学術セミナー開催案内

日　　時	： 2024(令和 6)年 11 月 8 日(金)16:00～17:30
場　　所	： 京都大学桂キャンパス A クラスターA2 棟 A2-303 号室
講 演 者	： Prof. Dr. Peter Hamm (Department of Chemistry, University of Zurich)
タイトル	： Universal behavior in the nonequilibrium response of photoactive proteins

［ 概要 ］次頁

［ 言語 ］英語

［ 実施方法 ］対面

［ 参加費用 ］無料

［ 事前申し込み ］不要

［ 主催 ］工学研究科化学工学専攻ソフトマター工学研究室

［ お問い合わせ先 ］

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後援・協力：本セミナーは、京都大学大学院エネルギー科学研究科「国際先端エネルギー科学研究教育センター」との後援・協力の下で実施します。

Academic Seminar Announcement

Date and Time: Friday, November 8th, 2024, 16:00~17:30

Location: Kyoto University Katsura Campus, A Cluster, Building A2, Room A2-303

Speaker: Prof. Dr. Peter Hamm (Department of Chemistry, University of Zurich)

Title: Universal behavior in the nonequilibrium response of photoactive proteins

Abstract is on next page.

[Language] English

[Format] In-person

[Participation fee] Free

[Pre-registration] Not required

[Organizer] Department of Chemical Engineering, Graduate School of Engineering, Soft Matter Engineering Laboratory

[Contact]

Department of Chemical Engineering, Graduate School of Engineering (Soft Matter Engineering)

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This seminar is held with the support and cooperation of the International Advanced Energy Science Research and Education Center, Graduate School of Energy Science, Kyoto University.

UNIVERSAL BEHAVIOR IN THE NONEQUILIBRIUM RESPONSE OF PHOTOACTIVE PROTEINS

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Over the last decade, we have performed time-resolved experiments on a wide set of photoactive proteins, both artificially photo-switchable proteins (i.e., various PDZ domains [1-3] and MCL-1/peptide complexes [4]), as well as naturally photo-switchable proteins (i.e., cyanobacteriochrome Slr1393-g3 [5,6] and TePixJ [7]). All these proteins have in common that they are relatively small, compact and rigid single domain proteins, but in terms of details of their structure, the embedded chromophore and their biological function they are in part very different. In either case, the embedded chromophore photo-isomerizes after electronic excitation, which is an ultrafast (i.e., femtosecond to a few picosecond) photochemical process. The essentially instantaneous conformational change initially perturbs the structure of the immediate protein environment of the chromophore. This local perturbation then "propagates" over the entire protein in a cascade of events, which spread over a wide range timescales from picosecond to milliseconds. Our spectroscopic method to study this phenomenon is transient (pump-probe) IR spectroscopy, in which an ultrafast visible or near-UV laser pulse excites the chromophore, and a properly delayed IR pulse probes the response of the protein at a later time. Experimental concepts have been developed that allow us to cover all relevant timescales from picoseconds to potentially seconds in one and the same experimental run [8]. In addition, we extract "lifetime spectra" from the experimental data, based on exponential fitting together with a maximum entropy method in order to identify kinetic processes [5]. Interestingly and very universally for all studied proteins [1-7], the "dynamical content" reveals discrete timescales, which are distributed roughly equidistantly on a logarithmic time-axis with about 0.8 lifetime-peaks/decade. All-atom molecular dynamics simulations can reproduce the effect for a given protein in a semi-quantitative manner [2]. However, the universal character of the response calls for more generic models, and ideas in that direction will be discussed.

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