



“The Revolution Revolution”

Werner Kühlbrandt, *Science*, 2014

“*Liberty Leading the People*”  
painted by Eugène Delacroix

# 構造データベースから見えてくる 電子顕微鏡による構造解析の動向

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CrSJ2018 ランチオンセミナー

2018-11-11 東工大

## Cryo-EM (3DEM) data in databanks

### 1. Comparison to crystallography

Methodology outline

[raw data] → [map] → [atomic model]

### 2. Comparison to NMR

Ensemble structure of molecule in solution

**Background:**

**Cryo-EM data in databanks**

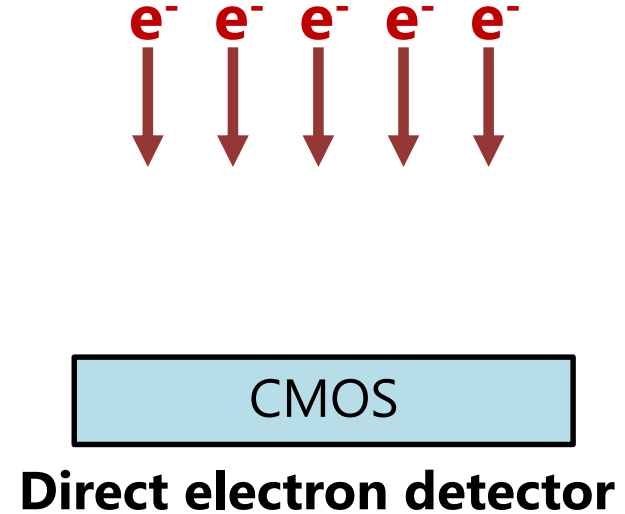
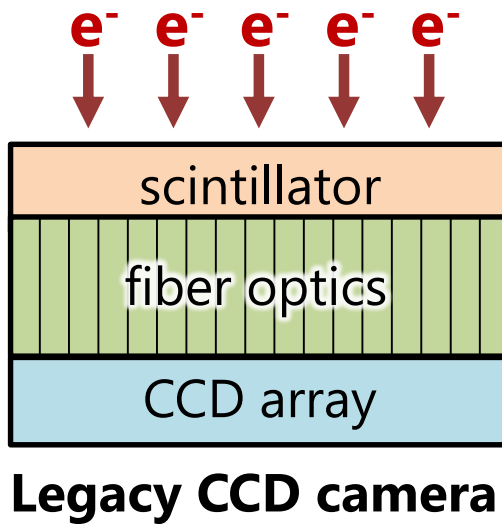
## Resolution

Submission Year	~ 2 A	~ 3 A	~ 5 A	~ 7 A	~ 10 A	~ 15 A	~ 23 A	~ 34 A	~ 51 A	~ 77 A	~ 115 A	~ 173 A	Total
2018	48	52	1032	138	112	168	183	87	33	20	11		1911
2017	11	56	933	234	199	93	81	114	43	45	89	14	1981
2016	20	35	668	212	231	91	154	101	46	3	8		1597
2015	4	21	333	70	127	81	128	83	43	7	3		973
2014	1	4	105	54	145	71	143	139	57	76	2		816
2013		1	45	41	107	94	144	96	70	19			653
2012			18	31	87	63	121	75	58	9			493
2011			10	11	80	78	89	46	13	9	3		355
2010		1	21	23	59	69	53	54	16		3		325
2009		1	16	13	43	46	43	21	5				198
2008			8	8	39	36	52	36	15	1			214
2007			3	3	46	37	40	26	12	1			175
2006			1		23	37	44	38	7	2			156
2005	1		1		20	26	34	20	1	2			106
2004		1	2	3	11	23	16	3			1		60
2003			3	1	9	21	10	26	3				75
2002					4	18	7	3	1	11			45

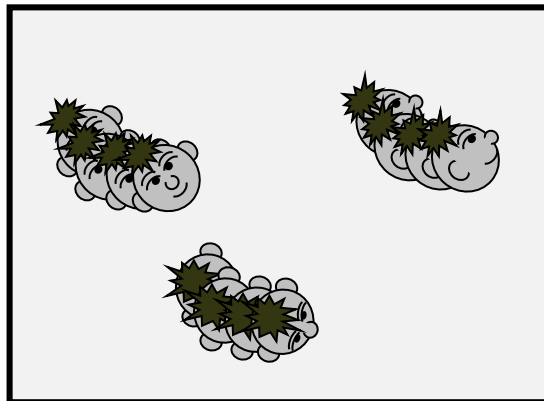
Number: EMDB & PDB entries

*EM Navigator statistics*

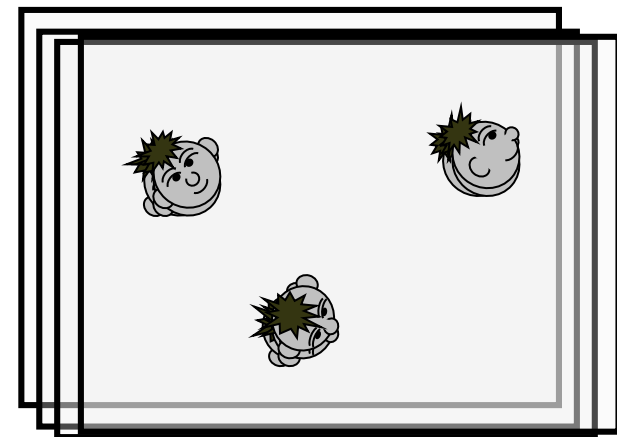
<https://pdj.org/emnavi/>



→ Resolution, sensitivity, & speed improved



Micrographs as movie



motion correction

## Resolution

Detector

Detector	~ 2 A	~ 3 A	~ 5 A	~ 7 A	~ 10 A	~ 15 A	~ 23 A	~ 34 A	~ 51 A	~ 77 A	~ 115 A	~ 173 A	Total
GATAN K2 SUMMIT	4	46	1372	250	187	55	28	38	6	14			2028
FEI FALCON II		20	678	173	138	77	54	25	5	7	5		1193
GATAN K2		40	591	148	168	58	43	60	47	3	15	3	1213
GATAN K2 QUANTUM	4	17	140	29	79	10	12	11	4		6		333
FEI FALCON III	1		102	10	6	3	9						131
KODAK SO163 FILM		4	96	76	370	356	318	205	36	12			1494
OTHER		10	87	16	20	12	11	27	10	3			201
GATAN ULTRASCAN 4000	1		31	41	112	249	343	122	70	63	84	11	1200
DIRECT ELECTRON DE-20		5	15	7	8	3	6	3	8				60
GATAN GENERIC	1	3	12	7	26	33	56	38	16	1			210
GATAN K2 BASE		1	12	10	6			1					30
DIRECT ELECTRON DE-12			12	6	9		2	1	1	1			32
FEI FALCON I		2	10	18	18	9	5	2	9				75
n/a	2		10	3	38	36	82	50	32	7			311
GENERIC FILM			8	2	6	4	17	4					41
TIETZ TEMCAM F416	71	21	6	13	41	10	128	139	60	74	2		589
DIRECT ELECTRON DE-16			6										6

