PATRICK TYLER GARRETT

contact@pgarrett.dev • pgarrett.dev • 0000-0002-8434-9693 • pgarrett-scripps

EDUCATION

Ph.D. Candidate in Bioinformatics 2021–Present

Scripps Research Skaggs Graduate School, La Jolla, CA

Expected: 2026 **Advisor:** John R. Yates III, Ph.D. **Focus:** Mass spectrometry–based proteomics **GPA:** 3.9

B.S. in Cognitive Science 2016–2020

University of California, San Diego, La Jolla, CA

June 2020

Specialization: Machine Learning and Neural Computation **Minor:** Computer Science **GPA:** Overall 3.6

EXPERIENCE

Graduate Researcher 2021–Present

Yates Laboratory, Scripps Research, La Jolla, CA

- Conduct doctoral research in mass spectrometry–based proteomics under John R. Yates III.
- Design Smart Acquisition Methods (SAMs) for Bruker timsTOF instruments, including hybrid DDA/PRM acquisition strategies driven by real-time database search.
- Built and maintained the open-source tacular-omics Python ecosystem (peptacular, spxtacular, pefftacular, paftacular, mzmlpy, tdfpy, psimodpy, unimodpy, uniprotptmpy).
- Provided cross-project computational support to Yates Lab and collaborators.

Research Technician 2019–2021

Yates Laboratory, Scripps Research, La Jolla, CA

- Developed a real-time search pipeline with Bruker Daltonics that enabled bidirectional communication between the timsTOF Pro PASEF API and the ProLuCID GPU search engine, supporting real-time decision-making during acquisition.
- Trained deep learning models for peptide property prediction (collisional cross-section, retention time, fragmentation) deployed inside the PaSER pipeline, including a mixture density network for peptide CCS distributions.
- Authored mass spectrometry data pre-processing tooling supporting downstream machine learning workflows across the lab.

Programmer 2019–2020

SPAWAR / NAVWAR, San Diego, CA

Clearance: Active Secret-level security clearance

- Built an automated network test environment using the Robot Framework, Python, and bash on a small development team within a classified lab environment.
- Owned scripting, bug triage, and system testing; contributed to network automation tooling and release processes.

AWARDS & HONORS

Grand Prize, Scripps Research Hackathon 2026

Scripps Research

PeerReviewAgents — a LangGraph agentic pipeline that simulates the full peer-review process, generating a decision letter with an accept/reject recommendation and requested revisions.

Edgington Endowed Fellowship 2022–2024

Skaggs Graduate School, Scripps Research

Three-year endowed graduate fellowship providing full tuition and stipend support, with the freedom to choose lab and research direction independent of grant funding.

PUBLICATIONS

Turner NP, Baboo S, **Garrett PT**, Diedrich JK, Bajo M, et al.
Rapid Histone Post-Translational Modification Analysis Using Alternative Proteases and Tandem Mass Tags.
Analytical Chemistry, 2026

Bassett PT, Nguyen B, Singh V, **Garrett PT**, Moresco JJ, et al.
Polymorphic IGLV6-57 AL amyloid fibrils and features of a shared folding pathway. PREPRINT
bioRxiv, 2025

Bamberger C, Jung T, **Garrett PT**, Yates JR
Correlative Analysis of Amino Acid Sites for Structure Elucidation with Covalent Protein Painting.
Journal of Proteome Research, 2025

Gomes FP, Durbin KR, Schauer KL, Nwachukwu J, Kobylski RR, **Garrett PT**, et al.
Native top-down proteomics enables discovery in endocrine-resistant breast cancer.
Nature Chemical Biology, 2025

Garrett PT, Turner NP, Nakorchevsky A, Pankow S, Yates JR
Mass spectrometry-based proteomics.
Elsevier (Book Chapter), 2025

Berndsen Z, Akhtar M, Thapa M, Vickers T, Schmitz A, **Garrett PT**, et al.
Repeat modules and N-linked glycans define structure and antigenicity of a critical enterotoxigenic E. coli adhesin.
PLoS Pathogens, 2024

McClatchy DB, **Garrett PT**, Jung T, Diedrich JK, Yates JR
Acid Cleavable Biotin-Alkyne Improves Sensitivity for Direct Detection of Biotin Labeled Peptides in Bioorthogonal Noncanonical Amino Acid Tagging Analysis.
Journal of Proteome Research, 2024

