Resource Summary Report

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Comprehensive Perl Archive Network

RRID:SCR_007253
Type: Tool

Proper Citation

Comprehensive Perl Archive Network (RRID:SCR_007253)

Resource Information

URL: http://www.cpan.org

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Description: Welcome to CPAN, where you you will find All Things Perl. CPAN is the Comprehensive Perl Archive Network, a large collection of Perl software and documentation. You can begin exploring from either http://www.cpan.org/, http://www.perl.com/CPAN/ or any of the mirrors listed at http://www.cpan.org/SITES.html. Note that CPAN is also the name of a Perl module, CPAN.pm, which is used to download and install Perl software from the CPAN archive. This FAQ covers only a little about the CPAN module and you may find the documentation for it by using perldoc CPAN via the command line or on the web at http://search.cpan.org/dist/CPAN/lib/CPAN.pm. Sponsors: CPAN works with the generosity and cooperation of hundreds of developers, over 100 participating mirrors, funet.fi donating the network bandwidth, storage space and computing power, volunteers who help keep everything together and users whose interest in Perl keep the archive alive and growing. Keywords: Comprehension, Perl, Archive, Software, Documentation,

Synonyms: CPAN

Resource Type: portal, topical portal, data or information resource

Funding:

Resource Name: Comprehensive Perl Archive Network

Resource ID: SCR_007253

Alternate IDs: nif-0000-30267

Record Creation Time: 20220129T080240+0000

Record Last Update: 20250417T065308+0000

Ratings and Alerts

No rating or validation information has been found for Comprehensive Perl Archive Network.

No alerts have been found for Comprehensive Perl Archive Network.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 59 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Boulton W, et al. (2024) SWAMPy: simulating SARS-CoV-2 wastewater amplicon metagenomes. Bioinformatics (Oxford, England), 40(9).

Schroeder WL, et al. (2021) Using EuGeneCiD and EuGeneCiM computational tools for synthetic biology. STAR protocols, 2(4), 100820.

Weso?owski W, et al. (2021) VCF2CAPS-A high-throughput CAPS marker design from VCF files and its test-use on a genotyping-by-sequencing (GBS) dataset. PLoS computational biology, 17(5), e1008980.

Wang L, et al. (2021) Sinbase 2.0: An Updated Database to Study Multi-Omics in Sesamum indicum. Plants (Basel, Switzerland), 10(2).

Schroeder WL, et al. (2021) Optimization-based Eukaryotic Genetic Circuit Design (EuGeneCiD) and modeling (EuGeneCiM) tools: Computational approach to synthetic biology. iScience, 24(9), 103000.

Du X, et al. (2020) 5-HT7 Receptor Contributes to Proliferation, Migration and Invasion in NSCLC Cells. OncoTargets and therapy, 13, 2139.

Schroeder WL, et al. (2020) Protocol for Genome-Scale Reconstruction and Melanogenesis Analysis of Exophiala dermatitidis. STAR protocols, 1(2), 100105.

Bonito G, et al. (2019) Fungal-Bacterial Networks in the Populus Rhizobiome Are Impacted by Soil Properties and Host Genotype. Frontiers in microbiology, 10, 481.

Weighill D, et al. (2019) Multi-Phenotype Association Decomposition: Unraveling Complex Gene-Phenotype Relationships. Frontiers in genetics, 10, 417.

Weighill D, et al. (2019) Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. Frontiers in genetics, 10, 487.

Tuskan GA, et al. (2018) Defining the genetic components of callus formation: A GWAS approach. PloS one, 13(8), e0202519.

Heigwer F, et al. (2018) Time-resolved mapping of genetic interactions to model rewiring of signaling pathways. eLife, 7.

Yim WC, et al. (2017) Divide and Conquer (DC) BLAST: fast and easy BLAST execution within HPC environments. PeerJ, 5, e3486.

Merkys A, et al. (2016) COD::CIF::Parser: an error-correcting CIF parser for the Perl language. Journal of applied crystallography, 49(Pt 1), 292.

Rhee DB, et al. (2015) toxoMine: an integrated omics data warehouse for Toxoplasma gondii systems biology research. Database : the journal of biological databases and curation, 2015, bav066.

Yu J, et al. (2015) PTGBase: an integrated database to study tandem duplicated genes in plants. Database : the journal of biological databases and curation, 2015.

O'Halloran DM, et al. (2015) PrimerView: high-throughput primer design and visualization. Source code for biology and medicine, 10, 8.

Hatton L, et al. (2015) Protein structure and evolution: are they constrained globally by a principle derived from information theory? PloS one, 10(5), e0125663.

Weighill DA, et al. (2015) 3-way networks: application of hypergraphs for modelling increased complexity in comparative genomics. PLoS computational biology, 11(3), e1004079.

Miya M, et al. (2015) MiFish, a set of universal PCR primers for metabarcoding environmental DNA from fishes: detection of more than 230 subtropical marine species. Royal Society open science, 2(7), 150088.