

Fig S2: Prediction scheme used in ANN

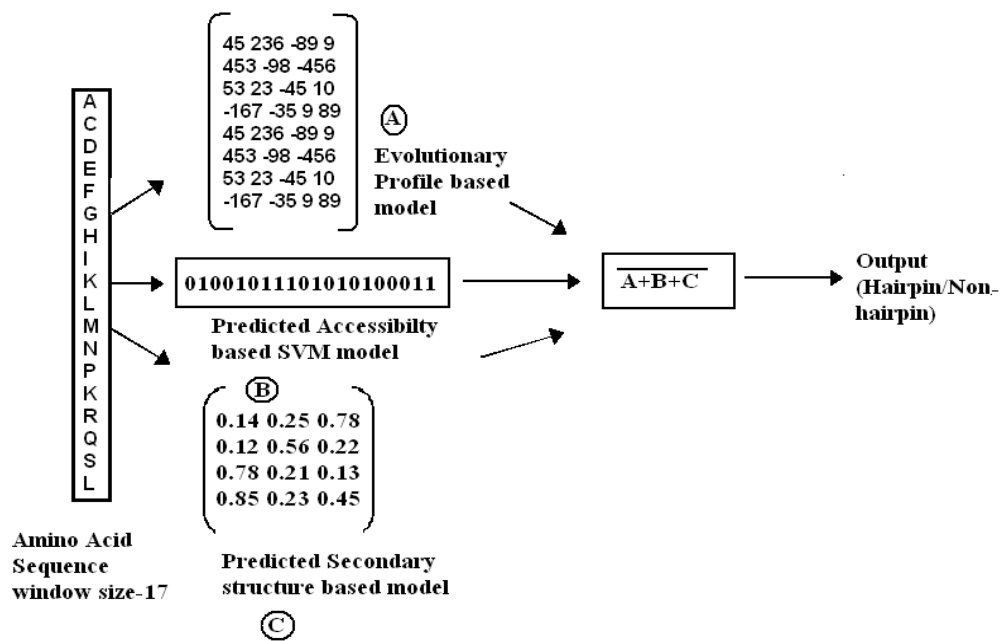


Fig S3: Overall prediction scheme for hybrid approach of SVM

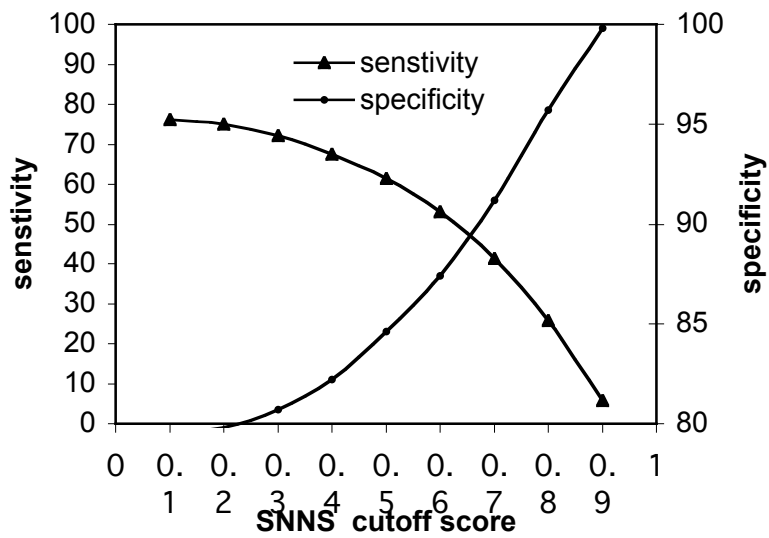


Fig S4: Consensus Prediction on 2880 protein dataset

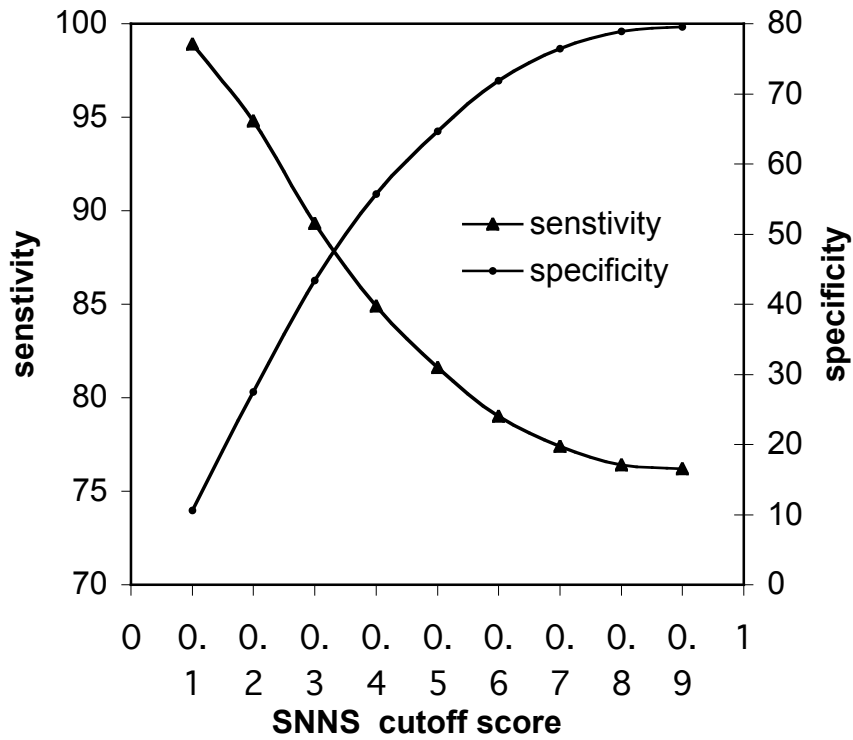


FIG S5: Combined Prediction on 2880 protein dataset

BhairPred *SVM based Method for prediction of β -hairpins in proteins*

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Email: only alphanumeric and underscore

Sequence Name:

Paste Sequence:

OR Upload Sequence file

Sequence format:

Prediction Approach: SVM

Threshold:

