Resource Summary Report

Generated by dkNET on Aug 16, 2026

Bioclipse

RRID:SCR_014914
Type: Tool

Proper Citation

Bioclipse (RRID:SCR_014914)

Resource Information

URL: http://www.bioclipse.net/

Proper Citation: Bioclipse (RRID:SCR_014914)

Description: Open source downloadable application which contains a framework for managing and analyzing chemical compounds, as well as supports editing in 2D, processing large collections of molecules in tables, calculate various types of properties, and more cheminformatics functionality. This software also is used for the management and analysis of biological sequences (DNA, RNA, and protein), and relates the chemical structures and a target and then describes them using mathematical descriptors and models them using statistical methods. Bioclipse is equipped with a scripting language (Bioclipse Scripting Language or BSL) which can be used to automate tasks or create reusable snippets that can be shared with others,

Resource Type: data processing software, software application, data analysis software, software resource

Keywords: framework, chemical, compound, 2d, molecule, cheminformatic, biological, dna, rna, protein, mathematical

Availability: Commercial

Resource Name: Bioclipse

Resource ID: SCR_014914

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260815T182454+0000

Ratings and Alerts

No rating or validation information has been found for Bioclipse.

No alerts have been found for Bioclipse.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Saraf MK, et al. (2021) Nongenomic effects of estradiol vs. the birth control estrogen ethinyl estradiol on signaling and cell proliferation in pituitary tumor cells, and differences in the ability of R-equol to neutralize or enhance these effects. Steroids, 168, 108411.

Fagerholm U, et al. (2021) Advances in Predictions of Oral Bioavailability of Candidate Drugs in Man with New Machine Learning Methodology. Molecules (Basel, Switzerland), 26(9).

O'Rourke A, et al. (2020) Mechanism-of-Action Classification of Antibiotics by Global Transcriptome Profiling. Antimicrobial agents and chemotherapy, 64(3).

Kónya Z, et al. (2018) Aralkyl selenoglycosides and related selenosugars in acetylated form activate protein phosphatase-1 and -2A. Bioorganic & medicinal chemistry, 26(8), 1875.

Gousiadou C, et al. (2018) Computational Analysis of LOX1 Inhibition Identifies Descriptors Responsible for Binding Selectivity. ACS omega, 3(2), 2261.

Kalhotra P, et al. (2018) Structure?Activity Relationship and Molecular Docking of Natural Product Library Reveal Chrysin as a Novel Dipeptidyl Peptidase-4 (DPP-4) Inhibitor: An Integrated In Silico and In Vitro Study. Molecules (Basel, Switzerland), 23(6).

Ravula P, et al. (2016) Design, synthesis, in silico toxicity prediction, molecular docking, and evaluation of novel pyrazole derivatives as potential antiproliferative agents. EXCLI journal, 15, 187.

Alvarsson J, et al. (2016) Large-scale ligand-based predictive modelling using support vector machines. Journal of cheminformatics, 8, 39.

Park G, et al. (2013) Multiphasic analysis of whole exome sequencing data identifies a novel mutation of ACTG1 in a nonsyndromic hearing loss family. BMC genomics, 14, 191.

Lapins M, et al. (2013) A unified proteochemometric model for prediction of inhibition of cytochrome p450 isoforms. PloS one, 8(6), e66566.

Townsend JA, et al. (2011) CMLLite: a design philosophy for CML. Journal of cheminformatics, 3(1), 39.

Willighagen EL, et al. (2011) Linking the Resource Description Framework to cheminformatics and proteochemometrics. Journal of biomedical semantics, 2 Suppl 1(Suppl 1), S6.

Cao YM, et al. (2011) Analysis of PCBs degradation abilities of biphenyl dioxygenase derived from Enterobacter sp. LY402 by molecular simulation. New biotechnology, 29(1), 90.

Carlsson L, et al. (2010) Use of historic metabolic biotransformation data as a means of anticipating metabolic sites using MetaPrint2D and Bioclipse. BMC bioinformatics, 11, 362.

Spjuth O, et al. (2010) Towards interoperable and reproducible QSAR analyses: Exchange of datasets. Journal of cheminformatics, 2(1), 5.

Wagener J, et al. (2009) XMPP for cloud computing in bioinformatics supporting discovery and invocation of asynchronous web services. BMC bioinformatics, 10, 279.

Kind T, et al. (2009) Software platform virtualization in chemistry research and university teaching. Journal of cheminformatics, 1, 18.