Table 3.

The prediction accuracy at family/superfamily/fold level for top 1, top 5 and top 10 predictions, on SCOP 2.06 test dataset

Type	Methods	Top1	Top5	Top10
Family (742 proteins)	DeepSF	75.87%	91.77%	95.14%
	PSI-BLAST	82.20%	84.50%	85.30%
Superfamily (1754 proteins)	DeepSF	72.23%	90.08%	94.70%
	PSI-BLAST	86.90%	88.40%	89.30%
Fold (37 proteins)	DeepSF	51.35%	67.57%	72.97%
	PSI-BLAST	18.90%	35.10%	35.10%