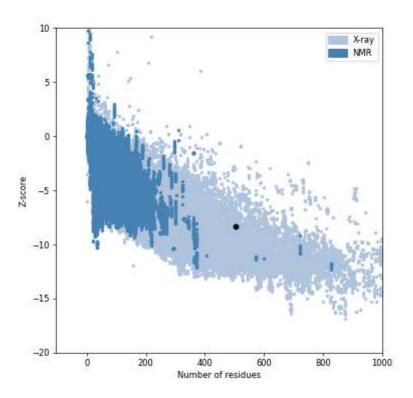
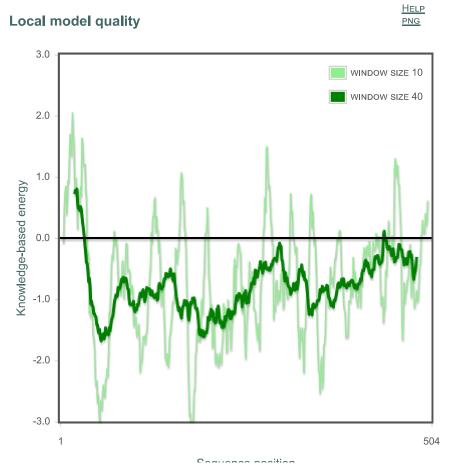


Please upload a structure in PDB format: 选择文件 未选择任何文件	<u>Help</u>
Alternatively you can specify a structure by entering its PDB code, chain identifier and NMR model number:	
PDB code:	
PDB CHAIN ID:	
PDB MODEL NUMBER:	
If you leave the fields for chain id or model number blank, the first chain of the first model found in the PDB file will be analysed. Analyse	
Results for MmcO.pdb, chain A, model 1 (504 aa)	
Overall model quality	<u>Help</u>
Z-Score: -8.31	

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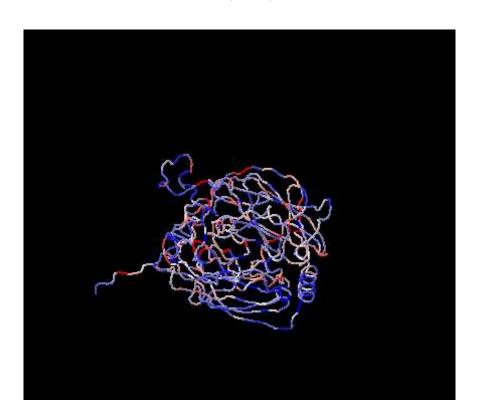














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- Wiederstein & Sippl (2007)
 ProSA-web: interactive web service for the recognition of errors in three-dimensional structures of proteins.
 - Nucleic Acids Research 35, W407-W410. [view]
- Sippl, M.J. (1993)
 Recognition of Errors in Three-Dimensional Structures of Proteins.
 Proteins 17, 355-362. [view]

This site is maintained by Markus Wiederstein. For comments and suggestions please contact prosa@came.sbg.ac.at



