

# Resource Summary Report

Generated by [NIF](#) on Aug 16, 2026

## Human PAML Browser

RRID:SCR\_007715

Type: Tool

### Proper Citation

Human PAML Browser (RRID:SCR\_007715)

### Resource Information

**URL:** <http://mendel.gene.cwru.edu/adamslab/cgi-bin/paml/pbrowser.py>

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**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 16, 2013. It provides access to the results of tests for positive selection in 14,000 human genes. Multiple alignments of protein-coding regions of genes from human and other mammals were extracted from whole-genome alignments available from UC-Santa Cruz. Each gene was analyzed using the maximum likelihood tests of selection using PAML. Branch, site, and branch+site tests were performed, each with at least one matching null model.

**Synonyms:** Human PAML Browser

**Resource Type:** data or information resource, database

**Keywords:** positive selection, protein

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Human PAML Browser

**Resource ID:** SCR\_007715

**Alternate IDs:** nif-0000-02996

**Record Creation Time:** 20220129T080243+0000

**Record Last Update:** 20260815T182858+0000

### Ratings and Alerts

No rating or validation information has been found for Human PAML Browser.

No alerts have been found for Human PAML Browser.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

McDermott JE, et al. (2012) Topological analysis of protein co-abundance networks identifies novel host targets important for HCV infection and pathogenesis. BMC systems biology, 6, 28.