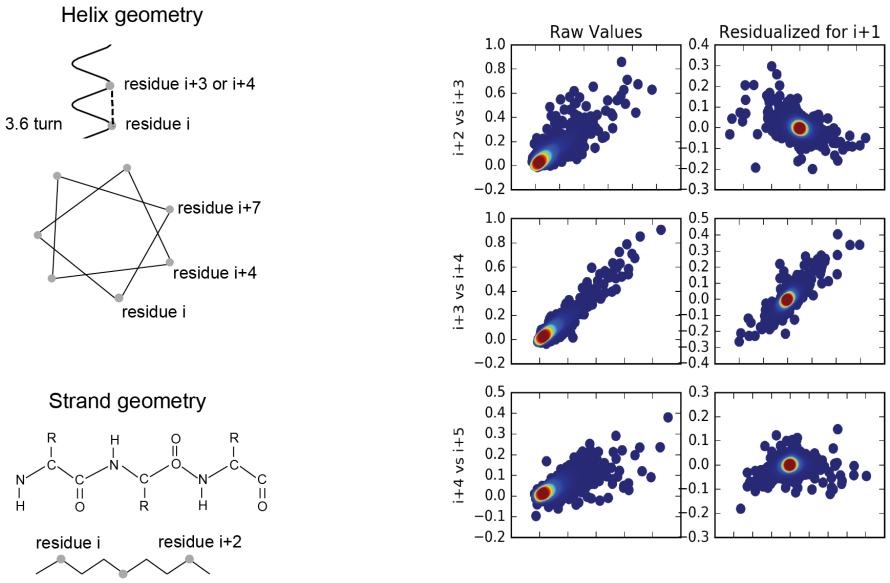
Figure S2.

A. Secondary structure propensity score reflects helical and strand geometry.



B. Prediction set distribution of disorder and valdiation precisions by disorder.

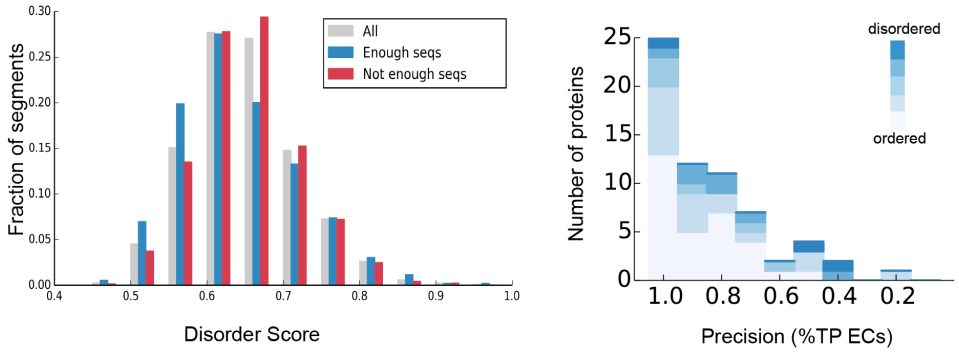


Figure S2.
(A) Secondary structure propensity score reflects helical and strand geometry. Schematic representation of α-helical and β-strand geometries (left). Correlation of mean neighboring EC scores (i.e. i+2 and i+3) across ~3800 PFAM families before and after residualizing for i+1 scores (right) demonstrate that mean i+3 and i+4 scores remain correlated even after correcting for the mean i+1 score in each PFAM family (Experimental Procedures).
(B) Prediction set disorder distribution and validation set precisions by disorder. Our prediction set is representative of disordered segments in the human proteome, with disorder score only slightly biasing the probability that an alignment contains enough sequences for EC analysis. Overall performance in predicting experimental contacts for the 83 proteins with known structures with varying overall disorder (fraction of disordered residues marked as blue gradient).