

Creating Experimental and Computational Tools to Devise Novel Protein Therapeutics

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[Gabriel Rocklin, PhD](#), is an assistant professor of [Pharmacology](#) and a member of the [Robert H. Lurie Comprehensive Cancer Center](#) of Northwestern University. He is also a faculty member at Northwestern's [Center for Synthetic Biology](#), where his [lab](#) develops high-throughput methods for protein biophysics and protein design, with a focus on protein therapeutics.

Q&A

What are your research interests?

I am interested in how protein sequences determine protein phenotypes such as structure, folding stability, conformational dynamics, binding affinity for small molecules and other proteins.

What is the ultimate goal of your research?

The goal of our lab is to develop experimental and computational tools to explore these sequence-phenotype relationships. We have both fundamental and applied sides of the lab. We investigate sequence-phenotype relationships as well as use our approaches to design new proteins for many applications. Our ultimate goal is to create computational and experimental tools that empower protein design research around the world, as well to develop new classes of protein therapeutics.

How did you become interested in this area of research?

I first became interested in biochemistry in high school. I saw pictures of protein structures in textbooks and was astonished at their complexity. When I was in college, several breakthroughs in computational protein design made the field very exciting for me, although I ended up not pursuing protein design research until I was a postdoc. One of my biggest surprises as a postdoc came when I asked 10 different people in our lab the best way to design new proteins. I got 10 very different answers! And there really wasn't any way to know who was correct. So that pushed me into developing new high-throughput experimental methods. These methods now make it possible to systematically examine protein design methods on a huge scale.

What types of collaborations are you engaged in across campus (and beyond)?

I think collaboration is one of the best parts of science. For now, my collaborations at Northwestern are with other members at the Center for Synthetic Biology, including [Mike Jewett](#), [Josh Leonard](#) and [Neil Kelleher](#). But as our applied projects develop, we will be excited to find new collaborators in disease areas where protein therapeutics could be beneficial. We also have a great collaboration on the other side of the river with Tobin Sosnick at the University of Chicago. Apart from those, the entire protein design field is extremely collaborative. Our lab is a member of RosettaCommons, a unique international consortium of labs that contribute to the development of the Rosetta software for protein modeling and design. This organization fosters social connections and lines of communication between over 50 labs worldwide. This ultimately promotes collaboration over competition. This helps smooth down the harshest aspects of science and helps the field progress much faster.

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