Christopher Hughes

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Google Scholar Citations
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LinkedIn Profile

Relevant Skills

Research and Leadership Abilities

- Extensive experience with all aspects of the development and continuous operation of a mass spectrometry core facility, including: instrument acquisition, maintenance, repair, and optimization; protocol optimization and SOP development; day-to-day project management for a large and diverse customer base; construction of cost models and financial management; preparation of applications to pursue funding initiatives.
- Skilled in the application of proteomics, metabolomics, DNA/RNA sequencing, and other technologies (e.g. microscopy, flow cytometry, mass cytometry, molecular biology methods) towards the study of complex biological systems.
- Expertise in the use bioinformatic languages, such as R, Python, and C#, for the analysis of proteomics, DNA/RNA sequencing, and metabolomics data. Proficient with Adobe Illustrator for the creation of high quality figures and rich schematics.
- Extensive experience transitioning project ideas and preliminary findings into complete applications for granting agencies, such as CIHR, CFI, NSERC, CRS, and NIH.

Current Role

2018-present | **Staff Scientist and Mass Spectrometry Service Specialist**
BC Cancer

In this role with Dr. Poul Sorensen, my primary responsibilities include the independent conception, development, funding acquisition for, execution, and supervision of studies examining mechanisms of cancer cell adaptation mediated by modification of mRNA translation, with a particular emphasis on the RNA-binding protein YB-1. Studying the oncogenic properties of Ewing sarcoma with a specific focus on patterns in the expression of transcript and protein isoforms specific to this cancer type, with additional effort focused on the putative tumour suppressor DLG2.

Selected Publications

2021 Zhang, H., **Hughes, C.S.** *et al*, Proteomic screens for suppressors of anoikis identify IL1RAP as a promising surface target in Ewing sarcoma *Cancer Discovery.* PMID: 34021002

2019 **Hughes, C.S.**, Sorensen, P.H., Morin, G.B. A Standardized and Reproducible Proteomics Protocol for Bottom-up Quantitative Analysis of Protein Samples using SP3 and Mass Spectrometry *Methods in Mol. Biol.*. PMID: 30852816

2019 **Hughes, C.S.**, Moggridge, S., Mueller, T., Sorensen, P.H., Morin, G.B., Krijgsveld, J. Single-pot, Solid-phase-enhanced Sample Preparation for Proteomics Experiments *Nature Protocols.* PMID: 30464214

2019 Kovalchik, K.A., Colborne, S., Spencer, S., Sorensen, P.H., Chen, D.D.Y., Morin, G.B., **Hughes, C.S.**$^{\diamond}$, RawTools: Rapid and Dynamic Interrogration of Orbitrap Data Files for Mass Spectrometer System Management *J. Prot. Res.*. PMID: 30462513

2018 Moggridge, S., Sorensen, P.H., Morin, G.B., **Hughes, C.S.**$^{\diamond}$ Extending the Compatibility of the SP3 Paramagnetic Processing Approach for Proteomics *J. Prot. Res.*. PMID: 29565595

2018 **Hughes, C.S.**, Morin, G. Using Public Data for Comparative Proteome Analysis in Precision Medicine Studies *Proteomics.* PMID: 28887829

2017 **Hughes, C.S.**, Spicer, V., Krokhin, O.V., Morin, G.B., Investigating Acquisition Performance on the Orbitrap Fusion When Using Tandem MS/MS/MS Scanning with Isobaric Tags *J. Prot. Res.*. PMID: 28418257

2017 **Hughes, C.S.**, Zhu, C., Spicer, V., Krokhin, O.V., Morin, G. Evaluating the Characteristics of Reporter Ion Signal Acquired in the Orbitrap Analyzer for Isobaric Mass Tag Proteome Quantification Experiments *J. Prot. Res.*. PMID: 28418254

2016 **Hughes, C.S.**, McConechy, M., Cochrane, D., Nazeran, T., Karnezis, A., Huntsman, D., Morin, G. Biomarker Discovery from High Resolution Proteomic Analysis of Fixed Ovarian Tumor Tissue Samples. *Scientific Reports.* PMID: 27713570

