

Resource Summary Report

Generated by [dkNET](#) on Aug 17, 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: 20260815T183225+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 [dkNET](#) .

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.

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.

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

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.