CHRISTINE YIWEN YEH

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EDUCATION

MD/PhD Biomedical Informatics, Stanford University   2020 -

- *PhD Thesis Co-advisors: Sylvia Plevritis, Livnat Jerby*

MS Biomedical Informatics, Stanford University   2016 - 2017
BSH Molecular, Cellular, and Developmental Biology (Honors), Stanford University   2012 - 2016

ACTIVE RESEARCH PROJECTS

- Integrative spatiotemporal modeling of high grade serous ovarian carcinoma

- Characterizing the Interactome of B-cell lymphoma after CAR-T cell therapy using graph-based machine learning

- Generalized latent representation learning of spatio-molecular cell communication in biological tissues GitHub

PROFESSIONAL EXPERIENCE

Computational Biologist (Associate)   Jul 2017 - Aug 2020
D. E. Shaw Research   *New York, NY*

- Lead the computational biology arm of several proprietary drug discovery programs
- Helped develop a drug for advanced/metastatic solid tumors; currently in phase 1 clinical trials (NCT04252339)
- Discovered two early drug candidates for type II diabetes treatment
- Developed algorithms for novel computational biochemistry analyses
- Deconvolved the catalytic mechanism of a well-validated type II diabetes protein using molecular dynamics simulations and machine learning

Research Assistant   Jun 2014 - Jun 2017
Michael Snyder Lab and Sharon Pitteri Lab, Stanford School of Medicine   *Stanford, CA*

- Designed and oversaw interdisciplinary research collaborations between Snyder and Pitteri labs
- Employed integrated multi-omics to elucidate the molecular underpinnings of several biological phenomena in human health and disease, including: pregnancy, breast cancer, type II diabetes, and N-glycanase deficiency
- led international sample processing teams for the Human Personalized Omics Profiling project at the Taipei, Taiwan (2016) and Dublin, Ireland (2017) iterations of the Human Proteome Organization World Congress

Bioinformatics Research Intern   Jun 2016 - Sep 2016
Genentech   *South San Francisco, CA*

- Discovered the functional and biochemical functions of protein arginine methyltransferases in the context of various cancers and complex neurological disorders
- Built computational analysis infrastructure for mass-spectrometry data in an early drug discovery pipeline

AWARDS

Stanford Graduate Fellowship, Stanford Vice Provost of Graduate Education   2020 -

- *Multi-year full support for outstanding students pursuing a doctorate in science and engineering*

PhD Abstract Competition Finalist, Human Proteome Organization World Congress   2017

- *Top 8 graduate student abstracts chosen based on excellence*

AWARDS (CONT.)

Firestone Medal for Excellence in Research, Stanford Vice Provost of Undergraduate Education 2016
- *Awarded to top undergraduate honors theses in science and engineering at Stanford*

Stanford Award of Excellence, Stanford Alumni Association 2016
- *Awarded to top Stanford students in leadership and dedication to the university*

Conference Travel Award, Stanford Undergraduate Advising and Research 2016
- *Full travel award to present research at the American Society of Mass Spectrometry 2016 Annual Conference*

Canary Center Research Fellowship, Canary Center for Cancer Early Detection 2015
- *Fellowship to support research for biomarker discovery*

Major Grant for Honors Research, Stanford Undergraduate Advising and Research 2015
- *Award to support Undergraduate Honors theses*

Undergraduate Summer Research Fellowship, Stanford Bio-X, Interdisciplinary Biosciences Institute 2014
- *Award to support interdisciplinary summer research*

PUBLICATIONS

Yu, A; Li Y; Li, I; Ozawa, MG; **Yeh, CY**; Chiou, AE; Trope, WL; Taylor, J; Shrager, J; Plevritis, SK. Reconstructing co-dependent cellular crosstalk in lung adenocarcinoma using REMI **Science Advances** (2022)

Yeh, CY; Izaguirre, J; Greisman, J; Willmore, L; Maragakis, P; Shaw, DE. A conserved motif controls the kinetics of the Protein Tyrosine Phosphatase 1B catalytic cycle. ***Under Internal Review*** (2022)

