

Michael E. Meadow, PhD

PhD Scientist | Translational Protein Biologist | MD Candidate
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Professional Summary

PhD scientist, physician-in-training, and translational protein biologist with 12 years of experience across quantitative proteomics, protein turnover, ubiquitin biology, and translational neuroscience. Developed Proteome Birthdating, a single-sample NeuCode SILAC LC-MS/MS platform for measuring proteome-wide turnover and molecular age. Research integrates discovery biology across more than 20 mammalian species, patient-derived disease models, and preclinical therapeutic research.

Education

MD Candidate — University of Rochester School of Medicine & Dentistry	<i>Expected 2027</i>
PhD, Cellular, Developmental & Molecular Biology — University of Rochester	<i>2025</i>
BS, Microbiology, Immunology & Molecular Genetics, summa cum laude — UCLA Honors College	<i>2018</i>

Core Expertise

Molecular & Cellular Biology — Ubiquitin-proteasome system; autophagy; proteostasis; mammalian primary-cell culture; and patient-derived iPSC/hESC differentiation.

Quantitative Proteomics — LC-MS/MS; NeuCode and SILAC metabolic labeling; PTM enrichment; multiplexed, targeted, and turnover proteomics; protein-turnover kinetics; and large-scale data analysis.

Translational Neuroscience — Rare neurogenetic diseases, common neurodegenerative disorders, and neuro-oncology; preclinical CNS cell therapy; and comparative disease and aging models.

Professional Experience

Doctoral Scientist (PhD) — University of Rochester	Rochester, NY
Vera Gorbunova & Sina Ghaemmaghani Labs	2021–2025

- Developed Proteome Birthdating, a single-sample LC-MS/MS method that measures global protein turnover and partitions proteins by molecular age. Showed that ubiquitination preferentially targets newly synthesized proteins; published in *Molecular & Cellular Proteomics* (2024) and *Bio-protocol* (2025).
- Directed comparative proteomics across more than 20 mammalian species and identified SIRT6 C-terminal phosphorylation associated with maximum lifespan; co-first author, *GeroScience* (2026).
- Applied quantitative proteomics to human Alzheimer's disease samples and an amyloidosis-prone rodent model, examining species-specific oxidative-damage responses in neurodegeneration.

Laboratory Assistant — UCLA	Los Angeles, CA
William E. Lowry Lab	2018–2019

- Generated glial-enriched progenitors from patient-derived iPSCs across five donor lines for a preclinical white-matter-stroke cell-therapy program; co-author, *Stem Cell Research* (2021).

Undergraduate Researcher — UCLA	Los Angeles, CA
S. Thomas Carmichael Lab	2016–2018

- Contributed to a hydrogel-delivered interneuron progenitor therapy for cortical stroke through preclinical efficacy studies, behavioral analysis, and histology.

Undergraduate Researcher — UCLA	Los Angeles, CA
James Wohlschlegel Lab	2015–2018

- Characterized the KCTD7 interactome, defining ubiquitin-proteasome-autophagy crosstalk underlying a neurodegenerative disorder; co-author, *Annals of Neurology* (2018).

Research Volunteer — Rutgers Robert Wood Johnson Medical School	New Brunswick, NJ
Kiran Madura Lab	2014–2015

- Investigated the molecular response of the ubiquitin-conjugating enzyme Ubc7 to protein damage in the endoplasmic reticulum.

Technical Skills

Software & Data Analysis — Proteome Discoverer, MaxQuant, Skyline, and FragPipe; Python, Mathematica, and R for data processing, analysis, and visualization; protein structure modeling and molecular docking.

Instrumentation & Proteomics Workflows — Orbitrap and Astral LC-MS/MS method development; NeuCode/SILAC labeling; fractionation; ubiquitin and phosphopeptide enrichment; and targeted and DIA acquisition.

Laboratory Techniques — Mammalian and primary-cell culture; iPSC/hESC differentiation; CRISPR editing; immunoprecipitation and co-immunoprecipitation; Western blotting; qPCR; and molecular cloning.

