

## Scientist, Computational Biology

**Manifold Bio is a well-funded, VC-backed biotech startup with a mission to invent next-generation technologies to design drugs that will improve and save patient lives.** We are innovators in creating DNA and protein multiplexing technologies to engineer biological systems. Our team is highly collaborative and interdisciplinary. We are located in the Pagliuca Harvard Life Lab, a well-equipped modern lab space with a rich community of companies building cutting-edge technologies.

As a Computational Biologist, you'll support Manifold's team by designing and analyzing high-throughput experiments. You'll contribute to advancing our multiplex protein engineering platform and the design of novel protein therapeutic drugs. By adding your computational and scientific expertise to an interdisciplinary team, your role will be critical to developing world-changing methods for protein engineering.

*Note: The list of Desired Experiences and Capabilities below may not match every candidate exactly, and we're eager to train the right candidates for this role. Please apply if you meet at least two thirds of the criteria.*

### Responsibilities

- Work closely with Manifold's experimental team to iteratively design experiments and interpret results
- Design novel libraries of protein therapeutic designs to be experimentally tested
- Perform data analysis to identify patterns in the mapping from sequence to function
- Create next-generation tools – e.g. algorithms, models, software pipelines, or experimental approaches – that yield step changes in our ability to engineer protein therapeutics
- Maintain high-quality documentation of your discoveries in the form of written reports, technical presentations, electronic lab notebooks, code and software documentation

### Desired Experience and Capabilities

- PhD (or equivalent experience) in genetics, systems biology, biochemistry, computational biology, quantitative biology, or similar field; interdisciplinary work is of special interest
- 2+ years of professional and/or graduate school experience working with biological sequences or systems; wet lab experience is a plus
- Strong understanding of statistics fundamentals
- Proficiency with at least one programming language (Python preferred); a willingness to adapt to our Python / jupyter / AWS stack. Knowledge of best practices for software development (version control, test-driven development and good documentation habits) is preferred.
- First-hand technical experience in any of the following disciplines: bioinformatics, sequence analysis, Next Generation Sequencing (NGS) analysis, statistics, probabilistic modeling, machine learning, protein engineering, design of antibody or other binder libraries, biophysical modeling, Rosetta, or other quantitative modeling of biological systems
- Ability to meet the demands of multiple concurrent projects, and work efficiently in a fast-paced, high-growth environment
- A deep passion for science and developing new methods

**If you're excited to build a platform that combines these technologies to revolutionize how protein therapeutic discovery happens, please reach out to [careers@manifold.bio](mailto:careers@manifold.bio).**

*We value different experiences and ways of thinking and believe the most talented teams are built by bringing together people of diverse cultures, genders, and backgrounds.*