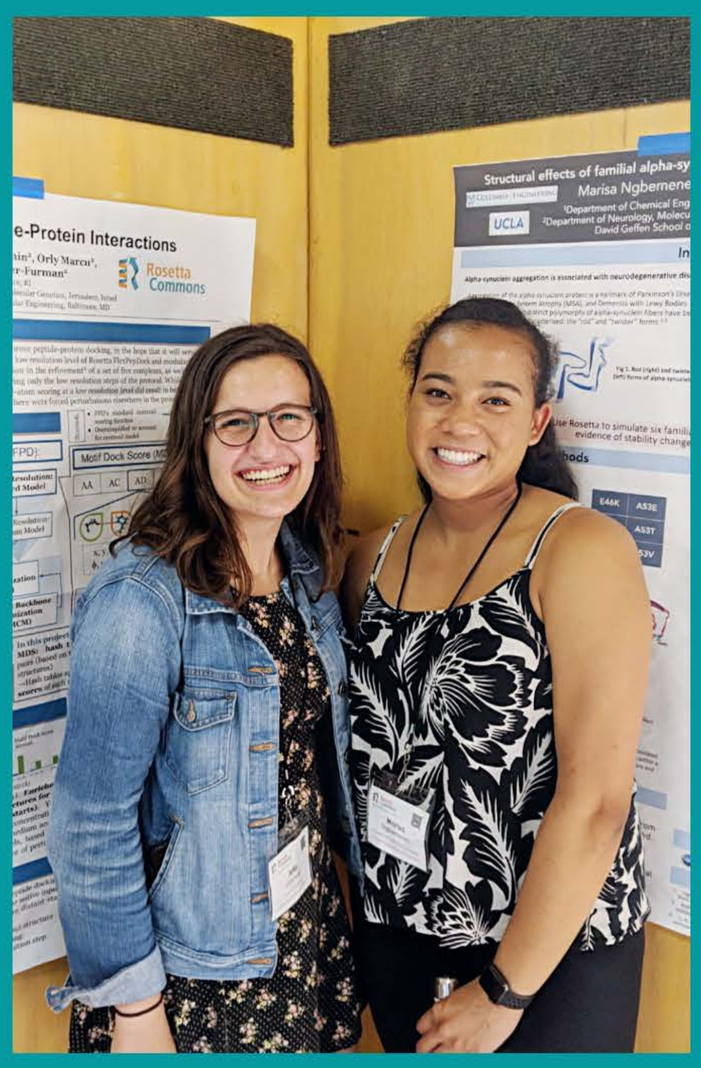
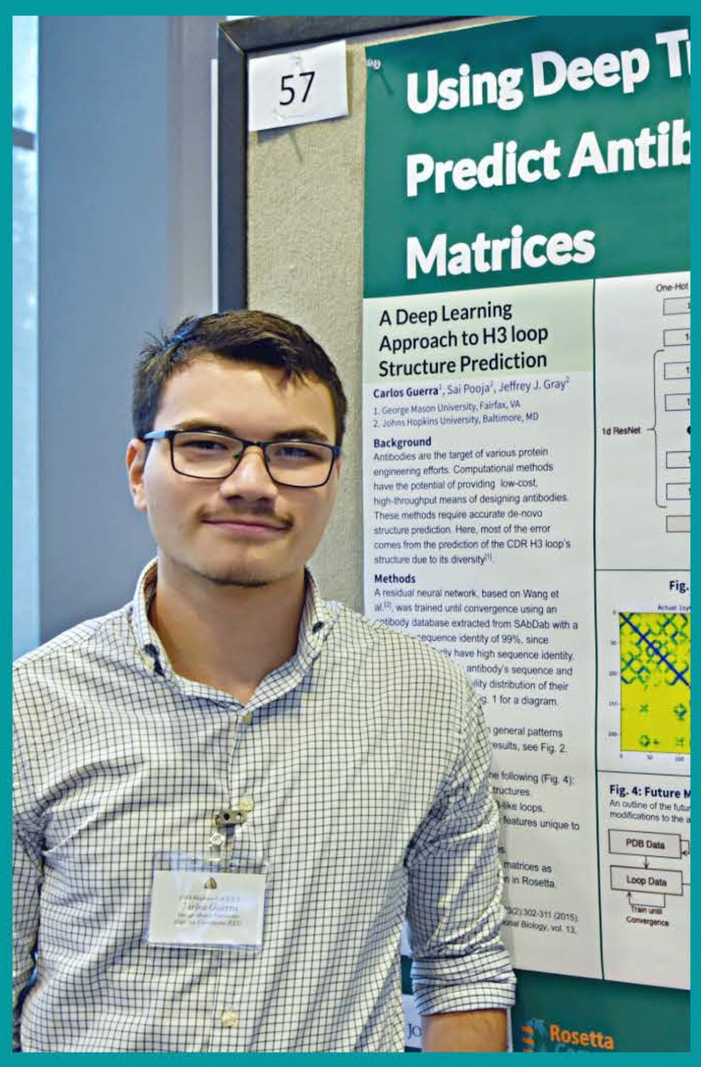




