

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: data or information resource, topical portal, portal

Resource Name: Comprehensive Perl Archive Network

Resource ID: SCR_007253

Alternate IDs: nif-0000-30267

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260803T040502+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 101 mentions in open access literature.

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

Wang Y, et al. (2025) Designing self-adaptative cyclized polyacrylonitrile-polyethyleneimine conjugates enhance uranium extraction from natural seawater. *Nature communications*, 16(1), 9249.

Giustini C, et al. (2025) A Mitochondrially Related Plastidial Transporter Regulates Photosynthesis in the Diatom *Phaeodactylum tricornutum*. *Physiologia plantarum*, 177(6), e70640.

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

Olkkonen E, et al. (2023) Analysis of population structure and genetic diversity in low-variance Saimaa ringed seals using low-coverage whole-genome sequence data. *STAR protocols*, 4(4), 102567.

Calderon Toledo C, et al. (2023) Circulation of enterotoxigenic *Escherichia coli* (ETEC) isolates expressing CS23 from the environment to clinical settings. *mSystems*, 8(5), e0014123.

Liu X, et al. (2023) Early Emotional Experiences and Prosocial Behavior among Chinese Adolescents: The Roles of Psychological Suzhi and Subjective Socioeconomic Status. *Behavioral sciences (Basel, Switzerland)*, 13(4).

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

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.

Emerson IA, et al. (2021) DCMP: database of cancer mutant protein domains. *Database : the journal of biological databases and curation*, 2021(2021).

- Wesołowski 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 X, et al. (2021) Preparation and Electrical Properties of Polyacrylonitrile Based Porous Carbon by Different Activation Methods. *Molecules* (Basel, Switzerland), 26(12).
- 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.
- O'Halloran DM, et al. (2020) Module for SWC neuron morphology file validation and correction enabled for high throughput batch processing. *PloS one*, 15(1), e0228091.
- Weighill D, et al. (2019) Wavelet-Based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. *Frontiers in genetics*, 10, 487.
- Carlotti T, et al. (2019) An OCARI-Based Wireless Sensor Network for Heat Measurements during Outdoor Fire Experiments. *Sensors* (Basel, Switzerland), 19(1).
- 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.
- Cooper CI, et al. (2018) Valection: design optimization for validation and verification studies. *BMC bioinformatics*, 19(1), 339.