NAVIGO PROTEINS

www.navigo-proteins.com

Navigo Proteins GmbH is an established, successful, growing innovative biotechnology company with a strong foundation in experimental protein engineering and the development of proprietary affinity ligand technologies, located in Halle/Saale, Germany. Our core strength lies in experimental discovery, high-throughput screening, and the engineering of next-generation proteins for applications in biotherapeutics, diagnostics and bioprocessing, and cutting-edge computational approaches. We combine deep expertise in protein science with modern AI-driven methods to design and optimize next-generation protein therapeutics.

To strengthen our team, we are looking for a

Protein Engineer AI (m/f/d)

This is an exciting opportunity to join a growing team at an early stage of expansion and help shape the future of our AI-driven protein engineering platform. Building on a recently established internal capability in AI and computational protein engineering, supported by strong in-house computational infrastructure, we are now expanding this area to further scale its impact across our protein engineering programs and enable deeper integration into experimental workflows. The successful candidate can expect a multifaceted job with personal responsibilities, good development opportunities and a long-term career perspective, as well as a sociable working atmosphere in a motivated team with flat hierarchies.

Your tasks:

- Apply AI-driven protein engineering methods to support protein design projects
- Apply physics-based modelling approaches (Rosetta/PyRosetta) together with cutting-edge generative AI methods, protein language models (PLMs), and structure prediction technologies to drive protein design, optimization and engineering efforts
- Develop and maintain Python-based analysis scripts, workflows, and computational pipelines
- Analyze protein sequence, structure, and experimental datasets to guide design decisions
- Collaborate with computational and experimental scientists to support design-build-test-learn cycles
- Evaluate and benchmark emerging AI and computational biology methodologies
- Contribute to the development of internal tools and infrastructure for protein engineering applications
- Present findings and recommendations to project teams

Your requirements:

- PhD or Postdoctoral experience in AI-based Protein Engineering and computational protein design
- Solid foundation in biochemistry, biology or chemistry
- Experience with state-of-the-art AI & physics-based methods for proteins, including:
    - AI and Generative protein design models – BindCraft, BoltzGen, RFDiffusion
    - Structure prediction and protein representation learning approaches – AlphaFold, Boltz, Protenix etc
    - Protein Language Models (PLMs)
    - Protein modelling tools such as Rosetta/PyRosetta
- Strong Python programming and scripting skills, including development of analysis workflows and computational pipelines
- Experience in using Linux-based computing environments
- Strong capability to understand complex biological problems and formulate them into well-defined computational questions using AI and modelling approaches, while bridging computational innovation with experimental protein engineering

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- Curiosity about advances in generative AI, with the ability to rapidly learn and apply new methods to protein engineering projects in a fast-paced research environment
- Strong motivation to solve challenging protein design problems in real-world, time-constrained, and shifting-priority settings
- Fluent in English
- Strong communication and teamwork skills, with the ability to collaborate effectively across computational and experimental disciplines and different business units

- Advantageous:
    - Knowledge of German
    - Experience working with Linux-based multi-GPU servers for machine learning training, inference, and large-scale computational workflows
    - Familiarity with GPU resource management, job scheduling, and workload distribution in shared compute environments
    - Experience managing Python environments and software dependencies using tools such as Conda, Mamba, Docker or virtual environments
    - Exposure to high-performance computing (HPC) environments and workload managers such as SLURM (beneficial but not required)
    - Experience working with large biological datasets and AI/ML workflows
    - Familiarity with cloud computing platforms and distributed computing environments
    - Knowledge of software development best practices, including version control (Git), reproducible research workflows, and collaborative code development

If this sounds like an exciting opportunity to you, we are looking forward to reviewing your application, including your salary expectations and your earliest availability.

Your advantages:

- Attractive remuneration
- Social benefits, success-participation, and company pension schemes
- Flexible working hours, home office possible, good work-life balance
- Job Bike
- Company and team events