Protein/Protein Interface Design

Cyrus automates the *Rosetta* Protein/Protein Interface Design (PPID) software protocols as a set of easy-to-use, SaaS offerings to computationally design:

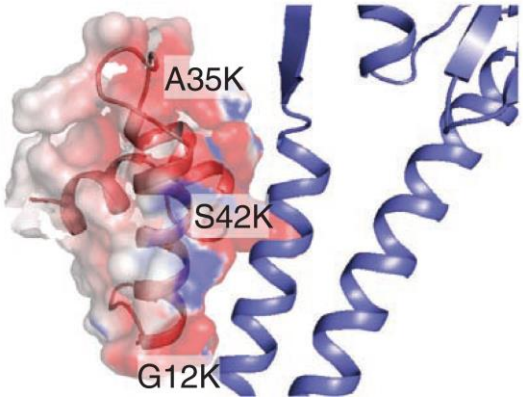
- Optimization of protein binding affinity
- New protein target binding activity in previously inactive proteins
- Rapid Non-Antibody-Protein based therapeutics and diagnostics

The only experimentally proven Protein/Protein Interface Design Software

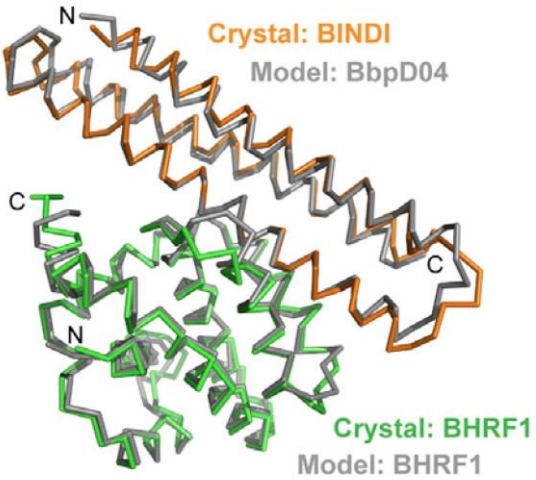
The only software to ever create proteins that bind to protein targets with nanomolar affinity and verification by crystal structures.

Experimentally proven to rapidly optimize existing protein/protein affinity

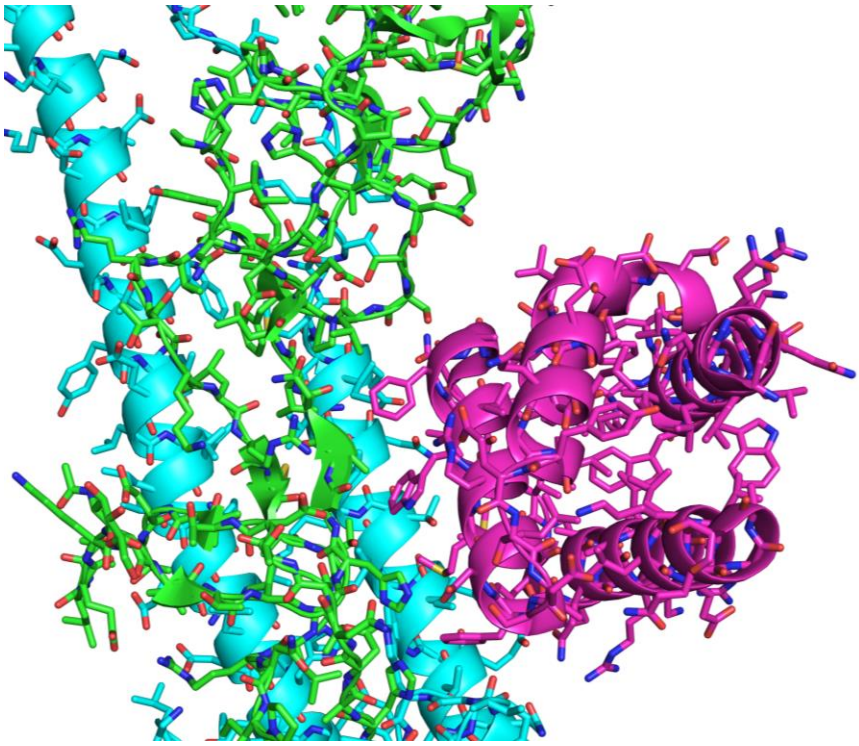
Computationally explore a vast range (>10^{13}) of mutations to design new sequences with optimized affinity that traditional screening approaches cannot discover.



Discover mutations not found by traditional screening
Proven in the computational re-design of a higher affinity Hemagglutinin binding protein (1).



Numerous Crystal-Structure validations
Design of several nanomolar affinity binders, including an inhibitor of an Epstein-Barr viral Bcl-2 protein (3).



Breakthrough Science
First computationally designed protein binders to an invariant region on the surface of influenza, with affinity similar to antibodies (2).

(1) *Whitehead, T.A., et al. "Optimization of affinity, specificity and function of designed influenza inhibitors using deep sequencing." Nature Biotechnology 30 (6), 543 - 548 (2012).*
(2) *Fleishman, S. J. et al. "Computational design of proteins targeting the conserved stem region of influenza hemagglutinin". Science vol. 332, 816–821 (2011).*
(3) *Procko, E. et al. "A computationally designed inhibitor of an Epstein-Barr viral Bcl-2 protein induces apoptosis in infected cells". Cell vol. 157, 1644–1656 (2014).*