

Resource Summary Report

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Family Pairwise Search - Protein Family Classification

RRID:SCR_007202

Type: Tool

Proper Citation

Family Pairwise Search - Protein Family Classification (RRID:SCR_007202)

Resource Information

URL: <http://fps.sdsc.edu/>

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Description: Family Pairwise Search (FPS) is a protein homology detection algorithm that combines sequence similarity scores from a pairwise alignment algorithm such as Smith-Waterman or BLAST. Source code and a web server are available. This is a method for scoring a query sequence against a family of sequences. (Note: the query sequence may alternatively be a sequence, a GCG profile or a BLAST checkpoint file.) FPS compares the query sequence individually (pairwise) to each sequence in the family and then combines the pairwise scores into an overall score for the match. This site provides access to * a web server to allow you to use FPS to search various protein family libraries for matches to a protein sequence, * an overview of the FPS algorithm, * a description of the inputs and outputs for the FPS server, * a sample output from the FPS server, and * a release notes for FPS, and * links to several papers about FPS, and * the FPS source code for non-commercial use. * COPYRIGHT information and how to license FPS for commercial use is described here.

Abbreviations: FPS

Synonyms: Family Pairwise Search

Resource Type: service resource, software resource, source code

Funding: National Biomedical Computation Resource

Resource Name: Family Pairwise Search - Protein Family Classification

Resource ID: SCR_007202

Alternate IDs: nlx_20019

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260912T200146+0000

Ratings and Alerts

No rating or validation information has been found for Family Pairwise Search - Protein Family Classification.

No alerts have been found for Family Pairwise Search - Protein Family Classification.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Walsh TP, et al. (2008) SCANPS: a web server for iterative protein sequence database searching by dynamic programming, with display in a hierarchical SCOP browser. Nucleic acids research, 36(Web Server issue), W25.

Kapitonov VV, et al. (2003) The esterase and PHD domains in CR1-like non-LTR retrotransposons. Molecular biology and evolution, 20(1), 38.