# Kevin P. Erazo Castillo

Computational Biologist/Chemist

*Bay Area, California*

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## Education

**University of Illinois at Urbana-Champaign** — *Champaign, IL*

MS in Computer Science - Data Science — *2022 - Present*

GPA: 4.0 / 4.0

**Stanford University** — *Stanford, CA*

PhD in Chemistry — *2015 - 2022*

GPA: 3.71 / 4.0

**Massachusetts Institute of Technology** — *Cambridge, MA*

B.S. in Chemistry and Biology — *2011 - 2015*

GPA: 4.6 / 5.0

## Experience

**Brightseed Bio** — *South San Francisco, CA*

Computational Biologist/Chemist — *2022 - Present*

- Led the design and development of (deep learning) transformer models for *de novo* annotation of small molecule metabolites from high-resolution mass spectra.
- Performed standard metabolomics analysis (from raw files to putative annotations) and ligand-based bioactivity prediction for multiple partnership programs.
- Initiated the computational biology journal club to discuss recent research developments and possible new directions for internal projects.

**Snyder Lab** — *Stanford, CA*

Graduate Research Assistant — *2019 - 2022*

- Applied DDA and DIA mass spectrometry techniques to profile the serum lipidome, proteome and metabolome of patients with (and without) Segmental Graft Dysfunction (SGD).
- Performed single/multi-omics analysis and integration with clinical and demographic data to identify differentially regulated pathways in SGD and predict liver rejection.
- Coordinated with clinical (UPenn) and research (Stanford) stakeholders to define project outcomes and managed the research agenda within Snyder Lab.

**Khosla Lab** — *Stanford, CA*

Graduate Research Assistant — *2016 - 2019*

- Characterized small molecule activators of 6-Deoxyerythronolide B Synthase (DEBS) turnover — their structure, function, binding, and possible mechanisms of action — to optimize *in vitro* antibiotic production.
- Investigated the structure and conformational changes of partial and hybrid DEBS constructs via X-ray crystallography and FRET strategies, respectively.

## Relevant Coursework

**University of Illinois at Urbana-Champaign**

Computer Science & Data Science

- CS 598: Deep Learning for Healthcare
- CS 416: Data Visualization
- CS 447: Natural Language Processing

**Stanford University**

Machine Learning & Statistical Modeling

- CS 229: Machine Learning
- STATS 200: Introduction to Statistical Inference
- CS 373: Statistical & Machine Learning Methods for Genomics
- STATS 315A: Modern Applied Statistics: Learning
- CS 273B: Deep Learning in Genomics and Biomedicine
- CS 161: Design and Analysis of Algorithms

## Publications

By Recency

- Shen, X. *et al*. Multi-omics microsampling for the profiling of lifestyle-associated changes in health. *Nature Biomedical Engineering* (2023).
- Kevin Paul Erazo Castillo, Michael Snyder, Carolyn R. Bertozzi, and Chaitan Khosla. *Multi-Omic Characterization of Segmental Graft Dysfunction in Liver Transplant Patients*. 2022. <https://purl.stanford.edu/fr977vj0087>.
- Sanchez-deAlcazar, D., Mejias, S. H., Erazo, K., Sot, B. & Cortajarena, A. L. Self-assembly of repeat proteins: Concepts and design of new interfaces. *Journal of Structural Biology* **201**, 118–129 (2018).
- Mejías, S. H. *et al*. Repeat protein scaffolds: Ordering photo- and electroactive molecules in solution and Solid State. *Chemical Science* **7**, 4842–4847 (2016).

## Skills

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|---|---|
| **Programming** | Python (primary), R |
| **Data Science** | NumPy, Pandas, Scikit-learn, SciPy, statsmodels \|\| Tydiverse, glmnet, Limma |
| **Deep Learning** | PyTorch, Keras, Tensorflow |
| **Cheminformatics** | RDKit, OpenBabel, AutoDock, PyMol |
| **Environments** | Mac, Linux, AWS, AWS-Sagemaker |
| **Biochemistry** | Plasmid design, heterelogous expression, assay development, protein crystallography, small molecule synthesis |
| **Languages** | English, Spanish |