Number: EMDB & PDB entries

*EM Navigator statistics*

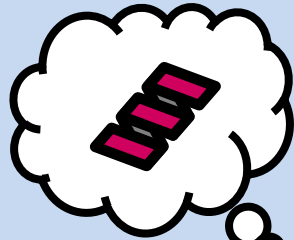
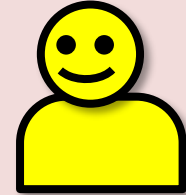
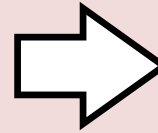
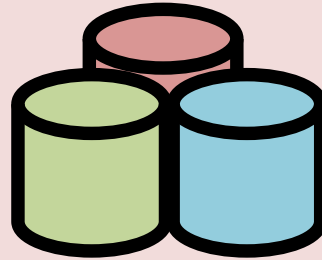
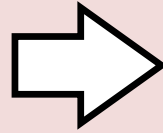
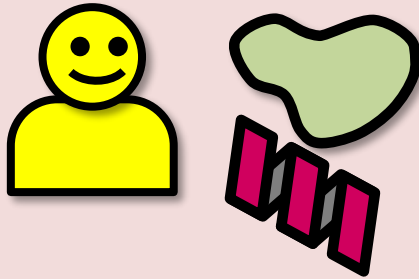
<https://pdbj.org/emnavi/>



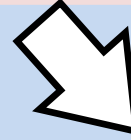
Deposition

PDB, EMDB,  
& BMRB

Archive  
distribution



Search



Visualization





*EM Navigator*

<https://pdj.org/emnavi/>

**EM Navigator** - 3D electron microscopy data navigator -

**Browse 3DEM data**

Keywords / EMDB-ID / PDB-ID

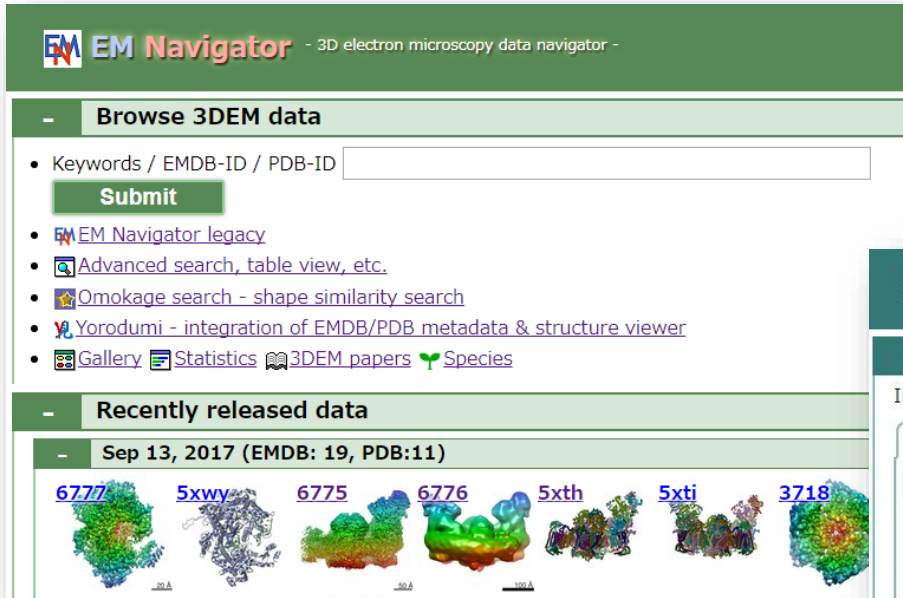
**Submit**

- [EM Navigator legacy](#)
- [Advanced search, table view, etc.](#)
- [Omokage search - shape similarity search](#)
- [Yorodumi - integration of EMDB/PDB metadata & structure viewer](#)
- [Gallery](#) [Statistics](#) [3DEM papers](#) [Species](#)

**Recently released data**

Sep 13, 2017 (EMDB: 19, PDB:11)

[6777](#) [5xwy](#) [6775](#) [6776](#) [5xth](#) [5xti](#) [3718](#)



**Yorodumi** - PDB/EMDB/SASBDB browser -

**Open data**

ID or keywords:  **Submit**

**Random choices** **Recently viewed**

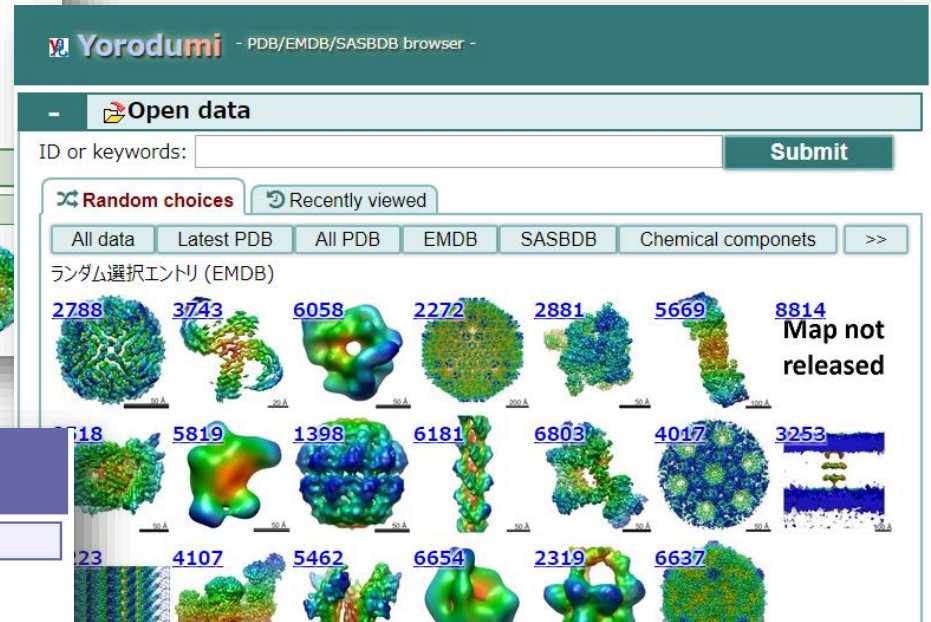
All data Latest PDB All PDB EMDB SASBDB Chemical componets >>

ランダム選択エントリ (EMDB)

[2788](#) [3743](#) [6058](#) [2272](#) [2881](#) [5669](#) [8814](#)  
Map not released

[5118](#) [5819](#) [1398](#) [6181](#) [6803](#) [4017](#) [3253](#)

[23](#) [4107](#) [5462](#) [6654](#) [2319](#) [6637](#)



