

HTML Templates

The ModFOLD9 Server Results

Please cite the ModFOLD9 paper:

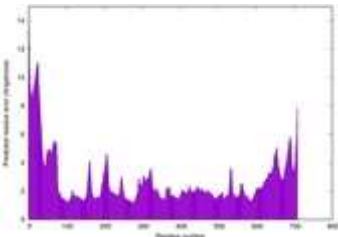

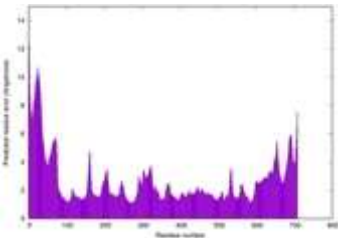

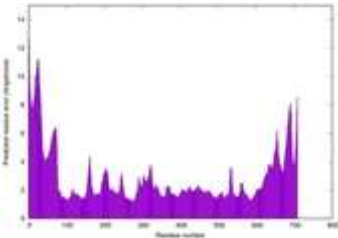

McGuffin, L.J. and Alharbi, S.M.A. (2024) ModFOLD9: a web server for independent estimates of 3D protein model quality. Journal of Molecular Biology, In press. [DOI](#) [PubMed](#)

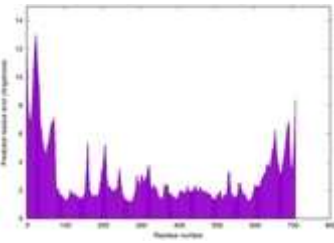

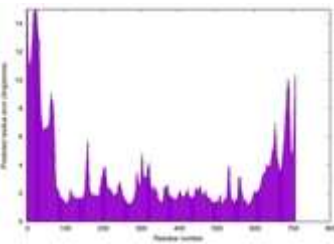

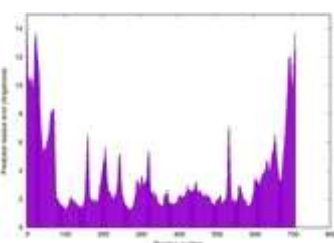
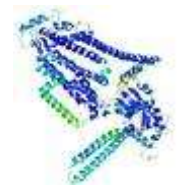
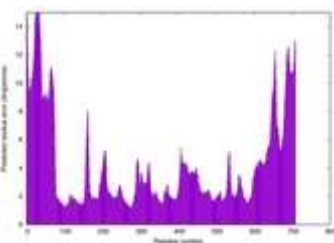
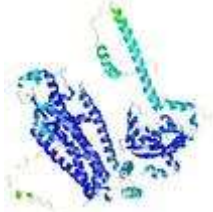
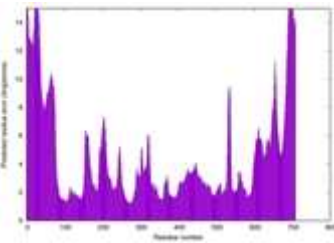
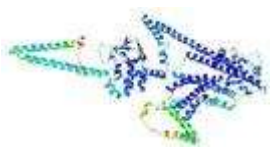
Click on the links below to download machine readable results files:

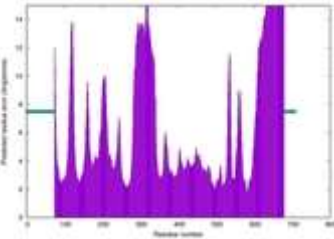

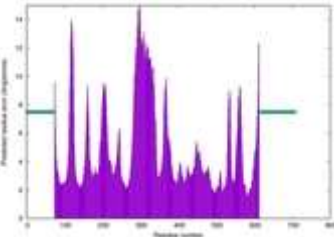

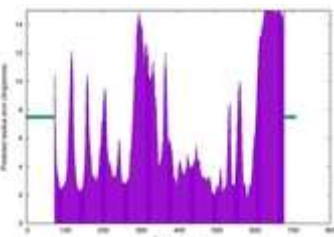

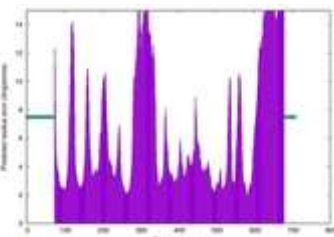

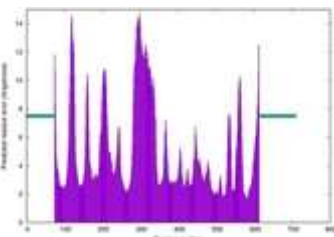

[Download Quality Assessment file](#) (raw model quality prediction scores in CASP QA format)