Greisman, J*; Willmore, L*; **Yeh, CY***; Giordanetto, F; Shahamadtar, S; Nisonoff, H; Maragakis, P; Shaw, DE. Discovery and Validation of the binding poses of allosteric fragment hits to Protein Tyrosine Phosphatase 1B: from Molecular Dynamics to X-Ray Crystallography. ***Under Internal Review*** (2022) *Authors Contributed Equally

Piening, BD; Zhou, W.; Contrepois, K; Röst, H; Gu Urban, GJ; Mishra, T; Hanson, BM; Leopold, S; **Yeh, CY**; ... Pitteri, S; Sodergren, E; McLaughlin, TL; Weinstock, GM; Snyder, MP Integrative Personal Omics Profiles During Periods of Weight Gain and Loss. **Cell Systems** (2018)

Going, CC; Alexandrova, L; Lau, K; **Yeh, CY**; Feldman, D; Pitteri, SJ Vitamin D supplementation decreases serum 27-hydroxycholesterol in a pilot breast cancer trial. **Breast Cancer Research and Treatment** (2017)

Yeh, CY*; Adusumilli, R*; Kullolli, M; Mallick, P; John EM; Pitteri, SJ Assessing biological and technological variability in protein levels measured in pre-diagnostic plasma samples of women with breast cancer. **Biomarker Research** (2017) *Authors Contributed Equally

TEACHING

BIOMEDIN 217: Translational Bioinformatics, Graduate Teaching Assistant	2022
BIOC 205: Molecular Foundations of Medicine, Graduate Teaching Assistant	2021, 2022
BIO 118: Genetic Analysis of Biological Processes, Head Teaching Assistant	2017
Enrichment Program at APEX for Youth, Volunteer Saturday 4th Grade Teacher	2018-2020

CONFERENCE PRESENTATIONS

- The DFG motif controls WPD loop transitions in the catalytic mechanism of Protein Tyrosine Phosphatase 1B
  The Biophysical Society Annual Meeting, *Baltimore, MD* 2019

- Drug Discovery in 4D – Supercomputing fragment binding to Protein Tyrosine Phosphatase 1B
  Big Data in Precision Health, *Stanford, CA* 2018

- Uncovering the molecular underpinnings of NGLY1 disease through personalized proteomics and glycoproteomics profiling
  Human Proteome World Congress, *Dublin, Ireland* 2017

- Vitamin D supplementation decreases serum 27-hydroxycholesterol and expression of CYP27A1 in tumors of breast cancer patients
  Canary Symposium at Stanford, *Stanford, CA* 2017

- Integrating glycoproteomics in the comprehensive multi-omics profiling of obesity-mediated progression to type II diabetes
  Human Proteome World Congress, *Taipei, Taiwan* 2016

- Characterizing the interactome of human protein arginine methyltransferases with affinity purification mass spectrometry
  Genentech Summer Symposium, *South San Francisco, CA* 2016

- Integrating glycoproteomics in the comprehensive multi-omics profiling of obesity-mediated progression to type II diabetes
  American Society of Mass Spectrometry, *San Antonio, TX*

- Translating integrative personalized omics profiling in type II diabetes and other metabolic diseases
  Human Proteome World Congress, *Vancouver, Canada* 2015

LEADERSHIP AND OUTREACH

Pre-admissions Mentoring Program Director, Stanford Biomedical Informatics 2020 - Present

- launched peer-to-peer application mentoring program for prospective applicants who identify as underrepresented minorities in STEM
- trained graduate students in inclusive mentorship

COVID-19 Transition Coordinator, Pacific Free Clinic 2021 - 2022

- worked with executive team of students and faculty to transition the free clinic from telehealth to in-person medical services for an underresourced community in San Jose, CA

Chair, Women of D. E. Shaw Research 2017 - 2020

- managed all functions of the employee resource group
- spearheaded professional development, diversity, and inclusion initiatives

Executive Committee Member, Biomedical Computation at Stanford (BCATS) Conference 2016 - 2017

- designed the conference program for the 17th annual conference
- solicited internationalspeakers (leaders in the field of biocomputational research)
- organized 200+ attendees on conference day

LETTERS EARNED

Letter of Nomination for Outstanding Students for Overseas Scholarships (Rhodes, Gates etc.)
Anonymous Stanford Faculty 2015

Letter of Congratulations for Extraordinary High Achievement in Statistical Methods
Professor Ewart Thomas 2013