

第 1377 回生物科学セミナー

日時: 5 月 17 日(月) 16:00-17:30

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演題: Proteomes in 3D

Biological processes are regulated by molecular events, such as intermolecular interactions, chemical modification and conformational changes, which do not affect protein levels and therefore escape detection in classical proteomic screens. Reasoning that these events affect protein structure, we tested whether a global readout of protein structure could detect various types of functional alterations simultaneously and in situ. We tested this idea using limited proteolysis coupled to mass spectrometry (LiP-MS), which monitors structural changes in thousands of proteins within a complex, native-like environment. In bacteria adapting to different nutrient sources and in yeast responding to acute stress, the structural readout, visualized as structural barcodes, captured enzyme activity changes, allosteric regulation, phosphorylation, protein aggregation and protein complex formation, with the resolution of individual regulated functional sites such as binding and active sites. Comparison with prior knowledge, including flux, phosphoproteomics and metabolomics data, showed that LiP-MS detects many known functional alterations within well-studied pathways. It suggested novel metabolite-protein interactions and enabled identification of a fructose-1,6-bisphosphate-based regulatory mechanism of glucose uptake in *E. coli*. The structural readout dramatically increases the coverage of classical protein expression profiling, generates mechanistic hypotheses, better links holistic and reductionist approaches, and paves the way for a new in situ structural systems biology.

場所: 本セミナーはZoomで行います。

参加希望のかたは、UTAS シラバス詳細情報の「オンライン授業内容」で zoom の URL をご確認ください。
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