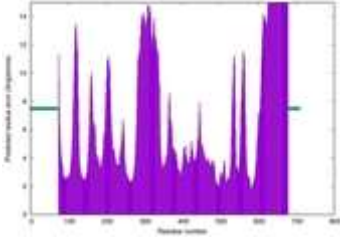

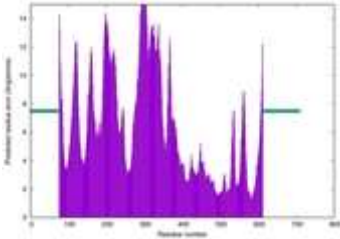

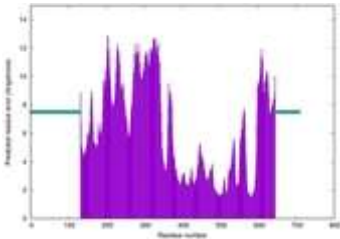

[Make a compressed file containing all evaluated 3D models](#) (models are in PDB format with predicted per-residue errors in the B-factor column)

Results will be available for 21 days after job completion (subject to server capacity)

Graphical ModFOLD9 results for NoName Help					
Rank	Model ID	Confidence and P-value	Global model quality score	Residue quality plots	3D view of local quality
1	IntFOLD701.pdb	CERT: 3.159E-4	0.6200	<div></div> <div>View and download</div>	<div></div> <div>View model in 3D and download</div> <div>Fix errors using ReFOLD3</div>
2	CNGC6AlphaFold.pdb	CERT: 3.53E-4	0.6141	<div></div> <div>View and download</div>	<div></div> <div>View model in 3D and download</div> <div>Fix errors using ReFOLD3</div>
3	IntFOLD702.pdb	CERT: 4.2E-4	0.6048	<div></div> <div>View and download</div>	<div></div> <div>View model in 3D and download</div> <div>Fix errors using ReFOLD3</div>

4	IntFOLD703.pdb	CERT: 4.829E-4	0.5974	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>
5	swissmodel02.pdb	CERT: 5.541E-4	0.5901	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>
6	ESMFold.pdb	CERT: 8.915E-4	0.5648	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>
7	RoseTTAFold2.pdb	HIGH: 1.296E-3	0.5449	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>
8	OmegaFold.pdb	HIGH: 2.204E-3	0.5166	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>

9	modeller04.pdb	UNCERT: 1.017E-1	0.3120	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>
10	modeller07.pdb	UNCERT: 1.071E-1	0.3090	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>
11	modeller06.pdb	UNCERT: 1.188E-1	0.3029	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>
12	modeller05.pdb	UNCERT: 1.349E-1	0.2954	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>
13	modeller02.pdb	UNCERT: 1.403E-1	0.2931	 <p>View and download</p>	 <p>View model in 3D and download</p> <p>Fix errors using ReFOLD3</p>

14	modeller01.pdb	UNCERT: 1.531E-1	0.2879	<div><div>View and download</div></div>	<div><div>View model in 3D and download</div><div>Fix errors using ReFOLD3</div></div>
15	modeller03.pdb	UNCERT: 2.46E-1	0.2580	<div><div>View and download</div></div>	<div><div>View model in 3D and download</div><div>Fix errors using ReFOLD3</div></div>
16	swissmodel01.pdb	UNCERT: 3.346E-1	0.2354	<div><div>View and download</div></div>	<div><div>View model in 3D and download</div><div>Fix errors using ReFOLD3</div></div>

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