Rosetta Commons

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.

Students learn the inner details of PyRosetta and the community coding environment. Students perform research in a molecular modeling and design laboratory, developing new algorithms and discovering new science. Interns are mentored by faculty and graduate students.

The Program:

* One week of Rosetta Code School
* Eight weeks of hands-on research
* One week at the Rosetta Conference to close the summer.

The sponsor, NSF, covers housing, travel expenses, and a stipend.

APPLY AT ROSETTACOMMONS.ORG/ABOUT/INTERN
QUESTIONS? EMAIL CAMILLE MATHIS AT CMATHIS@JHU.EDU

*Pending 2020 renewal

ROSETTA COMMONS
SUMMER 2020 INTERNSHIPS

Neoleukin
Seattle, WA
De Novo Protein Design for Immunotherapeutics

King lab
University of Washington
Seattle, WA
Breaking symmetry in the computational design of self-assembling protein nanomaterials

Baker Lab
University of Washington
Seattle, WA
Design of self-assembling protein nanomaterials: three-dimensional crystals

Stein Lab
University of Copenhagen
København, Denmark
Accurate prediction of protein stability changes on homology models

Fomekong Group
EMD Serono Research
& Development Institute
Billerica, MA
Using Rosetta to build better drugs

Arzeda Corporation
Seattle, WA
Enzyme design for the production of performance improving sustainable chemicals

Kellogg lab
Cornell University
Ithaca, NY
Combining CryoEM and Rosetta to inform protein structure and dynamics

Cooper Lab
Northeastern University
Boston, MA
Citizen Science Games in Protein Folding and Design

Das Lab
Stanford University
Stanford, CA
Modeling and designing RNA at high resolution

Karanicolas Lab
Fox Chase Cancer Center
Philadelphia, PA
Designing targeted protein degraders

Bahl Lab
Institute for
Protein Innovation
Harvard Medical School
Boston, MA
Engineering antibodies with enhanced properties

GlaxoSmithKline
Collegeville, PA
Designing better biomolecules faster

Kortemme Lab
UCSF
San Francisco, CA
Phenotypic prediction and design of allosteric small molecule sensors

Smith Lab
Wesleyan University
Middletown, CT
Elucidation of protein dynamics from Nuclear Magnetic Resonance (NMR) structural data

Gray Lab
Johns Hopkins University
Baltimore, MD
Glycoengineering for immunotherapy and biofuels

Horowitz Lab
University of Denver
Denver, CO
Biochemistry puzzles for science education

