

MS10-P12 Analyzing protein-protein contacts at the PDB-wide level

Guido Capitani¹, Jose Duarte^{1,2}, Kumaran Baskaran¹, Nikhil Biyani¹, Spencer Bliven^{1,3}

1. Paul Scherrer Institute, Villigen, Switzerland
2. ETH Zurich, Switzerland
3. University of California San Diego, USA

email: guido.capitani@psi.ch

As of March 2015, the Protein Data Bank [1] contains more than 105'000 entries: it reached this size largely thanks to the technical advances of macromolecular crystallography in the last 10-15 years. The complexity and diversity of macromolecular crystal structures, however, often make it challenging to establish which of the protein-protein contacts observed in a crystal do bear biological relevance and which ones are lattice contacts. We tackled this problem by creating a general protein interface classification method (EPPIC, Evolutionary Protein-Protein Interface Classifier, www.eppic-web.org [2]). EPPIC analyzes all interfaces in a crystal and classifies them as biological or as crystal contacts by analyzing their evolutionary footprint (or lack thereof). It also uses a geometric interface classification criterion based on our definition of interface core residue [3]. We are now using EPPIC to analyze protein-protein contacts on a PDB-wide scale. To that end, we assembled an automated computational pipeline to run our program on the entire PDB and store the results in a relational database [4], containing about 880'000 interfaces to date. The EPPIC approach, PDB-wide computational pipeline and selected results will be presented.

[1] Berman HM, Henrick K & Nakamura H, *Nature Structural Biology*, 2003, 10, 98

[2] Duarte JM, Srebniak A, Schärer M & Capitani G, *BMC Bioinformatics*, 2012, 13, 334

[3] Schärer, MA, Grütter MG & Capitani G, *Proteins*, 2010, 78, 2707-13

[4] Baskaran K, Duarte JM, Biyani N, Bliven S & Capitani G, 2014, *BMC Structural Biology*, 14, 22

Keywords: Structural bioinformatics, EPPIC, protein-protein interfaces, crystal contacts

MS11. Hybrid approaches

Chairs: Guillermo Montoya, Jan Pieter Abrahams

MS11-P1 Application of magnetically oriented microcrystal array to X-ray and neutron crystallography

Shu Tsukui¹, Fumiko Kimura¹, Tsunehisa Kimura¹

1. Division of Forest and Biomaterials Science, Graduate School of Agriculture, Kyoto University, Kitashirakawa, Sakyo-ku, Kyoto 606-8502, Japan

email: tsukui.shu.52w@st.kyoto-u.ac.jp

The diffraction method is powerful to elucidate the crystal structure of substances at atomic resolution. It is a prerequisite to prepare single crystals large enough for the acquisition of single crystal data. Owing to the synchrotron facilities, the sizes required for X-ray crystallography are getting smaller and smaller, as small as several tens micrometers in size, but yet it is difficult for many substances to crystalize to this size. Size restriction is much severer in neutron crystallography; for example, single crystals of millimeter sizes or more are required in case of proteins.

We have proposed a new technique that enables to convert microcrystals to pseudo-single crystals. Microcrystals are biaxially aligned by using magnetic fields to obtain a magnetically oriented microcrystal array (MOMA). The magnetic susceptibility of biaxial crystals (triclinic, orthorhombic and monoclinic crystal systems) has susceptibility tensor with three different principal values, χ_1 , χ_2 , and χ_3 (we assume $\chi_1 > \chi_2 > \chi_3$). The principal axes corresponding to c_1 and c_3 are referred to as easy and hard magnetization axes, respectively. The easy axis aligns parallel to the applied static field, while the hard axis aligns parallel to the z axis when a magnetic field rotation in the xy plane is applied. Combination of these two magnetic fields (referred to as modulated rotating magnetic field) causes three-dimensional alignment of microcrystals.

Orthorhombic hen egg-white lysozyme (HEWL) microcrystals (5-10 μm) were chosen for a model study. The HEWL microcrystals were suspended in a suspension liquid medium (whether ultra-violet curable resin or hydrosol). A capillary containing the microcrystal suspension was subjected to a modulated rotation in the center of 8 T superconducting magnet to achieve 3D alignment. The 3D alignments were consolidated by photo-polymerization of the UV-curable resin or gelation of the hydrosol to obtain MOMAs. X-ray diffraction measurements were carried out at Spring-8. The diffraction images shown in **FIG. 1** were obtained, from which the crystal structure at resolutions higher than 2.0 Å was obtained. Neutron diffraction measurements were carried out on deuterated MOMA prepared in a similar way. Diffraction spots were observed.