InterMap3D: predicting and visualizing co-evolving protein residues

InterMap3D predicts co-evolving protein residues and plots them on the 3D protein structure. Starting with a single protein sequence, InterMap3D automatically finds a set of homologous sequences, generates an alignment and fetches the most similar 3D structure from the Protein Data Bank (PDB). It can also accept a user-generated alignment. Based on the alignment, co-evolving residues are then predicted using three different methods: Row and Column Weighing of Mutual Information, Mutual Information/Entropy and Dependency. Finally, InterMap3D generates high-quality images of the protein with the predicted co-evolving residues highlighted.

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