

Vojtěch Klusák

Searching for the connection
between structure of a protein
and its stability

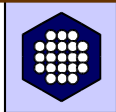
Institute of Organic Chemistry and Biochemistry (IOCB),
Department of Molecular Modeling
and
Center for Biomolecules and Complex Molecular Systems

problems:

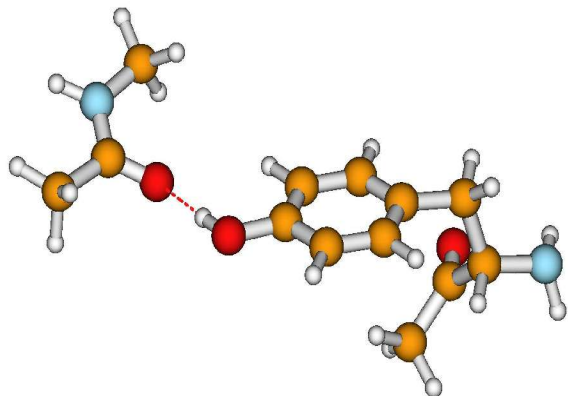
weak interactions

ligand protein complexes

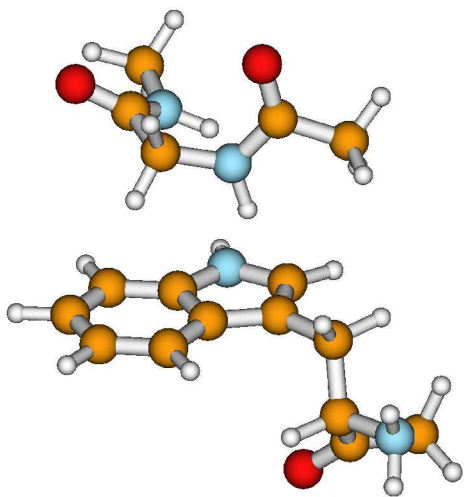
protein structure stabilization in general



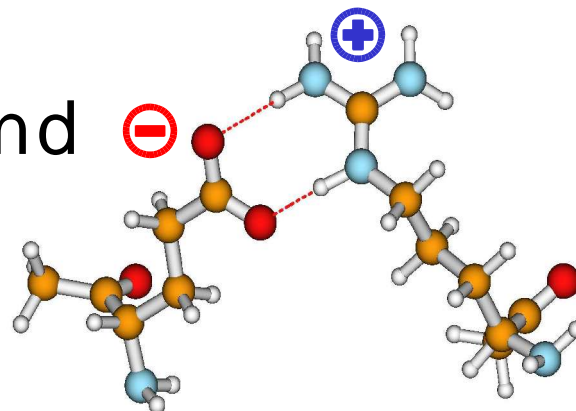
types of interactions:



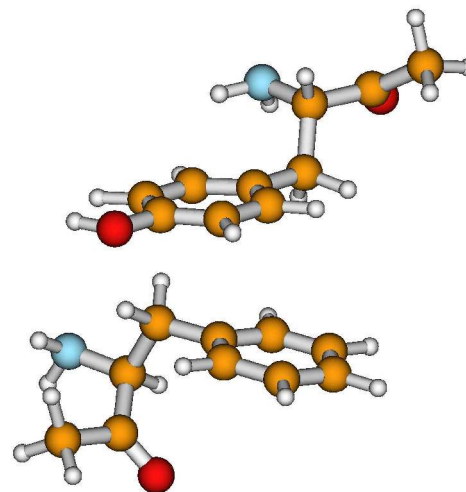
hydrogen bond



ionic bond



dispersion interaction

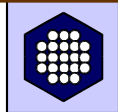


methods:

