



**Biophysics Seminar**  
**at the 57<sup>th</sup> Annual Meeting of Biophysical Society of Japan**  
11:30-12:20, 24 September (Tue), Room G (Ivory)

**1. Recent activities of PDBj and wwPDB**

**PDBj と wwPDB の最近の活動について**

**Genji Kurisu**

**Institute for Protein Research, Osaka University**

The PDBj (PDB Japan, <https://pd bj.org/>) is a core member of the worldwide Protein Data Bank (wwPDB, <https://wwpdb.org/>) and processes the deposited data from researchers in Asian and Middle-east regions. In order to promote the recent “Data Science”, the wwPDB is introducing several new policies: (i) Collection of ORCID (Open Researcher and Contributor ID: <http://orcid.org/>) for contact authors has started already and login using ORCID will be implemented in 2019, (ii) Visualization of ligand validation and electron density maps in the wwPDB validation report was improved, (iii) PDBx/mmCIF format became mandatory for MX deposition from July 1st, this year. These issues will be introduced at the Seminar.

**2. New tools for editing and annotating structural data**

**Gert-Jan Bekker**

**Institute for Protein Research, Osaka University**

Ever since the introduction of PDBx/mmCIF, the shadow of death has been looming over the legacy PDB flat-file format. From July 1st 2019, deposition of PDBx/mmCIF formatted files has become mandatory. However, as many users are still used to the legacy flat-file format, we have developed a PDBx/mmCIF editor to help users transition to the new format. The editor doesn't require any installation and can be used from within a web browser at <https://pd bj.org/cif-editor>. Users can load local files to edit and save them again, while the tool validates the data with the dictionary. Concurrently, we have also developed a new archive for computationally obtained data, which incorporates the same PDBx/mmCIF editor in addition to our WebGL based molecular viewer Molmil for visualization. The Biological Structure Model Archive is available at <https://bsma.pd bj.org>, where published entries can be freely downloaded, while new entries can be submitted using users' ORCID ID.