CSCB Seminar Series

DUKE NUS GRADUATE MEDICAL SCHOOL SINGAPORE

Title:

"Gene-drug interaction screens in isogenic cell models."

Abstract:

With the complete molecular characterization of the major cancer types in sight, it is clear that only a minority of the cancer genes represent readily accessible drug targets. Furthermore, mechanistic biomarkers that predict response to targeted therapies remain scant. We employ large-scale chemical genetic screens in isogenic cells to systematically uncover gene-drug interactions in cancer. For instance, using a panel of engineered cell lines we have recently identified several known and novel breast cancer vulnerabilities and a mechanism of resistance to drugs inhibiting the PI3K/mTOR pathway. We have performed similar screens in an isogenic model that captures the genetic landscape of lung adenocarcinoma. In addition, I will present our efforts concerning the generation of a collection of haploid human knockout cells covering the majority of expressed genes that represents a powerful platform empowering haploid genetics in human cells.

Date:

11 Dec 2013 (Wednesday)

Time:

12:00 PM to 1:00 PM

Venue:

Conference Room 4D, Level 4
Duke-NUS Grad Med Sch
8 College Road, S169857

(Opposite Singapore General Hospital, Block 6/7)

Host:

Mathijs VOORHOEVE Ph.D.
Assistant Professor
Program in Cancer & Stem Cell Biology
Duke-NUS Graduate medical School Singapore

"No registration is required."
Any enquiry, pls contact:
Jamie Liew (Tel: 6516 6954)

Speaker & Biography:

Sebastian Nijman, Ph.D.
CeMM Principal Investigator
CeMM Research Center for Molecular Medicine
Vienna

Dr. Sebastian Nijman was studied medical biology at Utrecht University and specialized in Molecular Biology and Biochemistry in the labs of Hans Bos and Rene Medema. Sebastian also holds a Masters of Arts degree from the University of Maastricht (Science, Society and Technology Studies) and was involved in clinical research at a Contract Research Organization. In the lab of Rene Bernards at the Netherlands Cancer Institute, he performed his PhD work, focusing on functional genetic screens in cancer-relevant pathways. He performed the first RNAi screen in mammalian cells that led to the identification of the cylindromatosis tumor suppressor as a regulator of NF-kappaB signaling. This work has led to a rational therapeutic approach for treating cylindromatosis and is one of his major achievements so far. In 2006 he joined the lab of Todd Golub at The Broad Institute of Harvard and MIT, USA. There he developed novel genomic approaches to discover the functions of genes and identify new angles for cancer treatment. Since joining CeMM, Sebastian's research is mostly focused on the identification and understanding of cancer vulnerabilities using chemical genetic screens.