CSCB Seminar Series

DUKE NUS GRADUATE MEDICAL SCHOOL SINGAPORE

Title:

"Uses of functional genomics in cancer research."

Abstract:

Dr. René Bernards (Professor and Head, Division of Molecular Carcinogenesis, The Netherlands Cancer Institute, The Netherlands) will supplement his seminar at Frontiers in Cancer Singapore (Nov 7th; "Using Functional Genetics to Optimize the Treatment of Cancer") with a less formal talk at Duke-NUS. He will give an overview of what his lab has done with siRNA and shRNA in oncology, with more emphasis on the research aspects of their findings. Moreover, in this seminar, he hopes that there will be more active audience participation in discussions on using functional genomics in cancer research.

Date:

8 Nov 2013 (Friday)

Time:

12:00 NN to 1:00 PM

Venue:

Amphitheatre, Level 2
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:

René Bernards, Ph.D.
Professor
Group leader, Head of Division
Molecular Carcinogenesis
Netherlands Cancer Institute
Amsterdam, The Netherlands

Biography:

René Bernards received his Ph.D. in 1984 from the University of Leiden. He joined the Laboratory of Robert Weinberg at the Whitehead Institute in Cambridge, USA for his postdoctoral training. He worked with Stephen Friend on the isolation of the retinoblastoma tumor suppressor gene. He was appointed assistant professor at the Massachusetts General Hospital Cancer Center in 1988. In 1992 he joined the Netherlands Cancer Institute.

His scientific accomplishments include the development of MammaPrint, the first clinically-used gene expression profile for breast cancer. To bring this discovery to the clinic he co-founded "Agendia", a genomics-based diagnostic company that started offering the first microarray-based diagnostic test for the clinical management of breast cancer in 2004. His laboratory also developed the first shRNA vector for gene silencing in mammalian cells and used this vector to create a genome-scale library of shRNA vectors. His laboratory has used this vector collection to identify biomarkers of response to cancer drugs and to identify particularly powerful drug combinations for the treatment of cancer. Some of the combination therapies suggested by these genetic screens are currently showing promise in the clinic.