

Project Report

Proteomes Interactomes and Biological Networks

December 5, 2019

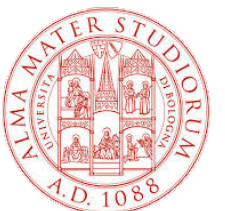
Emidio Capriotti

<http://biofold.org/>



**Biomolecules
Folding and
Disease**

Department of Pharmacy and
Biotechnology (FaBiT)
University of Bologna



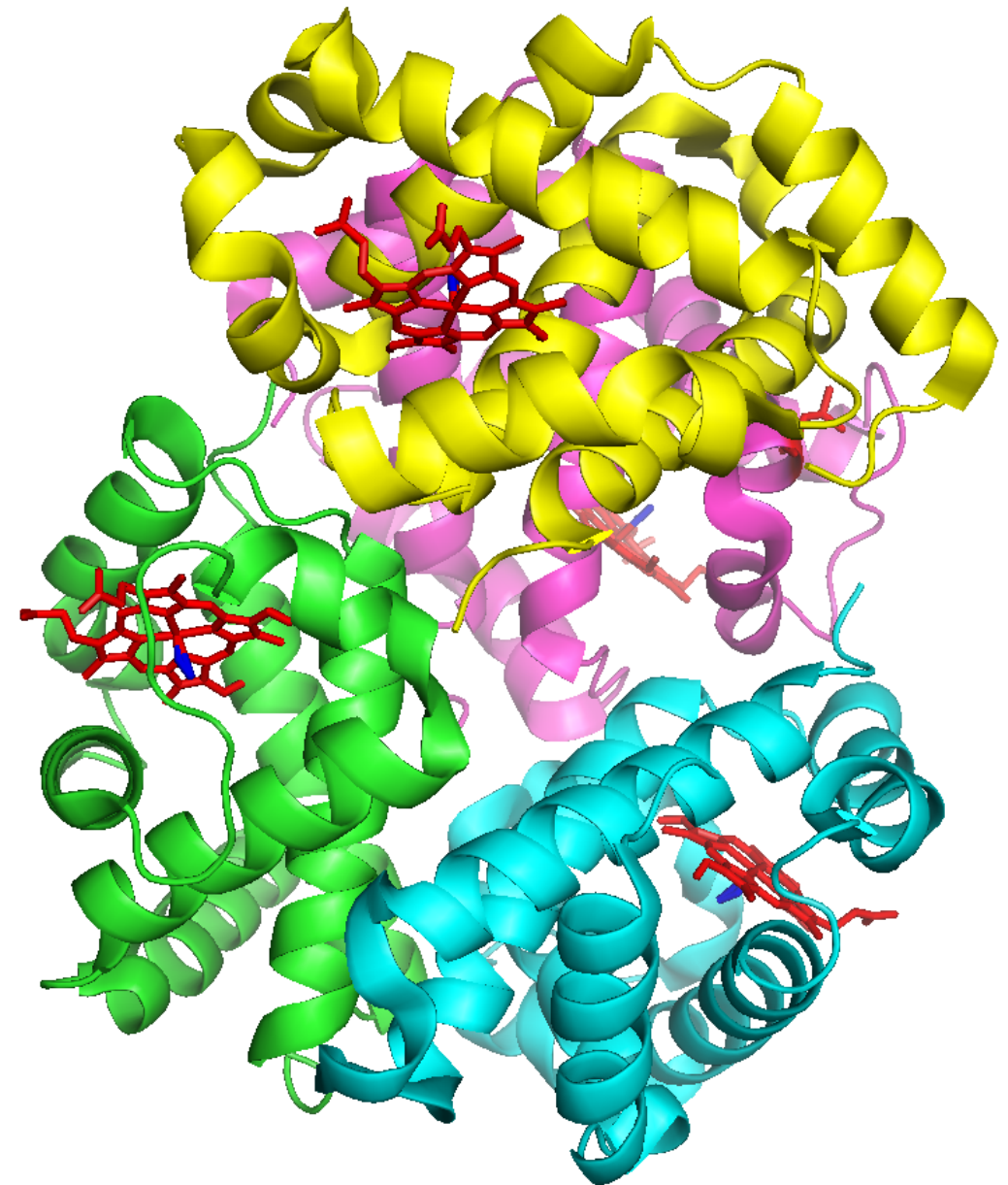
Report Outlines

- Title
- Abstract: Summary of the work
- Introduction: Description of the Hemoglobin function
- Methods: Detailed information about the methodologies used for the analysis
- Results: Quantitative results of the analysis
- Discussion: Short summary of the results
- References: List of articles and web pages
- Supplementary Materials: Information not included in the main report

Introduction

Description of the hemoglobin function and the protein complex

- Oxygen transport
- Tetramer composed by 2 types of monomers (α and β subunits)
- Each monomer interact with a Heme group



Methods

Detailed description of the data and methodologies used for the development of the project.

- **Details about the protein structure** used for the analysis of the Hemoglobin complex (1GZX).
- **Programs** used for the analysis of complex.
- Procedure used for the analysis of the hemoglobin complex: Calculation of the **physical interactions** (heme-monomers and between monomers) and the **surface of interaction** between monomers.

Results (I)

Quantitative results of the analysis divided in two main parts:

- Analysis of the **physical interactions** heme and oxygen groups and monomers and between monomers. What are the atoms and residues below 3.5 Å?

The mean donor-acceptor distances in protein secondary structure elements are close to 3.0 Å. Since many pdb files lack hydrogen atoms, the presence of an **energetically significant hydrogen bond** can be inferred when a probable **donor and acceptor are within 3.5 Å of each other** (https://proteopedia.org/wiki/index.php/Hydrogen_bonds).

The distance between the residues participating in the **salt bridge is less than 4 Å** (https://proteopedia.org/wiki/index.php/Salt_bridges).

Table (I)

Heme - monomer interactions:

Chain	Residue	Hetero	Atoms ($\leq 3.5\text{\AA}$)
A	HIS58	OXY1143	NE2-O2,
	HIS87	HEM1142	NE2-FE,

Interactions between monomers:

Chain1	Residue1	Chain2	Residue2	Atoms ($\leq 3.5\text{\AA}$)
A	ARG141	C	ASP526	NH2-OD2,

Highlights the salt bridges that stabilizes the interactions and show some figures

Results (II)

Quantitative results of the analysis divided in two main parts:

- Analysis of the **surface of interaction** between monomers and the lost of accessibility of the single residues

Calculate the surface of interaction for each pair of chains to calculate which **chains has stronger interaction**.

Determine the possible **interaction hot-spots** considering the **hydrophobic residues** with large value of relative solvent accessibility lost.

Table (II)

Surface of interaction between monomers:

Chain1	Chain2	SA (Å ²)
A	B	994

Lost relative solvent accessibility for each residue

Chain	Residue	RSA(M)	RSA(C)	RSA(M)-RSA(M)
A	LEU34	0.74	0.44	0.31

Show the residues with more than 10% of difference and highlight the hydrophobic residues with high difference

Facultative Problem

Using the protein-protein interaction network from IntAct database:

- Extract the sub network of interactions between human proteins from Uniprot database. (Use “uniprotkb” as a key for the identifiers).
- Calculate the degree, betweenness and clustering coefficient for the α and β subunits of the hemoglobin.
- Identify the proteins with direct interactions and calculate degree, betweenness and clustering coefficient for the interacting proteins.