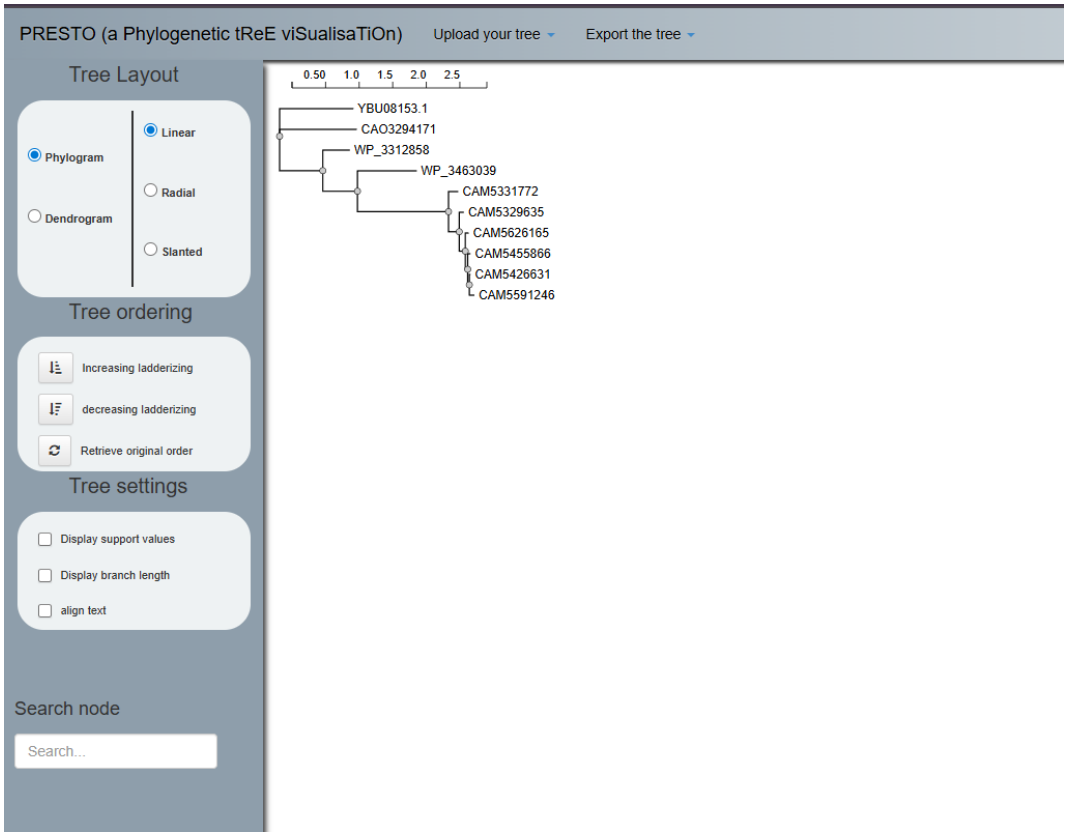
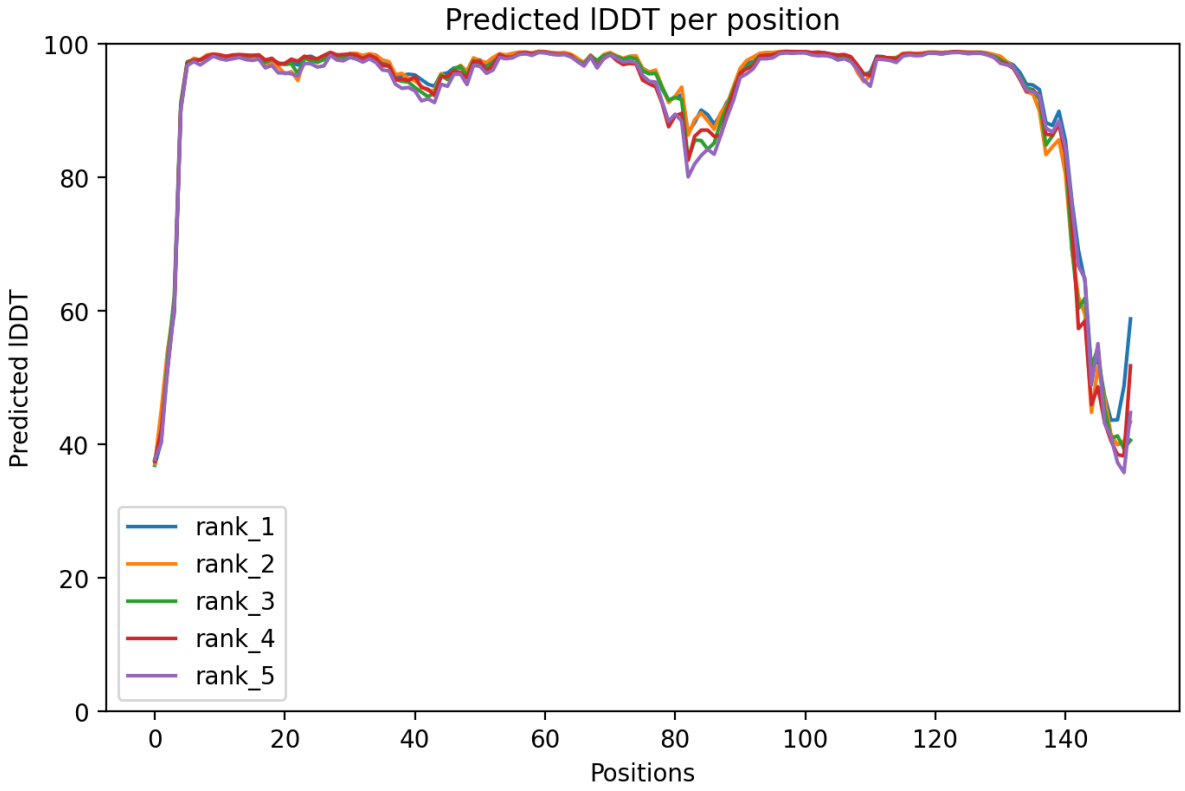
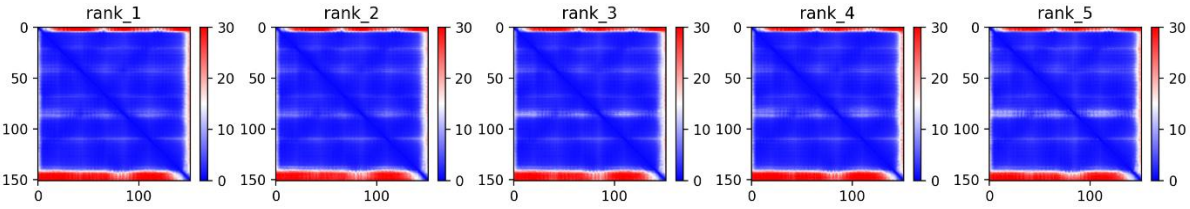
