

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

TempEst

RRID:SCR_017304

Type: Tool

Proper Citation

TempEst (RRID:SCR_017304)

Resource Information

URL: <https://beast.community/tempest>

Proper Citation: TempEst (RRID:SCR_017304)

Description: Software tool for investigating temporal signal and clocklikeness of molecular phylogenies. Used for visualization and analysis of temporally sampled sequence data to assess whether there is sufficient temporal signal in data to proceed with phylogenetic molecular clock analysis, and to identify sequences whose genetic divergence and sampling date are incongruent. Not available for downloading as of August 8, 2019.

Synonyms: Path-O-Gen, tempest

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [DOI:doi.org/10.1093/ve/vew007](https://doi.org/10.1093/ve/vew007)

Keywords: temporal, signal, clocklikeness, molecular, phylogeny, visualization, analysis, temporally, sampled, sequenced, data, identify, genetic, incongruent

Funding: ERC Grant ;
EU Seventh Framework Programme

Availability: Restricted

Resource Name: TempEst

Resource ID: SCR_017304

Old URLs: <http://tree.bio.ed.ac.uk/software/tempest/>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260912T195851+0000

Ratings and Alerts

No rating or validation information has been found for TempEst.

No alerts have been found for TempEst.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 166 mentions in open access literature.

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

Delgado-Suarez EJ, et al. (2026) Emergence of multidrug-resistant blaCTX-M-65/gyrA_D87Y clones among the circulating Salmonella Infantis population in Mexico. Microbial genomics, 12(2).

Chang W, et al. (2026) Identification of a novel second-generation HIV-1 circulating recombinant form, CRF182_0708, in Yunnan, China. BMC infectious diseases, 26(1).

Metcalf B, et al. (2026) The rise and spread of invasive emm49 Streptococcus pyogenes in the USA. Microbial genomics, 12(1).

Raghuram V, et al. (2026) Genomic surveillance of Salmonella enterica serotype Minnesota strains from poultry products imported into South Africa. Microbial genomics, 12(2).

Wu H, et al. (2026) Whole-genome analysis of a novel Pandoraea sputorum lineage causing high-mortality bloodstream infections. Microbial genomics, 12(6).

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.

Cacciabue M, et al. (2026) The whole genome analysis of four Orf virus strains from Europe and South America. Virus evolution, 12(1), veag004.

Magassouba N, et al. (2026) Two years of SARS-CoV-2 genomic surveillance capacity development in Guinea. Scientific reports, 16(1).

Santos MS, et al. (2026) A comprehensive analysis of the SARS-CoV-2 omicron variant in Tocantins State, Brazil, and tracing the spread of the XBB.1.18.1 lineage. Brazilian journal of microbiology : [publication of the Brazilian Society for Microbiology], 57(1).

Seo Y, et al. (2026) Genomic Insights into Ciprofloxacin-Resistant Enteropathogenic Escherichia coli ST752 in Republic of Korea: A One Health Perspective on Its Emergence and Transmission. Antibiotics (Basel, Switzerland), 15(3).

Puenpa J, et al. (2026) Genomic Characterization and Evolutionary Dynamics of SARS-CoV-2 Lineage NB.1.8.1 in Thailand, 2025. *Viruses*, 18(4).

Wang Y, et al. (2026) Geographic and cross-species transmission of Mamastroviruses from multiple hosts. *Animal microbiome*, 8(1).

Wu Z, et al. (2026) HIV-1 molecular transmission networks among MSM in Ningxia, China (2018-2024): insights into local transmission dynamics and drug resistance. *Frontiers in microbiology*, 17, 1766785.

Li Y, et al. (2026) Epidemiological characterization and phylogenetic analysis of human metapneumovirus isolated from children in Ningbo, China, 2020-2024. *Microbial genomics*, 12(6).

Zamunér CFC, et al. (2025) Evolution and spread of *Xanthomonas citri* subsp. *citri* in the São Paulo, Brazil, citrus belt inferred from 758 novel genomes. *Microbial genomics*, 11(1).

Payne CJ, et al. (2025) Genomic diversity and evolutionary patterns of *Edwardsiella ictaluri* affecting farmed striped catfish (*Pangasianodon hypophthalmus*) in Vietnam over 20 years. *Microbial genomics*, 11(2).

Dong X, et al. (2025) Genomic insights into the rapid rise of *Pseudomonas aeruginosa* ST463: A high-risk lineage's adaptive strategy in China. *Virulence*, 16(1), 2497901.

Rößler S, et al. (2025) Evidence for early circulation of the M1UK sublineage of *Streptococcus pyogenes* in Germany, 2015-2023. *Emerging microbes & infections*, 14(1), 2576587.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

McCrone JT, et al. (2025) Evidence of latency reshapes our understanding of Ebola virus reservoir dynamics. *bioRxiv* : the preprint server for biology.