## **Resource Summary Report**

Generated by dkNET on Apr 26, 2025

# **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 resource, software repository

Keywords: code, developer

Funding:

Resource Name: Google Code

Resource ID: SCR\_005786

Alternate IDs: nlx\_149265

**Record Creation Time:** 20220129T080232+0000

**Record Last Update**: 20250422T055254+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 451 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

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.

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

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.

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

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.

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.

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

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.

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

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

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

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

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

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

Foster JM, et al. (2013) LipidHome: a database of theoretical lipids optimized for high throughput mass spectrometry lipidomics. PloS one, 8(5), e61951.