

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

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

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

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

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: 20260804T043447+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 1120 mentions in open access literature.

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

Gorman LM, et al. (2026) Coral Venom and Toxins as Protection Against Crown-of-Thorns Sea Star Attack. *Molecular ecology*, 35(1), e70202.

Nascimento JPM, et al. (2026) Arrival of Oropouche Virus in a Nonendemic Area in Northeastern Brazil, 2024. *Journal of medical virology*, 98(1), e70780.

Zhang L, et al. (2025) Phylogeography Analysis Reveals Rabies Epidemiology, Evolution, and Transmission in the Philippines. *Molecular biology and evolution*, 42(2).

Li Y, et al. (2025) Epidemiological and molecular characteristics of human parainfluenza virus in southern China during 2016-2020. *Virologica Sinica*, 40(2), 157.

Ma Y, et al. (2025) Epidemic dynamics and clinical characteristics of HIV-1 CRF07_BC_N and CRF07_BC_O in Shanghai, 2017-2023. *Virulence*, 16(1), 2554301.

Benkovi? D, et al. (2025) Genetic Diversity of Canine Circovirus Detected in Wild Carnivores in Serbia. *Veterinary sciences*, 12(6).

Dubrulle J, et al. (2025) Effect of Land-Use on Hantavirus Infection Among Introduced and Endemic Small Mammals of Madagascar. *Ecology and evolution*, 15(4), e70914.

Fay EJ, et al. (2025) Evolutionary and functional analyses reveal a role for the RHIM in tuning RIPK3 activity across vertebrates. *eLife*, 13.

- Wei Y, et al. (2025) Genetic and codon usage analyses reveal the evolution of the seoul virus. *Frontiers in genetics*, 16, 1544577.
- Azbazdar ME, et al. (2025) Genetic Evolution of the Hemagglutinin Genes of Seasonal Influenza A Viruses in Türkiye Between 2017 and 2023. *Influenza and other respiratory viruses*, 19(7), e70134.
- Yuan Y, et al. (2025) From transmission to adaptive evolution: genomic surveillance of Getah virus. *Frontiers in cellular and infection microbiology*, 15, 1513392.
- George S, et al. (2025) Evolutionary dynamics and molecular epidemiology of H1N1 pandemic 2009 influenza A viruses across swine farms in Denmark. *Virus evolution*, 11(1), veaf014.
- Salles MMA, et al. (2025) Ancient Introgression Explains Mitochondrial Genome Capture and Mitonuclear Discordance Among South American Collared *Tropidurus* Lizards. *Molecular ecology*, 34(21), e70130.
- Gomaa AE, et al. (2025) Genome-Wide Variation Profile of the Genus Tobamovirus. *Viruses*, 17(9).
- Legrand A, et al. (2025) Evolutionary characterization of antiviral SAMD9/9L across kingdoms supports ancient convergence and lineage-specific adaptations. *Nature ecology & evolution*, 9(12), 2206.
- Sianga-Mete R, et al. (2025) Viral genome sequence datasets display pervasive evidence of strand-specific substitution biases that are best described using non-reversible nucleotide substitution models. *eLife*, 12.
- Qian X, et al. (2025) The Potassium Utilization Gene Network in *Brassica napus* and Functional Validation of BnaZSHAK5.2 Gene in Response to Potassium Deficiency. *International journal of molecular sciences*, 26(2).
- Legrand A, et al. (2025) Ancient convergence with prokaryote defense and recent adaptations to lentiviruses in primates characterize the ancestral immune factors SAMD9s. *bioRxiv : the preprint server for biology*.
- Schubert N, et al. (2025) Sex-Dependent Influence of Major Histocompatibility Complex Diversity on Fitness in a Social Mammal. *Molecular ecology*, 34(18), e70058.
- Wangui J, et al. (2025) Molecular Analysis of Human Respiratory Syncytial Virus Group B Strains Isolated in Kenya Before and During the Emergence of Pandemic Influenza A/H1N1. *Influenza and other respiratory viruses*, 19(2), e70082.