Resource Summary Report

Generated by dkNET on May 19, 2025

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: database, data or information resource

Keywords: positive selection, protein

Funding:

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: 20250519T204732+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.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.