

A.

PremPS Method Help Results Download Contact

PremPS - Predicting the Effects of Mutations on Protein Stability

PremPS evaluates the effects of single mutations on protein stability by calculating the changes in unfolding Gibbs free energy. It can be applied to a large number of tasks, including finding functionally important variants, understanding their molecular mechanisms and protein design. 3D structure of a protein is required for this method.

Step 1 - Select Protein

Input PDB code: Bioassembly 1st
 Example: 1YU5 Asymmetric Unit

Crystal structure of Native Sperm Whale myoglobin from low ionic strength environment (Form 1)

Upload PDB file: no file selected
 Formal description for uploaded file

School of Biology & Basic Medical Sciences, Southern University
 150 Hainan Road, Suzhou, Jiangsu, 215123 P.R. China

B.

Step 2 - Select Protein Chains

PDB id: 1U7S
Chain A : Myoglobin

Chains

C.

Step 3 - Select Mutations

PDB id: 1U7S
Chains
Chain A : Myoglobin

Manually select

Specify One or More Mutations:

Chain to Mutate	Residue	Mutant Residue	View in Structure
Chain A	Q 26 (GLN)	A (ALA)	<input type="button" value="View"/>
Chain A	L 104 (LEU)	D (ASP)	<input type="button" value="View"/>
Chain A	R 118 (ARG)	C (CYS)	<input type="button" value="View"/>

Need mutant structure for each mutation? It takes more time!

Add or Remove Mutations

Manually select

Upload Mutation List: no file selected

Need mutant structure for each mutation? It takes more time!

Manually select

Alanine Scanning

Need mutant structure for each mutation? It takes more time!