

INTRODUCTION TO PROTEINS

Andrea Giansanti

Dipartimento di Fisica, Sapienza Università di Roma

Andrea.Giansanti@roma1.infn.it

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DIPARTIMENTO DI FISICA



SAPIENZA
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- SEQUENCE->STRUCTURE/UNSTRUCTURE->DYNAMICS-FUNCTIONS

JOURNALS

PROTEINS

PROTEIN SCIENCE

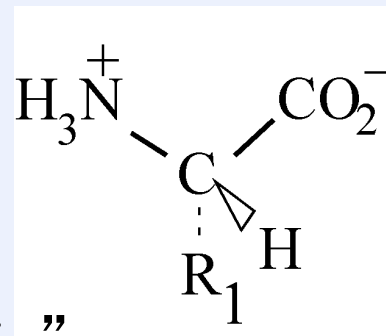
JOURNAL OF MOLECULAE BIOLOGY

Proteopedia https://proteopedia.org/wiki/index.php/Main_Page

Proteins

- From the Greek “proteios” meaning “of first importance”
- The basic building blocks of almost all living organisms
- Constitute the majority of the cell (see biology by numbers), and perform nearly all enzymatic activities
- Composed of 20 naturally occurring amino-acids

varying moiety
called “side chain”



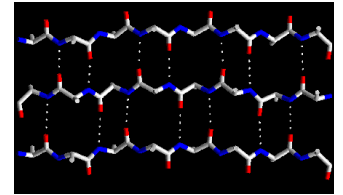
Hierarchy of Protein Structure

Primary 1°

AKSDQPWFAGLE

Linear chain made of 20 possible amino acids

Secondary 2°



Alpha-helices, beta-sheets, turns

Tertiary 3°



Motifs, domains

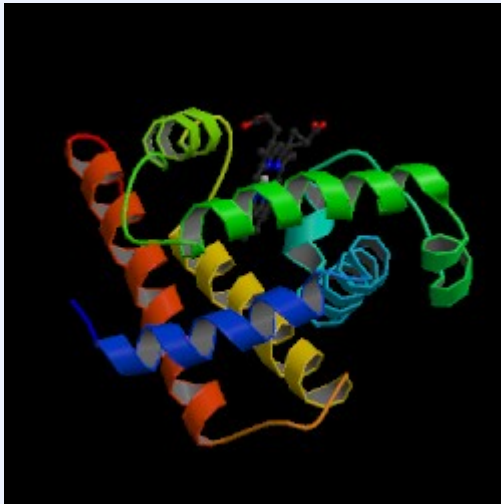
Quaternary 4°



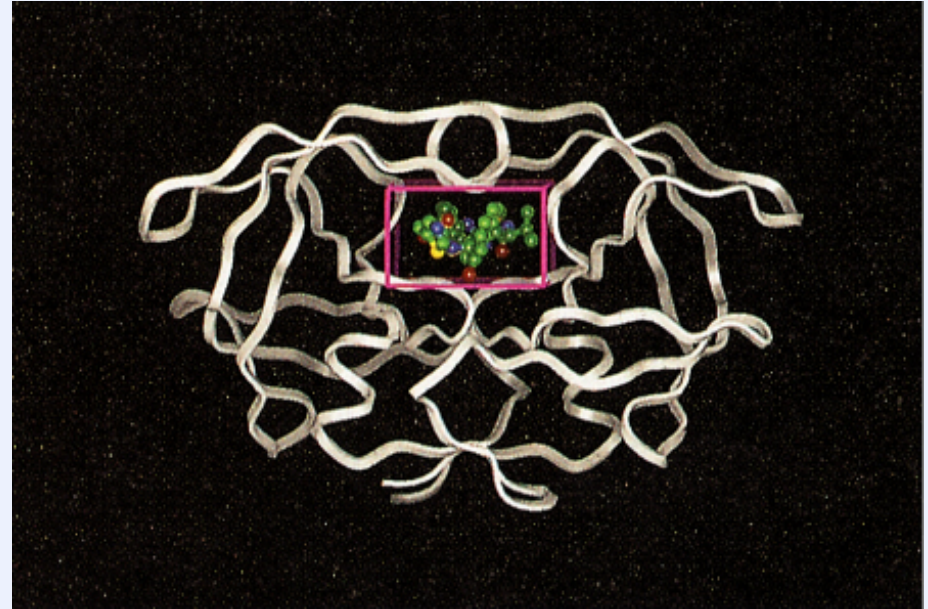
Oligomers, complexes

Structure/Unstructure

is quite basic in protein science



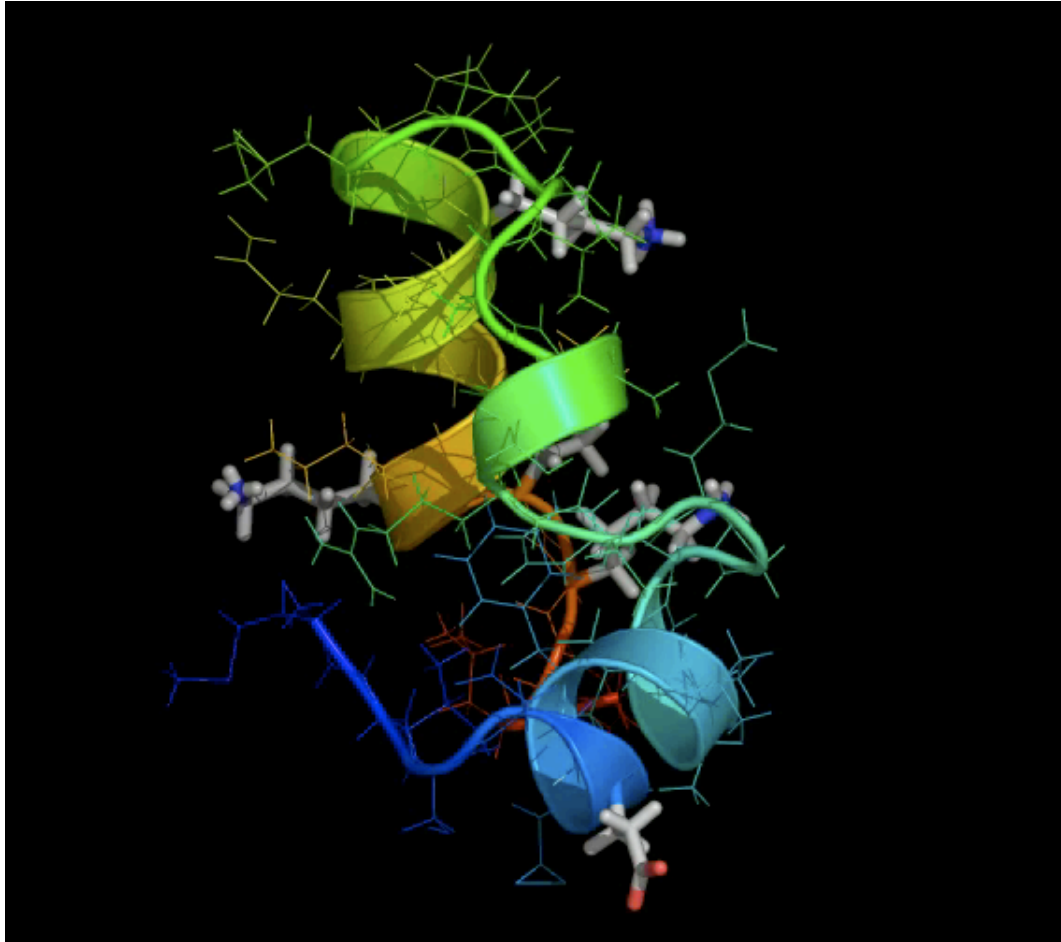
Myoglobin (1958) x-ray structure M.F. Perutz



Viral proteases are targets of the molecular design of inhibitor drugs such as Ritonavir, capable of blocking the active site of the enzyme and to contribute to the containment of HIV epidemics.

The Protein Data Bank (www.pdb.org)





Sequence->Structure->Function
