

Resource Summary Report

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Lazarus IDE

RRID:SCR_014362

Type: Tool

Proper Citation

Lazarus IDE (RRID:SCR_014362)

Resource Information

URL: <http://www.lazarus-ide.org>

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Description: A cross-platform integrated development environment (IDE) for Free Pascal. It contains a class library (LCL) that supports rapid application development for native code on numerous platforms, processor architectures and operating systems.

Abbreviations: Laz

Synonyms: Lazarus, Lazarus integrated development environment

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

Keywords: software development environment, software development tool, pascal, object pascal, integrated development environment, ide, class library, lcl

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

Resource Name: Lazarus IDE

Resource ID: SCR_014362

Alternate URLs: <http://lazarus.freepascal.org>

License: Free Pascal License (GPL with linking exceptions)

License URLs: http://wiki.lazarus.freepascal.org/FPC_modified_LGPL

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Ratings and Alerts

No rating or validation information has been found for Lazarus IDE.

No alerts have been found for Lazarus IDE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Claret JL, et al. (2024) Despite structural identity, ace-1 heterogenous duplication resistance alleles are quite diverse in Anopheles mosquitoes. *Heredity*, 132(4), 179.

Filatov DA, et al. (2024) ProSeq4: A user-friendly multiplatform program for preparation and analysis of large-scale DNA polymorphism datasets. *Molecular ecology resources*, 24(5), e13962.

Rastetter EB, et al. (2022) N and P constrain C in ecosystems under climate change: Role of nutrient redistribution, accumulation, and stoichiometry. *Ecological applications : a publication of the Ecological Society of America*, 32(8), e2684.

Warren PA, et al. (2022) The impact of choice discriminability and outcome valence on visual decision making under risk. *Vision research*, 199, 108073.

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.

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

Naefgen C, et al. (2022) Given the option, people avoid incongruent responses in a dual-tasking situation. *Acta psychologica*, 228, 103626.

Sharpe SM, et al. (2020) Goosegrass Detection in Strawberry and Tomato Using a Convolutional Neural Network. *Scientific reports*, 10(1), 9548.

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.

Yu J, et al. (2019) Weed Detection in Perennial Ryegrass With Deep Learning Convolutional Neural Network. *Frontiers in plant science*, 10, 1422.

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

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.

Hoppe K, et al. (2017) Sequential Modulations in a Combined Horizontal and Vertical Simon Task: Is There ERP Evidence for Feature Integration Effects? *Frontiers in psychology*, 8, 1094.

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.

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

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

Mendyk A, et al. (2015) From Heuristic to Mathematical Modeling of Drugs Dissolution Profiles: Application of Artificial Neural Networks and Genetic Programming. *Computational and mathematical methods in medicine*, 2015, 863874.

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.