

Resource Summary Report

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hPATM

RRID:SCR_006224

Type: Tool

Proper Citation

hPATM (RRID:SCR_006224)

Resource Information

URL: <http://bioinformatics.biol.uoa.gr/hPATM/>

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Description: A web tool, based on a heuristic transformation of the original global pairwise and local pairwise alignment algorithms, offers objective alignments for transmembrane protein sequences. hPATM takes advantage of the information offered by the knowledge of the position of transmembrane segments, by experiment or prediction. The heuristic approach may reveal similarities between diverge sequences with low percentages of identity and similarity. The produced alignments, based on common structural scaffolds derived by the transmembrane segments of the sequence, can be used to spot conserved non-transmembrane segments or as a basis for the production of 3-D models via homology modelling. The hPAFAG algorithm is based on the heuristic transformation of the Needleman & Wunsch and Smith & Waterman algorithms, featuring affine gap penalties. The heuristic transformation is based on two extra features: * a heuristic bonus, added to the score when two amino acids that belong to transmembrane segments are aligned. * a heuristic gap penalty, subtracted from the score when a gap is opened in a transmembrane segment. This way transmembrane segments are anchored (not by force, but by more strict alignment) together, allowing the pairwise alignment to focus on non-transmembrane segments. This web server offers a friendly interface for the hPATM command line version. The algorithm was implemented in PERL and the source code of the command line version is available on request by the authors.

Abbreviations: hPATM

Synonyms: Heuristic Pairwise alignment for Transmembrane Proteins, hPATM - heuristic pairwise alignment for transmembrane proteins

Resource Type: service resource, source code, data analysis service, software resource, production service resource, analysis service resource

Keywords: heuristic, pairwise alignment, transmembrane protein, protein, algorithm, transmembrane, alignment, transmembrane segment, fasta

Availability: All rights are reserved for the whole or part of the program. Permission to use, Copy, And modify this software and its documentation is granted for academic use provided that authors are properly cited.

Resource Name: hPATM

Resource ID: SCR_006224

Alternate IDs: nlx_151775

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260731T042720+0000

Ratings and Alerts

No rating or validation information has been found for hPATM.

No alerts have been found for hPATM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.