Resource Summary Report

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An Integrated Multiple Structure Visualization and Multiple Sequence Alignment Application

RRID:SCR_001646
Type: Tool

Proper Citation

An Integrated Multiple Structure Visualization and Multiple Sequence Alignment Application (RRID:SCR_001646)

Resource Information

URL: http://ilyinlab.org/friend/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Friend is a bioinformatics application designed for simultaneous analysis and visualization of multiple structures and sequences of proteins and/or DNA/RNA. The application provides basic functionalities such as: structure visualization with different rendering and coloring, sequence alignment, and simple phylogeny analysis, along with a number of extended features to perform more complex analyses of sequence structure relationships, including: structural alignment of proteins, investigation of specific interaction motifs, studies of protein-protein and protein-DNA interactions, and protein super-families. Friend is also useful for the functional annotation of proteins, protein modeling, and protein folding studies. Friend provides three levels of usage; 1) an extensive GUI for a scientist with no programming experience, 2) a command line interface for scripting for a scientist with some programming experience, and 3) the ability to extend Friend with user written libraries for an experienced programmer. The application is linked and communicates with local and remote sequence and structure databases.

Synonyms: FRIEND

Resource Type: rendering software, data visualization software, software resource, software application, data analysis software, data processing software

Defining Citation: PMID:16076889

Keywords: alignment, analysis, bioinformatics, database, dna, interaction, motif, phylogeny, protein, rna, scientist, sequence, structure, super-family, visualization, bio.tools

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: An Integrated Multiple Structure Visualization and Multiple Sequence Alignment Application

Resource ID: SCR_001646

Alternate IDs: biotools:friend, nif-0000-10149

Alternate URLs: https://bio.tools/friend

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250425T055210+0000

Ratings and Alerts

No rating or validation information has been found for An Integrated Multiple Structure Visualization and Multiple Sequence Alignment Application.

No alerts have been found for An Integrated Multiple Structure Visualization and Multiple Sequence Alignment Application.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.