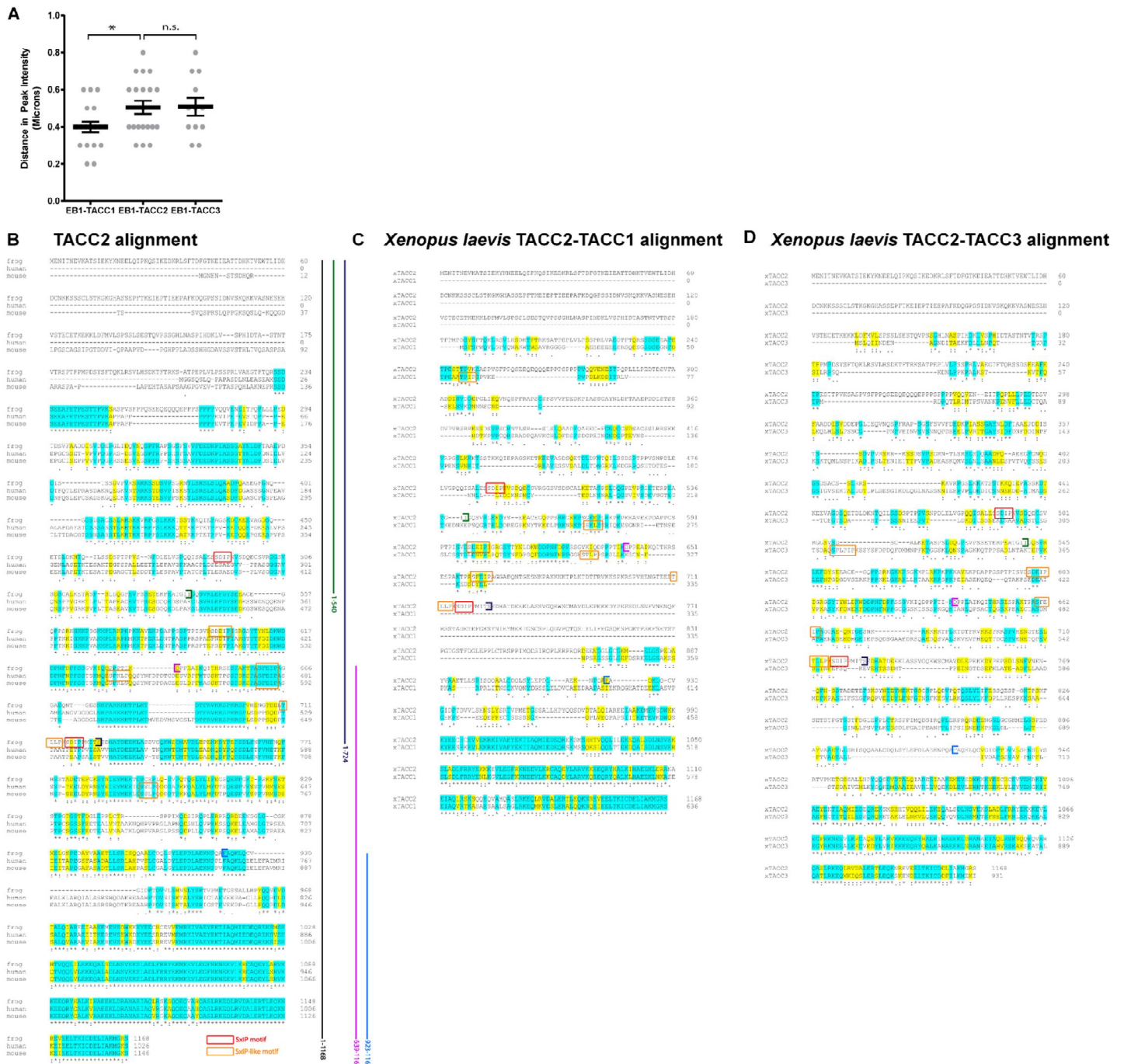


Supplemental Materials

Molecular Biology of the Cell

Rutherford et al.



Supp Fig 1. *Xenopus laevis* TACC2 is orthologous to mammalian TACC2 proteins and shows sequence conservation with other *Xenopus* TACC proteins. (A) Quantification of distances in peak intensity values for EB1 and TACC family members. (B) Sequence alignments of TACC2 in frog, human (GenBank AAC64968.2), and mouse (NP_996738.2). Human TACC2 shows 56% sequence similarity to frog TACC2; mouse TACC2 shows 51% sequence similarity to frog TACC2. There is an identical SxIP-like motif (SFEIP) found in all three TACC2 sequences, as well as very strong sequence conservation evident in the C-terminal regions of the proteins. TACC2 truncated proteins are noted. Vertical lines on right side designate the sequence encompassed by the various constructs, in addition to the colored brackets within the sequence to show the beginning and ends of the constructs. (C) Sequence alignment of *Xenopus* TACC2 to *Xenopus* TACC1 (GenBank AKJ88110.1) shows 40% sequence similarity, with sequence conservation noticeably concentrated within the TACC domain-containing C-terminal regions of the proteins. (D) Sequence alignments of *Xenopus* TACC2 and TACC3 (NP_001081964.1) show 30% sequence similarity between the family members, with strong sequence conservation also concentrated the C-terminal regions of the

proteins. Blue highlights identical residues, while yellow highlights similar residues. Red boxes mark SxIP motifs in TACC2. Orange boxes mark SxIP-like motifs.