

Resource Summary Report

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Perl Programming Language

RRID:SCR_018313

Type: Tool

Proper Citation

Perl Programming Language (RRID:SCR_018313)

Resource Information

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

Proper Citation: Perl Programming Language (RRID:SCR_018313)

Description: Software tool to accompany existing resources such as Python programming language resource and comprehensive Perl archive network (CPAN) resource. Perl is family of two high level, general purpose, interpreted, dynamic programming languages. Perl refers to Perl 5, but from 2000 to 2019 it also referred to its redesigned sister language, Perl 6, before name was officially changed to Raku in October 2019.

Synonyms: Perl 5, Perl 6, Raku

Resource Type: software resource, programming language

Keywords: Programming language

Availability: Free, Available for download, Freely available

Resource Name: Perl Programming Language

Resource ID: SCR_018313

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260812T044343+0000

Ratings and Alerts

No rating or validation information has been found for Perl Programming Language.

No alerts have been found for Perl Programming Language.

Data and Source Information

Usage and Citation Metrics

We found 382 mentions in open access literature.

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

Jiménez-Sánchez A, et al. (2026) Transcriptomic Plasticity Is a Hallmark of Metastatic Pancreatic Cancer. *Cancer research*, 86(7), 1769.

Liang L, et al. (2026) Construction and validation of a prognostic model for lung adenocarcinoma based on necrotic cell death triggered by sodium overload-related coexpressed genes. *Frontiers in genetics*, 17, 1763705.

He P, et al. (2026) Integrated expression quantitative trait loci and Mendelian randomization analyses of the candidate genes and pathways identified for myocardial infarction. *Frontiers in molecular biosciences*, 13, 1693113.

Moretti S, et al. (2026) MetaNetX: a bridge between metabolic resources for enhanced curation and multi-omics data harmonization. *Nucleic acids research*, 54(D1), D617.

Kong F, et al. (2026) Differential effects of HDAC8 targeting on Foxp3+ Tregs and effector T cells promote antitumor immunity. *JCI insight*, 11(3).

Zhou Y, et al. (2026) Quercetin-Fe nanodots inhibit cervical cancer cell proliferation by targeting PCNA. *Cancer nanotechnology*, 17(1), 2.

Chen H, et al. (2026) Novel dual regulatory roles of RpoA in quorum sensing regulation and social behavior switching in *Pseudomonas aeruginosa*. *mBio*, 17(5), e0003226.

Hu G, et al. (2026) Design and Validation of a Predictive Model for Hepatocellular Carcinoma Based on Genes With Differential Expression Driven by DNA Methylation. *International journal of genomics*, 2026, 2729004.

Feng W, et al. (2026) Integrative multi-omics identifies a glycosylation-based prognostic framework and nominates ALG3 for targeted therapy in bladder cancer. *Discover oncology*, 17(1).

Dong C, et al. (2026) Investigation of molecular immune regulation mechanisms and therapeutic target prediction in pancreatic cancer based on bioinformatics and genetics. *Clinics (Sao Paulo, Brazil)*, 81, 100952.

Choi N, et al. (2026) Novel mechanisms of chemosensory adaptation to the cave environment. *bioRxiv : the preprint server for biology*.

Zhang S, et al. (2026) A tumor microenvironment-focused signature based on m6A and lactylation modification predicts prognosis and immunotherapy response in hepatocellular carcinoma. *Discover oncology*, 17(1).

Kong F, et al. (2025) MEF2D regulates T-cell function via CD70-CD27 signaling and promotes immune evasion in hepatocellular carcinoma. *Journal of immunology* (Baltimore, Md. : 1950), 214(11), 3162.

Zhen Q, et al. (2025) Erucic Acid, Derived by *Lactobacillus Crispatus*, Induces Ferroptosis in Cervical Cancer Organoids Through the PPAR- γ Signaling Pathway. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(48), e12599.

Li W, et al. (2025) Identification of critical biomarkers and immune infiltration in preeclampsia through bioinformatics and machine learning methods. *BMC pregnancy and childbirth*, 25(1), 136.

Xiao J, et al. (2025) Integrated single-cell analysis reveals the regulatory network of disulfidptosis-related lncRNAs in bladder cancer: constructing a prognostic model and predicting treatment response. *Frontiers in oncology*, 15, 1527036.

Li Z, et al. (2025) The Methylation and Expression of LINC00511, an Important Angiogenesis-Related lncRNA in Stomach Adenocarcinoma. *International journal of molecular sciences*, 26(5).

Ma J, et al. (2025) Effective energy harvesting of Yak by regulating the glucose and lipid metabolism in liver to adapt to the plateau environment. *Scientific reports*, 16(1), 944.

Zhang W, et al. (2025) Uncovering a fibroblast differentiation-based keloid classification by integration of single-cell and bulk RNA sequencing. *Communications biology*, 8(1), 1387.

Zou Y, et al. (2025) Identification of palmitoylation-related lncRNAs as prognostic biomarkers and immune modulators in HCC. *Discover oncology*, 16(1), 1878.