

LIA SERRANO

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EDUCATION

University of Wisconsin-Madison, Madison, WI
Doctor of Philosophy-PhD. Student, Chemistry

September 2020-Present

Northeastern University, Boston, MA
Bachelor of Science degree, Biochemistry
Minor in Psychology
Major GPA: 3.51/4.0, Overall GPA: 3.50/4.0
Latin Honors: *Cum Laude*

January 2015-May 2018

LABORATORY SKILLS

LC-MS/MS, cell lysis, immunoprecipitation, tryptic digestion, metabolite extraction, Immobilized Metal Affinity Chromatography (IMAC), protein concentration assays (Bradford, BCA), high-throughput and automation assay development for proteomics

WORK EXPERIENCE

University of Wisconsin-Madison, Madison, WI
Research Intern, Analytical Chemistry

February 2020-August 2020

- Assisted in multi-omic sample preparation for large-scale LC-MS quantitative experiments
- Drove early development of lipidomic LC-MS acquisition methods for enhanced structural definition
- Analyzed and presented mass spectrometry data in group meetings

Neon Therapeutics, Cambridge, MA
Research Associate, Proteomics

May 2018-November 2019

- Assisted production and analysis of HLA-I and HLA-II peptidomics data to inform a bioinformatic neoantigen predictor for a personalized cancer vaccine
- Adapted immunoprecipitation method to a plate-based format for high-throughput sample processing
- Developed Immobilized Metal Affinity Chromatography (IMAC) assay to identify HLA-phosphopeptides as potential therapeutic targets
- Analyzed and presented proteomics data to program/company-wide meetings

Acceleron Pharma, Cambridge, MA
Co-Op, Bioanalytical Development

July 2017-December 2017

- Developed a standardized immuno-affinity LC-MS/MS assay for measuring drug (human Fc Fusion proteins/monoclonal antibodies) concentrations in serum from multiple preclinical species
- Presented projects in monthly Bioanalytical Development and mass spectrometry group meetings
- Assisted optimization of Beckman Coulter automated liquid handler for high-throughput processing

OpGen, Inc., Woburn, MA
Co-Op, Research and Development

January 2016-September 2016

- Designed tolerance, stability, and optimization experiments to develop a Peptide Nucleic Acid Fluorescent *in situ* Hybridization (PNA-FISH) diagnostic assay for rapid detection of blood-borne pathogens
- Tested functionality of diagnostic kits using fluorescence microscopy

- Prepared and maintained bacterial and yeast cultures in blood, broth, and agar mediums

Northeastern University, Boston, MA

January 2017-May 2017

Biology II Teaching Assistant

- Administered two Biology II lab sections
- Wrote and delivered lectures for each lab, supervised the section, held weekly office hours
- Evaluated student performance through wet-lab participation, reports, and quizzes

INSTRUMENTATION

University of Wisconsin-Madison, Madison, WI

February- August 2020

Instrument: UltiMate 3000 HPLC coupled to Orbitrap Fusion Lumos mass spectrometer

Software: Thermo software (Xcalibur, Freestyle, Tune)

- Routinely operated, calibrated, and troubleshooted

Instrument: Vanquish Binary Pump coupled to a Q Exactive Orbitrap HF mass spectrometer

Software: Thermo software (Xcalibur, Freestyle, Tune, Compound Discoverer, TraceFinder)

- Routinely operated, calibrated, and troubleshooted

Neon Therapeutics, Cambridge, MA

May 2018-November 2019

Instrument: Easy nLC 1200 coupled to Orbitrap Fusion Lumos mass spectrometer

Software: Thermo software (Xcalibur, Freestyle, Tune)

- Designed DDA acquisition methods on Xcalibur
- Created database searches for different kinds of proteomic data (SILAC-labeled, PTM analysis) using Spectrum Mill
- Operated and calibrated instrument using Tune
- Operated and set-up High Field Asymmetric Waveform Ion Mobility (FAIMS) Pro Interface

Acceleron Pharma, Cambridge, MA

July-December 2017

Instrument: Shimadzu Nexera UHPLC system coupled to a Sciex TripleTOF6600 (QTOF) mass spectrometer

Software: AB SCIEX software (Analyst, PeakView, MultiQuant)

- Used Skyline (target list), PeakView (*in-silico* digest visualization), and a corroborating open-source proteomic database to optimize the selection of drug-specific peptide transitions in the context of matrix proteome
- Optimized acquisition methods in AnalystTF for sensitive and accurate quantitation of drug specific transitions
- Wrote quantitation methods in MultiQuant and evaluated response curves to inform assay optimization strategies

RELEVANT COURSES

Northeastern University

Protein Chemistry (graduate level), Advanced Genomics, Spectroscopy of Organic Compounds, Physical Chemistry, Biology Capstone

May Institute: Computation and Statistics for Mass Spectrometry and Proteomics

Beginner's Statistics in R, Targeted Proteomics in Skyline

POSTERS/PUBLICATIONS

Serrano LR, Abelin JG, Barthelme D, Oslund RC, Creech AL, Colson T, Goulding SP, Rothenberg DA, McGann CD, Ting YS, Nasrullah Y, Sridar J, Harjanto D, Malloy M, Arieta CM, Rooney MS. A novel HLA-peptide profiling workflow called MAPTAC (Mono-Allelic-Purification-with-Tagged-Allele-Constructs) leverages mass spectrometry to improve neoantigen prediction.

Mass Spectrometry in the Health and Life Sciences: Molecular and Cellular Proteomics, 2019, San Francisco, CA.

Abelin JG, Harjanto D, Malloy M, Suri P, Colson T, Goulding SP, Creech AL, **Serrano LR**, Nasir G, Nasrullah Y, McGann CD, Addona TA, Arieta CM, Rooney MS, et al. Defining HLA-II Ligand Processing and Binding Rules with Mass Spectrometry Enhances Cancer Epitope Prediction. *Immunity*. 2019; **51**(4):766-779

Overmyer, K.A., Shishkova, E., Miller, I.J., Balnis, J., Bernstein, M.N., PetersClarke, T.M., Meyer, J.G., Quan, Q., Muehlbauer, L.K., Trujillo, E.A., He, Y., Chopra, A., Chieng, H.C., Tiwari, A., Judson, M.A., Paulson, B., Brademan, D.R., Zhu, Y., **Serrano, L.R.**, Linke, V., Drake, L.A., Adam, A.P., Schwartz, B.S., Singer, H.A., Swanson, S., Mosher, D.F., Stewart, R., Coon, J.J., Jaitovich, A., Large-scale Multi-omic Analysis of COVID-19 Severity, *Cell Systems* (2020), doi: <https://doi.org/10.1016/j.cels.2020.10.003>.