BIOGRAPHICAL SKETCH

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NAME	POSITION TITLE
Lau, Ken	Assistant Professor of Cell and Developmental Biology
eRA COMMONS USER NAME ksklau	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
University of Toronto	PhD	2002-2008	Proteomics and Bioinformatics
Massachusetts General Hospital	Postdoctoral Fellowship	2008-2013	Systems Biology/ Intestinal Biology

A. Personal Statement.

I have a strong overall interest in studying how environmental information is integrated by heterogeneous cell populations to generate complex pathological behaviors *in vivo*. Under multivariate input conditions, what are the rules or logic that cells follow to arrive at behavioral decisions? How are decisions occurring at the single cell level translated into tissue level disease phenotypes? We wish to address these questions for diseases, for example, inflammatory bowel diseases (IBDs), that clearly involve complex repertoires of components and are consequently poorly understood and managed. We utilize cutting-edge experimental and computational tools to address the issues of multifactorial complexity arising *in vivo*. Through my Ph.D. training in the Bioinformatics and Proteomics program at the University of Toronto and my postdoctoral fellowship at MIT/MGH, I have obtained expertise in various mathematical and computational techniques for analyzing large datasets. In addition, I have designed and conducted the experiments (including animal experiments) to obtain the datasets used for building the mathematical models. The marriage of my mathematical and experimental backgrounds gives me the unique ability to oversee projects that directly involve mathematical modeling and experimentation. My research program will follow two broadly defined directions. First, we will use multiplex experimental techniques and computational modeling to decipher how individual cells in the mouse intestinal mucosa make response decisions as a function of their local environments. We surmise that in IBD where there is a dysregulated interaction between the epithelium and the underlying immune system, interpretation of an alternative environment through the cells' signaling networks result in pathological cell response decisions, which when propagated over many interacting cells, integrate into a macroscopic disease state. Secondly, to prove causality, we will reverse-engineer the healthy and disease state through primary *ex vivo* epithelial cultures with reconstituted immune components. From these *in vivo* and *ex vivo* studies, we will gain a much better understanding of the complexity in IBD, and will be able to rationally design interventions that manage complexity. In collaboration with clinicians at Vanderbilt, we will verify the principles of signaling in human patient samples, with the hope of translating our critical findings into multi-targeted therapies.

B. Positions and Honors.

Position and Employment

2002 - 2008	Graduate Student, Proteomics and Bioinformatics, Mount Sinai Hospital and University of Toronto
2008 - 2013	Postdoctoral Fellow, Pathology, Massachusetts General Hospital and Harvard Medical School
2008 - 2013	Postdoctoral Affiliate, Bioengineering, Massachusetts Institute of Technology
2013 - present	Assistant Professor, Cell and Developmental Biology, Vanderbilt University Medical Center

Honors

1999-2000	University of Toronto Scholarship
1999-2000	Chancellor Scholarship in Life Sciences
1999-1999	Elizabeth Kingston Scholarship

2002-2002 OSAP Millennium Scholar
2002-2006 Postgraduate Scholar, Natural Sciences and Engineering Research Council of Canada
2002-2002 Trinity College Graduation Award
2006-2007 Medical Research Fellow, Bank of Montreal
2006-2007 Baden-Havard Endowment Fund
2008-2008 Beckman-Coulter Prize
2009-2009 Biovision Fellow
2009-2012 Robert Black Fellow, Damon Runyon Cancer Research Foundation
2012-2013 MGH Toteston Award

