

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

Defining Citation: [PMID: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/>

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 24 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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

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.

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.

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.

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

Xu Z, et al. (2022) Two entry tunnels in mouse TAAR9 suggest the possibility of multi-entry tunnels in olfactory receptors. Scientific reports, 12(1), 2691.

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.

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

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).

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

Venisse JS, et al. (2021) Genome-Wide Identification, Structure Characterization, and Expression Pattern Profiling of the Aquaporin Gene Family in *Betula pendula*. *International journal of molecular sciences*, 22(14).

Swanson NA, et al. (2021) Cryo-EM structure of the periplasmic tunnel of T7 DNA-ejectosome at 2.7 Å resolution. *Molecular cell*, 81(15), 3145.

Yang HC, et al. (2021) Temperature effect on water dynamics in tetramer phosphofructokinase matrix and the super-arrhenius respiration rate. *Scientific reports*, 11(1), 383.

Baeza M, et al. (2021) Identification of Stress-Related Genes and a Comparative Analysis of the Amino Acid Compositions of Translated Coding Sequences Based on Draft Genome Sequences of Antarctic Yeasts. *Frontiers in microbiology*, 12, 623171.

Fan J, et al. (2021) Crystal structures of LeuT reveal conformational dynamics in the outward-facing states. *The Journal of biological chemistry*, 296, 100609.

Jiang D, et al. (2021) Open-state structure and pore gating mechanism of the cardiac sodium channel. *Cell*, 184(20), 5151.

Melnikova DN, et al. (2021) Effect of Point Mutations on Structural and Allergenic Properties of the Lentil Allergen Len c 3. *Membranes*, 11(12).

Jiang D, et al. (2020) Structure of the Cardiac Sodium Channel. *Cell*, 180(1), 122.

Jones BJ, et al. (2020) Larger active site in an ancestral hydroxynitrile lyase increases catalytically promiscuous esterase activity. *PloS one*, 15(6), e0235341.