20年を迎えたPDBj

- 50年を迎えようとするPDBでの位置づけ -

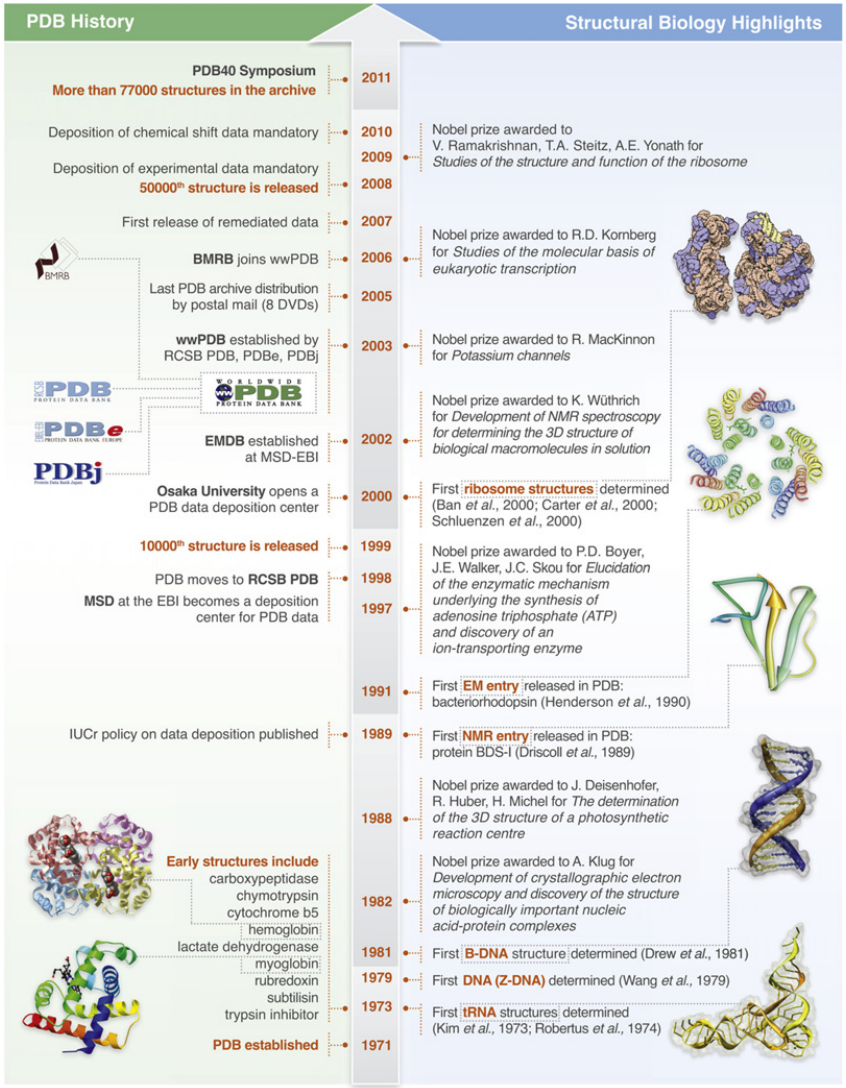
栗栖源嗣

大阪大学蛋白質研究所

wwpdb.org

2021年でProtein Data Bankは50年

PDBj 20 Year Anniversary



Structure
Meeting Review

Cell PRESS

The Protein Data Bank at 40: Reflecting on the Past to Prepare for the Future

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[3]Protein Data Bank Japan, Institute for Protein Research, Osaka University, 3-2 Yamadaoka, Suita, Osaka, 565-0871, Japan
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DOI 10.1016/j.str.2012.01.010

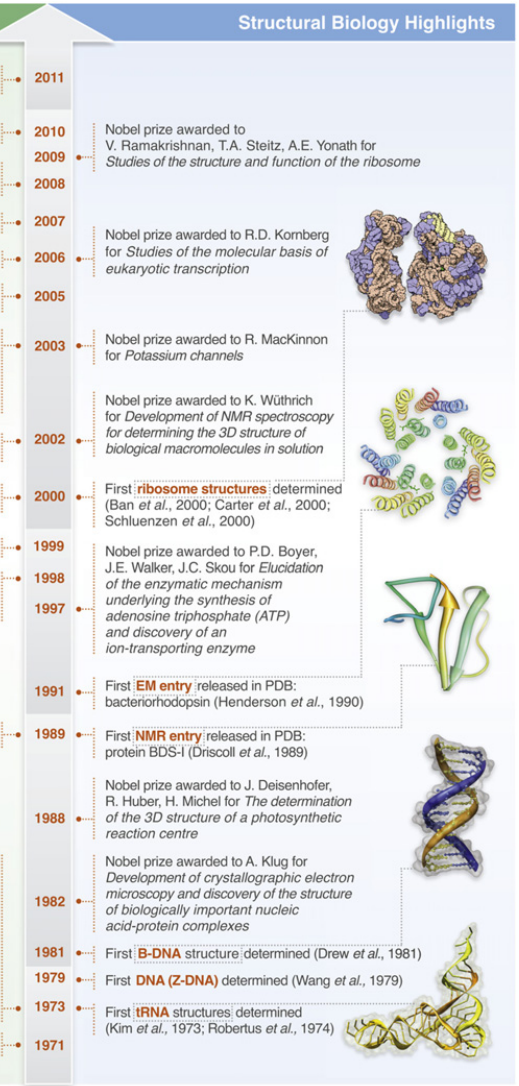
A symposium celebrating the 40th anniversary of the Protein Data Bank archive (PDB), organized by the Worldwide Protein Data Bank, was held at Cold Spring Harbor Laboratory (CSHL) October 28–30, 2011. PDB40's distinguished speakers highlighted four decades of innovation in structural biology, from the early era of structural determination to future directions for the field.

Structural biology was born in Cambridge, England in the 1950s, when the race to the DNA double helix reached the finish line (Franklin and Gosling, 1953; Watson and Crick, 1953; Wilkins et al., 1953) and the first three-dimensional (3D) crystal structures of hemoglobin and myoglobin (Kendrew et al., 1958; Perutz et al., 1960) were determined. In the years that followed, a slow of rain, snow (yes, snow in New York in October), and wind pelting on the tent in which they were displayed, they engendered lively discussions until the very last minute of the meeting.

The program boasted 19 distinguished speakers. Several speakers who had been a part of that early era of structural biology described their experiences determining structures

Berman et al., Structure **20**, 391-396 (2012)

最初期のアジアからの寄与



tural location and by their characteristic combinations of somatic sensory and motor inputs. All three nuclei project in a spatially overlapping manner to parietal cortex and terminate in the cortical layers as summarized in Fig. 2. This arrangement of somatic sensory and motor thalamocortical fiber systems in the marsupial opossum stands in contrast to that reported for placental mammals with the use of comparable techniques; for example, in the cat, the ventral posterior nucleus projects to layers IV and III of postcruciate cortex, while VL projects only to precruciate cortex (6). These anatomical species differences were predicted by parallel differences in physiological mapping results in the opossum and cat (3, 7). In the opossum, the convergent projections from separate sensory and motor thalamic nuclei onto a single cortical area comprise an adequate anatomical correlate for a functionally amalgamated sensory-motor area.

The identification of three separate thalamic inputs to sensory cortex is not unique to the somatic sensory system of the opossum, since more than one input has already been reported for opossum visual cortex and hedgehog visual, auditory, and somatic sensory cortices (8). In sensory systems of both species, the results demonstrate that more than one thalamic influence is operating directly on each "column" of sensory cortex. Multiple thalamic inputs that terminate in different combinations of cortical layers provide a probable anatomical substrate for the variety of responses evoked in cortex after stimulation of different thalamic nuclei. For example, the restricted VP projection provides a reasonable substrate for the primary evoked response while the diffuse CIN projection may well underlie the recruiting response first discovered by Morison and Dempsey (1). However, further studies which combine anatomical and physiological techniques are necessary in order to more closely correlate physiological responses with their anatomical substrate.

