

Resource Summary Report

Generated by [NIF](#) on Sep 5, 2026

PHAST

RRID:SCR_003204

Type: Tool

Proper Citation

PHAST (RRID:SCR_003204)

Resource Information

URL: <http://compugen.bscb.cornell.edu/phast/>

Proper Citation: PHAST (RRID:SCR_003204)

Description: A freely available software package for comparative and evolutionary genomics that consists of about half a dozen major programs, plus more than a dozen utilities for manipulating sequence alignments, phylogenetic trees, and genomic annotations. For the most part, PHAST focuses on two kinds of applications: the identification of novel functional elements, including protein-coding exons and evolutionarily conserved sequences; and statistical phylogenetic modeling, including estimation of model parameters, detection of signatures of selection, and reconstruction of ancestral sequences. It consists of over 60,000 lines of C code.

Abbreviations: PHAST

Synonyms: Phylogenetic Analysis with Space/Time Models

Resource Type: software resource

Defining Citation: [PMID:21278375](#), [DOI:10.1093/bib/bbq072](#)

Keywords: evolutionary genomic, evolution, genomics, sequence alignment, phylogenetic tree, genomic annotation, functional element, protein-coding exon, conserved sequence, phylogenetic modeling, ancestral sequence, c

Funding: NIH ;

David and Lucile Packard Foundation ;

NHGRI ;

University of California Biotechnology Research and Education Program ;

NSF DBI-0644111;

NIGMS R01-GM082901-01

Availability: Free, Available for download, Freely available

Resource Name: PHAST

Resource ID: SCR_003204

Alternate IDs: OMICS_01557

Alternate URLs: <https://sources.debian.org/src/phast/>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260903T234600+0000

Ratings and Alerts

No rating or validation information has been found for PHAST.

No alerts have been found for PHAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 69 mentions in open access literature.

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

Navratilova P, et al. (2026) Epigenome and interactome profiling uncovers principles of distal regulation in the barley genome. *Cell genomics*, 6(1), 101037.

Sarebanzadeh K, et al. (2026) Dispersion of LPG from spherical storage tanks: Power-law scaling and comparative analysis of LFL vs. 50% LFL. *PloS one*, 21(2), e0341322.

Ke Q, et al. (2026) Population and pangenome analyses uncover the evolutionary dynamics of the peroxidase gene family in barley. *BMC genomics*, 27(1).

Wang G, et al. (2026) Phylogeny of waterfowl (Anseriformes) constructed using genome sequences provides insights into topological incongruences. *Molecular biology and evolution*, 43(2).

Cazottes E, et al. (2026) Remodeling of XIST regulatory landscape during primate evolution. *Science advances*, 12(3), eadw5839.

Breen MS, et al. (2026) Trisomy 21 Drives ADARB1 Overexpression and Premature RNA Recoding in the Developing Fetal Brain. *Nature communications*, 17(1).

Cai T, et al. (2026) Intermolecular 3'UTR-3'UTR interactions drive Wnt gene activation through heteromeric protein assembly. *bioRxiv : the preprint server for biology*.

Ivan J, et al. (2026) Selecting a Window Size for Phylogenomic Analyses of Whole Genome Alignments Using AIC. *Systematic biology*, 75(1), 100.

Wang Z, et al. (2026) Genomic adaptations for tail-length evolution in arboreal snakes. *Molecular biology and evolution*, 43(2).

Luo Y, et al. (2025) mRNA 3'UTRs chaperone intrinsically disordered regions to control protein activity. *bioRxiv : the preprint server for biology*.

Hawkins MB, et al. (2025) Establishment, conservation, and innovation of dorsal determination mechanisms during the evolution of vertebrate paired appendages. *bioRxiv : the preprint server for biology*.

Ye C, et al. (2025) Predicting functional constraints across evolutionary timescales with phylogeny-informed genomic language models. *bioRxiv : the preprint server for biology*.

Cicconardi F, et al. (2025) Convergent Molecular Evolution Associated With Repeated Transitions to Gregarious Larval Behavior in Heliconiini. *Molecular biology and evolution*, 42(8).

Zhang Z, et al. (2025) Evolution of cetacean-specific conserved non-coding elements suggests their role in the limb changes during secondary aquatic adaptation. *BMC biology*, 23(1), 216.

Guo W, et al. (2025) Pygmy sperm whale multi-omics data reveal hypoxia adaptations in deep-diving cetaceans. *BMC biology*, 24(1), 20.

He C, et al. (2025) Large-scale Genome Analyses Provide Insights into Hymenoptera Evolution. *Molecular biology and evolution*, 42(10).

Trigila AP, et al. (2025) Comparative genomics sheds light on mammalian and avian gene regulation and phenotypic evolution. *Nature communications*, 16(1), 9111.

Kim IV, et al. (2025) Chromatin loops are an ancestral hallmark of the animal regulatory genome. *Nature*, 642(8069), 1097.

Teterina AA, et al. (2025) Pervasive Conservation of Intron Number and Other Genetic Elements Revealed by a Chromosome-level Genome Assembly of the Hyper-polymorphic Nematode *Caenorhabditis brenneri*. *Genome biology and evolution*, 17(3).

Miri Karam Z, et al. (2024) Identification of a Novel Deletion Variant (c.2999_3005delTGTGTGT/p.Asn1000SerfsTer4) in NPHP4 Associated With Nephronophthisis-4. *Journal of clinical laboratory analysis*, 38(11-12), e25077.