

Resource Summary Report

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PHAST

RRID:SCR_003204

Type: Tool

Proper Citation

PHAST (RRID:SCR_003204)

Resource Information

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

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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: 20260905T132459+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 [Kravitz](#) .

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.

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

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).

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

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

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.

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

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).

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.