

Resource Summary Report

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Free Pascal Compiler

RRID:SCR_014360

Type: Tool

Proper Citation

Free Pascal Compiler (RRID:SCR_014360)

Resource Information

URL: <http://www.freepascal.org>

Proper Citation: Free Pascal Compiler (RRID:SCR_014360)

Description: Free Pascal is a 32, 64 and 16 bit professional Object Pascal compiler targeting multiple processor architectures and operating systems. Documentation, including guides and manuals, are available on the website.

Abbreviations: FPC, FPK

Resource Type: software development environment, software resource, software development tool, software application

Keywords: software development environment, software development tool, compiler, pascal, object pascal

Availability: Free for download as source code, Pre-compiled for multiple platforms

Resource Name: Free Pascal Compiler

Resource ID: SCR_014360

License: Free Pascal License (GPL with linking exceptions)

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260804T043541+0000

Ratings and Alerts

No rating or validation information has been found for Free Pascal Compiler.

No alerts have been found for Free Pascal Compiler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Liegel N, et al. (2024) The effect of performance contingent reward prospects flexibly adapts to more versus less specific task goals. *Psychophysiology*, 61(12), e14678.

Zhang Q, et al. (2023) A multi-threaded approach to genotype pattern mining for detecting digenic disease genes. *Frontiers in genetics*, 14, 1222517.

Nilsson AS, et al. (2022) Cocktail, a Computer Program for Modelling Bacteriophage Infection Kinetics. *Viruses*, 14(11).

Dietrich JW, et al. (2022) SPINA Carb: a simple mathematical model supporting fast in-vivo estimation of insulin sensitivity and beta cell function. *Scientific reports*, 12(1), 17659.

Alexandrowicz RW, et al. (2020) The diffusion model visualizer: an interactive tool to understand the diffusion model parameters. *Psychological research*, 84(4), 1157.

Adams ES, et al. (2019) Self-organizing conflicts: Group assessment and the spatio-temporal dynamics of ant territory battles. *Behavioural processes*, 162, 119.

Kostanyan AE, et al. (2018) An easy-to-use calculating machine to simulate steady state and non-steady-state preparative separations by multiple dual mode counter-current chromatography with semi-continuous loading of feed mixtures. *Journal of chromatography. A*, 1552, 92.

Dell'Ariccia G, et al. (2018) Flexible migratory choices of Cory's shearwaters are not driven by shifts in prevailing air currents. *Scientific reports*, 8(1), 3376.

Šimkus R, et al. (2018) Phoretic interactions and oscillations in active suspensions of growing *Escherichia coli*. *Royal Society open science*, 5(5), 180008.

Tinker NA, et al. (2016) Haplotag: Software for Haplotype-Based Genotyping-by-Sequencing Analysis. *G3 (Bethesda, Md.)*, 6(4), 857.

Fuentes-Pananá EM, et al. (2016) Assessment of Epstein-Barr virus nucleic acids in gastric but not in breast cancer by next-generation sequencing of pooled Mexican samples. *Memorias do Instituto Oswaldo Cruz*, 111(3), 200.

Lee W, et al. (2016) Integrative NMR for biomolecular research. *Journal of biomolecular NMR*, 64(4), 307.

Dufour CM, et al. (2015) Space use variation in co-occurring sister species: response to environmental variation or competition? *PloS one*, 10(2), e0117750.

Tol JP, et al. (2015) Automatic interactive optimization for volumetric modulated arc therapy planning. *Radiation oncology* (London, England), 10, 75.

Nevozhay D, et al. (2014) Cheburator software for automatically calculating drug inhibitory concentrations from in vitro screening assays. *PloS one*, 9(9), e106186.

Janik M, et al. (2012) Determination of the minimum measurement time for estimating long-term mean radon concentration. *Radiation protection dosimetry*, 152(1-3), 168.

Benhamou S, et al. (2011) Dynamic approach to space and habitat use based on biased random bridges. *PloS one*, 6(1), e14592.

Honma A, et al. (2008) Optimal-foraging predator favors commensalistic Batesian mimicry. *PloS one*, 3(10), e3411.

de Jong A, et al. (2006) BAGEL: a web-based bacteriocin genome mining tool. *Nucleic acids research*, 34(Web Server issue), W273.

van Hijum SA, et al. (2005) Projector 2: contig mapping for efficient gap-closure of prokaryotic genome sequence assemblies. *Nucleic acids research*, 33(Web Server issue), W560.