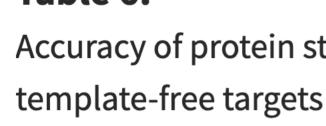
## Accuracy of protein structure predictions on 95

Table 6.



**Methods** 

DeepSF

**HHSearch** 

TM-score

Max

0.54

0.52

Mean

0.27

0.25

Std

0.07

0.08

Min

0.15

0.11