H. KILLACKEY
F. EBNER

Section of Neurosciences, Division of Biological and Medical Sciences, Brown University, Providence, Rhode Island 02912

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10. Supported by NINDS grant NS-06551 and fellowship NS-50714 (to H.F.K.). We thank E. W. Swick and E. DiPalma for assistance.

13 June 1972

Three-Dimensional Structure of Yeast Phenylalanine Transfer RNA: Folding of the Polynucleotide Chain

Abstract. At 4 Å resolution the polynucleotides in yeast phenylalanine transfer RNA are seen in a series of electron dense masses about 5.8 Å apart. These peaks are probably associated with the phosphate groups, while lower levels of electron density between segments of adjacent polynucleotide chains are interpreted as arising from hydrogen-bonded purine-pyrimidine base pairs. It is possible to trace the entire polynucleotide chain with only two minor regions of ambiguity. The polynucleotide chain has a secondary structure consistent with the cloverleaf conformation; however, its folding is different from that proposed in any model. The molecule is made of two double-stranded helical regions oriented at right angles to each other in the shape of an L. *One end of the* L *has the CCA acceptor; the anticodon loop is at the other end, and the dihydrouridine and TψC loops form the corner.*

Transfer RNA (tRNA) has a key role in the translation of the polynucleotide sequences of messenger RNA into the polypeptide sequences of protein. A considerable body of information has accumulated regarding these molecules but up to the present time the three-dimensional folding of the polynucleotide chain was unknown. Eight years ago Holley and his collaborators sequenced alanine tRNA from yeast and pointed out that the sequence could be folded into a clover[illegible] formation in which there are f[illegible] paired stem regions connect[illegible] loops (*1*). Approximately 4[illegible] molecules from various sourc[illegible] now been sequenced, and all [illegible] can be arranged in a similar c[illegible] arrangement. We have been [illegible] out an x-ray diffraction ana[illegible] yeast phenylalanine tRNA (2[illegible] sequence is known (*3*). Recentl[illegible] scribed the heavy atom de[illegible] which allowed us to calculate [illegible] dimensional electron density [illegible] 5.5 Å resolution (*4*). That [illegible] lowed us to discern the extern[illegible] of portions of the molecule and [illegible] short segments of the polyn[illegible] chain. We have continued t[illegible] and now report our interpret[illegible] the electron density map at 4.[illegible] lution which allows us to d[illegible] the positions of most of the p[illegible] groups in the nucleotides [illegible] phenylalanine tRNA. The pot[illegible] tide chain has been traced and its three-dimensional folding is presented.

Yeast phenylalanine tRNA crystallizes in an orthorhombic unit cell, space group $P2_12_12_1$, $a = 33$ Å, $b = 56$ Å, and $c = 161$ Å, with four molecules in the unit cell (*2*). The methods used in preparing crystals of yeast phenylalanine tRNA, and the chemistry of the isomorphous heavy atom replacements have been described (*4*). Three types of heavy atom derivatives containing plat-

19 JANUARY 1973

Note that both too little and too much mixing will reduce production, the latter by increasing the critical depth below that which will support net growth of phytoplankton. How increasing levels of atmospheric CO_2 from fossil fuel burning and forest destruction will affect climate-related ocean mixing and hence future plankton production and fisheries harvests is not clear.

This study was supported by the US Department of Energy and the NSF. We thank C. J. Lorenzen and G. Rowe for unpublished data and S. Horrigan and B. Bowden for reviewing the manuscript.

Received 23 July; accepted 2 October 1979.

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Molecular structure of a left-handed double helical DNA fragment at atomic resolution

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* Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139
† Department of Organic Chemistry, Gorlaeus Laboratories, University of Leiden, The Netherlands

The DNA fragment d(CpGpCpGpCpG) crystallises as a left-handed double helical molecule with Watson–Crick base pairs and an antiparallel organisation of the sugar phosphate chains. The helix has two nucleotides in the asymmetric unit and contains twelve base pairs per turn. It differs significantly from right-handed B-DNA.

Crystallisation and structure solution

The ammonium salt of the deoxy hexamer d(CG)$_3$ was prepared by a slight modification of the recently developed[11] phosphotriester approach. The crystals were grown from a solution containing 30 mM sodium cacodylate buffer (pH 7.0), 10 mM spermine tetrachloride, 15 mM $MgCl_2$ and 2 mM d (CG)$_3$ using the vapour diffusion method as developed for tRNA crystallisation[9]. The precipitating agent was 5% isopropanol. Crystals [illegible] over a period of [illegible] 0.7 × 0.5 mm were [illegible] als were mounted [illegible] droplet of mother [illegible] ace group $P2_12_12_1$ [illegible] $c = 44.58$ Å. The [illegible] ng reflections in [illegible] which suggested [illegible] nes perpendicular [illegible] we estimated that [illegible] nucleotides in the [illegible] ered and complete [illegible] solution of 0.9 Å

J. Biochem., 70, 913–924 (1971)

The Crystal Structure of Bonito (Katsuo) Ferrocytochrome *c* at 4 Å Resolution

Tamaichi ASHIDA, Tatzuo UEKI,* Tomitake TSUKIHARA,**
Akio SUGIHARA,*** Tsunehiro TAKANO
and Masao KAKUDO

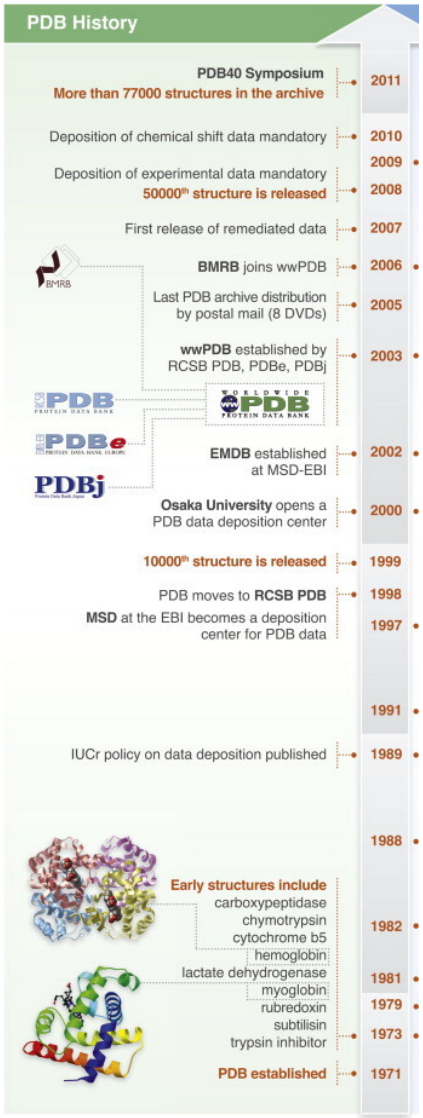
Institute for Protein Research, Osaka University, Osaka

Received for publication, March 10, 1971

The crystal structure of bonito ferrocytochrome *c* has been studied at 4 Å resolution on the basis of two isomorphous heavy atom derivatives ($K_3UO_2F_5$ and K_2PtCl_4). The crystal of bonito ferrocytochrome *c* belongs to an orthorhombic system with a space group of $P2_12_12_1$. The unit cell dimensions are: $a = 57.54$, $b = 84.71$ and $c = 37.74$ Å. The crystal contains two kinds of molecules which are nearly equivalent to each other *via* the pseudo-twofold axis along the a axis.

