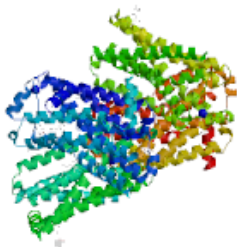


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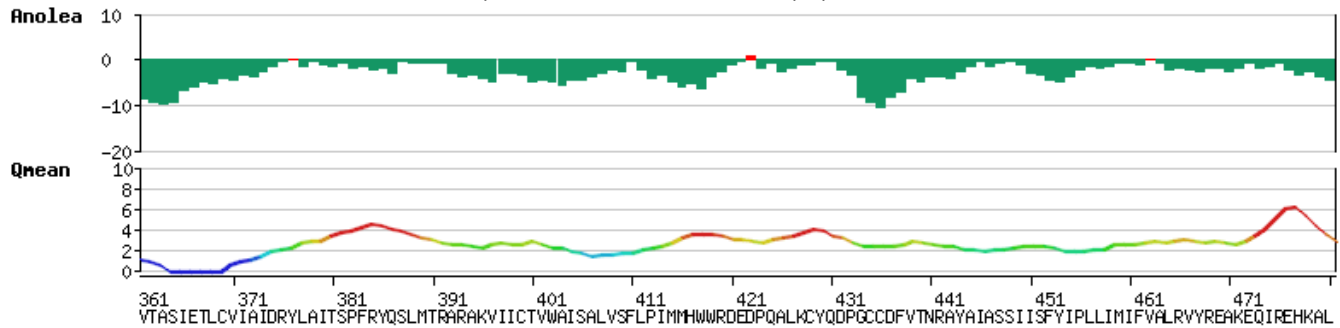
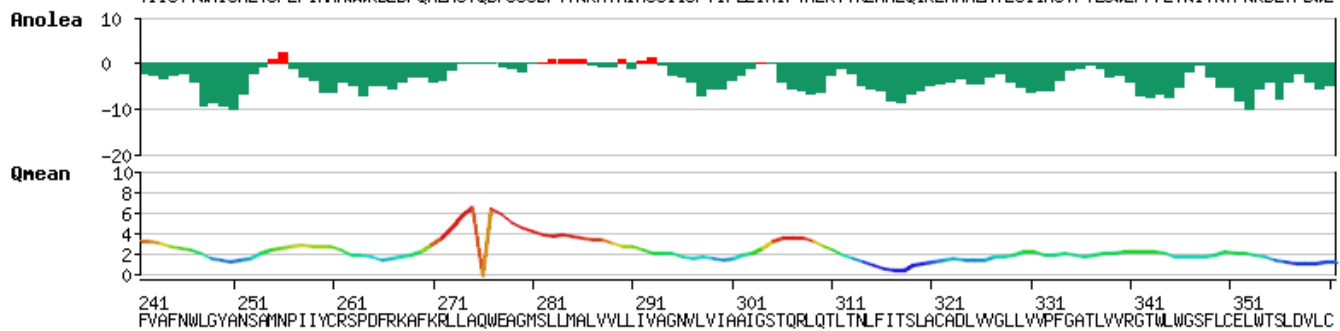
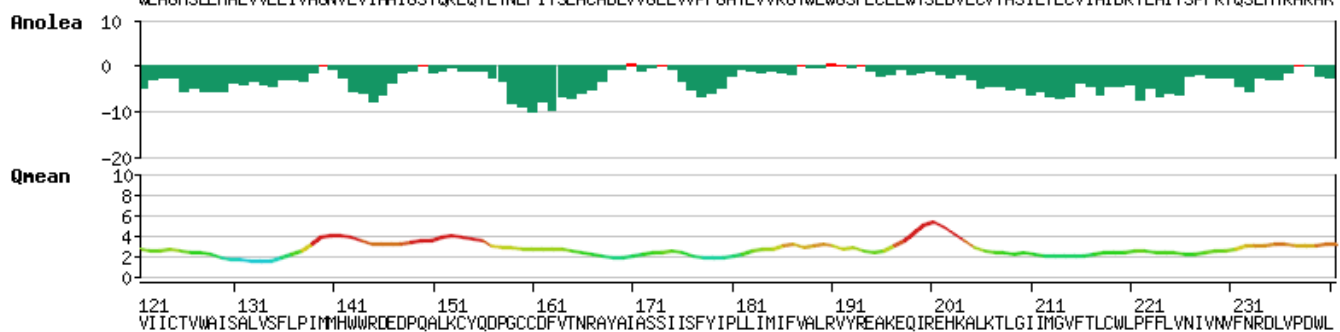
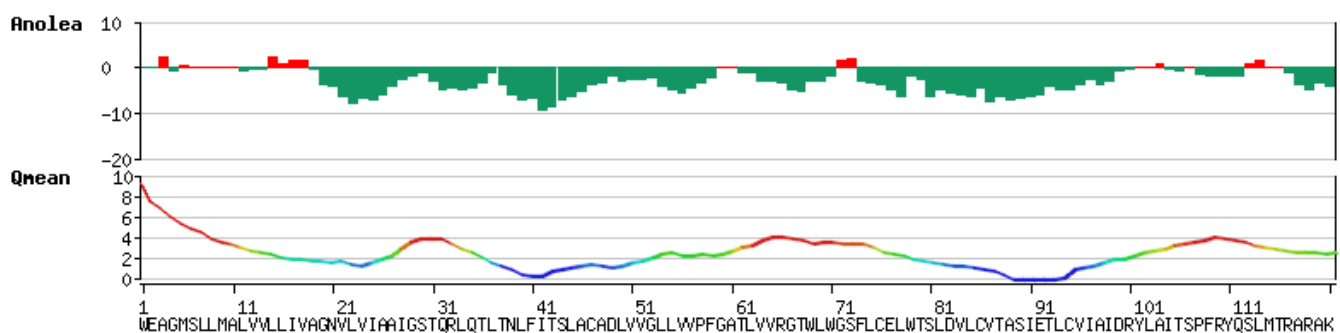
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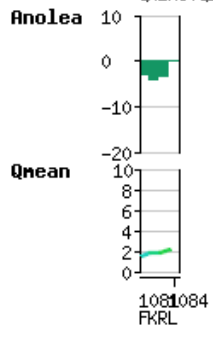
