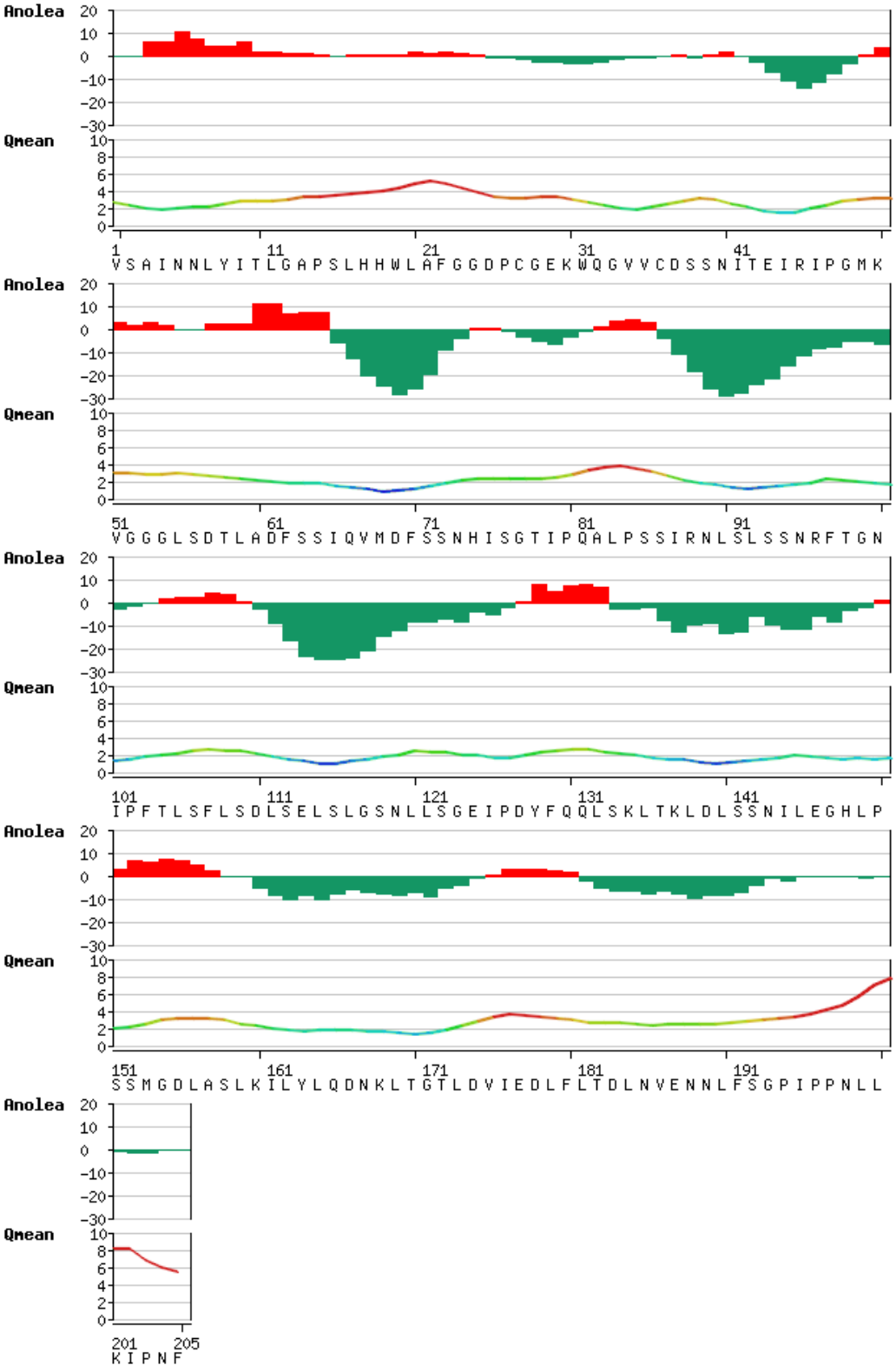



If you publish results using ANOLEA, please cite the following paper:
*Melo, F. and Feytmans, E. (1998) Assessing Protein Structures with a Non-local Atomic Interaction Energy. Journal of Molecular Biology 277, 1141-1152*

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.*

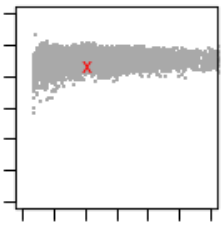
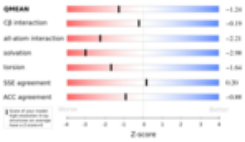
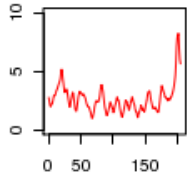
## Global Scores:

## 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 | Estimated absolute model quality | Score components | Coloring by residue error | Residue error plot |
| 0.655 |  <br>Z-Score: -1.237<br>Plot 1: [save png]<br>Plot 2: [save png] |  <br>[save png] |  |  <br>[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 | -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.