

# Resource Summary Report

Generated by [dkNET](#) on Aug 14, 2026

## Fastml

RRID:SCR\_016092

Type: Tool

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### Proper Citation

Fastml (RRID:SCR\_016092)

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### Resource Information

**URL:** <http://fastml.tau.ac.il/>

**Proper Citation:** Fastml (RRID:SCR\_016092)

**Description:** Web application for the reconstruction of ancestral sequences. It computes maximum likelihood ancestral sequence reconstruction based on the phylogenetic relations between homologous sequences.

**Synonyms:** The FastML Server

**Resource Type:** web application, data access protocol, software resource, web service

**Defining Citation:** [PMID:22661579](#)

**Keywords:** ancestral, amino-acid, sequence, reconstruction, phylogenetic, relation, accurate, bio.tools

**Funding:** Israel Science Foundation 878/09;  
Bioinformatics Center at Tel-Aviv University

**Availability:** Free, Freely available

**Resource Name:** Fastml

**Resource ID:** SCR\_016092

**Alternate IDs:** biotools:fastml, OMICS\_08650

**Alternate URLs:** <https://bio.tools/fastml>, <https://sources.debian.org/src/fastml/>

**License:** GNU General Public License

**Record Creation Time:** 20220129T080328+0000

**Record Last Update:** 20260814T042935+0000

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## Ratings and Alerts

No rating or validation information has been found for Fastml.

No alerts have been found for Fastml.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 111 mentions in open access literature.

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

Yamamoto N, et al. (2026) Evolutionary remodeling of the FXR binding pocket drove functional divergence and ligand discrimination. *Molecular biology and evolution*, 43(2).

Zhang P, et al. (2026) Resurrection and characterization of ancestral xylose transporters enhance the capability of xylose uptake in the mixed sugar co-fermentation of Recombinant *Saccharomyces cerevisiae*. *Bioresources and bioprocessing*, 13(1), 1.

Derouiche L, et al. (2026) Mitochondrial DNA Variation of the Striped Hyena (*Hyaena hyaena*) in Algeria and Further Insights into the Species' Evolutionary History. *Genes*, 17(1).

Zhao L, et al. (2025) Exploring the Stability and Substrate Profile of Transaminase from *Silicibacter pomeroyi* with Ancestral Sequence Reconstruction. *Chembiochem : a European journal of chemical biology*, 26(13), e202500155.

Jin GT, et al. (2025) A de novo Gene Promotes Seed Germination Under Drought Stress in *Arabidopsis*. *Molecular biology and evolution*, 42(1).

Seppely M, et al. (2025) Impact of Phylogenetic Method Choice on Indel Analyses in HIV-1 Subtype B. *Genome biology and evolution*, 17(6).

Lewitus E, et al. (2025) HIV-1 Vif global diversity and possible APOBEC-mediated response since 1980. *Virus evolution*, 11(1), veae108.

Wallmann A, et al. (2025) Structural and evolutionary determinants of Argonaute function. *Nucleic acids research*, 53(18).

Walker-Hale N, et al. (2025) Multiple transitions to high l-DOPA 4,5-dioxygenase activity reveal molecular pathways to convergent betalain pigmentation in Caryophyllales. *The New phytologist*, 247(1), 341.

Hart NS, et al. (2025) Widespread and Convergent Evolution of Cone Monochromacy in Galeomorph Sharks. *Molecular biology and evolution*, 42(3).

Luo T, et al. (2024) Men with a history of commercial heterosexual contact play essential roles in the transmission of HIV-1 CRF55\_01B from men who have sex with men to the general population in Guangxi, China. *Frontiers in cellular and infection microbiology*, 14, 1391215.

Vakirlis N, et al. (2024) Ancestral Sequence Reconstruction as a Tool to Detect and Study De Novo Gene Emergence. *Genome biology and evolution*, 16(8).

Delic S, et al. (2024) The Evolutionary Origins and Ancestral Features of Septins. *bioRxiv : the preprint server for biology*.

Lu Z, et al. (2024) Evolution of optimal growth temperature in Asgard archaea inferred from the temperature dependence of GDP binding to EF-1A. *Nature communications*, 15(1), 515.

Delic S, et al. (2024) The evolutionary origins and ancestral features of septins. *Frontiers in cell and developmental biology*, 12, 1406966.

Huang CY, et al. (2024) Subfunctionalization of NRC3 altered the genetic structure of the Nicotiana NRC network. *PLoS genetics*, 20(9), e1011402.

Hu G, et al. (2024) Improving the Quality of Wheat Flour Bread by a Thermophilic Xylanase with Ultra Activity and Stability Reconstructed by Ancestral Sequence and Computational-Aided Analysis. *Molecules (Basel, Switzerland)*, 29(8).

Lewitus E, et al. (2024) HIV-1 Gag, Pol, and Env diversified with limited adaptation since the 1980s. *mBio*, 15(3), e0174923.

Yada T, et al. (2024) A putative scenario of how de novo protein-coding genes originate in the *Saccharomyces cerevisiae* lineage. *BMC genomics*, 25(Suppl 3), 834.

Iglhaut C, et al. (2024) Please Mind the Gap: Indel-Aware Parsimony for Fast and Accurate Ancestral Sequence Reconstruction and Multiple Sequence Alignment Including Long Indels. *Molecular biology and evolution*, 41(7).