

PATRICK TYLER GARRETT

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Bioinformatics Ph.D. candidate in mass spectrometry-based proteomics, building open-source computational tools, real-time acquisition methods, and machine-learning models for next-generation proteomics.

EDUCATION

Ph.D. Candidate in Bioinformatics

2021–Present

Scripps Research Skaggs Graduate School, La Jolla, CA

Expected: Fall 2026 **Advisor:** John R. Yates III, Ph.D. **Focus:** Mass spectrometry-based proteomics

B.S. in Cognitive Science

2016–2020

University of California, San Diego, La Jolla, CA

Specialization: Machine Learning and Neural Computation **Minor:** Computer Science

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 (Summer Internship)

2019–2020

SPAWAR / NAVWAR, San Diego, CA

Clearance: Previously held 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

Garrett PT, Diedrich JK, Yates JR

dnoise: Fast, In-Place Denoising of Bruker timsTOF Data with an Ion-Mobility Streak Filter. SUBMITTED

bioRxiv / Journal of the American Society for Mass Spectrometry, 2026, doi:10.5281/zenodo.21959649

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, doi:10.1021/acs.analchem.6c01147

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.

Nature Communications, 2026, doi:10.1038/s41467-026-75958-x

Bamberger C, Jung T, Garrett PT, Yates JR

Correlative Analysis of Amino Acids Sites for Structure Elucidation with Covalent Protein Painting.

Journal of Proteome Research, 2025, doi:10.1021/acs.jproteome.5c00072

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, doi:10.1038/s41589-025-01866-8

Garrett PT, Turner NP, Nakorchevsky A, Pankow S, Yates JR

Mass spectrometry-based proteomics.

Reference Module in Life Sciences, 2025, doi:10.1016/b978-0-323-99507-8.00013-5

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, doi:10.1371/journal.ppat.1012241

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, doi:10.1021/acs.jproteome.4c00616

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, doi:10.1101/2023.05.08.539897

Garrett PT, Yates JR

Peptacular: A ProForma 2.1 compliant Python package for amino acid sequence analysis. SUBMITTED

Journal of Open Source Software, doi:10.5281/zenodo.21960384

Garrett PT, Yates JR

spxtacular: A chainable Python library for mass spectrum processing. SUBMITTED

Journal of Open Source Software, doi:10.5281/zenodo.21986851

SOFTWARE

tacular-omics

A permissively licensed Python ecosystem for computational proteomics, spanning peptidoform manipulation, spectral search, instrument I/O, and modification ontologies.

home.tacular.dev

Live portal hosting interactive proteomics web apps built on the tacular-omics ecosystem.

sage-plus

Experimental downstream Sage distribution for mass-spectrometry search workflows, MCP-based tooling, and active Rust development.

rustypaper

Structure-aware conversion of born-digital scientific PDFs to Markdown, Typst, and JSON using fast, CPU-only Rust tooling.

peptacular v3.2.0

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

doi:10.5281/zenodo.21960384

spxtacular 0.5.0

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

doi:10.5281/zenodo.21986851

spectrl 1.0.0

Compact, URL-safe interchange for sharing mass spectra in links, QR codes, notebooks, and publications.

doi:10.5281/zenodo.21986776

sequoia-boost 0.2.0

Pure Rust gradient-boosted decision trees with multiple construction algorithms, model serialization, and TreeSHAP support.

doi:10.5281/zenodo.21968436

paftacular v1.1.1

Parsing, serialization, and analysis of PSI mzPAF peak annotations.

doi:10.5281/zenodo.21960114

mzmlpy v0.6.0

Lightweight library for parsing mzML mass spectrometry data.

doi:10.5281/zenodo.21960080

dnoise v0.1.0

Structural-prior denoising of Bruker timsTOF .d files in a Rust command-line tool and library.

doi:10.5281/zenodo.21959649

tdfpy v3.0.0

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

doi:10.5281/zenodo.21959585

PeerReviewAgents v0.2.0

Multi-agent LLM peer-review framework simulating a specialist journal editorial board.

doi:10.5281/zenodo.21781896

tacular v1.1.0

Lookup library for core omics datatypes, controlled vocabularies, and post-translational modifications.

doi:10.5281/zenodo.21269547

SERVICE

Member

2025–Present

Proteomics Standards Initiative (PSI)

Contributed to ProForma 2.1, mzPaf, and PSI-MOD.

Reviewer

Journal of Proteome Research (JPR) and *Journal of Open Source Software (JOSS)*

Peer-reviewed proteomics manuscript and open-source software submissions.

SKILLS

Languages: Python (Polars, pandas, Numba, sklearn), Rust (PyO3, maturin, rayon)

Proteomics: DDA Search (Sage, ProLuCID), DIA Search (DIA-NN), Bruker timsTOF data (PRM, DDA, DIA), mzML, PSI Formats (ProForma, mzPaf, mzML, mzIdentML, mzTab), PTM ontologies (PSI-MOD, Unimod, UniProt PTM), Quantitative analysis (LFQ, TMT, SILAC, CPP)

Machine Learning: Deep learning (Keras, Transformers, RNN, CNN), Traditional ML (SKlearn, Xgboost), Fine-tuning, parameter search, and hyperparameter optimization

Other: Git, GitHub, GitHub Actions, CI/CD, Docker, Proxmox, Containers, Networking, Linux, HPC, Slurm, Claude code, Skills, MCP, LangGraph

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.