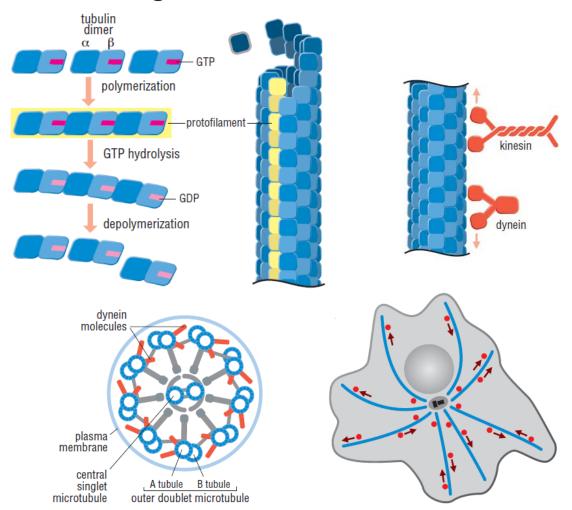
FUNCTIONAL SITES IN PROTEIN STRUCTURES

Dr. Zhiyi Wei SUSTC

The three-dimensional structure of a protein determines its function

We are focusing on biochemical function



Molecular recognition

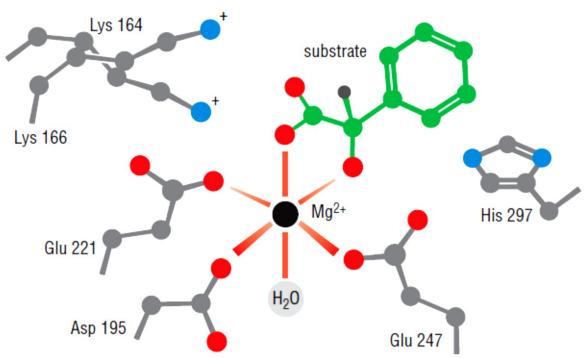
- Almost everything in your body can be recognized by proteins
 - Macromolecules or large assembly
 - DNA/RNA, protein, glycan, lipid bilayer
 - Small molecules
 - Nucleotide (like ATP), ion (like Ca²⁺), various organic chemicals (like Heme and vitamin), water, gas, or even proton.
- The functions of all proteins depend on the ability to bind ligands
 - Nomenclature of ligand (in my class hereafter): refers to those interacting molecules other than proteins
- Recognition features of proteins
 - High specificity
 - Can be versatile or selective
- Recognition is achieved by complementary binding
 - Complementarity of shape
 - Complementarity of weak interactions

Functional Site

- Protein structures provide specialized microenvironments for molecular recognition
 - Binding site
 - Active site (involved in catalysis)
- The microscopic environment of the site
 - Usually a cavity, pocket, or cleft
 - Providing a different chemical environment from the bulk solution around the protein
 - Hydrophobic for hydrophobic ligand or protein
 - Charged for reverse-charged ligand or protein

Active Site

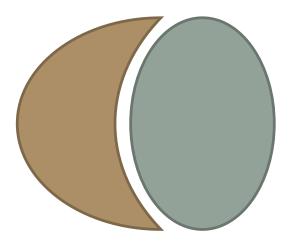
- Asymmetric pocket on or near the surface of a macromolecule that promotes chemical catalysis when the appropriate substrate binds
 - Creating an environment which is very difficult to achieve in free solution
- General acid-base catalysis
 - Protons are transferred between donating or accepting atoms on the substrate and key basic and acidic side chains



