Sikao Guo, Ph.D.

COMPUTATIONAL BIOPHYSICIST | RESEARCH SCIENTIST

sikaoguo@gmail.com | linkedin.com/in/sikaoguo | sikaoguo22.github.io | U.S. Permanent Resident (no sponsorship required)

PROFESSIONAL SUMMARY

Computational biophysicist with 6+ years of postdoctoral and research-engineering experience developing mechanistic models and computational methods for protein conformational sampling, biomolecular self-assembly, structural bioinformatics, and stochastic reaction-diffusion. Integrates molecular structures, kinetic data, statistical mechanics, and all-atom validation to generate testable predictions. Led first-author studies in PLOS Computational Biology, eLife, and Journal of Computational Chemistry, et al.

PROFESSIONAL EXPERIENCE

Inria **Jul 2025 - Present**

Research Engineer *Sophia Antipolis, France*

- Developed an inverse-kinematics C++17/Python sampler that generalized fixed-end loop closure to fixed, single-end, and fully released protein-backbone sampling, enabling conformational exploration of loops, fragments, and intrinsically disordered regions.
- Introduced SE(3)-based endpoint moves, shifted tripeptide frames, residue-specific Ramachandran priors, and spatial-hash clash detection; redesigned searches spanning 100,000+ loop-closure combinations to retain reproducible feasible ensembles.
- Built an all-atom validation workflow integrating AttnPacker, AMBER99SB/OBC2 OpenMM minimization, PhiSiCal-Checkup, MDS/clustering, and hard QC; benchmarked 224 SBL structures against 249 BBFlow structures and generated 1,000 androgen-receptor IDR conformers, with 727 passing final score filters.
- Architected AutoCLIP, a specification-driven Model-View-Presenter framework that converts one GUI design into VMD, PyMOL, and web applications; deployed nine structural-biology tools and replaced separate application-platform implementations with reusable application specifications and platform generators.
- Established cross-platform CI/CD, packaging, and a 232-test validation suite across Linux and macOS, supporting reproducible release of research methods to scientific users.

Johns Hopkins University **Jan 2020 - Jun 2025**

Assistant Research Scientist (2025); Postdoctoral Fellow (2020-2024) *Baltimore, MD*

- Led development and validation of MPI NERDSS, scaling particle-based reaction-diffusion and reversible self-assembly to 96 CPUs with approximately 90x acceleration on 20,000-particle systems while preserving serial kinetics and diffusion.
- Co-developed ioNERDSS, an automated PDB/mmCIF-to-coarse-grained simulation workflow using interface geometry, KD-trees, reaction generation, sequence alignment, and ML-assisted affinity initialization; benchmarked it across 44,000+ PDB structures and 3- to 720-subunit assemblies.
- Led a first-author clathrin-assembly study that reproduced experimental kinetics and predicted an approximately 25-trimer critical nucleus and 0.7-0.8 uM adaptor threshold, explaining why adaptor-poor lattices abort.
- Built cryo-ET-informed stochastic models of approximately 3,700-subunit HIV Gag/Gag-Pol lattices, identifying a -12 to -8 kBT stability window and cofactor-timing rules that reduce kinetic trapping and support testable viral-maturation hypotheses.

Institute of Physics, Chinese Academy of Sciences **Sep 2014 - Dec 2019**

Doctoral Researcher *Beijing, China*

- Developed a mechanochemical state-transition model of dimeric kinesin that reproduced force- and ATP-dependent velocity, dwell time, run length, and processivity across six perturbation classes and predicted head-specific loads for optical-trapping tests.
- Implemented stochastic Runge-Kutta and Monte Carlo simulations across an approximately 45 pN bidirectional load range, resolving directional asymmetry and slip/catch-slip detachment kinetics consistent with independent datasets.
- Built nucleotide-state kinesin-microtubule complexes from four PDB structures and ran 200+ ns of GROMACS/AMBER99SB simulations with umbrella sampling, PMF, and WHAM to test ATP-driven head coordination.

EDUCATION

Ph.D. in Physics | Institute of Physics, Chinese Academy of Sciences | Beijing, China | Sep 2014 - Dec 2019
B.S. in Physics | Nankai University | Tianjin, China | Sep 2010 - Jun 2014

SELECTED PUBLICATIONS

Full publication list: Google Scholar

- **Guo S**, Sarti E, Cazals F. A Unified, Cross-Platform Framework for Automatic GUI and Plugin Generation in Structural Bioinformatics and Beyond. *arXiv preprint, 2026.* arXiv:2602.16047
- **Guo S**, Korolija N, et al. Parallelization of Particle-Based Reaction-Diffusion Simulations Using MPI. *Journal of Computational Chemistry, 2025.* doi:10.1002/jcc.70132
- Ying YM, Sang M, et al., including **Guo S**. Transforming Macromolecular Structures into Simulations of Self-Assembly with ioNERDSS. *bioRxiv preprint, 2026.* doi:10.64898/2026.01.27.702082
- **Guo S**, Saha I, Saffarian S, Johnson ME. Structure of the HIV Immature Lattice Allows for Essential Lattice Remodeling within Budded Virions. *eLife, 2023.* doi:10.7554/eLife.84881
- **Guo S**, Sodt AJ, Johnson ME. Large Self-Assembled Clathrin Lattices Spontaneously Disassemble without Sufficient Adaptor Proteins. *PLOS Computational Biology, 2022.* doi:10.1371/journal.pcbi.1009969

SELECTED OPEN-SOURCE SOFTWARE

AutoCLIP — specification-driven GUI generation for VMD, PyMOL, and web (GitHub | Docs)
NERDSS-MPI — parallel particle-based reaction-diffusion simulator (GitHub | Guide)
ioNERDSS — PDB/mmCIF-to-simulation modeling workflow (GitHub | Docs)

TECHNICAL EXPERTISE

Research Areas: computational biophysics, structural bioinformatics, protein conformational sampling, IDRs, biomolecular self-assembly, membrane-associated assembly
Modeling & Methods: MCMC, inverse kinematics and tripeptide loop closure, Brownian dynamics, coarse-grained modeling, kinetic/ODE/PDE modeling, molecular dynamics, statistical validation, MDS and clustering
Programming & Scientific Computing: C++17, Python, MPI/OpenMPI, NumPy, SciPy, Biopython, Eigen, CGAL, OpenMM, GROMACS, Linux, Git, pytest, Docker