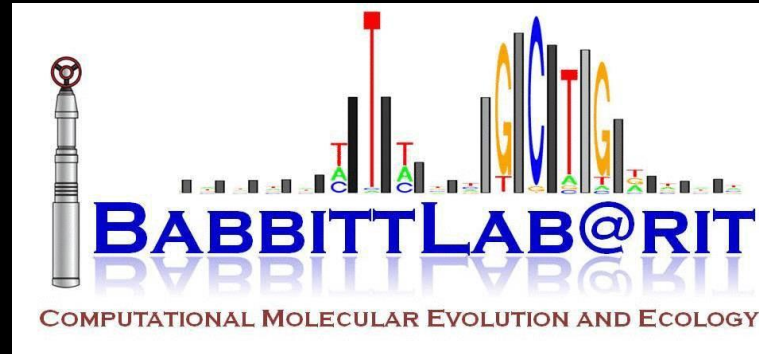


Dr. Gregory A. Babbitt



some of our students



Erin Coppola BME



Jamie Mortensen BME



Justin Liao BME



Mohammed Alawad
Bioinformatics



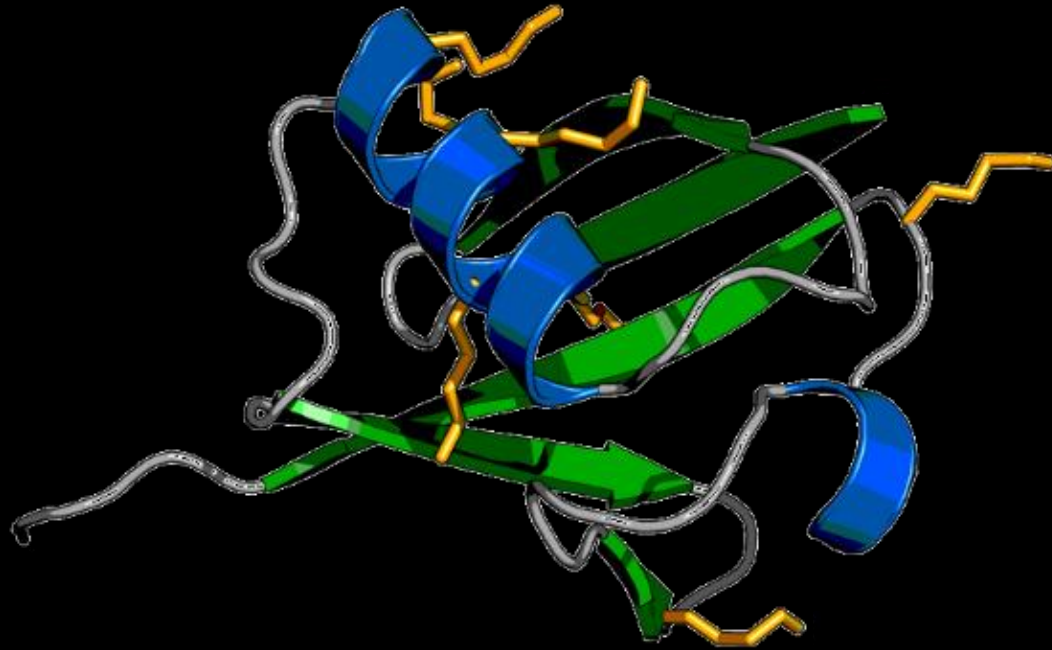
Katharina Schulze
Bioinformatics

We are a mostly “dry-bench” or computer-based laboratory studying the evolution of the molecular components of cells. Biophysics and biochemistry underlies all molecular processes in the cell, but only some molecular structure and behavior, genetic and epigenetic, can contain information that is subject to heritable change over potentially deep timescales.

