

EMDB & EMPIAR Archives



Jack Turner

EMDB

Outline



Archives & EMDB Website

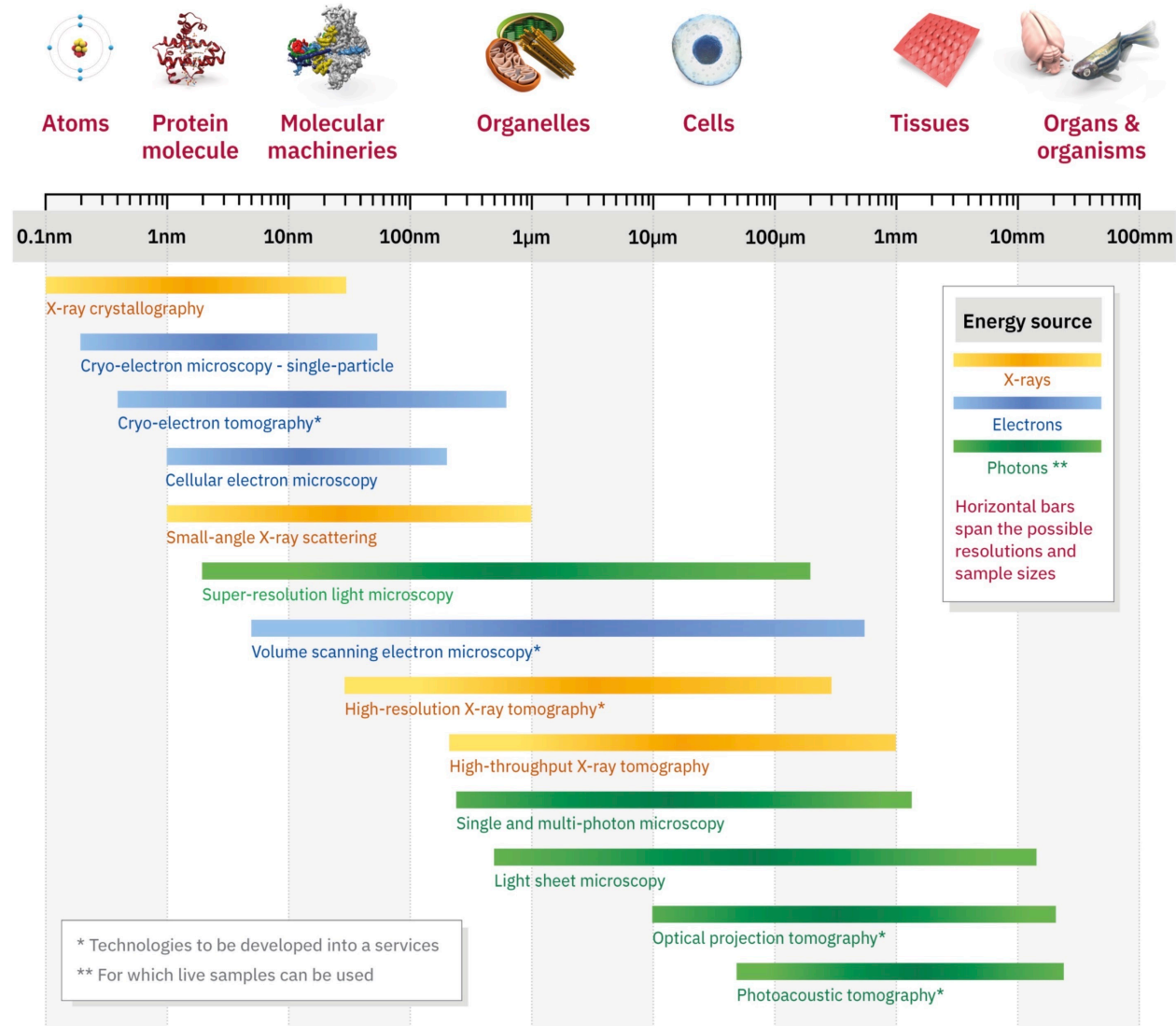


EMDB Deposition

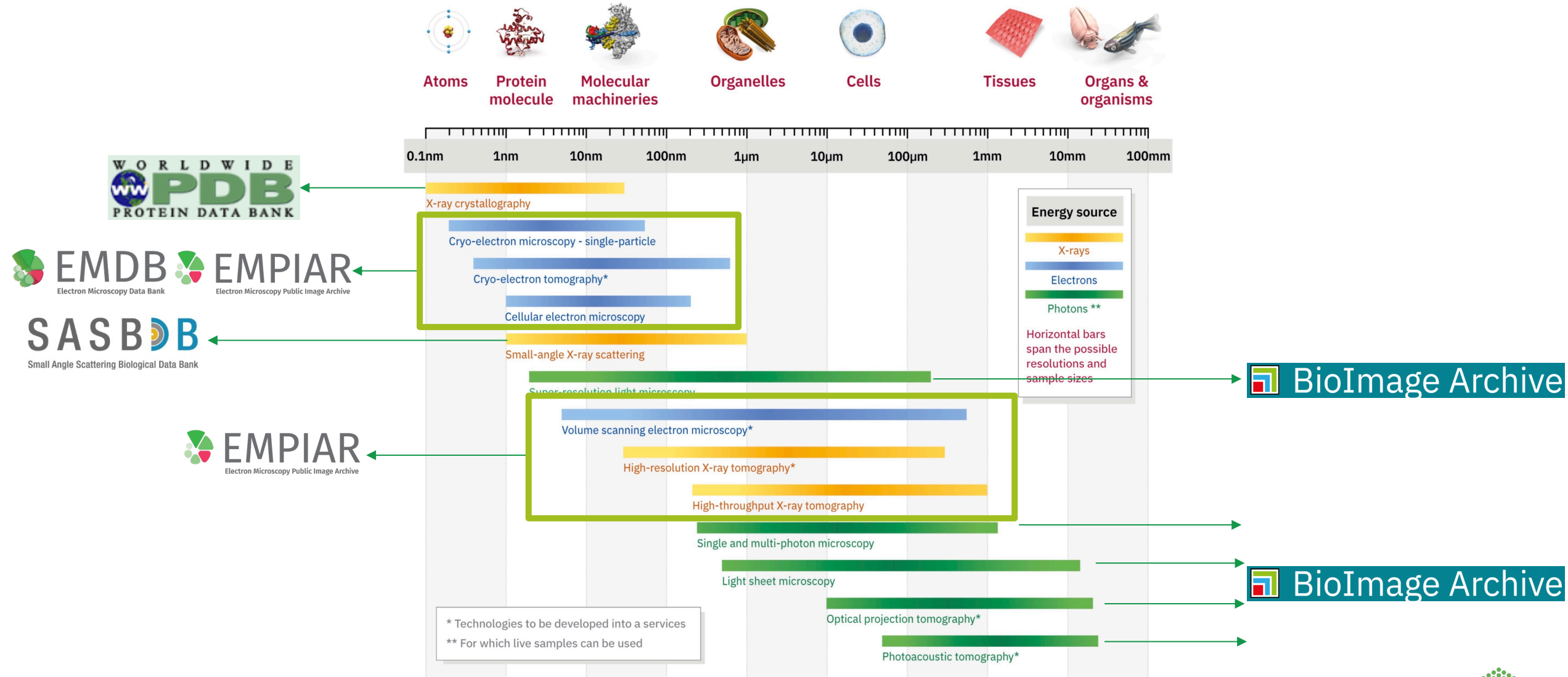


EMPIAR Deposition

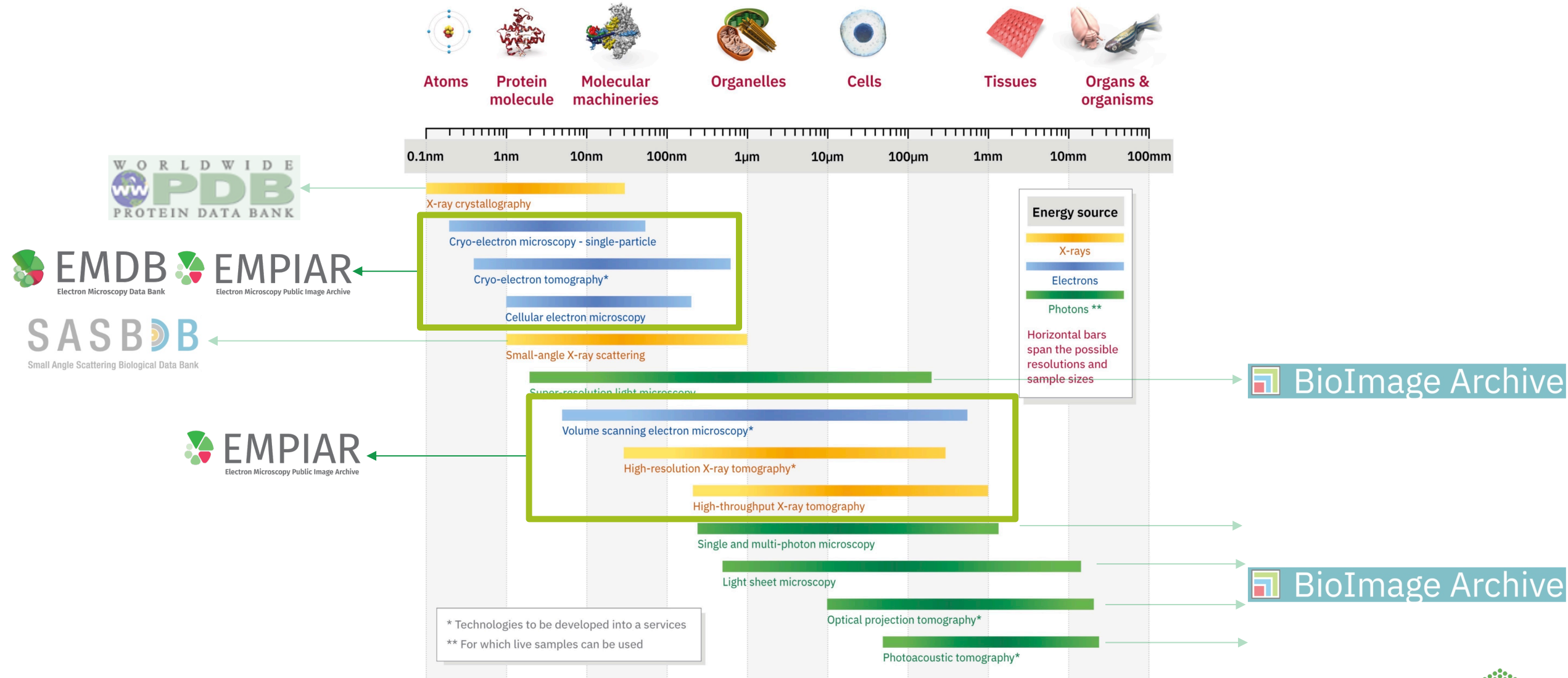
Archiving across scales



Archiving across scales



Archiving across scales

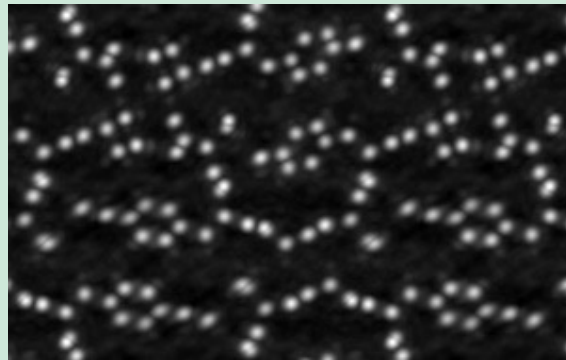


The Electron Microscopy Data Bank - EMDB

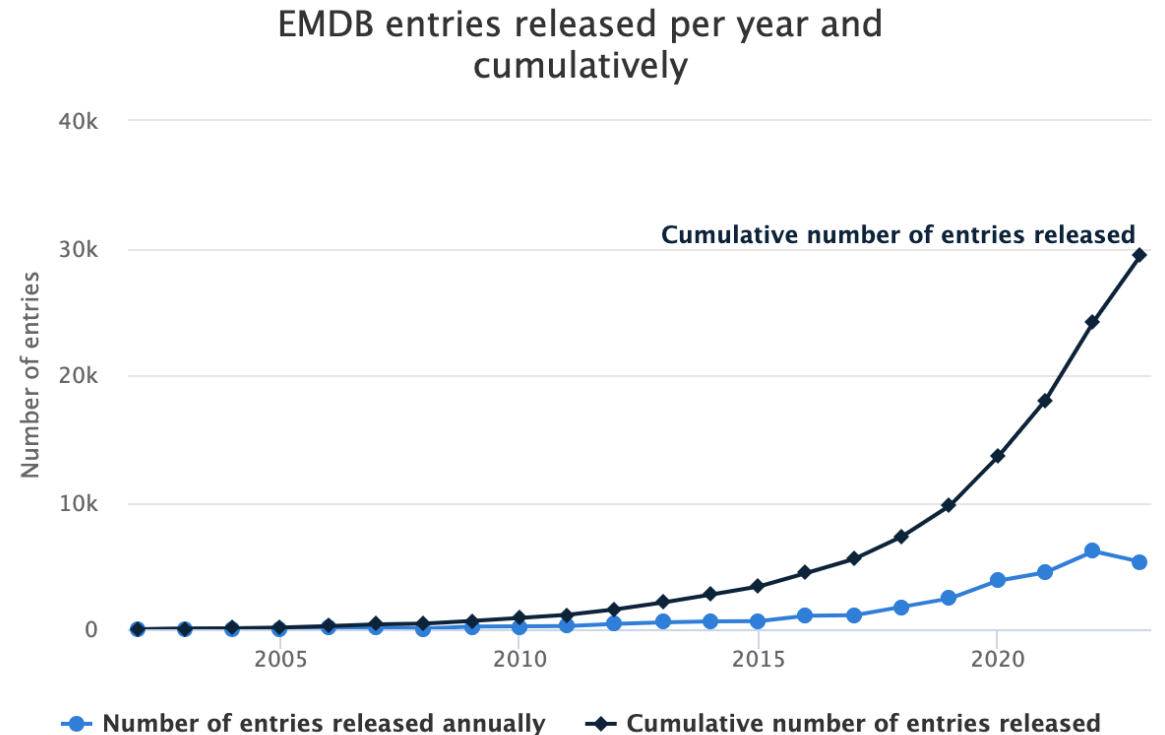
- Established in 2002 at EMBL-EBI
- wwPDB Partner
- Electron microscopy volume maps and Tomograms
- All data is freely and openly available under a CC0 license



EMD-15182



EMD-0698



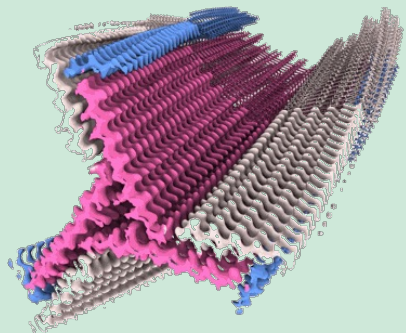
EMDB – continued growth of the archive

