Bornberglab
Molecular Evolution and Bioinformatics

Masters thesis project

Evolution of Globular Proteins in Early Biology

Identification of Ancient Oligopeptide Repeats

Background: 50 years ago Dayhoff proposed that modern globular proteins evolved from spontaneously formed short peptides which then organized into complexes that could then be joined to form early proteins at the origin of life (see figure).

Objectives: The project will involve identification and formal characterization of fossil oligopepetide repeats in a family of ancient proteins. Additionally, the changes that occurred to the repeats will be formally analyzed

Requirements:

- Adequate completion and grades in Biochemistry and/or Biotechnology courses
- Interest in or ability to write computer code
- Interest in protein structure, evolution, and/or enzyme function

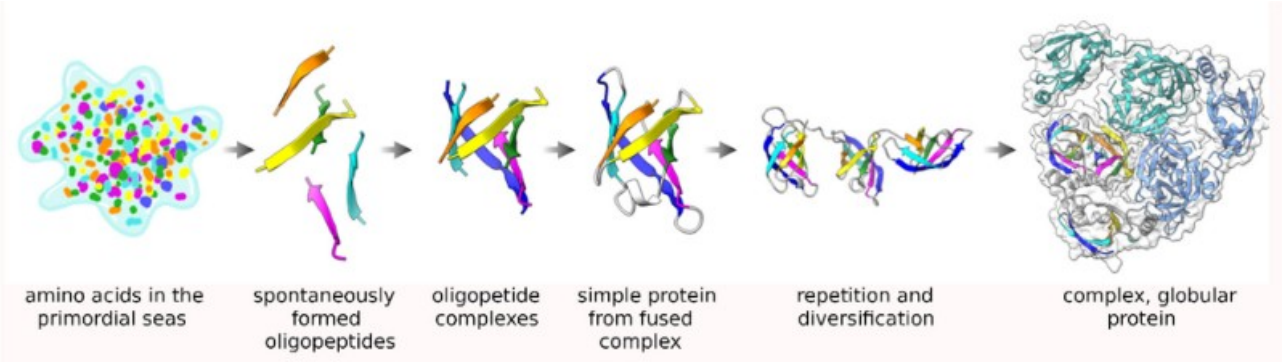

Figure 1: Dayhoff's hypothesis for the evolution of early proteins from non-living materials

Methods:

- Bioinformatic sequence and statistical analysis (*i.e.* MSA, dot plots, *etc.*)
- Protein structure visualization and analysis software (*i.e.* PyMol, DSSP, etc.)

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Molecular Evolution and Bioinformatics group (http://bornberglab.org/)

Selected Literature:

1) Eck, R.V., Dayhoff, M.O. "Evolution of the Structure of Ferredoxin Based on Living Relics of Primitive Amino Acid Sequences" Science **152,** 363 (1966)
2) Romero, M.I.R., Rabin, A., Tawfik, D. S., "Functional Proteins from Short Peptides: Dayhoff's Hypothesis Turns 50" Angew. Chem. Int. Ed. **55,** 15966 (2016)