

Table S1: Prediction results with Thornton's dataset using SVM

Where **AA**: amino acid sequence; **MSA**: multiple sequence alignment; **ACC_O**: observed accessibility (DSSP); **ACC_P**: predicted accessibility; **SS_O**: secondary structure observed (DSSP); **SS_P**: Secondary Structure Predicted (PSIPRED)

Approach	Percent Coverage		Percent Probability		Accuracy	MCC
	$Q_{o(H)}$	$Q_{o(Nh)}$	$Q_{p(H)}$	$Q_{p(Nh)}$		
AA	68.1	63.2	69.4	62.0	65.9	0.31
MSA (1)	77.3	65.7	73.4	70.7	72.1	0.44
AA + ACC_O (2)	78.04	57.06	69	68.12	68.6	0.36
AA + SS_O (3)	65.6	75.1	76.3	64.3	69.9	0.41
Hybrid (1+2+3)	78.8	70.6	76.6	73.3	75.1	0.49
AA + ACC_P (4)	70.8	59.4	68.0	62.8	65.7	0.30
AA + SS_P (5)	60.76	74.8	74.7	61.0	67.1	0.36
Hybrid (1+4+5)	81.5	58.3	70.5	72.4	71.1	0.41

Table S2: Prediction results with Thornton's dataset using ANN

Where **AA**: Amino Acid sequence; **MSA**: Multiple Sequence Alignment; **ACC_O**: Observed Accessibility (DSSP); **ACC_P**: Predicted Accessibility; **SS_O**: Secondary Structure observed (DSSP); **SS_P**: Secondary Structure Predicted (PSIPRED)

Approach	QoH	QoNh	Accuracy	QpH	QpNh	Sh	Snh	MCC
AA	45.7	71.9	58.1	69.1	51.2	5.9	16.2	0.19
MSA	45.8	75.9	59.3	70	53.3	6.9	20	0.23
AA + SS_O	67.7	75.8	71.3	77.4	65.9	14.7	9.9	0.43
AA+ SS_P	55.6	75.8	62.7	70.4	56.8	8.8	11	0.27
AA + ACC_O	55.8	73.5	63.5	72.2	57.7	9.5	13.1	0.28
AA + ACC_P	46.6	68.5	57.1	65.1	51.2	4.8	13.1	0.16
Seq-Str network(SS_P)	55.1	74.8	63.9	73.3	57.8	9.7	14.7	0.31
Seq-Str network(SS_O)	64.9	74.3	69.1	75.7	63.4	13.1	9.5	0.39