The main structural features of bonito ferrocytochrome *c* molecule, such as the size and shape, the pathway of the polypeptide chain, and the orientation and the environment of the heme group, appear to be similar to those of horse ferricytochrome *c*, although it is suggested that the side-chain conformation at the surface

Berman et al., Structure **20**, 391-396 (2012)



1971

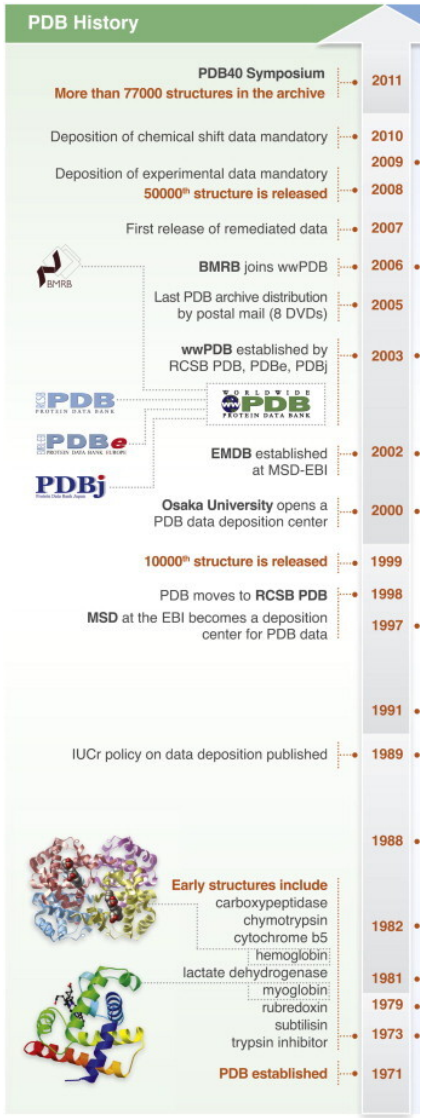
Data-In :	n/a	BNL	BNL
Data-Out :	n/a	BNL	CCDC

CRYSTALLOGRAPHY

Protein Data Bank

A repository system for protein crystallographic data will be operated jointly by the Crystallographic Data Centre, Cambridge, and the Brookhaven National Laboratory. The system will be responsible for storing atomic coordinates, structure factors and electron density maps and will make these data available on request. Distribution will be on magnetic tape in machine-readable form whenever possible. There will be no charge for the service other than handling costs. Files will be updated as new material is received. The total holding will be announced annually in the organic

Nature New Biology **233**, page 223 (1971)



1977

Data-In : BNL BNL BNL

Data-Out : Tokyo BNL CCDC

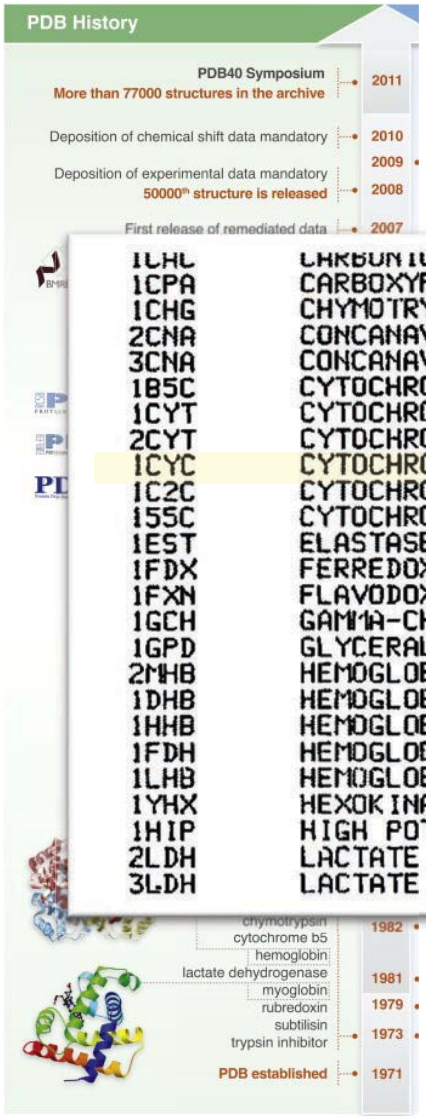
J. Mol. Biol. (1977) **112**, 535–542

The Protein Data Bank: A Computer-based Archival File for Macromolecular Structures

The Protein Data Bank is a computer-based archival file for macromolecular structures. The Bank stores in a uniform format atomic co-ordinates and partial bond connectivities, as derived from crystallographic studies. Text included in each data entry gives pertinent information for the structure at hand (e.g. species from which the molecule has been obtained, resolution of diffraction data, literature citations and specifications of secondary structure). In addition to atomic co-ordinates and connectivities, the Protein Data Bank stores structure factors and phases, although these latter data are not placed in any uniform format. Input of data to the Bank and general maintenance functions are carried out at Brookhaven National Laboratory. All data stored in the Bank are available on magnetic tape for public distribution, from Brookhaven (to laboratories in the Americas), Tokyo (Japan), and Cambridge (Europe and worldwide). A master file is maintained at Brookhaven and duplicate copies are stored in Cambridge and Tokyo. In the future, it is hoped to expand the scope of the Protein Data Bank to make available co-ordinates for standard structural types (e.g. α-helix, RNA double-stranded helix) and representative computer programs of utility in the study and interpretation of macromolecular structures.

The Protein Data Bank† (1971,1973) was established in 1971 as a computer-based archival file for macromolecular structures. The purpose of the Bank is to collect,

