UCSF Chimera can display Ramachandran plots. (Found under Favorites/Model Panel/Ramachandran plot). Ramachandran violations indicate that an amino acid within a polypeptide chain has spatially-incompatible backbone dihedral angles in the vicinity of the peptide bonds connecting successive amino acids. To illustrate that this type of plot can be used to check the quality of an experimentally determined protein structure you will look at three protein structures: PDB codes 5A9Z, 1EMA and 1IX9.   
Which of these structures show many outliers?

What could be a reason for this?

Answers: 5A9Z shows the most outliers in these three proteins , the reason could be the outlier residues do not have a stable phi:psi angle value and thus they are predicted to be conformationaly unstable.

If you excluded the structure with a high proportion of outliers, can you predict any difference in secondary structure elements between the remaining two structures from the Ramachandran plots?

Answers: the Ramachandan plot of 1IX9 shows less amino acid dots in the beta-sheet than protein 1EMA, on contrary, more amino acids display right hand alpha-helix for 1IX9. These two proteins show pretty much the same amount of amino acids in left hand alpha-helix.

Go to the PDB database (https://www.rcsb.org/) and look at the wwPDB validation graph on the Structure Summary page. Do you get a similar information on the relative quality of the three structures as you did from the Ramachandran analysis?

They are similar in terms of Ramachandran outliers.  
  
(c) Finally you should analyze the structure of green fluorescent protein (GFP, use the PDB code in the above example). Make an illustration that show the hydrogen bond interactions between the GFP chromophore and the rest of the protein.

Answers: As the picture shown below, the GFP chromophore interacts with the rest of the protein by the two hydrogen bonds.

