

Resource Summary Report

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MOLEonline

RRID:SCR_018314

Type: Tool

Proper Citation

MOLEonline (RRID:SCR_018314)

Resource Information

URL: <http://mole.upol.cz>

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Description: Interactive web based tool for analyzing biomacromolecular channels, tunnels and pores. Enables two modes of calculation with one dedicated to analysis of channels and another for transmembrane pores. Can use PDB and mmCIF formats. Can analyze biomacromolecular structures stemming from NMR, X-ray and cryo-EM techniques. Interconnected with PDBe, CSA, ChannelsDB, OPM, UniProt to help setup and analysis of acquired results. Provides analytics for detection and structural characterization of channels and information about their physicochemical features.

Synonyms: MOLEonline 2.0

Resource Type: analysis service resource, data access protocol, production service resource, service resource, software resource, web service

Defining Citation: [PMID:29718451](https://pubmed.ncbi.nlm.nih.gov/29718451/)

Keywords: biomacromolecular channel, analysis, biomacromolecular pore, biomacromolecular tunnel, transmembrane pore analysis, analysis, biomacromolecular structure, physicochemical feature

Availability: Free, Freely available

Resource Name: MOLEonline

Resource ID: SCR_018314

Alternate URLs: <https://mole.upol.cz/online/>

Old URLs: <http://old.mole.upol.cz/>

Record Creation Time: 20220129T080339+0000

Ratings and Alerts

No rating or validation information has been found for MOLEonline.

No alerts have been found for MOLEonline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 36 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Yokoyama T, et al. (2026) Val109 and Ile170 contribute to channel function in Guillardia theta-derived anion channelrhodopsins. Scientific reports, 16(1).

Montanucci L, et al. (2025) Ligand distances as key predictors of pathogenicity and function in NMDA receptors. Human molecular genetics, 34(2), 128.

Lee SH, et al. (2025) Discovery to Engineering of Mycotoxin Deoxynivalenol Degrading Enzymes Based on the Specialized Glyoxalase I. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(29), e02914.

Toay S, et al. (2025) Genetic mutations disrupt the coordinated mode of tyrosinase's intra-melanosomal domain. Protein science : a publication of the Protein Society, 34(8), e70209.

Vela-Amieva M, et al. (2025) The Arg108Cys Variant of Methylmalonyl-CoA Mutase: Clinical Implications for the Mexican Population Based on Molecular Dynamics and Docking. International journal of molecular sciences, 26(7).

Toay S, et al. (2025) Genetic mutations disrupt the coordinated mode of tyrosinase intra-melanosomal domain. bioRxiv : the preprint server for biology.

Špačková A, et al. (2024) ChannelsDB 2.0: a comprehensive database of protein tunnels and pores in AlphaFold era. Nucleic acids research, 52(D1), D413.

Li G, et al. (2024) Yeast metabolism adaptation for efficient terpenoids synthesis via isopentenol utilization. Nature communications, 15(1), 9844.

Zmysliá M, et al. (2024) A nanoengineered tandem nitroreductase: designing a robust prodrug-activating nanoreactor. RSC chemical biology, 6(1), 21.

Aleo SJ, et al. (2024) Genetic variants affecting NQO1 protein levels impact the efficacy of idebenone treatment in Leber hereditary optic neuropathy. Cell reports. Medicine, 5(2),

101383.

Schott K, et al. (2024) Unplugging lateral fenestrations of NALCN reveals a hidden drug binding site within the pore region. *Proceedings of the National Academy of Sciences of the United States of America*, 121(22), e2401591121.

Kalkan Ö, et al. (2023) Heterologous expression, purification and structural features of native *Dictyostelium discoideum* dye-decolorizing peroxidase bound to a natively incorporated heme. *Frontiers in chemistry*, 11, 1220543.

Cooper BF, et al. (2023) Phospholipid transport to the bacterial outer membrane through an envelope-spanning bridge. *bioRxiv : the preprint server for biology*.

Ward J, et al. (2023) VEO-IBD NOX1 variant highlights a structural region essential for NOX/DUOX catalytic activity. *Redox biology*, 67, 102905.

Brünger T, et al. (2023) Conserved patterns across ion channels correlate with variant pathogenicity and clinical phenotypes. *Brain : a journal of neurology*, 146(3), 923.

Maksaev G, et al. (2023) Blockade of TRPV channels by intracellular spermine. *The Journal of general physiology*, 155(5).

Ushio K, et al. (2022) Boric acid transport activity of human aquaporins expressed in *Xenopus* oocytes. *Physiological reports*, 10(1), e15164.

Uno S, et al. (2022) Diverse reaction behaviors of artificial ubiquinones in mitochondrial respiratory complex I. *The Journal of biological chemistry*, 298(7), 102075.

Tayade R, et al. (2022) Genome-Wide Identification of Aquaporin Genes in Adzuki Bean (*Vigna angularis*) and Expression Analysis under Drought Stress. *International journal of molecular sciences*, 23(24).

Cerdan AH, et al. (2022) Lateral fenestrations in the extracellular domain of the glycine receptor contribute to the main chloride permeation pathway. *Science advances*, 8(41), eadc9340.