SAAMBE-3D

Running predictions of ΔΔG due to single mutation (1)

User Input Mutations

- The *Single Mutation* option allows the user to submit one single mutation for prediction.
  - Users are required to provide a wild-type structure by uploading **(3)** a file in pdb format.
  - Details on the single mutation should be provided: **(5)** *residue* position, **(6)** *mutated chain*, **(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 PDB file.
- The *Mutation List* 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 uploading **(4)** a file in pdb format.
  - The list of single-point mutations must be input **(7)** by uploading a file containing the mutation information (*chain* identifier, *residue position, wild-type* residue code and *mutant* residue code). The file format requires one mutation per line (split by space). A sample file is also provided.

Results

Single Mutation

- The predicted ΔΔG for a single-point mutation will be displayed on the bottom of the same page.

Multiple single mutations
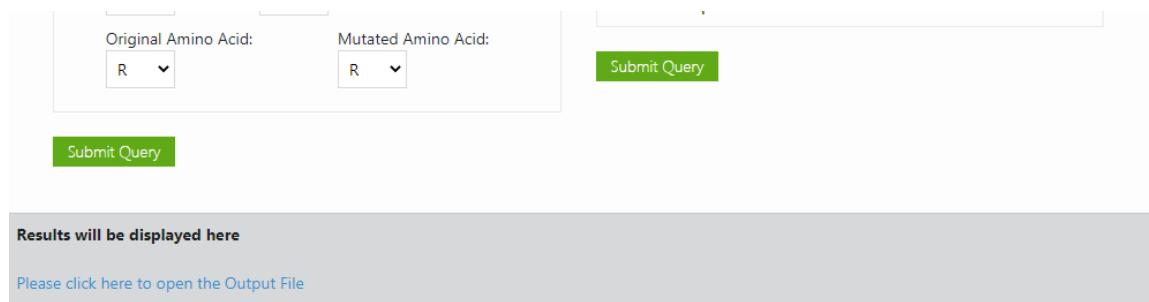
- The predicted ΔΔG for the multiple single mutations will be showed on the bottom of the same page. Users can download the output file.

Predict whether the given mutation is disruptive or non-disruptive **(2)**

The input is exactly the same as the predictions of ΔΔG, and the result is displayed in the same position (bottom).