Clinical Experience & Leadership

Neuro-Oncology: Sustained clinical involvement under Nimish A. Mohile, MD, including clinic, multidisciplinary tumor board, and division research conferences.

Clinical Honors & Humanities: Letters of Achievement (top 10%) in Anatomy, Neurology, and Pharmacology; Medical Humanities Certificate Pathway candidate (2019–present).

Leadership: MSTP Admissions Committee (2021–2023); Human Structure & Function Tutor (2020–2021); Research Interest Group Vice President (2020–present); and UR Well Student Run Clinics (2019–present).

Awards & Honors

Awards: US HUPO Travel Award (2024); ABTA Medical Student Summer Fellowship (2021); AAN Medical Student Research Scholarship (2021); LANS Research Competition, Finalist (2018); Faculty Women's Club & Stout Memorial Scholarships (2015–2017); and Toshiba ExploraVision Competition, Honorable Mention (2014).

Posters: FASEB Ubiquitin & Ubiquitin-like Proteins (2024); US HUPO (2024); MD/PhD National Student Conference, Poster Prize (2024); UR Biology Retreat (2023–2026); UR Aging Day (2023–2026); CSHL Mechanisms of Aging (2022); URMG Genetics Day (2022); URMG MSRS (2019–2026); Northeast Physician-Scientist Student Symposium (2019); UCLA Stem Cell Symposium (2018); UCLA Neurology Science Day, 1st Place Undergraduate Poster (2018); MIMG Undergraduate Poster Symposium (2018); UCLA Undergraduate Research Day (2017–2018); and North Jersey Regional Science Fair, 2nd Place Poster Microbiology (2015).

Presentations: Invited Bio-protocol Webinar (2025); FASEB Ubiquitin & Ubiquitin-like Proteins (2024); US HUPO Lightning Talk (2024); URMG MSTP Retreat (2022–2023); and LANS Research Competition (2018).

Selected Publications

- **Meadow ME*, Gigas J*, et al.** Long-lived mammals contain more phosphorylation sites in the SIRT6 C-terminus that enhance PARP1 interaction and resistance to oxidative stress. *GeroScience*. 2026. *Co-first.
- Jain A, Mayeen N, **Meadow ME**, et al. Structural proteomics reveals that misfolded nascent proteins expose buried lysines for ubiquitination and rapid proteasomal degradation. *Cell Reports*. 2026;45(7):117620.
- *Abstract.* Lee YS, **Meadow ME**, et al. Proteomic characterization of methionine sulfoxide reductase (MSR)-deficient cells. *Journal of Biological Chemistry Supplement*. 2026;302(5).
- **Meadow ME, et al.** Proteome Birthdating: A single-sample approach for measuring global turnover dynamics and “protein age.” *Bio-protocol*. 2025;15(9):e5296.
- Martinez JC, et al. (including **Meadow ME**). cGAS-deficient mice display premature aging associated with derepression of LINE1 elements and inflammation. *Nature Aging*. 2026. doi:10.1038/s43587-026-01206-y.
- **Meadow ME, et al.** Proteome birthdating reveals age-selectivity of protein ubiquitination. *Molecular & Cellular Proteomics*. 2024;23(7):100791.
- McCabe M, et al. (including **Meadow ME**). Assessing the effectiveness of a primary-care-provider office-based intervention for increasing organ-donor registration rates in two New York State counties. *Progress in Transplantation*. 2022;32(4):292–299.
- Llorente IL, Hatanaka E, **Meadow ME**, et al. Reliable generation of glial-enriched progenitors from human fibroblast-derived iPSCs. *Stem Cell Research*. 2021;55:102458.
- Metz KA, et al. (including **Meadow ME**). KCTD7 deficiency defines a distinct neurodegenerative disorder with a conserved autophagy-lysosome defect. *Annals of Neurology*. 2018;84(5):766–780.