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

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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.

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

MS11. Hybrid approaches

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

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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.

These results show that a combination of MOMAs with X-ray and neutron diffraction measurement is of great use for single crystal analyses of protein crystals that do not grow to required sizes.

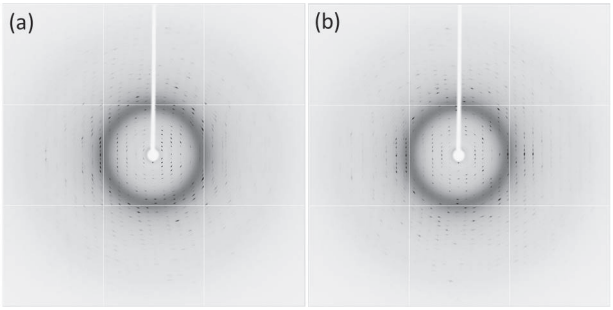

Figure 1. X-ray diffraction images, (a) and (b), taken at two different angles 90° apart. The edges of the images correspond to resolution of 1.79 Å. The averaged full width of half maximum (FWHM) of the diffraction spots are 2.14 and 2.77° for (a) and (b), respectively.

Keywords: X-ray crystallography, Neutron crystallography, Micro-crystallography, Magnetic orientation

MS11-P2 Adsorption of hydrocarbons in the porous borohydride framework γ-$Mg(BH_4)_2$

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The first porous hydride, γ-$Mg(BH_4)_2$, was discovered recently [1]. It has about 1/3 of space in a form of small pores available to guest molecules, such as H_2, N_2 or CH_2Cl_2 [1]. It is expected that the hydridic nature of the borohydride ligands, exposed by $H^{\delta-}$ into the pores, gives rise to specific guest-host interactions and thus to a selectivity of adsorption. In this work we study adsorption of methane, ethane, propane and butane into γ-$Mg(BH_4)_2$.

In situ X-ray diffraction data show that only methane and ethane are adsorbed into the pores, while propane and butane are too large to enter. Variable temperature diffraction under different gas pressures allowed us not only to localize the guests, but also to extract the isosteric heats of adsorption directly from the diffraction data [1, 2]. Neutron powder diffraction was done on doubly isotopically substituted γ-$Mg(^{11}BD_4)_2$, loaded with CD_4 (NIST) and C_2H_6 (HZB). Accurate localization of the guest molecules allows to determine the nature and the role of the guest-host interactions.

On saturation, 2/3 of methane and ethane molecules are adsorbed per Mg atom. The isosteric heats of adsorption, 22 (CH_4) and 32 (C_2H_6) kJ/mol of gas, allow to store 15–30 weight % of fuel gases at room temperature. This work will be complemented by volumetric studies of the adsorption enthalpies, as well as by theoretical calculations aiming to understand perfectly clear the nature of the intermolecular interactions.

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Keywords: adsorption, in situ powder diffraction, porous hydride, thermodynamics