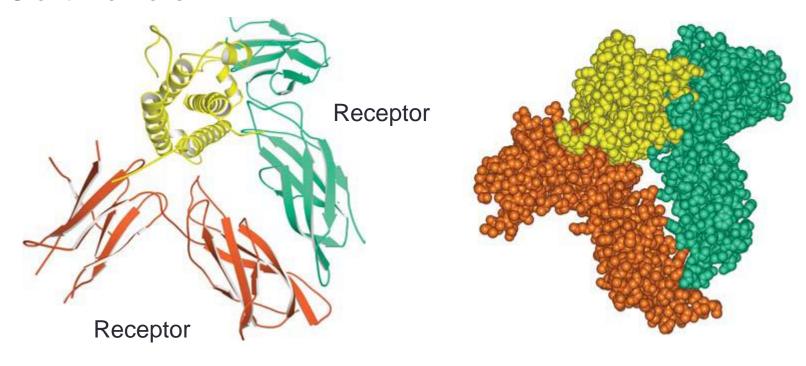
The active site of mandelate racemase

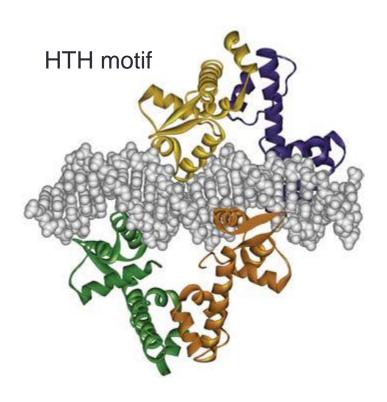
Location of binding sites

 Binding sites for macromolecules on a protein's surface can be concave, convex, or flat

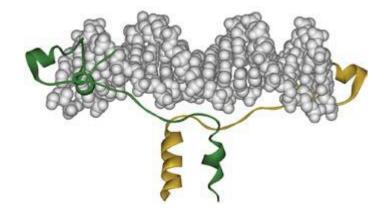


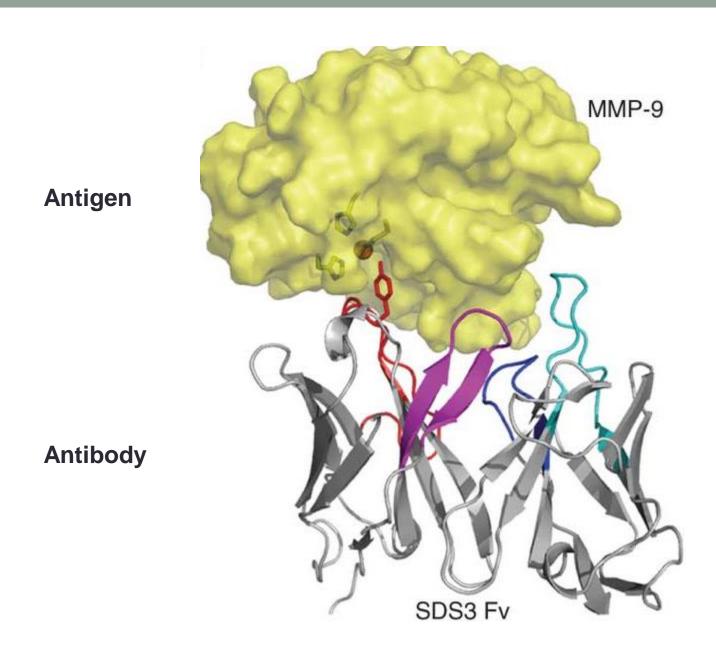
Growth hormone





Zinc finger

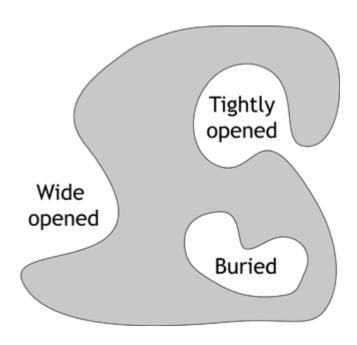


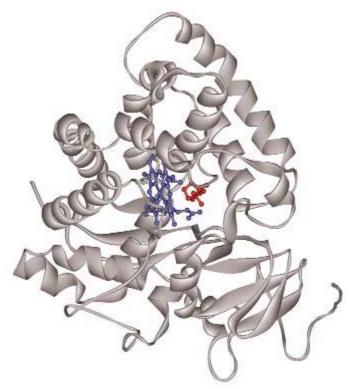


Sela-Passwell, et. al., Nat Medicine (2012)

