

Resource Summary Report

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[EMDataResource.org](#)

RRID:SCR_003207

Type: Tool

Proper Citation

EMDataResource.org (RRID:SCR_003207)

Resource Information

URL: <http://www.emdataresource.org/>

Proper Citation: EMDataResource.org (RRID:SCR_003207)

Description: Portal for deposition and retrieval of cryo electron microscopy (3DEM) density maps, atomic models, and associated metadata. Global resource for 3 Dimensional Electron Microscopy structure data archiving and retrieval, news, events, software tools, data standards, validation methods.

Abbreviations: EMDB, EMDataResource

Synonyms: EMDataResource, EMDResource, EMDB, EMDataBank.org, EMDataBank - Unified Data Resource for 3DEM, EMDataBank

Resource Type: data repository, portal, service resource, storage service resource, data or information resource, project portal

Defining Citation: [PMID:20935055](#), [PMID:20888470](#)

Keywords: deposition, retrieval, cryo, electron, microscopy, 3DEM, density, maps, atomic, model, metadata, structure

Funding: NIGMS R01 GM079429;
BBSRC BBG022577

Availability: Free, Freely available

Resource Name: EMDataResource.org

Resource ID: SCR_003207

Alternate IDs: r3d100010552, nif-0000-30776

Alternate URLs: <https://doi.org/10.17616/R3T61P>

Old URLs: EMDataBank.org

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260817T040344+0000

Ratings and Alerts

No rating or validation information has been found for EMDataResource.org.

No alerts have been found for EMDataResource.org.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 183 mentions in open access literature.

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

Lv N, et al. (2026) IgG-Bridging-Seeded Synergistic Aggregation of SARS-CoV-2 Spikes Underlies Potent Neutralization by a Low-Affinity Antibody. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(11), e17192.

Bose P, et al. (2026) Structural basis of secreted acid phosphatase polymerization in the *Leishmania* parasite. *Protein science : a publication of the Protein Society*, 35(5), e70591.

Hong Q, et al. (2026) Structural insight into the assembly and D antigenicity of polio type 1 stabilized virus-like particles. *NPJ vaccines*, 11(1).

Li H, et al. (2025) Molecular mechanisms of the viral encoded chaperone 100K in capsid folding and assembly of adenovirus. *Nature communications*, 16(1), 4013.

Zyla DS, et al. (2025) Stabilized Full-Length Measles Fusion Protein Elicits Potent Immunity and Protection In Vivo. *bioRxiv : the preprint server for biology*.

Manik MK, et al. (2025) Structural basis for TIR domain-mediated innate immune signaling by Toll-like receptor adaptors TRIF and TRAM. *Proceedings of the National Academy of Sciences of the United States of America*, 122(2), e2418988122.

Wang L, et al. (2025) Human Coronavirus HKU1 Neutralizing Monoclonal Antibodies Target Diverse Epitopes Within and Around the TMPRSS2 Receptor Binding Site. *bioRxiv : the preprint server for biology*.

Schendel SL, et al. (2025) A global collaboration for systematic analysis of broad-ranging antibodies against the SARS-CoV-2 spike protein. *Cell reports*, 44(4), 115499.

Manger S, et al. (2025) How does *Mycoplasma pneumoniae* scavenge lipids from its host membranes? *Science advances*, 11(40), eady4746.

Li X, et al. (2025) Structure-guided design of native-like HIV Env Single Chain Trimers for enhanced stability, immunogenicity, and versatile vaccine delivery. *bioRxiv : the preprint server for biology*.

Nan X, et al. (2024) Exploring distinct modes of inter-spike cross-linking for enhanced neutralization by SARS-CoV-2 antibodies. *Nature communications*, 15(1), 10578.

Gambelli L, et al. (2024) Structure of the two-component S-layer of the archaeon *Sulfolobus acidocaldarius*. *eLife*, 13.

Kochańczyk T, et al. (2024) Structural basis for transthiolation intermediates in the ubiquitin pathway. *Nature*, 633(8028), 216.

Hickey KL, et al. (2024) Temporal control of acute protein aggregate turnover by UBE3C and NRF1-dependent proteasomal pathways. *bioRxiv : the preprint server for biology*.

Sofer S, et al. (2024) Perturbed N-glycosylation of *Halobacterium salinarum* archaeum filaments leads to filament bundling and compromised cell motility. *Nature communications*, 15(1), 5841.

Wang X, et al. (2024) DiffModeler: Large Macromolecular Structure Modeling in Low-Resolution Cryo-EM Maps Using Diffusion Model. *bioRxiv : the preprint server for biology*.

Rubio AA, et al. (2024) Bispecific antibodies with broad neutralization potency against SARS-CoV-2 variants of concern. *bioRxiv : the preprint server for biology*.

Li R, et al. (2024) Multivalent interactions between fully glycosylated influenza virus hemagglutinins mediated by glycans at distinct N-glycosylation sites. *Npj viruses*, 2(1), 48.

Xu D, et al. (2024) Vaccine design via antigen reorientation. *Nature chemical biology*, 20(8), 1012.

Solorio-Kirpichyan K, et al. (2024) Cryo-EM structure of histidyl-tRNA synthetase-like domain reveals activating crossed helices at the core of GCN2. *PNAS nexus*, 3(12), pgae528.