 Sequence->Function-> Structure
 AND/OR DYNAMICS

Pioneers:

H. Frauenfelder, G. Careri,
 G. Weber, (early seventies)
 M. Karplus (1977)

Early review

[Nature. 1990 Oct 18;347\(6294\):631-9.](#)

[Molecular dynamics simulations in biology.](#)

[Karplus M, Petsko GA..](#)

Molecular dynamics--the science of simulating the motions of a system of particles--applied to biological macromolecules gives the fluctuations in the relative positions of the atoms in a protein or in DNA as a function of time. Knowledge of these motions provides insights into biological phenomena such as the role of flexibility in ligand binding and the rapid solvation of the electron transfer state in photosynthesis. Molecular dynamics is also being used to determine protein structures from NMR, to refine protein X-ray crystal structures faster from poorer starting models, and to calculate the free energy changes resulting from mutations in proteins.

Domain Boundaries, Reliability of
Present Methods and Promising
Avenues, Suggested Reading

Problem 3 Function Prediction
Introduction to the Problem, The
Definition of Biological Function,
The Function Vocabulary, Protein
Names, Text Mining, Transferring
Functional Annotations by
Similarity, Transcriptomics,
Proteomics, Promising Avenues,
Suggested Reading

Problem 4 Protein Structure
Prediction
Introduction to the Problem,
Energetic Calculations of Protein
Structures (Energy Calculation,

Water forms a hydration shell around proteins.

*The properties of this bound water are
still the subject of many experimental
and theoretical investigations.*