

Miri Krupkin, PhD

Principal Structural & Computational Biologist

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PROFESSIONAL SUMMARY

Interdisciplinary Structural Biologist and Computational Scientist with 10+ years of expertise decoding macromolecular assemblies across biological scale—from catalytic proto-ribosomes and the 2.5-MDa translation machinery to massive viral genomic RNAs (>9,000 nt). Backed by elite training at **Stanford, MIT, and Weizmann** (Direct Ph.D. with Nobel Laureate Ada Yonath; Leading Edge Fellow 2025). Proven track record developing production-grade structural validation software (**Python, SciPy, BioPython, PyTest**), determining atomic-resolution Cryo-EM/ET and X-ray structures in industry co-development campaigns (**Pfizer, Nabriva**), and engineering platform solutions for unstable RNA transcripts. Experienced in leading cross-functional consortia (**NIH, Gates Foundation**) to translate complex empirical ground truth into actionable computational architectures.

CORE TECHNICAL EXPERTISE

Computational Structural Biology & AI Infrastructure: Generative model benchmarking (AlphaFold 3, Rosetta) and empirical validation pipelines; Python (vectorized NumPy, SciPy, BioPython, pandas, PyTest) and MATLAB; Hungarian algorithm multi-chain assignment, coarse-grained P-backbone superimposition, RASA/pLDDT biophysical profiling, py3Dmol visualization, REST APIs (RCSB, EBI), and Linux/Slurm HPC (Stanford Sherlock).

Structural Biology & Imaging: Cryo-EM (SPA), Cryo-ET (in situ tomography), and macromolecular X-ray crystallography. End-to-end execution from sample vitrification and automated collection (Titan Krios 300 kV, Glacios 200 kV, SerialEM, at Synchrotrons: SLAC, ESRF, SLS, Diamond) to high-resolution reconstruction and modeling (CryoSPARC, RELION, IMOD, AreTomo, Coot, ChimeraX).

Biophysics & Dynamic Conformational Kinetics: Real-time single-molecule TIRF microscopy and Zero-Mode Waveguide (ZMW / PacBio RS) instrumentation. Custom microfluidic flow cells, targeted macromolecular surface immobilization (enzymatic labeling, bio-orthogonal click chemistry), and non-equilibrium kinetic profiling of dynamic RNA/protein conformational transitions.

Regulatory & Consortium Governance: CITI & HIPAA Certified, IRB & BSL-2 Compliance, cross-functional leadership, and executive reporting across multi-institutional consortia (NIH CHEETAH, Gates Foundation).

PRODUCTION SOFTWARE SUITES & OPEN-SOURCE ASSETS

FoldCheck Suite ([FoldCheck-RNA](#) & [FoldCheck-Pro](#)) | Lead Architect & Developer

Python, NumPy, SciPy, BioPython, REST APIs, PyTest | 2026

- **Algorithmic Validation:** Engineered open-source testing suites evaluating generative macromolecular predictions (AlphaFold 3) against empirical Cryo-EM and crystallographic ground truth.
- **Asymmetric Quaternary Pairing (FoldCheck-Pro):** Implemented the Hungarian algorithm to resolve asymmetric heterodimer subunit pairing (HIV-1 RTase p66/p51) and integrated pLDDT/RASA surface classification.
- **Topological RNA Superimposition (FoldCheck-RNA):** Implemented coarse-grained phosphorus (P) backbone alignment to capture global fold geometry past local torsion noise, paired with a 30+ non-canonical modification registry for large RNAs (>9,000 nt).

RESEARCH & PROFESSIONAL EXPERIENCE

Research Structural Biology & RNA/Protein Platforms | Stanford School of Medicine

Elisabetta and Joseph Puglisi labs | 2019 – Present

- **Long-Transcript Platform Innovation:** Engineered a proprietary large-scale RNA stabilization protocol eliminating solution precipitation for highly structured transcripts (>9,000 nt), enabling downstream biophysical characterization and multi-lab distribution (yielding 2 papers in preparation).
- **VLP Packaging & Ultrastructure Profiling:** Built a modular synthetic RNA packaging platform encapsidating full-length viral RNAs into Virus-Like Particles (VLPs); validated encapsidation efficiency and viral mechanics using in situ cryo-ET and single-molecule fluorescence microscopy.
- **Overcoming Translation Bottlenecks (NAR Cover Paper, 2022):** Spearheaded Cryo-EM structural determination of ribosome-bound synthetic tRNA complexes; identified core steric clashes during A-to-P translocation and executed structure-guided rational point mutations that relieved steric hindrance and improved kinetics.
- **Automated Pipeline Deployment:** Built automated Python and MATLAB data pipelines integrating custom image analysis and kinetic fitting routines, eliminating manual bottlenecks across multi-gigabyte Cryo-EM and single-molecule datasets.
- **Consortium Leadership:** Served as primary technical presenter within the NIH-funded CHEETAH HIV consortium, delivering data-driven milestones to international research leaders; supervised 3 graduate researchers across VLP and assay workflows (3 papers published).