*Yorodumi*

**Omokage search** - Shape similarity search of macromolecules -

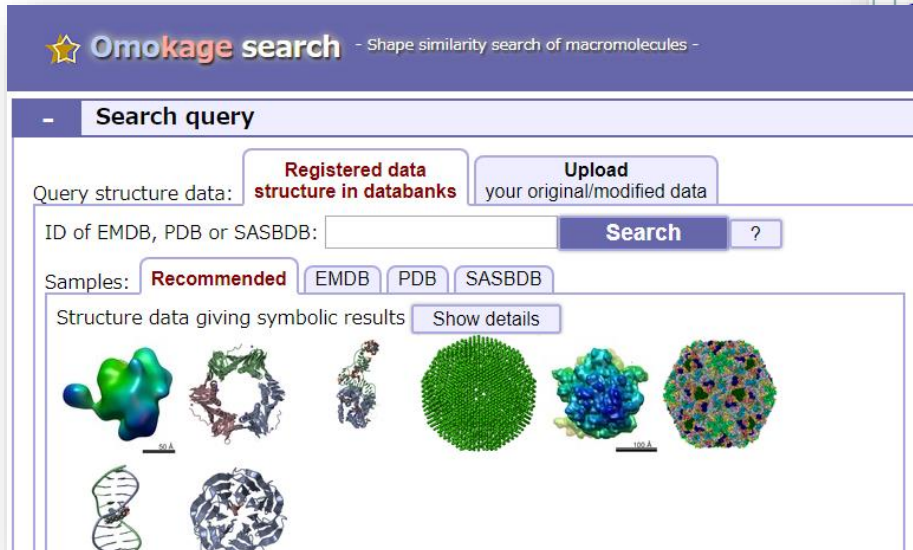
**Search query**

Query structure data: **Registered data structure in databanks** **Upload** your original/modified data

ID of EMDB, PDB or SASBDB:  **Search** ?

Samples: **Recommended** EMDB PDB SASBDB

Structure data giving symbolic results **Show details**



*Omokage search*



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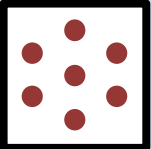
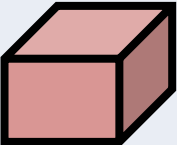





03/22/2017

## Archival PDBx/mmCIF Version V4 to V5 Update in the Protein Data Bank

The wwPDB is preparing the update of PDBx/mmCIF model files for all entries in the PDB archive to V5 version of the PDBx/mmCIF dictionary. When completed, all PDB model files will have better organized content and will conform to the revised data model used within the wwPDB OneDep System. A list of changes will be available at the wwPDB website (<https://www.wwpdb.org/documentation/remediation>). Since January

News in wwPDB website  
[www.wwpdb.org](http://www.wwpdb.org)

# **Comparison to crystallography**

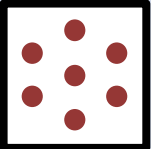
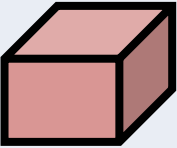




		Crystallography	3DEM
 Raw data	Aligned?	Yes	<b>No</b>
	Phase?	<b>No</b>	Yes
↓		Initial model/phase required	Initial map can help
 Density map	 Refine		 Refine
↓			Initial model required for low-res. data
 Atomic model	 Refine		 Refine

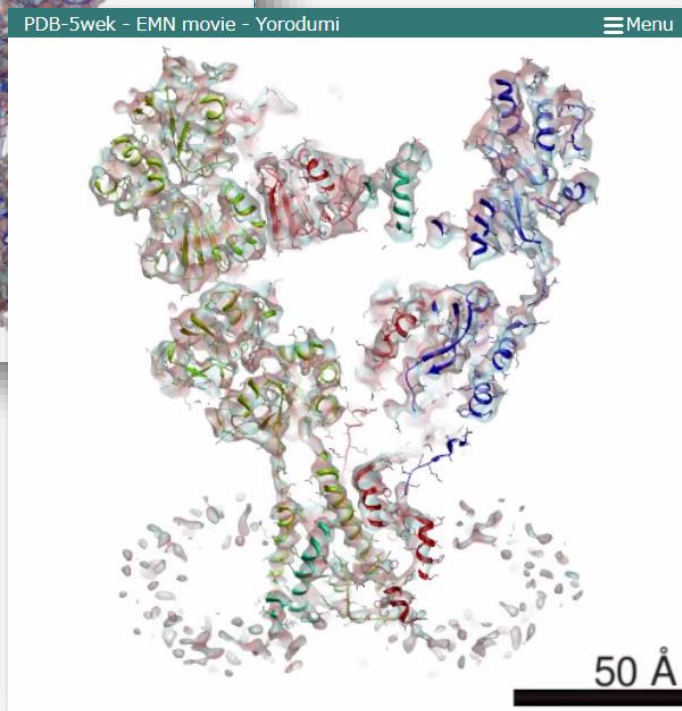
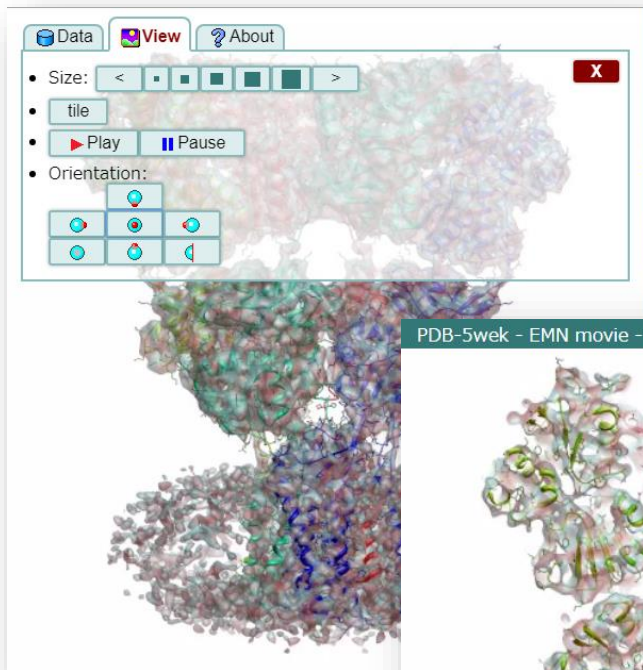
PHENIX v2411 is used for refinement

Processing				
<b>Software</b>	<b>Name:</b> PHENIX / <b>Version:</b> dev_2411: / <b>Classification:</b> refinement			
<b>CTF correction</b>	<b>Type:</b> PHASE FLIPPING AND AMPLITUDE CORRECTION			
<b>3D reconstruction</b>	<b>Resolution:</b> 3.2 Å / <b>Resolution method:</b> FSC 0.143 CUT-OFF / <b>Number of particles:</b> 238758 / <b>Symmetry type:</b> POINT			
<b>Refine</b>	<b>Refine ID</b>	<b>Highest resolution</b>		
	1	3.20		
	ELECTRON MICROSCOPY			
<b>Refine LS restraints</b>	<b>Refine ID</b>	<b>Type</b>	<b>Dev ideal</b>	<b>Number</b>
	ELECTRON MICROSCOPY	f_bond_d	0.010	10528
	ELECTRON MICROSCOPY	f_angle_d	1.201	14384
	ELECTRON MICROSCOPY	f_dihedral_angle_d	11.771	8615
	ELECTRON MICROSCOPY	f_chiral_restr	0.063	1619
	ELECTRON MICROSCOPY	f_plane_restr	0.005	1642

