

Course Project: Structural Analysis

Proteomes Interactomes and Biological Networks

December 2, 2019

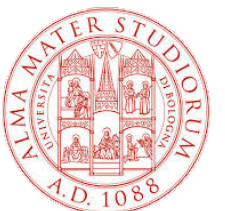
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<http://biofold.org/>



**Biomolecules
Folding and
Disease**

Department of Pharmacy and
Biotechnology (FaBiT)
University of Bologna

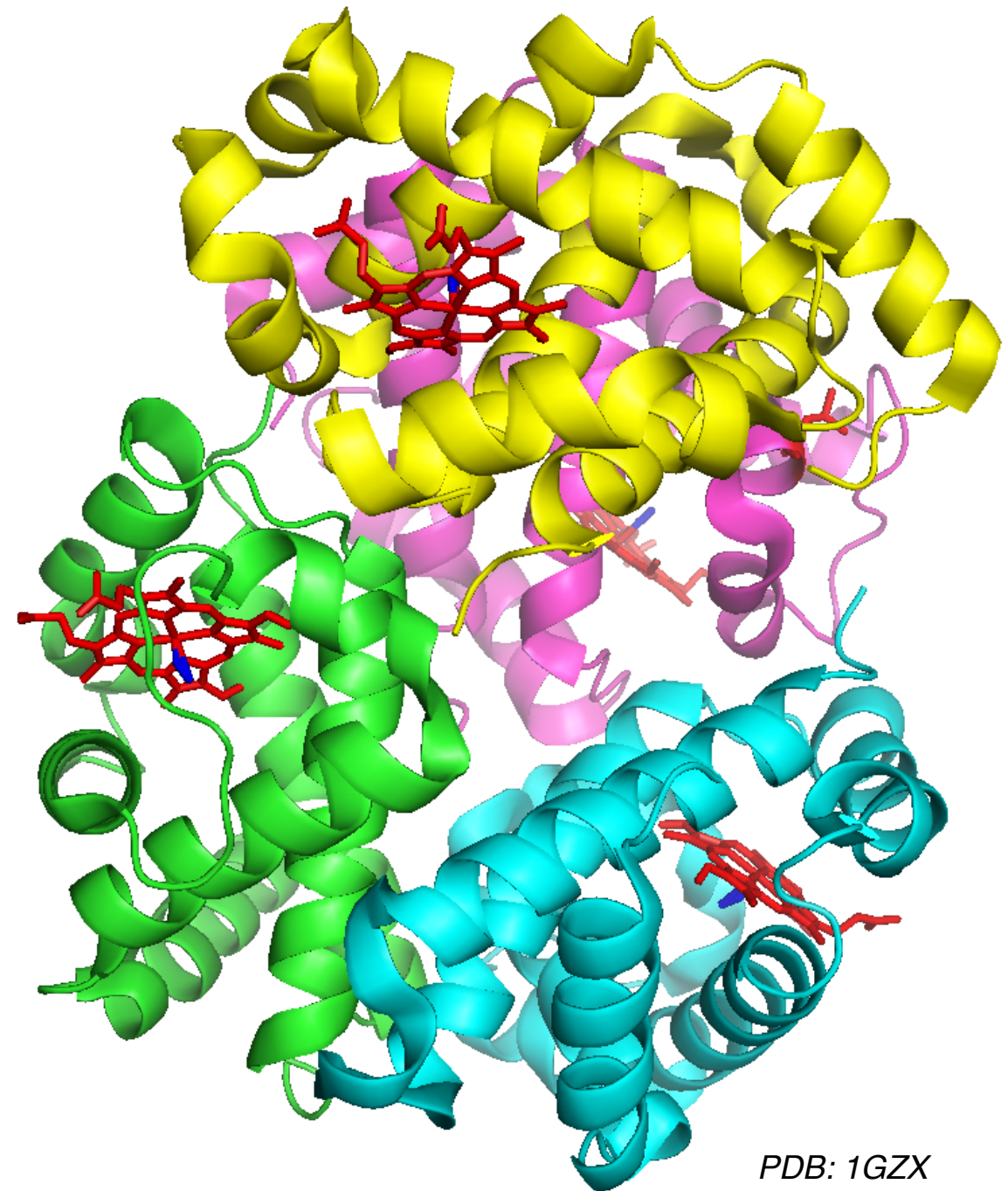


Hemoglobin

Hemoglobin is an oxygen-transport protein. It is a tetramer composed by **two subunits designated α and β** , with stoichiometry $\alpha_2\beta_2$.

