

“Instruction: How to use this tool”

- This tool is only for protein not for DNA/RNA or any other biomolecules.
- PDB format of protein file is supported. No HEATM record should be in protein file.
- Single chain PDB is preferred.
- Multiple structures can be uploaded by keeping structures in a single directory and compressing them into TAR zipped format.
- In order to receive email notification, the user can provide email-address
- User can use job Id to know the status of structure.

Note: As this tool is to detect native/native like structure from pool of decoys so only multiple structures submission will be meaningful.

Explanation of Result:

Successful execution of this tool gives six different files as output, following is explanation of each files:

- result_pcSM: Name of top ten structures selected by pcSM along with their parameters value
- result_pcSM_all: Name of all structures with their parameters value
- result_pcSM.xls: Name of top ten structures selected by pcSM along with their parameters value in Excel format.
- result_pcSM_all.xls: Name of all structures with their parameters value in Excel format.
- result_pcSM.html: Name of top ten structures selected by pcSM along with their parameters value in HTML form
- result_pcSM_all.html: Name of all structures with their parameters value in HTML format.