

Luncheon Seminar at the 56th Annual Meeting of Biophysical Society of Japan

September 16 (Sun), 11:45 ~ 12:35, D site (Room A36, Bldg. A)

1. Making full use of the wwPDB validation reports

wwPDB 検証レポートの活用法

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wwPDB validation reports provide an assessment of structure quality which shows that obtained structure model is consistent with experimental data and how the model agrees to the widely accepted criteria at atomic level. It is essential resource not only for structural interpretation of original publication, but also development of bioinformatics, and drug discovery. In order to improve accessibility and usability, we developed two semantic versions of the wwPDB validation reports, PDBx/mmCIF compatible XML and RDF, respectively. I will outline the basic concepts of the new archives and explain the effective way to use them through case-study.

2. Introduction to NIG Supercomputer and DDBJ

遺伝研スパコンとDDBJの紹介

Masanori Arita

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DDBJ is a part of International Nucleotide Sequence Database (INSD) in collaboration with NCBI and ENA/EBI since 1987. Our service includes next-generation sequence data in Sequence Read Archive, research projects in BioProject, biological sources and materials in BioSample, and personal genomes in JGA. More than half of our computing resource is open to domestic researchers (and foreign collaborators), and > 500 registered users from > 120 institutions perform their own research free of charge. Modern research requires a complicated software environment and we keep providing the up-to-date system for all scientists in Japan.