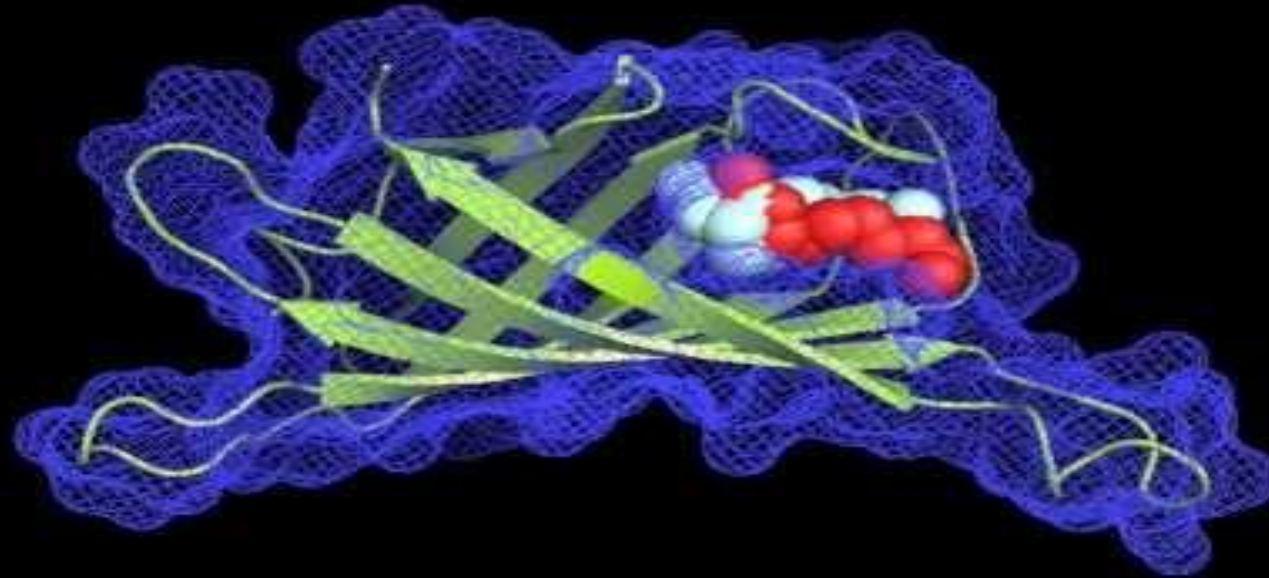


Our long-term research goals are aimed at a more biophysically-grounded understanding of molecular evolution in the cell. We combine biophysical and molecular evolutionary modeling to investigate the boundary between evolvable and non-evolvable biophysics.

