

Project 9.2. Lysine deserts as a universal mechanism to escape premature proteins degradation

Supervisor: dr hab. Wojciech Pokrzywa

Institute: International Institute of Molecular and Cell Biology in Warsaw

Laboratory: Laboratory of Protein Metabolism in Development and Aging

WWW:<https://www.iimcb.gov.pl/en/research/laboratories/31-laboratory-of-protein-metabolism-in-development-and-aging-pokrzywa-laboratory>

Background:

Eukaryotic cells use degradation systems such as the ubiquitin-proteasome (UPS) system to remove unwanted proteins. UPS mediates proteolysis by attaching the small protein ubiquitin to the target protein, using a cascade of enzymes in a process called ubiquitination. Ubiquitin is attached primarily to a specific amino acid in the target protein - lysine. Recent studies have shown that the yeast protein Slx5 avoids UPS due to the extensive, lysine-free region in the so-called lysine desert. Such a lysine desert may be a part of the uncharacterized strategy used by proteins to avoid premature degradation. As a result of our initial analyzes, we found various lysine deserts among the proteins of both simple and complex organisms. Many of these proteins are associated with the UPS, suggesting a protective mechanism against self-determination for degradation. However, we have also found lysine deserts in proteins involved in fundamental cellular processes such as transcription.

Aim:

The overall objective of these studies is to understand the common occurrence of proteins with lysine deserts using evolutionary and structural bioinformatics analyzes supported by experimental methods. The theoretical part will consist of a quantitative analysis of the evolutionary preservation of lysine deserts in a number of taxonomic groups, followed by a qualitative analysis of their biological functions. Selected proteins will also be analyzed via molecular simulations to understand the dynamics of lysine desert exposure under selected conditions. The most promising candidates obtained from bioinformatics analyzes will be subjected to experimental tests using human cell lines and animal model *Caenorhabditis elegans*.

Requirements:

- Master's degree in biological sciences/bioinformatics
- experience in programming (Python/R), omics data analysis and cluster computing
- knowledge of biological databases, biochemistry, molecular biology, evolutionary and structural bioinformatics of proteins
- fluency in English
- strong motivation for scientific work (documented internships and apprenticeships in scientific institutes)
- ability to organize working time independently
- systematic work
- experience in molecular modeling and/or laboratory work/*C. elegans* maintenance is an advantage