

Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

Augur

RRID:SCR_023964

Type: Tool

Proper Citation

Augur (RRID:SCR_023964)

Resource Information

URL: <https://github.com/nextstrain/augur>

Proper Citation: Augur (RRID:SCR_023964)

Description: Software package to track evolution from sequence and serological data. Provides collection of commands which are designed to be composable into larger processing pipelines.

Synonyms: augur

Resource Type: software resource, software toolkit

Keywords: track evolution, sequence, serological data.

Availability: Free, Available for download, Freely available

Resource Name: Augur

Resource ID: SCR_023964

Alternate URLs: <https://sources.debian.org/src/augur/>,
<https://docs.nextstrain.org/projects/augur/en/stable/>

License: GNU Affero General Public License

Record Creation Time: 20230824T050210+0000

Record Last Update: 20260919T195616+0000

Ratings and Alerts

No rating or validation information has been found for Augur.

No alerts have been found for Augur.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 88 mentions in open access literature.

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

Mapunda LA, et al. (2026) The genomic diversity of SARS-CoV-2 Omicron lineages collected during routine sentinel surveillance in Tanzania between November 2022 and July 2023. BMC genomics, 27(1).

Koel B, et al. (2026) Emergence and antigenic characterisation of influenza A(H3N2) viruses with hemagglutinin substitutions N158K and K189R during the 2024/25 influenza season. bioRxiv : the preprint server for biology.

Hernández-Ortiz OH, et al. (2026) Hybrid and Vaccine-Induced Immunity Against SARS-CoV-2 in a Cohort of Hospitalized Patients from the Metropolitan Aburrá Valley, Colombia. Vaccines, 14(5).

Daodu RO, et al. (2026) Lassa virus live tracking and lineage assignment: how nextstrain can enhance surveillance and public health in Africa and beyond. Emerging microbes & infections, 15(1), 2640699.

Xu B, et al. (2026) Fiber-type vulnerability and proteostasis reprogramming in skeletal muscle during pancreatic cancer cachexia. JCI insight, 11(6).

Cho AY, et al. (2026) Wild birds drive the introduction, maintenance, and spread of H5N1 clade 2.3.4.4b high pathogenicity avian influenza viruses in Spain, 2021-2022. Virus evolution, 12(1), veag006.

Sonti S, et al. (2026) Patient-derived lung organoids from bronchoalveolar lavage capture epithelial heterogeneity and disease biology in bronchopulmonary dysplasia. Redox biology, 90, 104057.

Granger K, et al. (2026) Single-nuclei RNA-sequencing uncovers sexually divergent exercise signatures partially mimicked by TFEB overexpression in mouse skeletal muscle. bioRxiv : the preprint server for biology.

Monamele CG, et al. (2026) Genome characterization of the SARS-CoV-2 omicron in Cameroon. BMC infectious diseases, 26(1).

Tewari D, et al. (2026) Genotype Diversity of Highly Pathogenic Avian Influenza H5N1 Clade 2.3.4.4b in Pennsylvania Poultry During Disease Outbreak from April 2022 to March 2023. Viruses, 18(5).

Asaduzzaman M, et al. (2026) Unravelling the dengue surge in South Asia during 2000-2023: pattern, trend, genomics, and key determinants. Epidemiology and infection, 154, e28.

Phong KT, et al. (2026) Single cell RNA-sequencing reveals that testosterone reduces estrogen signaling in the healthy human mammary gland. *Journal of mammary gland biology and neoplasia*, 31(1).

Dakroub F, et al. (2026) Genomic and clinical epidemiology of SARS-CoV-2 in Lebanon: a prospective multicenter study 2020-2024. *BMC infectious diseases*, 26(1).

Hua L, et al. (2026) Myeloid-Derived CD38 Mediates Age-Related Endometrial Aging Through NAD⁺ Depletion. *Aging cell*, 25(1), e70356.

Adegaju MS, et al. (2026) Structural analysis of antigenic variation and adaptive evolution of the H5N1 neuraminidase gene. *PLoS computational biology*, 22(1), e1013903.

Li SH, et al. (2026) Childhood immunological imprinting of cross-subtype antibodies targeting the hemagglutinin head domain of influenza viruses. *Cell host & microbe*, 34(5), 873.

Pereira JS, et al. (2025) Unravelling dengue serotype 3 transmission in Brazil: evidence for multiple introductions of the 3III_B.3.2 lineage. *Virus evolution*, 11(1), veaf034.

Gnimadi TAC, et al. (2025) Genetic Diversity and Spatiotemporal Distribution of SARS-CoV-2 Variants in Guinea: A Meta-Analysis of Sequence Data (2020-2023). *Viruses*, 17(2).

Soriano JE, et al. (2025) A neuronal architecture underlying autonomic dysreflexia. *Nature*, 646(8087), 1167.

Akin E, et al. (2025) In-vitro characterization of 2019-24 Influenza B Viruses reveals increased temperature-dependent fitness in later timepoints independent of antigenic drift. *medRxiv* : the preprint server for health sciences.