

Resource Summary Report

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Electron Microscopy Data Bank at PDBe (MSD-EBI)

RRID:SCR_006506

Type: Tool

Proper Citation

Electron Microscopy Data Bank at PDBe (MSD-EBI) (RRID:SCR_006506)

Resource Information

URL: <http://www.ebi.ac.uk/pdbe/emdb/>

Proper Citation: Electron Microscopy Data Bank at PDBe (MSD-EBI) (RRID:SCR_006506)

Description: Repository for electron microscopy density maps of macromolecular complexes and subcellular structures at Protein Data Bank in Europe. Covers techniques, including single-particle analysis, electron tomography, and electron (2D) crystallography.

Abbreviations: EMDB at PDBe

Synonyms: MSD-EBI, Electron Microscopy Data Bank at Protein Data Bank in Europe, Electron Microscopy DataBank, Electron Microscopy Data Bank at PDBe (MSD-EBI), Electron Microscopy Data Bank at PDBe

Resource Type: analysis service resource, data analysis service, data or information resource, data repository, database, production service resource, service resource, storage service resource

Keywords: electron microscopy, density map, macromolecule, complex, subcellular structure, single-particle analysis, electron tomography, electron crystallography, macromolecular complex, structure, protein, protein binding, electron, electron configuration, tomography, microscopy, gold standard

Funding: NIH

Availability: Public

Resource Name: Electron Microscopy Data Bank at PDBe (MSD-EBI)

Resource ID: SCR_006506

Alternate IDs: r3d100010562, nlx_149453

Alternate URLs: <https://doi.org/10.17616/R3HP57>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260905T132555+0000

Ratings and Alerts

No rating or validation information has been found for Electron Microscopy Data Bank at PDBe (MSD-EBI).

No alerts have been found for Electron Microscopy Data Bank at PDBe (MSD-EBI).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 153 mentions in open access literature.

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

Füzik T, et al. (2026) Structures of asymmetric particles of tick-borne encephalitis virus provide insight into flavivirus assembly and maturation. *Science advances*, 12(27), eaee4765.

Shen C, et al. (2025) Deciphering the molecular mechanism of the bacterial division motor TolQRA. *Cell discovery*, 11(1), 87.

Shikimachi R, et al. (2025) Structural basis for E3 ubiquitin ligase UHRF1 binding to nucleosome core particle and histone H3 ubiquitination. *The Journal of biological chemistry*, 301(12), 110894.

Gaynes MN, et al. (2025) Cryo-EM Structure of the Cyclase Domain and Evaluation of Substrate Channeling in a Bifunctional Class II Terpene Synthase. *bioRxiv : the preprint server for biology*.

Wang Y, et al. (2025) Structural basis of the RNA-mediated Retron-Eco2 oligomerization. *Cell discovery*, 11(1), 73.

Little M, et al. (2025) Interaction of cardiac leiomodins with the native cardiac thin filament. *PLoS biology*, 23(1), e3003027.

Liu ZK, et al. (2025) Structural basis for aerobic anoxygenic photosynthesis in the reaction center-light-harvesting 1 (RC-LH1) supercomplex of *Dinoroseobacter shibae*. *Communications biology*, 8(1), 1565.

Hu J, et al. (2025) Establishing a universal IVRP method for quadrivalent HPV vaccines to replace in vivo potency tests. *NPJ vaccines*, 10(1), 55.

Riel EB, et al. (2025) The cryo-EM structure and physical basis for anesthetic inhibition of the THIK1 K2P channel. *Proceedings of the National Academy of Sciences of the United States of America*, 122(14), e2421654122.

Kikuchi A, et al. (2025) Cryo-EM reveals evolutionarily conserved and distinct structural features of plant CG maintenance methyltransferase MET1. *Nature communications*, 16(1), 8524.

Zhang F, et al. (2025) Cryo-EM structure and oligomerization of the human planar cell polarity core protein Vangl1. *Nature communications*, 16(1), 135.

Pérez-Illana M, et al. (2025) Aviadenovirus structure: A highly thermostable capsid in the absence of stabilizing proteins. *PLoS pathogens*, 21(10), e1013553.

Yang X, et al. (2025) Structural insights into the catalytic mechanism of ammonia monooxygenase. *Nature communications*, 17(1), 508.

Tian X, et al. (2025) Molecular mechanism of PINK1 regulation by the Hsp90 machinery. *Nature communications*, 16(1), 10801.

Wu T, et al. (2025) Critical role of extracellular loops in differential modulations of TTX-sensitive and TTX-resistant Nav channels. *Proceedings of the National Academy of Sciences of the United States of America*, 122(32), e2510355122.

Li H, et al. (2025) The deubiquitinating enzyme Otu1 releases substrates from the conserved initiation complex of the Cdc48/p97 ATPase for proteasomal degradation. *bioRxiv : the preprint server for biology*.

Christianson B, et al. (2025) Characterization of the Structure and Function of the Photosynthetic RC-LH1 Core Supercomplex From *Rhodospirillum rubrum*. *Physiologia plantarum*, 177(3), e70275.

Cui Y, et al. (2025) Bacterial Hachiman complex executes DNA cleavage for antiphage defense. *Nature communications*, 16(1), 2604.

McIntire WE, et al. (2024) G protein $\gamma 4$ as a structural determinant of enhanced nucleotide exchange in the A2AAR-Gs complex. *Research square*.

Li X, et al. (2024) Structures and organizations of PSI-AcpPCI supercomplexes from red tidal and coral symbiotic photosynthetic dinoflagellates. *Proceedings of the National Academy of Sciences of the United States of America*, 121(7), e2315476121.