

Resource Summary Report

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Datamonkey

RRID:SCR_010278

Type: Tool

Proper Citation

Datamonkey (RRID:SCR_010278)

Resource Information

URL: <http://www.datamonkey.org/>

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Description: Web-based suite of phylogenetic analysis tools for use in evolutionary biology. Web application for comparative analysis of sequence alignments using statistical models. Used for analyzing evolutionary signatures in sequence data. Datamonkey 2.0 provides curated collection of methods for interrogating coding-sequence alignments for imprints of natural selection, packaged as a responsive (i.e. can be viewed on tablet and mobile devices), fully interactive, and API-enabled web application.

Synonyms: , Datamonkey 2.0, datamonkey.org

Resource Type: data access protocol, software resource, source code, web service

Defining Citation: [PMID:15713735](#), [PMID:20671151](#), [PMID:29301006](#)

Keywords: comparative analysis of sequence alignments, analyzing evolutionary signatures, sequence data,

Funding: Canadian Institutes of Health Research ;
NIAID AI43638;
NIAID AI47745;
NIAID AI57167;
NIGMS R01 GM093939;
NIGMS U01 GM110749;
NSF ;
University of California at San Diego

Availability: Free, Available for download, Freely available

Resource Name: Datamonkey

Resource ID: SCR_010278

Alternate IDs: nlx_156937

Alternate URLs: <https://github.com/veg/datamonkey-js>

Record Creation Time: 20220129T080257+0000

Record Last Update: 20260905T132638+0000

Ratings and Alerts

No rating or validation information has been found for Datamonkey.

No alerts have been found for Datamonkey.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1260 mentions in open access literature.

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

Urban-Olivares J, et al. (2026) The Copepoda mitogenome as a dynamic evolutionary landscape. PloS one, 21(6), e0350115.

Dong W, et al. (2026) Identification and genomic characterization of a goose astrovirus in Henan Province, China. Frontiers in veterinary science, 13, 1806778.

Ramírez-Castañeda V, et al. (2026) Snakes (Colubridae: Erythrolamprus) With a Complex Toxic Diet Show Convergent yet Highly Heterogeneous Voltage-gated Sodium Channel Evolution. Genome biology and evolution, 18(4).

Le Corf A, et al. (2026) Genomic and functional adaptations in the guanylate-binding protein GBP5 highlight specificities of bat antiviral innate immunity. PLoS biology, 24(4), e3003760.

Lin Y, et al. (2026) Genomic characterization of a Chinese bovine papillomavirus isolate and its L1-based phylogenetic placement in a global dataset. Frontiers in veterinary science, 13, 1839050.

Calvo EP, et al. (2026) Unexpected diversification of DENV2 genotype III in Colombia: New Insights and application of the globalized nomenclature. PloS one, 21(2), e0343528.

Maachi A, et al. (2026) Multiple origins and functions: evolutionary pathways of HSP70 proteins in viruses. The Journal of general virology, 107(3).

Putaporntip C, et al. (2026) Contrasting evolutionary trajectories of pyrimethamine resistance in human and zoonotic malaria parasites. *Malaria journal*, 25(1).

Hrmova M, et al. (2026) Dormancy Versus Germination: 3D Protein Modeling and Evolutionary Analyses Define the Roles of Genetic Variants in the Barley MKK3 Enzyme. *International journal of molecular sciences*, 27(1).

Carvalho JL, et al. (2026) Escaping Constraints to Innovate: Maternal Neofunctionalization in a HoxB4 Duplicate. *Journal of experimental zoology. Part B, Molecular and developmental evolution*, 346(2), 141.

Jardim-Messeder D, et al. (2026) The Road so Far: Tracing the Molecular Evolution of Hexokinase Family in Metazoa. *Genome biology and evolution*, 18(3).

Lee MG, et al. (2026) Boundary-associated propagation of a processed pseudogene dissects pre-existing limitations of genome annotation in the T2T era. *Mobile DNA*, 17(1).

López-Astacio RA, et al. (2026) Distinct evolutionary patterns of endemic and emerging parvoviruses and the origin of a new pandemic virus. *Proceedings of the National Academy of Sciences of the United States of America*, 123(16), e2515274123.

Shirai T, et al. (2026) Molecular Evolution of the Fusion (F) Genes in Human Metapneumovirus Genotype B. *Microorganisms*, 14(2).

Luan Q, et al. (2026) Genetic variability and phylogenetic analysis of the VP2 gene of feline parvovirus in Harbin. *Frontiers in veterinary science*, 13, 1783463.

Han S, et al. (2026) Evidence of Relaxed Selection in the Mitochondrial Genomes of Phototrophic Paulinella Lineages. *Genome biology and evolution*, 18(3).

Jallow MM, et al. (2026) Epidemiology, Genomic Diversity, and Evolutionary Dynamics of Human Metapneumovirus Over 7 Years of Integrated Community- and Hospital-Based Sentinel Surveillance in Senegal, 2018-2024. *Influenza and other respiratory viruses*, 20(7), e70290.

Lee DY, et al. (2026) Genomic and phylogenetic characterization of severe fever with thrombocytopenia syndrome virus in companion animals in Korea, 2023-2024. *PLoS neglected tropical diseases*, 20(6), e0014305.

Mizukoshi F, et al. (2026) Phylogenetic Analyses of RdRp Region and VP1 Gene in Human Norovirus Genotype GII.17[P17] Variants. *Microorganisms*, 14(4).

Nalça AR, et al. (2026) Evolutionary Patterns of the Genes Involved in the Integrity and Segregation of Chromosomes in Sawflies (Hymenoptera: Symphyta). *Ecology and evolution*, 16(6), e73748.