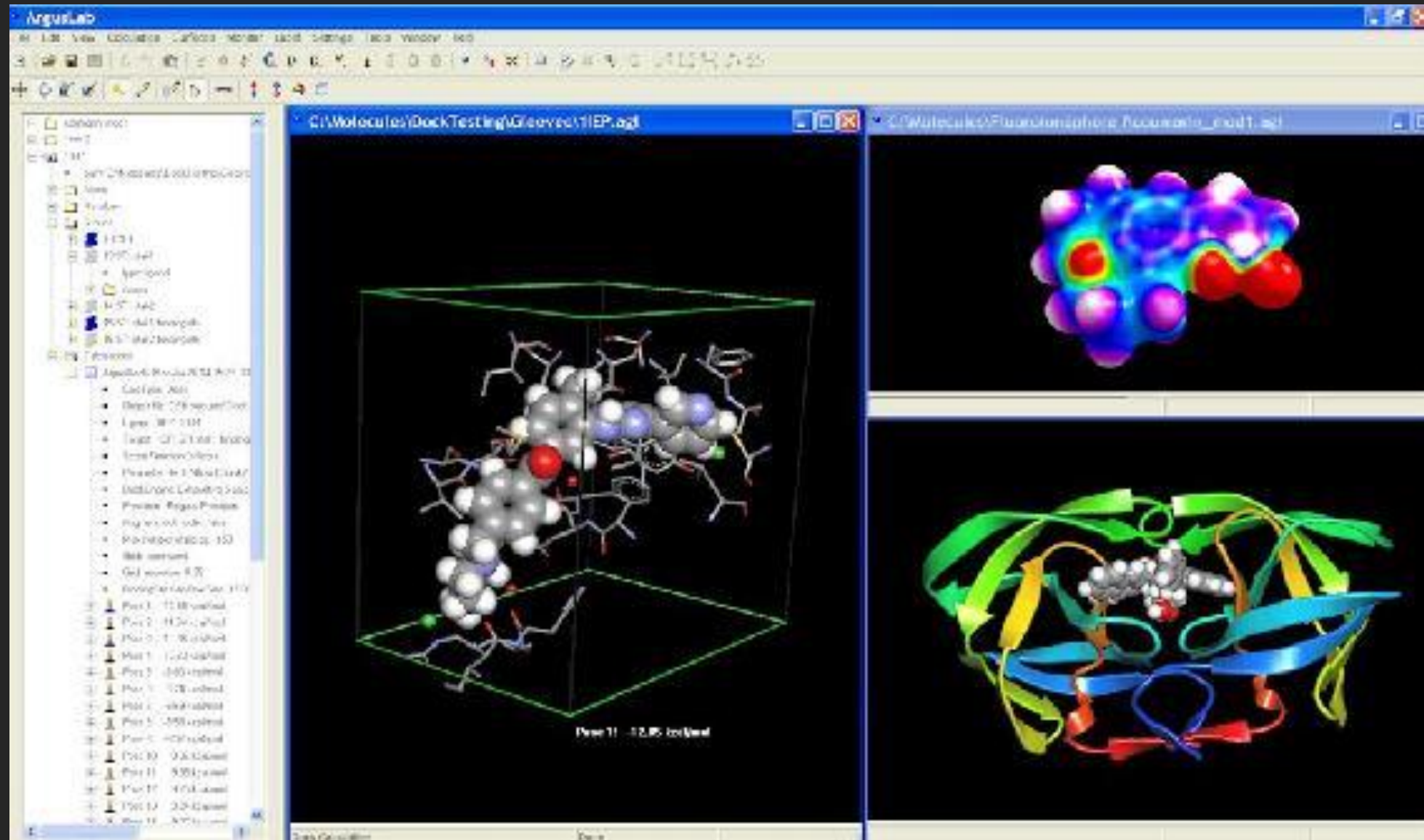
ubiquitin structure



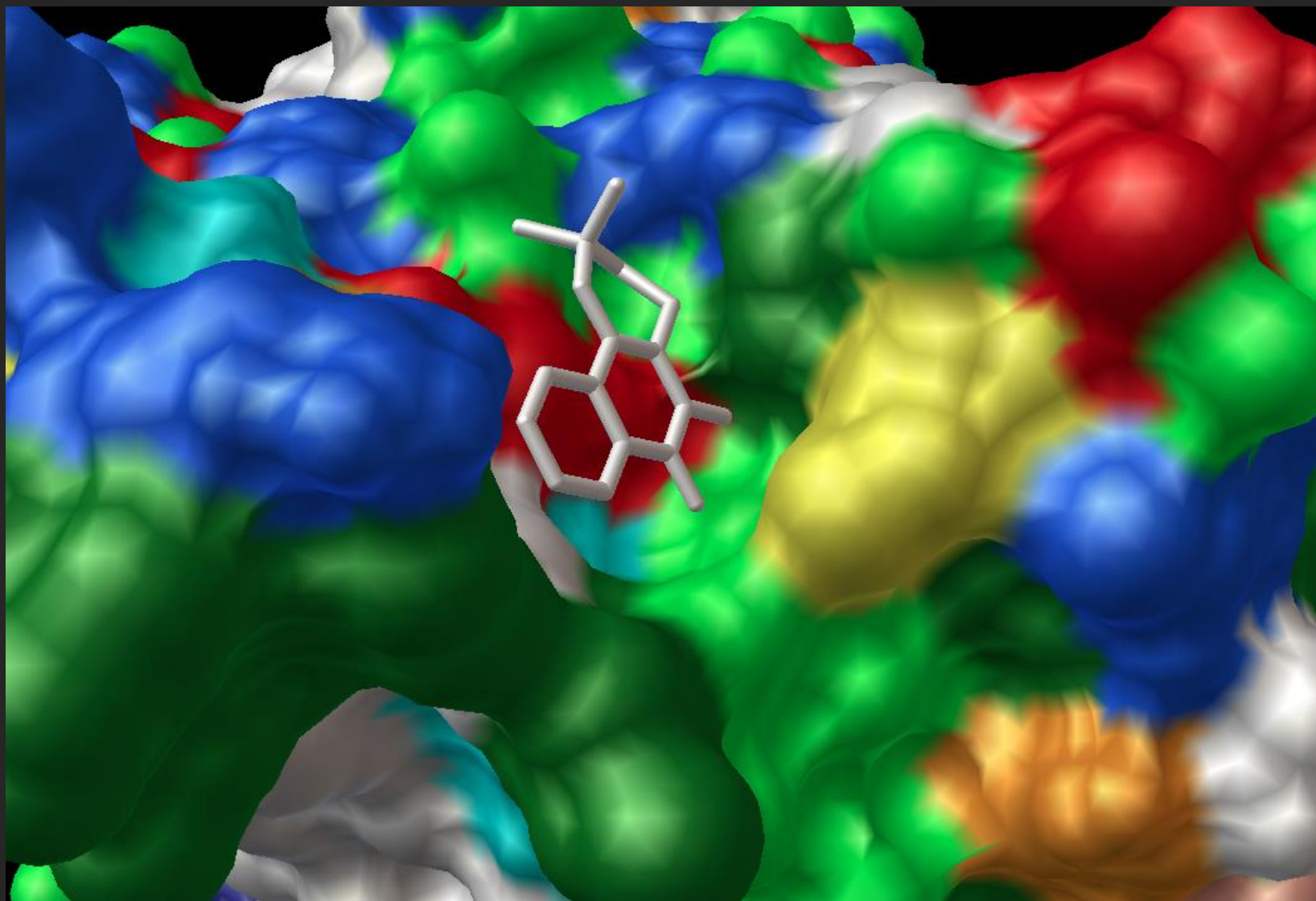
Introduction to Molecular Docking Simulation