EMDB	2022	2021	2020
Released entries	6,131 (+37%)	4,488 (+17%)	3,831
Deposited entries	8,366 (+35%)	6,210 (+36%)	4,568
Total entries	24,187 (+34%)	18,058 (+33%)	13,583
Total size (TB)	8.9	4.5	2.9

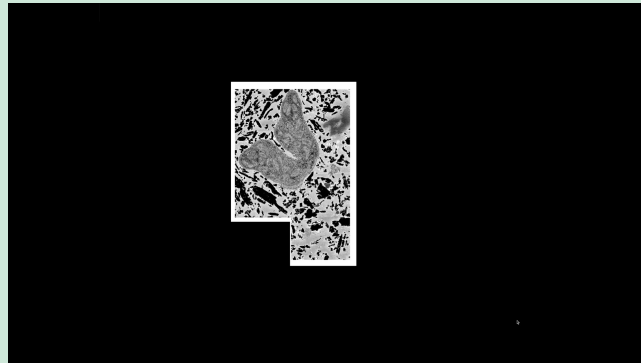
- Milestone of **30,000** release entries reached in February 2023
 - Exponential growth, doubling time **~2 – 2.5 years**
 - If this continues **50k** entries in **2025** and **100k** entries in **2028**

Electron Microscopy Public Image Archive - EMPIAR

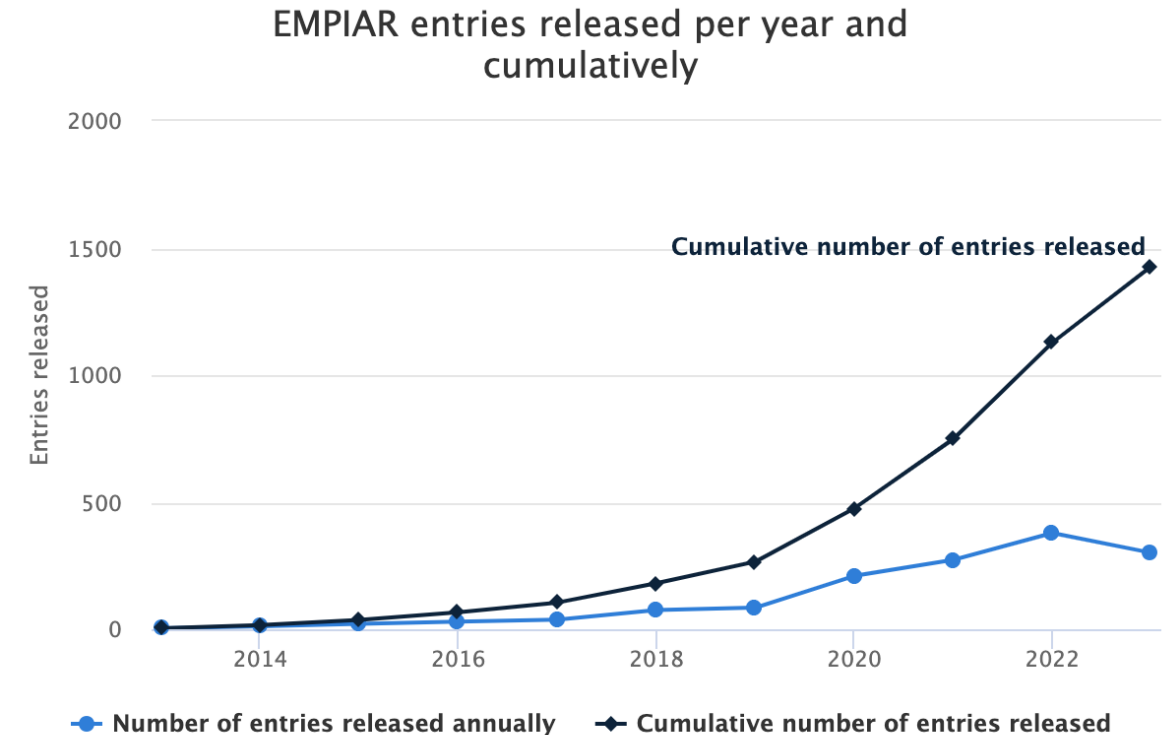
- Raw imaging data used to produce maps found in the EMDB
- Volume EM techniques and X-ray tomography and microscopy
- All data is freely and openly available under a CC0 license



