# Enzyme Re-Design

*Computational Enzyme/Ligand Interaction Design*

Cyrus automates the *Rosetta* enzyme design software protocol as an easy-to-use, SaaS offering to computationally design:

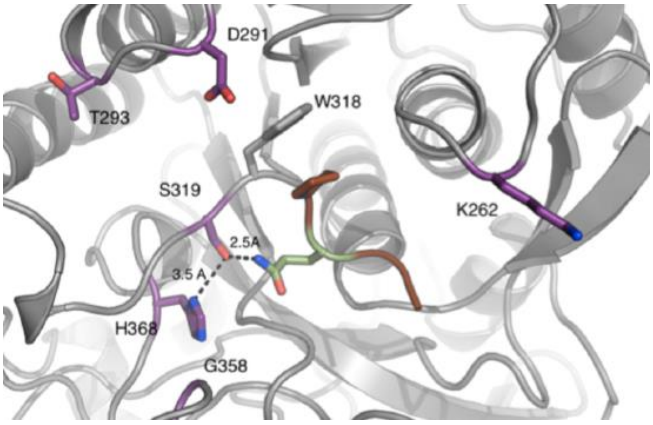
- New enzyme activity in previously inactive proteins
- Sub-nanomolar binding affinity to small molecules in previously inactive proteins
- Alteration of enzymatic activity and specificity

## The only experimentally proven enzyme design software

The only software to ever create small-molecule binding proteins with sub-nanomolar affinity verified by crystal structures.

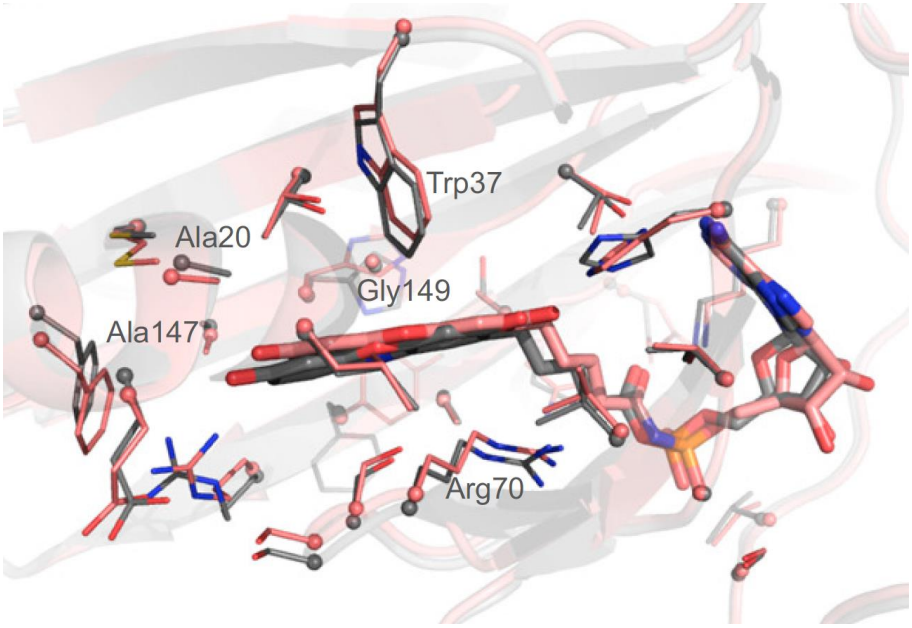
## Identify active enzymes where screening fails

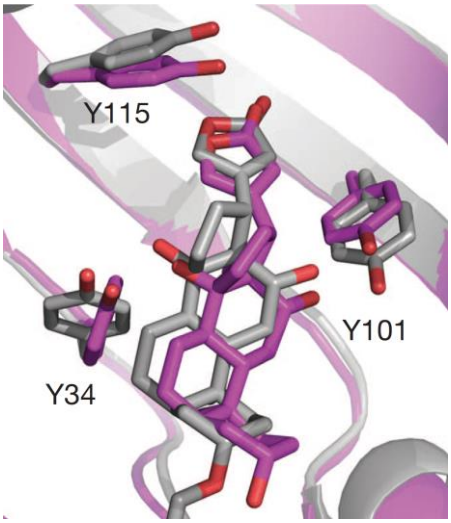
Computationally explore a vast range (>$10^{13}$) of mutations to design new sequences with desired activity that traditional screening approaches cannot discover.




***Highly Value IP Development (PVP Biologics)***

Proven in the re-design of a protease for activity on gluten (gliadinase enzyme) (2)




***Computational success where screening fails***

Proven success in identifying new enzyme variants for a resorufin ligase where surface display approaches did not identify active variants (1)

***Breakthrough Science***

- First "de novo" small-molecule binding protein in an inactive scaffold (3)
- First in a series of as-yet-unpublished computationally designed small-molecule binders


*(1) Liu et al. "Computational design of a red fluorophore ligase for site-specific protein labeling in living cells." PNAS, E4551-E4559 (2014).*
*(2) Wolf. et al. "Engineering of Kuma030: a gliadin peptidase that rapidly degrades immunogenic gliadin peptides in gastric conditions". JACS 137, 13106-13113 (2015).*
*(3) Tinberg. et al. "Computational design of ligand-binding proteins with high affinity and selectivity". Nature 501, 212-216 (2013).*