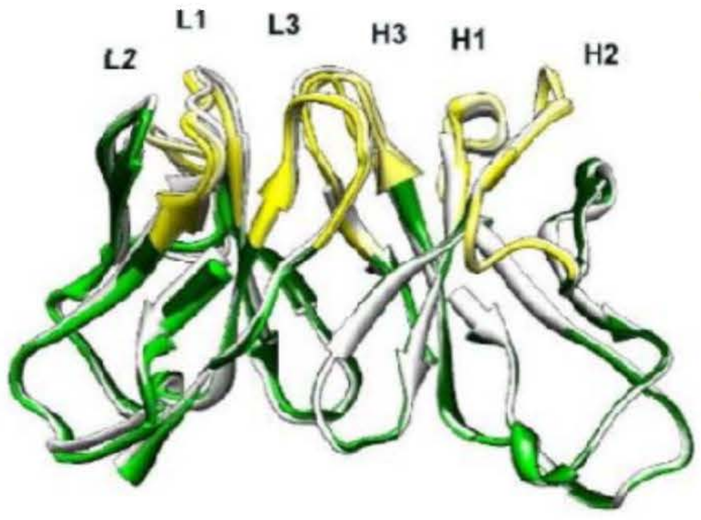
Slusky Lab
University of Kansas
Lawrence, KS
Enzyme design for environmental remediation

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

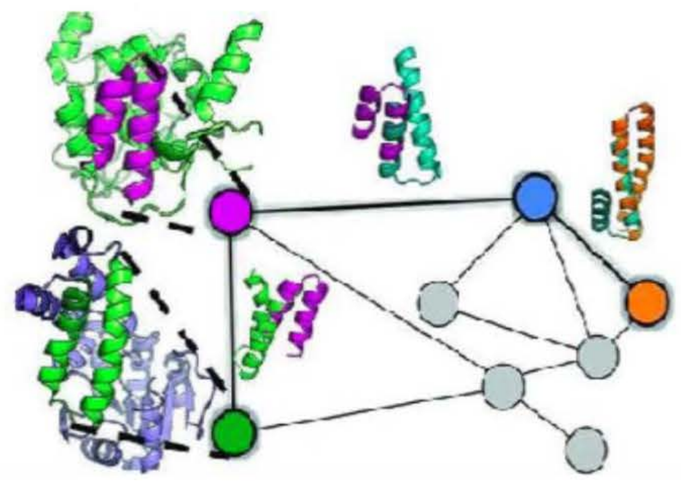
- de novo protein design
- drug design
- materials design
- structure prediction of biological macromolecules and macromolecular complexes

The Rosetta Community Goals:

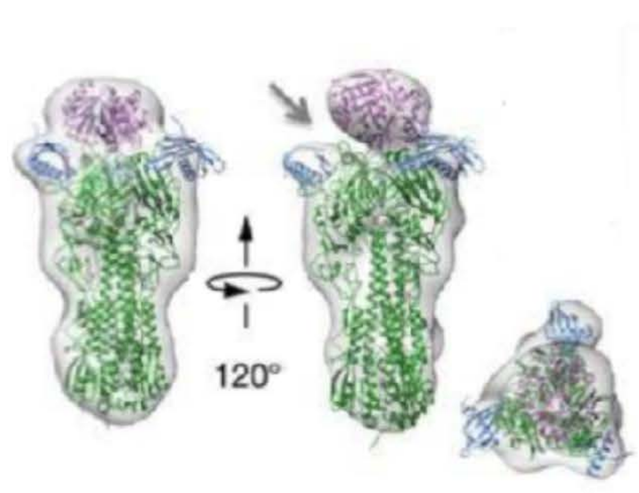
- understand marcromlecular interactions
- design custom molecules
- develop efficient ways to search conformation and sequence space
- find broadly useful energy functions for various biomolecular representations
- treat diseases and create new molecular technologies



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



Design of proteins by "sewing" to recombine substructures.



Design of a hemagglutinin-binding trimer that protects against the flu.