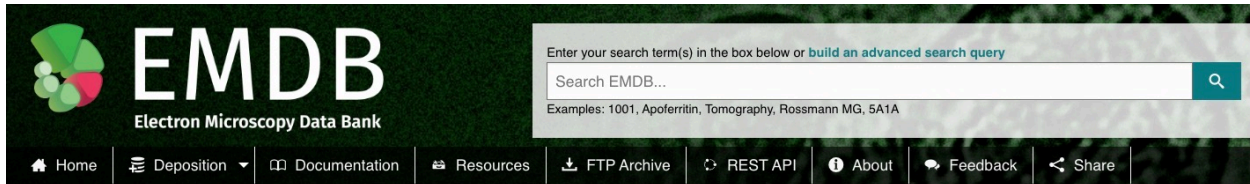
EMPIAR-11278/EMD-14167



EMPIAR-10310



The Electron Microscopy Data Bank - Website



EMDB
Electron Microscopy Data Bank

Enter your search term(s) in the box below or [build an advanced search query](#)

Search EMDB...

Examples: 1001, Apoferritin, Tomography, Rossmann MG, 5A1A

Home | Deposition | Documentation | Resources | FTP Archive | REST API | About | Feedback | Share

EMDB (the Electron Microscopy Data Bank) is a public repository for electron cryo-microscopy maps and tomograms of macromolecular complexes and subcellular structures. It covers a variety of techniques, including single-particle analysis, electron tomography, sub-tomogram averaging, fibre diffraction and electron crystallography. [More...](#)

As of 06 September 2023, EMDB contains 29495 entries ([latest entries](#), [trends](#)).

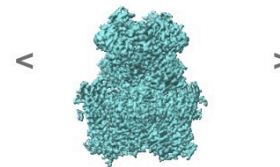
EMDB News

- 21 December 2022: EMDB proudly announces the EMICSS resource. It provides weekly updated cross-reference information for all EMDB entries to other resources (including PDB, EMPIAR, Europe PMC, UniProt, AlphaFold DB and many more.) Read more here: emdb-empiar.org/emicss.
- 12 October 2022: EMDB Validation Analysis (VA) is officially launched at <https://www.ebi.ac.uk/emdb/va/>. It is available as a local stand-alone package and is coming soon to CCP-EM. The tutorial on how to use the VA information is on [EMDB YouTube channel](#). A full description of VA functionality is published in [Acta Crystallographica Section D](#).

Quick links

- EMDB Policies
- Talks & Tutorials
- Validation Analysis
- Chart builder
- EMICSS
- Volume Browser
- EMDB Citations
- EMPIAR
- PDBe
- BioImage Archive
- EMDataResource
- EM Navigator
- 3D EM History

Recent Entries (Show all)

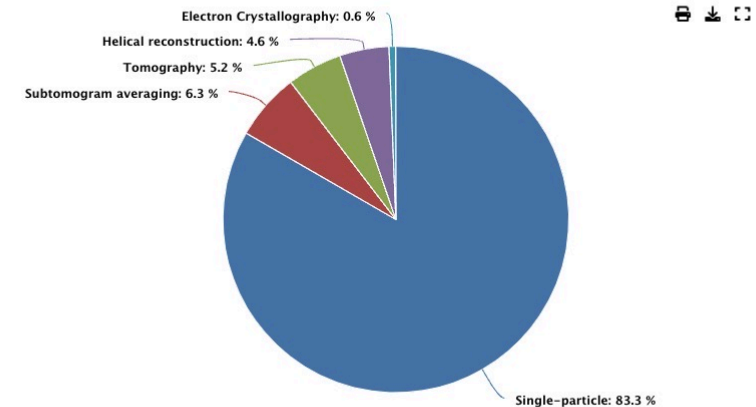


EMD-40748 [1/127]
Structure of LBD-TMD of AMPA receptor GluA2

Explore EMDB

Select a graph from the pull-down menu. Click on any element of a graph to see the corresponding list of EMDB entries.

EM Method



Explore EMDB

Select a graph from the pull-down menu. Click on any element of a graph to see the corresponding list of EMDB entries.

Organism

12.5k

<https://www.ebi.ac.uk/emdb/>

The Electron Microscopy Data Bank - Website

Powerful Search

EMDB
Electron Microscopy Data Bank

Enter your search term(s) in the box below or build an advanced search query
Search EMDB

Example: 1001,Apoferritin, Tomography, Rosemann MG, SARA

Edit your search query here and hit Return to execute it:
`xref_ALPHAFOLD:[* TO *] NOT fitted_pdbs:[* TO *]`

Filter By
Number of entries released by year

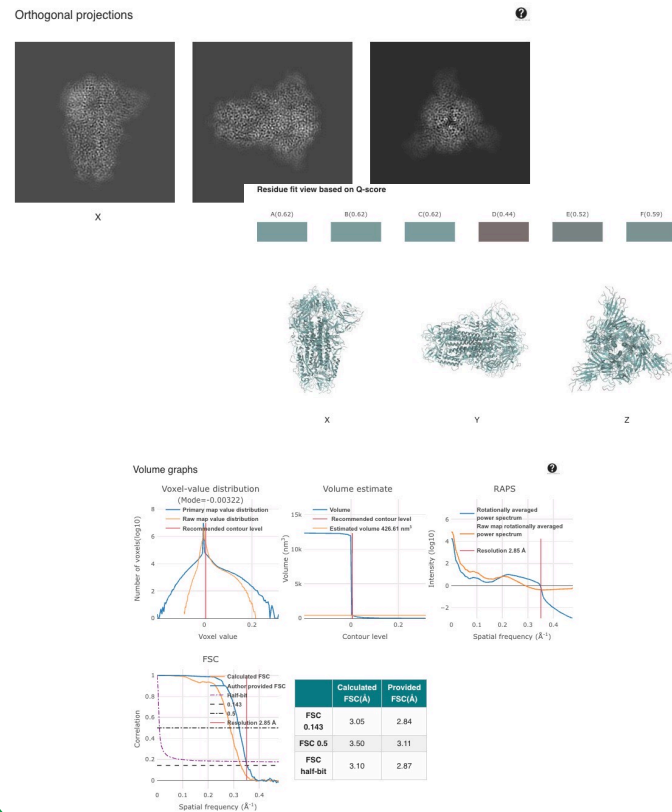
Current Database
EMDB (11058)

Edit your search query here and hit Return to execute it:
`xref_ALPHAFOLD:[* TO *] NOT fitted_pdbs:[* TO *]`

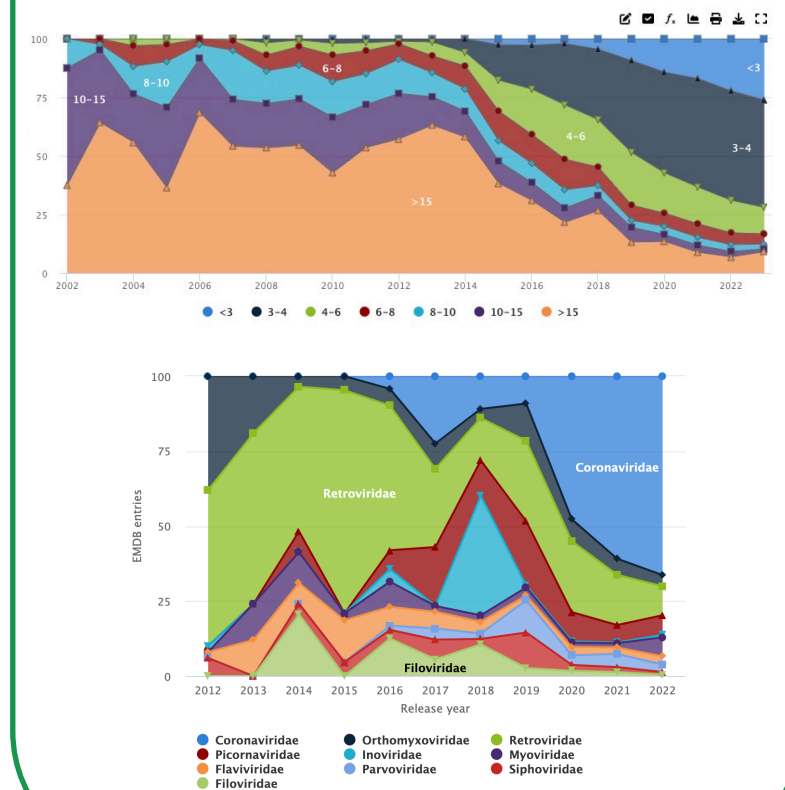
EMPIAR-11561
Cryo-electron microscopy structure of HeLa cell

