

Fig S2: Prediction scheme used in ANN

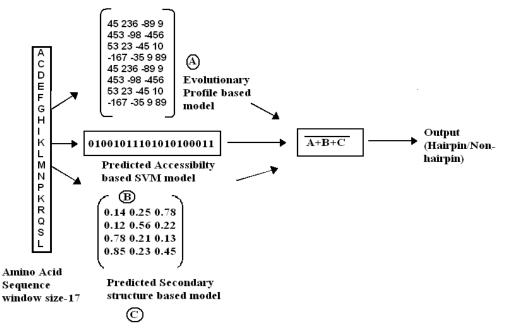


Fig S3: Overall prediction scheme for hybrid approach of SVM

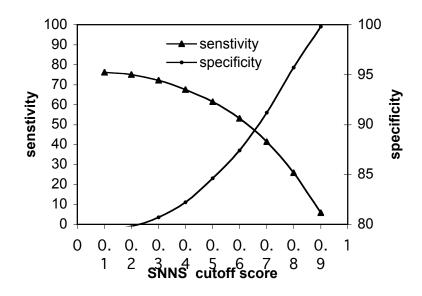


Fig S4: Consensus Prediction on 2880 protein dataset

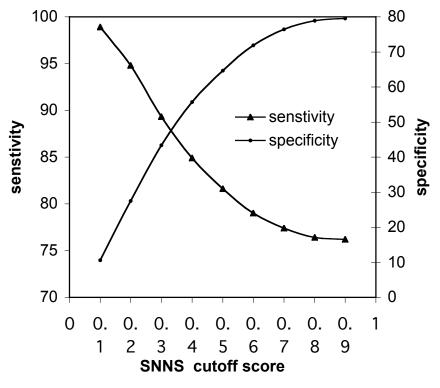


FIG S5: Combined Prediction on 2880 protein dataset

ShairPred	in proteins			
	Submission	Prediction Method	References	Team
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lome		Submission		1NXB-Neurotoxin
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	Prediction			
	Approach	SVM 💿		
	Threshold			
		0.0 💌		
		Run Prediction Reset		

Figure S6: Submission form of BhairPred server

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Prediction Results			
Method of prediction	SVM		
Threshold value of Prediction	0.5		
Input Protein Sequence	MAGDAVQSEPRSWSLLEQLGLAGADLAAPGVQQQLELERERLKREIRKELKL KEGAENLRRATTDLGRSLAPVELLLRGSARRLDLLHQQLQELHAHVVLPDPA AGSDATQSLAEGSPICSSTNLSRVAGLEKQLAIELKVKQGAENMIQTYSNGSS KDRKLLLTAQQMLQDSKTKIDIIRMQLRRALQALQAGELESQAAPDEAQGDP ELGAVELRIEELRHHFRVEHAVAEGAKNVLRLLSGAKAPDRKAVSEAQEKLT ESNQKLGLLRESLERRLGELPADHPKGRLLREELTAASSSAFSAILPGPFPATH YSTLSKPAPLTGTLEVRVVGCKNLPETIPWSPPSVGASGTPESRTPFLSRPAR GLYSRSGSLSGRSSLRGEAENATEVSTVLKLDNTVVGQTAWKPCGPNAWDQ		
sipred Predicted Secondary Structure	СССССССССССССННННННСССССССССНННННННННН		
Raw Sheet-Coil-Sheet atterns(predicted from PSI- PRED)	VVLPDPAAGSDATQSLAEGSPIC TVLKLDNTV TVVGQTAW		
Final Sheet-Coil-Sheet Pattern	EVSTVLKLDNTVVGQTA LKLDNTVVGQTAWKPCG		
Prediction	pattern 1 is not a predicted Beta-haipin		
Prediction	pattern 2 is not a predicted Beta-hairpin		

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.