In vivo genome editing for high resolution mapping of endogenous proteins in the mammalian brain

A scalable method to image endogenous proteins is essential for integrative understanding of a cell at the molecular level. Recently, we developed a simple and generalizable technique to image endogenous proteins with high accuracy in the brain (Cell, 2016). The technique, termed SLENDR, uses in vivo genome editing to insert a sequence encoding an epitope tag or a fluorescent protein to a gene of interest by CRISPR-Cas9-mediated homology-directed repair (HDR), enabling to image endogenous proteins with a tag. Single-cell, HDR-mediated genome editing was achieved by delivering the editing machinery to dividing neuronal progenitors through in utero electroporation. SLENDR allows us to rapidly determine the localization and dynamics of many endogenous proteins in various cell types, regions and ages in the brain, providing a powerful tool suitable for large-scale analyses on a broad spectrum of proteins.

Speaker:

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Date: Monday, July 25, 2016
Time: 12:00 - 13:00
Venue: 1F Auditorium, IIIS Building
University of Tsukuba

Light refreshments will be served

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