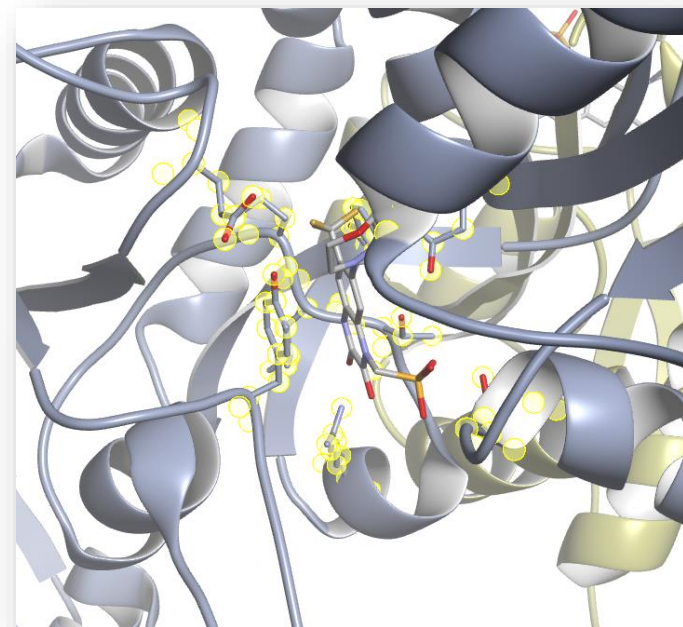
Restraint parameters during refinement

Screenshot of *Yorodumi*  
data: PDB-5ool

		Crystallography	3DEM
 Raw data	Aligned?	Yes	<b>No</b>
	Phase?	<b>No</b>	Yes
↓		Initial model/phase required	Initial map can help
 Density map		 Refine	 Refine
↓			
 Atomic model			 Refine



Map-model fitting  
as movie








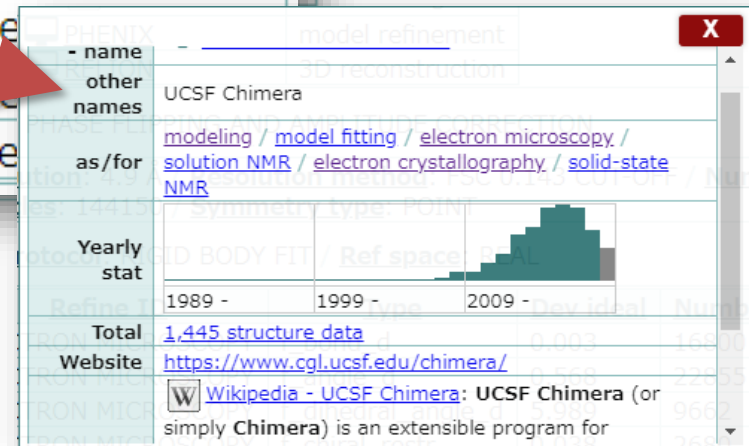
*Yorodumi-Molmil*  
Ligand binding site  
focus view

EMDB-8819  
PDB-5wek

<b>Buffer solution</b>	pH: 8				
<b>Buffer component</b>	<b>ID</b>	<b>Conc.</b>	<b>Name</b>	<b>Formula</b>	<b>Buffer ID</b>
	1	150 mM	sodium chloride	NaCl	1
	2	20 mM	Tris	C <sub>4</sub> H <sub>11</sub> NO <sub>3</sub>	1
	3	0.1 % w/v	digitonin	digitonin	1

Buffer solution details

<b>EM software</b>	<b>ID</b>	<b>Name</b>	<b>Category</b>
	2	 <a href="#">SerialEM</a>	image acquisition
	7	 <a href="#">Coot</a>	model fitting
	8	 <a href="#">UCSF Chimera</a>	model refinement
	11	 <a href="#">PHENIX</a>	model fitting
	15	 <a href="#">RELION</a>	3D reconstruction

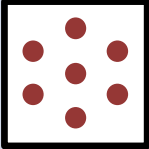
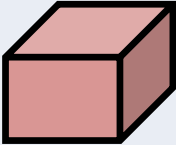



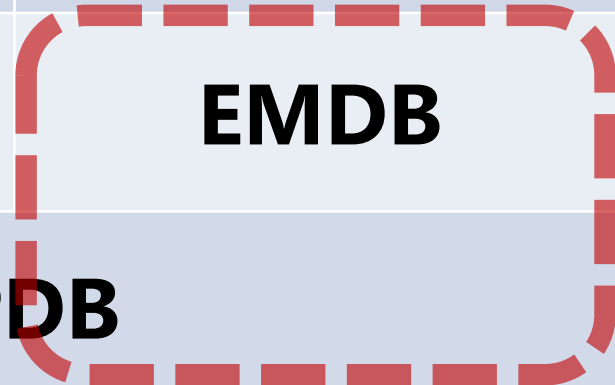
- name  
 other names  
 as/for  
 Yearly stat  
 Total  
 Website

UCSF Chimera  
[modeling / model fitting / electron microscopy / solution NMR / electron crystallography / solid-state NMR](#)  
 1,445 structure data  
<https://www.cgl.ucsf.edu/chimera/>  
[Wikipedia - UCSF Chimera](#): UCSF Chimera (or simply Chimera) is an extensible program for

Software details



	Crystallography	3DEM (incl. electron crystallography)
 Raw data	-	<b>EMPIAR</b>
 Density map	<b>PDB</b> (structure factor)	<b>EMDB</b>
 Atomic model		<b>PDB</b>



*EM Navigator*

The screenshot shows the EMPIAR website interface. At the top, there is a navigation bar with 'EMBL-EBI' logo and links for 'Services', 'Research', 'Training', and 'About us'. Below this is the EMPIAR logo and the title 'Electron Microscopy Public Image Archive'. A secondary navigation bar includes 'EMPIAR home', 'Deposition', 'REST API', 'FAQ', 'About EMPIAR', 'Share', and 'Feedback'. The main content area features a descriptive paragraph about EMPIAR, a 'Deposit your data' link, and a 'Browse and download' link. Below this is a search bar and a table of datasets. The table has columns for 'Dataset', 'Title', 'Authors', and 'Related EMDB/PDB entries'. One dataset is visible: EMPIAR-10115, titled 'Tilt-series of e. coli carrying the ple7 plasmid', by Swulius MT, Jensen GJ. To the right, there are 'Quick links' to EMDB, PDBe, and EMDataBank, and 'EMPIAR citations'.

EMBL-EBI

Services Research Training About us

**EMPIAR**

Electron Microscopy Public Image Archive

EMPIAR home Deposition REST API FAQ About EMPIAR Share Feedback

EMPIAR, the Electron Microscopy Public Image Archive, is a public resource for raw, 2D electron microscopy images. Here, you can browse, upload, and download and reprocess the thousands of raw, 2D images used to build a 3D structure. [More ...](#)

[Deposit your data](#) in EMPIAR to share it with the structural biology community.

Browse and [download](#) EMPIAR datasets using the table below.

