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# The PyRosetta Interactive Platform For Protein Structure Prediction And Design A Set Of Educational Modules

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PyRosetta is an interactive Python-based interface to the powerful Rosetta molecular modeling suite. It enables users to design their own custom molecular modeling algorithms using Rosetta sampling methods and energy functions. PyRosetta was created at Johns Hopkins University by Jeffrey J. Gray, Sergey Lyskov, and the PyRosetta Team.

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PyRosetta (<http://www.pyrosetta.org>) is a Python-based interactive platform for accessing the objects and algorithms within the Rosetta protein structure prediction suite. Rosetta, developed by a consortium of laboratories in the Rosetta Commons, has an unmatched variety of functionalities and is one of the most accurate protein structure prediction and design approaches. The workshops teach how to measure and manipulate protein conformations, calculate energies in low- and high ...

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>>from rosetta import \* >>init() PyRosetta has primarily two modes of use: interactive mode and script mode. Interactive-mode uses IPython and allows the user to type in PyRosetta commands in real-time. It is excellent for learning to use PyRosetta or running simple commands quickly.

### **Table of Contents - Johns Hopkins University**

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