The four subunits of hemoglobin sit roughly at the corners of a tetrahedron, facing each other across a cavity at the center of the molecule. **Each of the subunits contains a heme prosthetic group.**

Each individual heme molecule contains one Fe^{2+} atom. The **heme group binds oxygen** while still attached to the hemoglobin monomer.

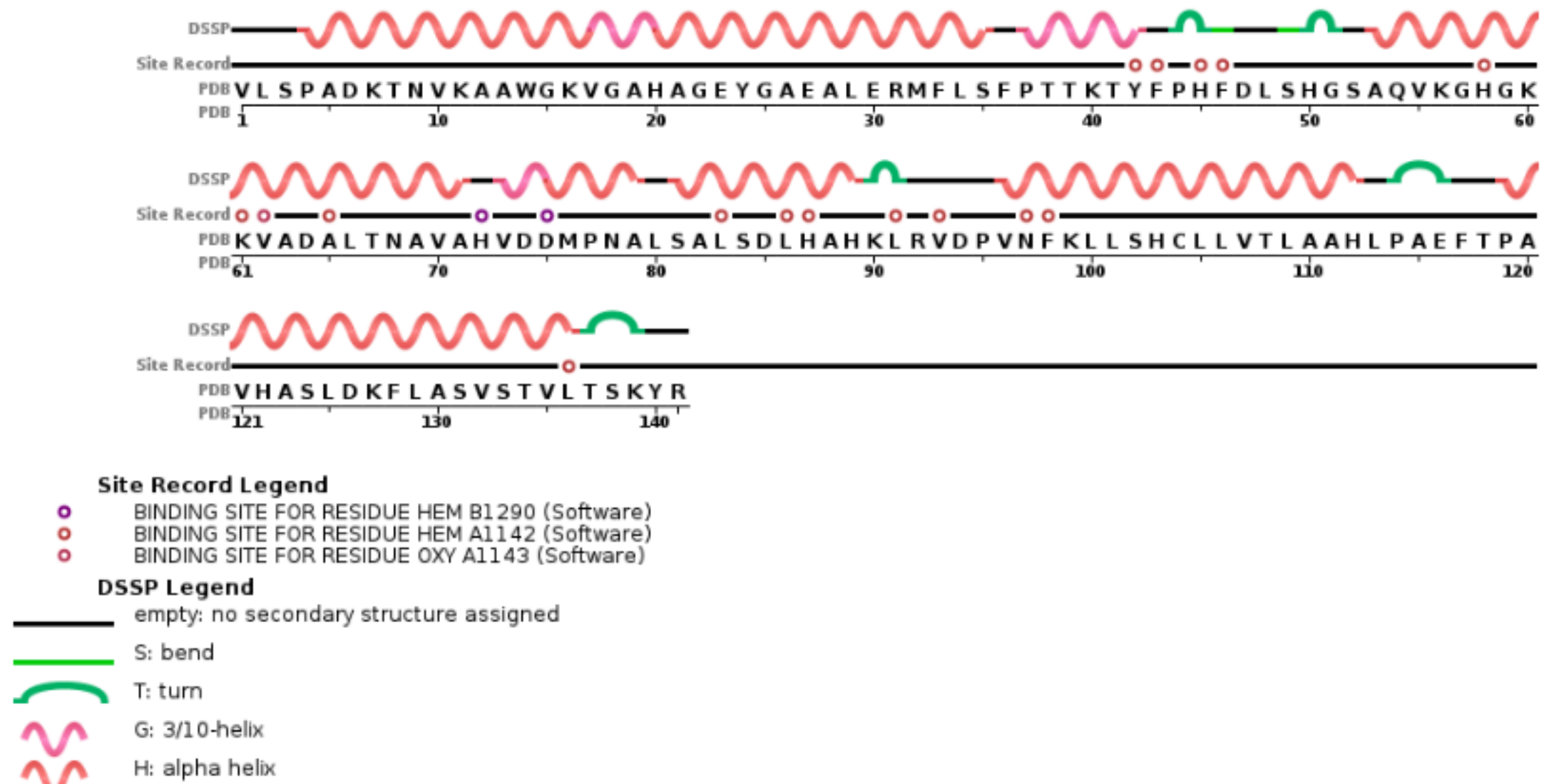


PDB: 1GZX

Subunit Alpha

All-alpha chain A and C of the PDB structure 1GZX composed by 141 residues

