Computational Protein Stabilization

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 protein point mutants faster and more accurately than FEP.
- Category-leading performance in quantitatively calculating energy change upon point mutation.
- Experimentally proven protein stabilization algorithms.

Highest prediction accuracy and confidence

Cyrus delivers software that is refined and tested on large experimental data sets. Cyrus has recently released an improved version of the protein mutational free energy calculator in Rosetta, based on work from the DiMaio lab at UW (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 (2,3).

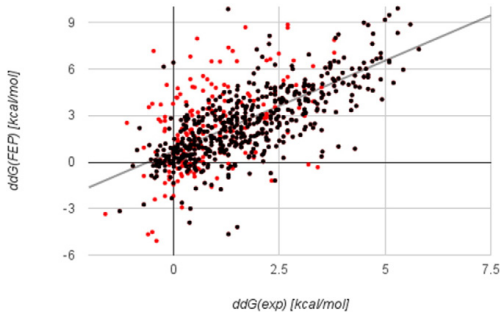
Rosetta / Bench ΔΔG is fast and accurate

	Rosetta***	FEP*	CC/PBSA**	EGAD**	Imutant2**	FoldX**
Exp't correlation	0.69	0.63	0.56	0.59	0.54	0.50
# data points	1210	712	478	1065	933	1200

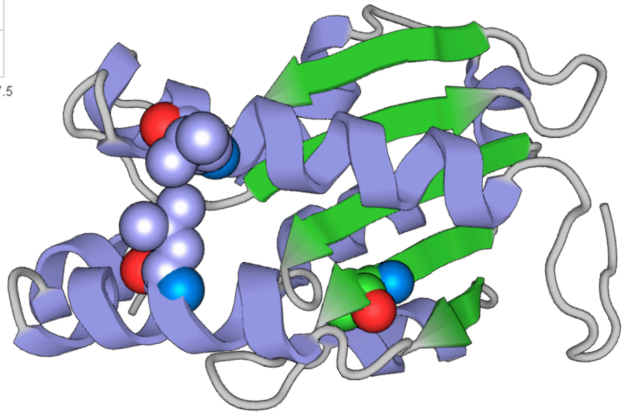
Predictions for the FoldX experimentally stability data set (Guerois, Nielson & Serrano *JMB* **320** 369 (2002)
*From: Steinbrecher, Zhu, Wang, Abel, Negron, Pearlman, Feyfant, Duan & Sherman *JMB* **429** 948 (2017)
From: Potapov, Cohen & Schreiber *PEDS* **22 553 (2009)
***From: Kellogg, Leaver-Fay & Baker *Proteins* **79** 830 (2011)

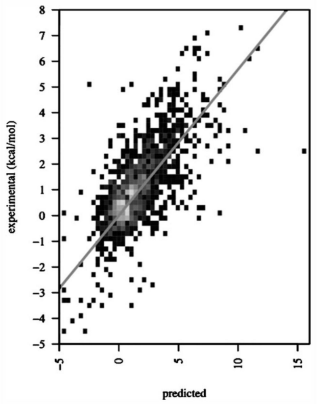
FEP* Throughput: 2-4 mutations/day Per GPU card

Rosetta*** Bench: Throughput: 5,000-10,000 mutations/day



Predicted vs experiment:





(1) Park et al. J. Chem Theory Computation vol. 12 p. 6201 (2016); (2) Lau et al. JBC vol. 293, p. 13224 (2018); (3) Jacak et al. Proteins vol. 80, p. 825 (2012)