IQSE AMO QO Seminar Series

Tuesday, May 7th, 2024, 11:30AM ZOOM & IQSE seminar room (MPHY 578)

Pizza will be served for IQSE members at 11:00 am. The talk will start around 11:30 AM

Narangerel Altangerel

(IQSE TAMU)

Thermostable Raman Interaction Profiling (TRIP)

ABOUT THE SPEAKER: Dr. Altangerel received her PhD from the department of Physics and Astronomy at Texas A&M University in 2017 under Prof. Marlan Scully. She continues as a postdoctoral researcher with Dr. Marlan Scully at Institute of Quantum Science and Engineering and Dr. Philip Hemmer at Electrical and Computer Engineering Department, Texas A&M University. Her research has focused on advancing Raman spectroscopy for solving significant challenges in biological, medical, and agricultural fields. Her pioneering work includes detecting plant abiotic stresses, distinguishing drought tolerance in corn genotypes. Also, she developed techniques to detect bacteria and biomolecules in animal feces, predict animal diets, and identify animal species. Additionally, she devised methods for non-invasive detection of protein interactions and estimation of protein structures and binding affinities. Her contributions demonstrate the wide-ranging applications of Raman spectroscopy in diverse scientific domains.

EVENT DETAILS: Development of a simple, label-free screening technique capable of precisely and directly sensing interaction-in-solution over a size range from small molecules to large proteins such as antibodies could offer an important tool for researchers and pharmaceutical companies in the field of drug development. In this work, we present a thermostable Raman interaction profiling (TRIP) technique that facilitates low-concentration and low-dose screening of binding between protein and ligand in physiologically relevant conditions. TRIP was applied to eight protein-ligand systems, and produced reproducible high-resolution Raman measurements, which were analyzed by principal component analysis (PCA) [1]. TRIP was able to resolve time-dependent binding between 2,4-dinitrophenol (DNP) and transthyretin (TTR), and analyze biologically relevant SARS-CoV-2 spike-antibody interactions. Also, TRIP was successfully applied to estimate amino acid composition and secondary structure of unknown proteins by coupling with multiple linear regression (MLR) [2]. In order to validate the approach, the Raman spectra of seven known proteins of varying sizes by utilizing their amino acid frequencies and the Raman spectra of 20 amino acids. These constructed spectra exhibited a close resemblance to the measured Raman spectra. Specific vibrational modes tied to free amino and carboxyl termini of the amino acids disappeared as signals linked to secondary structures emerged under TRIP conditions. Furthermore, the technique is used (inversely) to successfully estimate amino acid compositions and secondary structures of unknown proteins across a range of sizes, achieving impressive accuracy ranging between 1.47% and 5.77% of root mean square errors (RSME). These results extend the uses for TRIP beyond interaction profiling, to probe amino acid composition and structure.

ZOOM information:

https://tamu.zoom.us/j/98156251523?pwd=QVdSdGxtL1UyY0g1L083SU5QR0QrUT09

Meeting ID: 981 5625 1523
Passcode: 297578

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