Release date: 2018-01-10
Dataset size: 1.1 GB
Fungus: HIKH
Müller: CW
To Be Published: No
Image sets: Tilt series, Tilt series

Validation



Statistics



<https://www.ebi.ac.uk/emdb/>

Electron Microscopy Public Image Archive - EMPIAR

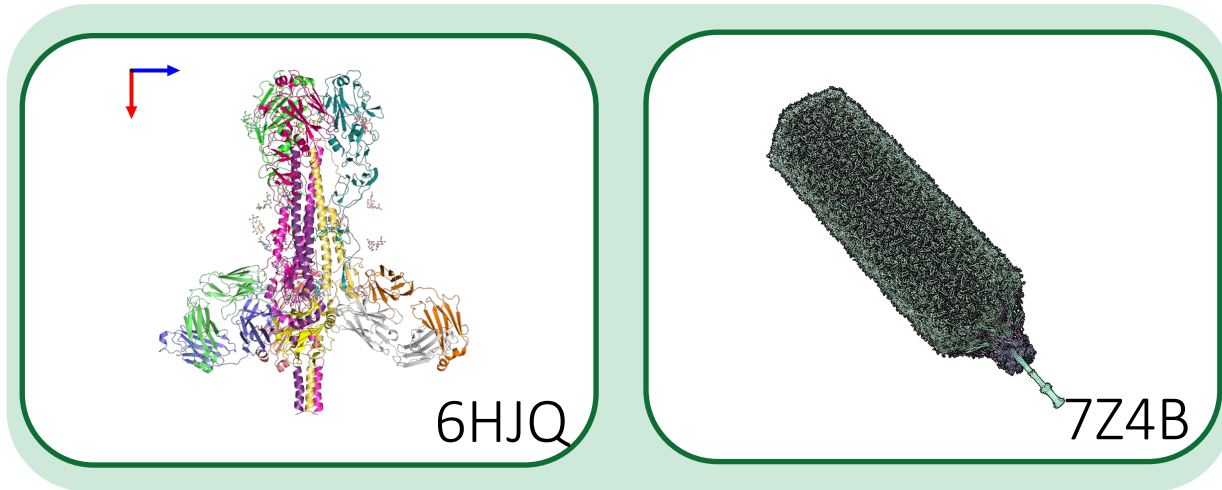
EMPIAR	2022	2021	2020
Released entries	376 (+39%)	273 (+30%)	210
Deposited entries	436 (+51%)	288 (+3%)	280
Released size (TB)	903 (+15%)	788 (+75%)	450
Total entries	1129 (+51%)	750 (+57%)	477
Total size (TB)	2,399	1,496	707

- 1 PB in June 2021
- 2PB and 1,000th entry in 2022
- **3 PB 2023**

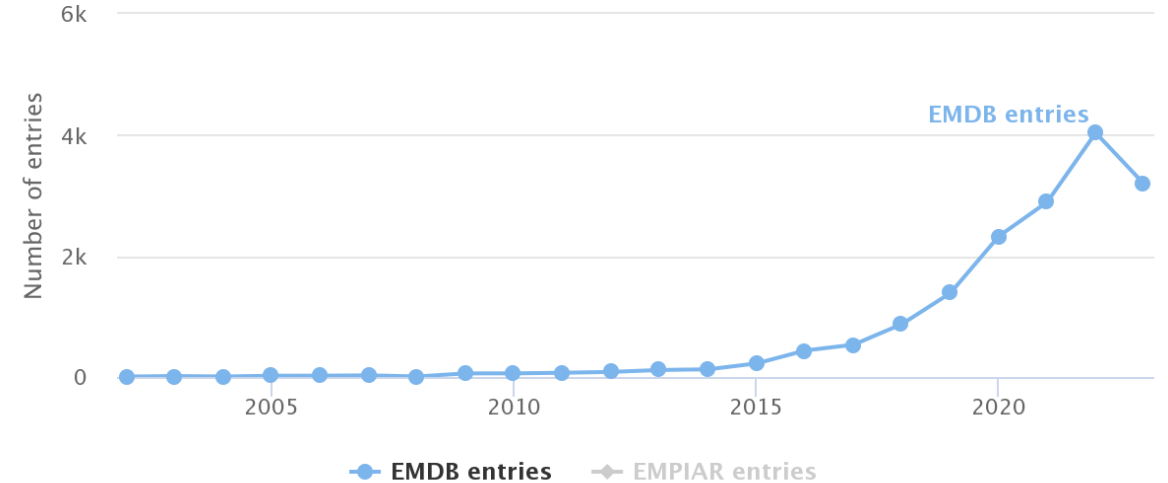
Protein Data Bank - PDB



- Archiving Coordinate models from EM, X-ray and NMR
- All data is freely and openly available under a CC0 license



Number of entries released by year



~16,500 entries

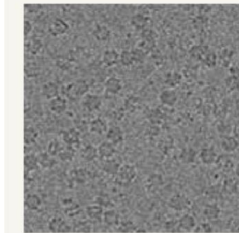
EMDB, EMPIAR & PDB Summary

- Archive the full electron microscopy (EM) processing workflow
- EMPIAR – Supporting development of software and scientists
- EMDb – Refined EM structures and tomograms
- PDB - Coordinate models from X-ray, EM and NMR

MODELLING IN ICE

In cryo-electron microscopy (cryo-EM), thousands of raw EM images are collected and computationally analysed to build up a density map that reflects the shape of the protein.

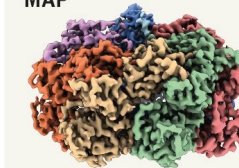
RAW IMAGE



Where to share data

Electron Microscopy Public Image Archive (EMPIAR)

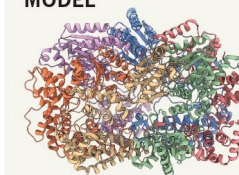
MAP



Electron Microscopy Data Bank (EMDB)

This map is then combined with the known protein sequence to create a final model showing the placement of atomic groups.

MODEL



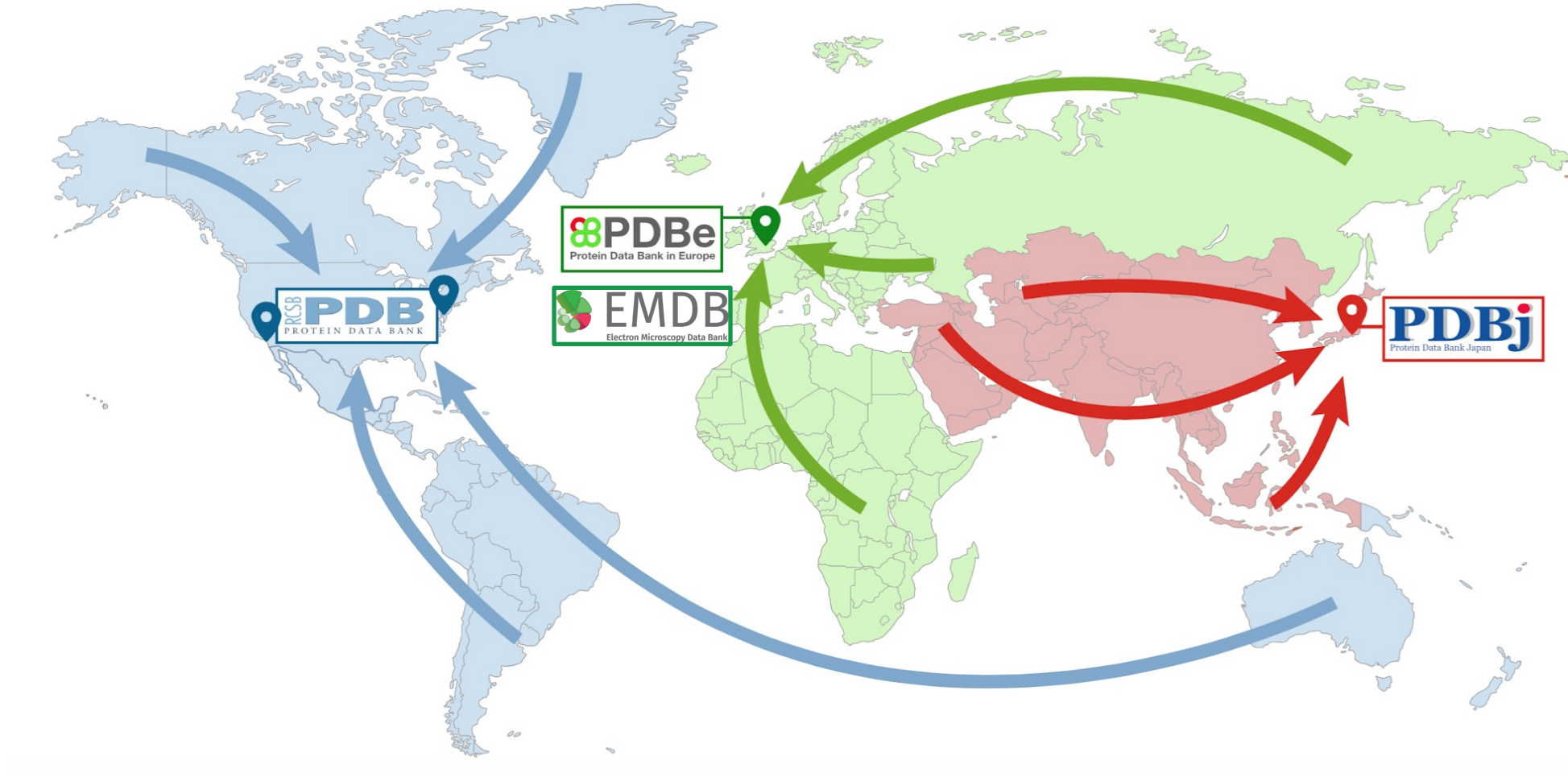
Protein Data Bank (PDB)

