

If you publish results using ANOLEA, please cite the following paper:

Melo, F. and Feytmans, E. (1998) Assessing Protein Structures with a Non-local Atomic Interaction Energy. *Journal of Molecular Biology* 277, 1141-1152

If you publish results from QMEAN, please cite the following paper:

Benkert, P., Schwede, T. and Tosatto, S.C.E. (2009). QMEANclust: Estimation of protein model quality by # combining a composite scoring function with structural density information. *BMC Struct Biol.* 2009 May 20;9:35.

**Global Scores:**

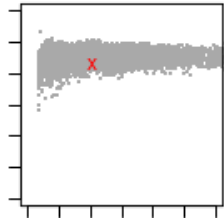
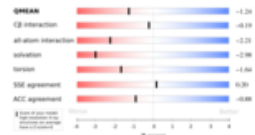

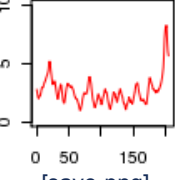
**DFire:** [top](#)

dfire\_energy: -241.77

If you publish results from DFire, please cite the following paper:

Zhou, H., and Zhou, Y. (2002). Distance-scaled, finite ideal-gas reference state improves structure-derived potentials of mean force for structure selection and stability prediction. *Protein Sci.* 11:2714-2726.

**QMEAN:** [?](#) [top](#)

Global scores			Local scores	
QMEANscore6 <a href="#">?</a>	Estimated absolute model quality <a href="#">?</a>	Score components <a href="#">?</a>	Coloring by residue error <a href="#">?</a>	Residue error plot <a href="#">?</a>
0.655	 <p>Z-Score: -1.237 Plot 1: <a href="#">[save png]</a> Plot 2: <a href="#">[save png]</a></p>	 <p><a href="#">[save png]</a></p>		 <p><a href="#">[save png]</a></p>
			All residues error: <a href="#">[save jpg]</a> <a href="#">[save pdb]</a>	Energy profile: <a href="#">?</a> <a href="#">[save raw scores]</a>

The QMEAN6 score is a composite score consisting of a linear combination of 6 terms (estimated model reliability between 0-1). The pseudo-energies of the contributing terms are given below together with their Z-scores with respect to scores obtained for high-resolution experimental structures of similar size solved by X-ray crystallography:

Scoring function term	Raw score	Z-score
C_beta interaction energy	-95.47	-0.19
All-atom pairwise energy	-2596.88	-2.21
Solvation energy	2.08	-2.98
Torsion angle energy	-32.51	-1.64
Secondary structure agreement	84.4%	0.20
Solvent accessibility agreement	74.6%	-0.88
QMEAN6 score	0.655	-1.24

If you publish results from QMEAN, please cite the following paper:

Benkert P, Biasini M, Schwede T. (2011). "Toward the estimation of the absolute quality of individual protein structure models." *Bioinformatics*, 27(3):343-50.

If you publish results using SWISS-MODEL, please cite the following papers:

Arnold K., Bordoli L., Kopp J., and Schwede T. (2006). The SWISS-MODEL Workspace: A web-based environment for protein structure homology modelling. *Bioinformatics*, 22,195-201.

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