

Maria Nikitina

Molecular biologist · Protein engineering · Structural computation

Baden-Baden, Germany · +49 176 63786735 · maria.nikitina.bio@gmail.com

Experimental biology
Sequence–structure reasoning
AI-assisted research workflows

EXPERIENCE

Independent research <i>Analogy-guided protein engineering</i> - Developing a literature-grounded framework for identifying mechanistic analogies across biological systems and translating them into explicit, testable protein-engineering hypotheses. - Connecting cross-domain reasoning with sequence/structure analysis, engineering criteria, and experimental validation for activity, stability, expression, folding, and regulation.	2026–present Developing
University of Groningen · Fürst Lab <i>Computational structural biology</i> - Built a high-throughput Boltz workflow for predicting and prioritizing protein–protein complexes on a SLURM-managed HPC cluster. - Integrated pLDDT/ipTM, interface geometry, RMSD comparison, and evolutionary conservation to rank candidates for experimental validation.	Dec 2025–Mar 2026 Groningen, NL
University of Natural Resources and Life Sciences <i>Master's thesis · synthetic promoters</i> - Designed and tested synthetic promoter variants activated by <i>Agrobacterium tumefaciens</i>-induced plant defense responses to increase recombinant protein accumulation. - Combined cis-motif analysis, cloning, transient expression in <i>Nicotiana benthamiana</i>/BY-2 cells, and quantitative mRNA/protein measurements; designs reached approximately 80% of the 35S reference in <i>N. benthamiana</i>.	Jan–May 2025 Vienna, AT
University of Natural Resources and Life Sciences <i>Research internship · recombinant proteins</i> - Designed a vector library targeting different subcellular compartments to investigate folding and disulfide-bond formation in snake venom metalloproteinases. - Established expression, extraction, quantitative analysis, BY-2 testing, and laboratory SOPs.	Feb–Dec 2024 Vienna, AT
Technical University of Munich <i>Research internship · population genomics</i> Analyzed <i>Magnaporthe oryzae</i> population structure from SNP data using PCA, t-SNE, UMAP, and DAPC.	Mar–Jun 2024 Munich, DE
Newcastle University <i>Erasmus research project · Rubisco evolution</i> Studied adaptive evolution of Rubisco across marine ecosystems using BLAST, sequence alignment, Python, and phylogenetic analysis.	Sep 2023–Jan 2024 Newcastle, UK
Max Planck Institute of Biochemistry <i>Bachelor's thesis · HPLC–MS metabolomics</i> Developed a noise-reduction protocol for HPLC–MS/Orbitrap data collection and improved data quality for downstream quantitative analysis.	Mar–Aug 2022 Martinsried, DE

RESEARCH SOFTWARE AND AI

HPC Protein Partner Screening AI-assisted prioritization of candidate partners from UniProt annotations, followed by Boltz complex prediction, SLURM GPU arrays, output auditing, structural controls, and transparent ranking.
CitationTool Local-first evidence retrieval for scientific claims using page-aware text extraction, DOI detection, BM25 ranking, and optional opt-in AI review.
FASTA Research Toolkit Tested tools for protein/DNA validation, sequence preparation, local alignment, and evolutionary analysis with deterministic, privacy-conscious workflows.

ADDITIONAL EXPERIENCE

Omegamatrix GmbH Laboratory assistant · gas-chromatographic Omega Index analysis	Apr 2022–Aug 2023
Max Planck Neuroscience · Kornfeld Lab 3D electron-microscopy annotation of zebra finch synaptic structures	Jul 2021–Jul 2022
Helios Clinic Clinical and laboratory assistant · patient registration and real-time PCR sampling	Feb–Sep 2021
Karlsruhe Botanical Garden Seasonal assistant	Jun–Jul 2019

EDUCATION

Technical University of Munich M.Sc. Molecular Biotechnology	2022–2026
Ludwig Maximilian University of Munich B.Sc. Biology	2019–2022

RESEARCH FOCUS

Protein engineering
Sequence–structure–function relationships
Recombinant protein expression
Protein folding and stability
Disulfide-rich proteins
Structural interaction prediction
Evolutionary reasoning
Analogy-guided design

SKILLS

Recombinant expression
Promoter and vector design
Site-directed mutagenesis
Subcellular targeting
Molecular cloning
Protein extraction and quantification
SDS–PAGE · Western blot
HPLC–MS · GC

TOOLS

Boltz · PyMOL · YASARA
Python · R · Bash
BLAST · MAFFT · ClustalW
PCA · t-SNE · UMAP · DAPC
SLURM · HPC · Git · GitHub
Automated research workflows

INDEPENDENT PROJECTS

Human Archives Founder and builder of a voice-first iOS product for capturing, transcribing, structuring, and resurfacing ideas with AI-assisted organization.
Population Structure Workbench Ploidy-aware SNP workflow with strict QC, LD pruning, PCA diagnostics, and bootstrap-based cluster stability.

SOCIAL

github.com/ariaixian
linkedin.com/in/maria-n-972194228

LANGUAGES

English · full professional
German · full professional
Russian · native/bilingual

ACTIVITIES

iGEM Munich 2023
The Entrepreneurial Group Munich
LMU Munich Chess Club
Kunstbunter Kinderspaß volunteer organizer