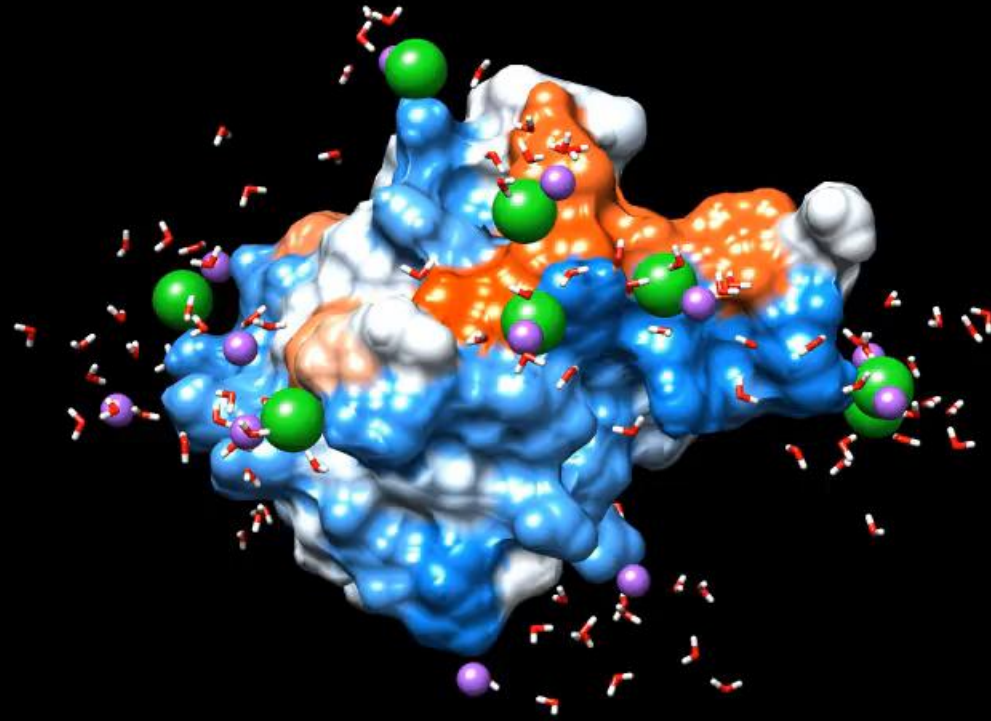
Drug docking surveys of small molecule libraries

