

MAIN FIGURES

Figure 1. Co-evolutionary analysis of disordered segments in the human proteome.

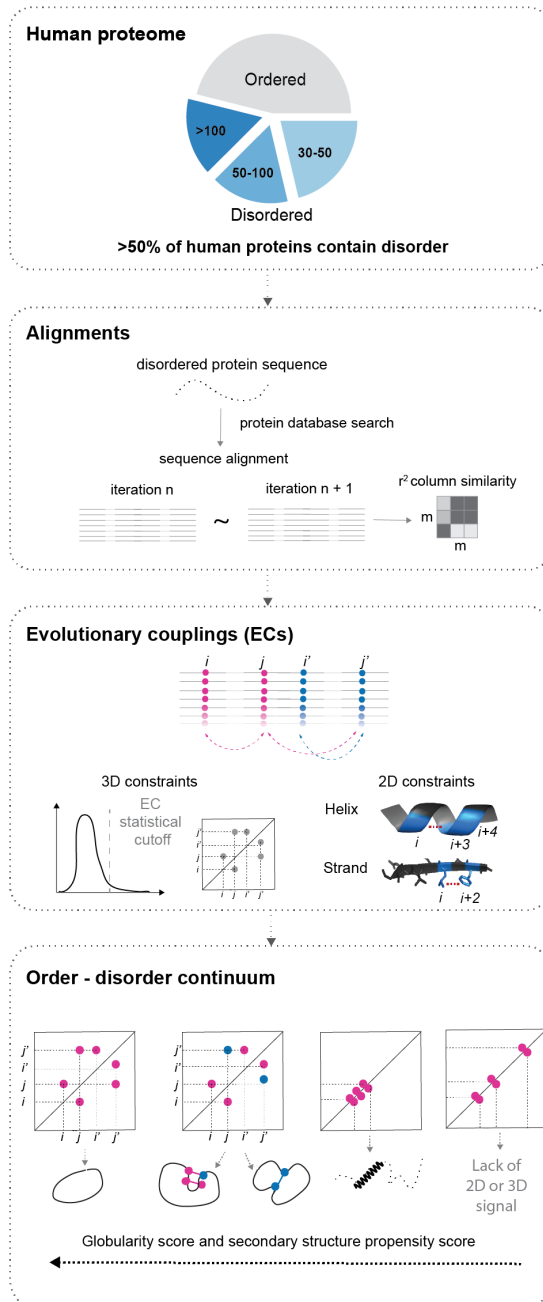


Figure 1. Co-evolutionary analysis of disordered segments in the human proteome.

First we identify contiguous regions of disorder, secondly we search for similar sequences and select robust alignments; thirdly we calculate evolutionary couplings for each alignment using an updated algorithm to compute significant long range ECs and secondary structure propensity from short-range ECs. Finally we assess these predictions to reveal the likelihood of secondary and tertiary structure (**Experimental Procedures**).