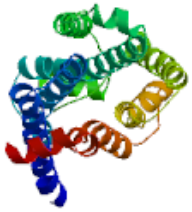
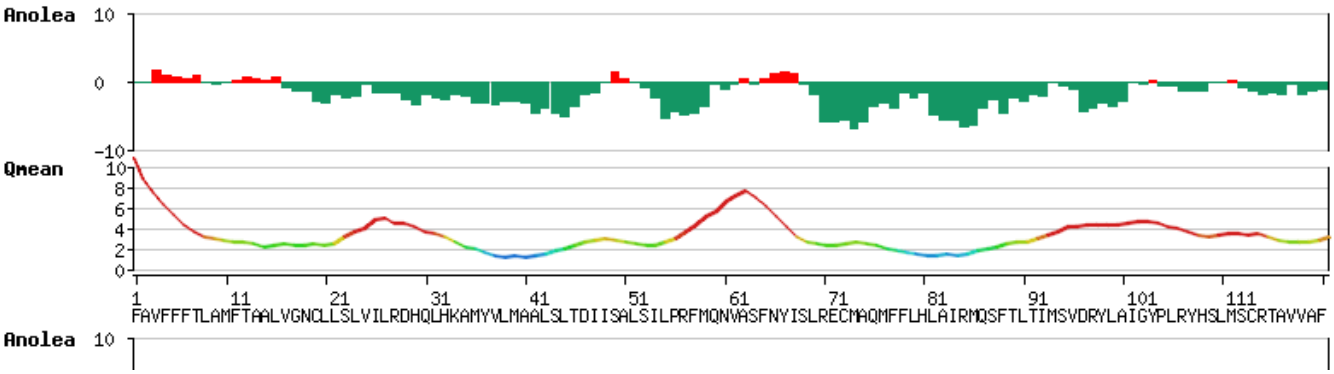
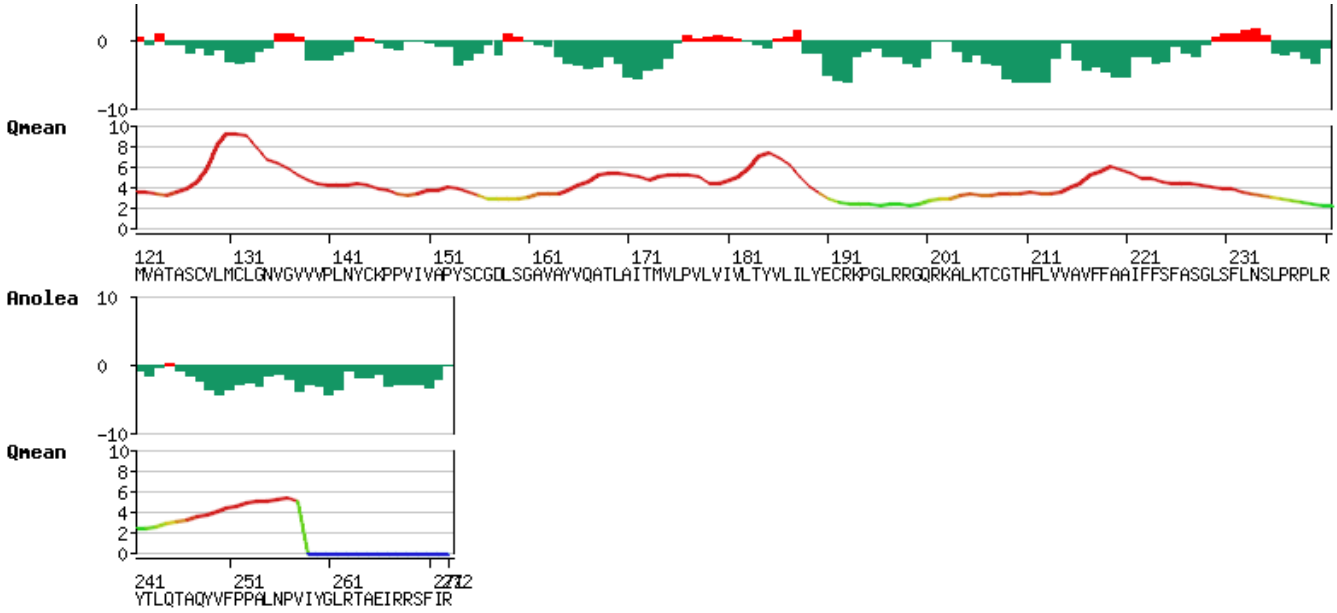
Workunit: P000010 SLOR1 vt4 based model



[Anolea] [DFire] [QMEAN]

Local Scores: [+/-]





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.

DFire: [+/-]

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dfire_energy:   -408.53
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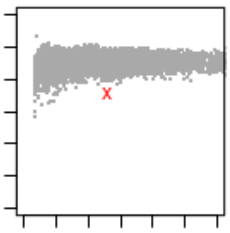
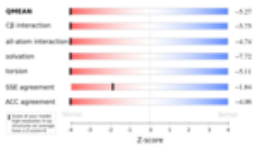
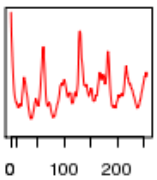
QMEAN6: [+/-]

Global scores			Local scores	
QMEANscore6	Estimated absolute model quality	Score components	Coloring by residue error	Residue error plot
0.277	 Z-Score: -5.266 Plot 1: [save png] Plot 2: [save png]	 [save png]		 [save png]
			All residues error: [save jpg] [save pdb]	Energy profile: [save raw scores]

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	110.50	-5.75
All-atom pairwise energy	1239.49	-4.74
Solvation energy	44.54	-7.72
Torsion angle energy	13.05	-5.11
Secondary structure agreement	72.0%	-1.84

Solvent accessibility agreement	57.6%	-4.06
QMEAN6 score	0.277	-5.27

References:

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.

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.