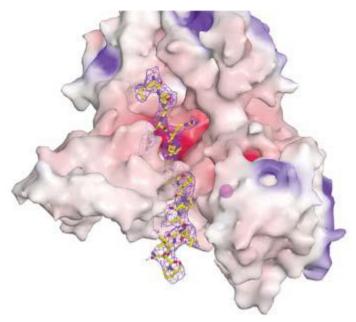
Location of binding sites

 Binding sites for small ligands are clefts, pockets or cavities



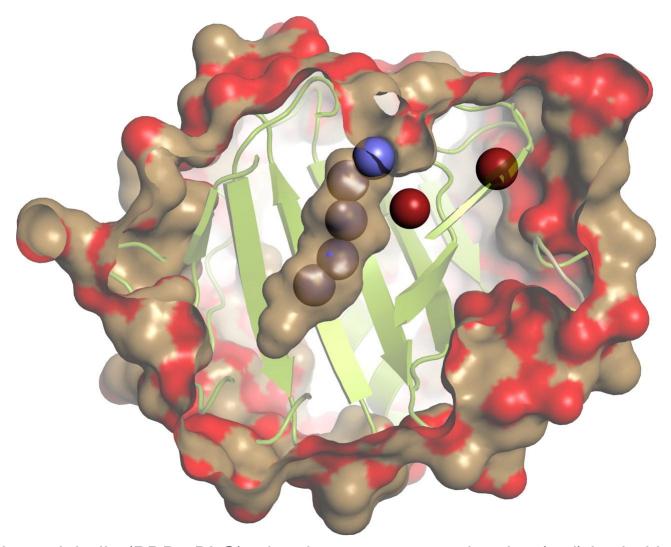


bacterial cytochrome P450 with its substrate camphor bound



Substrate binding to anthrax toxin lethal factor

BIO446 Protein Structure and Function

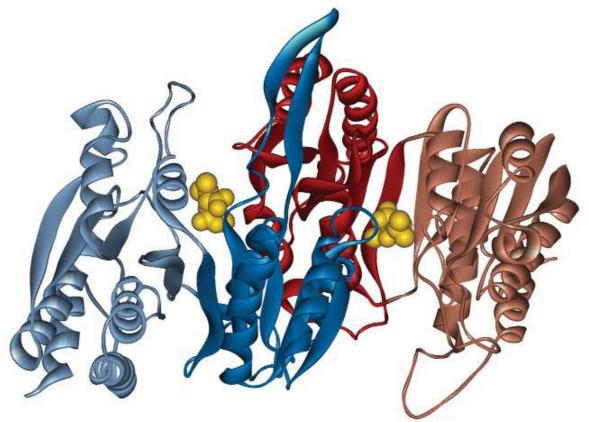


β-lactoglobulin (PDB 3BLG), showing two water molecules (red) buried in small polar cavities and five water molecules (blue) modeled in the nonpolar calyx.

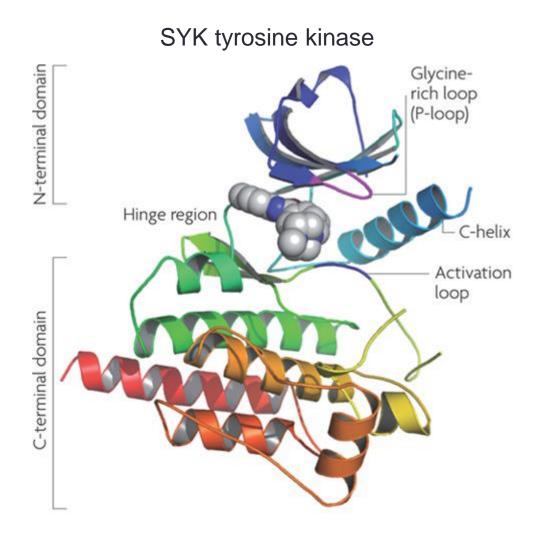
Qvist, et al. PNAS (2008)

Location of active sites

Catalytic sites often occur at domain and subunit interfaces



Dimeric bacterial enzyme 3-isopropylmalate dehydrogenase. The active sites are indicated by the bound cofactor NADPH.

