Supporting Information

Richards et al. 10.1073/pnas.1322892111

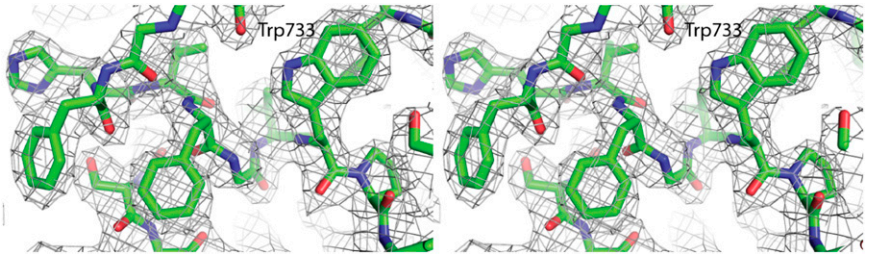

Fig. S1. Stereo image showing a representative area (in the blade12-C region) of the electron density map for the 2.6-Å structure of the echinoderm microtubule-associated protein (EMAP)-like (EML1) TAPE (tandem atypical propeller in EMLs) domain. Wire mesh shows the 2mFo-DFc map contoured at 1.0 σ.

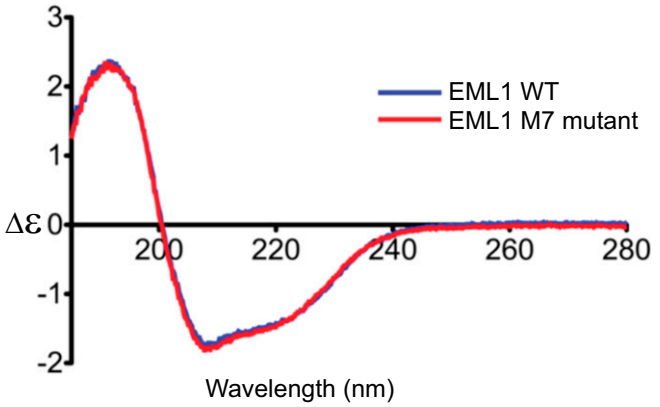

Fig. S2. Circular dichroism (CD) spectra of full-length EML1 wild-type and M7 mutant. The similarity of the M7 mutant's CD spectrum to that of the WT protein indicates that the mutation of seven surface residues in the M7 mutant has not resulted in disruption to the folding of the TAPE domain. CD spectra were collected using 0.25 mg/mL samples of full-length EML1 WT and M7 mutant in 10 mM Na phosphate (pH 7.5), 50 mM NaF in a 0.05-cm path-length quartz cell at 20 °C on a Chiroscan+ instrument (Applied Photophysics).