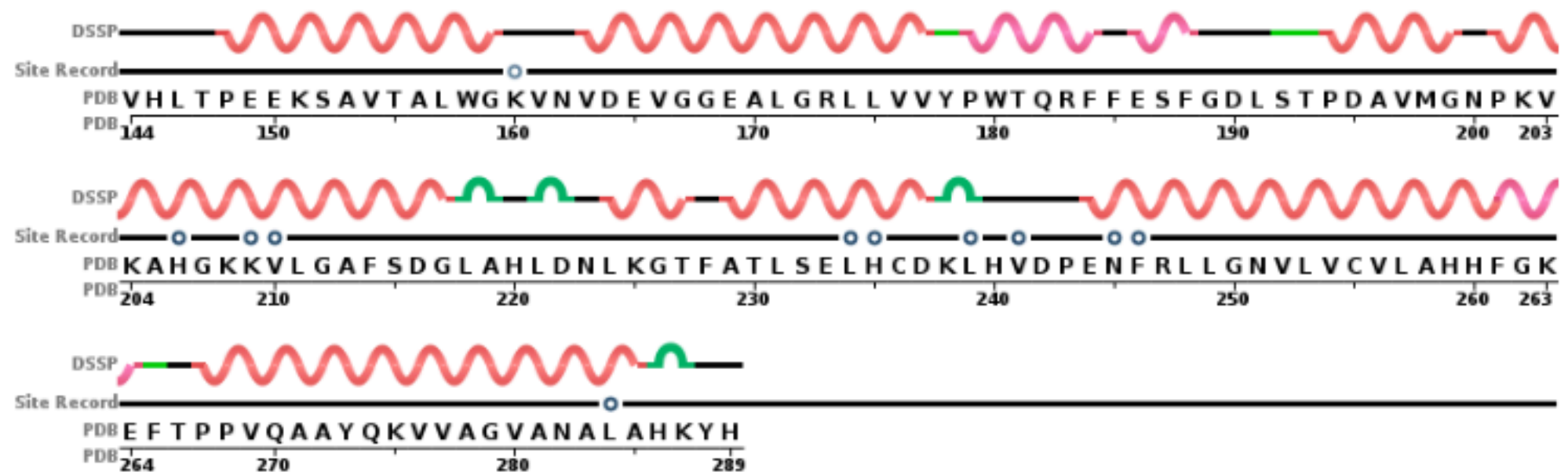
Sequence Chain View



Subunit Beta

All-alpha chain B and D of the PDB structure 1GZX composed by 146 residues






Sequence Chain View



Site Record Legend

- BINDING SITE FOR RESIDUE HEM C1542 (Software)
- BINDING SITE FOR RESIDUE HEM B1290 (Software)

DSSP Legend

- | | |
|---|--|
|  | empty: no secondary structure assigned |
|  | S: bend |
|  | T: turn |
|  | G: 3/10-helix |
|  | H: alpha helix |

