



**Post-Doctoral Position available in EXTRACELLULAR MATRIX and MOONLIGHTING PROTEASE DEGRADOMICS: IDENTIFICATION AND CHARACTERISATION OF NOVEL PROTEASE SUBSTRATES**

**OVERALL LAB, University of British Columbia, Vancouver BC, Canada.**

A postdoctoral position is available for a candidate to study novel substrates of proteases, in particular matrix metalloproteinases (MMPs). The OVERALL LAB has pioneered a number of cutting edge proteomics methods (degradomics: including **TAILS** (Nature Biotechnology, Nature Protocols), **C-TAILS** (Nature Methods, Nature Protocols), **PICS** (Nature Biotechnology), **TopFIND** database (Nature Methods)) for the analysis of protein termini and identification of protease substrates in healthy and diseased tissue (e.g. arthritis (Cell Reports), skin inflammation (Science Signaling), innate and acquired immunity (Nature Communications), and viral infection (Nature Medicine)). Moonlighting proteins that have canonical roles inside the cell that are secreted by non-conventional means are a priority. The candidate will elucidate the roles of these novel and unexpected substrates in cell regulation before and after proteolytic processing. Thus we will decipher how tissue pathologies, particularly inflammatory diseases, autoimmunity and immunodeficiencies, and cancer, are driven by proteases (e.g. MMPs, ADAMs, ADAMTS, cathepsins, viral proteases) and bioactive substrates that modulate signaling feedback loops with emphasis on connective tissues, the extracellular matrix and immune cells.

The candidate should have a practical background in protease biology, extracellular matrix biology, inflammation, and immunobiology. Experience in a variety of biological systems is an asset as the candidate will use biochemical methods, mammalian cell tissue culture and murine models to elucidate the roles of moonlighting proteins and the effects of proteolytic processing as well as determining whether cleavage creates new functions. Biological assays will include angiogenesis, chemotaxis, cell migration and invasion assays, proinflammatory cytokine production. Further characterization of the significance of proteolytic processing *in vivo* will be determined by developing selected reaction monitoring (SRM) assays and neoepitope antibodies to establish the prevalence of proteolytic processing in healthy and inflamed/diseased tissues using mass spectrometry, immunohistochemistry and by developing ELISA-type assays. It is anticipated that some of the identified proteoforms will be useful as biomarkers for disease diagnosis. A significant portion of the lab is dedicated to degradomics, utilizing and developing liquid chromatography tandem mass spectrometry techniques (LC-MS/MS). Thus there is the opportunity for the candidate to use proteomics to address the roles of moonlighting substrates and the applicant will be trained in this.

The lab is situated in the Centre for Blood Research (<http://cbr.ubc.ca/>) in the Life Sciences Centre (<http://lsi.ubc.ca/>) at the University of British Columbia in Vancouver.

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