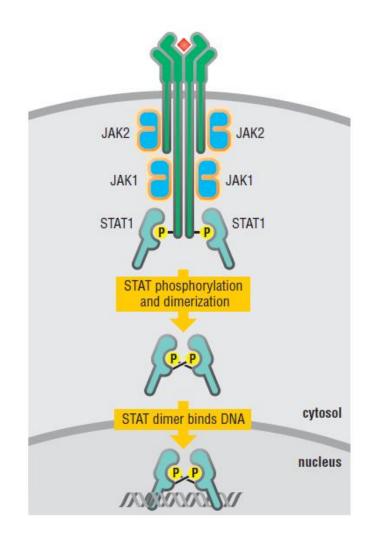


Nature Reviews | Drug Discovery

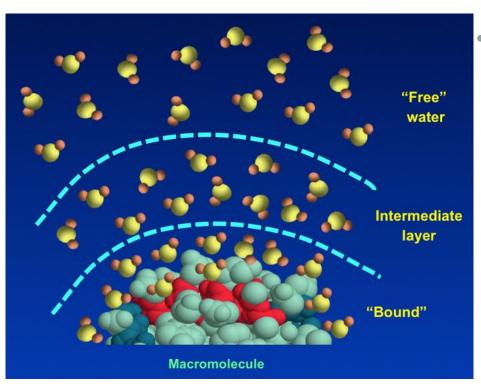
Chico, et. al., Nat Rev Drug Discovery (2009)

Nature of binding sites

- Binding sites generally have a higher than average amount of exposed hydrophobic surface
- Binding sites for small molecules are usually concave and partly hydrophobic
- Weak interactions can lead to an easy exchange of partners



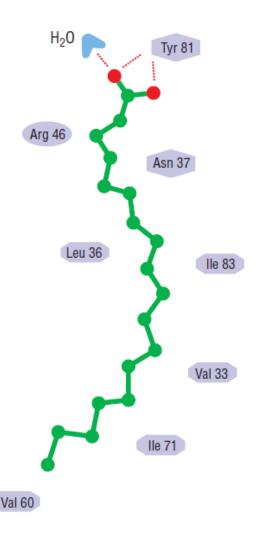
Nature of binding sites



- Displacement of water drives binding events
 - The enthalpic cost of releasing the surface waters
 - Depending on the microenvironment
 - Polar interaction is stronger in an environment of reduced polarity than in aqueous solution

Nature of binding sites

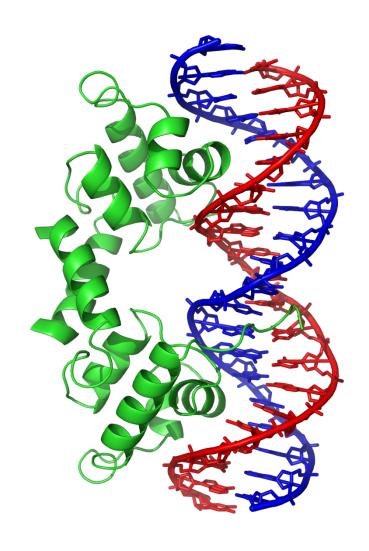
- High binding affinity usually means high specificity, but sometimes...
- Contributions to binding affinity
 - Hydrophobic interactions
- Contributions to binding specificity
 - Anisotropic or directional forces
 - Hydrogen bonding



