

## Computational Scientist, DNA & Protein Library Design

**Manifold Bio is a biotech company pursuing a pipeline of protein therapeutics using novel molecular measurement technologies and library-guided protein engineering.** Our drug discovery engine is differentiated by massively parallel screening *in vivo* from the beginning of our discovery process. This unique platform is powered by a proprietary protein barcoding technology that allows multiplexed protein quantitation at unprecedented scale and sensitivity. We combine this and other high-throughput protein engineering approaches with computational design to create antibody-like drugs and other biologics. Our world-class team of protein engineers, biologists, and computational scientists are working together to aim the platform at therapeutic opportunities where precise targeting is the key to overcoming clinical challenges.

### Position

**Manifold Bio is seeking an exceptional Computational Scientist to join our growing Compute team.** You will work closely with experimental and hybrid scientists designing and analyzing libraries and high-throughput experiments. Your efforts will contribute to advancing our multiplex protein engineering platform and the design of novel protein therapeutics. You will be expected to own and independently advance projects in areas related to your deep expertise such as protein design, DNA library design, or machine learning/biophysical modeling from MPRA data. You will work closely with our CSO and our other computational scientists to onboard new capabilities that advance the M-Design platform for data-driven engineering of drugs with desired properties.

### Responsibilities

- Work closely with Manifold's scientific teams to design maximally informative DNA-encoded libraries
- Collaborate on designing high-throughput experiments and analyze/interpret results
- Perform data analysis to identify patterns in the mapping from sequence to function
- Create tools, algorithms, models, and data pipelines to support our Compute and experimental teams
- Proactively share your findings with colleagues through high-quality documentation and discussions

### Qualifications

- PhD and/or 4+ years of equivalent experience in computational biology, bioinformatics, genomics, systems/synthetic biology, protein engineering, or a similar field working with biological sequences or systems; wet lab experience is a plus
- First-hand experience with any of the following: DNA/Protein sequence analysis, computational protein design, probabilistic modeling, machine learning, biophysical modeling, or antibody design
- Experience with the design and analysis of massively parallel reporter assays (MPRAs)
- Experience designing DNA libraries for binders, DMS, or equivalent high-throughput experiments
- Experience working with Next Generation Sequencing (NGS) data
- Strong understanding of statistics fundamentals
- Fluency in one or more programming languages, Python preferred
- Basic familiarity with version control, test-driven development, and Unix computing
- Ability to meet the demands of multiple concurrent projects in a fast-paced research environment
- Outstanding written and verbal communication skills
- 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.*