MINGZHAO LIU

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SUMMARY OF SKILLS

Programming knowledge in **C**, **C#**, **C++**, **Java**, **Python**, **Perl**, **SQL**, **MongoDB**, **HTML**, **JavaScript**, **LISP**, **Prolog**, **PHP** and **R**

Experienced in working with **Rosetta** protein modeling suite

Experienced in working in **GxP**, and **FDA regulated** environments

Experienced in working with **Git, SVN,** and **Mercurial** version control systems

Experienced in working in **Windows** and **Unix** environments

Effective presenter, communicator, writer, and public speaker

Efficient at coordinating across multiple groups for requirements

Strong independent and autodidactic worker

EDUCATION

Ramapo College of New Jersey – Mahwah, NJ

Bachelor of Science: Bioinformatics, May 2016, *Magna cum laude*

Bachelor of Science: Computer Science, May 2016, *Magna cum laude*

WORK EXPERIENCE

Pfizer Inc. - Pearl River, NY

Senior System Analyst, Research Informatics, Dec. 2018– Current

System Analyst, Research Informatics, Jan. 2017 – Dec 2018

Support Vaccines R&D laboratories by through developing, supporting, and validating applications

- Develop and design systems to manage, analyze, and report laboratory data in our Laboratory Information Management System (LIMS)
- Create and provide ad hoc reports in Oracle Database using **SQL**
- Perform benchmarks on system performance and follow up to optimize problematic processes
- Design and create tools to visualize and prioritize the Research Informatics support ticket queue using **Java** and **JavaScript**, with rapid prototyping using **PHP**
- Coordinating multiple laboratory groups to gather requirements for new assay systems
- Provide end user support for clients using Research Informatics systems
- Validate and document newly deployed/changed/upgraded systems and environments

RESEARCH EXPERIENCE

A Bioinformatic Approach to Investigate a Relationship between Cis-Regulatory U-Rich and G-quadruplex Motifs Involved in Mammalian Polyadenlation

School of Theoretical and Applied Sciences – Ramapo College of New Jersey

Undergraduate Researcher, Jan. 2014 – July 2016

Developed genome-wide analysis tools using **Java**, **JavaScript**, **C++**, and **Python**

- Web service with a **C++** backend and **Python** database access, on a **Node.js** webserver
- Performed programmatic alignments of sequence data using Needleman-Wunsch algorithm
- Extracted and stored nucleic acid sequence data and annotations using **MongoDB**
- Presented research project at Student Research Symposium, MACUB conference, and RNA Conference 2016

Marburg Virus Antibody Modeling using Comparative Modeling

Center for Structural Biology – Vanderbilt University & RosettaCommons

Developer of Rosetta, powerful macromolecule structure prediction and design software

Research Intern, May. 2015 – Aug. 2015

NSF funded research internship through RosettaCommons

- Trained to understand Rosetta protein modeling suite and develop algorithms for protein folding
- Developed a protocol for efficient large scale comparative modeling of antibodies
- Accesses underlying Rosetta **C++**functions for modeling, **XML** for input of user parameters
- Integration with PyMOL using **Python**
- Increased automation using **Perl** and **Bash** scripts
- Benchmarked the efficacy of comparative modeling techniques
- Presented Research at RosettaCON