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Probing the small-scale protein motions with a laboratory X-ray

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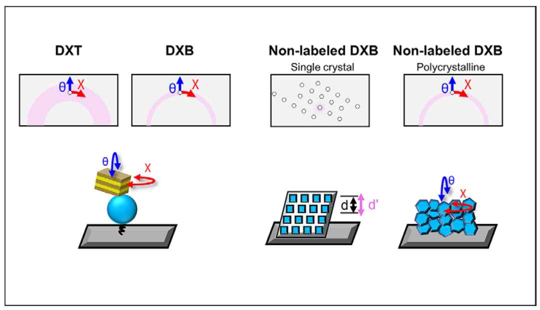
An ordinary laboratory X-ray could be used to characterize the molecular motions of a wide variety of biological molecules.



Directly measuring molecular motion could lead to a better understanding of protein behaviors, so techniques that can characterize a wide variety of substances would be useful. Arai et al. reported a method allowing scientists to directly measure molecular motion using a normal laboratory X-ray.

The authors used a method called diffracted X-ray blinking and found their technique could observe the movements of adsorbed proteins, protein crystals, and powder polymer in real time. The technique could characterize motions at a picometer length scale and a maximum time resolution of 50 milliseconds.

Surprisingly, they showed semicrystalline molecules moved more than adsorbed protein molecules, even with a more rigid structure. The team also observed the molecular motion of a crystallized antifreeze protein counterintuitively increased when the temperature was decreased.

“Such unusual motion increase at low temperature may be needed to bind an ice crystal,” said co-author Tatsuya Arai.

Diffracted X-ray blinking works by measuring the X-ray diffraction intensity of a material over time. To characterize molecular motions for noncrystalline substances, which do not yield a characteristic X-ray diffraction pattern, the authors first attached nanocrystals onto the biological molecules. Nanoparticle labels were not required for crystalline materials, since their structure already results in an X-ray diffraction pattern.

Arai said the authors plan to show the robustness of their technique by characterizing the molecular motions of even more biological materials, including proteins, polymers, and crystals. They also plan to study whether time resolution better than 50 milliseconds can be achieved – for instance, by measuring highly crystalline materials with strong diffraction patterns.

Source: “Laboratory diffracted x-ray blinking to monitor picometer motions of protein molecules and application to crystalline materials,” by Tatsuya Arai, Rena Inamasu, Hiroki Yamaguchi, Daisuke Sasaki, Ayana Sato-Tomita, Hiroshi Sekiguchi, Kazuhiro Mio, Sakae Tsuda, Masahiro Kuramochi, and Yuji C. Sasaki, *Structural Dynamics* (2021). The article can be accessed at https://doi.org/10.1063/4.0000112.