

Resource Summary Report

Generated by [RRID](#) on Aug 4, 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: software toolkit, software application, data processing software, data analysis software, software resource

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: EU Seventh Framework Programme ;
ERC Grant

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: 20260804T043650+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 152 mentions in open access literature.

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

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).

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).

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.

Shi S, et al. (2025) Comparative analysis of codon usage bias and host adaptation across avian metapneumovirus genotypes. *Poultry science*, 104(9), 105428.

Minna Z, et al. (2025) Divergent transmission dynamics and drug resistance evolution of HIV-1 CRF01_AE and CRF07_BC in Tianjin, China (2013-2022). *Virology journal*, 22(1), 137.

Van der Roest B, et al. (2025) Phylodynamic inference suggests introductions as main driver of Mpox Clade II outbreak in 2022 in Slovenia. *Epidemiology and infection*, 153, e115.

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

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

Gustani-Buss EC, et al. (2025) Dispersal dynamics and introduction patterns of SARS-CoV-2 lineages in Iran. *Virus evolution*, 11(1), veaf004.

Li X, et al. (2025) Evaluation of global distribution, genetic evolution, and mammalian infectivity and pathogenicity of H13 and H16 avian influenza viruses. *Emerging microbes & infections*, 14(1), 2482695.

Gu SH, et al. (2025) Molecular characterization and evolutionary analysis of human adenovirus type 55, related to febrile respiratory illness in the South Korean military. *Virus genes*, 61(4), 432.

Zhang F, et al. (2025) Tracking international and regional dissemination of the KPC/NDM co-producing *Klebsiella pneumoniae*. *Nature communications*, 16(1), 5574.

White RT, et al. (2025) 20 years later: unravelling the genomic success of New Zealand's home-grown AK3 community-associated methicillin-resistant *Staphylococcus aureus*. *Microbial genomics*, 11(7).

Iqbal BN, et al. (2025) Molecular Epidemiology of SARS-CoV-2 Detected from Different Areas of the Kandy District of Sri Lanka from November 2020-March 2022. *Viruses*, 17(9).

Sánchez-Nava J, et al. (2025) Inferring Geographic Spread of Flaviviruses Through Analysis of Hypervariable Genomic Regions. *Tropical medicine and infectious disease*, 10(10).

Maya L, et al. (2025) Epidemiology and Evolution of Bovine Viral Diarrhea Virus (BVDV) in Uruguay: A 10-Year Study. *Viruses*, 17(10).

Chen K, et al. (2025) Global genomic survey of *Salmonella* Kentucky: discovery of a chromosomeborne blaNDM-5 and the emergence of ST314, an MDR clone mediated by the IncR plasmid. *Emerging microbes & infections*, 14(1), 2576588.

Jayadas TTP, et al. (2025) The Re-emergence of Chikungunya in Sri Lanka: A Genomic investigation. *medRxiv : the preprint server for health sciences*.

Zhang YQ, et al. (2025) Genetic and Pathogenic Characterization of a Porcine Deltacoronavirus Strain Isolated in Zhejiang Province, China. *Transboundary and emerging diseases*, 2025, 4084814.