Show  entries Search:

Dataset	Title	Authors	Related EMDB/PDB entries
<a href="#">EMPIAR-10115</a>	Tilt-series of e. coli carrying the ple7 plasmid	Swulius MT, Jensen GJ [Pubmed: <a href="#">22904287</a> ] [DOI: <a href="#">10.1128/jb.00505-12</a> ]	

Quick links

- [EMDB](#)
- [PDBe](#)
- [EMDataBank](#)

[EMPIAR: Quick tour](#)

EMPIAR citations

[Quantitative analysis of 3D alignment quality: its impact on soft-validation, particle pruning and](#)

EMPIAR webpage by EMBL-EBI

# **Comparison to NMR**

Nikkei biotech  
cryo-EM issue  
Feb, 2017

日経バイオテック  
Nikkei Biotechnology & Business

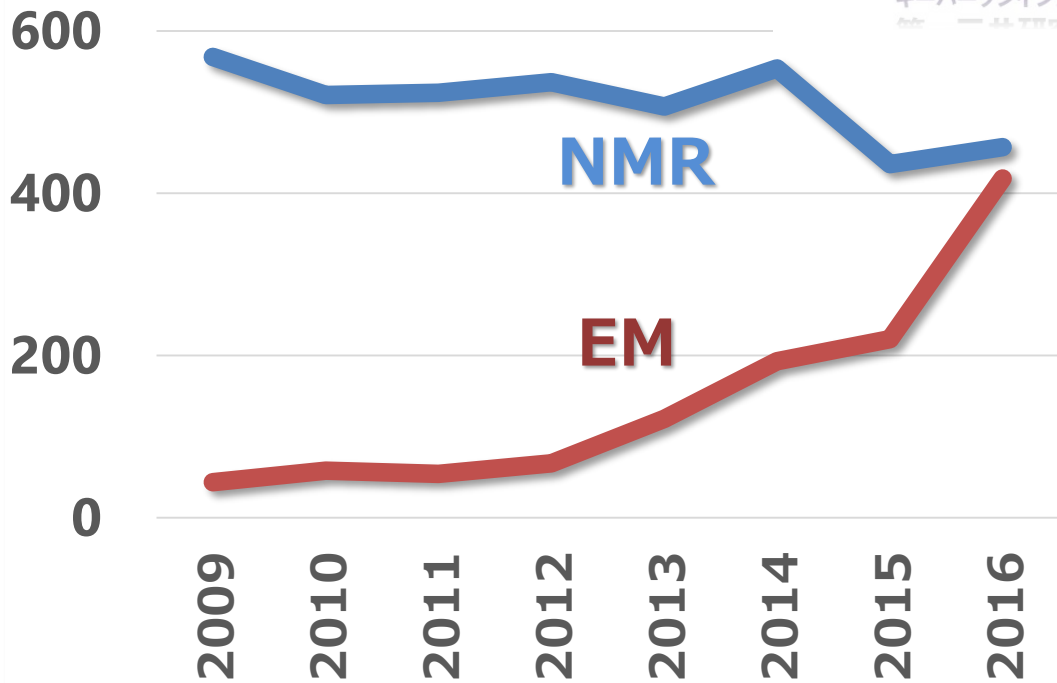
2017  
02  
27

特集

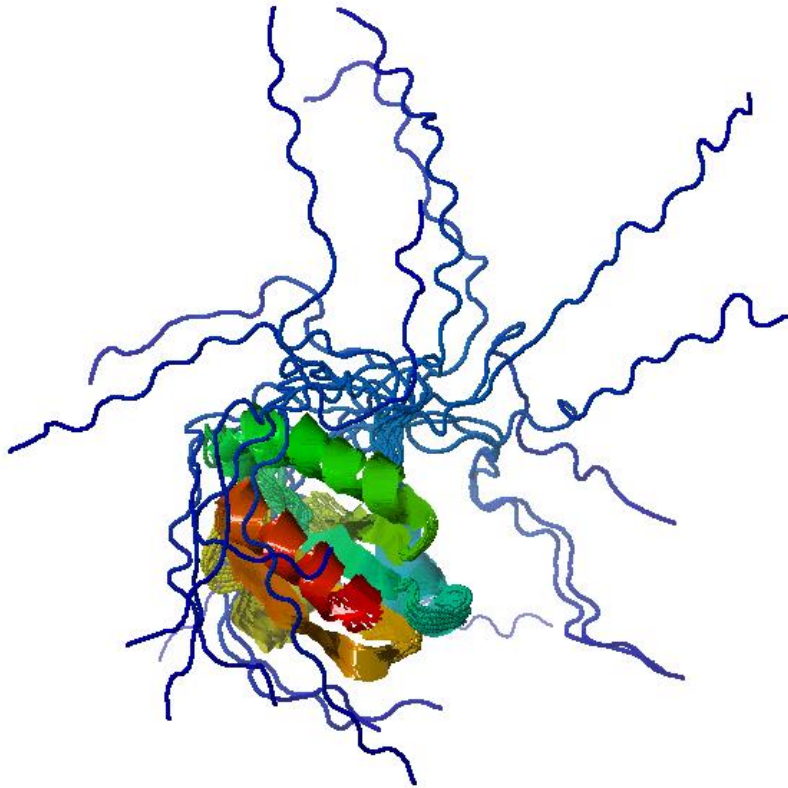
クライオ電子顕微鏡

キーパーソンインタビュー

第 1 回 藤原 誠



PDB yearly deposition  
NMR vs. EM



