

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 ;

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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: 20260725T190537+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 58 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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.

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.

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

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

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).

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

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.

Lyu R, et al. (2024) Quantitative analysis of cis-regulatory elements in transcription with KAS-ATAC-seq. *Nature communications*, 15(1), 6852.

Zhang C, et al. (2024) A Novel Splice Site Mutation in the FBN2 Gene in a Chinese Family with Congenital Contractural Arachnodactyly. *Biochemical genetics*, 62(4), 2495.

Teterina AA, et al. (2024) Pervasive conservation of intron number and other genetic elements revealed by a chromosome-level genomic assembly of the hyper-polymorphic nematode *Caenorhabditis brenneri*. *bioRxiv : the preprint server for biology*.

Zhang Y, et al. (2024) A trade-off in evolution: the adaptive landscape of spiders without venom glands. *GigaScience*, 13.

Zuo MY, et al. (2022) A novel de novo TBX20 variant in a 6-year-old Chinese girl with left ventricular noncompaction: a case report. *Translational pediatrics*, 11(2), 311.

Di Genova A, et al. (2022) A molecular phenotypic map of malignant pleural mesothelioma. *GigaScience*, 12.

Zhang K, et al. (2021) Caspases Switch off the m6A RNA Modification Pathway to Foster the Replication of a Ubiquitous Human Tumor Virus. *mBio*, 12(4), e0170621.

Zhang S, et al. (2021) Long Non-coding RNA Signatures Associated With Liver Aging in Senescence-Accelerated Mouse Prone 8 Model. *Frontiers in cell and developmental biology*, 9, 698442.

Liu X, et al. (2021) TBK1 variants in Chinese patients with amyotrophic lateral sclerosis. *Neurobiology of aging*, 97, 149.e9.

Zeng B, et al. (2020) Exploration of Long Non-coding RNAs and Circular RNAs in Porcine Milk Exosomes. *Frontiers in genetics*, 11, 652.