Bernstein *et al., J. Mol. Biol.*, **112**, 535-342, 1979

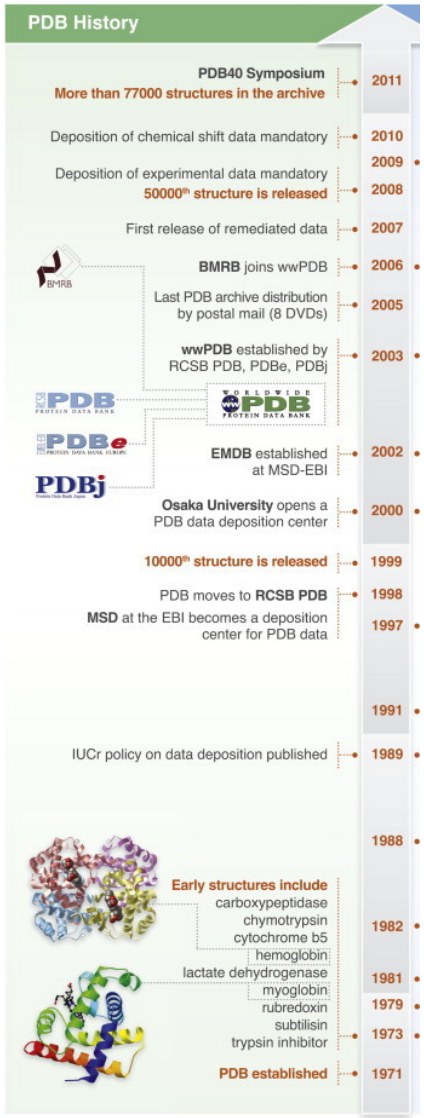


1977

TABLE 1

Protein data bank holdings

IDENT CODE	MOLECULE	DEPOSITOR	STATUS CODE
1ADK	ADENYLATE KINASE	G. SCHULZ	A
1ADH	ALCOHOL DEHYDROGENASE (ADP-RIB)	C.-I. BRANDEN	
2ADH	ALCOHOL DEHYDROGENASE (ORTHOPHEN)	C.-I. BRANDEN	
2CHA	ALPHA-CHYMOTRYPSIN (TOSYL)	D. BLOW	R
3CHA	ALPHA-CHYMOTRYPSIN	A. TULINSKY	
1FAB	ANTIGEN BINDING FRAGMENT (NEW)	R. POLJAK	
1REI	BENCE-JONES IMMUNOGLOBULIN REI	D. EPP, R. HUBER	
1CHL	CARBONIC ANHYDRASE C	N. KANNIAN	
1CPA	CARBOXYPEPTIDASE A	W. LIPSCOMB	
1CHG	CHYMOTRYPSINOGEN	J. KRAUT	
2CNA	CONCANAVALIN A	G. REEKE, G. EDELMAN	N
3CNA	CONCANAVALIN A	K. HARDMAN	R
1B5C	CYTOCHROME B5	F. S. MATHEWS	
1CYT	CYTOCHROME C (ALBACORE, OXIDIZED)	R. DICKERSON	
2CYT	CYTOCHROME C (ALBACORE, REDUCED)	R. DICKERSON	
1CYC	CYTOCHROME C (BONITO, HEART)	M. KAKUDO	
1C2C	CYTOCHROME C2	J. KRAUT	
155C	CYTOCHROME C550	R. TIMKOVICH	
1EST	ELASTASE	H. WATSON	
1FDX	FERREDOXIN	L. JENSEN	
1FXN	FLAVODOXIN (CLOSTRIDIUM MP)	M. LUDWIG	
1GCH	GAMMA-CHYMOTRYPSIN	COHEN, DAVIES, SILVERTON	P
1GPD	GLYCERALDEHYDE-3-P-DEHYDROGENASE(LOBSTR)	M. ROSSMANN	N
2MHB	HEMOGLOBIN (HORSE, AQUO MET)	LADNER, HEIDNER, PERUTZ	RP
1DHB	HEMOGLOBIN (HORSE, DEOXY)	M. PERUTZ, G. FERMI	
1HHB	HEMOGLOBIN (HUMAN, DEOXY)	M. PERUTZ, G. FERMI	
1FDH	HEMOGLOBIN (HUMAN, FETAL, DEOXY)	J. FRIER	
1LHB	HEMOGLOBIN (LAMPREY)	W. HENDRICKSON	
1YHX	HEXOKINASE (YEAST) BIII	T. STEITZ	B
1HIP	HIGH POTENTIAL IRON PROTEIN	J. KRAUT	
2LDH	LACTATE DEHYDROGENASE	M. ROSSMANN	PD
3LDH	LACTATE DEHYDROGENASE/NAD/PYRUVATE	M. ROSSMANN	PD
7PAP	PAPAIN (BZOXY-PHE-ALA,CYS-25)	J. DRENTH	
1PGK	PHOSPHOGLYCERATE KINASE (YEAST)	H. WATSON	A
2PGK	PHOSPHOGLYCERATE KINASE (HORSE)	P. EVANS, D. PHILLIPS	B
1PAB	PREALBUMIN (HUMAN, PLASMA)	S. OATLEY, D. PHILLIPS	
1RNS	RIBONUCLEASE S	H. WYCKOFF	
2RXN	RUBREDOXIN	L. JENSEN	ND
1SNS	STAPHYLOCOCCAL NUCLEASE	F. A. COTTON, E. HAZEN	
1SGB	STREPTOMYCES GRISEUS PROTEINASE B	M. JAMES	A
1SBT	SUBTILISIN BPN'	J. KRAUT	
2SBT	SUBTILISIN NOVO	J. DRENTH	
1SOD	SUPEROXIDE DISMUTASE	J. AND D. RICHARDSON	A
1TLN	THERMOLYSIN (UNREFINED)	B. MATTHEWS	
2TLN	THERMOLYSIN (REFINED)	B. MATTHEWS	
1SRX	THIOREDOXIN	B.-O. SODERBERG	A
1TNA	TRANSFER RNA (YEAST, PHE)	J. SUSSMAN, S.-H. KIM	N
2TNA	TRANSFER RNA (YEAST, PHE)	M. SUNDARALINGAM	P
3TNA	TRANSFER RNA (YEAST, PHE)	JACK, LADNER, KLUG	P
1TIM	TRIOSE PHOSPHATE ISOMERASE	I. WILSON, D. PHILLIPS	
1PTN	TRYPSIN (NATIVE, PH8)	FEHLHAMMER,BODE,SCHWAGER	N
2PTB	TRYPSIN(BENZAMIDINE INHIBITED, PH7)	FEHLHAMMER,BODE,SCHWAGER	RN
1PTC	TRYPSIN/TRYPSIN INHIBITOR COMPLEX	BODE ET AL.	N



1979

Data-In : BNL BNL BNL

Data-Out : Osaka, CSIRO BNL CCDC

THE PROTEIN DATA BANK

NEWSLETTER

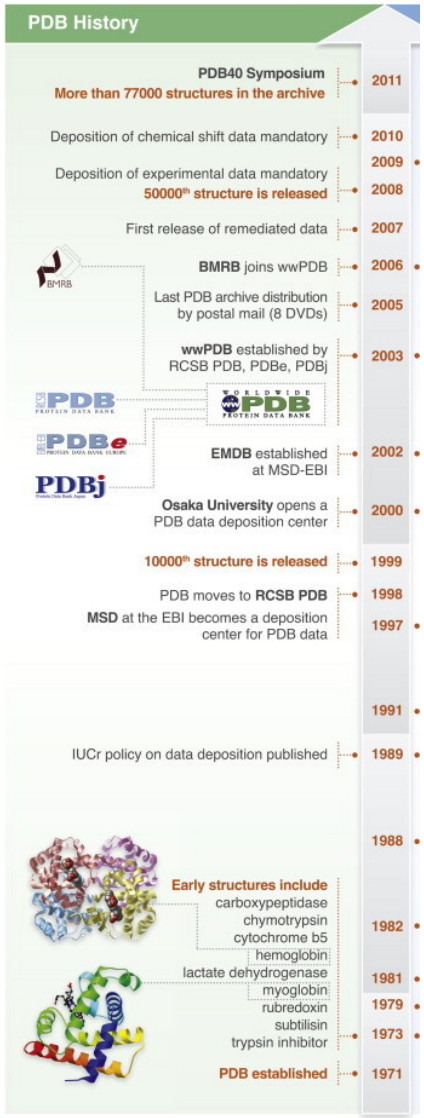
Number 10 October 1979

This brief newsletter provides up-to-date holdings information (Tables 1-5) and a Request Form. A full Newsletter will be distributed in January, and any of the persons listed below will be happy to answer inquiries.

We would like Japanese users to note that the center of Data Bank activity in Japan has been transferred to the Institute for Protein Research at Osaka University. Professor Masao Kakudo of Osaka has assumed the data distribution functions formerly carried out by Professor Mitsuo Tasumi of the University of Tokyo. We wish to thank Professor Tasumi for all his efforts on behalf of the Bank.

It is expected that the Protein Data Bank be ackno
publications which result from work making use of the Ba
In citing the Protein Data Bank in print, we suggest tha
be included to F. C. Bernstein, T. F. Koetzle, G. J. B.
E. F. Meyer, Jr., M. D. Brice, J. R. Rodgers, O. Kennard
and M. Tasumi, J. Mol. Biol. 112, 535-42 (1977). When p
published describing structures for which coordinates ha
we suggest that this same citation be used and our addre

Area	Address of Center		
The Americas	Protein Data Bank Chemistry Department Brookhaven National Laboratory Upton, New York 11973 USA	F. C. T. F. E. Ab	
Europe and Worldwide	University Chemical Laboratory Lensfield Road Cambridge CB2 1EW, England	O. Kennard S. Bellard	0223-66499
Australia	CSIRO Div. of Chemical Physics P. O. Box 160 Clayton, Victoria 31368 AUSTRALIA	B. J. Poppleton	
Japan	Institute for Protein Research Osaka University 5311, Yamada-Kami, Suita Osaka, Japan	M. Kakudo	(06) 877-5111 ext. 3836



Data-In : BNL/RCSB BNL/RCSB EBI

Data-Out : Osaka BNL, RCSB EBI

1998

1105

Acta Cryst. (1998). D**54**, 1105–1108

Deposition of Macromolecular Structures

Peter A. Keller,* Kim Henrick, Philip McNeil, Stuart Moodie and Geoffrey J. Barton

