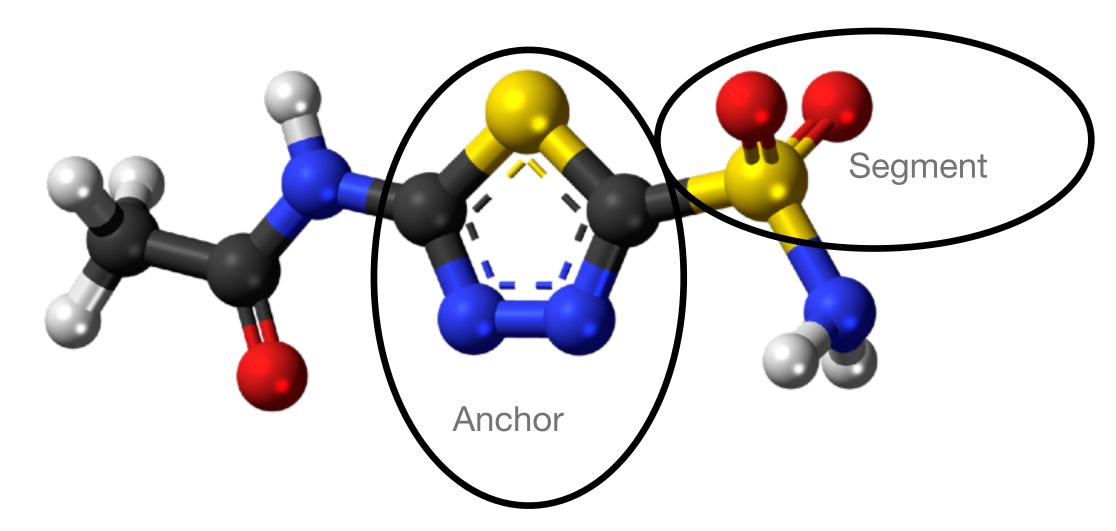


UCSF DOCK is based on anchor-and-grow



- Receptor spheres and rigid "anchor" in ligand
 - represented as graph of atoms separated by distances
 - docking is search for isomorphic subgraph
- Until the molecule is complete, segments are iteratively
 - added to the anchor and
 - pruned if the energy is too high
- Complete structures are locally minimized