©nature

Deposition



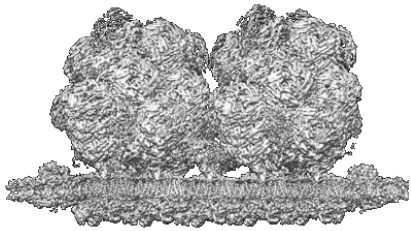
Onedep – A unified deposition system for EM, X-ray and NMR



EMDB - Methodologies

Single Particle

Double-PBS-PSII-PSI-LHCs megastructure



EMD-33658

[1]

Author List:
You X, Zhang X,
Cheng J, Xiao YN,
Sun S, Sui SF

Subtomogram Averaging

DNA Origami Signpost



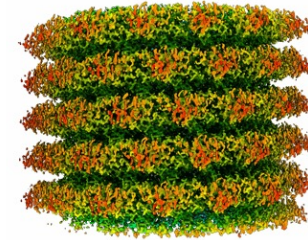
EMD-12188

[2]

Author List: Silvester
E, Vollmer B, Prazak V,
Vasishthan D, Machala EA,
Whittle C, Black S, Bath J,
Turberfield AJ, Gruenewald
K, Baker LA

Helical Reconstruction

Tobacco Mosaic Virus

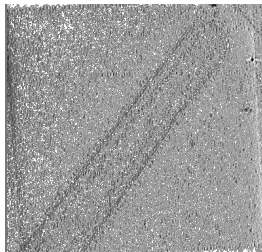


EMD-16572

Author List:
Bhella D, Love AJ,
Streetley J,
Taliensky M,
McGeachy K,
Bukharova T

Tomography

Syncytial Virus Filamentous Virion



EMD-13856

[3]

Author List:
Conley MJ,
Vijaykrishnan S,
Bhella D

Electron Crystallography

Metarhodopsin I



EMD-1079

[4]

Author List:
Ruprecht JJ,
Mielke T, Vogel
R, Villa C,
Schertler GFX

[1] You, X., Zhang, X., Cheng, J. et al. In situ structure of the red algal phycobilisome-PSII-PSI-LHC megastructure. Nature 616, 199–206 (2023). <https://doi.org/10.1038/s41586-023-05831-0>

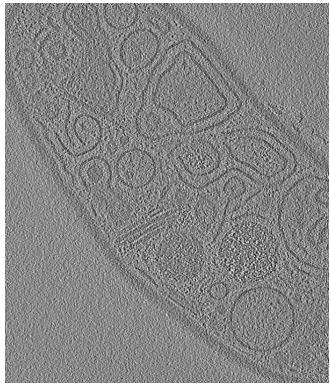
[2] Silvester, E., Vollmer, B., Pražák, V., Vasishthan, D., Machala, E. A., Whittle, C., Black, S., Bath, J., Turberfield, A. J., Grünewald, K., & Baker, L. A. (2021). DNA origami signposts for identifying proteins on cell membranes by electron cryotomography. Cell, 184(4), 1110–1121.e16. <https://doi.org/https://doi.org/10.1016/j.cell.2021.01.033>

[3] The EMBO Journal (2022) 41: e109728 <https://doi.org/10.15252/emboj.2021109728>

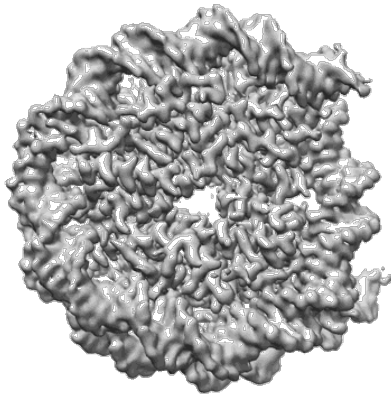
[4] Ruprecht, J.J., Mielke, T., Vogel, R., Villa, C. and Schertler, G.F. (2004), Electron crystallography reveals the structure of metarhodopsin I. The EMBO Journal, 23: 3609–3620. <https://doi.org/10.1038/sj.emboj.7600374>

