

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 8, 2026

GenomeMatcher

RRID:SCR_011800

Type: Tool

Proper Citation

GenomeMatcher (RRID:SCR_011800)

Resource Information

URL: <http://www.ige.tohoku.ac.jp/joho/gmProject/gmhome.html>

Proper Citation: GenomeMatcher (RRID:SCR_011800)

Description: A graphical interface for comparative genomics.

Abbreviations: GenomeMatcher

Resource Type: software resource

Resource Name: GenomeMatcher

Resource ID: SCR_011800

Alternate IDs: OMICS_00936

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260808T185935+0000

Ratings and Alerts

No rating or validation information has been found for GenomeMatcher.

No alerts have been found for GenomeMatcher.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 65 mentions in open access literature.

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

Yano H, et al. (2026) Giant linear plasmids in *Mycobacterium avium* harbour a tRNA array unit. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Arashida H, et al. (2026) Genome Plasticity Depends on Positions both Inside and Outside of the Symbiosis Island of *Bradyrhizobium diazoefficiens*. *Microbes and environments*, 41(1).

Taniguchi I, et al. (2026) Global population structure of Shiga toxin-producing *Escherichia coli* O103:H2 and the variation in their major virulence factor-encoding genetic elements. *Microbial genomics*, 12(1).

Konno Y, et al. (2026) Symbiosis Islands of *Bradyrhizobium* Determine Relationships with Host Legumes *Lespedeza cuneata* and *Glycine max*. *Microbes and environments*, 41(1).

Hisatsune J, et al. (2025) *Staphylococcus aureus* ST764-SCCmecII high-risk clone in bloodstream infections revealed through national genomic surveillance integrating clinical data. *Nature communications*, 16(1), 2698.

Takeuchi T, et al. (2025) Antigenic variation is caused by long plasmid segment conversion in a hard tick-borne relapsing fever *Borrelia miyamotoi*. *PLoS pathogens*, 21(9), e1013514.

Yasuoka K, et al. (2025) Genome Analysis of Japanese *Yersinia pseudotuberculosis* Strains Isolated From Kawasaki Disease Patients and Other Sources and Their Phylogenetic Positions in the Global *Y. pseudotuberculosis* Population. *Microbiology and immunology*, 69(3), 182.

Ichikawa K, et al. (2025) CGC1, a new reference genome for *Caenorhabditis elegans*. *Genome research*, 35(8), 1902.

Abdela AA, et al. (2025) Transcription of Nitrogen Fixation Genes Is Enhanced at Unfavorably High Oxygen Concentrations for Diazotrophic Growth in a Methane-oxidizing Bacterium. *Microbes and environments*, 40(4).

Kaneko T, et al. (2025) Novel *Escherichia coli* phages representing a distinct genus within the subfamily Stephanstirmvirinae: genome and host range characteristics. *Archives of virology*, 171(1), 18.

Fernandes IdA, et al. (2025) TccP4: a novel effector identified in the *Escherichia albertii* strain 1551-2 required for attaching and effacing lesion formation on infected Nck-null cells. *Microbiology spectrum*, 13(3), e0205524.

Matsumura E, et al. (2025) Single-cell genomics of single soil aggregates: methodological assessment and potential implications with a focus on nitrogen metabolism. *Frontiers in microbiology*, 16, 1557188.

Liu S, et al. (2024) Production of a Bacteriocin Like Protein PEG 446 from *Clostridium tyrobutyricum* NRRL B-67062. *Probiotics and antimicrobial proteins*, 16(4), 1411.

Bromfield ESP, et al. (2024) *Bradyrhizobium ontarionense* sp. nov., a novel bacterial symbiont isolated from *Aeschynomene indica* (Indian jointvetch), harbours photosynthesis, nitrogen fixation and nitrous oxide (N₂O) reductase genes. *Antonie van Leeuwenhoek*, 117(1), 69.

Yano H, et al. (2024) Nationwide genome surveillance of carbapenem-resistant *Pseudomonas aeruginosa* in Japan. *Antimicrobial agents and chemotherapy*, 68(5), e0166923.

Katahira K, et al. (2024) Mobile genetic element-driven genomic changes in a community-associated methicillin-resistant *Staphylococcus aureus* clone during its transmission in a regional community outbreak in Japan. *Microbial genomics*, 10(7).

Yasuda Y, et al. (2024) Highly Reduced Complementary Genomes of Dual Bacterial Symbionts in the Mulberry Psyllid *Anomoneura mori*. *Microbes and environments*, 39(3).

Ichikawa K, et al. (2024) CGC1, a new reference genome for *Caenorhabditis elegans*. *bioRxiv* : the preprint server for biology.

Yano H, et al. (2024) Mobile class A β -lactamase gene bla GMA-1. *Microbiology spectrum*, 12(1), e0258923.

Mizutani M, et al. (2024) Identification of An7 as a positive awn regulator from two wild rice species. *Breeding science*, 74(3), 247.