## Experiment

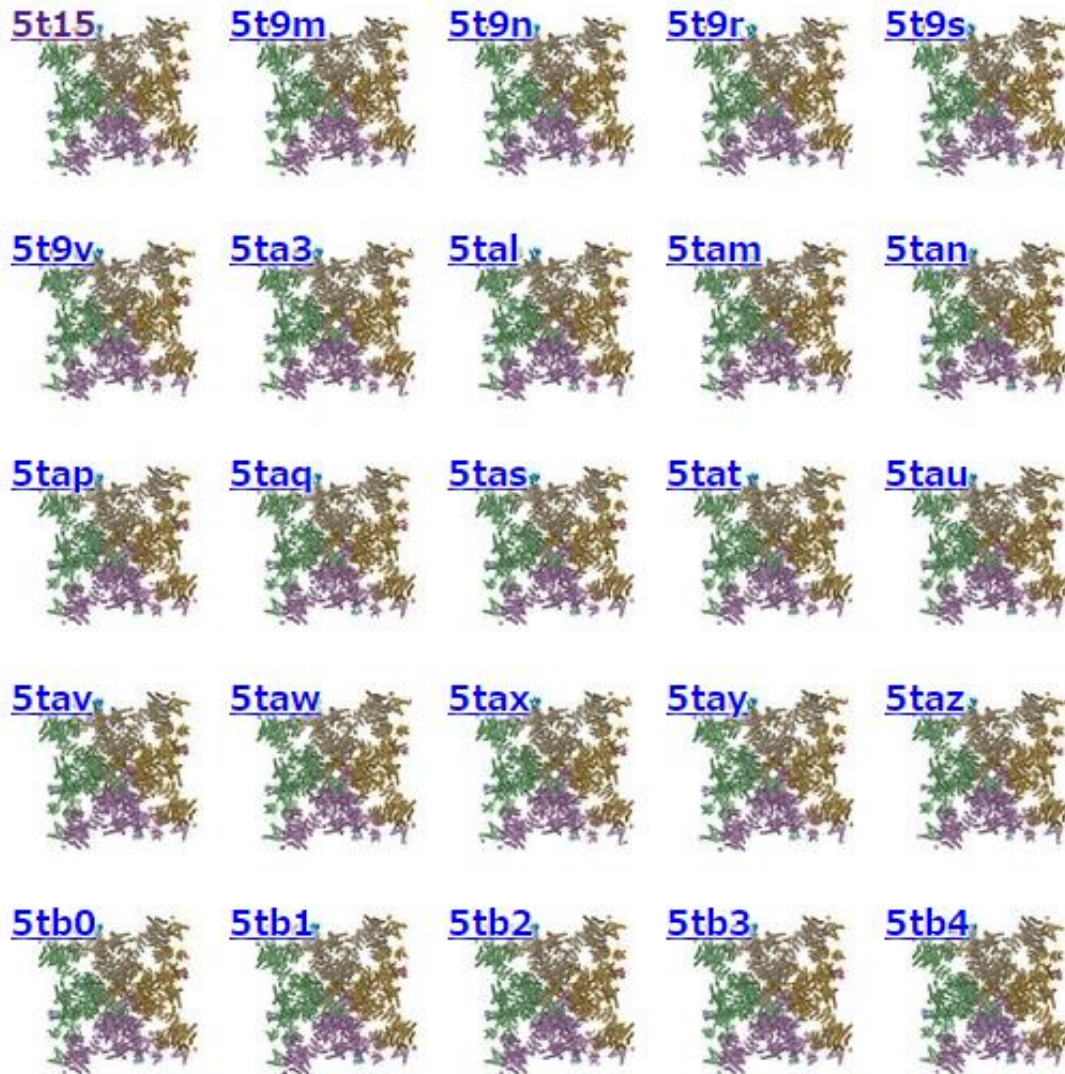
1 sample condition  
100 conformers

## Deposition

20 conformers  
1 entry

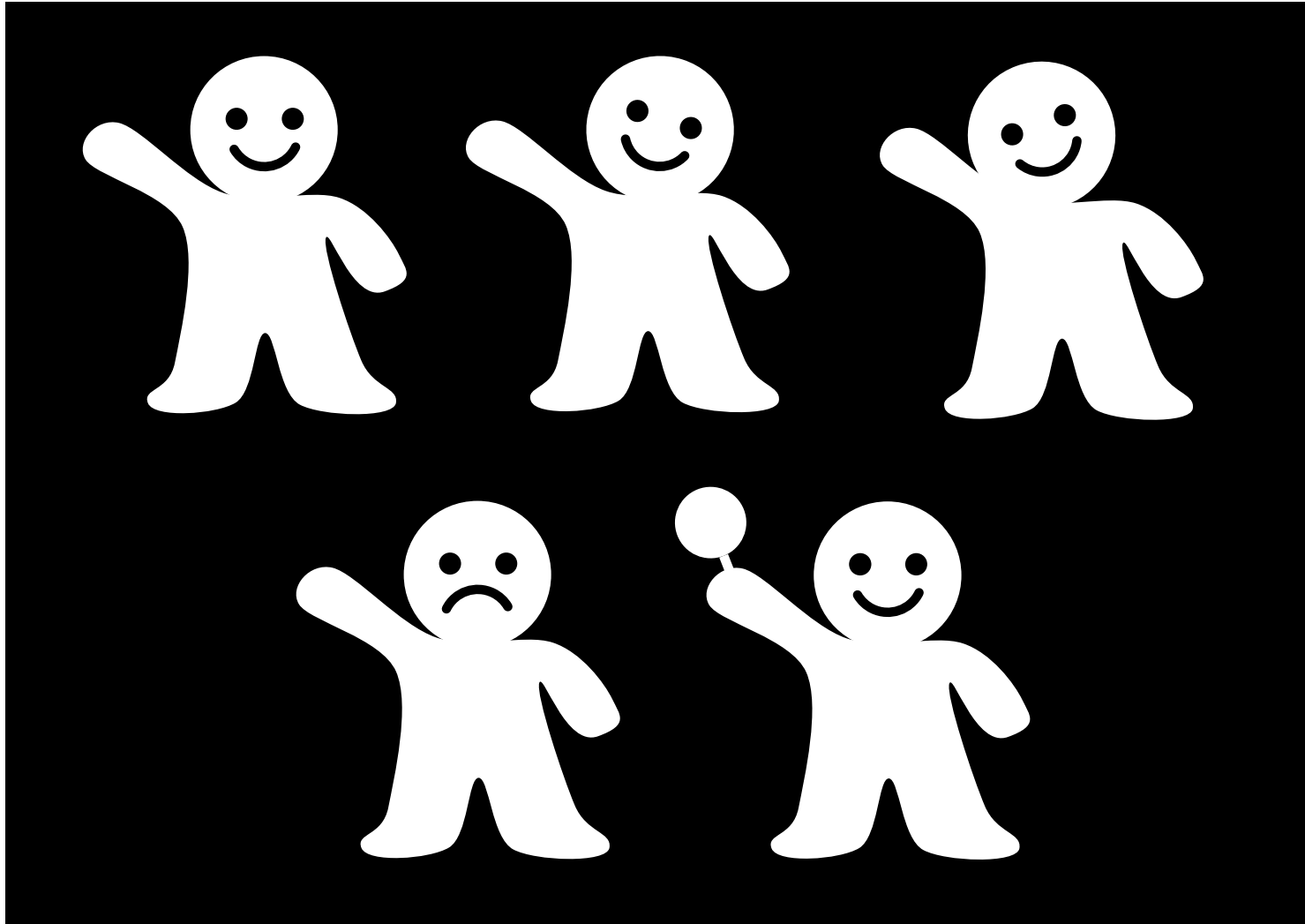
PDB-6ali

putative thioredoxin

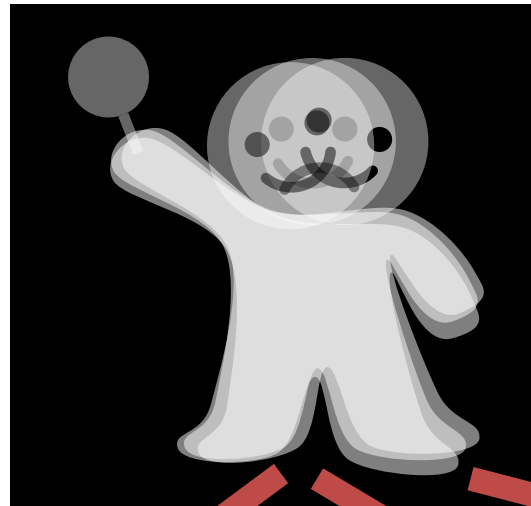


5 samples  
x (1 all + 4 classes)  
= 25 PDB entries

Ryanodine receptor  
(calcium channel)  
des Georges *et al.*,  
*Cell*, 2016

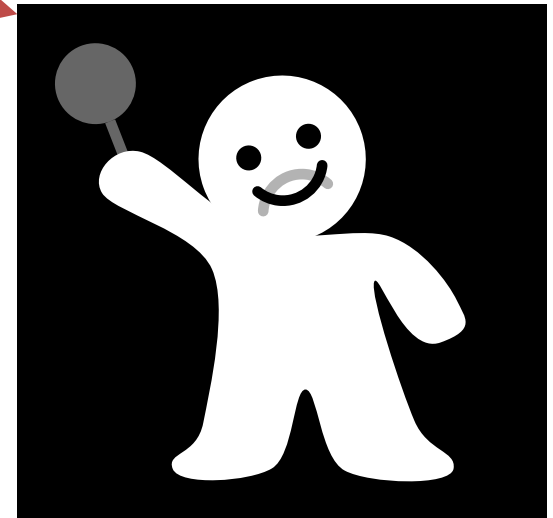
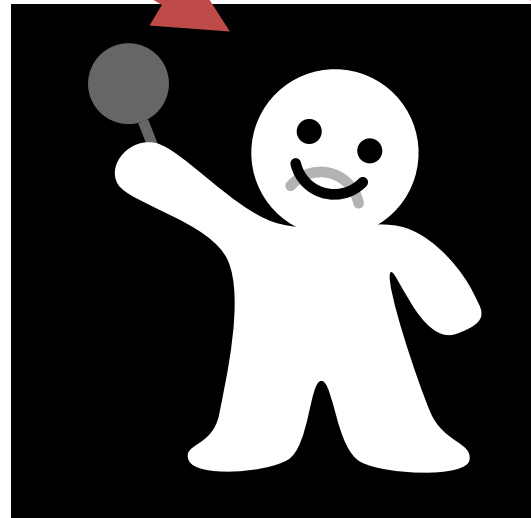
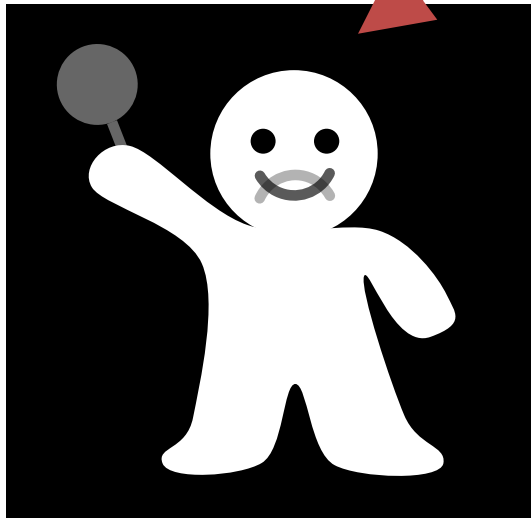


flexibility, heterogeneity & inoccupancy  
in molecular assembly



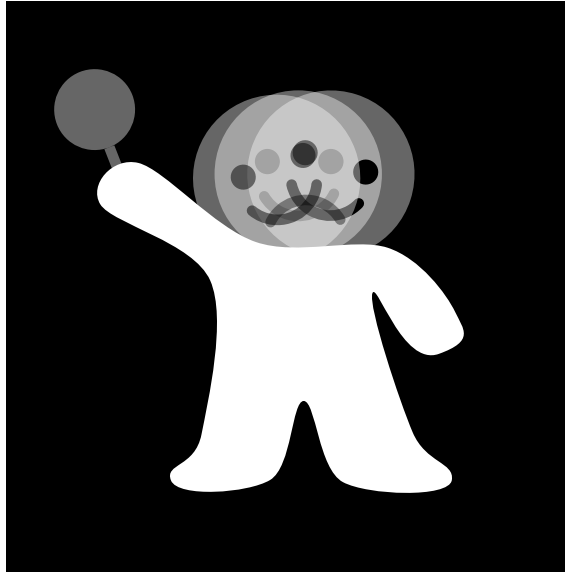
Global & unclassified average

Classification

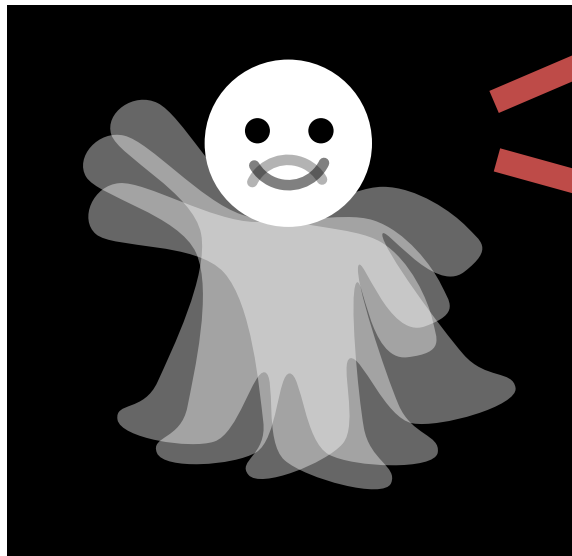


Class averages

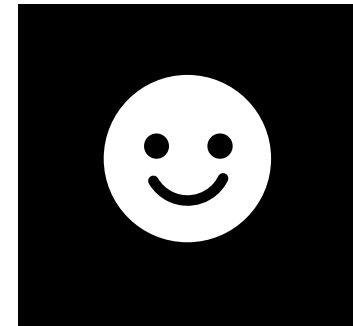




Local (masked)  
average



Classification



