

Table S3: DeepFold results on the 38 β -proteins in the test set with and without orientation restraints in terms of the average TM-score/RMSD and the percent of correctly folded models (TM-scores ≥ 0.5) for the 221 benchmark proteins. The p -values were calculated using paired, two-sided Student's t-tests.

Method	TM-score (p -value)	RMSD (p -value)	Correct Folds
GE+Cont+Dist	0.590 (1.5E-04)	8.42 (3.4E-04)	60.5%
GE+Cont+Dist+Orien	0.706 (*)	6.12 (*)	86.8%