

Resource Summary Report

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Google Code

RRID:SCR_005786

Type: Tool

Proper Citation

Google Code (RRID:SCR_005786)

Resource Information

URL: <http://code.google.com/>

Proper Citation: Google Code (RRID:SCR_005786)

Description: Developer tools, APIs and resources. Search developers.google.com and code.google.com.

Abbreviations: Google Code

Resource Type: software repository, software resource

Keywords: code, developer

Resource Name: Google Code

Resource ID: SCR_005786

Alternate IDs: nlx_149265

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260905T133235+0000

Ratings and Alerts

No rating or validation information has been found for Google Code.

No alerts have been found for Google Code.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 452 mentions in open access literature.

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

Dominguez RL, et al. (2024) Population-Based Study of Gastric Cancer Survival and Associations in Rural Western Honduras. *Cancer epidemiology, biomarkers & prevention* : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 33(12), 1578.

Wren JD, et al. (2017) Use it or lose it: citations predict the continued online availability of published bioinformatics resources. *Nucleic acids research*, 45(7), 3627.

Schoebel CN, et al. (2014) Population history and pathways of spread of the plant pathogen *Phytophthora plurivora*. *PloS one*, 9(1), e85368.

Rozen-Gagnon K, et al. (2014) Alphavirus mutator variants present host-specific defects and attenuation in mammalian and insect models. *PLoS pathogens*, 10(1), e1003877.

Wilson G, et al. (2014) Best practices for scientific computing. *PLoS biology*, 12(1), e1001745.

Santhanam J, et al. (2014) Immune-mediated competition in rodent malaria is most likely caused by induced changes in innate immune clearance of merozoites. *PLoS computational biology*, 10(1), e1003416.

Hasmats J, et al. (2014) Assessment of whole genome amplification for sequence capture and massively parallel sequencing. *PloS one*, 9(1), e84785.

Wang Y, et al. (2014) Comparison of metatranscriptomic samples based on k-tuple frequencies. *PloS one*, 9(1), e84348.

Ansari MA, et al. (2014) Inference of the properties of the recombination process from whole bacterial genomes. *Genetics*, 196(1), 253.

Hennessey J, et al. (2014) Trends in the production of scientific data analysis resources. *BMC bioinformatics*, 15 Suppl 11(Suppl 11), S7.

Daunizeau J, et al. (2014) VBA: a probabilistic treatment of nonlinear models for neurobiological and behavioural data. *PLoS computational biology*, 10(1), e1003441.

Wang YZ, et al. (2014) Exploring candidate genes for pericarp russet pigmentation of sand pear (*Pyrus pyrifolia*) via RNA-Seq data in two genotypes contrasting for pericarp color. *PloS one*, 9(1), e83675.

Park S, et al. (2014) Aberrant CDK4 amplification in refractory rhabdomyosarcoma as identified by genomic profiling. *Scientific reports*, 4, 3623.

Shinzato C, et al. (2014) A snapshot of a coral "holobiont": a transcriptome assembly of the scleractinian coral, *Porites*, captures a wide variety of genes from both the host and symbiotic zooxanthellae. *PloS one*, 9(1), e85182.

Babur ??, et al. (2014) Pattern search in BioPAX models. *Bioinformatics* (Oxford, England), 30(1), 139.

Gillard GB, et al. (2014) The transcriptome of the NZ endemic sea urchin *Kina* (*Evechinus chloroticus*). *BMC genomics*, 15, 45.

Kellner N, et al. (2014) The SPF27 homologue Num1 connects splicing and kinesin 1-dependent cytoplasmic trafficking in *Ustilago maydis*. *PLoS genetics*, 10(1), e1004046.

Oktem IM, et al. (2014) Dobrava-Belgrade virus in *Apodemus flavicollis* and *A. uralensis* mice, Turkey. *Emerging infectious diseases*, 20(1), 121.

Zhang X, et al. (2014) Identification of three novel mutations in the FRMD7 gene for X-linked idiopathic congenital nystagmus. *Scientific reports*, 4, 3745.

Andor N, et al. (2014) EXPANDS: expanding ploidy and allele frequency on nested subpopulations. *Bioinformatics* (Oxford, England), 30(1), 50.