EMDB Deposition - Types

Map Only



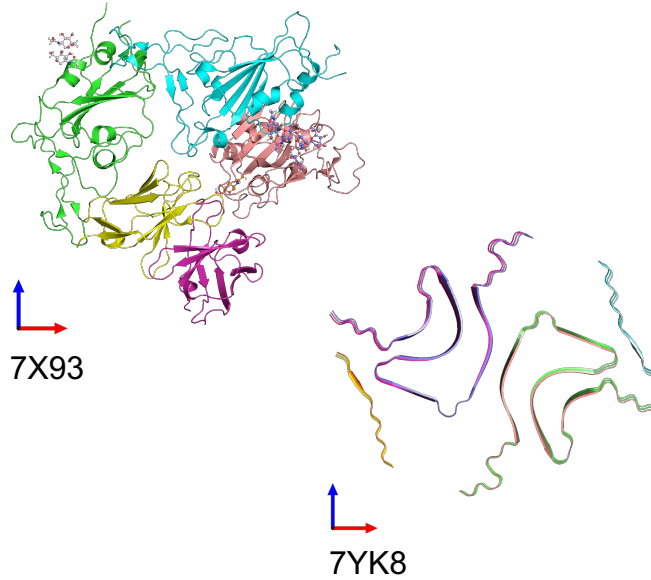
EMD-16202



EMD-29854

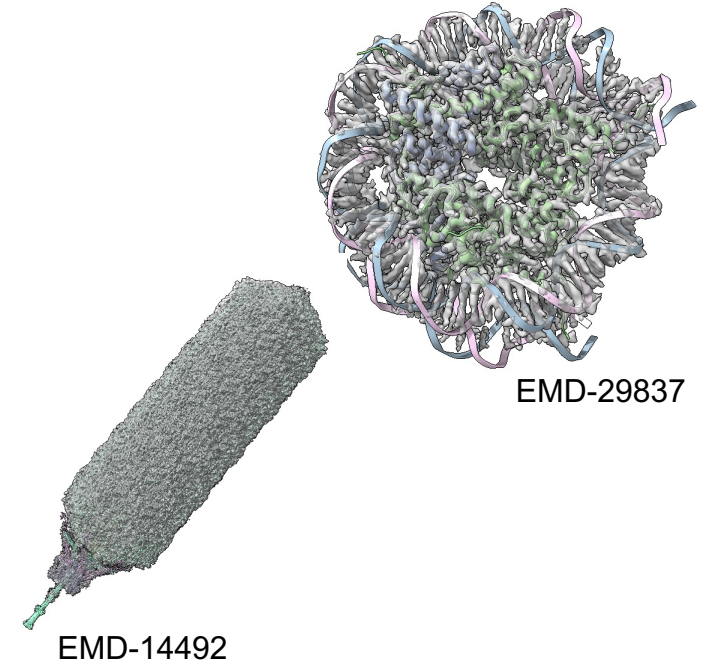
All Methodologies

Model Only



All methodologies
except Tomography

Map + Model

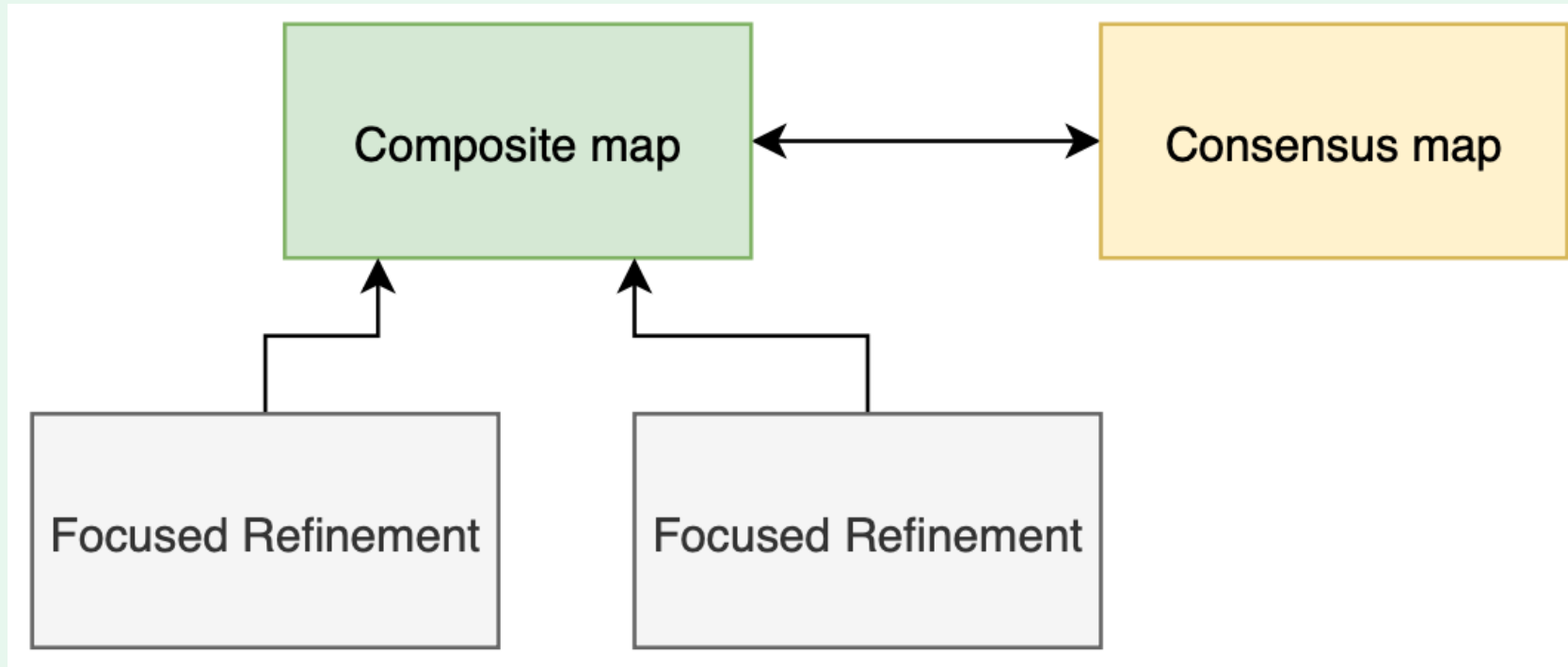


All methodologies
except Tomography

Must have associated map!

EMDB Deposition – Composite Map

- Composite Map - Generated by combining multiple focused refinements
- Focused Refinement – A refinement focused on an area of map
- Consensus map – A refinement of the whole map without focusing on any region



EMDB Deposition – Brain Page

wwPDB OneDep System

Existing deposition

Deposition ID

Password

[Log in](#)


[Forgot Password](#)

[Sign in with ORCID](#)

Validation server

Have you checked your data at the stand-alone validation server?
validate.wwpdb.org

wwPDB regions



For requests such as entry release or citation updates, please login to the deposition system and send us a message through the communications section

If you have any other feedback, please write to us at deposit-help@mail.wwpdb.org
At this time this deposition system does not work with Internet Explorer versions 8 or less.

Warning: Please note that the current system does not support having multiple sessions open at the same time. To switch between existing sessions please log out using opened deposition.

On initiation of a deposition session the wwPDB OneDep system will provide the Corresponding Author with a deposition session password. Responsibility for managing the access information to each deposition session Investigator(s).

Your e-mail address

Password (optional, or we will provide one)
This is a shared "group password"
(6 to 16 alphanumeric characters)

Country/Region [Reset](#)

Experimental method

- X-Ray Diffraction
- Electron Microscopy
 - Helical
 - Single particle
 - Subtomogram averaging
 - Tomography
- Solution NMR
- Neutron Diffraction
- Electron Crystallography
- Solid-state NMR
- Fiber Diffraction

Are you depositing coordinates with this submission?
 No, experimental data only
 Yes

Has the associated map been deposited previously?
 No
 Yes

Is this a composite map deposition?
 No
 Yes

Requested accession codes
 PDB EMDb BMRB

Please copy this code: **65952**

Privacy policy
 Tick to indicate that you have read and accepted the wwPDB policy on personal data privacy, including what data wwPDB collects, how the data is stored and shared. www.wwpdb.org/about/privacy

[Start deposition](#)

Experimental method

- X-Ray Diffraction
- Electron Microscopy
 - Helical
 - Single particle
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 - Tomography
- Solution NMR
- Neutron Diffraction
- Electron Crystallography
- Solid-state NMR
- Fiber Diffraction

Are you depositing coordinates with this submission?
 No, experimental data only
 Yes

Has the associated map been deposited previously?
 No
 Yes

Is this a composite map deposition?
 No
 Yes

EMDB Deposition - ORCID Login


Existing deposition

Deposition ID

Password

[Log in](#)

[Forgot Password](#)

 [Sign in with ORCID](#)

Deposition list							
Depositions available to 0000-0012-3456-789X							
Deposition ID	Entry ID	Entry Title	Created	Site	Status	Last login	
D_1292111636	7axh	Crystal structure of the hPXR-LBD in complex with alpha-zearalanol	17/03/2023	RCSB	PROC	17/03/2023	
D_1292111623	7ax8	Crystal structure of the hPXR-LBD in apo form (P43212 SG)	09/01/2023	PDBe	AUTH	16/03/2023	
D_1292100980	6qvt	CMP-Sialic acid bound structure the human ST6Gal1	14/07/2022	PDBj	HPUB	22/09/2022	
D_1292100979	6qvs	Unliganded structure of the human wild type ST6Gal1...	04/03/2019	PDBe	REL	15/05/2020	
D_1200009063	6fwu	Crystal structure of human wild type B4GalT1 in apo-closed dimeric form	07/03/2018	PDBe	REL	03/02/2019	
D_1290050811	4adp	HCV-J6 NS5B POLYMERASE V405I MUTANT	02/01/2012	RCSB	REL	-	
D_1290044331	2xi3	HCV-H77 NS5B Polymerase Complexed With GTP	25/06/2010	PDBj	REL	-	
D_1290044262	2xhu	HCV-J4 NS5B Polymerase Orthorhombic Crystal Form	21/06/2010	RCSB	REL	-	

EMDB Deposition – File Upload Page

Navigation

- ✓ Instructions
- ✓ Communication
- ! File upload

Log out

File upload

Electron microscopy upload information

- Mandatory submission: Map (3D volume) file , Image file(s)
- Strongly recommended: Fourier shell correlation curve (FSC) file(s)
- Optional: Additional map (3D volume) file(s), Mask (3D volume) file(s)
- The above files will be made publicly available upon release of the map

Based on a previous wwPDB deposition

Do you want to import information from a previous wwPDB deposition? Yes No

Previous deposition ID:

Previous deposition password:

What data items would you like to transfer from a previous deposition?

Contact information	<input type="checkbox"/>
Entry authors	<input type="checkbox"/>
Citation information	<input type="checkbox"/>
Grant information	<input type="checkbox"/>
Electron microscopy experimental information	<input type="checkbox"/>

General upload instructions

- Click 'Browse' or 'Choose File' to upload your file. Once the file is uploaded, select the file type from the pull-down list. If you have uploaded more than one file
- After pressing "Continue deposition", you must review the summary page carefully as it will tell you whether your data has been uploaded and interpreted correctly.
- The gzip and bzip2 compression formats are supported for all uploaded files. Archive formats such as tar and windows ZIP archives are not supported.

Map upload instructions

- Uploaded map and masks (CCP4 or MRC map formats only) will be converted to the Electron Microscopy Data Bank map format. For large maps the conversion maybe slow - we appreciate your patience.
- If you wish to upload files larger than 1.5Gb, please try first. If it fails, please contact us through the communication tab to obtain alternate upload options.
- Map must have positive densities (contrast), irrespective to the type of electron microscope images (negative stain, or frozen-hydrated). If the contrast density for the map is found to be negative, a scale factor of (-1) will be applied to map convention recommended by Heymann et al. J. Struct. Biol. 2005 (2):196-207
- Image of your map (500x500 pixel, white background preferred) must be free from copyright restrictions. This image will be displayed on the atlas pages for your entry when the map is released.
- FSC curve files (XML format) can be generated via [this server](#), or using software packages such as EMAN2, RELION or Bsoft. An example of a FSC curve file is available [here](#)

Choose File

⚠ Please provide/select one map file (Spider map format is not allowed). Please provide your half maps. Please provide/select one image of your map.

⚠ Deposition of a FSC file is strongly encouraged.

Based on a previous wwPDB deposition

Do you want to import information from a previous wwPDB deposition? Yes No

Previous deposition ID:

Previous deposition password:

What data items would you like to transfer from a previous deposition?