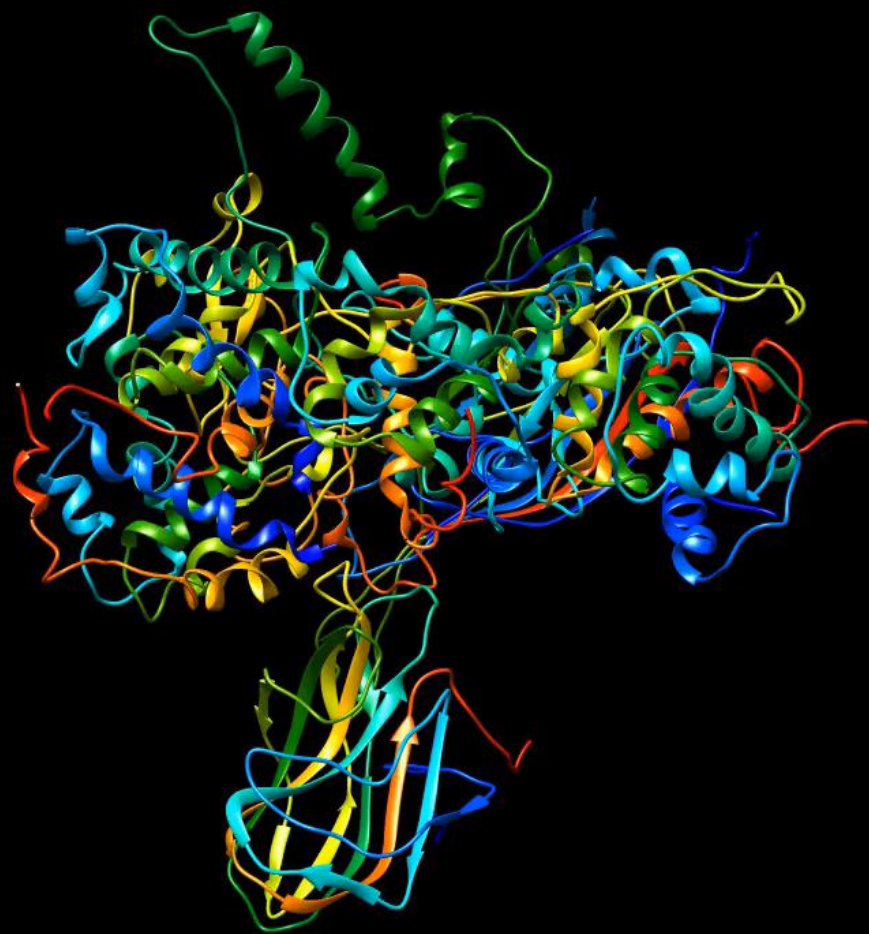


Drug docking surveys of small molecule libraries

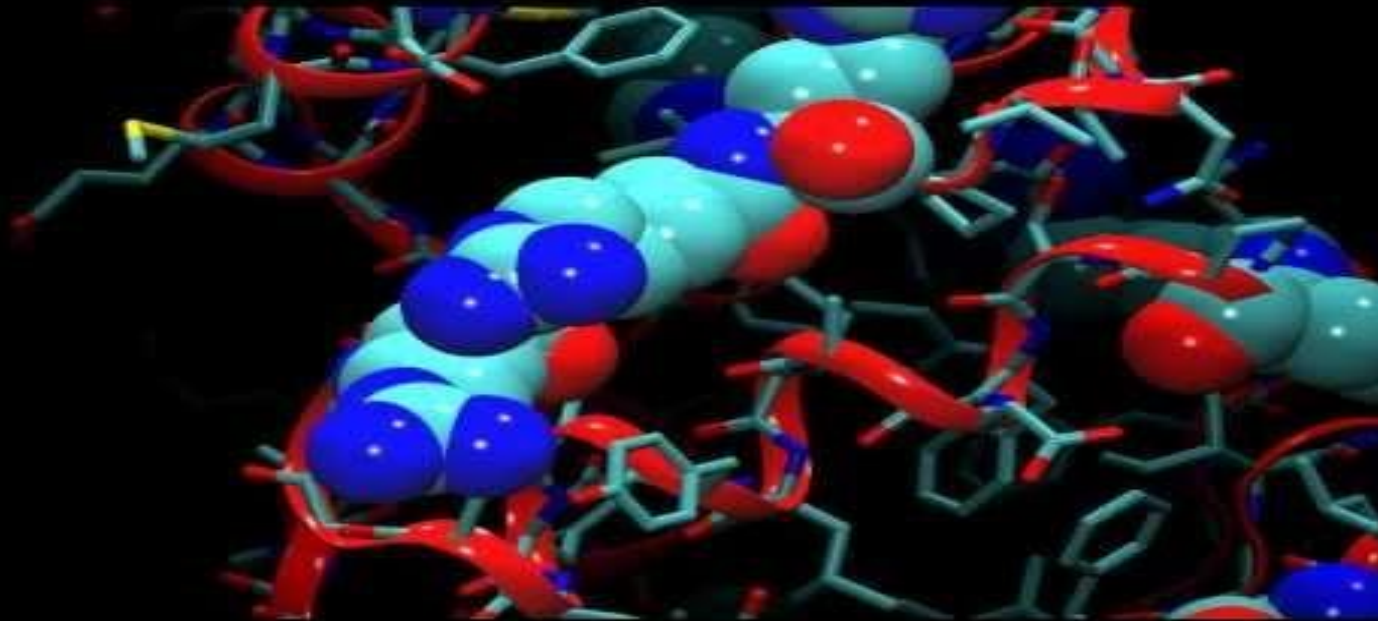


ubiquitin in explicit solvent MD simulation

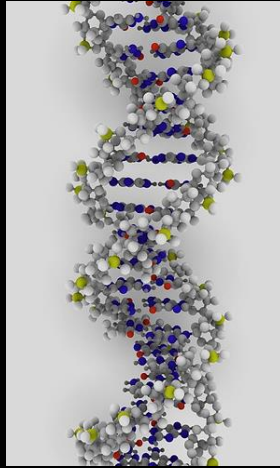




Introduction to Molecular Dynamics



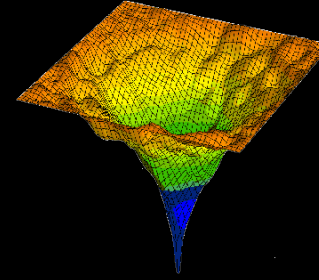
Anatomy of a molecular dynamic simulation



