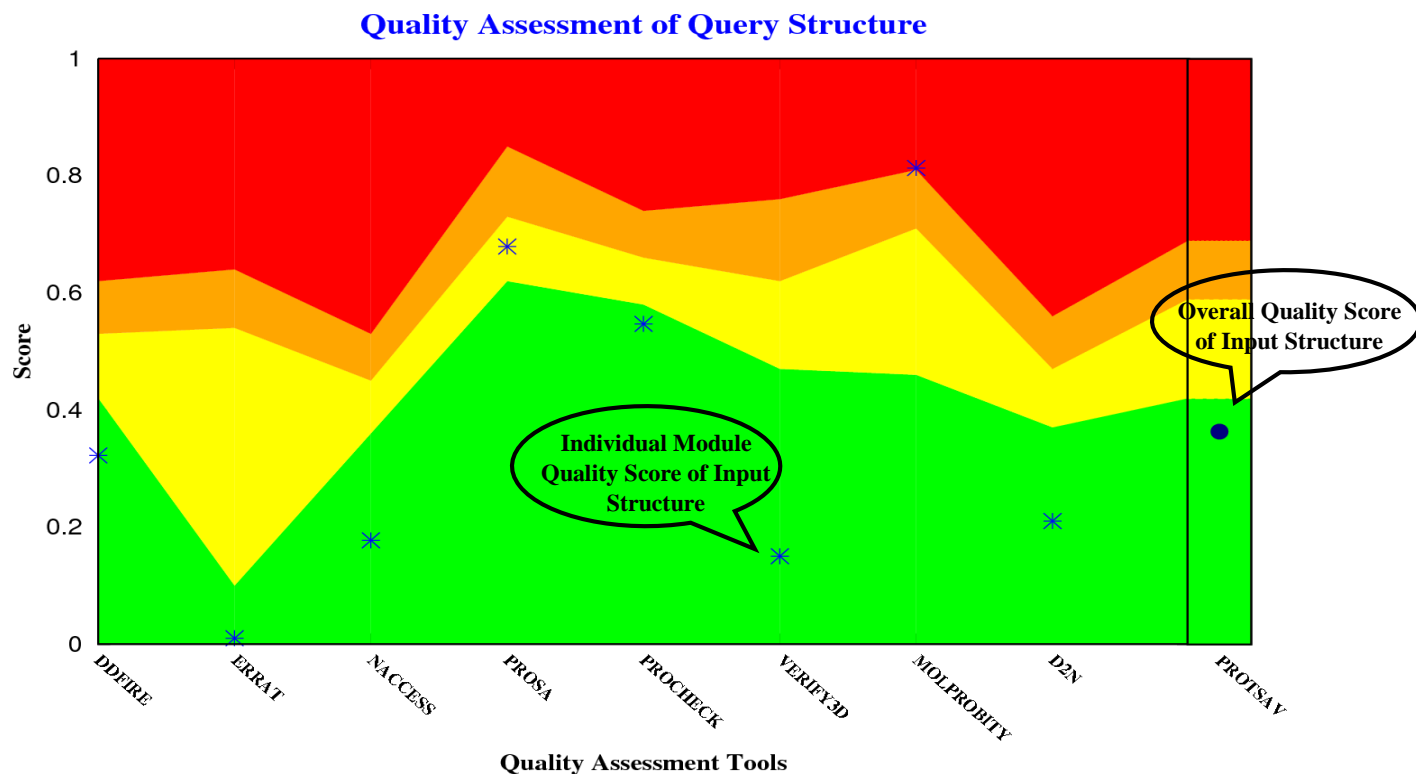


# User's Guide for ProTSAV

- ❖ User can perform quality assessment of single protein structure or multiple protein structure.
- ❖ User should submit the structure in pdb file format and it should not have missing residues. Missing residues in start or end of pdb file are acceptable.
- ❖ User should select all the modules to get accurate quality assessment, although user can select any number of modules according to choice.
- ❖ In case of single pdb file user will get a color plot representing quality of input protein structure as shown in figure below. Green color indicates the input structure to be in 0-2 Å rmsd, yellow color indicates 2-5 Å, orange color indicates 5-8 Å and red color indicates input structure to be beyond 8 Å.



- ❖ Along with the color representation of quality assessment of input protein (downloadable on direct click on it), user can download results of individual module selected at submission.
- ❖ On an average ProTSAV take around 50-60 seconds for performing quality assessment of single protein structure depending upon the size of protein structure.
- ❖ In case of multiple protein structures (maximum upto 100), user should submit all the structures in the form of zipped file and should furnish an email id for receiving the results. In the results user will be provided with rankings of submitted multiple structures as shown below:

SAMPLE_2	ProtSAV1	0.133857
SAMPLE_3	ProtSAV2	0.143714
SAMPLE_4	ProtSAV3	0.172
SAMPLE_1	ProtSAV4	0.341143
SAMPLE_7	ProtSAV5	0.372857
SAMPLE_5	ProtSAV6	0.377571
SAMPLE_6	ProtSAV7	0.382571

In first column, name of submitted pdb file is given, in second column ProTSAV ranking is given, in third column overall quality score is given.

- ❖ In case of multiple protein structures, the time taken will be longer.

For any query or suggestion please feel free to write us at:

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