CISPred: Consensus Integrated Protein Structure Prediction

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Protein structure prediction is one of the most significant problems in bioinformatics. Currently, there are many tools that predict protein secondary structures, or find protein structural motifs and some specific structural segments. Sometimes the tool results are different or contradictory. CISPred is a consensus protein structure prediction system that integrates results of individual tools to provide consensus predictions.

CISPred is a web-based prediction system that users can submit queried amino acids to from a web browser, and the prediction results are sent back to users by email. CISPred integrates selected existing tools (THREADER, SSPRO, PSIPRED, and PATMATMOTIFS) and databases (PROSITE and PDBFINDER) concurrently on a high performance 164-processor SUN Cluster in the Faculty of Computer Science.

CISPred has an 83% average 3-state accuracy (Q3 score) on 109 CASP (Critical Assessments of Techniques for protein Structure Prediction experiment) sequences, and has an 89% average 3-state accuracy on 1758 randomly selected sequences.