Contact information

Entry authors

Citation information

Grant information

Electron microscopy experimental information

EMDB Deposition – Deposition Interface

Deposition unlocked

List requirements

All items

Mandatory items

Navigation

- ✓ Instructions
- ✓ Communication
- ⚠ Re-upload files
- ✓ Upload summary
- Admin
 - ✓ Contact information
 - ✓ Grant information
 - ✓ Release status
 - ✓ Entry title & author
 - ✓ Citation information
- Macromolecules
 - ✓ 1) T-complex protein 1 subur
 - ✓ 2) T-complex protein 1 subur
 - ✓ 3) T-complex protein 1 subur
 - ✓ 4) T-complex protein 1 subur
 - ✓ 5) T-complex protein 1 subur
 - ✓ 6) T-complex protein 1 subur
 - ✓ 7) Nanobody Nb18
 - ✓ 8) T-complex protein 1 subur
 - ✓ 9) T-complex protein 1 subur
 - ✓ 10) Actin, cytoplasmic 2
 - ✓ 11) Phosducin-like protein 3
- EM sample
 - ✓ Overall sample description
- EM experiment
 - ✓ Specimen preparation
 - ✓ Microscopy
 - ✓ Image recording
 - ✓ Reconstruction
 - ✓ Fitting interpretation
- ✓ Ligands
- ✓ Assembly
- ✓ Related entries
- ✓ Validation reports
- ✓ Summary & conditions
- Downloads & reports
 - All files
 - Generated mmCif

Log out

Re-upload files

General upload instructions

- Click 'Browse' or 'Choose File' to upload your file. Once the file is uploaded, select the file type from the pull-down list. If you have uploaded more than one file of each type, use the check box to select which file should be used.
- After pressing "Continue deposition", you must review the summary page carefully as it will tell you whether your data has been uploaded and interpreted correctly.
- The gzip and bzip2 compression formats are supported for all uploaded files. Archive formats such as tar and windows ZIP archives are not supported.

Coordinate upload instructions

- Coordinate files should be deposited in mmCIF format.
- Phenix, Refmac and Buster support direct output of mmCIF files (please see www.wwpdb.org/deposition/PDBxDeposit for instructions).
- Please use the latest version of your refinement software to ensure compatibility with the OneDep system.
- If your refinement software does not export mmCIF files we encourage you to use `pdb_extract` to prepare an mmCIF formatted file.
- See www.wwpdb.org/deposition/preparing-pdbx-mmCIF-files for more details.

Map upload instructions

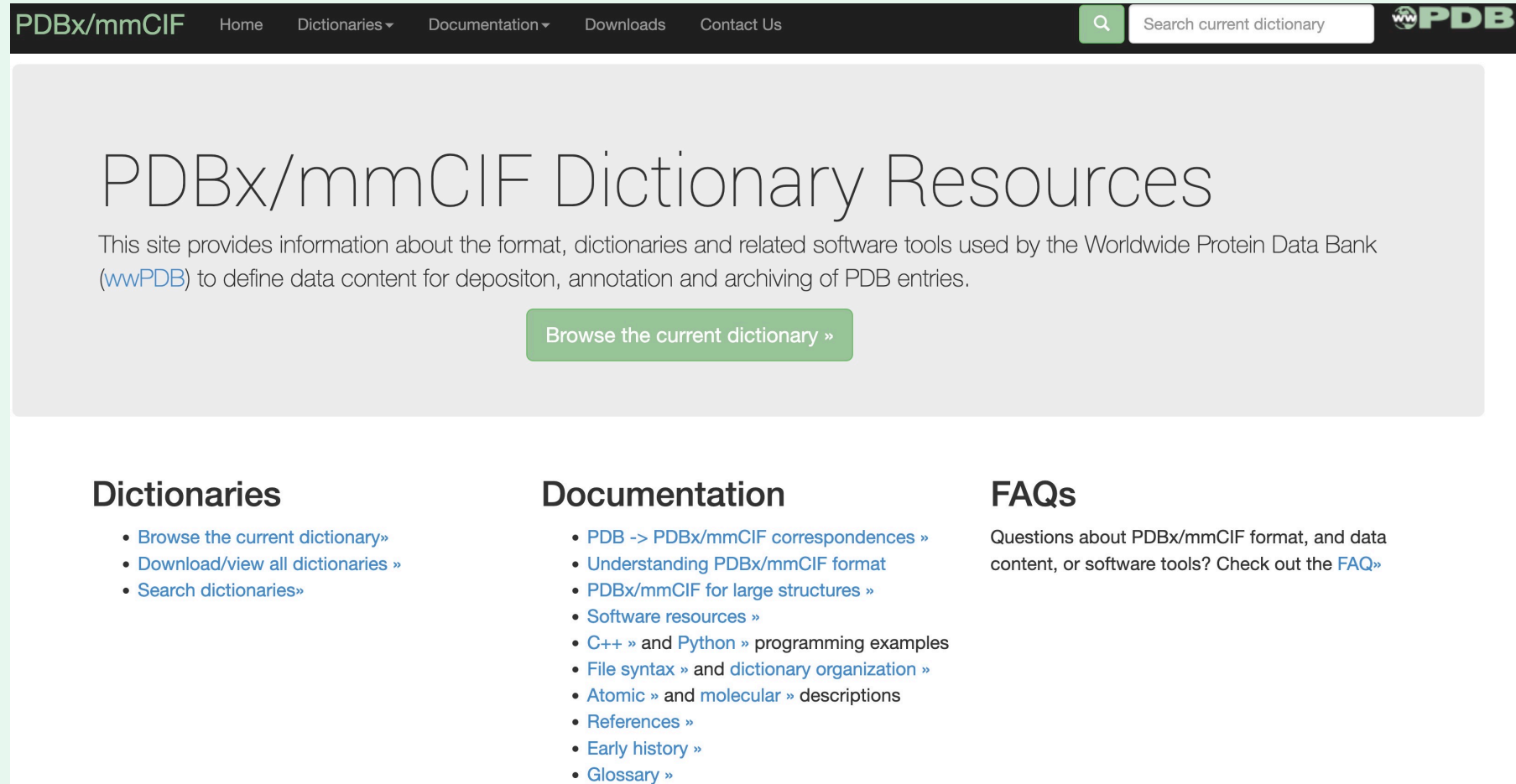
- Uploaded map and masks (CCP4 or MRC map formats only) will be converted to the Electron Microscopy Data Bank map format. For large maps the conversion maybe slow - we appreciate your patience.
- If you wish to upload files larger than 1.5Gb, please try first. If it fails, please contact us through the communication tab to obtain alternate upload options.
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- Image of your map (500x500 pixel, white background preferred) must be free from copyright restrictions. This image will be displayed on the atlas pages for your entry when the map is released.
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Choose File

	Converted file name	Author's file name	Upload date/time (UTC)	File size	File type
Previous upload	<input checked="" type="checkbox"/> D_8000211489_em-volume_P1.map.V2	Error retrieving original map name	2022-02-08 11:41	87.81 MB	<div style="border: 1px solid #ccc; padding: 2px;">EM map (MRC/CCP4 format)</div> Pixel spacing (Å)*: <input type="text"/> Contour level*: <input type="text"/> Short description: <div style="border: 1px solid #ccc; height: 40px; width: 100%;"></div>
Previous upload	<input checked="" type="checkbox"/> D_8000211489_img-embd_P1.png.V1	D_1292113241_img-embd-upload_P1.jpg	1970-01-20 00:45	211.41 KB	<div style="border: 1px solid #ccc; padding: 2px;">Entry image for public display</div>
Previous upload	<input checked="" type="checkbox"/> D_8000211489_model_P1.cif.V12	D_1292113241_model_P1.cif.V17	1970-01-20 00:45	8.95 MB	<div style="border: 1px solid #ccc; padding: 2px;">Coordinates (mmCIF format)</div>
Previous upload	<input checked="" type="checkbox"/> D_8000211489_em-half-volume_P2.map.V2	Error retrieving original map name	2022-02-08 11:42	87.81 MB	<div style="border: 1px solid #ccc; padding: 2px;">EM half map (MRC/CCP4 format)</div> Pixel spacing (Å)*: <input type="text"/> Contour level*: <input type="text"/> Short description: <div style="border: 1px solid #ccc; height: 40px; width: 100%;"></div>

EMBL-EBI

EMDB Deposition - mmCIF file



PDBx/mmCIF Home Dictionaries Documentation Downloads Contact Us 

PDBx/mmCIF Dictionary Resources

This site provides information about the format, dictionaries and related software tools used by the Worldwide Protein Data Bank ([wwPDB](#)) to define data content for deposition, annotation and archiving of PDB entries.

