Table 8 Average alignment accuracies for 36 strict similarities

Method	All alignments % Res-Res	All alignments % Sec-Sec	Ignoring α/β barrels % Res-Res	Ignoring α/β barrels % Sec-Sec
MAP (DSSP)	35	75	39	86
MAP (PHD)	15	43	15	49
THREADER	11	37	13	50