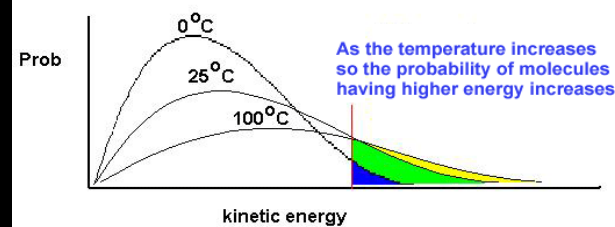
structure =
ideal or PDB



minimization of potential
energy surface (relaxation)



heating applied to all bonds



How might one statistically
compare results between
MD production runs?

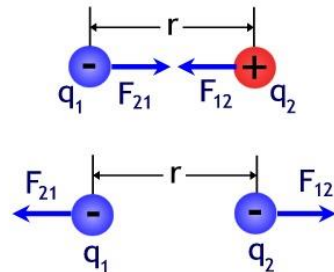


movies and statistics
rendered from atomic
vector trajectories

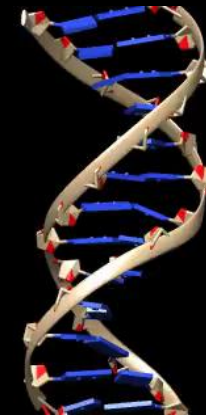
bonded atoms



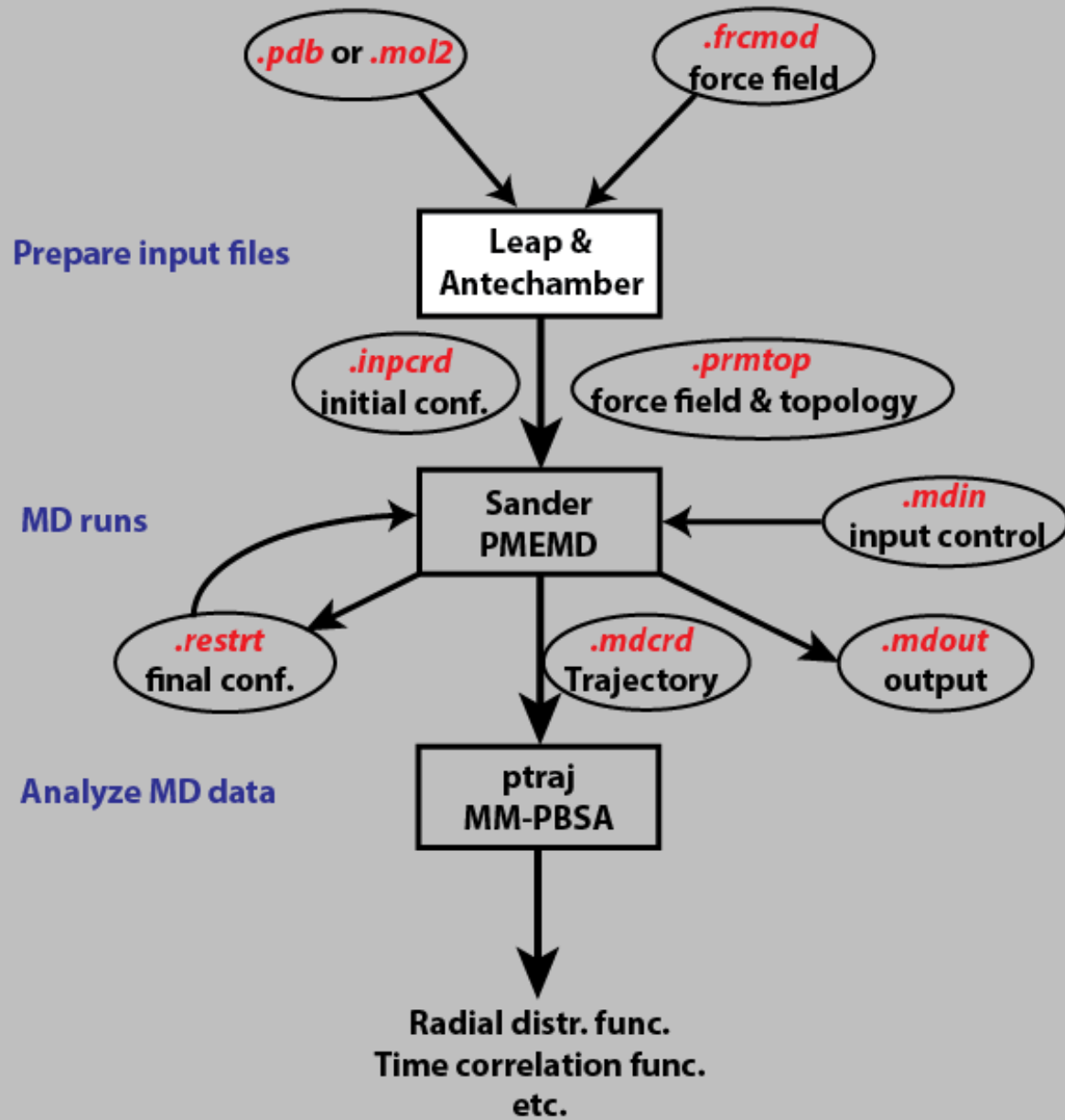
non-bonded atom



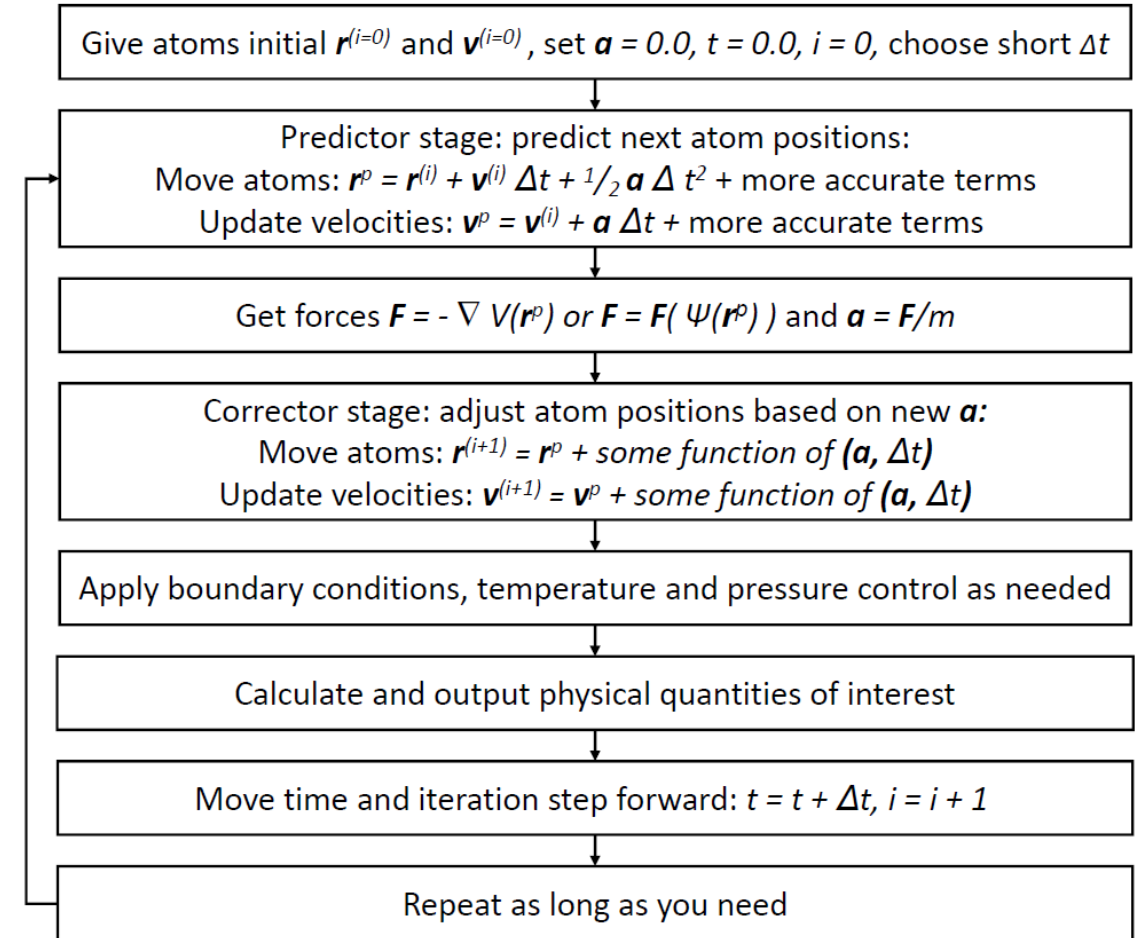
MD equilibration and
production run(s)
track Newtonian
mechanics stepped
out in femtoseconds



