

Christopher Hughes

christopher.hughes@dal.ca

Nationality: Canadian

[Google Scholar Citations](#)

[GitHub](#)

6144 Willow Street
B3K 1M2 Halifax, Canada

[LinkedIn Profile](#)

Relevant Skills

Research and Leadership Abilities

- Experience working with a broad range of clinical samples, including tissues and fluids, to facilitate their examination for drug tracking, biomarker discovery, or broader biological analyses.
- Skilled in the application of proteomics, metabolomics, DNA/RNA sequencing, and other technologies (e.g. microscopy, flow cytometry, mass cytometry, other molecular biology methods such as qPCR, Western blotting) towards the study of complex biological systems.
- Extensive expertise with the operation, maintenance, and utilization of mass spectrometers towards their application in the study of a broad range of molecular 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.
- Experience transitioning project ideas and preliminary findings into complete applications for granting agencies, such as CIHR, CFI, NSERC, CRS, Alex's Lemonade Stand, and NIH.
- Skilled in the conception, development, management, and execution of small and large scale research projects comprising individuals or collaborative teams of researchers working towards completion of set aims.

Current Role

2023-present

Manager, Biological Mass Spectrometry Core

Dalhousie University

In this role, I am tasked with all aspects of management of a mass spectrometry 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

- 2024 Lizardo, M., **Hughes, C.S.** *et al*, Pharmacologic inhibition of eIF4A blocks NRF2 synthesis to prevent osteosarcoma metastasis *Clin. Cancer Research*. PMID: 39078310
- 2023 Zhang, H.F., Delaidelli, A., Javed, S., Turgu, B., Morrison, T., **Hughes, C.S.** *et al* A MYCN-independent mechanism mediating secretome reprogramming and metastasis in MYCN-amplified neuroblastoma *Science Advances*. PMID: 37611092
- 2023 Johnson, F.D., **Hughes, C.S.** *et al*, Tandem mass tag-based thermal proteome profiling for the discovery of drug-protein interactions in cancer cells *STAR Protocols*. PMID: 36856765
- 2023 Asleh, K., Negri, G.L., Spencer, S.E., Colborne, S., **Hughes, C.S.** *et al* Proteomic analysis of archival breast cancer clinical specimens identifies biological subtypes with distinct survival outcomes *Nat. Communications*. PMID: 35173148
- 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

◇ - denotes senior authorship.

Selected Grants and Awards

| | |
|------|---|
| 2024 | Implementing a pan-Canadian standardized mass spectrometry-based proteomics approach for the analysis of clinical cancer samples: validation using archived breast cancer specimens for biomarker discovery. Agency: Terry Fox Marathon of Hope, Role: co-applicant |
| 2024 | Investigating mechanistic roles of a novel onco-fusion driven transcript isoform in Ewing sarcoma. Agency: Alex's Lemonade Stand Innovation Fund, Role: co-applicant |
| 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 |

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 |

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 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 |