

# Resource Summary Report

Generated by [dkNET](#) on Aug 25, 2026

## hPATM

RRID:SCR\_006224

Type: Tool

---

### Proper Citation

hPATM (RRID:SCR\_006224)

---

### Resource Information

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

**Proper Citation:** hPATM (RRID:SCR\_006224)

**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:** analysis service resource, data analysis service, production service resource, service resource, software resource, source code

**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:** 20260821T193800+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.