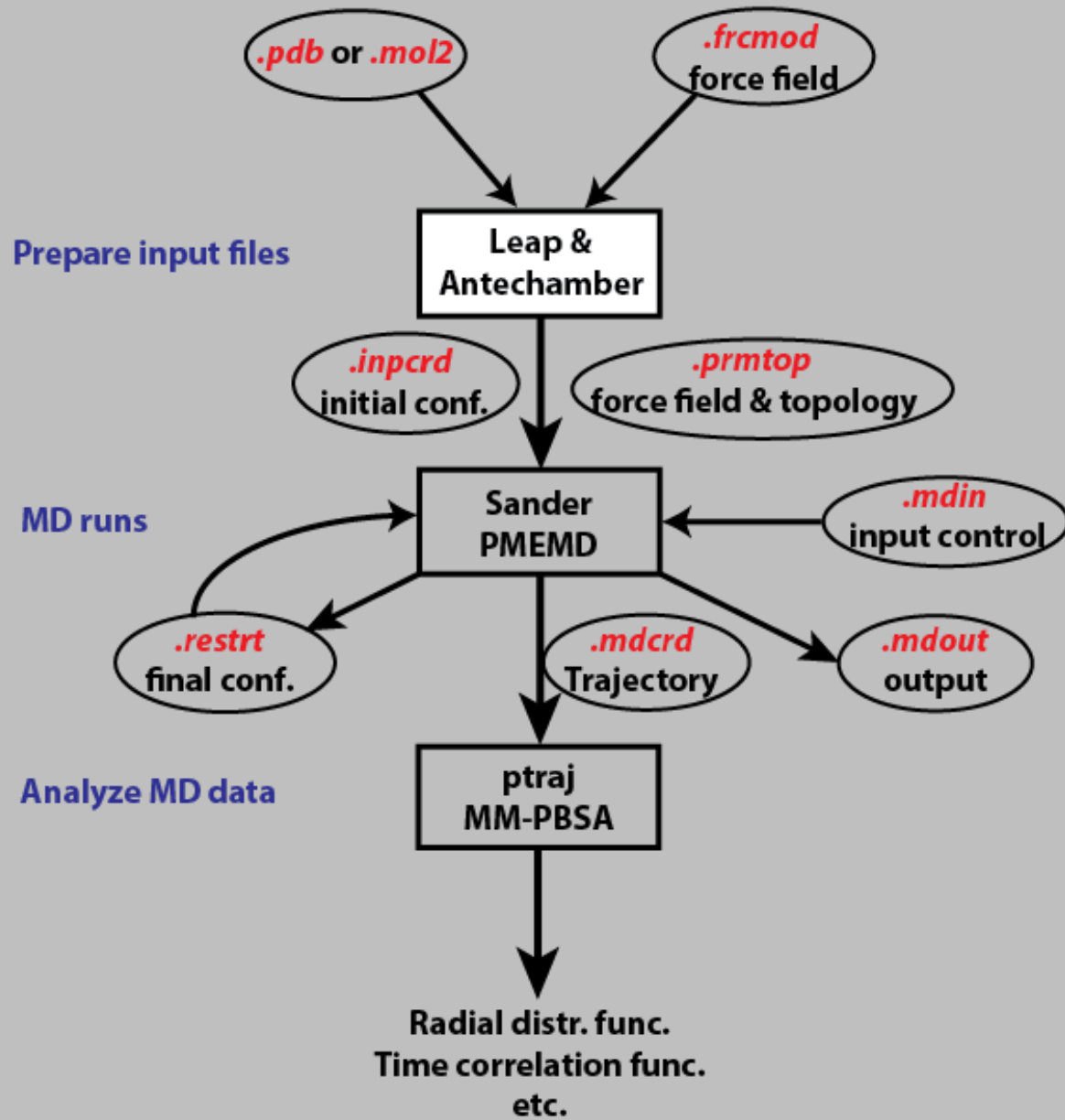
AMBER flowchart



Simplified schematic of the molecular dynamics algorithm



AMBER flowchart



Simplified schematic of the molecular dynamics algorithm

