Michael Smith Laboratories

Brian Ellis

Professor Emeritus

CONTACT

Office Phone Number 604-822-3451
Email Addresses bee@mslubc.ca
UBC Mailing Address 2185 East Mall Vancouver, British Columbia Canada V6T1Z4
Website  http://www.ellislab.mslubc.ca/

OFFICE

Building MSL
Room Number 235

LAB

Name Ellis Lab

PROFESSIONAL

Associated Departments Botany; Land and Food Systems (Plant Science)

Professional Profile Ph.D. (1969) University of British Columbia

Research Area Protein phosphorylation-dephosphorylation cycles create crucial molecular switches that help to control virtually all aspects of cell biology. We work with the major plant model, Arabidopsis thaliana, to explore the organization and regulation of protein kinase-based signaling pathways. These help regulate development within specialized tissues and organs (e.g. fibre cells, stomata, pollen); they also monitor and respond to environmental cues (e.g. pathogen attack, cold, high salt). MAP kinase (MAPK) cascades, in particular, form dynamic kinase signaling modules that integrate inputs from many sources: receptor kinases, hormones, reactive oxygen species (ROS) and calcium fluxes, and translate these into effective physiological responses. Any individual MAPK can help regulate a range of cellular processes, probably through the formation of function-specific multi-protein complexes. An important focus of our work is defining the factors that control the activity and functional specificity of MAPK modules. These include their subcellular locations, interacting partner proteins, and connections to other signaling pathways. We also serve as the lead laboratory for the CREATE (NSERC) post-graduate training project, “Working on Walls” (WoW). WoW (http://wow.mslubc.ca) provides an enriched scientific and professional training environment for graduate students and postdoctoral fellows specifically interested in
plant cell wall biology. The seven participating laboratories are located in the Michael Smith Laboratories, the Department of Botany, the Centre for High Throughput Biology and the Department of Wood Science at UBC, as well as the Department of Biology at the University of Victoria. Our research collaborator network extends around the world. For our MAPK studies as well as our WoW projects, we use a wide range of tools and approaches, including transcriptomics and proteomics, live cell imaging, cell-based reporter systems, site-directed mutagenesis, RNAi and microRNA gene silencing and the full suite of genetic, biochemical and molecular biology techniques.

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