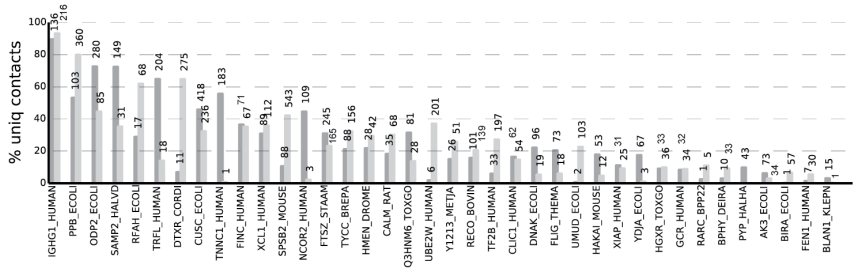
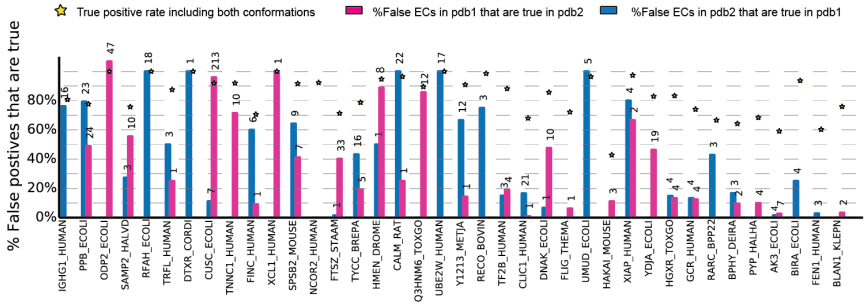
Figure S3. Prediction accuracy for proteins with alternative states (38 proteins, Table S2A)

A.



B.



C.

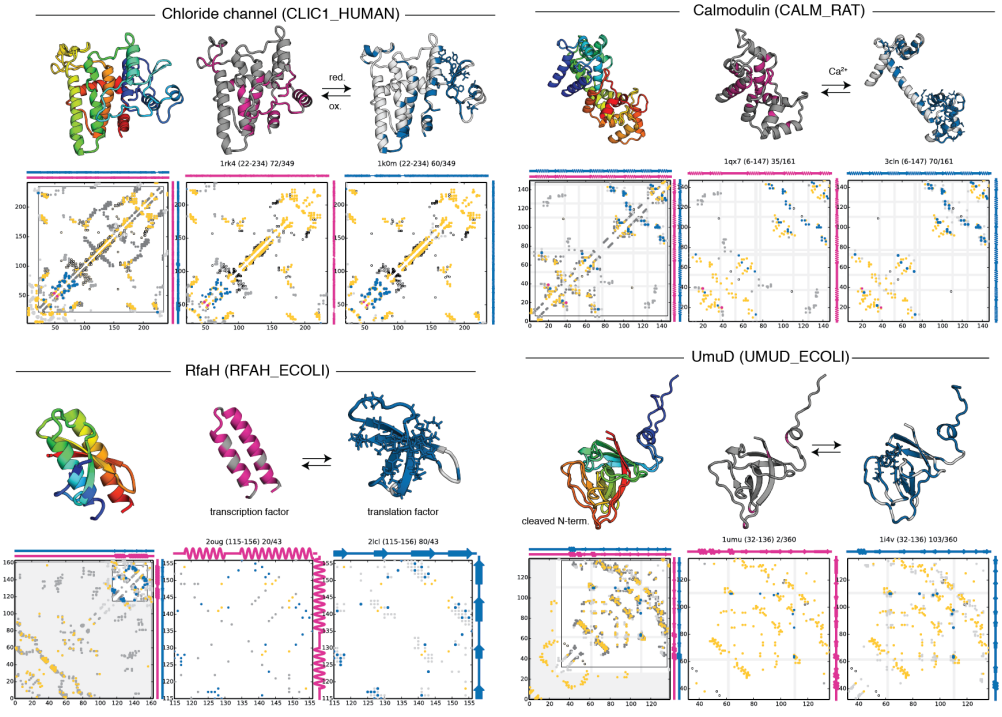


Figure S3. Prediction accuracy for proteins with alternative states (38 proteins, Table S2A).
(A) Comparison of alternative structural states. The fractions of contacts (number of contacts are indicated above the bars) that are unique to the first (dark grey) or second (light grey) conformations. Unique contacts were defined as residue-residue distances <5Å in one conformation and >8Å in the other conformation. **(B) Overall performance in predicting alternative contacts.** The fraction of false positives that are actually true positives in the alternative conformation (blue bars - considering only the first conformation (dark grey in a)); and pink bars - considering the second conformation only (light grey in a)). For instance 100% means that all the false positive ECs mapped on one conformation are actually true contacts in the other conformation. Overall true positive rates are shown as yellow stars (considering both states). **(C)** Highlighted structural details of 4 proteins. Left panel: overlay of the two structures. Middle panel: unique contacts of the first structure. Right panel: unique contacts of the second structure. Unique ECs of the first and second structures are pink and blue spheres respectively; common ECs are yellow circles, while false positive ECs are black empty circles. Secondary structure annotations (by dssp) are drawn for the first and second structures as pink and blue cartoons. TP ECs were calculated on the overlapping regions of the structure only (black box in left panel). Regions that are missing from the experimental structure are colored with grey background. The contact maps and predicted ECs for all proteins in our dataset (**Table S2A**) are available on the web supplement (https://marks.hms.harvard.edu/disorder/).