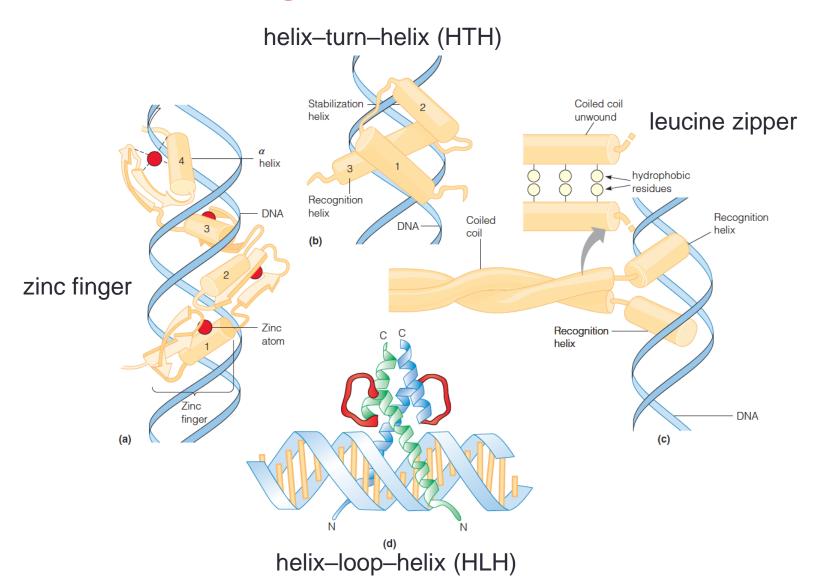
Protein-DNA interaction

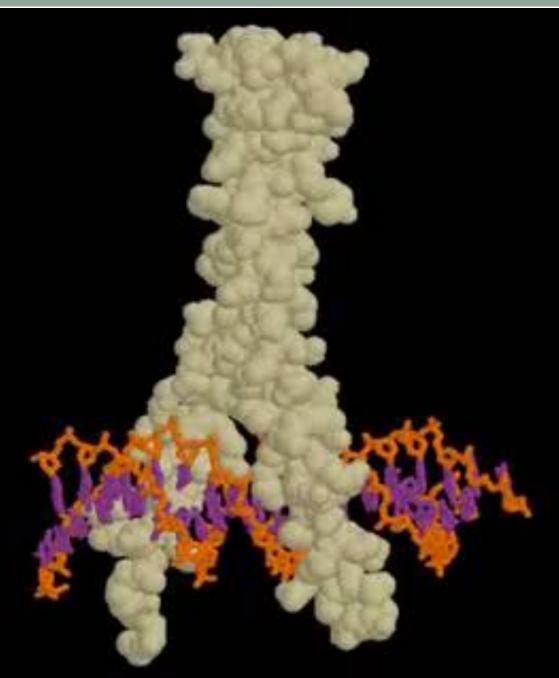
- DNA replication
- DNA modification
- DNA repair
- Transcription
- Chromosome modeling

