83rd WPI IIIS Seminar

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

It is essential to image endogenous proteins for the better understanding of cells at 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:

Dr. Jun Nishiyama

Neuronal Signal Transduction Group,

Max Planck Florida Institute for Neuroscience

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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