Molecular Evolution and Bioinformatics



## **Bachelor thesis project**

# **Analysis of Protein Repeats**

# Evolution of Cryptic Oligo-peptide Repeats

**Background:** Oligo-peptide repeats are short (20-50 residues) stretches of highly conserved sequence found in multiple copies within a single peptide chain. About 25-35% of all proteins contain oligo-peptide repeats although many of these have gone unnoticed, even in proteins with known structures. We have identified thousands of clusters of proteins that contain these cryptic oligo-peptide repeats.

**Objectives:** The student will focus on one of these clusters, studying, analyzing, and categorizing one of these repeat clusters. The repeat will be formally defined and its evolutionary relationship to other proteins will be determined.

### **Requirements:**

- Adequate completed coursework and interest in biochemistrz
- Adequate completed coursework and interest in math and statistics
- Programming skills in one or more languages (*e.g.* R, Python, C++, FORTRAN, etc.)

### Methods:

- Creation of multiple sequence alignments
- Statistical analysis of protein sequence features

**Figure 1:** Examples of oligo-peptide repeat proteins. Each repeat unit is colored individually for easy recogniton.







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#### **Selected Literature:**

- 1) Schuler, A., Bornberg-Bauer, E. "Evolution of Protein Domain Repeats in Metazoa" *Mol. Biol. Evol.* **33,** 3170 (2016)
- 2) Kajava, A.V. "Tandem repeats in proteins: from sequence to structure" *J. Struct. Biol.* **179,** 279 (2012)
- 3) Merski, M. et al. "Self-analysis of repeat proteins reveals evolutionary conserved patterns" *BMC Bioinformatics* **21,** 179 (2020)