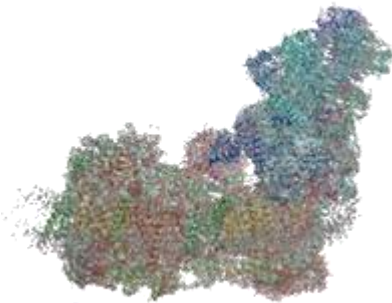
Local (masked)  
classification

# Respiratory "megacomplex"

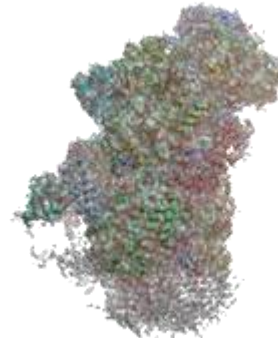
<b>EMDB</b>	6776	6776	6773	6772	6771	6774
<b>PDB</b>	5xti	5xth	5xtd	5xtc	5xtb	5xte
<b>res. (Å)</b>	17.4	3.9	3.7	3.7	3.4	3.4



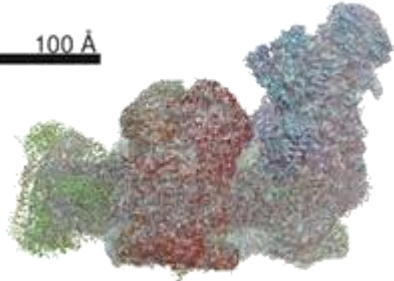
100 Å



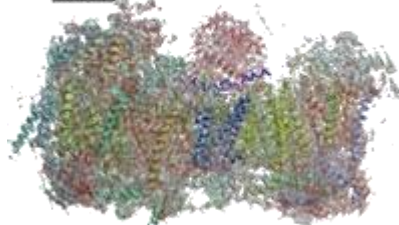
50 Å



50 Å



50 Å



50 Å



50 Å

## Database of citation of structure data

### Search result

**List of structure papers**

Showing 1 - 20 of 281 items for **keywords:** respiratory

**Architecture of Human Mitochondrial Respiratory Megacomplex I2III2IV2.**

[Cell](#), Vol. 170, Issue 6, Page 1247-1257.e12, Year 2017  
[Runyu Guo](#) / [Shuai Zong](#) / [Meng Wu](#) / [Jinke Gu](#) / [Maojun Yang](#)  
 Methods: EM (single particle)

