## **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 segmets, 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 nontransmembrane 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 segmens are aligned. \* a heuristic gap penalty, substracted 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: source code, service resource, production service resource, data analysis

service, analysis service resource, software resource

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

#### Funding:

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Resource Name: hPATM

Resource ID: SCR\_006224

Alternate IDs: nlx\_151775

**Record Creation Time:** 20220129T080235+0000

Record Last Update: 20250429T055038+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.