

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

Easyfig

RRID:SCR_013169

Type: Tool

Proper Citation

Easyfig (RRID:SCR_013169)

Resource Information

URL: <http://easyfig.sourceforge.net/>

Proper Citation: Easyfig (RRID:SCR_013169)

Description: A Python application for creating linear comparison figures of multiple genomic loci with an easy-to-use graphical user interface (GUI).

Abbreviations: Easyfig

Resource Type: software resource

Resource Name: Easyfig

Resource ID: SCR_013169

Alternate IDs: OMICS_00907

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260801T190456+0000

Ratings and Alerts

No rating or validation information has been found for Easyfig.

No alerts have been found for Easyfig.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1101 mentions in open access literature.

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

Tian R, et al. (2026) Emergence and genomic characterization of mcr-8.2-positive *Klebsiella pneumoniae* from layer chickens in Xinjiang, China. *Poultry science*, 105(1), 106190.

Figueroa Y, et al. (2026) STEC in the natural environment of Uruguay: genomic surveillance and environmental circulation in the framework of One Health. *Microbiology spectrum*, 14(1), e0315325.

Yeki S, et al. (2026) Sex-Specific doublesex Regulation Targeting the Color-Patterning Gene *h* Underlies the Evolution of Wing Sexual Dimorphism in the Harlequin Ladybug *Harmonia axyridis*. *Evolution & development*, 28(1), e70028.

Hu Y, et al. (2026) Global epidemiological and genetic characteristics of carbapenem-resistant *Escherichia coli* carrying blaIMP. *Microbiology spectrum*, 14(1), e0324425.

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

Xu L, et al. (2025) Genomic Insights into the Pathogenicity of Hypervirulent *Aeromonas hydrophila* Strain D4 Isolated from Diseased Blunt Snout Bream with the Epidemic Sequence Type 251 Clones. *Pathogens (Basel, Switzerland)*, 14(6).

Liu JQ, et al. (2025) Genome-Based Reclassification of Two *Haloarcula* Species and Characterization of *Haloarcula montana* sp. nov. *Biology*, 14(6).

Ma Y, et al. (2025) Tracing the evolutionary trajectory of the IncP-2 plasmid co-harboring blaIMP-45 and blaVIM-1: an outbreak of *Pseudomonas aeruginosa* co-producing IMP-45 and VIM-1 carbapenemases in China. *Frontiers in cellular and infection microbiology*, 15, 1623241.

Biedrzycka M, et al. (2025) Carbapenemase-Producing Enterobacterales from Patients Arriving from Ukraine in Poland, March 2022-February 2023. *Infectious diseases and therapy*, 14(2), 401.

Jiang H, et al. (2025) Prevalence and characterization of class I integrons in multidrug-resistant *Escherichia coli* isolates from humans and food-producing animals in Zhejiang Province, China. *BMC microbiology*, 25(1), 76.

Fujii A, et al. (2025) Comprehensive analysis of bacteriocins produced by clinical enterococcal isolates and their antibacterial activity against Enterococci including VRE. *Scientific reports*, 15(1), 4846.

Dumjahn L, et al. (2025) Dual-use virulence factors of the opportunistic pathogen *Chromobacterium haemolyticum* mediate hemolysis and colonization. *mBio*, 16(5), e0360524.

Becerra-Aparicio F, et al. (2025) Whole Genome Sequencing Analysis of *Klebsiella pneumoniae* Isolates from Health Care-Associated Bacteremia of Urinary Origin in Spain:

Findings from the Multicenter ITUBRAS-2 Cohort Study. Open forum infectious diseases, 12(4), ofaf164.

Kyrkou I, et al. (2025) *Pseudomonas aeruginosa* maintains an inducible array of novel and diverse prophages over lengthy persistence in cystic fibrosis lungs. FEMS microbiology letters, 372.

Fu S-Y, et al. (2025) Optimizing phage therapy for carbapenem-resistant *Enterobacter cloacae* bacteremia: insights into dose and timing. Antimicrobial agents and chemotherapy, 69(4), e0168324.

Kim EJ, et al. (2025) Bacteriophage cocktail LEC2-LEC10 for broad-spectrum control of pathogenic and uncharacterized *Escherichia coli* in fresh produce. Frontiers in microbiology, 16, 1594533.

Gan X, et al. (2025) Whole Genome Sequencing-Based Taxonomic Identification of Dulcitol-Positive *Cronobacter dublinensis* subsp. *beijingensis* subsp. nov. and *Cronobacter dublinensis* subsp. *infanticibi* subsp. nov. from Infant Cereals in China. Current microbiology, 82(10), 477.

Ho TT, et al. (2025) The potential novel bacteriophages against multidrug-resistant *Edwardsiella tarda* isolates from striped catfish *Pangasianodon hypophthalmus*. Scientific reports, 15(1), 37229.

Lu Y, et al. (2025) Comparative genomics of *Nocardia tsunamensis* IFM 10818, a new source of the antibacterial macrolide nargenicin A1. Microbiology spectrum, 13(12), e0122025.

Xu Y, et al. (2025) Prevalence and genetic characterization of Gram-positive bacteria carrying linezolid resistance genes in vegetables. Environmental microbiome, 20(1), 144.