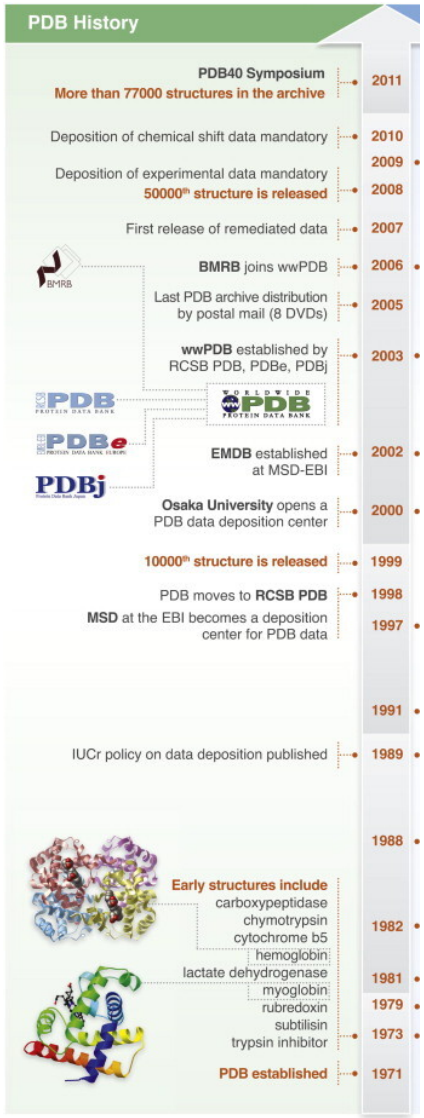
Macromolecular Structure Database Group, EMBL Outstation, European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, England. E-mail: msd@ebi.ac.uk

(*Received 6 March 1998; accepted 18 June 1998*)

Table 24.1.3.2. *PDB mirror sites as of May 1999*

Official PDB mirror sites
Argentina: University of San Luis
Australia: Australian National Genomic Information Service, Sydney; The Walter and Eliza Hall Institute of Medical Research, Melbourne
Brazil: ICB UFMG, Inst. de Ciencias Biologicas, Univ. Federal de Minas Gerais
China: Institute of Physical Chemistry, Peking University, Beijing
France: Institut de Génétique Humaine, Montpellier
Germany: GMD, German National Research Center for Information Technology, Sankt Augustin
India: Bioinformatics Centre, University of Pune
Israel: Weizmann Institute of Science, Rehovot
Japan: Institute of Protein Research, Osaka University
Poland: ICM Interdisciplinary Centre for Modelling, Warsaw University
Taiwan: National Tsing Hua University, HsinChu
United Kingdom: Cambridge Crystallographic Data Centre, Cambridge; EMBL Outstation, EBI, Hinxton
United States: Bio Molecular Engineering Research Center, Boston University; North Carolina Supercomputing Center, Research Triangle Park; University of Georgia, Athens, Georgia; PDB at Brookhaven National Laboratory

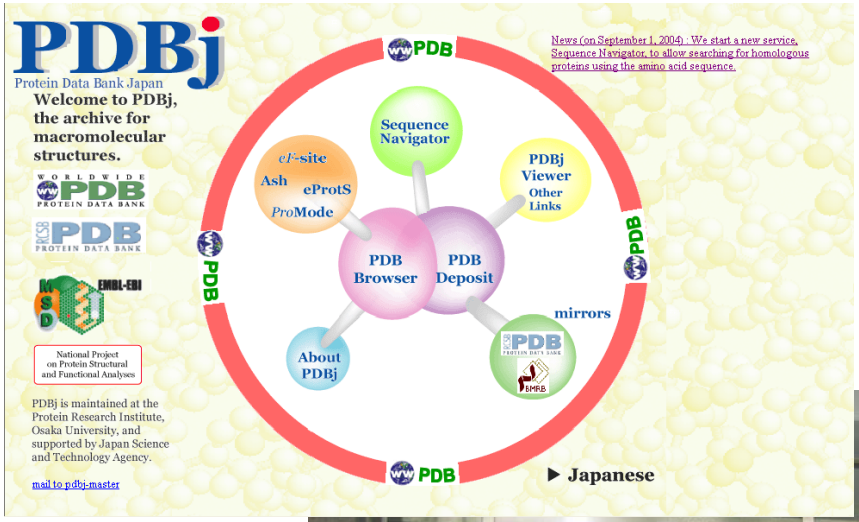
Sussmann *et al.*,
International Table of Crystallography Vol F, 1999



Data-In : Osaka RCSB EBI

Data-Out : Osaka RCSB EBI

2000



PDBj 20 Year Anniversary

PDB History

- 2011 — PDB40 Symposium; More than 77000 structures in the archive
- 2010 — Deposition of chemical shift data mandatory
- 2009 — Deposition of experimental data mandatory
- 2008 — 50000th structure is released
- 2007 — First release of remediated data
- 2006 — BMRB joins wwPDB
- 2005 — Last PDB archive distribution by postal mail (8 DVDs)
- 2003 — wwPDB established by RCSB PDB, PDBe, PDBj
- 2002 — EMDB established at MSD-EBI
- 2000 — Osaka University opens a PDB data deposition center
- 1999 — 10000th structure is released
- 1998 — PDB moves to RCSB PDB
- 1997 — MSD at the EBI becomes a deposition center for PDB data
- 1991
- 1989 — IUCr policy on data deposition published
- 1988
- 1982 — Early structures include carboxypeptidase, chymotrypsin, cytochrome b5, hemoglobin
- 1981 — lactate dehydrogenase, myoglobin
- 1979 — rubredoxin, subtilisin
- 1973 — trypsin inhibitor
- 1971 — PDB established

Data-In : wwPDB Worldwide PDB Protein Data Bank

Data-Out : Osaka RCSB EBI

2003

AGREEMENT

between

RESEARCH COLLABORATORY FOR STRUCTURAL BIOINFORMATICS (RCSB),
Piscataway New Jersey, Rockville Maryland, and La Jolla California

and

MACROMOLECULAR STRUCTURE DATABASE (MSD), Hinxton United Kingdom

and

PROTEIN DATA BANK JAPAN, Osaka Japan

to form the

Worldwide Protein Data Bank (wwPDB)

Effective DateJuly 1, 2003

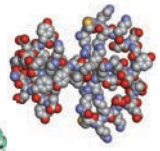
By signing this agreement, all members agree to accept the terms contained within.

	RCSB	MSD	PDBj
Name	Helen M. Berman	Kim Henrick	Haruki Nakamura
Signature			
Date	June 30, 2003	June 19, 2003	June 9, 2003

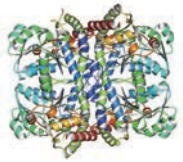
	Institutional Official	Institutional Official	Institutional Official
Name	Michael E. Breton	Janet Thornton	Katsuya Nagai
Signature			
Date	6-30-03	June 19, 2003	June 9, 2003

