PhD student

The Institute of Biochemistry and Biophysics PAS is looking for a PhD student for 28 months to develop methods and functional analyses in the project „LCRPlatform: new algorithms and methods for the comprehensive identification, categorization, and annotation of protein low complexity regions" funded by National Science Centre.

Low complexity regions (LCRs) are protein fragments with a low diversity of amino acids. Although about 14% of proteins contain such fragments, for many years low complexity regions were ignored by the scientific community and treated as non-functional parts of a proteome. While the function of most LCRs is still a mystery, recent evidences suggest that LCRs often play important roles in structure stability preservation, protein-RNA interactions, phase separation, adhesion, transduction of conformational information, membrane interactions, DNA binding, the binding of metals by cysteine, histidine, or charge clusters, in driving the formation of membraneless organelles through phase separation and some other processes. LCRs are also directly involved in the development of various diseases including neurodegenerative diseases and cancer.

Here we propose a first effort to systematically predict LCR functions. This relies on the development of new algorithms for finding and clustering similar LCRs that take into account different characteristics of low complexity protein sequences. Specifically, we will develop novel methods specializing in these different and complementary aspects of LCRs, such as homorepeats, short-tandem repeats or fused LCRs. A new LCR database will collect the analysis results for an integrated prediction of LCR function.

Scope of work:

- Data preparation: proteomic data aquisition, parsing, unification.
- Programme writing: development of the MotifLCR tool and LCRPlatform.
- Data characteristics: write scripts and compute the protein/cluster characteristics, perform literature and domain databases searches.
- Data integration: build a framework for data integration.

Keywords:

- Low complexity regions,
- compositionally biased regions,
- protein functions,
- programming,
- databases,
- bioinformatics

Qualifications:

- Scripting.
- Biological databases and data formats.
- Programming.
- Protein analyses.

- Functional analysis of protein data (in silico).
- Evolutionary biology.
- Very good knowledge in the field of low complexity regions of proteins.
- Very good knowledge in the field of non-globular protein science.
- Good knowledge of the English language

NCN call for proposals type: OPUS – ST

Deadline for submitting offers: September 17, 2021, 23:59

The form of submitting offers: email

Required documents:

- CV
- Motivation letter with justification of the matching to the project
- Copy of masters' degree diploma
- Letter of support from the master thesis supervisor
- a declaration of consent to the processing of personal data

Starting work from: October 01,2021

The conditions of employment: scholarship in the amount of PLN 3 420,00 gross / month

Additional information:

Applications should be sent by e-mail to the project manager: prof. dr hab. Marcin Grynberg, **greenb@ibb.waw.pl**.

Selected candidates will be invited to an interview, which will be held on September 21-22 at the Institute of Biochemistry and Biophysics of the Polish Academy of Sciences in Warsaw or remotely via the Internet messenger, depending on the epidemiological situation.