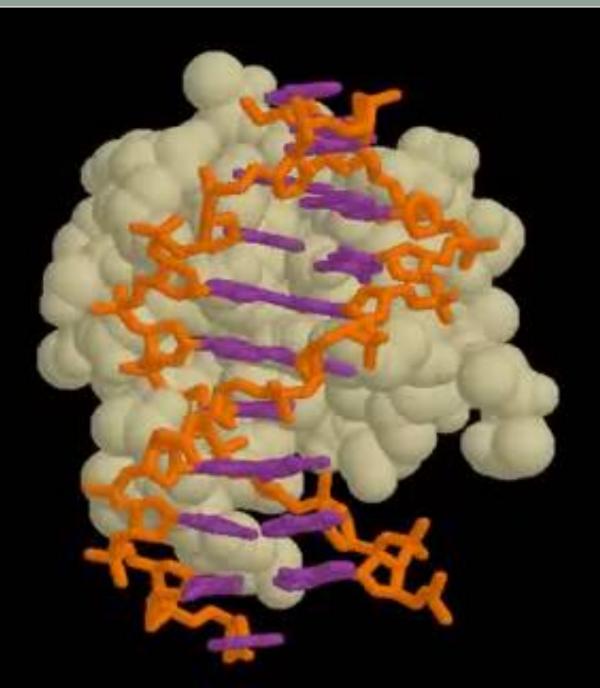
•



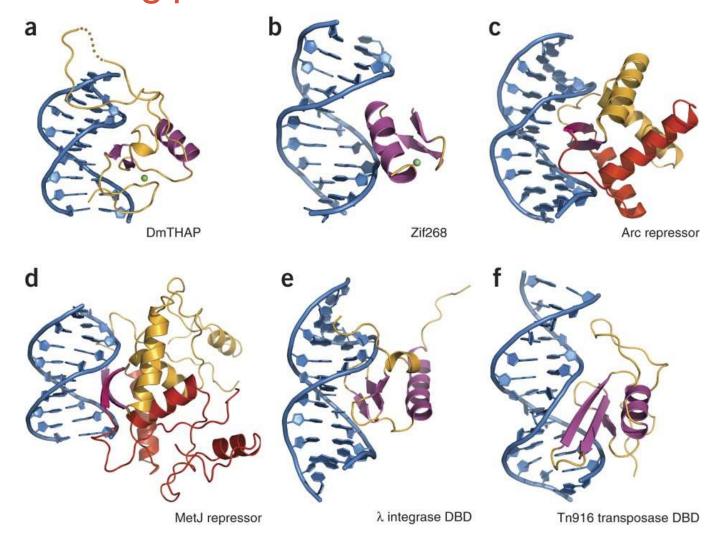
DNA binding motifs and domains



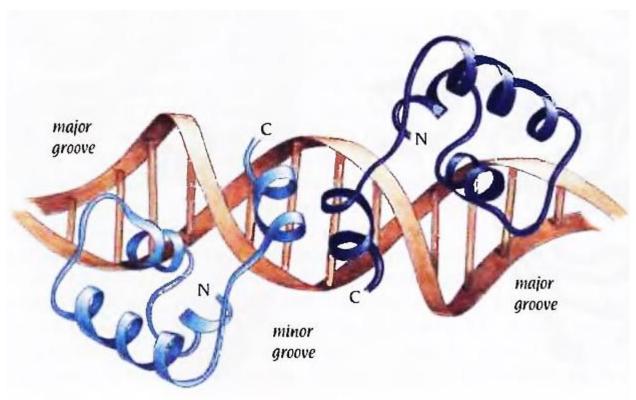




The major grooves provide binding sites for DNA binding proteins

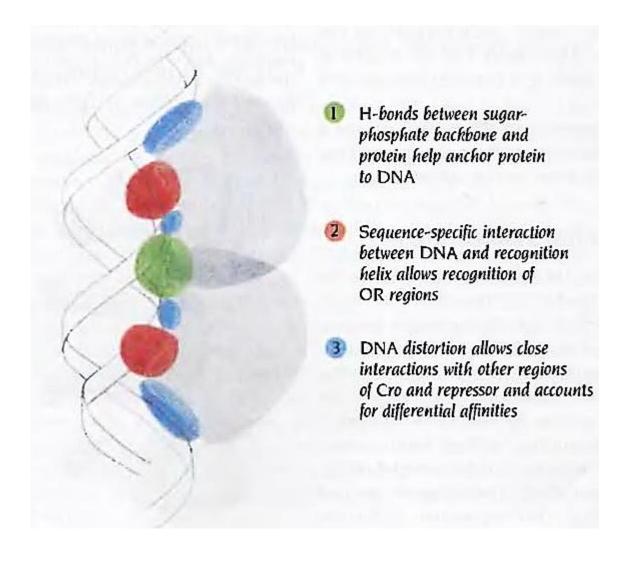


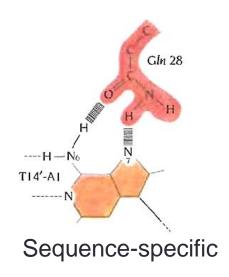
The minor grooves may be also involved in binding

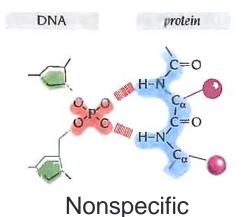


The lac repressor binds to both the major and minor grooves of DNA for distortion of the B-DNA structure

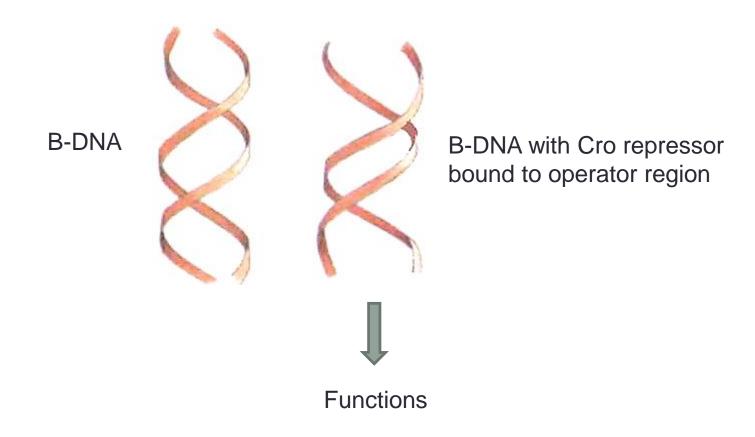
Main features of DNA interaction with HTH motif







Proteins impose precise distortions on DNA conformations in complexes



Protein-RNA interaction

- Interaction with mRNA
 - Transcription
 - Translation
 - Translocation/transport
- Interaction with tRNA
 - Translation
- Interaction with rRNA
 - Translation
- RNA editing
 - Splicing
- RNA interference
- DNA editing