2014 **Hughes, C.S.**, Foehr, S., Garfield, D., Furlong, E.E., Steinmetz, L.M., Krijgsveld, J. Ultrasensitive proteome analysis using paramagnetic bead technology. *Molecular Systems Biology.* PMID: 25358341

2012 **Hughes,C.S.** and Krijgsveld, J. Developments in quantitative mass spectrometry for the analysis of proteome dynamics. *Trends in Biotechnology.* PMID: 23107010

2012 **Hughes, C.S.** *et al.* Mass spectrometry-based proteomic analysis of the matrix microenvironment in pluripotent stem cell culture. *Mol. Cell. Prot.*. PMID: 23023296

$\diamond$ - denotes senior authorship.

Selected Education and Professional Experience

2014–2018 Group Leader, **Genome Sciences Centre, BC Cancer**

Managed the Mass Spectrometry Proteomics Platform. Involved the development, execution, analysis, and management of research projects utilizing mass spectrometry to study a range of experimental models. Developed and optimized protocols and SOPs for a wide variety of sample analysis types that cater to the facility user base. Optimized, maintained, and repaired hardware housed in the core facility. Managed administrative and financial aspects of the core facility. Prepared grant applications for funding to acquire new equipment and support research and other technical development projects.

2012–2014 Post-Doctoral Researcher, **European Molecular Biology Laboratory**

Performed integrative studies that utilized genomics, transcriptomics, and proteomics to study dynamic molecular systems.

Selected Grants and Awards

2022 Examining onco-fusion-driven expression of transcript and protein isoforms that underpin fitness relationships essential for Ewing sarcoma tumor formation. **Agency:** Sarcoma Foundation of America, **Role:** co-applicant

2021 Ewing sarcoma progression and spreading are controlled by selected protein production events that are regulated by modified forms of the YB-1 oncoprotein. **Agency:** MGI, **Role:** co-applicant

2016 Fixed tissue proteomics (FTP) applied to create a pragmatic clinical decision aid for endometrial cancer. **Agency:** CCSRI, **Role:** co-applicant

2016 Breast cancer classification and marker identification by comprehensive proteomic analysis. **Agency:** CBCF, **Role:** co-applicant

2016 High-resolution analysis of phenotypic fitness using genome-wide CRISPR editing coupled to quantitative mass spectrometry. **Agency:** BCPN, **Role:** co-applicant

Patents

2014 **Title:** Proteomic sample preparation using paramagnetic beads

Inventors: Hughes, C.S.*, Krijgsveld, J., Steinmetz, L.

Publication number: WO2015118152A1, US20170074869A1, CA2938907A1, EP3102612A1

Filing date: 2015-02-09

* - denotes majority inventor

Selected Presentations

Poster	CCRC 2019 **Title:** A subcellular atlas of translation machinery reveals novel roles for the RNA binding protein YB-1
Oral	Personalized Oncogenomics Clinical Research Session 2016 **Title:** Proteomics and Metabolomics in Personalized Oncogenomics
Oral	BCPN 2016 **Title:** High Resolution Proteomic Analysis of Ovarian FFPE Tumour Tissues using TMT-MS3 on an Orbitrap Fusion for Clinical Research
Poster	ASMS 2015 **Title:** Enhanced processing of FFPE tissue for clinical proteomics using SP3
Poster	ASMS 2014 **Title:** Single-tube sample preparation workflows for Ultra-sensitive Proteomics
Oral	Nordic Proteomics Meeting 2014 **Title:** Single-tube sample preparation workflows for Ultra-sensitive Proteomics
Poster	Proteostasis Discussion 2013 **Title:** Studying the dynamics of proteome homeostasis using Hyperplexed mass spectrometry

References

Additional references available upon request.

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Relationship: Previous supervisor

Dr. Gilles Lajoie
Western University, London, Canada
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Relationship: Ph.D. supervisor