

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

PHP

RRID:SCR_025974

Type: Tool

Proper Citation

PHP (RRID:SCR_025974)

Resource Information

URL: <https://www.php.net/>

Proper Citation: PHP (RRID:SCR_025974)

Description: Popular general-purpose scripting language that is especially suited to web development.

Synonyms: Hypertext Preprocessor

Resource Type: programming language, software resource

Keywords: scripting language, web development,

Availability: Free, Freely available

Resource Name: PHP

Resource ID: SCR_025974

Record Creation Time: 20241024T053301+0000

Record Last Update: 20260815T042944+0000

Ratings and Alerts

No rating or validation information has been found for PHP.

No alerts have been found for PHP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Li T, et al. (2026) TriticeaeExpDB: a centralized transcriptomic resource for Triticeae research. BMC genomics, 27(1).

Baskaran SP, et al. (2026) sCentInDB: a database of essential oil chemical profiles of Indian medicinal plants. Molecular diversity, 30(1), 789.

Khan A, et al. (2026) HMPV-TherResDB: Comprehensive human metapneumovirus (HMPV) database for sequence-structure annotations, vaccine resources, and therapeutics research. Virus research, 363, 199665.

de Araujo AT, et al. (2026) KitBase Expanded: An Integrated Genomic and Phenotypic Resource for 3,268 Fast-Neutron-Irradiated Rice Mutants. Database : the journal of biological databases and curation, 2026.

Ospina OE, et al. (2025) spatialGE Is a User-Friendly Web Application That Facilitates Spatial Transcriptomics Data Analysis. Cancer research, 85(5), 848.

Pagoni M, et al. (2025) Integrated Pharmacogenetic Signature for the Prediction of Prostatic Neoplasms in Men With Metabolic Disorders. Cancer genomics & proteomics, 22(2), 285.

Hakamata Y, et al. (2025) The effectiveness and neurobiological actions of memory bias modification: a randomized controlled trial. Psychological medicine, 55, e386.

Zou X, et al. (2025) Impact of rare non-coding variants on human diseases through alternative polyadenylation outliers. Nature communications, 16(1), 682.

Chen C, et al. (2025) VirulentHunter: deep learning-based virulence factor predictor illuminates pathogenicity in diverse microbial contexts. Briefings in bioinformatics, 26(3).

Haruay S, et al. (2025) Amoebic Dysentery in Northeastern Thailand: Contributing Factors in Border Provinces (2019-2023). Iranian journal of parasitology, 20(2), 268.

Wang ?? C, et al. (2025) PSIA: A Comprehensive Knowledgebase of Plant Self-incompatibility. Genomics, proteomics & bioinformatics, 23(3).

Saini P, et al. (2025) CyExpDB: a web-based multi-species tissue-specific gene expression platform for functional genomics in Cyprinidae fish. Database : the journal of biological databases and curation, 2025.

Grimalda G, et al. (2025) Money counts: effects of monetary vs. purely numerical values on the mental representation of quantities. Psychological research, 89(2), 85.

Gowers PA, et al. (2025) A qualitative study of coach mentoring dentists in difficulty from a mentor perspective. British dental journal, 238(9), 720.

Wei M, et al. (2025) TRAIT: A Comprehensive Database for T-cell Receptor-antigen Interactions. *Genomics, proteomics & bioinformatics*, 23(3).

Azhar R, et al. (2025) PAHG: the database of human multi-gene families. *BMC genomic data*, 26(1), 74.

Wang W, et al. (2024) scEccDNAdb: an integrated single-cell eccDNA resource for human and mouse. *Database : the journal of biological databases and curation*, 2024.

Yang P, et al. (2024) AlliumDB: a central portal for comparative and functional genomics in Allium. *Horticulture research*, 11(2), uhad285.

Shi Q, et al. (2024) DRED: A Comprehensive Database of Genes Related to Repeat Expansion Diseases. *Genomics, proteomics & bioinformatics*, 22(5).

Jeusset L, et al. (2023) ViCloD, an interactive web tool for visualizing B cell repertoires and analyzing intraclonal diversities: application to human B-cell tumors. *NAR genomics and bioinformatics*, 5(2), lqad064.