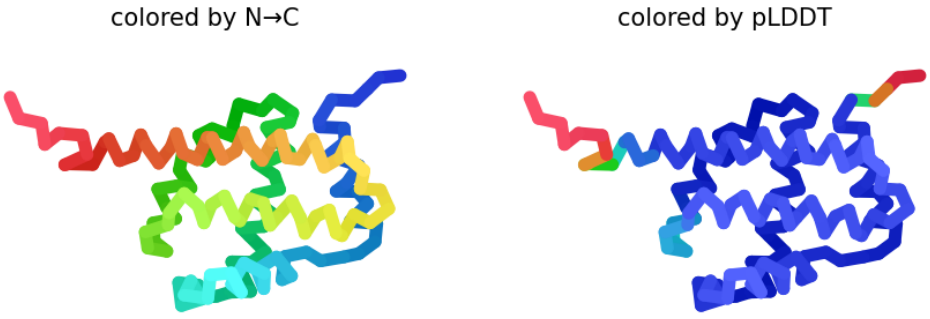
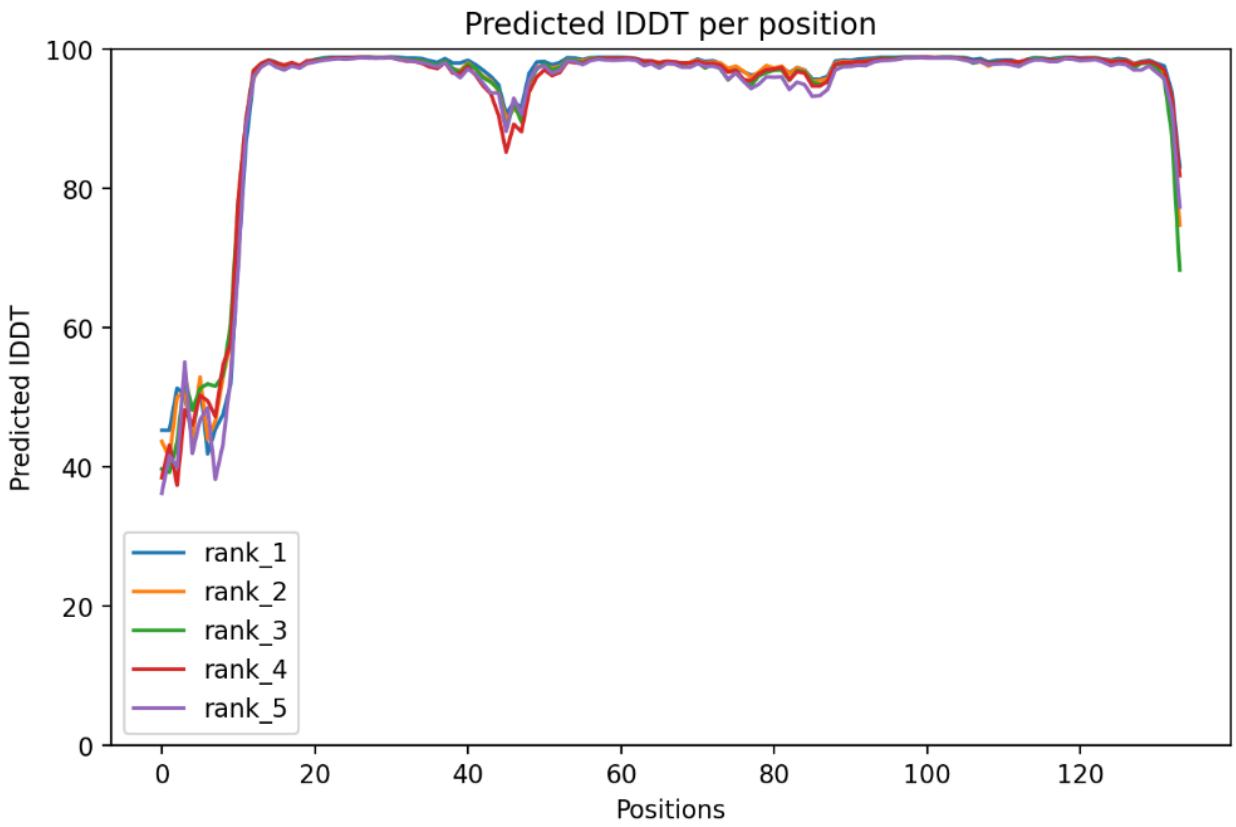

