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Local and Dynamic Investigations for Bio-soft materials at SPring-8

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In addition to the static crystallographic information regarding a 3D structure of proteins, dynamic information regarding a protein's conformational changes would be helpful in elucidating the molecular mechanisms that regulate protein functions, such as ion channel gating and ligand-induced receptor activation. Such local and dynamic information can be obtained using optical microscopy with recently developed single molecule techniques, and we think that the technique with synchrotron X-rays would be more powerful technique because of its brilliance, its short wavelength of light, and its transparency.

Small-angle X-ray scattering (SAXS) is one of well-established technique to investigate the nanoscale structure of protein under physiological conditions and structural changes in response to various external conditions and we have probed a compact intermediate state of calmodulin in the process of target binding [1,2] etc. And we have proposed a single molecule technique that utilizes synchrotron X-rays to monitor the internal motions of a single protein. We call it diffracted X-ray tracking (DXT) and it can detect atomic-scale dynamic motion of the protein at the single molecular level with several tens of microseconds time resolution [3]. In DXT, a target protein is labeled with a nanocrystal with a size of several tens of nanometers and the motions of the nanocrystal coupled with the protein's motions are recorded as the trajectories of diffraction spots from the nanocrystal [4-6].

At the seminar, we will present recent progress of such investigation for biomolecules

References

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