**Next steps**

**7au\_eos\_mpnn-2\_lig\_3**

1. Do the two mutations LZX suggested
   1. directly change in program and dock
   2. use original post-protein mpnn AF3 template then send to ligand mpnn, but bias the two amino acids towards the ones LZX wanted
      1. Best high temp design doesn’t work
      2. Best side chain packing design has one with no clash and no h-bonds with substrate at a new binding spot. i.e. everything different.
   3. use the vinodock best model as template for ligand mpnn.
      1. Some sequences were chosen for higher ligand confidence and just slightly lower overall confidence than best score
2. Trying manually redesigning the active site for eosin and then diffuse around it.