# Elly Poretsky, PhD

Computational Biologist
Postdoctoral Fellow

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## Summary

I'm a biologist and bioinformatician with expertise in plant immunity, comparative genomics and computational protein methods. I received my Ph.D. from UC San Diego where I characterized a maize anti-herbivory receptor, peptide hormones, and metabolomic biosynthetic pathways. In my current position as a SCINet post-doc fellow at USDA, I apply state-of-the-art methods in protein structure prediction, protein language models and molecular docking to improve protein function annotations. My work includes developing an ML model for protein phosphorylation prediction, and frameworks for protein-protein and protein-ligand interaction analyses. I strive for reproducible and open science, making my work accessible though GitHub, web-apps, and Docker containers.

## Education

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|---|---|---|
| University of California, San Diego | 2015-2021 | Ph.D. Biology |
| The Open University, Israel | 2010-2014 | B.S. Biology |

## Experience

**2023 –**  **Post-doctoral SCINet Fellow, GrainGenes Group**
US Department of Agriculture, Western Regional Research Center, Albany, CA
- Developed a ML model for phosphorylation prediction with protein language models
- Developed an analysis framework for predicted pan-interactome networks
- Studying enzyme-ligand interaction using molecular docking and dynamic simulation
- Apply LangChain with ChatGPT to automate GWAS result curation from PDFs

**2021 – 22**  **Post-doctoral Researcher, Schmelz Lab**
Biological Sciences, UC San Diego, La Jolla, CA
- Extracted and analyzed maize root terpenoid specialized metabolites
- Analyzed maize root microbiome data and conducted antimicrobial assays
- Comparative analysis of transcriptomic, metabolomic and GWAS data (>200 lines)

**2015 – 21**  **Ph.D. Student, Huffaker Lab**
Biological Sciences, UC San Diego, La Jolla, CA
- Characterized a GWAS candidate receptor for anti-herbivory in maize
- Characterized a family of maize peptide hormones and their CRISPR KO receptors
- Developed MutRank, an R Shiny gene coexpression analysis web-app
- Conducted a comparative genomic and GWAS analysis of maize enzyme clusters

## Skills

**Computing:** Python, R, Bash, SLURM, Docker, Snakemake, git, SQL
**Bioinformatics:**
    **Proteins:** Structure prediction (AlphaFold2, ESMfold, ColabFold), alignment (FoldSeek), protein language models (ProtT5, ESM), small molecule docking (DiffDock, DynamicBind)
    **Transcriptomic:** HISAT2, BWA, gene coexpression analysis, enrichment analysis
    **Genomic:** BLAST, Diamond, HMMER, InterProScan, phylogeny, synteny, variant calling
**Statistics:** Machine learning, GWAS, classical stats, linear and mixed models
**Biochemistry:** Protein extraction, western blotting, Co-IP, enzymatic bioassays
**Molecular Biology:** Cloning, DNA/RNA extraction, RT-qPCR, Illumina sequencing
**Analytical Chemistry:** Metabolite extraction, MS and FID data analysis, HPLC purification
**Data analysis apps:** Dash, Shiny, Jupyter Widgets, Custom LLM ChatBots

# Funding and Awards

2016-18     NIH Cellular and Molecular Genetics Training Grant
2016     Helmsley Scholarship for a Cold Spring Harbor Laboratory
2015-16     Graduate Assistance in Areas of National Need

# Presentations

2024 Harnessing the predicted maize pan-interactome for putative gene function prediction and prioritization of candidate genes for important traits. **SCINet Fellows Conference**, Agricultural Research Center, Beltsville, MD

2023 PhosBoost: Predicting Plant Protein Phosphorylation using Protein Language Models and Gradient Boosting Trees. **Annual UC Systemwide Bioengineering Symposium**, UC Berkeley, CA

2021 Uncovering the Genetic Basis of Maize Sensitivity to Herbivore-Associated Fatty-acid Amino-acid Conjugates. **Annual Maize Genetics Conference**, online

2019 Uncovering the Genetic Basis of Maize Sensitivity to Herbivore-Associated Fatty-acid Amino-acid Conjugates. **Departmental Plant Talks Seminar**, UC San Diego, CA

2018 Within spitting distance: Zeroing in on how plants recognize herbivore attack. **Annual CMG Research Colloquium**, UC San Diego, CA