**Immunogenicity and structures of a rationally designed prefusion M**

[Proc. Natl. Acad. Sci. U.S.A.](#), Vol. 114, Issue 35, Page E7348-E7357, Year 2017  
[Jesper Pallesen](#) / [Nianshuang Wang](#) / [Kizzmekia S Corbett](#) / [Daniel Wrapp](#) / [Hannah L Turner](#) / [Christopher A Cottrell](#) / [Michelle M Becker](#) / [Lingshu Wang](#) / [Erica L Andres](#) / [Arminja N Kettenbach](#) / [Mark R Denison](#) / [James D Chappell](#) / [B Ward](#) / [Jason S McLellan](#)  
 Methods: EM (single particle) / X-ray diffraction

**Yorodumi Papers** - Database of articles cited by EMDB/PDB/SASBDB data -

**+ Search query**

**- Structure paper**

	Title
<b>Journal, issue, pages</b>	Architecture of Human Mitochondrial Respiratory Megacomplex I2III2IV2 <a href="#">Cell</a> , Vol. 170, Issue 6, Page 1247-1257.e12, Year 2017
<b>Publish date</b>	Aug 23, 2017
<b>Authors</b>	<a href="#">Runyu Guo</a> / <a href="#">Shuai Zong</a> / <a href="#">Meng Wu</a> / <a href="#">Jinke Gu</a> / <a href="#">Maojun Yang</a>
<b>External links</b>	<a href="#">PubMed:28844695</a> / <a href="#">Publisher's page</a>
<b>Methods</b>	EM (single particle)
<b>Resolution</b>	3.4 - 17.4 A

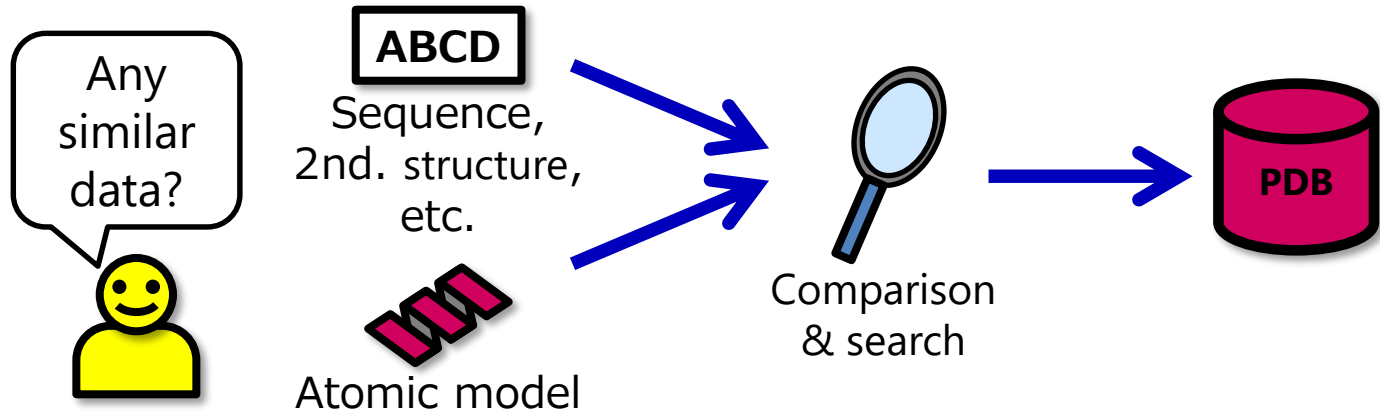
**EMDB-6771:** [▶ Movie](#) [▶ Structure viewer](#)  
 Cryo-EM structure of human respiratory complex I matrix

**EMDB-6772:** [▶ Movie](#) [▶ Structure viewer](#)  
 Cryo-EM structure of human respiratory complex I transmembrane domain

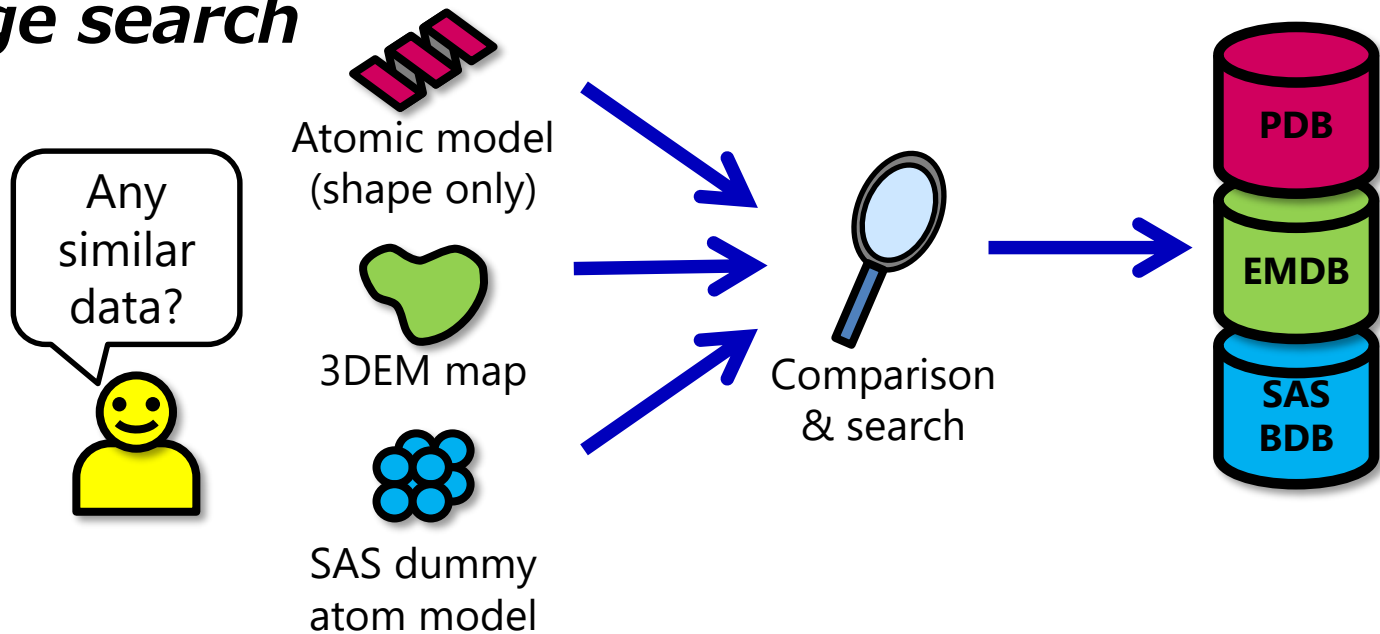
**EMDB-6773:** [▶ Movie](#) [▶ Structure viewer](#)  
 Cryo-EM structure of human respiratory complex I transmembrane domain

Details of data entries

## Typical ones (e.g. Structure Navigator of PDBj)



## Omokage search



# Enjoy cryo-EM data with PDBj services!

***EM Navigator*** <https://pdbj.org/emnavi/>

***Yorodumi*** <https://pdbj.org/yorodumi/>

***Omokage search*** <https://pdbj.org/omokage/>