C. Selected peer-reviewed publications.

1. Lau, KS, Mantas, M, Chass, GA, Ferretti, FH, Estrada M, Zamarbide G, Csizmadia, IG. . Ab initio and DFT conformational analysis of selected flavones: 5,7-dihydroxyflavone (chrysin) and 7,8-dihydroxyflavone. Can J Chem, 7(80), 845-855, 2002
2. Cheung, J, Estivill, X, Khaja, R, MacDonald, JR, Lau, K, Tsui, LC, Scherer, SW. Genome-wide detection of segmental duplications and potential assembly errors in the human genome sequence. Genome Biol, 4(4), R25, 2003
3. Lau, KS, Partridge, EA, Grigorian, A, Silvescu, CI, Reinhold, VN, Demetriou, M, Dennis, JW. Complex N-glycan number and degree of branching cooperate to regulate cell proliferation and differentiation. Cell, 129(1), 123-34, 2007
4. Mendelsohn, R, Cheung, P, Berger, L, Partridge, E, Lau, K, Datti, A, Pawling, J, Dennis, JW. Complex N-glycan and metabolic control in tumor cells. Cancer Res, 67(20), 9771-80, 2007
5. Beheshti Zavareh, R, Lau, KS, Hurren, R, Datti, A, Ashline, DJ, Gronda, M, Cheung, P, Simpson, CD, Liu, W, Wasylishen, AR, Boutros, PC, Shi, H, Vengopal, A, Jurisica, I, Penn, LZ, Reinhold, VN, Ezzat, S, Wrana, J, Rose, DR, Schachter, H, Dennis, JW, Schimmer, AD. Inhibition of the sodium/potassium ATPase impairs N-glycan expression and function. Cancer Res, 68(16), 6688-97, 2008
6. Katz, D, Ito, E, Lau, KS, Mocanu, JD, Bastianutto, C, Schimmer, AD, Liu, FF. Increased efficiency for performing colony formation assays in 96-well plates: novel applications to combination therapies and high-throughput screening. Biotechniques, 44(2), ix-xiv, 2008
7. Lau, KS, Dennis, JW. N-Glycans in cancer progression. Glycobiology, 18(10), 750-60, 2008
8. Lau, KS, Khan, S, Dennis, JW. Genome-scale identification of UDP-GlcNAc-dependent pathways. Proteomics, 8(16), 3294-302, 2008
9. Dennis, JW, Lau, KS, Demetriou, M, Nabi, IR. Adaptive regulation at the cell surface by N-glycosylation. Traffic, 10(11), 1569-78, 2009
10. Lau, KS, Haigis, KM. Non-redundancy within the RAS oncogene family: insights into mutational disparities in cancer. Mol Cells, 28(4), 315-20, 2009
11. Lau, KS, Juchheim, AM, Cavaliere, KR, Philips, SR, Lauffenburger, DA, Haigis, KM. In vivo systems analysis identifies spatial and temporal aspects of the modulation of TNF-a-induced apoptosis and proliferation by MAPKs. Sci Signal, 4(165), ra16, 2011
12. Mkhikian, H, Grigorian, A, Li, CF, Chen, HL, Newton, B, Zhou, RW, Beeton, C, Torossian, S, Tatarian, GG, Lee, SU, Lau, K, Walker, E, Siminovitch, KA, Chandy, KG, Yu, Z, Dennis, JW, Demetriou, M. Genetics and the environment converge to dysregulate N-glycosylation in multiple sclerosis. Nat Commun, 334, 2011
13. Lau, KS, Cortez-Retamozo, V, Philips, SR, Pittet, MJ, Lauffenburger, DA, Haigis, KM. Multi-scale in vivo systems analysis reveals the influence of immune cells on TNF-a-induced apoptosis in the intestinal epithelium. PLoS Biol, 10(9), e1001393, 2012
14. Lau, KS, Zhang, T, Kendall, KR, Lauffenburger, D, Gray, NS, Haigis, KM. BAY61-3606 affects the viability of colon cancer cells in a genotype-directed manner. PLoS One, 7(7), e41343, 2012
15. Lau, KS, Schrier, SB, Gierut, J, Lyons, J, Lauffenburger, DA, Haigis, KM. Network analysis of differential Ras isoform mutation effects on intestinal epithelial responses to TNF-a. Integr Biol (Camb), 5(11), 1355-65, 2013
16. Miraldi, ER, Sharfi, H, Friedline, RH, Johnson, H, Zhang, T, Lau, KS, Ko, HJ, Curran, TG, Haigis, KM, Yaffe, MB, Bonneau, R, Lauffenburger, DA, Kahn, BB, Kim, JK, Neel, BG, Saghatelian, A, White, FM. Molecular network analysis of phosphotyrosine and lipid metabolism in hepatic PTP1b deletion mice. Integr Biol (Camb), 5(7), 940-63, 2013