Thu., **24 October**, 4:00pm

Jukhyun Bio Auditorium(RM.121)

English

Functional Analyses of Genes from High-Throughput Screens

Speaker | Jaesang Kim

Affiliation | Ewha Womans University

Host | Prof. Chang-Duk Jun

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Education/Experience

1983-1987   A.B. in Chemistry, Harvard University, Cambridge, MA, USA
1989-1996   Ph.D. in Biology, Massachusetts Institute of Technology, Cambridge, MA, USA
1996-2002   Postdoctoral Fellow, Division of Biology, California Institute of Technology, USA
2002-2012   Assistant/Associate Professor, Division of Molecular Life Sciences, Ewha Womans University, Korea
2012-present   Professor, Division of Molecular Life Sciences, Ewha Womans University, Korea

🎙 Speaker
Prof. Jaesang Kim

Abstract

High-throughput data from various omics screens are providing large numbers of candidate genes involved in various cellular processes including carcinogenesis. Their candidacy however needs to be validated by a series of relevant experiments using in vitro and in vivo systems. Several such efforts carried out in our laboratory will be presented. The first will concern T-cell lymphoma. RHOA p.Gly17Val mutation and CTLA4-CD28 gene fusion are found in a large proportion of patients suffering from T-cell lymphoma. We have generated transgenic animal models whose phenotype indicate their usefulness as experimental models. The second will be non-small cell lung carcinoma which represents number 1 killer among all cancers. We have identified several oncogene and tumor suppressor candidates and carried out functional analyses. Vamp2-NRG1 represents a novel fusion oncogenes while TNNC1, best known for its role in muscle contraction, turns out to be a tumor suppressor of prognostic value.