

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

SynTView

RRID:SCR_011939

Type: Tool

Proper Citation

SynTView (RRID:SCR_011939)

Resource Information

URL: <http://genopole.pasteur.fr/SynTView/>

Proper Citation: SynTView (RRID:SCR_011939)

Description: An interactive multi-view genome browser for next-generation comparative microorganism genomics.

Abbreviations: SynTView

Resource Type: software resource

Keywords: bio.tools

Resource Name: SynTView

Resource ID: SCR_011939

Alternate IDs: OMICS_01500, biotools:syntview

Alternate URLs: <https://bio.tools/syntview>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260912T195742+0000

Ratings and Alerts

No rating or validation information has been found for SynTView.

No alerts have been found for SynTView.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

L??-Bury P, et al. (2023) Yersiniomics, a Multi-Omics Interactive Database for Yersinia Species. Microbiology spectrum, 11(2), e0382622.

Bussotti G, et al. (2018) Leishmania Genome Dynamics during Environmental Adaptation Reveal Strain-Specific Differences in Gene Copy Number Variation, Karyotype Instability, and Telomeric Amplification. mBio, 9(6).

Gonzalez-Hilarion S, et al. (2016) Intron retention-dependent gene regulation in Cryptococcus neoformans. Scientific reports, 6, 32252.

Drini S, et al. (2016) Species- and Strain-Specific Adaptation of the HSP70 Super Family in Pathogenic Trypanosomatids. Genome biology and evolution, 8(6), 1980.

Glaser P, et al. (2016) Demography and Intercontinental Spread of the USA300 Community-Acquired Methicillin-Resistant Staphylococcus aureus Lineage. mBio, 7(1), e02183.

Bouchez V, et al. (2015) New Data on Vaccine Antigen Deficient Bordetella pertussis Isolates. Vaccines, 3(3), 751.

Lechat P, et al. (2013) SynTView - an interactive multi-view genome browser for next-generation comparative microorganism genomics. BMC bioinformatics, 14, 277.