Speaker: Alexis Komor

Title:
Enabling the functional genomics field with base editors

Abstract:
Most genome-editing technologies introduce double-stranded DNA breaks (DSBs) at a target locus as the first step to gene correction. These methods are typically inefficient at point mutation correction and induce an abundance of random insertions and deletions (indels) at the target locus from the cellular response to DSBs. Here I will describe an alternate method to perform genome editing, base editing. Base editing works through the engineering of fusions of CRISPR/Cas9 and ssDNA modifying enzymes. The resulting fusions retain the ability to be programmed with a guide RNA and do not induce DSB but rather mediate the direct conversion of cytosine to uracil (thereby effecting a C•G to T•A substitution) or adenosine to inosine (effecting an A•T to G•C substitution). I will describe our efforts to characterize the mechanisms by which base editors work, and our work using base editors to elucidate the mechanisms of genetic diseases caused by single nucleotide variants.