

Resource Summary Report

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Piggy

RRID:SCR_015941

Type: Tool

Proper Citation

Piggy (RRID:SCR_015941)

Resource Information

URL: <https://github.com/harry-thorpe/piggy>

Proper Citation: Piggy (RRID:SCR_015941)

Description: Pipeline for analyzing intergenic regions in bacteria. It is designed to be used in conjunction with Roary (<https://github.com/sanger-pathogens/Roary>).

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

Keywords: intergenic, region, bacterial, analysis, gene, genome, assembly

Funding: Medical Research Council

Availability: Free, Available for download

Resource Name: Piggy

Resource ID: SCR_015941

License: GNU General Public License v3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260805T044346+0000

Ratings and Alerts

No rating or validation information has been found for Piggy.

No alerts have been found for Piggy.

Data and Source Information

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Cheng C, et al. (2025) What Kinds of Computations Can Young Children Perform Over Non-Symbolic Representations of Small Quantities? *Open mind : discoveries in cognitive science*, 9, 25.

Vasco M, et al. (2025) Economic preferences and cognitive abilities among teenagers in Spain. *Scientific data*, 12(1), 7.

Matlock W, et al. (2025) *Escherichia coli* phylogeny drives co-amoxiclav resistance through variable expression of TEM-1 beta-lactamase. *Nature communications*, 16(1), 8669.

Low TCH, et al. (2025) The ORB2 RNA-binding protein represses translation of its target transcripts during the *Drosophila* maternal-to-zygotic transition via its functionally conserved Zinc-binding 'ZZ' domain. *bioRxiv : the preprint server for biology*.

Baker M, et al. (2024) Convergence of resistance and evolutionary responses in *Escherichia coli* and *Salmonella enterica* co-inhabiting chicken farms in China. *Nature communications*, 15(1), 206.

Frantsuzova E, et al. (2024) Genomic, Phylogenetic and Physiological Characterization of the PAH-Degrading Strain *Gordonia polyisoprenivorans* 135. *Biology*, 13(5).

Maciel-Guerra A, et al. (2024) Core and accessory genomic traits of *Vibrio cholerae* O1 drive lineage transmission and disease severity. *Nature communications*, 15(1), 8231.

Jones H, et al. (2023) A reductionist paradigm for high-throughput behavioural fingerprinting in *Drosophila melanogaster*. *eLife*, 12.

Akansu EF, et al. (2023) Tethered Balloon-Borne Turbulence Measurements in Winter and Spring during the MOSAiC Expedition. *Scientific data*, 10(1), 723.

Chalka A, et al. (2023) The advantage of intergenic regions as genomic features for machine-learning-based host attribution of *Salmonella Typhimurium* from the USA. *Microbial genomics*, 9(10).

Pribbenow C, et al. (2022) Postsynaptic plasticity of cholinergic synapses underlies the induction and expression of appetitive and familiarity memories in *Drosophila*. *eLife*, 11.

Sassi M, et al. (2022) Forecasting *Staphylococcus aureus* Infections Using Genome-Wide Association Studies, Machine Learning, and Transcriptomic Approaches. *mSystems*, 7(4), e0037822.

Eslahi AV, et al. (2022) Global prevalence of *Trichinella* in pigs: A systematic review and meta-analysis. *Veterinary medicine and science*, 8(6), 2466.

Liu R, et al. (2021) In Vivo Clonal Analysis Reveals Development Heterogeneity of Oligodendrocyte Precursor Cells Derived from Distinct Germinal Zones. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 8(20), e2102274.

Colquhoun RM, et al. (2021) Pandora: nucleotide-resolution bacterial pan-genomics with reference graphs. *Genome biology*, 22(1), 267.

Suresh A, et al. (2021) Evolutionary Dynamics Based on Comparative Genomics of Pathogenic *Escherichia coli* Lineages Harboring Polyketide Synthase (pks) Island. *mBio*, 12(1).

Cheney L, et al. (2021) Multilevel Genome Typing Describes Short- and Long-Term *Vibrio cholerae* Molecular Epidemiology. *mSystems*, 6(4), e0013421.

Bohr LL, et al. (2021) Genome reorganization during emergence of host-associated *Mycobacterium abscessus*. *Microbial genomics*, 7(12).

Luo L, et al. (2021) Elucidation of global and national genomic epidemiology of *Salmonella enterica* serovar Enteritidis through multilevel genome typing. *Microbial genomics*, 7(7).

Caicedo-Montoya C, et al. (2021) Pan-Genome of the Genus *Streptomyces* and Prioritization of Biosynthetic Gene Clusters With Potential to Produce Antibiotic Compounds. *Frontiers in microbiology*, 12, 677558.