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 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: -332.64

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 	Estimated absolute model quality 	Score components 	Coloring by residue error 	Residue error plot 
0.659	 <p>Z-Score: -1.207                      Plot 1: <a href="#">[save png]</a>                      Plot 2: <a href="#">[save png]</a></p>	 <p>[save png]</p>		 <p>[save png]</p>
			All residues error: <a href="#">[save jpg]</a> <a href="#">[save pdb]</a>	Energy profile:  <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	-74.39	-1.16
All-atom pairwise energy	-5563.18	-1.29
Solvation energy	-7.37	-2.21
Torsion angle energy	-14.64	-3.50
Secondary structure agreement	83.5%	0.26
Solvent accessibility agreement	78.9%	-0.28
QMEAN6 score	0.659	-1.21

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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