

# PATRICK TYLER GARRETT

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Bioinformatics Ph.D. candidate and scientific software engineer focused on mass spectrometry-based proteomics. I build high-performance, open-source Python — GPU-accelerated spectral search, Bruker timsTOF I/O, and ProForma-compliant peptidofom tooling — and train deep-learning models for peptide property prediction. Creator of the open-source taclar-omics ecosystem; co-author on 9 publications including *Nature Chemical Biology* and *Analytical Chemistry*.

## SKILLS

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**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)

## EXPERIENCE

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**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.

**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.

**Programmer** 2019–2020

*SPAWAR / NAVWAR, San Diego, CA*

- 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.

## SELECTED SOFTWARE

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**taclar-omics** — A permissively licensed Python ecosystem for computational proteomics, spanning peptidofom manipulation, spectral search, instrument I/O, and modification ontologies. *peptacular*, *spxtacular*, *mzmlpy*, *tdfpy*, *ExclusionMS*

## EDUCATION

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**Ph.D. Candidate in Bioinformatics** 2021–Present

*Scripps Research Skaggs Graduate School, La Jolla, CA*

**B.S. in Cognitive Science** 2016–2020

*University of California, San Diego, La Jolla, CA*

## SELECTED PUBLICATIONS

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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

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

**Garrett PT** peptacular: a ProForma 2.1-compliant peptidofom manipulation library. *Journal of Open Source Software*

*Full list of 9 publications available in CV.*

## AWARDS & HONORS

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Grand Prize, Scripps Research Hackathon— *Scripps Research* 2026

Edgington Endowed Fellowship— *Skaggs Graduate School, Scripps Research* 2022–2024