

Protein Family Alignment Annotation Tool

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1 Introduction.

PFAAT is a JAVA based application designed to facilitate the analysis and annotation of large protein families. Since its release in 2003, a number of feature enhancements have been added: 1). Improved synchronization and selection between alignment sequences, tree nodes, and structural elements. 2). Sequence annotation now includes 10 synonyms, a user defined web link, and an unlimited number of user defined annotations. 3). Sequences can be sorted and filtered by residue composition in a column, sequence name, and percent identity. 4). A number of published residue properties are available for the analysis of binding sites. 5). Novel algorithms to analyze sequence conservation. 6). Cluster IDs can be assigned via a vertical bar on the tree viewer. 7) Tree branches can be colored by cluster ID, sequence annotation, and user designation.

2 Software and files.

PFAAT is available from <http://pfaat.sourceforge.net/>.

3 Figures and Tables.

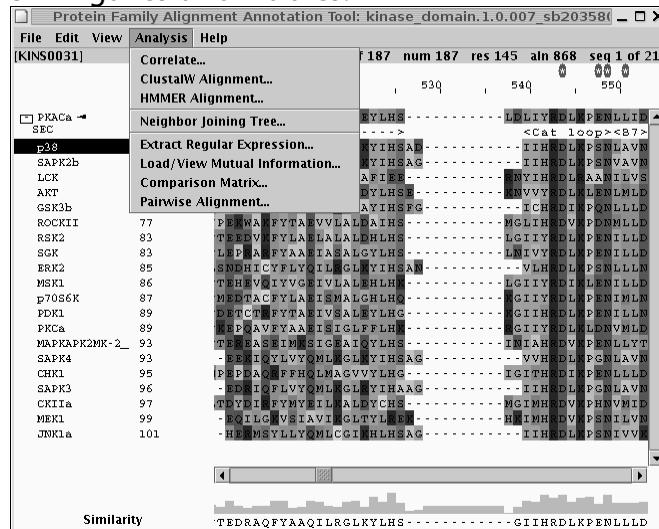


Figure 1: Snapshot of PFAAT.

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