# Publications

2024 **Poretsky E**\*, Cagirici HB\*, Andorf CM, Sen TZ. Harnessing the predicted maize pan-interactome for putative gene function prediction and prioritization of candidate genes for important traits. **G3: Genes, Genomes, Genetics**

2023 **Poretsky E**, Andorf CM, Sen TZ. PhosBoost: Improved phosphorylation prediction recall using gradient boosting and protein language models. **Plant Direct**

2023 Saldivar EV, Ding Y, **Poretsky E**, Bird S, Block AK, Huffaker A, Schmelz EA. Maize terpene synthase 8 (ZmTPS8) contributes to a complex blend of fungal-elicited antibiotics. **Plants**

2022 Poosapati S, **Poretsky E**, Dressano K, Ruiz M, Vazquez A, Sandoval E, Estrada-Cardenas A, Duggal S, Lim JH, Morris G, Szczepaniec A, Walse SS, Ni X, Schmelz EA, Huffaker A. A sorghum genome-wide association study (GWAS) identifies a WRKY transcription factor as a candidate gene underlying sugarcane aphid (*Melanaphis sacchari*) resistance. **Planta**

2022 Murphy KM\*, **Poretsky E**\*, Liu H, Micic N, Nyhuis A, Bohlmann J, Schmelz EA, Zerbe P, Huffaker A, Bjarnholt N. Shielding the oil reserves: the scutellum as a source of chemical defenses. **Plant Physiology**

2021 **Poretsky E**, Ruiz M, Ahmadian N, Steinbrenner AD, Dressano K, Schmelz EA, Huffaker A. Comparative analyses of responses to exogenous and endogenous antiherbivore elicitors enable a forward genetics approach to identify maize gene candidates mediating sensitivity to herbivore-associated molecular patterns. **The Plant Journal**

2020 **Poretsky E**, Dressano K, Weckwerth P, Ruiz M, Char SN, Shi D, Abagyan R, Yang B, Huffaker A. Differential activities of maize plant elicitor peptides as mediators of immune signaling and herbivore resistance. **The Plant Journal**

2020 **Poretsky E**, Huffaker A. MutRank: an R shiny web-application for exploratory targeted mutual rank-based coexpression analyses integrated with user-provided supporting information. **PeerJ**.

2020 Ding Y, Weckwerth PR, **Poretsky E**, Murphy KM, Sims J, Saldivar E, Christensen SA, Char SN, Yang B, Tong AD, Shen Z. Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity. **Nature Plants**

2020 Dressano K, Weckwerth PR, **Poretsky E**, Takahashi Y, Villarreal C, Shen Z, Schroeder JI, Briggs SP, Huffaker A. Dynamic regulation of Pep-induced immunity through post-translational control of defence transcript splicing. **Nature plants**

2019    Ding Y, Murphy KM, **Poretsky E**, Mafu S, Yang B, Char SN, Christensen SA, Saldivar E, Wu M, Wang Q, Ji L. Multiple genes recruited from hormone pathways partition maize diterpenoid defences. **Nature Plants**

2019    Fong SH, Carlin DE, Ozturk K, Ideker T, … **Poretsky E**, Qin Y, Rideout D and Zhou J. Strategies for Network GWAS Evaluated Using Classroom Crowd Science. **Cell Systems**

2015    Brandt B, Munemasa S, Wang C, Nguyen D, Yong T, Yang PG, **Poretsky E**, Belknap TF, Waadt R, Alemán F, Schroeder JI. Calcium specificity signaling mechanisms in abscisic acid signal transduction in Arabidopsis guard cells. **Elife**

# Teaching and Mentorship

| Year | Description |
|------|-------------|
| 2023 | Protein Function and Phenotype Prediction (2-day workshop, USDA) |
| 2022 | Summer Training Academy for Research Success (STARS) program, UC San Diego |
| 2021-22 | Research Opportunity and Orientation for Transfer Students program, UC San Diego |
| 2021-22 | Mentored one Master's student, UC San Diego |
| 2019 | Instructional Assistant. BILD1 - The Cell, UC San Diego |
| 2018 | Summer Training Academy for Research Success (STARS) program, UC San Diego |
| 2018 | Instructional Assistant. BILD2 - Multicellular Life, UC San Diego |
| 2017 | Instructional Assistant. BIMM101 - Recombinant DNA Techniques, UC San Diego |
| 2016-22 | Mentored five summer high school students, UC San Diego |
| 2016-17 | Mentored two summer high school students, UC San Diego |