FeatureMap3D - a tool to map protein features and sequence conservation onto homologous structures in the PDB - DTU Orbit (12/05/2017)

FeatureMap3D is a web-based tool that maps protein features onto 3D structures. The user provides sequences annotated with any feature of interest, such as post-translational modifications, protease cleavage sites or exonic structure and FeatureMap3D will then search the Protein Data Bank (PDB) for structures of homologous proteins. The results are displayed both as an annotated sequence alignment, where the user-provided annotations as well as the sequence conservation between the query and the target sequence are displayed, and also as a publication-quality image of the 3D protein structure with the selected features and sequence conservation enhanced. The results are also returned in a readily parsable text format as well as a PyMol (http://pymol.sourceforge.net/) script file, which allows the user to easily modify the protein structure image to suit a specific purpose. FeatureMap3D can also be used without sequence annotation, to evaluate the quality of the alignment of the input sequences to the most homologous structures in the PDB, through the sequence conservation colored 3D structure visualization tool. FeatureMap3D is available at: http://www.cbs.dtu.dk/services/FeatureMap3D/.

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