The Jena Library of Biological Macromolecules (JenaLib) has served the scientific and educational communities since 1993. It is a freely accessible internet resource aimed at a better dissemination of information on three-dimensional biopolymer structures with an emphasis on visualization and analysis. It provides access to all structure entries at the Protein Data Bank (PDB) and the Nucleic Acid Database (NDB).

**Introduction and Aim**

An automated alignment between UniProt sequences and the sequences extracted from the PDB coordinates allows the mapping of any kind of sequence-based information onto 3D structures. Besides single amino acid polymorphisms (SAP) from the UniProtKB database and ProSite motifs also exon and exon-exon boundary information extracted from Ensembl and Pfam domains are mapped onto 3D structures.

This information as well as SCOP and CATH domains and active sites and ligands can be visualized by the Jmol-based Jena3D viewer (jena3d.fli-leibniz.de). JenaLib offers a Google-like QuickSearch option and allows the user-controlled generation of entry lists. Tree browsers facilitate the navigation through SCOP, CATH and Pfam hierarchical trees. Recently we have started to offer tools for the statistical analysis of structure sets, the determination of mean distances between amino acid Calpha atoms being the first example.

**Selected Features**

**Jena3D Viewer - Homepage**

**Classification Tree Browser**

**Exon Mapping and Visualization**

**Sequence/Alignment View – Data Integration**

**Sequence Pattern Search – Protein/Nucleic Acid**

Visualization of exons mapped to PDB entry 11Z2 in the JenaLib Jmol classification tree browser (mainly collapsed).

The alignment view of PDB entry 1JM7 is shown. The integrated display of structural features like SCOP domains, SAPs from UniProtKB/CancerSNP (amino acid sidechains; wt – magenta, mutated – cyan) can be controlled individually.

Sequence pattern search in PDB sequences. 100% identical sequences are grouped (non-redundant set). Left: input form Right: example output (incomplete).

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