





RESEARCH EXPERIENCE FOR UNDERGRADUATES

A Cyberlinked Program in Computational Biomolecular Structure & Design

Interns in this geographically-distributed REU program participate in research using the Rosetta Commons software. The Rosetta Commons software suite includes algorithms for computational modeling and analysis of protein structures. It has enabled notable scientific advances in computational biology.







- + Learn the inner details of PyRosetta and the community coding environment
- + Perform research in a molecular modeling and design laboratory, developing new algorithms and discovering new science
- + Receive mentoring from faculty and graduate students

The Program:

- * One week of Rosetta Code School
- * Eight weeks of hands-on research
- * One week at the Rosetta Conferenceto close the summer. *NSF covers housing, travel expenses, and a stipend.

Apply at rosettacommons.org/about/intern Questions? Email Camille Mathis at cmathis@jhu.edu

* The program will be offered virtually in the event of a resurgence of COVID-19

ROSETTA COMMONS SUMMER 2021 INTERNSHIPS Correia Lab École Polytechnique Fédérale de Lausanne Lausanne, Switzerland Deciphering protein surface fingerprints for functional prediction and design Furman Lab Hebrew University Jerusalem, Israel How do post-translational modifications change the communication of a protein with its partners? Baker Lab University of Washington Seattle, WA Designing new protein switches for synthetic biology applications Gront Lab University of Warsaw Warsaw, Poland Rosetta on the Web: Homology Modelling and other applications Kellogg & Zanghellini Cornell University Ithaca, NY Design of novel transposases for scarless DNA-insertion using Roset Khare lab Rutgers University New Brunswick, NJ Designing stimulus-respo Karanicolas Lab Fox Chase Cancer Center Philadelphia, PA Designing small-molecules that brea down cancer-driving proteins Siegel Lab University of California, Davis enzymes for targeted chemotherapy Computational enzyme design Rocklin Lab Northwestern University Chicago, IL pplying high-throughput experi-ental data to guide computational protein design Boston, MA Whitehead Lab University of Colorado, Boulder Crowdsourcing protein folding and design oteins targeting infectious diseases and cancers Kortemme Lab UCSF San Francisco, CA Computational design of proteins with tunable and controllable geometries Lindert Lab Gray Lab Johns Hopkins University Baltimore, MD Antibody engineering by deep learning Ohio State University Columbus, OH Structure Modeling using Mass Spec Data Kuhlman Lab University of North Carolina, Chapel Hill Chapel Hill, NC Design of Dengue Virus Subunit Vaccine Mills Lab Arizona State University Tempe AZ Computational design of proteins containing functional non-canonical Jha Lab @ Los Alamos National Laboratory Las Alamos, NM Protein design for small molecule sensing

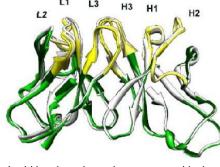
oping Educational Biochemistry Puzzles in Foldit

The Rosetta software has made scientific advances in computational biology, including:

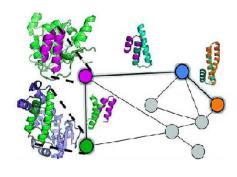
- · de novo protein design
- · drug design
- · materials design
- structure prediction of biological macromolecules and macromolecular complexes

The Rosetta Community Goals:

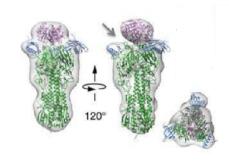
- understand marcromlecular interactions
- design custom molecules
- · develop efficient ways to search conformation and sequence space
- find broadly useful energy functions for various biomolecular representations
- treat diseases and create new molecular technologies



Antibody structures predicted de novo with sub-angstrom loop conformations.



Design of proteins by "sewing" to recombine substructures.



Design of a hemagglutininbinding trimer that protects against the flυ.