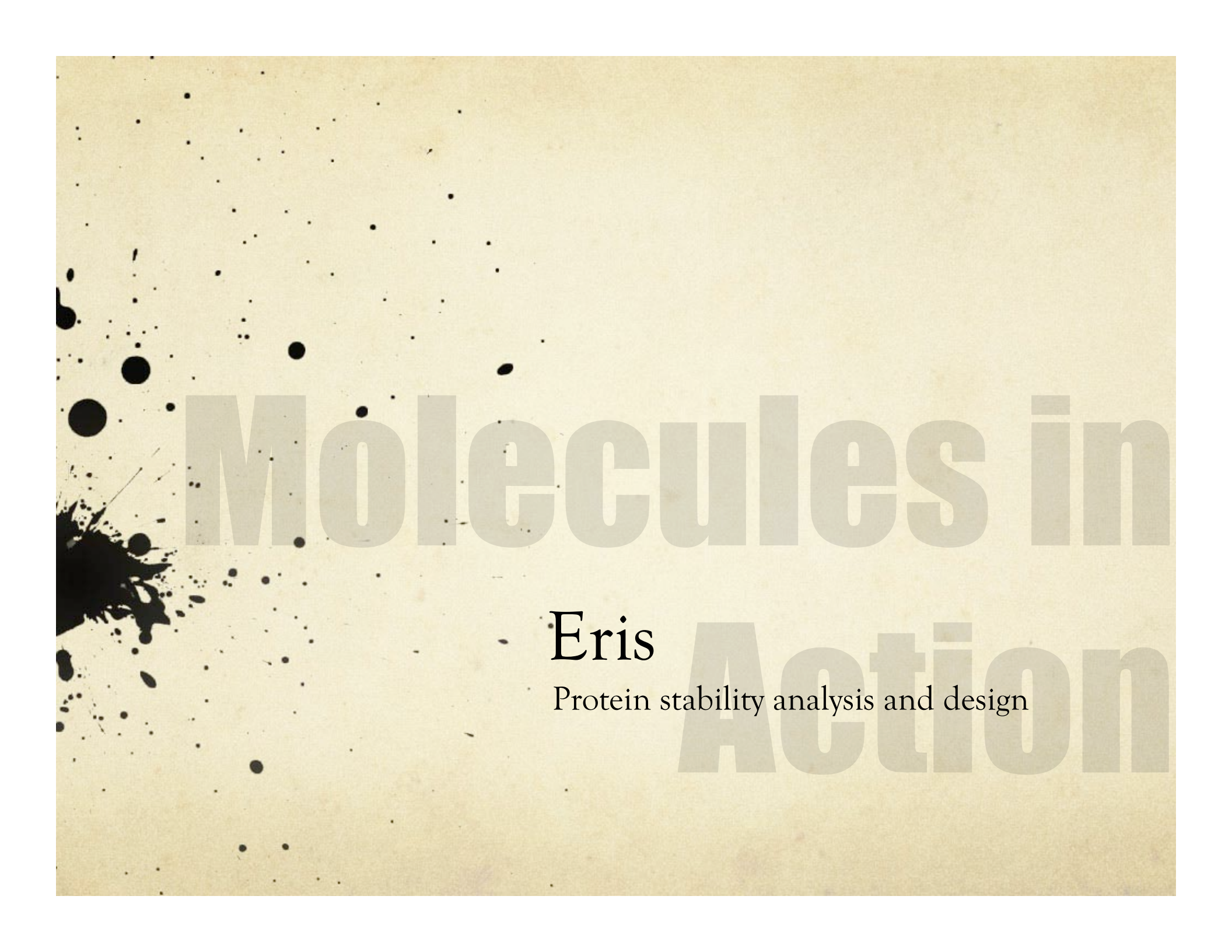




Molecules in

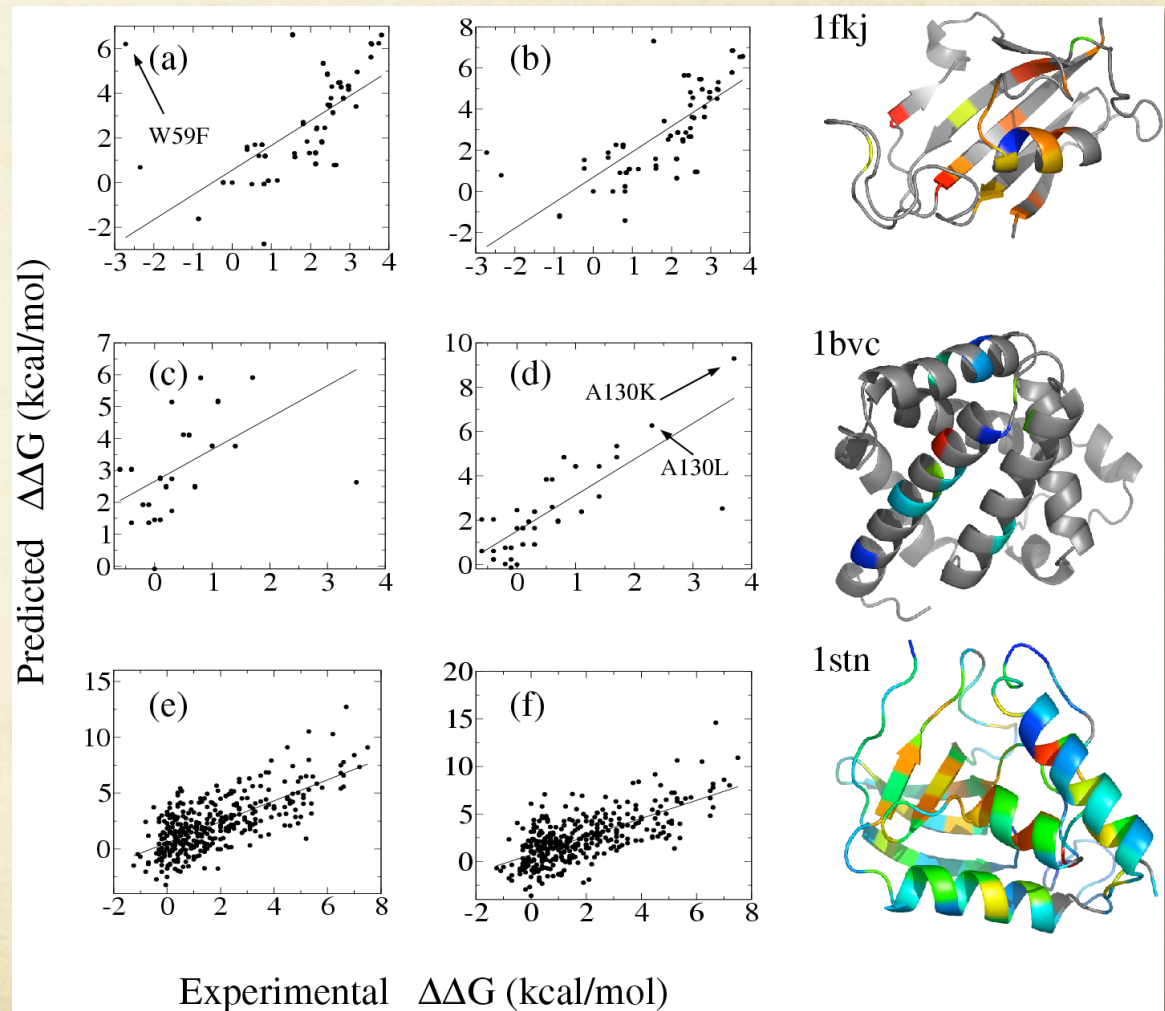
Eris

Protein stability analysis and design

Action

Eris

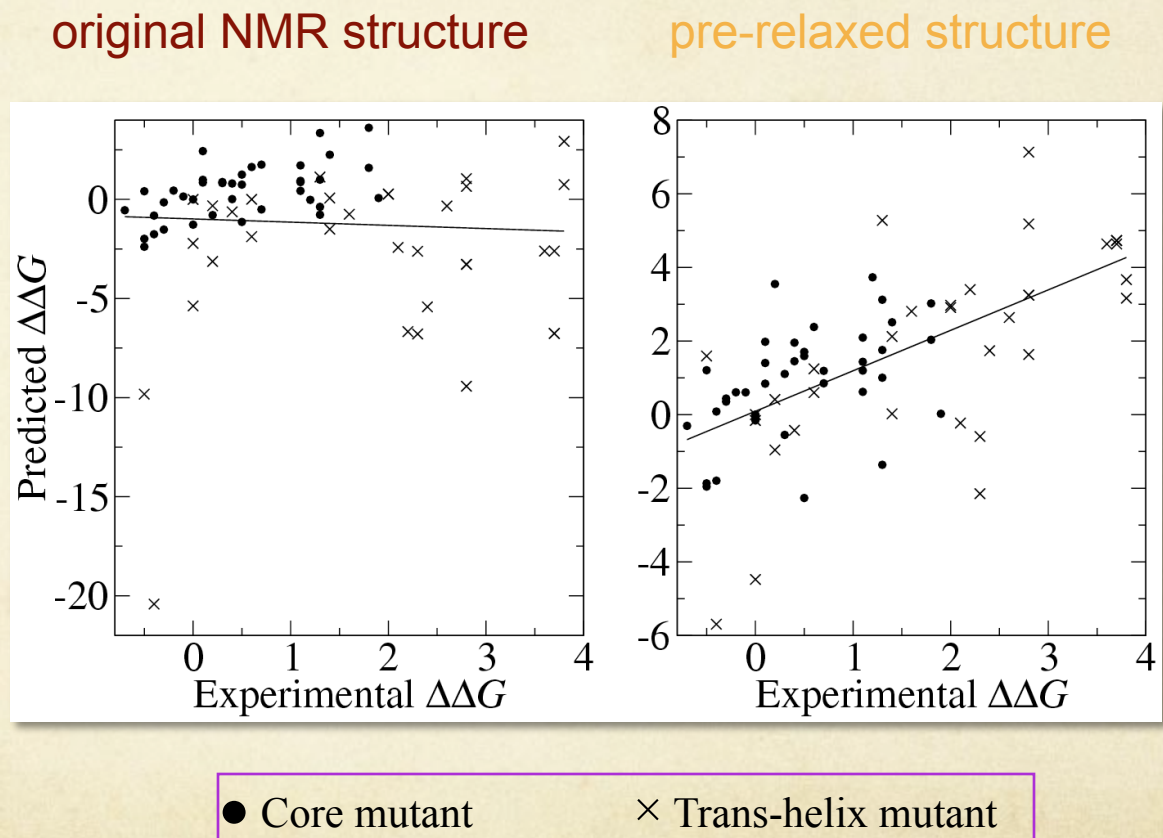
- Eris server calculates the change of the protein stability induced by mutations ($\Delta \Delta G$) utilizing the recently developed Medusa modeling suite.
- The $\Delta \Delta G$ values of a large dataset (>500), calculated and compared with the experimental data, feature significant correlations (~ 0.8).



Eris

- Eris allows refinement of the protein structure when high-resolution structures are not available.
- Compared with many other stability prediction servers, Eris is not trained using protein stability data and is valid for a wide range of proteins.
- Eris models backbone flexibility, which turns out to be crucial for $\Delta \Delta G$ estimation of small-to-large mutations.

Structural refinement improves $\Delta \Delta G$ estimation.



Eris

Eris stand-alone package is commercially available and includes the following functions:

- **[ddg]** Estimates the changes in protein stability upon point mutations, using either fixed or flexible backbone method.
- **[fixed backbone design]** For a given protein backbone conformation, identifies an amino sequence that minimizes energy of this conformation (fixed-backbone redesign).
- **[flexible backbone design]** For a given protein backbone conformation, identifies an amino sequence that minimizes energy of this conformation with the ability to locally perturb this conformation (flexible-backbone redesign).
- **[scan]** For a given protein conformation and a given amino acid position, identifies a substitute amino acid that minimizes this conformation.

Eris



<http://moleculesinaction.com/eris>