

Christopher Hughes

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Nationality: Canadian

[Google Scholar Citations](#)

[GitHub](#)

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Relevant Skills

Research and Leadership Abilities

- Expertise in the operation, maintenance, and repair of HPLC systems from a variety of vendors, including troubleshooting a variety of issues stemming from the HPLC itself, or the hardware it operates in cooperation with.
- 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.

Current Role

2023-present	Manager, Biological Mass Spectrometry Core Dalhousie University
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In this role, I am tasked with all aspects of management of a core facility catering to a wide range of individuals researching a diverse set of topics. My responsibilities include study conception and design, instrument operation/maintenance/calibration/repair, funding acquisition, project management, facility management, training and knowledge dissemination, and personnel management.

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.**[◇], RawTools: Rapid and Dynamic Interrogation 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.**[◇] 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

◇ - denotes senior authorship.

Selected Education and Professional Experience

2018–2023	Staff Scientist and Mass Spectrometry Service Specialist, Sorensen lab, BC Cancer Primary responsibilities included the independent conception, development, funding acquisition for, execution, and supervision of studies examining mechanisms of cancer cell adaptation mediated by modification of mRNA translation.
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.
2007–2012	PhD in Biochemistry, Western University, Canada

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
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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