

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 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: 20260905T132716+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

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

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.