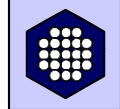
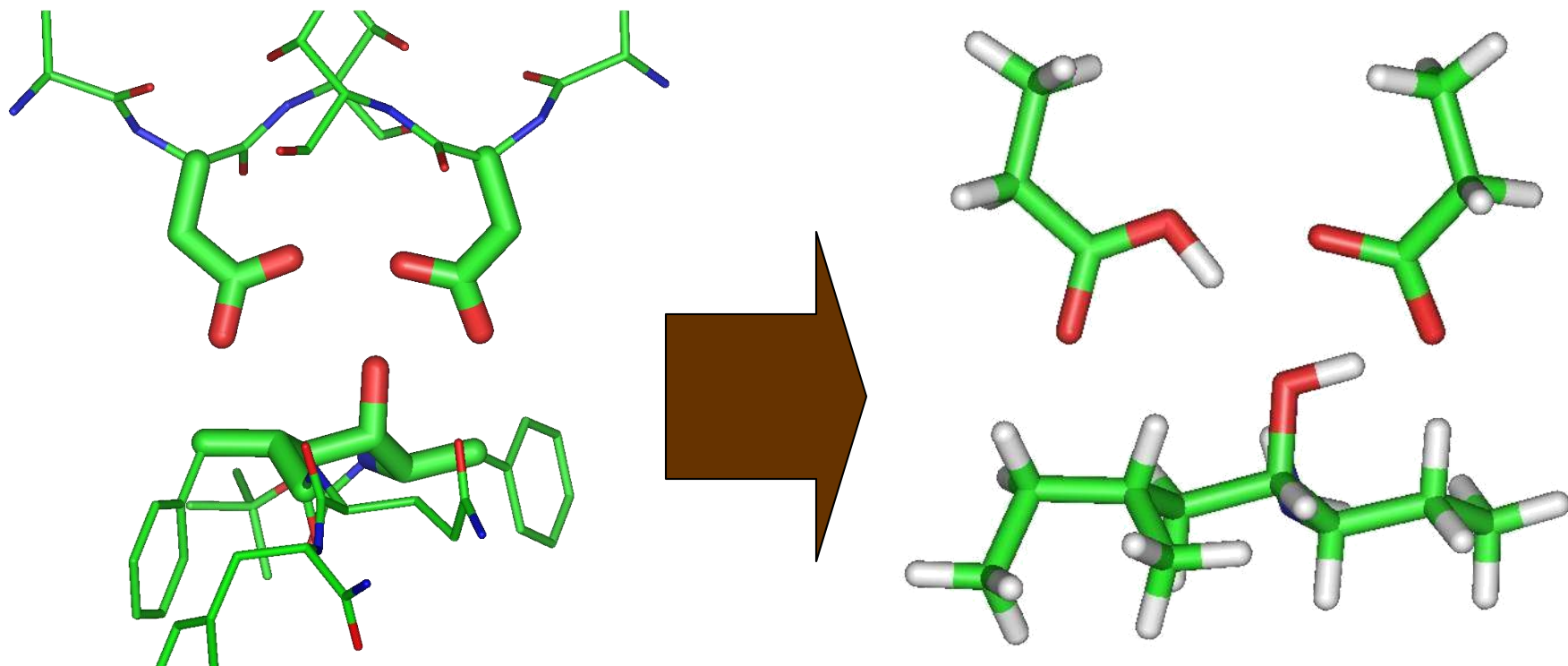
mainly Quantum mechanics (MP2, CCSD(T))

also empirical methods (AMBER, DFT-TB)

Fragmentation



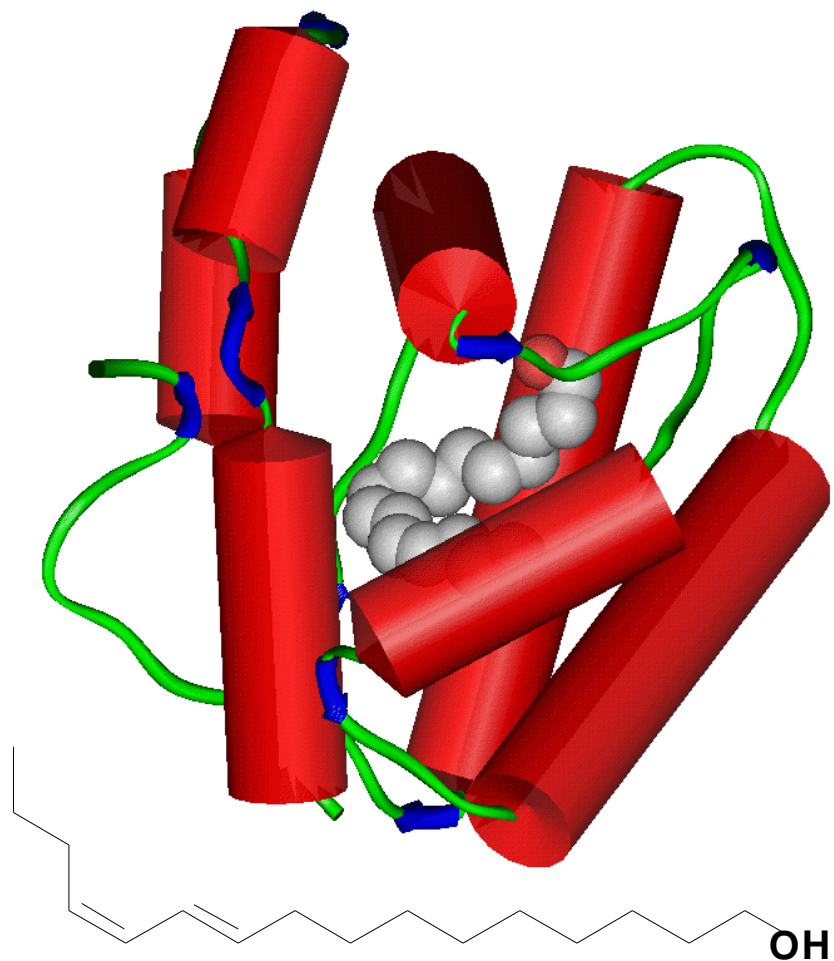
Fragmentation:



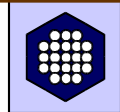
projects:

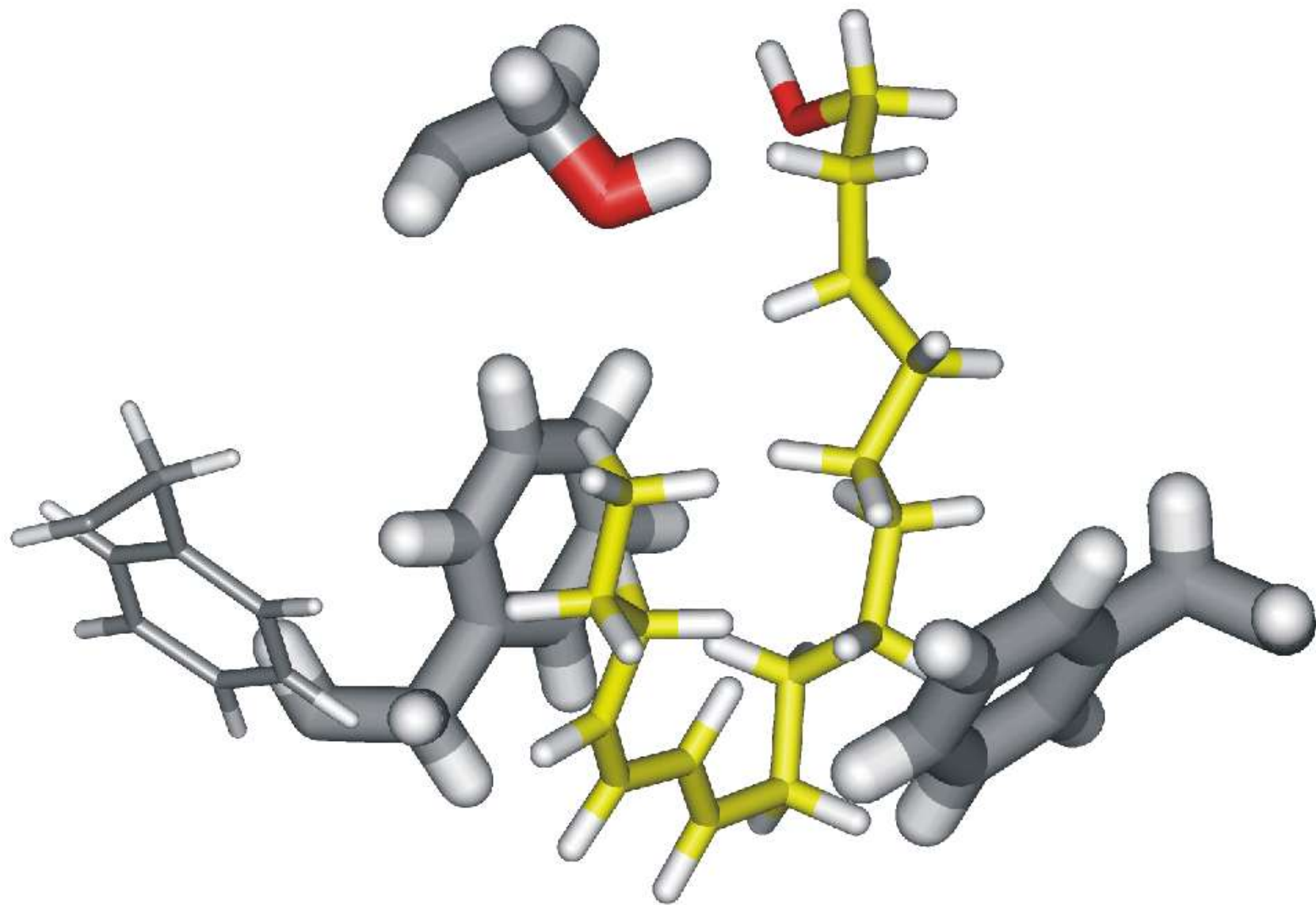
BmPBP: *Bombyx mori* Pheromone Binding

Protein
Bombykol: (10 E, 12 Z) - hexadekadien -1-ol



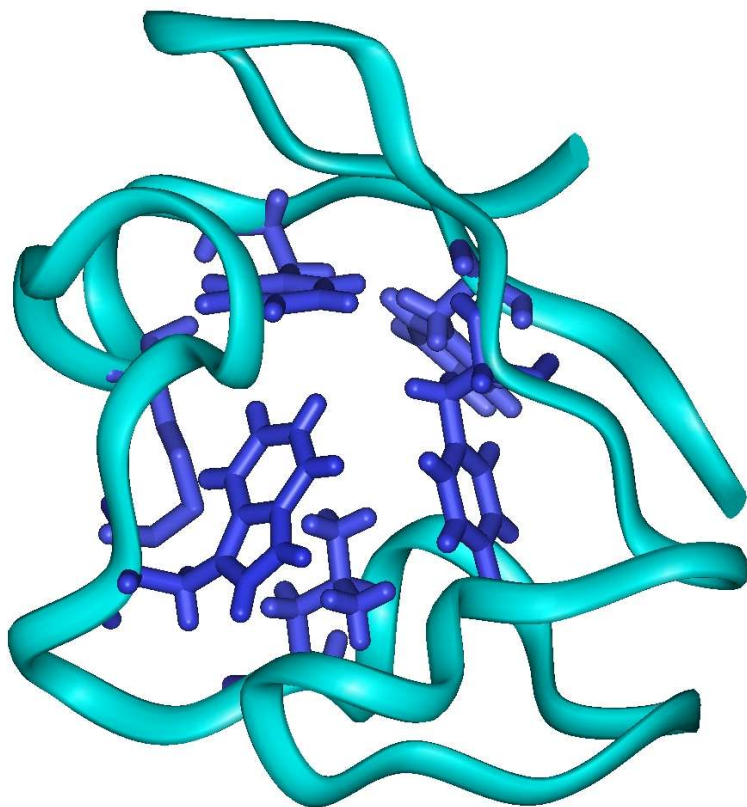
- Do the molecules interact anyhow?
- How to prepare analogs of the pheromone?





project:

role of hydrophobic core of rubredoxin (*desulfovibrio vulgaris*)



- Phe30 interacts more than 4 times stronger than one common H bond (23 vs. 5 kcal/mol)
- Structure of the cluster is important

Vondrášek J, Bendová L., **Klusák V.**, Hobza P. J Am. Chem. Soc. 2005; 127: 2615-2619.



project:
comparison of rubredoxin of *pyrococcus furiosus*
 (thermophile)
 and rubredoxin of *desulfovibrio vulgaris*
 (mesophile)

	1	2	3	4	5	6	7	8	9	..	n
1	X	X	X								
2	X	X	X	X							
3	X	X	X	X	X						
4		X	X	X	X	X					
5			X	X	X	X	X				
6				X	X	X	X	X			
7					X	X	X	X	X		
8						X	X	X	X	X	
9							X	X	X	X	X
..								X	X	X	X
n									X	X	X

- 66% homology
- identical fold
- high quality X-ray structures

Questions:

- Does the total sum correlate with thermostability?
- Which AAs are important for thermostability?

Acknowledgements:

Zdeněk Havlas

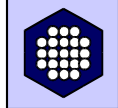
Jiří Vondrášek

Pavel Hobza

Luboš Rulíšek

Lada Bendová

Aleš Svatoš



projects:

Major Urinary Protein-I (MUP-I)