PDBjのあゆみ

PDBj で最初に登録処理した NMR 構造は
1EJQ（シンデカン 4）



PDBj で最初に登録処理した構造は 1GC0
（メチオニンγリアーゼ）でした



PDBj活動開始

実験データ必須化
PDB エントリー数 50,000 件達

PDB 設立 40 年
記念シンポジウム開催

PDBj 処理件数 20,000 件達成

結晶構造登録フォーマットとして
PDBx/mmCIF が必須化

2000 03 04 05 06 08 2010 11 13 15 17 19 2020

Promode
サービス開始

eF-site
サービス開始

BMRB が
wwPDB に合流

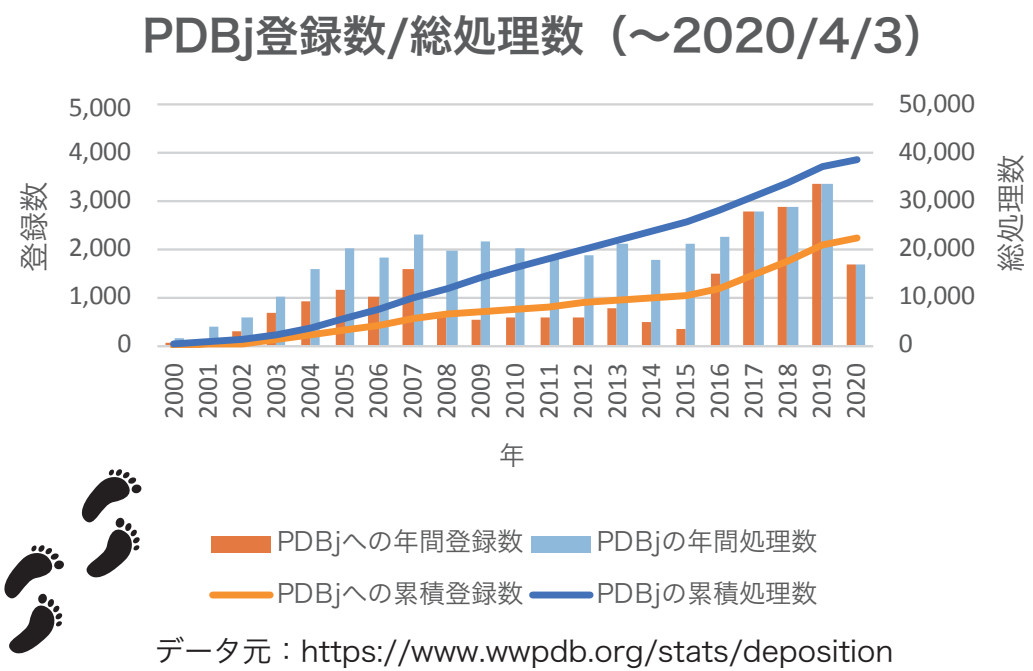
化学シフトデータ登録必須化

PDBj で OneDep 稼働

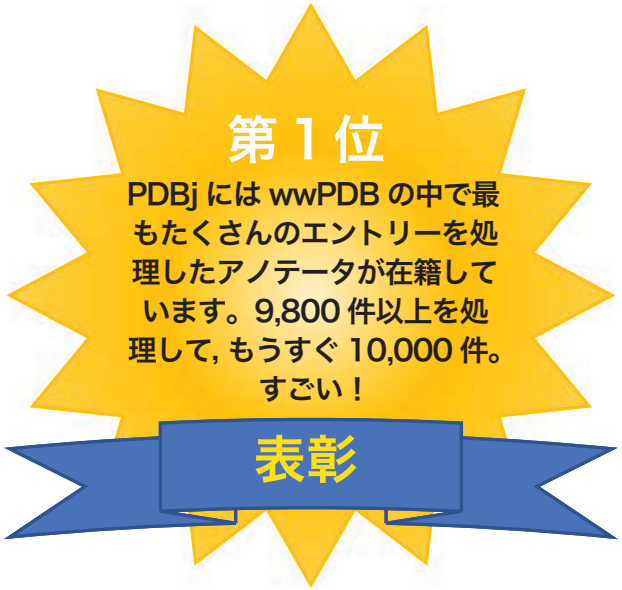
PDBj 新代表に栗栖 源嗣教授が就任

PDBj 発足 20 周年
PDBj 処理件数 40,000 件達成（予定）

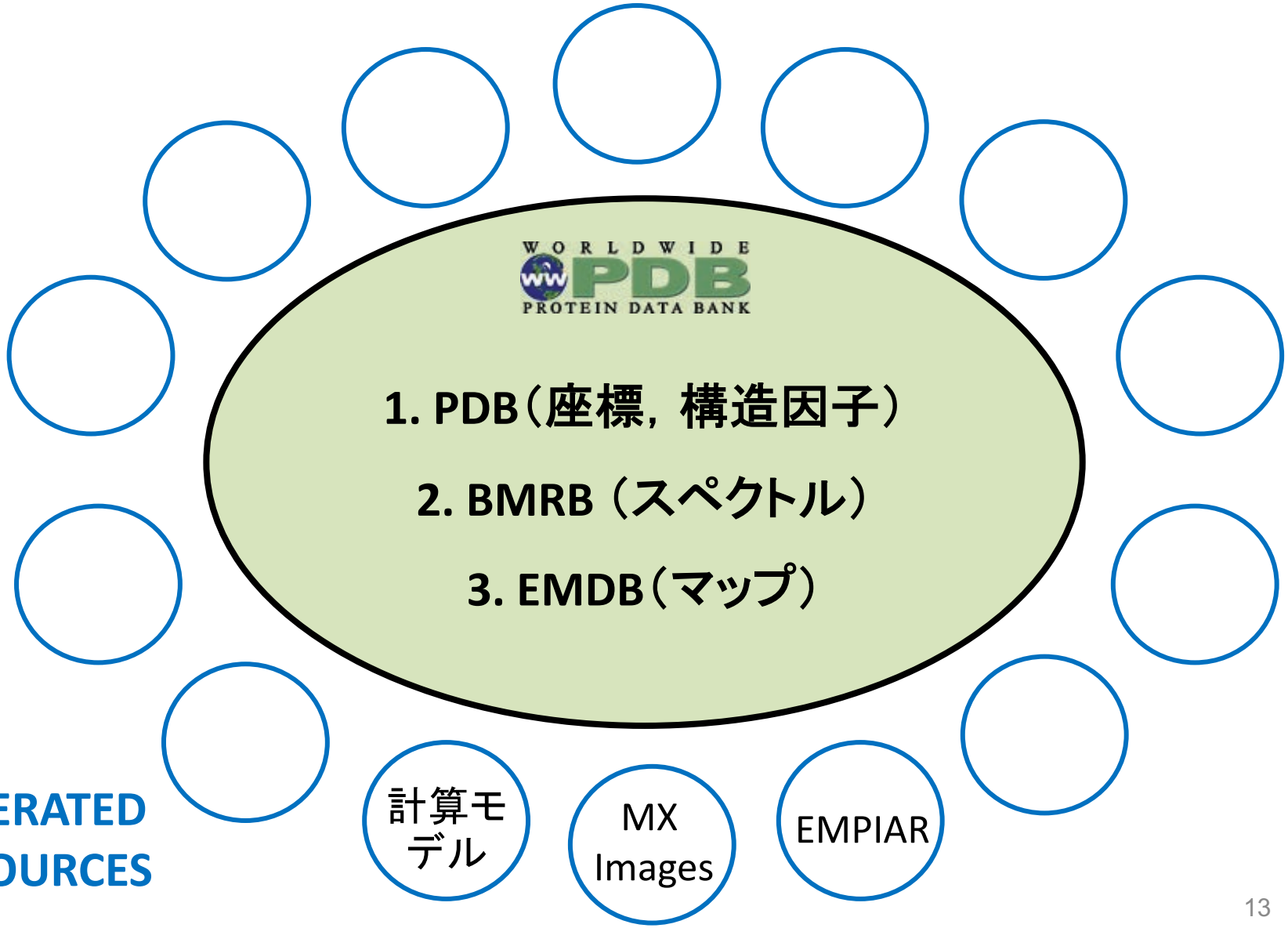
PDBjが積み上げた20年の実績



データ元：https://www.wwpdb.org/stats/deposition



PDBjは3つのwwPDBデータを管理

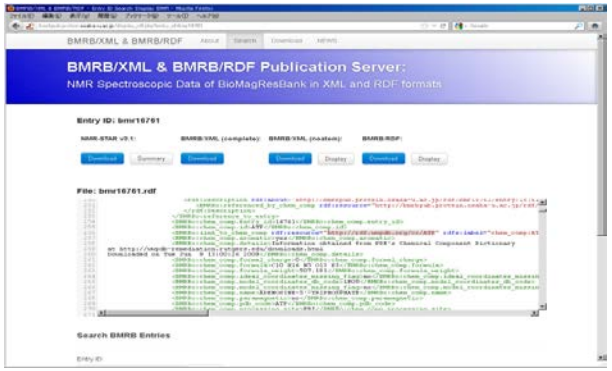


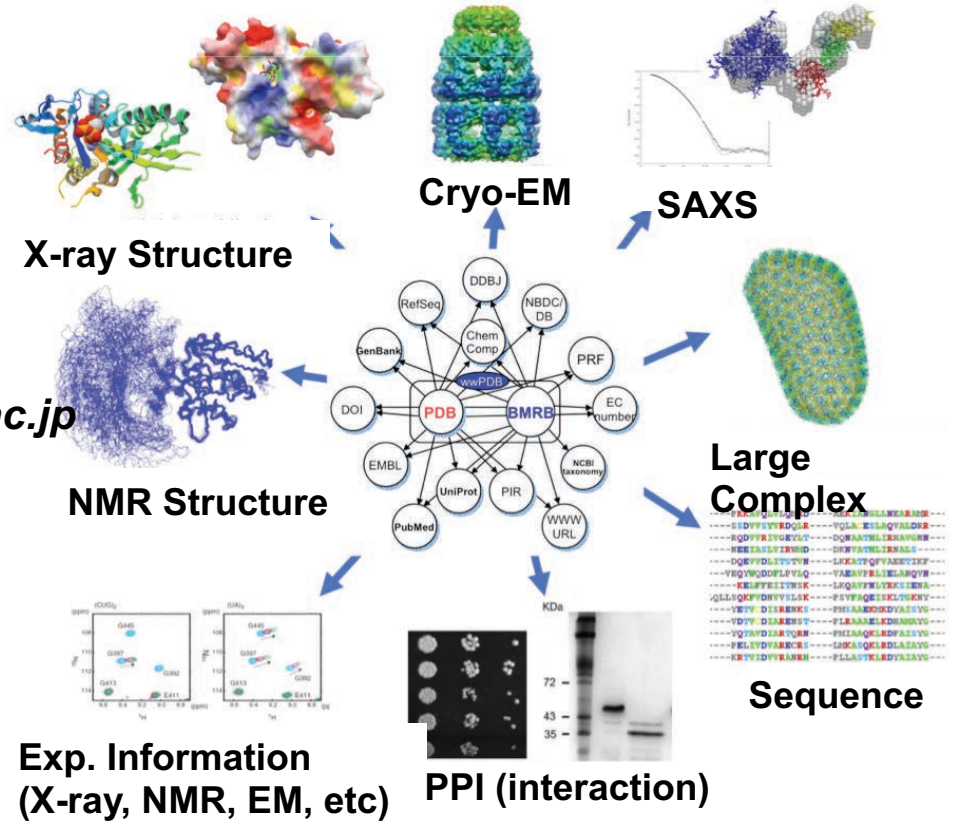
wwPDBにおけるRDF化の現状

wwPDB/RDF
http://rdf.wwpdb.org/

Kinjo et al. (2012) Nucl. Acids Res. 40, D453-D460.
Yokochi et al. (2016) J. Biomed. Semantics, 7:16.

BMRB/RDF
http://bmrbpub.protein.osaka-u.ac.jp






```
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  <rdf:type rdf:resource="http://purl.uniprot.org/core/Structure_Resource"/>
