Proteins constitute the molecular machinery of life, carrying out diverse functions that underlie nearly every biological process. The design of new proteins with tailored properties holds enormous promise for applications such as industrial biotechnology and therapeutic intervention for major diseases. In my thesis, I present a collection of tools that apply generative modeling to surpass existing methods of protein structure prediction and design and expand the protein design toolkit to novel modalities and applications using deep learning. To design novel protein structures, I developed ProteinSGM, one of the first applications of diffusion models for protein structure generation. Then, I present protein side-chain packing model named FlowPacker that outperforms baselines in both runtime and performance for accurate determination of side-chain conformations. Finally, I describe NCFlow, a method that integrates flow matching with AlphaFold3-based modeling to design peptides with non-canonical amino acids (ncAAs). This thesis provides a detailed overview of protein structure prediction and design during the first half of the 2020's, and serves as a testament to the transformative role of deep learning in reimagining the way we design and model proteins.