

Table S2: Justification of secondary structure predictors measured on PDB dataset (the reported numbers represent fraction of correctly predicted residues in a three state model - helix, sheet, coil)

method	consensus	spider3	psipred	predator	jnet	simpa	GOR IV
precision[%]	73.0	78.0	72.0	65.8	65.1	68.4	63.2