Protein Repair and Analysis Server: A Web Server to Repair PDB Structures, Add Missing Heavy Atoms and Hydrogen Atoms, and Assign Secondary Structures by Amide Interactions

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ABOUT CHAIN SELECTION

Users can specify a specific chain if they need to, otherwise all chains will be processed. The chain should be specified as a positive integer. PRAS will map the integer to alphabets. This is because a chain can start with any letter. Thus, 1 = the first chain, 2 = the second chain, 3 = the third chain, etc.

Note that if user makes an invalid selection (i.e., selecting a chain that does not exist in the file supplied) PRAS will notify user and then terminate the execution.

If user selects a specific chain, files generated from the assignment of secondary structure and plots of four Ramachandran types will be numbered 1 because there will be only one chain when the PRAS generated PDB or mmCIF structure is passed to these modules.