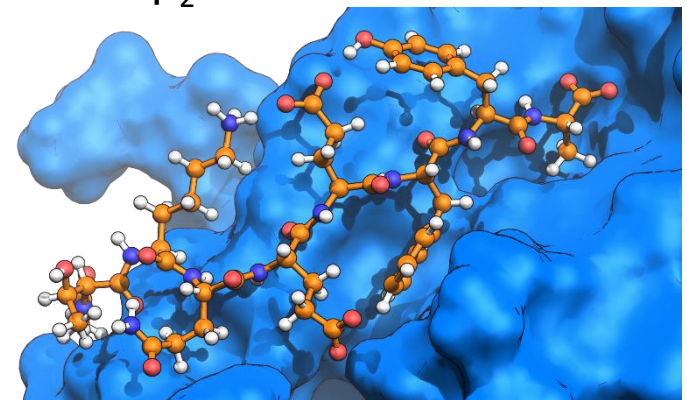
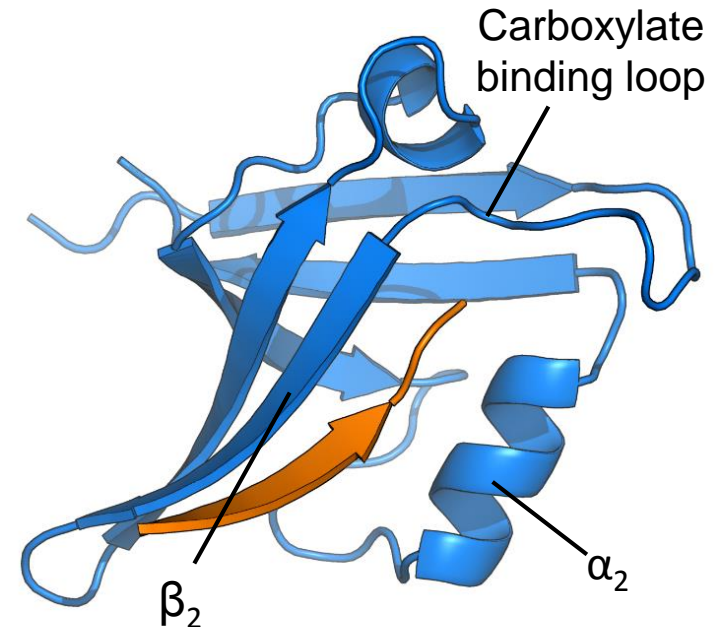


Structure of PDZ domains

- Around 80-100 residues
- Conserved structure:
 - 5/6 β -strands
 - 2 α -helices
- Recognize 4-7 C-terminal amino acids of their targets ($K_d \approx 10\text{-}80 \mu\text{M}$)
- β -sheet augmentation mechanism
- Binding groove formed by α_2 and β_2
- Carboxylate binding loop highly conserved



Tiam1 PDZ domain