Scientist, Modelling & Simulations

Zymeworks is a clinical-stage biopharmaceutical company dedicated to the discovery, development and commercialization of next-generation bispecific and multifunctional biotherapeutics, initially focused on the treatment of cancer. Zymeworks' suite of complementary therapeutic platforms and its fully-integrated drug development engine provide the flexibility and compatibility to precisely engineer and develop highly-differentiated product candidates.

About the Position

We are seeking a scientist interested in building a comprehensive computational protein modeling and data analytics platform for use in biologics engineering and drug discovery. At Zymeworks, scientists own the entire computational method development process, from devising the algorithms, through coding the implementation, to direct application in drug development. The successful candidate may be hired at a junior or senior level depending on experience.

This position will report to our Modelling & Simulations Group Lead and is based in our Vancouver, BC location.

Responsibilities

- Develops and applies protein engineering and design algorithms
- Develops, validates, and documents software that implements protein modelling and optimization methods
- Develops and applies data analysis, data mining, and machine learning methods for protein engineering
- Works closely with the software engineering team to meet software quality requirements
- Collaborates with protein engineering and therapeutic development teams to effectively apply protein engineering and data analysis software for lead optimization
- Collaborates with external industrial and academic partners
- Participates in the preparation of patents and publications

Required Qualifications

- A Ph.D. in Physics, Chemistry, Applied Math, Computer Science or a related field and a minimum of 4 years' post-graduate experience developing and implementing protein modeling algorithms
- Method development experience in any of the following areas: Fragment assembly, homology modeling, or other protein structure prediction techniques, force field/potential development, protein structure optimization, molecular dynamics/Monte Carlo simulation, antibody modeling
- Highly motivated with an exceptional interest in the development and application of modeling, data mining, and simulation methods for biologics engineering and drug discovery
- Proficient in at least one of C, C++, Java, or Fortran, and proficient in a scripting language (eg

Python, Perl, Ruby)
- Fluent in written and spoken English

Desirable Qualifications:

- Experience optimizing numerically intensive code
- Protein bioinformatics experience, including but not limited to: Prediction of protein properties from sequence data, Extraction of residue co-evolution data from sequence data, Binding target prediction/identification from sequence data
- Experience implementing and applying machine learning methods to protein modeling problems. Areas of interest include: clustering methods and other unsupervised learning techniques (eg SOMs, kernel PCA, ICA), regression and classification methods (eg random forests, Gaussian process regression, GBMs)
- Experience handling and analyzing high-throughput proteomic and genomic data

Why Work for Us?

Zymeworks' employees are passionate, engaged and extremely motivated to succeed. We are excited by the cutting-edge science and technology, the endless possibilities this union holds and the sheer opportunity to be a part of something big. To learn more about Zymeworks Inc. and our current openings, please visit our website at www.zymeworks.com.

We offer challenging career opportunities, competitive benefits and an environment that recognizes and rewards performance.

How to Apply

If you're interested in this challenging opportunity, please apply online at https://zymeworks.bamboohr.co.uk/jobs/view.php?id=71. Due to the high volume of applicants, only those selected for interviews will be contacted.