Program Lead & Postdoctoral Researcher I MIT

Gates Foundation Initiative I 2017 – 2019

- **Automated Image Processing Pipelines:** Engineered automated MATLAB and ImageJ segmentation pipelines for high-content multi-channel fluorescence microscopy, establishing quantitative physicochemical baselines for drug delivery across reconstituted mucin hydrogels (*Biomacromolecules* 2023, co-first author).
- **Clinical Regulatory Compliance:** Directed end-to-end clinical biospecimen procurement and hospital biobanking workflows under strict IRB, CITI, and HIPAA protocols; supervised 4 researchers across 3 peer-reviewed studies (including *JACS* Au, *Nat Commun*).
- **Consortium Governance:** Managed multi-institutional research milestones within a Gates Foundation initiative, synthesizing complex biophysical and microbiological data into structured monthly executive briefings.

Quantitative Researcher I Weizmann Institute of Science

Direct-Track PhD with *Ada Yonath (Nobel Laureate)* I 2009 – 2017

- **Structural Elucidation & SBDD Co-Development:** Determined atomic crystal structures of bacterial ribosomes complexed with novel orthosomycin, macrolide, and pleuromutilin therapeutics in active co-development with Pfizer and Nabriva Therapeutics; mapped drug-binding pockets and allosteric resistance pathways across 8 peer-reviewed papers (including co-first-author *PNAS* 2016).
- **Synchrotron Campaign Operations:** Directed 24-hour continuous operations across European synchrotron beamlines (ESRF France, SLS Switzerland, Diamond UK), executing real-time Python/Linux data-reduction pipelines with zero instrument downtime.
- **Prebiotic RNA Machine Engineering:** Supervised 16 graduate students and interns across sub-teams of 4 to design, synthesize, and biochemically validate synthetic proto-ribosomal RNA dimers capable of spontaneous peptide-bond formation, yielding 4 papers (*Phil Trans R Soc B*, *PNAS*, *NAR*).

LEADERSHIP, EDITORIAL GOVERNANCE & EVALUATION

People Leadership & Training: Mentored 22 direct graduate students and technicians, trained >50 scientific personnel across Stanford, MIT, and Weizmann; co-authored peer-reviewed papers with 14 mentees.

Scientific Review & Governance: Served as a handling editor and as a manuscripts peer for 16+ biological manuscripts across 5 journals. Headed evaluation committees across major scientific meetings (Bay Area RNA Conference, MIT-Harvard Symposium, *Frontiers in Chemistry Symposium*).

Conference Organization: Co-organized 4 major scientific symposia of 300+ attendees, coached >50 speakers on technical narrative clarity. Negotiated quotes/service contracts with external vendors and directly managed operational teams of 10+ personnel to execute large-scale events.

EDUCATION, AWARDS, & CERTIFICATIONS (selected)

PhD, Structural Biology I Weizmann Institute of Science (PhD direct track from MSc)

BSc, Chemistry (magna cum laude) I Bar-Ilan University

Competitive Fellowships: Secured >\$120,000 in competitive awards including Best Talk Award, the Cincinnati Children's Hospital Clinical Research fellowship, and The National Adams Ph.D. Fellowship.

Certifications: CITI Program (Human Subjects Research), HIPAA/HITECH Compliance.

Executive Management Training: Completed selective leadership tracks (Leading Edge Fellow, Compass Scholar) focused on organizational decision architectures, research governance frameworks, and structured team management.

SELECTED PUBLICATIONS & PRESENTATIONS

40+ Presentations & 20+ Peer-Reviewed Publications (*PNAS*, *Nature Communications*, *JACS*, *Current Opinion in Structural Biology*, *NAR*; full list on [PubMed](#)). Delivered strategic briefings to philanthropic donors and leadership across premier forums (Gates Foundation Consortium, NIH HIV Group, Chan Zuckerberg Biohub, New York Structural Biology Center). Selected publications:

- **Krupkin M**, et al. Packaging a Synthetic Full-length HIV viral RNA into Functional HIV Virions. (In preparation).
- Wagner CE*, **Krupkin M***, et al. Comparison of Physicochemical Properties of Native Mucus and Reconstituted Mucin Gels. *Biomacromolecules* (2023).
- **Krupkin M**, et al. Advances in understanding the initiation of HIV-1 reverse transcription. *Current Opinion in Structural Biology* (2020).
- **Krupkin M**, et al. Avilamycin and evernimicin induce structural changes in rProteins uL16 and CTC that enhance inhibition of A-site tRNA binding. *PNAS* (2016).

*Contributed equally to this work.