

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 [PRECISE-TBI](#) .

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.

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

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.

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.

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.

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.

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.

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.