

Resource Summary Report

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CueMol

RRID:SCR_019052

Type: Tool

Proper Citation

CueMol (RRID:SCR_019052)

Resource Information

URL: <http://www.cuemol.org/en/>

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Description: Software tool for macromolecular structure visualization. Molecular visualization framework to visualize crystallographic models of macromolecules. Used to visualize and create publication quality images of macromolecular structures with user friendly interfaces.

Synonyms: Que

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

Keywords: Macromolecular structure visualization, macromolecular crystallographic model visualization, molecular structure, molecular structure image, structure image

Availability: Free, Available for download, Freely available

Resource Name: CueMol

Resource ID: SCR_019052

Alternate IDs: <https://github.com/CueMol/cuemol2>,
<https://sourceforge.net/projects/cuemol/>

License: GPLv3

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260729T044450+0000

Ratings and Alerts

No rating or validation information has been found for CueMol.

No alerts have been found for CueMol.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Ueno A, et al. (2025) A cytokine-based designer enzyme with an abiological multinuclear metal center exhibits intrinsic and extrinsic catalysis. *Nature communications*, 16(1), 6781.

Kim J, et al. (2025) Structural insights into the selective recognition of RF-amide peptides by neuropeptide FF receptor 2. *EMBO reports*, 26(9), 2413.

Goto S, et al. (2024) Cryo-EM structures elucidate the multiligand receptor nature of megalin. *Proceedings of the National Academy of Sciences of the United States of America*, 121(22), e2318859121.

Jianwei L, et al. (2023) Structures of apo Cas12a and its complex with crRNA and DNA reveal the dynamics of ternary complex formation and target DNA cleavage. *PLoS biology*, 21(3), e3002023.

Noritsugu K, et al. (2023) Lysine long-chain fatty acylation regulates the TEAD transcription factor. *Cell reports*, 42(4), 112388.

Bulzu PA, et al. (2021) Heliorhodopsin Evolution Is Driven by Photosensory Promiscuity in Monoderms. *mSphere*, 6(6), e0066121.

Yonekura-Sakakibara K, et al. (2021) Seed-coat protective neolignans are produced by the dirigent protein AtDP1 and the laccase AtLAC5 in *Arabidopsis*. *The Plant cell*, 33(1), 129.

Bartsch A, et al. (2021) An antibiotic-resistance conferring mutation in a neisserial porin: Structure, ion flux, and ampicillin binding. *Biochimica et biophysica acta. Biomembranes*, 1863(6), 183601.

Wang B, et al. (2021) Structural basis for self-cleavage prevention by tag:anti-tag pairing complementarity in type VI Cas13 CRISPR systems. *Molecular cell*, 81(5), 1100.

Zarkadas E, et al. (2020) The Binding of Palonosetron and Other Antiemetic Drugs to the Serotonin 5-HT₃ Receptor. *Structure (London, England : 1993)*, 28(10), 1131.

Tanaka Y, et al. (2020) Crystal structure of a YeeE/YedE family protein engaged in thiosulfate uptake. *Science advances*, 6(35), eaba7637.

Inoue K, et al. (2020) Shining light on rhodopsin selectivity: How do proteins decide whether to transport H⁺ or Cl⁻? The Journal of biological chemistry, 295(44), 14805.

Miyauchi H, et al. (2017) Structural basis for xenobiotic extrusion by eukaryotic MATE transporter. Nature communications, 8(1), 1633.

Kasuya G, et al. (2016) Crystal structures of the TRIC trimeric intracellular cation channel orthologues. Cell research, 26(12), 1288.

Tanaka Y, et al. (2015) Crystal Structures of SecYEG in Lipidic Cubic Phase Elucidate a Precise Resting and a Peptide-Bound State. Cell reports, 13(8), 1561.

Hirano T, et al. (2015) Structure-based analysis of domain function of chitin oligosaccharide deacetylase from *Vibrio parahaemolyticus*. FEBS letters, 589(1), 145.

Taniguchi R, et al. (2015) Outward- and inward-facing structures of a putative bacterial transition-metal transporter with homology to ferroportin. Nature communications, 6, 8545.

Takeda H, et al. (2014) Structural basis for ion selectivity revealed by high-resolution crystal structure of Mg²⁺ channel MgtE. Nature communications, 5, 5374.

Kumazaki K, et al. (2014) Crystal structure of *Escherichia coli* YidC, a membrane protein chaperone and insertase. Scientific reports, 4, 7299.

Ishii R, et al. (2012) Structure of a dominant-negative helix-loop-helix transcriptional regulator suggests mechanisms of autoinhibition. The EMBO journal, 31(11), 2541.