J Biomol NMR (2008) 40:153–155
DOI 10.1007/s10858-008-9221-y

COMMUNICATION

BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions

John L. Markley · Eldon L. Ulrich · Helen M. Berman · Kim Henrick · Haruki Nakamura · Hideo Akutsu

Received: 4 January 2008 / Accepted: 18 January 2008 / Published online: 21 February 2008

Abstract We describe the role of the BioMagResBank (BMRB) within the Worldwide Protein Data Bank (wwPDB) and recent policies affecting the deposition of biomolecular NMR data. All PDB depositions of structures based on NMR data must now be accompanied by experimental restraints. A scheme has been devised that allows depositors to specify a representative structure and to define residues within that structure found experimentally to be largely unstructured. The BMRB now accepts coordinate sets representing three-dimensional structural models based on experimental NMR data of molecules of biological interest that fall outside the guidelines of the Protein Data Bank (i.e., the molecule is a peptide with 23 or fewer residues, a polynucleotide with 3 or fewer residues, a polysaccharide with 3 or fewer sugar residues, or a natural product), provided that the coordinates are accompanied by representation of the covalent structure of the molecule (atom connectivity), assigned NMR chemical shifts, and the structural restraints used in generating model. The BMRB now contains an archive of NMR data for metabolites and other small molecules found in biological systems.

Keywords Archived NMR data · Metabolomics · NMR structure · Structural restraints · Unstructured regions

J. L. Markley (✉) · E. L. Ulrich
BioMagResBank, Department of Biochemistry, University of Wisconsin-Madison, 433 Babcock Drive, Madison, WI 53706-1544, USA
e-mail: markley@nmrfam.wisc.edu

H. M. Berman
RCSB Protein Data Bank, Department of Chemistry and Chemical Biology, Rutgers, The State University of New Jersey, 610 Taylor Road, Piscataway, NJ 08854-8087, USA

K. Henrick
MSD, EMBL, MSD-EBI, EMBL Outstation-Hinxton, Cambridge CB10 1SD, UK

H. Nakamura · H. Akutsu
PDBj, Institute for Protein Research, Osaka University, 3-2 Yamadaoka, Suita, Osaka 565-0871, Japan

Organization. The BioMagResBank (BMRB, http://www.bmrb.wisc.edu/), the repository for experimental and derived data gathered from NMR spectroscopic studies of biological molecules (Ulrich et al. 2008), has been a member of the Worldwide Protein Data Bank (wwPDB, http://www.wwpdb.org/) since 2006 (Berman et al. 2003). Other wwPDB partners include the Research Collaboratory for Structural Biology (RCSB PDB, http://www.pdb.org/), the Protein Data Bank Japan (PDBj, http://www.pdbj.org/), and the Macromolecular Structure Database at the European Bioinformatics Institute (MSD EBI, http://www.ebi.ac.uk/msd/). These four groups work closely together with the goal of maintaining a single Protein Data Bank archive of macromolecular structural data that is freely and publicly available to the global community.

The wwPDB Advisory Committee (wwPDBAC), which provides oversight and advice, meets yearly and currently is chaired by Stephen K. Burley. This committee consists of the leaders of the four sites plus two scientists nominated by each of the four partner sites. Additional ex officio members include scientists representing various stakeholder communities (e.g., International Union of Crystallography, International Council on Magnetic Resonance in Biological Systems, electron microscopy, structural genomics) and representatives of the international funding agencies that support the wwPDB member sites.

On matters pertaining to NMR spectroscopy, the wwPDB is advised by members of the wwPDB NMR Task

Force (NMR TF), which is chaired by Robert Kaptein (a wwPDBAC member). Historically, members of this TF have been nominated by the wwPDB leadership. Additional interested persons are welcome to join and participate. The wwPDB NMR TF meets periodically (usually more than once each year) at international NMR conferences.

Data remediation. Together with other wwPDB partners, the BMRB participated in the recently completed remediation of the full PDB archive (Henrick et al. 2008). Among the changes was adoption of uniform atom nomenclature in accordance with longstanding IUPAC recommendations (Markley et al. 1998). BMRB's major contribution to the remediation was to parse and organize restraints for NMR structures into the NMR Restraints Grid (http://tang.bmrb.wisc.edu:8080/WebModule/MRGridServlet) (Doreleijers et al. 2005).

Requirement for structure factors and constraints. Over the past 2 years, the wwPDB organization, in consultation with other members of the crystallographic and NMR communities, reviewed policies concerning data deposition. These deliberations led to the decision, supported by the wwPDBAC and wwPDB NMR TF at their most recent meetings, that all PDB depositions must be accompanied by structure factors (for X-ray structures) and restraints (for NMR structures). These requirements, listed below, were formally announced on November 30, 2007, and are scheduled to go into effect on February 1, 2008.

- The wwPDB shall require deposition of structure factor amplitudes/intensities (for crystal structure depositions) and/or NMR restraints (for NMR structure depositions) in addition to atomic coordinates as a prerequisite for receiving a PDB ID.
- The wwPDB leadership shall inform the relevant journals of this new policy, and will suggest that Instructions to the Authors read as follows:

  "For papers describing structures of biological macromolecules, atomic coordinates and the associated experimental data (structure factor amplitudes/intensities and/or NMR restraints) must be deposited at a member site of the Worldwide Protein Data Bank (www.wwpdb.org): RCSB PDB (www.pdb.org), MSD-EBI (www.ebi.ac.uk/msd), PDBj (www.pdbj.org), or BMRB (www.bmrb.wisc.edu). The PDB ID should be included in the manuscript. Authors must agree to release the atomic coordinates and deposited experimental data when the associated article is published. Questions relating to depositions should be sent to info@wwpdb.org."

