

SAAMBE-SEQ

Running predictions

User Input Mutations

Prediction of $\Delta\Delta G$ over Single Mutation

Sequence Selection **1**

Predicting the effect of one mutation only for this protein complex
Please Provide the Mutated Chain Sequence

>fastaA **3**
FPTIPLSRLEKAMLRRAHRLHQLAFDITYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQ
QKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDEERIQLMGRLEDGSPRTG
QIFKQYTSKFDTNSHNDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF

Please Provide the Interaction Chain Sequence

>fastaB **4**
FSGSEATANLFRAPWSLQSVNPGKLTNSSKEPKFTKCRSPERETFSCHWTDEVHHGTKNLGP
IQLFYTRRNTQEWQEWKECPDYVVSAGENSICYFNSSFTSIWIPYCIKLTNSGGTVDEKCFSD
EIVQDPDPIALNWTLNVS LTGIHADIQVRWEAPRNADIQKGMWVLELQYKEVNETKW

OR,
Upload the sequence in FASTA format
[Click here to Download a sample FASTA format](#)

Upload the Mutated Chain Sequence
 5

Upload the Interaction Chain Sequence
 6

Mutation Details

Position: **7**

Original Amino Acid: **8**

Mutated Amino Acid: **9**

Sequence Selection **2**

Predicting the effect of multiple single mutations within the same protein complex - requires text file with mutations list
Please Provide the Mutated Chain Sequence

Please Provide the Interaction Chain Sequence

OR,
Upload the sequence in FASTA format
[Click here to Download a sample FASTA format](#)

Upload the Mutated Chain Sequence

Upload the Interaction Chain Sequence

Mutation Details

10

Upload a plain text file with one mutation per line, [click here](#) to view an example for reference

- The *Single Mutation* **(1)** option allows the user to submit one single mutation for prediction. User must provide two sequences corresponding to two protein chains.
 - Users are required to provide a wild-type sequence (the chain where the mutation is located) by pasting **(3)** a sequence in fasta format or uploading **(5)** a file in fasta format.
 - Users also are required to provide the interaction sequence of another chain by pasting **(4)** a sequence in fasta format or uploading **(6)** a file in fasta format.
 - Details on the single mutation should be provided: **(7)** *residue position*, **(8)** *wild type amino acid* and **(9)** *mutant amino acid* (using the one letter amino acid code). The residue position must be consistent with the sequence file.
- The *Mutation List* **(2)** option allows the user to submit a list of single mutations to be analyzed in batch.

- Similar to the *Single Mutation* option, a wild-type sequence is required and can be input by pasting a sequence in fasta format or uploading a file in fasta format.
- The list of single-point mutations must be input (**10**) by uploading a file containing the mutation information (*wild-type* residue code, *position* and *mutant* residue code). The file format requires one mutation per line (split by space). A sample file is also provided.

Results

Original Amino Acid:	Mutated Amino Acid:	
<input type="text" value="R"/>	<input type="text" value="R"/>	<input type="text"/>
<input type="button" value="Submit Query"/>		<input type="button" value="Submit Query"/>

Results will be displayed here

[Please click here to open the Output File](#)

Single Mutation and Multiple single mutations

- The predicted $\Delta\Delta G$ for mutation will be displayed on the bottom of the same page. Users can download the output file.