

Resource Summary Report

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Clinker

RRID:SCR_016140

Type: Tool

Proper Citation

Clinker (RRID:SCR_016140)

Resource Information

URL: <https://github.com/Oshlack/Clinker/wiki>

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Description: Software for a bioinformatics pipeline that generates a superTranscriptome from popular fusion finder outputs (JAFFA, tophatFusion, SOAP, deFUSE, Pizzly, etc). They can be then be either viewed in genome viewers such as IGV or through the included plotting feature developed with GViz.

Synonyms: Clinker - Fusion Super Transcript generator and Plotter

Resource Type: data processing software, data visualization software, software application, software resource

Keywords: fusion, chimeric, gene, bioinformatics, transcriptome, viewer, plotting, graph, visualization

Funding: Murdoch Children's Research Institute

Availability: Free, Available for download

Resource Name: Clinker

Resource ID: SCR_016140

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260805T044350+0000

Ratings and Alerts

No rating or validation information has been found for Clinker.

No alerts have been found for Clinker.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 286 mentions in open access literature.

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

Fernández-Fernández R, et al. (2025) Genomic Analysis of Bacteriocin-Producing Staphylococci: High Prevalence of Lanthipeptides and the Micrococcin P1 Biosynthetic Gene Clusters. Probiotics and antimicrobial proteins, 17(1), 159.

Howard-Varona C, et al. (2025) Infection and Genomic Properties of Single- and Double-Stranded DNA Cellulophaga Phages. Viruses, 17(3).

Guo Y, et al. (2025) Identification of a Biosynthetic Gene Cluster for the Production of the Blue-Green Pigment Xylindein by the Fungus Chlorociboria aeruginascens. Journal of natural products, 88(2), 233.

Simon V, et al. (2025) Functional and Pangenomic Exploration of Roc Two-Component Regulatory Systems Identifies Novel Players Across Pseudomonas Species. Molecular microbiology, 123(5), 439.

Borowicz M, et al. (2025) Tailocin-Mediated Interactions Among Soft Rot Pectobacteriaceae. Molecular ecology, 34(8), e17728.

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.

Benoit M, et al. (2025) Solanum pan-genetics reveals paralogues as contingencies in crop engineering. Nature, 640(8057), 135.

Kovacec V, et al. (2025) Genomic characterization of group B Streptococcus from Argentina: insights into prophage diversity, virulence factors and antibiotic resistance genes. Microbial genomics, 11(4).

Chen J, et al. (2025) Bacterial peptide deformylase inhibitors induce prophages in competitors. bioRxiv : the preprint server for biology.

Das J, et al. (2025) Genomic insights into novel predatory myxobacteria isolated from human feces. Microbiology spectrum, 13(7), e0214724.

Göpel L, et al. (2025) Genomic analysis of carbapenemase-encoding plasmids and antibiotic resistance in carbapenem-resistant Klebsiella pneumoniae isolates from Vietnam, 2021. Microbiology spectrum, 13(5), e0311524.

Morohoshi T, et al. (2025) Distribution and Characterization of the Novel Quorum-quenching Enzyme AiiB in Priestia megaterium Isolated from a Natural Environment.

Microbes and environments, 40(3).

O'Dea F, et al. (2025) Phenotypic and genomic analysis of the emerging poultry pathogen *Enterococcus cecorum* in UK isolates. *Microbial genomics*, 11(9).

Vincent CV, et al. (2025) Concanamycins Are Key Contributors to the Virulence of the Potato Common Scab Pathogen *Streptomyces scabiei*. *Molecular plant pathology*, 26(11), e70175.

Yagi N, et al. (2025) A Monitoring Method to Evaluate the Accumulation of Antimicrobial-Resistance Genes in Gram-Negative Bacteria Distributed in Environmental Water. *Environmental microbiology reports*, 17(6), e70265.

Withatanung P, et al. (2025) Genomic and functional characterization of a novel temperate Coventryvirus phage infecting *Staphylococcus pseudintermedius*. *Scientific reports*, 15(1), 45073.

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.

Choi D, et al. (2025) Strain-specific activation of aspergillic acid biosynthesis in *Aspergillus oryzae* NRRL 3483. *Scientific reports*, 15(1), 38755.

da Silva Fong D, et al. (2025) Identification and characterization of a novel papillomavirus in thornback skate (*Raja clavata*). *Microbial genomics*, 11(11).

Soto-Serrano A, et al. (2025) "Expanding the Lactococcal Cell Wall Polysaccharide Paradigm: Novel Structures and Metabolic Pathways in the Emerging Dairy Species *Pseudolactococcus laudensis* and *Pseudolactococcus raffinolactis*". *MicrobiologyOpen*, 14(6), e70133.