PRESTO (a Phylogenetic tReE viSualisaTiOn)
Upload your tree
Export the tree
Tree Layout
Phylogram
Dendrogram
Linear
Radial
Slanted
Tree ordering
Increasing ladderizing
decreasing ladderizing
Retrieve original order
Tree settings
Display support values
Display branch length
align text
Search node
Search...
0.50
1.0
1.5
2.0
2.5
YBU08153.1
CAO3294171
WP_3312858
WP_3463039
CAM5331772
CAM5329635
CAM5626165
CAM5455866
CAM5426631
CAM5591246

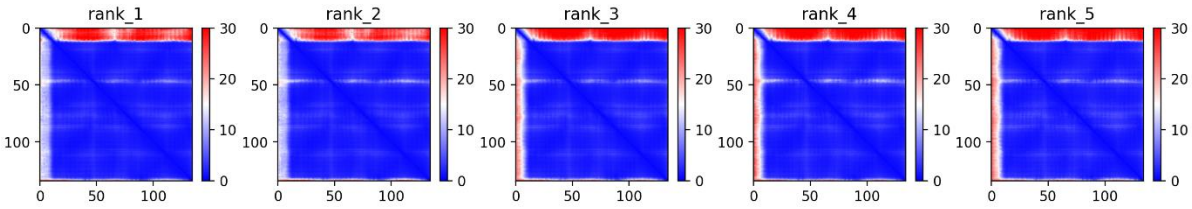

Predicted lDDT per position
Predicted lDDT
Positions
rank_1
rank_2
rank_3
rank_4
rank_5