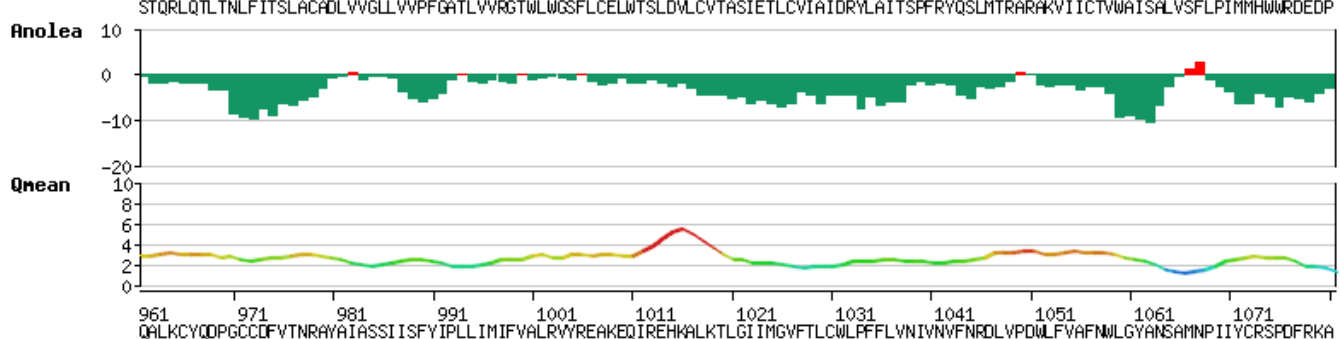
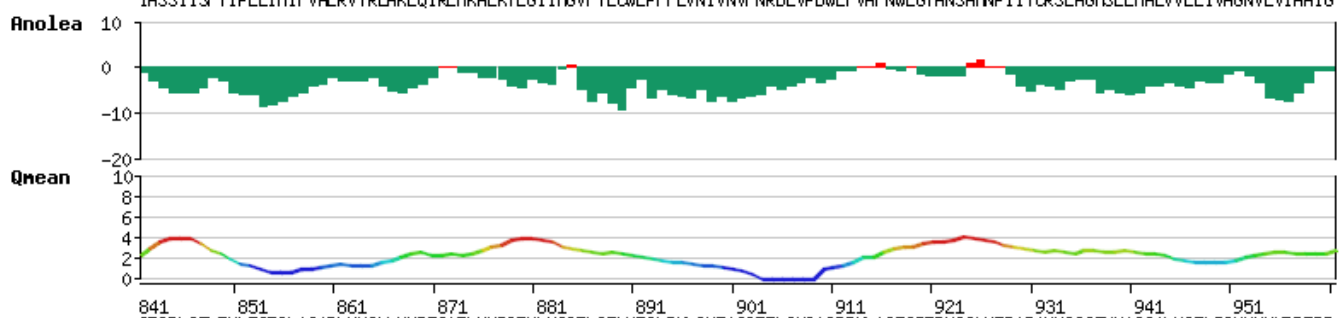
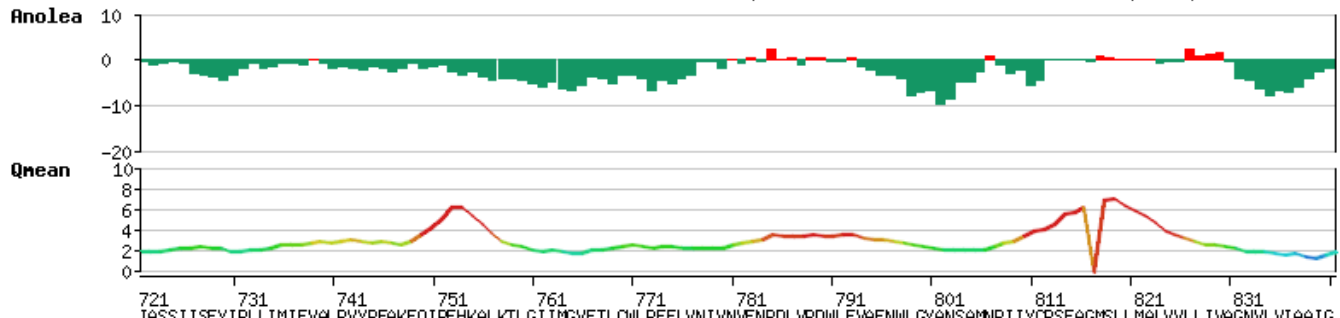
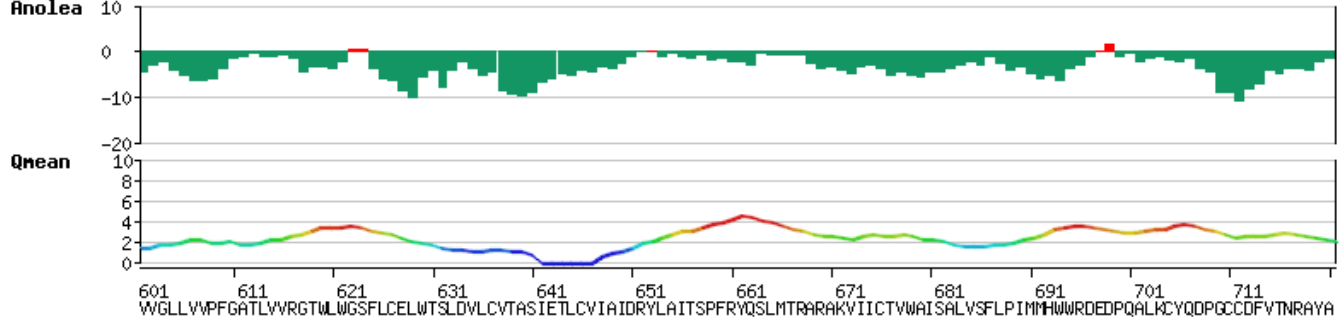
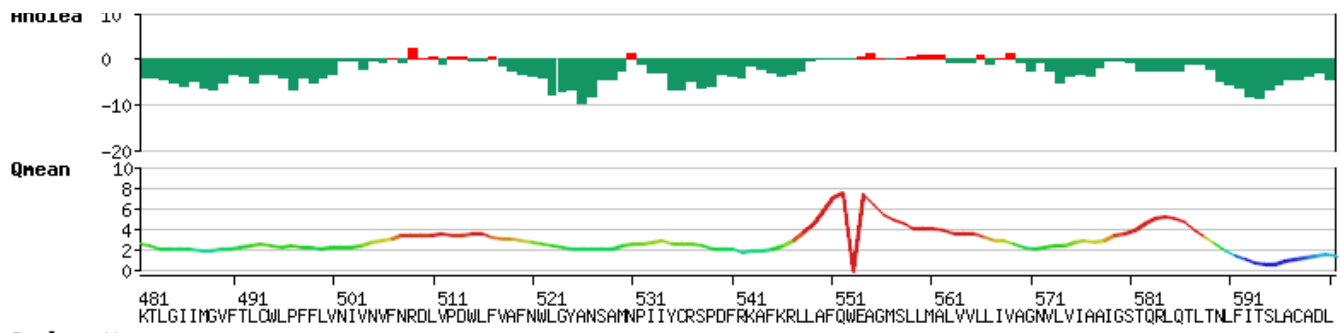
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[Anolea] [DFire] [QMEAN] ?

