




Cyrus automates a set of *Rosetta* protein design software protocols as an easy-to-use, SaaS offering proven to reliably identify stabilizing mutations in a wide variety of proteins:

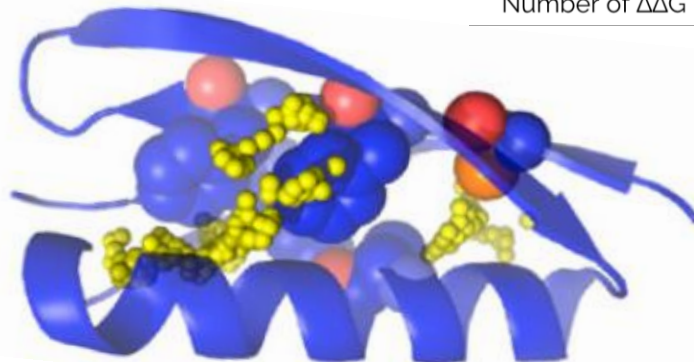
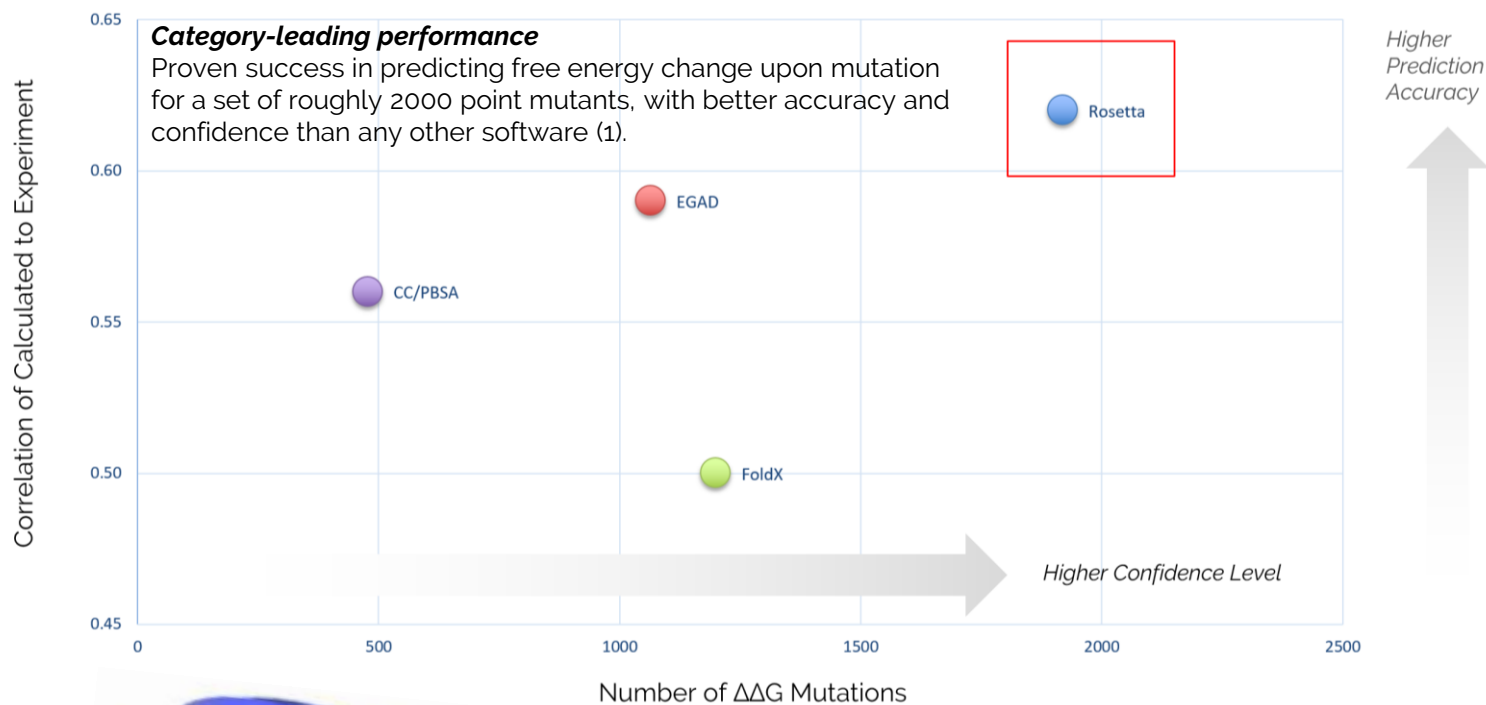
-  Correctly predict stabilizing single point mutants.
-  Category-leading performance in quantitatively calculating energy change upon point mutation.
-  Experimentally proven protein stabilization algorithms

Highest prediction accuracy and confidence

Only Cyrus delivers software that is refined and tested on large experimental data sets. Our protein mutational free energy predictor has been tested and developed for several years, outperforming similar tools (1).

Experimentally demonstrated thermo-stabilization

Thermo-stabilization is often achieved by re-designing a protein core. Our custom-built stabilization protocol has been experimentally validated on a number of proteins (2).



Experimentally demonstrated thermo-stabilization

- Algorithm to predict stabilizing protein core mutations (2)
- Aggressive *in silico* core re-sampling discovers mutations verified experimentally to stabilize proteins.

(1) Kellogg et al. "Role of conformational sampling in computing mutation-induced changes in protein structure and stability." *Proteins* 79, 830-838 (2010).
 (2) Borgo. et al. "Automated selection of stabilizing mutations in designed and natural proteins". *PNAS* 109, 1494-1499 (2012).