

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: service resource, data repository, data analysis service, storage service resource, data or information resource, database, production service resource, analysis 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: 20260731T042724+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 144 mentions in open access literature.

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

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.

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.

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

Little M, et al. (2025) Interaction of cardiac leiomodoin 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.

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

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

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.

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

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

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*.

Li X, et al. (2024) Structures and organizations of PSI-AcpPCl 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.

Wang P, et al. (2024) Molecular principles of the assembly and construction of a carboxysome shell. *Science advances*, 10(48), eadr4227.

Wang Q, et al. (2024) The architecture of substrate-engaged TOM-TIM23 supercomplex reveals preprotein proximity sites for mitochondrial protein translocation. *Cell discovery*, 10(1), 19.

Chi X, et al. (2024) Cryo-EM structures of the human NaS1 and NaDC1 transporters revealed the elevator transport and allosteric regulation mechanism. *Science advances*, 10(13), eadl3685.

Wang P, et al. (2024) Architectures of photosynthetic RC-LH1 supercomplexes from *Rhodobacter blasticus*. *Science advances*, 10(41), eadp6678.