  <database rdf:resource="http://purl.uniprot.org/database/PDB"/>
  <method rdf:resource="http://purl.uniprot.org/core/X-Ray_Crystallography"/>
  <resolution rdf:datatype="http://www.w3.org/2001/XMLSchema#float">2.10</resolution>
</rdf:Description>
```
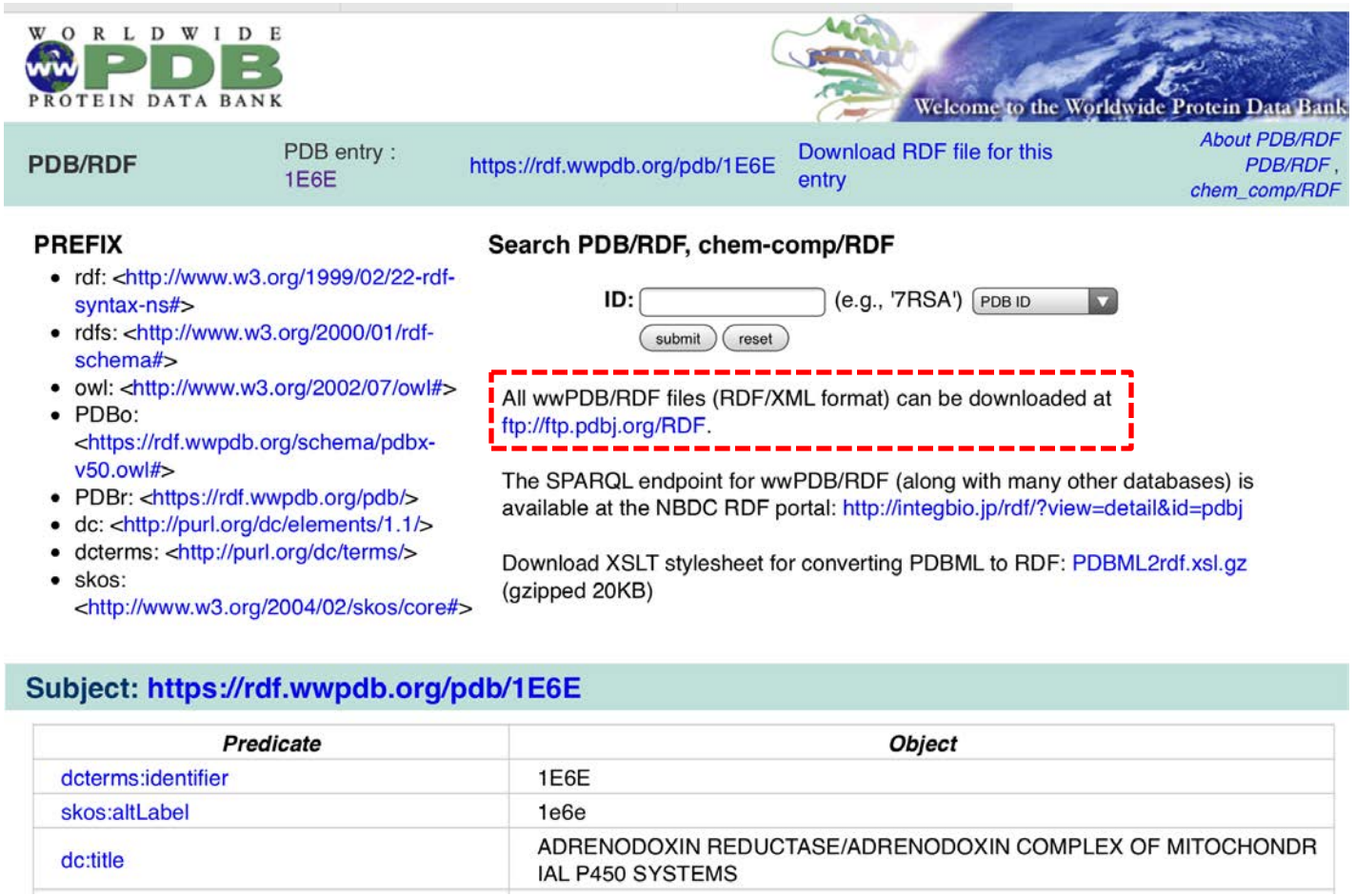

wwPDBでPDBjがRDFファイルを公開



WORLDWIDE PDB PROTEIN DATA BANK

Welcome to the Worldwide Protein Data Bank

PDB/RDF PDB entry : 1E6E https://rdf.wwpdb.org/pdb/1E6E Download RDF file for this entry *About PDB/RDF PDB/RDF , chem_comp/RDF*

PREFIX

- rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
- rdfs: <http://www.w3.org/2000/01/rdf-schema#>
- owl: <http://www.w3.org/2002/07/owl#>
- PDBo: <https://rdf.wwpdb.org/schema/pdbx-v50.owl#>
- PDBr: <https://rdf.wwpdb.org/pdb/>
- dc: <http://purl.org/dc/elements/1.1/>
- dcterms: <http://purl.org/dc/terms/>
- skos: <http://www.w3.org/2004/02/skos/core#>

Search PDB/RDF, chem-comp/RDF

ID: (e.g., '7RSA') PDB ID

submit reset

All wwPDB/RDF files (RDF/XML format) can be downloaded at ftp://ftp.pdbj.org/RDF.