rank_1
rank_2
rank_3
rank_4
rank_5


colored by N→C
colored by pLDDT

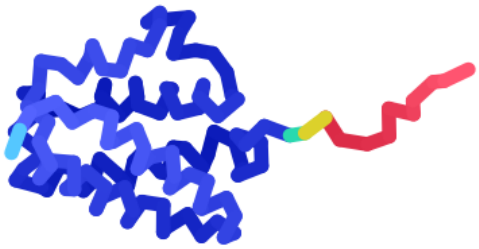
\


Predicted lDDT per position
Predicted lDDT
Positions
rank_1
rank_2
rank_3
rank_4
rank_5
0
20
40
60
80
100
120



colored by N→C

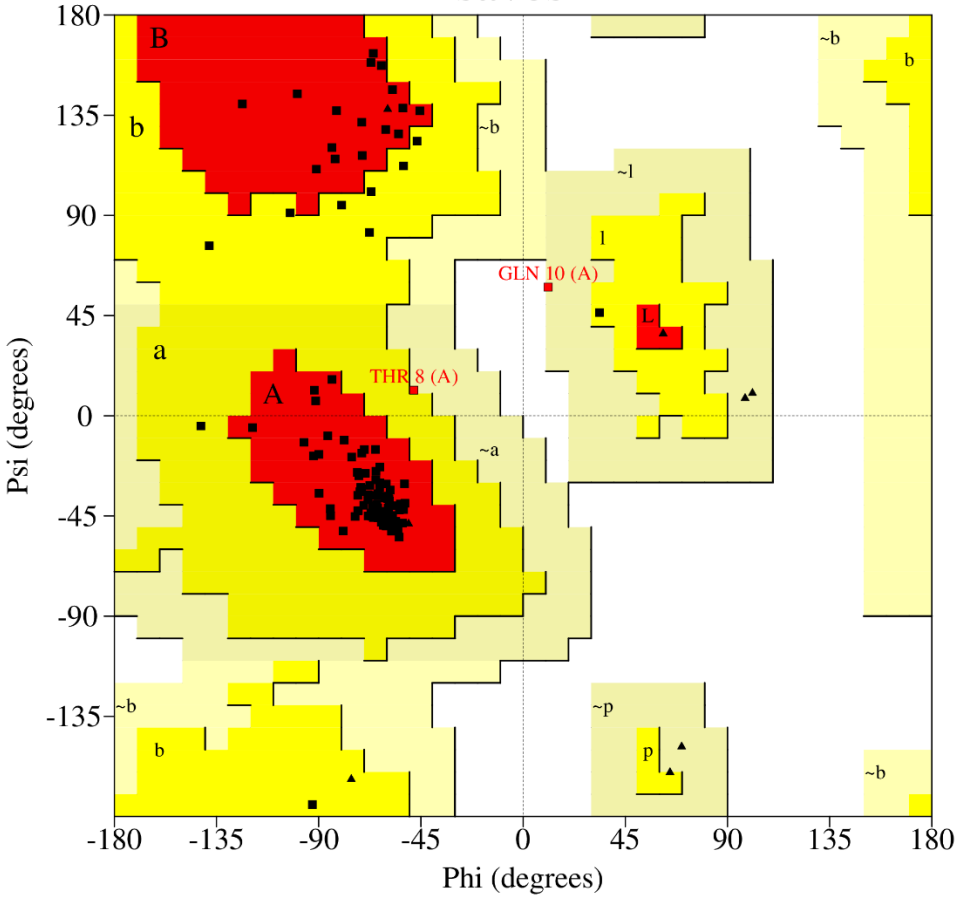
colored by pLDDT



PROCHECK

Ramachandran Plot

saves



Plot statistics

Residues in most favoured regions [A,B,L]	103	89.6%
Residues in additional allowed regions [a,b,l,p]	10	8.7%
Residues in generously allowed regions [~a,~b,~l,~p]	2	1.7%
Residues in disallowed regions	0	0.0%
Number of non-glycine and non-proline residues	115	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	10	
Number of proline residues	8	
Total number of residues	134	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

saves_01.ps