

数学与系统科学研究院

计算数学所学术报告

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报告题目:

**Integrative Biophysics of Estrogen
Receptor**

邀请人: 卢本卓 研究员

报告时间: **2017 年 6 月 28 日 (周三)**

上午 10:00-11:00

报告地点: **数学院南楼七层**

702 教室

Abstract:

Macromolecular interactions such as estrogen receptor (ER)—a key driver of breast cancer growth—provide the molecular underpinning for virtually every biological process. Despite decades of effort, however, structure determination of protein-protein complexes is still a daunting task for existing techniques due to size, stability, and/or complexity of protein complexes of interest. To advance the ability to characterize these complexes, we have established a multi-technique iSPOT platform by integrating scattering, footprinting, and computational docking, thereby determining a first median-resolution structure of the multi-domain ER complex. This iSPOT application has revealed a completely new protein fold of ER that is different from that of existing hormone receptors that provides a glimpse into the hidden cross-talk between the ER domains critical for the design of next drugs, while the data-driven iSPOT development provides a vital step for biomedical applications to many protein-protein complexes for years to come.

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