TEAD4_HUMAN       KKGGLKDLFERGPSNAFFLVKFWADLNTNIED---------EGSSFYGVSSQYESPENMI
TEAD2_BOVINE      KKGGLRELYDRGPPHAFFLVKFWADLNWGPSGEEVGAGG--SSGGFYGVSSQYESLEHMT
TEAD2_MOUSE       KKGGLRELYDRGPPHAFFLVKFWADLNWGPSAEEAGSSG--GGGGFYGVSSQYESRELMT
TEAD1_DANRE       KKGGLKELFGKGPQNAFFLVKFWADLNCNIQED---------SGSFYGVTSQYESSENMT
Sd_DROME          KSGGLKDLYEKGPQNAFYLVKCWADLNTDLTTGS-------ETGDFYGVTSQYESNENVV
                                                                  *
                                                         #
TEAD2_HUMAN       LTCSSKVCSFGKQVVEKVETERAQLEDGRFVYRLLRSPMCEYLVNFLHKLRQLPERYMMN
TEAD4_HUMAN       ITCSTKVCSFGKQVVEKVETEYARYENGHYSYRIHRSPLCEYMINFIHKLKHLPEKYMMN
TEAD2_BOVINE      LTCSSKVCSFGKQVVEKVETERAQLEDGRFVYRLLRSPMCEYLVNFLHKLRQLPERYMMN
TEAD2_MOUSE       LTCSSKVCSFGKQVVEKVETERAQLEDGRFVYRLLRSPMCEYLVNFLHKLRQLPERYMMN
TEAD1_DANRE       ITCSTKVCSFGKQVVEKVETEYARFENGRFVYKISRSPMCEYMINFIHKLKHLPEKYMMN
Sd_DROME          LVCSTIVCSFGKQVVEKVESEYSRLENNRYVYRIQRSPMCEYMINFIQKLKNLPERYMMN
                      : *       * *                     :*  :

TEAD2_HUMAN       SVLENFTILQVVTNRDTQELLLCTAYVFEVSTSERGAQHHIYRLVRD
TEAD4_HUMAN       SVLENFTILQVVTNRDTQETLLCIAYVFEVSASEHGAQHHIYRLVKE
TEAD2_BOVINE      SVLENFTILQVVTNRDTQELLLCTAYVFEVSTSERGAQHHIYRLVRD
TEAD2_MOUSE       SVLENFTILQVVTNRDTQELLLCTAYVFEVSTSERGAQYHIYRLVRD
TEAD1_DANRE       SVLENFTILLVVSNRETQETLLCMACVFEVSNSEHGAQHHIYRLVKD
Sd_DROME          SVLENFTILQVMRARETQETLLCIAYVFEVAAQNSGTTHHIYRLIKE
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