- 1P350 X線回折によるハエの体内脂肪結晶化の直接確認
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- 1aK14 Direct confirmation of fat crystallization in a fly body by means of X-ray diffraction
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Living things at the Temperate or Frigid Zone had acquired some mechanisms for surviving at low temperatures of winter during their long evolution process. For many animals, winter cause another problem, i.e., food less problem. Some insects diapauses to avoid this problem. Even during diapause, however, energy is needed for their basal metabolisms. Some overwintering insects accumulate fat, triacylglycerol (TG), in their bodies before winter and get energy from the hydrolysis reaction of TG catalyzed by lipase during diapause. When TG is solidified at low temperatures, the insects cannot get energy. Thus, TG crystallization is a serious problem for the insects, as well as ice formation in their body. We have been investigating the crystallization phenomena of TAG taking place in a fly body at low temperatures by means of X-ray diffraction. In previous study, we used dried dead flies [1]. In the present study, we tried to detect the crystallization of TAG using living flies. A cool-temperate fly species, *Drosophila triauraria*, was examined. To make the flies prepare for overwintering, the daylength condition before winter was created artificially by controlling time of lighting (10 h light, 14 h dark) at 15°C. Experiments were done on Beamline 40B2 of SPring-8. We succeeded in detecting the Bragg diffraction peaks from TAG crystals in a fly cooled down to -30°. At this temperature, however, the formation of ice happened in the fly body. As a result, the fly was killed. [1] Takahashi et al., J. Appl. Cryst., (2003), 36, 545-548.

- 1P352 位相差電子顕微における強位相物体の新理論
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A Novel Phase Contrast Theory to Justify the Phase Contrast Recovery for Strong Objects
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Various examples of highly contrasted images obtained with electron microscopes equipped with phase plates for biological specimens such as proteins, viruses, bacteria and cells have been reported. Then plausible but unexpected outcomes have emerged. One of the examples is high contrasted images of whole mount cyanobacterial cells with a thickness of about 1 micron meter. Considering the phase change induced by ice-embedded, unstained and unsectioned cells to be more than 10 π , the high contrast result is beyond the scope of the applicability formalized by Zernike, where weak phases far below 0.5 π is assumed. The desirable unexpected has recently been settled by taking the coherence of incident electron waves into account. In brief the weak object condition is tightly coupled with the formalism given by Zernike and valid only in the incoherence extreme of the incidence. As like holography, the incident coherence even dominates the appearance of phase contrast images. The new theory predicts that the coherence is fatal not only in the spatial resolution but also in the phase contrast. Experimental results to reveal the correlation between the contrast and the coherence are to be shown.

- 1P351 X線による1分子ダメージ評価
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Single Molecular Damage Evaluation with X-rays
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Many scientists try to observe individual internal motions of protein molecules in the range of micro-second or nano-second. The speed-up of these techniques is a back match to damage. Therefore, we must evaluate damages of individual single protein molecules in aqueous solutions. Here, we proposed single molecular detection system with X-rays in order to observe individual internal motions of protein molecules very accurately. In general, radiation damage in all X-ray observations is the biggest obstacle. X-ray experiments on biological or inorganic crystals show significant damage. Recently, we succeeded in vitro time-resolved x-ray observations of picometer-scale slow Brownian motions of individual protein molecules in aqueous solutions. In this single molecular detection system, which we call Diffracted X-ray Tracking (DXT), we observed the rotating motions of an individual nanocrystal, which is labeled to the specific site in individual protein molecules, using time-resolved Laue diffraction. DXT can monitor dynamics of the individual molecules or specific sites in individual single protein molecules. Now, we try to observe individual DNA molecules, myosin head molecules, denatured proteins, protein membranes (Bacteriorhodopsin and KcsA) and actin filament. Here, we paid attention to the width of x-ray energy, and accurately evaluated the movements of single molecules.

- 1P353 ラマン散乱およびテラヘルツ分光によるリゾチームおよびBPTI結晶の低振動数モードの観測
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Low frequency modes of crystalline lysozyme and BPTI observed by Raman scattering and terahertz time-domain spectroscopy
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Low frequency modes (LFM) of proteins have attracted much attention because their roles in protein functions are supposed to be crucial but still unclear. Recent progresses of protein dynamics simulations and experimental methods including terahertz time-domain spectroscopy (THzTDS) are expected to help us gain valuable insights of this problem. We performed Raman scattering spectroscopy for the LFM of two kinds of crystalline proteins: lysozyme and bovine pancreatic trypsin inhibitor (BPTI). We also successfully observed the LFM of lysozyme crystals by using THzTDS. Temperature dependence of the LFM were analyzed by the parameter fitting procedure on the basis of multiple damped oscillators. Common features were recognized between the spectra for lysozyme and BPTI: Drastic spectral changes in the lower-frequency region indicate anharmonic vibrational behavior of the LFM around physiological temperature. By employing a small number of components, the fitting well reproduces the temperature dependent spectral changes. In this procedures, the specified frequencies for the components are almost the same for both proteins. Comparison of observed spectra between Raman scattering and absorption spectra obtained by THzTDS for dry, semi-dry, and wet crystalline lysozyme revealed that there exists a simple relation between the spectral shapes of the absorption and the Raman scattering spectra. It was recognized that water molecules play a key role in anharmonic vibrational behavior of the LFM.