Announcement of post-doc scholarship at the Department of Clinical Sciences, division of infection medicine

Post-doctoral position in computational antibody optimization and peptide inhibitor design

We are seeking a highly motivated postdoctoral scientist to join the epIgG project, a cross-disciplinary collaboration between five labs from Sweden and Switzerland. The epIgG project aims at finding and characterizing IgG antibodies that interfere with pathogenic bacteria's ability to interact with host proteins. The molecular interactions between pathogens and their hosts are critical to the infection process and knowledge gained in this project will contribute to the resolution of the looming antimicrobial resistance crisis. As a member of this group, the post holder will gain access to an important scientific network with state-of-the-art technologies and will regularly interact with PIs, postdocs and graduate students from the member groups.

This specific postdoctoral research project will involve the identification, characterization and optimization of antigen-specific IgG antibodies by quantitative mass spectrometry and structural bioinformatics using primarily OpenMS and the Rosetta Macromolecular Modeling Software suite respectively. High-affinity antibodies will be expressed and characterized by protein docking followed by chemical crosslinking mass spectrometry, thereby identifying the epitope and the interaction conformation. This information is then used to optimize the binding affinity using computational protein design and evaluated using competition assays followed by quantitative mass spectrometry. Once key epitopes are determined, the postdoc will use computational peptide design design to predict inhibitors capable of disrupting the interaction between the bacterial and human protein. This knowledge will facilitate the improvement of therapies based on the humoral immune response, such as intravenous pooled polyclonal IgG (IVIG) therapy of sepsis or vaccination strategies.

Project description
The primary goal involved in the post-doctoral position is to conduct research and bring molecular modeling and protein design expertise to the epIgG group. More
specifically, the goals include developing a computational workflow to extract antibody peptide sequences from high-resolution mass spectrometry data and assemble these peptides to obtain the full antibody sequence. To assist the assembly, you will first build an antibody scaffold from known antibody structures and antibody sequences. Further, you will use Rosetta to redesign the naturally occurring antibodies for higher affinity and better expression. The post holder will collaborate closely with mass spectrometrists and immunologist to accomplish this task. To increase your chances in a future academic career as well as contribute to the group, you are expected to actively seek external funding. While the candidate is expected to focus on the computational aspects of this project, if interested, the opportunity will also be given to gain laboratory experience, assisting with experiments and measurements.

Reference number: V 2017/721

Scholarship period: The scholarship covers a period of 6 months with possibility of prolongation up to a maximum of 24 months in total.

Preliminary start date: Fall 2017

Supervisor/contact person: Lars Malmström, lars.malmstrom@med.lu.se, Johan Malmström, +46-768998232, johan.malmstrom@med.lu.se

Qualifications

- To be eligible for a post-doc scholarship at Lund University the recipient must hold a PhD degree within a relevant field. The PhD degree must not be from Lund University. The PhD degree must not be older than three year. The applicant must not have been employed at Lund University in the past two years.

Candidates should preferably have working experience in the following subjects:

- Ph.D. in Computational Biology, Computer Science or similar
- Programming languages such as Python and C++
- Protein design and structure modeling
- Statistics
- Good oral and written proficiency in English.

Additional skills that are strongly meriting:

- Experience with Rosetta Molecular Modeling Suite (rosettacommons.org)
- Experience with OpenMS
- Experience with Protein Design
Written application, including reference number, is to be sent via e-mail to the supervisor and must include the following:

- CV
- Personal letter stating the reasons why the study suits the applicant (maximum one page)
- List of publications
- References (2)
- Copy of the PhD diploma

Application deadline: 2017-10-17

Information regarding scholarships at Lund University

- The scholarship sum is paid out quarterly
- A scholarship awarded will be reviewed every six months
- Scholarships are tax-exempt
- Scholarships do not give rise to sickness benefits, compensation from the Social Insurance Office or retirement pension.
- A scholarship holder cannot be hired after the scholarship period due to tax reasons.

References:

1. Rosenberger, George; Liu, Yansheng; Rost, Hannes; Ludwig, Christina; Buil, Alfonso; Bensimon, Ariel; Soste, Martin; Spector, Tim; Dermitzakis, Emmanouil; Collins, Ben; Malmstrom, Lars; Aebersold, Ruedi; Inference and quantification of peptidoforms in large sample cohorts by SWATH-MS. Nat Biotechnol (2017)


4. Rost, Hannes; Liu, Yansheng; DAgostino, Giuseppe; Zanella, Matteo; Navarro, Pedro; Rosenberger, George; Collins, Ben; Gillet, Ludovic; Testa, Giuseppe; Malmstrom, Lars; Aebersold, Ruedi; TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. Nat Methods (2016)

5. Rost, Hannes; Rosenberger, George; Navarro, Pedro; Gillet, Ludovic; Miladinovic, Sasa; Schubert, Olga; Wolski, Witold; Collins, Ben; Malmstrom, Johan; Malmstrom, Lars; Aebersold, Ruedi; OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. Nat Biotechnol (2014)

7. Herzog, Franz; Kahraman, Abdullah; Boehringer, Daniel; Mak, Raymond; Bracher, Andreas; Walzthoeni, Thomas; Leitner, Alexander; Beck, Martin; Hartl, Franz-Ulrich; Ban, Nenad; Malmstrom, Lars; Aebersold, Ruedi; Structural probing of a protein phosphatase 2A network by chemical cross-linking and mass spectrometry. *Science* (2012)