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

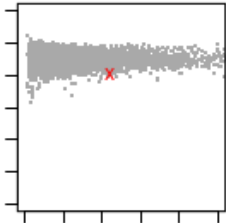
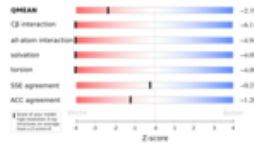
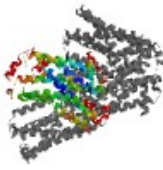
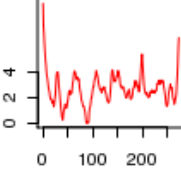
If you publish results from QMEAN, please cite the following paper:

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: [+/-]

dfire_energy: -1892.27

QMEAN6: [+/-]

Global scores			Local scores	
QMEANscore6	Estimated absolute model quality	Score components	Coloring by residue error	Residue error plot
0.528	 <p>Z-Score: -2.347 Plot 1: [save png] Plot 2: [save png]</p>	 <p>[save png]</p>	 <p>[save jpg] Chain: ← A → Z-score = -2.57</p>	 <p>[save png]</p>
			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	1014.94	-6.11
All-atom pairwise energy	14137.34	-4.94
Solvation energy	30.22	-4.05
Torsion angle energy	-35.21	-4.09
Secondary structure agreement	80.5%	-0.21
Solvent accessibility agreement	73.2%	-1.20
QMEAN6 score	0.528	-2.35

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.

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

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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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