The SPARQL endpoint for wwPDB/RDF (along with many other databases) is available at the NBDC RDF portal: http://integbio.jp/rdf/?view=detail&id=pdbj

Download XSLT stylesheet for converting PDBML to RDF: PDBML2rdf.xsl.gz (gzipped 20KB)

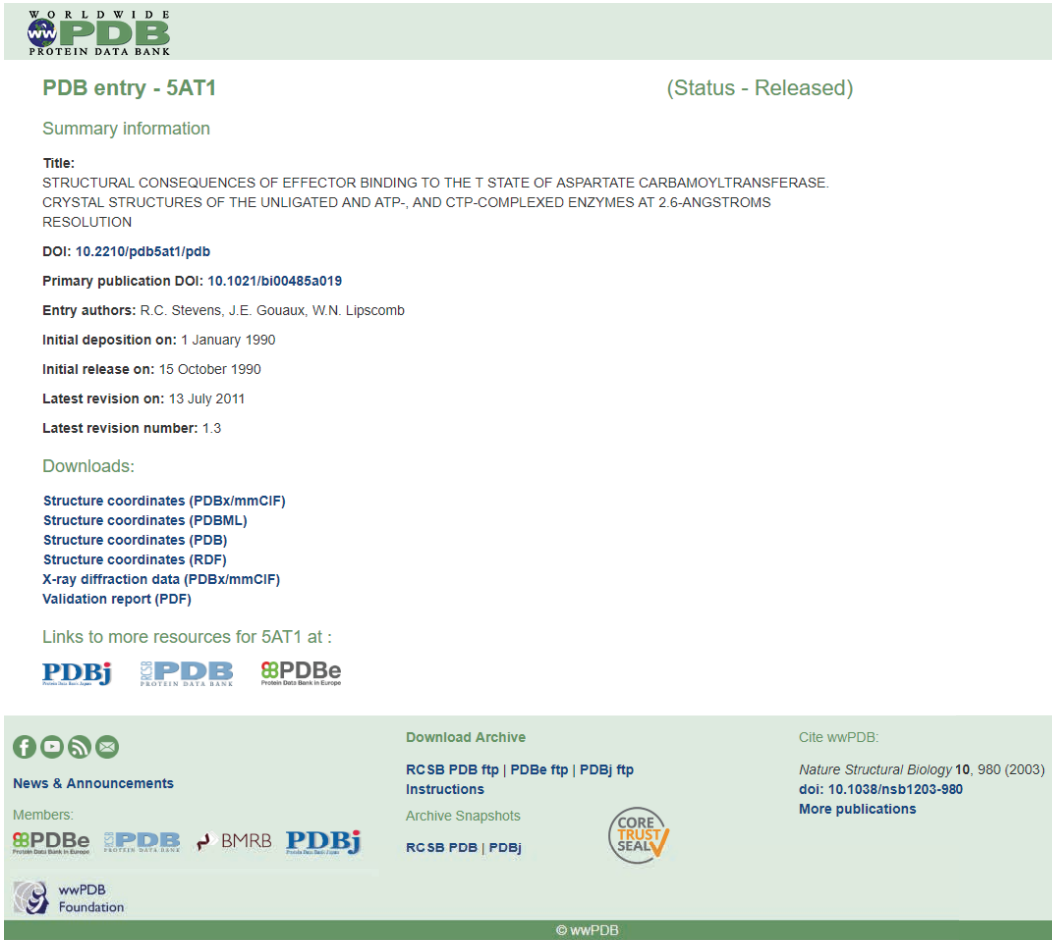
Subject: https://rdf.wwpdb.org/pdb/1E6E

Predicate	*Object*
dcterms:identifier	1E6E
skos:altLabel	1e6e
dc:title	ADRENODOXIN REDUCTASE/ADRENODOXIN COMPLEX OF MITOCHONDRIAL P450 SYSTEMS

wwPDB DOI landing page

Data-In :

Data-Out :



- 米国RCSB-PDBのPDBフォーマットファイルにDOIが紐づいていた e.g.10.2210/pdb5AT1/pdb
- wwPDB landing pageを作成し直接redirectするよう変更
- 各Journalに新しいリンクの更新を依頼

PDBj 構成員と協力者

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  - 加藤 和貴（大阪大学微生物病研究所・准教授） for MAFFTash
- **事務職員**
  - 佐久間 量子（大阪大学蛋白質研究所・特任事務職員）

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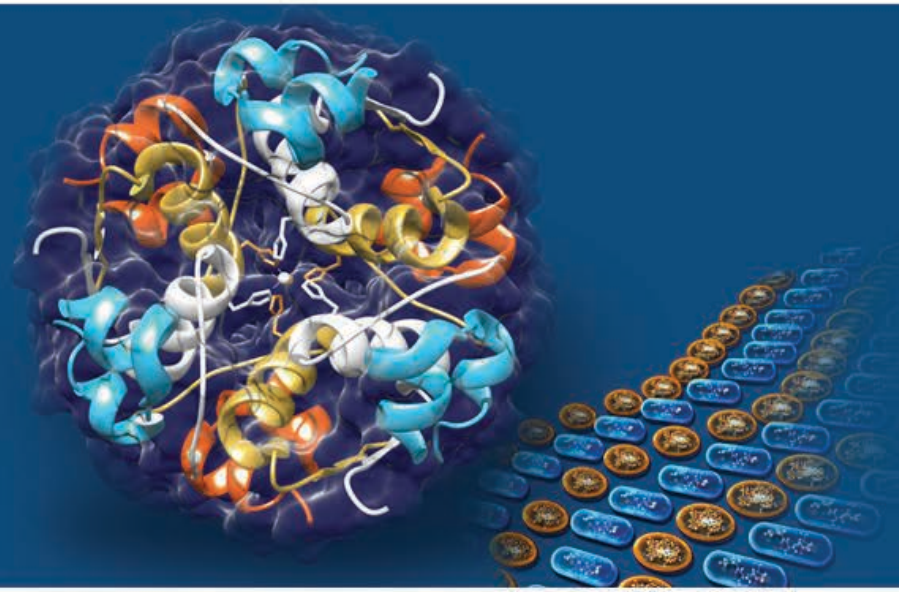
活動をサポートしていただける場合は，国際財団 **wwPDB Foundation**，もしくは **PDBj支援基金**へご寄付ください。



国際財団wwPDB Foundation

PayPal https://foundation.wwpdb.org/

本財団への寄付は，米国の免税措置の対象となります

Worldwide
Protein Data Bank
Foundation

PDBj支援基金（大阪大学未来基金）

https://www.miraikikin.osaka-u.ac.jp/916/

本基金への寄付は，日本の免税措置の対象となります

Acknowledgements

WORLDWIDE PDB PROTEIN DATA BANK

RCSB PDB PROTEIN DATA BANK

PDBe Protein Data Bank in Europe

PDBj Protein Data Bank Japan

BMRB