Baboo S, Diedrich J, Torres J, Copps J, Singh B, **Garrett PT**, et al.
Evolving spike-protein N-glycosylation in SARS-CoV-2 variants. PREPRINT
bioRxiv, 2023

Garrett PT
peptacular: a ProForma 2.1–compliant peptidoform manipulation library. SUBMITTED
Journal of Open Source Software

SOFTWARE

tacular-omics *(Maintainer)*
A permissively licensed Python ecosystem for computational proteomics, spanning peptidoform manipulation, spectral search, instrument I/O, and modification ontologies.

peptacular *(Author)*
Peptide sequence analysis built around ProForma 2.1 notation: mass calculation, fragment generation, and isotopic pattern prediction (first-author JOSS submission).

spxtacular *(Author)*
Mass spectrometry spectrum processing with a chainable Spectrum API: denoising, isotope deconvolution, neutral-mass conversion, fragment matching, and PSM scoring.

mzmlpy *(Author)*
Lightweight library for parsing mzML mass spectrometry data.

tdfpy *(Author)*
Parsing of Bruker timsTOF data (PRM, DDA, DIA) with 3D centroiding and noise filtering.

ExclusionMS *(Author)*
Web REST API for controlling inclusion/exclusion intervals in the PASEF API on the timsTOF Pro, backed by an interval-tree exclusion/inclusion/priority list.

SERVICE

Member 2025–Present
Proteomics Standards Initiative (PSI)
Contributed to ProForma 2.1, mzPaf, and PSI-MOD.

Reviewer
Journal of Open Source Software (JOSS)
Reviewed proteomics submissions.

SKILLS

Languages: Python (Polars, Numba CUDA, PyTorch, TensorFlow, Keras), Rust (PyO3)

Proteomics: DDA Search (Sage), DIA search (DIA-NN), Bruker timsTOF data (.d, .tdf, .paf), mzML, ProForma, PSI-MOD / Unimod / UniProt PTM ontologies, Quantitative analysis (LFQ and TMT)

Machine Learning: Deep learning for peptide property prediction (CCS, RT, MS2), Mixture density networks, GPU acceleration via Numba CUDA, Traditional ML (SKlearn, Xgboost)

TALKS

Transformers: Rise of the Attention-based network.
ASMS Bruker Workshop, 2021

Predicting Peptide Collisional Cross Sections with Transformer Networks
ASMS Bruker Breakfast Seminar, 2022

ExclusionMS: A Customizable & Real Time Exclusion List
US HUPO Student Lightning Talk, 2023

AI Usage In Science.
Scripps Seminar, 2026

POSTERS

Garrett PT, Park R, Yates JR
PepMPNN: CCS Prediction for any PTM
ASMS, 2021

Park R, **Garrett PT**, Marszałek W, Srikumar T, Brehmer S, Jung T, et al.
Application of TIMScore to De Novo Search Engine, DeepNovo in PaSER
ASMS, 2021

Park R, Brehmer S, Jung T, **Garrett PT**, Gnanasambandan V, Beauvais MA, et al.
Combining the Accurate Mass and Time Tag and Ion Mobility to Find Missing Peptides
US HUPO, 2021

Park R, **Garrett PT**, Brehmer S, Jung T, Gnanasambandan V, Beauvais MA, et al.
CCS-centric Protein Identification
US HUPO, 2021

Garrett PT, Park C, Park R, Jung T, Yates JR
FASTA-Suite: The Decoy Strategy Matters
Scripps Research Symposium, 2022

Garrett PT, Park R, Diedrich JK, Yates JR
PaSER Ex: Real Time Exclusion List
ASMS, 2023

Garrett PT, Jung T, Yates JR
Peptacular: Powering the Next Generation of Proteomics Web Apps
ASMS, San Diego, 2026

TEACHING & MENTORING

Research Mentor 2022–Present
Yates Laboratory, Scripps Research, La Jolla, CA

- Jeff Lane (undergraduate, Summer 2022) — benchmarked tree data structures for multidimensional storage and search of peptides by m/z, charge, ion mobility, and intensity (Arboretum).
- Daniel Lu (high-school student, 2024) — built a graphical user interface for the Sage proteomics search engine.
- Trevor Hernandez (high-school student, Summer 2025) — developed an XGBoost model predicting peptide charge-state likelihood across charge states 1–9.
- Daniel Lu (undergraduate, 2025) — built a Python-based PTM quantifier computing modification proportions across sites.