

Probing biology using computational binder design

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Proteins that bind a chosen target with high affinity and specificity are among the most versatile tools in biology, underpinning therapeutics, diagnostics, biosensors, and a growing range of applications across health and agriculture. Generating them has traditionally required slow, resource-intensive experimental campaigns. Our previously developed software BindCraft made protein binder design broadly accessible to biologists. Now, we introduce BindCraft2, which makes the process substantially faster, fully open, and far more general. Its central advance is breadth. From a single settings file, BindCraft2 can design against essentially any protein target, structured or disordered, a single target or several at once, and can be deliberately steered to avoid off-targets. Across all of these, it produces the full range of protein-based binder modalities, from de novo miniproteins to antibodies and nanobodies, oligomers, and cyclic peptides. In doing so, BindCraft2 brings the entire breadth of protein-based binder design into one open, easy-to-use framework, putting the design of a binder for any target, in any format, within routine reach for biology.