From Sea - Snake - *Laticauda semifaciata* revealing beta-hairpin motifs.

start Microsoft Office Shor... BhairPred - Bhairpin p... new Exceed 9:34 PM

Figure S6: Submission form of BhairPred server

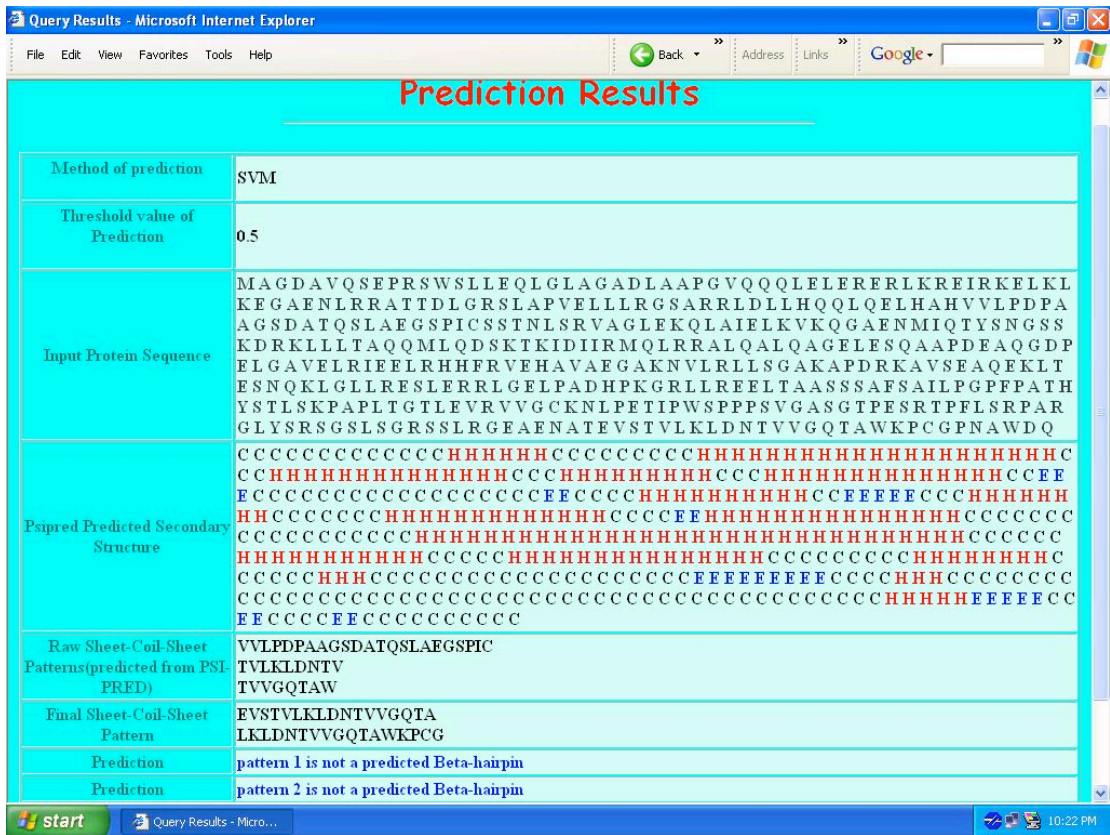


Figure S7: Result of prediction as displayed by server. The output displays the amino acid residues, their corresponding secondary structure (as predicted by PSIPRED or user defined; H for helix, E for extended sheet and C for coil), raw sheet-coil-sheet pattern extracted accordingly as described in paper, sheet-coil-sheet pattern of length 17 amino acid residues and finally whether these fixed length patterns are β -hairpin or not.