

Resource Summary Report

Generated by T1D on Sep 5, 2026

Genome Institue at Washington University

RRID:SCR_010259

Type: Tool

Proper Citation

Genome Institue at Washington University (RRID:SCR_010259)

Resource Information

URL: <http://genome.wustl.edu/genomes/>

Proper Citation: Genome Institue at Washington University (RRID:SCR_010259)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 17, 2022. Genome databases housed at the Genome Institute at Washington University. Included are genome databases from Humans/Primates, other vertebrates, microorganisms, plants and invertebrates.

Resource Type: data or information resource, database

Keywords: genome databases from Humans/Primates, vertebrates, microorganisms, plants, invertebrates.

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Genome Institue at Washington University

Resource ID: SCR_010259

Alternate IDs: nlx_156912

Record Creation Time: 20220129T080257+0000

Record Last Update: 20260904T000254+0000

Ratings and Alerts

No rating or validation information has been found for Genome Institue at Washington University.

No alerts have been found for Genome Institue at Washington University.

Data and Source Information

Usage and Citation Metrics

We found 114 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Zhao Q, et al. (2014) Identification of glutathione (GSH)-independent glyoxalase III from *Schizosaccharomyces pombe*. *BMC evolutionary biology*, 14, 86.

Bao G, et al. (2013) Genome Sequence of *Klebsiella oxytoca* M5a1, a Promising Strain for Nitrogen Fixation and Chemical Production. *Genome announcements*, 1(1).

Zandawala M, et al. (2013) Isolation and functional characterization of calcitonin-like diuretic hormone receptors in *Rhodnius prolixus*. *PloS one*, 8(11), e82466.

Ikeda D, et al. (2013) Lampreys have a single gene cluster for the fast skeletal myosin heavy chain gene family. *PloS one*, 8(12), e85500.

Jaber-Hijazi F, et al. (2013) Planarian MBD2/3 is required for adult stem cell pluripotency independently of DNA methylation. *Developmental biology*, 384(1), 141.

Dolled-Filhart MP, et al. (2013) Computational and bioinformatics frameworks for next-generation whole exome and genome sequencing. *TheScientificWorldJournal*, 2013, 730210.

Subirana JA, et al. (2013) A satellite explosion in the genome of holocentric nematodes. *PloS one*, 8(4), e62221.

Patnala R, et al. (2013) Candidate gene association studies: a comprehensive guide to useful in silico tools. *BMC genetics*, 14, 39.

Refai O, et al. (2013) Extension of the *Caenorhabditis elegans* Pharyngeal M1 neuron axon is regulated by multiple mechanisms. *G3 (Bethesda, Md.)*, 3(11), 2015.

Edwards JA, et al. (2013) *Histoplasma* yeast and mycelial transcriptomes reveal pathogenic-phase and lineage-specific gene expression profiles. *BMC genomics*, 14, 695.

Romeralo M, et al. (2013) Analysis of phenotypic evolution in *Dictyostelia* highlights developmental plasticity as a likely consequence of colonial multicellularity. *Proceedings. Biological sciences*, 280(1764), 20130976.

Wang Q, et al. (2013) Detecting somatic point mutations in cancer genome sequencing data: a comparison of mutation callers. *Genome medicine*, 5(10), 91.

Zhao G, et al. (2012) Conserved Motifs and Prediction of Regulatory Modules in *Caenorhabditis elegans*. *G3 (Bethesda, Md.)*, 2(4), 469.

Kuraku S, et al. (2012) Horizontal transfers of Tc1 elements between teleost fishes and their vertebrate parasites, lampreys. *Genome biology and evolution*, 4(9), 929.

Deakin JE, et al. (2012) Genomic restructuring in the Tasmanian devil facial tumour: chromosome painting and gene mapping provide clues to evolution of a transmissible tumour. *PLoS genetics*, 8(2), e1002483.

Ngamskulrungroj P, et al. (2012) Characterization of the chromosome 4 genes that affect fluconazole-induced disomy formation in *Cryptococcus neoformans*. *PloS one*, 7(3), e33022.

Yue M, et al. (2012) Diversification of the *Salmonella* fimbriae: a model of macro- and microevolution. *PloS one*, 7(6), e38596.

Barrantes I, et al. (2012) A next-generation sequencing approach to study the transcriptomic changes during the differentiation of *Physarum* at the single-cell level. *Gene regulation and systems biology*, 6, 127.

Ogilvie LA, et al. (2012) Comparative (meta)genomic analysis and ecological profiling of human gut-specific bacteriophage ϕ B124-14. *PloS one*, 7(4), e35053.

Fabre L, et al. (2012) CRISPR typing and subtyping for improved laboratory surveillance of *Salmonella* infections. *PloS one*, 7(5), e36995.