[Browse the current dictionary »](#)

Dictionaries

- [Browse the current dictionary»](#)
- [Download/view all dictionaries »](#)
- [Search dictionaries»](#)

Documentation

- [PDB -> PDBx/mmCIF correspondences »](#)
- [Understanding PDBx/mmCIF format](#)
- [PDBx/mmCIF for large structures »](#)
- [Software resources »](#)
- [C++ »](#) and [Python »](#) programming examples
- [File syntax »](#) and [dictionary organization »](#)
- [Atomic »](#) and [molecular »](#) descriptions
- [References »](#)
- [Early history »](#)
- [Glossary »](#)

FAQs

Questions about PDBx/mmCIF format, and data content, or software tools? Check out the [FAQ»](#)

<https://mmcif.wwpdb.org/>

EMDB Deposition - mmCIF file

```
#
_em_imaging.entry_id          EMD-90269
_em_imaging.id               1
_em_imaging.astigmatism      ?
_em_imaging.electron_beam_tilt_params ?
_em_imaging.residual_tilt    ?
_em_imaging.sample_support_id 1
_em_imaging.detector_id      1
_em_imaging.scans_id         1
_em_imaging.microscope_id    ?
_em_imaging.microscope_model 'FEI TITAN KRIOS'
_em_imaging.specimen_holder_type ?
_em_imaging.specimen_holder_model 'FEI TITAN KRIOS AUTOGRID HOLDER'
_em_imaging.details         ?
_em_imaging.date             ?
_em_imaging.accelerating_voltage 300
_em_imaging.illumination_mode 'FLOOD BEAM'
_em_imaging.mode             'BRIGHT FIELD'
_em_imaging.nominal_cs       2.7
_em_imaging.nominal_defocus_min 2000
_em_imaging.nominal_defocus_max 4000
_em_imaging.calibrated_defocus_min ?
_em_imaging.calibrated_defocus_max ?
_em_imaging.tilt_angle_min    ?
_em_imaging.tilt_angle_max    ?
_em_imaging.nominal_magnification ?
_em_imaging.calibrated_magnification ?
_em_imaging.electron_source   'FIELD EMISSION GUN'
_em_imaging.citation_id       ?
_em_imaging.temperature       ?
_em_imaging.detector_distance ?
_em_imaging.recording_temperature_minimum ?
_em_imaging.recording_temperature_maximum ?
_em_imaging.alignment_procedure 'COMA FREE'
_em_imaging.c2_aperture_diameter 50
_em_imaging.specimen_id       1
_em_imaging.cryogen           NITROGEN
#
```

```
_em_vitrification.entry_id      EMD-90269
_em_vitrification.id            1
_em_vitrification.sample_preparation_id ?
_em_vitrification.specimen_id   1
_em_vitrification.cryogen_name  ETHANE
_em_vitrification.humidity      ?
_em_vitrification.temp          ?
_em_vitrification.chamber_temperature ?
_em_vitrification.instrument    'FEI VITROBOT MARK IV'
_em_vitrification.method        ?
_em_vitrification.time_resolved_state ?
_em_vitrification.citation_id   ?
_em_vitrification.details       ?
#
```

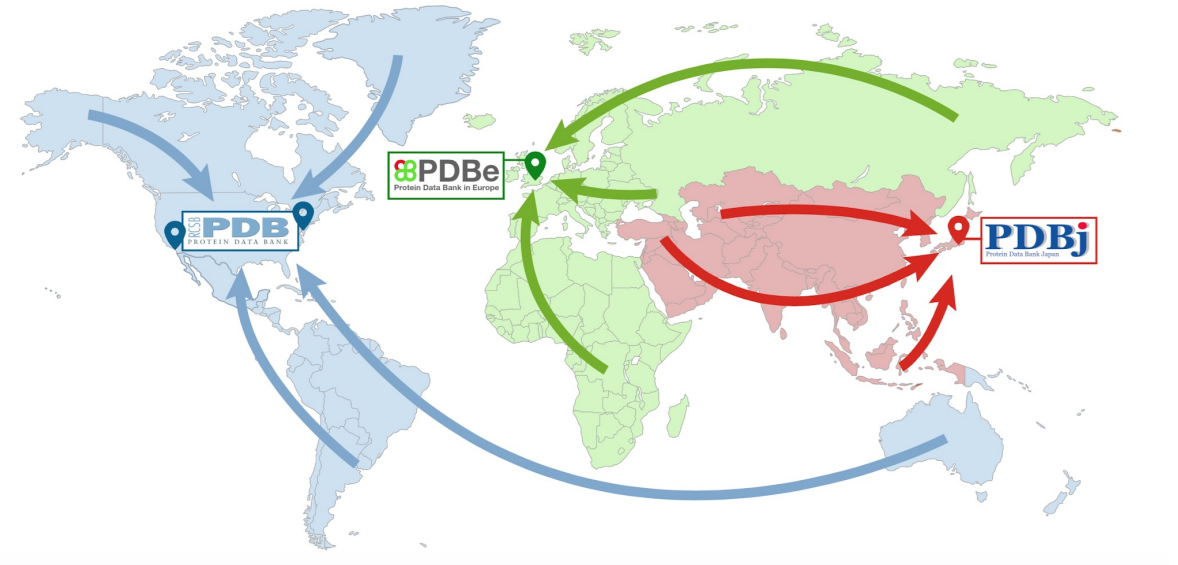
<https://mmcif.wwpdb.org/>

EMDB Deposition – Common communications

- The provided sequence should be the full sequence in the sample, including any unmodeled regions.
- Half-maps must be unmasked, unfiltered and unsharpened raw maps.
- Maps and models should all be present in the same coordinate space and overlay correctly.
- Defocus values must be in nm and positive values refer to defocus.
- Please reach out if you wish to deposit variability analysis data (cryoDRGN, 3Dflex, ...)

EMDB Deposition Summary

- Five methodologies
 - Single Particle
 - Subtomogram Averaging
 - Helical Reconstruction
 - Tomography
 - Electron Crystallography
- Composite map depositions must follow section 1.3 of EMDB Policy
- ORCID Login
- **mmCIF files are metadata files**



EMPIAR Deposition

EMPIAR Deposition Step-By-Step

1. Register as a new user on EMPIAR's deposition system
2. Sign-in & Create a New Deposition
3. Complete the Deposition Overview Page
4. Granting rights or transferring ownership of an entry
5. Main EMPIAR Data Upload page
 - a. Globus
 - b. Aspera Command Line
 - c. Aspera Web Interface
6. Complete the Associate image sets on the data page & Submit

EMPIAR Deposition Policies

- EMPIAR is relatively unstructured compared to EMDB
- Policies pages should be visited to understand accepted file types
- Supported Methods (more info on the policies pages):
 - i. EMDB - raw image data relating to structures deposited to the EMDB
 - ii. SBF-SEM - image data collected using serial block-face scanning electron microscopy (like the Gatan 3View system)
 - iii. SXT - image data collected using soft x-ray tomography
 - iv. FIB SEM - image data collected using focused ion beam scanning electron microscopy
 - v. IHM - integrative hybrid modelling data
 - vi. CLEM - correlative light-electron microscopy
 - vii. CLXM - correlative light X-ray microscopy
 - viii. MicroED - microcrystal electron diffraction
 - ix. ATUM-SEM - Automated Tape-collecting Ultramicrotome Scanning Electron Microscopy
 - x. Hard X-ray/X-ray microCT - Hard X-ray/X-ray micro-computed tomography
 - xi. ssET - serial section electron tomography

EMPIAR Deposition Setup

The screenshot shows the EMPIAR website's 'Deposition' page. At the top, there is a navigation bar with the EMPIAR logo and links for 'EMPIAR home', 'Deposition', 'Annotation', 'REST API', 'FAQ', 'About EMPIAR', 'Policies', 'Feedback', and 'Share'. Below the navigation bar, a grey box prompts users to 'Please sign in to get started' and provides links to 'login' and 'register'. The main content area is divided into three columns: 1. 'EMPIAR deposition system' with a stack of electron micrographs and a sub-link 'Begin/Continue an EMPIAR deposition'. 2. 'Annotate a segmentation' with a 3D red and yellow segmented structure and a sub-link 'Create and annotate an EMDB-SFF segmentation'. 3. 'SPW deposition system' with a list of 9 steps (1-9) and a sub-link 'Begin/Continue an SPW deposition'. On the right side, there is a 'License: PUBLIC DOMAIN' badge, 'Quick links' with social media icons, and a list of links: 'Browse EMPIAR', 'Sample-Preparation Widget', 'Volume Browser', 'Claim entries to your ORCID', 'Talks and Tutorials', 'EMPIAR Quick tour', 'Publications', 'Re-use case study', 'Statistics', 'EMPIAR in the news', 'Contact us', 'COVID-19 Data Portal', and 'EMDB'.

EMPIAR

EMPIAR home | **Deposition** | Annotation | REST API | FAQ | About EMPIAR | Policies | Feedback | Share

Please sign in to get started.
Proceed to the [login page](#) or [register an account](#).

EMPIAR deposition system
Begin/Continue an EMPIAR deposition

Annotate a segmentation
Create and annotate an EMDB-SFF segmentation

SPW deposition system
Begin/Continue an SPW deposition

License: PUBLIC DOMAIN

Quick links

- Browse EMPIAR
- Sample-Preparation Widget
- Volume Browser
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- Re-use case study
- Statistics
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- Contact us
- COVID-19 Data Portal
- EMDB

<https://www.ebi.ac.uk/empiar/deposition/choose-action/>

EMPIAR Deposition - Summary

1. Gather Information

- EMPIAR accepts various types of data, including multi-frame micrographs, frame-averaged micrographs, particle stacks and tilt series, as well as auxiliary files (*e.g.* particle selection coordinates)
 - Make a note of dataset details (*e.g.* # of images (or tilt-series), raw or processed, single or multi-frame, image format and dimensions, pixel spacing and type)

2. Organise your Data!

- Each data-type must be located in a separate directory (*e.g.* one for micrographs and one for particle stacks) and please sub-divide directories possessing more than 10,000 files

3. Setup Data Transfer Programs

- Aspera (<http://asperasoft.com>) and Globus (<https://www.globus.org>) efficiently and robustly transfer large data volumes (empiar.org/faq)

4. Deposit your Data and Metadata (empiar.org/deposition)

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