Chemical shift depositions remain optional. These bodies also considered a proposal by members of the community that NMR structure depositions be accompanied by a BMRB deposition of assigned chemical shifts. Although it was decided that this requirement should not be made mandatory at present, the wwPDB NMR TF strongly recommend that these valuable data be deposited.

Small molecule NMR structures. At its 2006 meeting, the wwPDBAC discussed the question of small molecule NMR structures that do not comply with PDB guidelines. X-ray structures of such compounds are commonly deposited in the Cambridge Structural Database (CSD, http://www.ccdc.cam.ac.uk/products/csd/), but no such archive is available for NMR structures. Subsequently, the wwPDBAC approached BMRB with a request that it consider supporting this effort. BMRB developed the following proposal, which was brought before its External Advisory Board in May 2007.

BMRB will consider accepting coordinate sets representing three-dimensional structural models provided that the following criteria are met:

1. The molecule falls outside the guidelines of the Protein Data Bank (i.e., the molecule is a peptide with 23 or fewer residues, a polynucleotide with 3 or fewer residues, a polysaccharide with 3 or fewer sugar residues, or a natural product)
2. The molecule is of biological interest
3. The structural model(s) are based on experimental NMR data
4. The coordinates are accompanied by:
   a. A representation of the covalent structure of the molecule (atom connectivity)
   b. Assigned NMR chemical shifts for the molecule
   c. Structural restraints used in generating the structural model

For depositions meeting these criteria, BMRB encourages that authors submit their primary (time-domain) data, tables of NOEs, and other relevant information

This policy was announced at the most recent meetings of the wwPDBAC and wwPDB NMR TF.

Small molecule NMR structures meeting the above criteria can be deposited at the SMSDep website developed by BMRB and PDBj-BMRB (http://smsdep.bmrb.wisc.edu/bmrb-adit/). With small molecule structure depositions, the BMRB accession code serves to identify the structure as well as the supporting NMR data (questions about small molecule NMR structure depositions should be addressed to bmrbhelp@bmrb.wisc.edu).

Depositor defined regions of local disorder in structures. At the request of the wwPDB NMR TF, BMRB created tags, enumerations, and formal PDBx dictionary (Westbrook et al. 2005) entries for the following purposes:

- To separately specify the single structural model chosen by the authors to best represent the solution structure and to describe how it was derived.
- To describe uncertainty in the structural model (on a per-residue basis) and to denote residues found experimentally to be largely unstructured.
- To describe uncertainty in the structural model (on a per-atom basis) both qualitatively and quantitatively depending on the available data.

A detailed draft was refined by RCSB PDB and circulated to the wwPDB NMR TF. These specifications make it possible for an author to clearly define those regions that are experimentally determined to be structured and those that are not. This information will be available in the mmCIF version of the PDB entry and can be used by software developers in displaying structures.

Metabolomics data at BMRB. In collaboration with the Madison Metabolomics Consortium and the Human Metabolome Database (HMDB, http://www.hmdb.ca/), BMRB has developed an archive of NMR data for metabolites and other small molecules found in biological systems (Ulrich et al. 2008). A metabolomics deposition tool under construction at BMRB will enable others to submit data to add to this collection. Compounds are cross-referenced to PDB ligands, and the spectral information should be of interest to scientists studying macromolecule:ligand complexes. The site is mirrored by PDBj and CERM in Florence, Italy.

References

Berman HM, Henrick K, Nakamura H (2003) Announcing the Worldwide Protein Data Bank. Nat Struct Biol 10:980

Doreleijers JF, Nederveen AJ, Vranken W, Lin J, Bonvin AM, Kaptein R, Markley JL, Ulrich EL (2005) BioMagResBank databases DOCR and FRED containing converted and filtered sets of experimental NMR restraints and coordinates from over 500 protein PDB structures. J Biomol NMR 32:1–12

Henrick K, Feng Z, Bluhm WF, Dimitropoulos D, Doreleijers JF, Dutta S, Flippen-Anderson JL, Ionides J, Kamada C, Krissinel E, Lawson CL, Markley JL, Nakamura H, Newman R, Shimizu Y, Swaminathan J, Velankar S, Ory J, Ulrich EL, Vranken W, Westbrook J, Yamashita R, Yang H, Young J, Yousufuddin M, Berman HM (2008) Remediation of the protein data bank archive. Nucleic Acids Res 36:D426–D433

Markley JL, Bax A, Arata Y, Hilbers CW, Kaptein R, Sykes BD, Wright PE, Wüthrich K (1998) Recommendations for the presentation of nmr structures of proteins and nucleic acids (iupac recommendations 1998). Pure Appl Chem 70:117–142

Ulrich EL, Akutsu H, Doreleijers JF, Harano Y, Ioannidis YE, Lin J, Livny M, Mading S, Maziuk D, Miller Z, Nakatani E, Schulte CF, Tolmie DE, Kent Wenger R, Yao H, Markley JL (2008) BioMagResBank. Nucleic Acids Res 36:D402–D408

Westbrook J, Henrick K, Ulrich EL, Berman HM (2005) Definition and exchange of crystallographic data. In: Hall SR, McMahon B (eds) International tables for crystallography, vol G. Springer, Dordrecht, The Netherlands, pp 195–198