Sequence Comparison

The alignment of the two sequences shows that they share ~44% of the residues

```
The best scores are:
HBB_HUMAN 147 bp                                n-w bits E(1)
                                                ( 147) 373 65.3 1.4e-161

>>HBB_HUMAN 147 bp                                (147 aa)
  n-w opt: 373  Z-score: 320.6  bits: 65.3 E(1): 1.4e-161
global/local score: 373; 43.6% identity (74.5% similar) in 149 aa overlap (1-142:1-147)

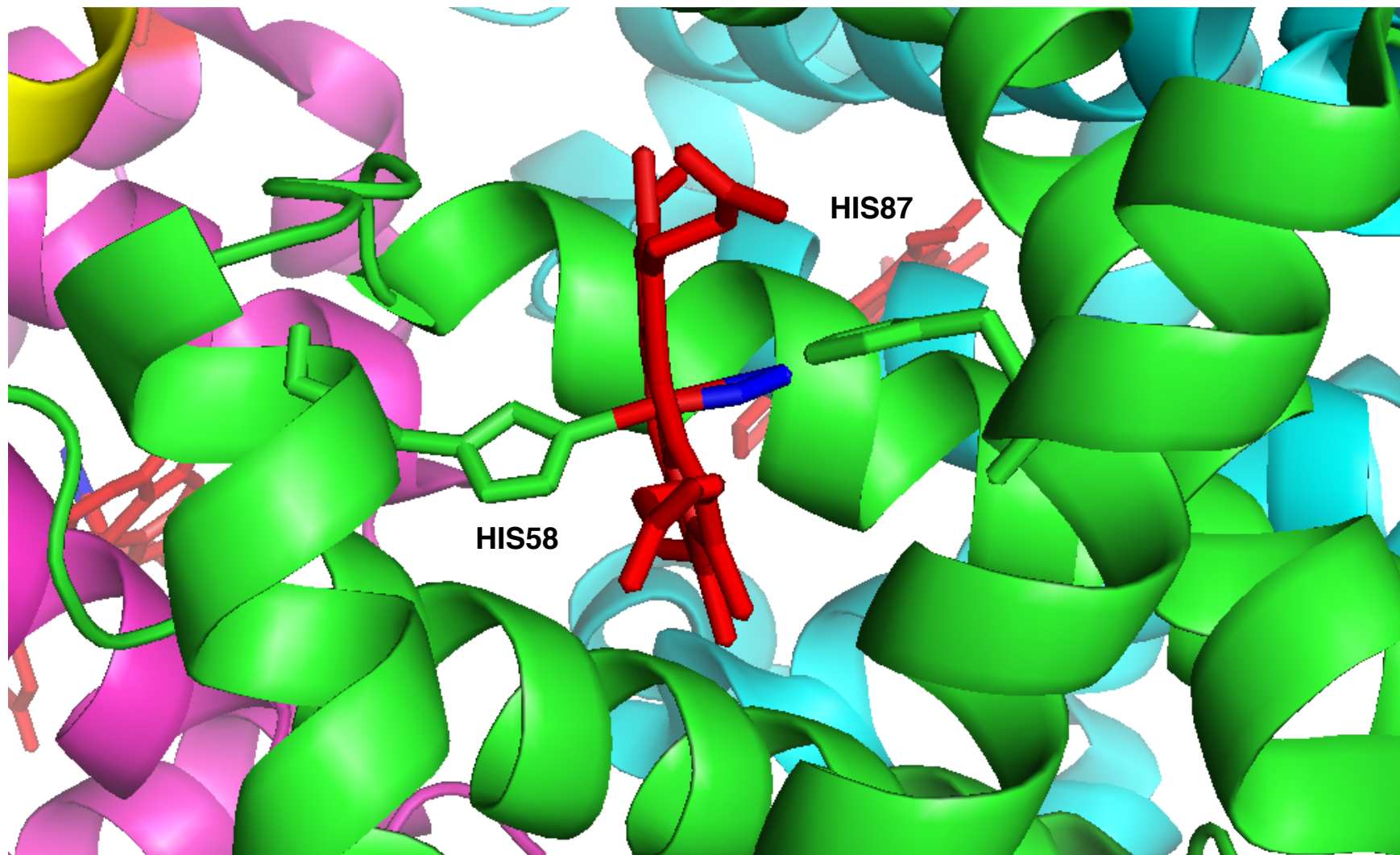
      10      20      30      40      50
HBA_HU MV-LSPADKTNVKAAWGKVGAGHAGEYGAEALERMFLSFPTTKTYFPHF-DLS-----HGS
      :: :: : : : : : : : : : : : : : : : : : : : : : : : : : :
HBB_HU MVHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDVAMGN
      10      20      30      40      50

      60      70      80      90     100     110
HBA_HU AQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAH
      . : : : : : : : : : : : : : : : : : : : : : : : : : : :
HBB_HU PKVKAHGKKVLGAFSDGLAHLNLKGTFFATLSELHCDKLHVDPENFRLLGNVLVCVLAHH
      60      70      80      90     100     110

      120     130     140
HBA_HU LPAEFTPAVHASLDKFLASVSTVLTSKYR
      . : : : : : : : : : : : : : : : : :
HBB_HU FGKEFTPPVQAAYQKVVAGVANALAHKYH
      120     130     140
```


Heme and Oxygen

Anchoring of the heme is facilitated by a **histidine nitrogen that binds to the iron**.
A **second histidine** is near the **bound oxygen**.



Problem 1

Given the PDB structure 1GZX for each one of the monomers:

- Considering a minimum atom distance of 3.5 Å, identify the residues in proximity of the heme and oxygen group.
- Using the same procedure identify the possible interacting residues among the monomers.
- Generate the dssp file of the whole structure and all substructure and calculate the surface of interaction between all the monomers.
- Evaluating the differences in relative solvent accessibility, identify the interacting residues among all the monomers.
- Compare the results obtained for each monomer.