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臺灣大學應用力學研究所
演 講 公 告

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主 講 人：涂熊林助研究員
中央研究院化學研究所

講　　題： Integrated approaches for quantitative bioanalysis: streamlined proteomics analysis and bio-interface engineering

摘　　要： 如附件

主 持 人： 張建成教授

時　　間： 112年12月11日（星期一）下午2時20分開始

地　　點： 臺灣大學應用力學研究所國際會議廳

☆☆ 歡迎聽講，敬請張貼 ☆☆

Integrated approaches for quantitative bioanalysis: streamlined proteomics analysis and bio-interface engineering

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Abstract：

Quantitative analysis of biological systems and associated components greatly facilitates our understanding of modern biological science. In this presentation, I would describe our effort in integrating analytical chemistry, bioengineering tools, and material chemistry for constructing platforms to investigate biological samples with quantitative insight. Specifically, I would first describe a recent strategy called Chip-DIA for streamlined single-cell proteomic analysis. The assay is composed of a custom chip and data-independent acquisition mass spectrometry (DIA-MS). Its analytical and proteomic profiling performance, as well its recent extension for profiling phosphoproteomics from the nanoscale (1-1000 cells) would be presented and discussed. Next, I would share our efforts in constructing different bio-interfaces to probe neurite outgrowth in primary neurons, which revealed a surface viscosity-dependent neuritogenesis during early neuronal development in-vitro. Following this, I will discuss the synthesis and utilization of pico-newton DNA tension probes to investigate tension amplitude of cortical neurons upon receiving different mechanical inputs. Our results shed light on complex biophysical mechanisms governing cell-interface interactions, providing insights to develop advanced functional bio-interfaces.