

MM 2018

Grading rubric for HW3

Homology modeling by hand.

10% for each of the following.

1. **Amino acid sequence is exactly that of the target.**
2. **Most of the backbone atoms and some side chain atoms have not moved from their template positions. (Fixed)**
3. **No sp³ amides, sp³ carbonyls, or sp² C-alphas**
4. **Structure is minimized. Sidechains have moved from template positions. Using gizcolorf , all sidechains are blue.**
5. **Two residue insertion is present. Bonds made correctly.**
6. **One-residue (not 2-residue) deletion.**
7. **No outliers in phi-psi plot**
8. **No outliers in bonds, bond angles, no D-amino acids.**
9. **Extra terminal residues removed.**
10. **All peptides are trans.**