
ALEXANDER HOWARD

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SUMMARY

I am a Ph.D. candidate at the University of California, Davis with seven years of experience designing and executing molecular and bioinformatic experiments across multiple model organisms. I am driven by my passion for innovation in biology and want to apply my interdisciplinary research background to improving human wellness through bioinformatics, machine learning, and molecular biology.

EDUCATION

2022 – 2027

**PhD in Biochemistry, Molecular, Cellular & Developmental Biology
with a Designated Emphasis in Biotechnology (to be awarded June 2027)**

Institution - University of California, Davis

Dissertation - “Utilizing Bioinformatics, Directed Evolution, and Machine Learning to Engineer Expanded Disease Resistance against *Magnaporthe oryzae* in *Oryza sativa*”

Dissertation Advisor - Dr. Pamela Ronald

D.E.B. Advisor - Dr. Denneal Jamison-McClung

2018 – 2022

BS in Biotechnology with a minor in statistics

Institution - University of Nevada, Reno

Advisors - Dr. Grant Cramer and Dr. Jeff Harper

PROFESSIONAL SKILLS

COURSES/CERTIFICATIONS

2024 - “Hands-on Biotic Stress Resistance Evaluation” at the

International Rice Research Institute in Los Baños, Philippines

2023 - UC Davis DataLab Bioinformatics and AI Collaboratory Workshop

RESEARCH

Cloning and genetics - DNA extraction/purification, restriction enzyme cloning, Gibson assembly, Golden Gate assembly, PCR, qPCR, RNA-seq

Protein engineering - Protein purification, SDS-PAGE, yeast surface display, yeast two-hybrid, directed evolution, fluorescence-activated cell sorting, fluorescent microscopy

Plant research - *A. thaliana*, *N. benthamiana*, *O. sativa*, *V. vinifera*, agroinfiltration, disease/pest and drought stress assays, field sample collection and harvesting

DATA ANALYSIS

Coding - R, Python, Unix, Conda

Bioinformatics - Bulk/single-cell RNA-seq analysis, reference-based genome assembly, variant calling, sequence alignment, phylogenetic analysis, sequence/structure homology searches, protein structure modeling

Modeling/machine learning - Protein language modeling (ESM-2), LLM fine-tuning and transfer learning, HuggingFace, scikitlearn, AlphaFold2/3

	Data management/analysis - High-performance computing, custom database creation and maintenance, QA/QC, data visualization, statistical analysis
LAB/PROJECT MANAGEMENT	<p>Laboratory conduct - SOP development, biosafety/sterile technique, regulated materials handling and disposal</p> <p>Laboratory management - Inventory management, sample/strain maintenance, greenhouse maintenance, lab member training, regulatory permitting</p> <p>Team coordination - Google Workspace, Slack, Zoom, Microsoft Teams</p>
SCIENTIFIC COMMUNICATION	<p>Technical writing - Effective manuscript and grant writing</p> <p>Data presentation - Clear and confident data visualization, posters, PowerPoints, public speaking, and communication with experts and laypeople</p>
<u>RESEARCH EXPERIENCE</u>	
2023 – Current	<p>Graduate Student Researcher, University of California - Davis Laboratory of Dr. Pamela Ronald Project - “Utilizing Bioinformatics, Directed Evolution, and Machine Learning to Engineer Expanded Disease Resistance against <i>Magnaporthe oryzae</i> in <i>Oryza sativa</i>” Lab management – I coordinated lab technicians to help maintain research facilities and materials, developed optimized SOPs, trained researchers/technicians on SOPs, and lead grant writing related to the research project. Research - Pik-1 is an immune receptor in rice that protects against infection by blast fungus. Unfortunately, some blast strains can escape detection by all characterized Pik-1 receptor variants, leaving rice vulnerable to infection. I used directed evolution to screen a library of Pik-1 variants for strong binding against these escaping blast strains. I then fine-tuned a protein language model on this data to predict the recognition properties of Pik-1 variants of interest. Using reference-based genome assembly and variant calling, I identified unique variants of Pik-1 across thousands of rice genomes. My fine-tuned machine learning models predicted that one variant, SHZ-2, had broader pathogen recognition than any other Pik-1 variant currently used by rice breeders. I have been using fluorescent microscopy, agroinfiltration, and blast inoculations to verify that this SHZ-2 variant is functional and capable of providing novel blast recognition properties. Overall, my goal with this research is to identify a novel Pik-1 variant that can protect against fungal pathogen variants of concern and can be used in rice breeding programs to enhance crop disease resistance.</p>
2021 – 2022	<p>Undergraduate Research Scientist, University of Nevada - Reno Laboratory of Dr. Jeff Harper Project - “Structural prediction and analysis of CDPKs in <i>A. thaliana</i> pollen to identify sources of differential substrate specificity”</p>

Research - Calcium-dependent protein kinases (CDPKs) are an important component of cellular signaling in pollen for structure formation and fertility. Several homologous CDPKs are active in pollen, and each show unique substrate specificities. I was tasked with experimentally modeling the structure of two CDPKs – one with high substrate promiscuity and another with highly substrate selectivity. Using sequence homology and protein modeling tools, I identified key differing residues with the highest potential impact on substrate specificity. These target residues were used by the lab to explore how modifying or swapping these residues may impact CDPK substrate specificity and, in extension, their signaling in pollen.

2018 – 2021

Undergraduate Research Scientist, University of Nevada - Reno

Laboratory of Dr. Grant Cramer

Project - “Analysis of differential 3’UTR splicing in *V. vinifera* varieties under drought stress conditions”

Lab management – During my time in the lab I independently trained three other undergraduate students on how to code in R, apply the RNA-seq pipeline, and run statistical analyses on their data.

Research skills - mRNA transcripts are post-transcriptionally regulated via the 3' untranslated region (3'UTR) to tune transcript longevity, subcellular localization, and rate of translation. I utilized RNA-sequencing and a specialized 3'UTR-calling software to explore the differential 3'UTR splicing that occurs in grapevine tissue under drought stress. I found that drought tolerant varieties of grapevine consistently used shorter, less-regulated 3'UTRs under drought conditions while drought susceptible varieties used longer, more-regulated 3'UTRs when under drought. These results indicated that 3'UTR splicing may play a role in how grapevines respond to droughts and could be a strategy for improving crop resilience against various environmental stressors.

HONORS, AWARDS AND FELLOWSHIPS

2025

Jastro-Shields Award

Stipend scholarship awarded to outstanding graduate students in recognition of their potential to carry out research projects related to the mission of the College of Agricultural and Environmental Sciences.

Keystone Symposia “Future of Science” Award

Travel funding award offered to select Keystone conference attendees showcasing groundbreaking research in their field.

2024

Henry A. Jastro Award

Research scholarship awarded to excellent graduate students conducting research in the College of Agricultural and Environmental Sciences.

SCIENTIFIC COMMUNICATION

PUBLICATIONS/PRE-PRINTS

Integration of crop modeling and sensing into molecular breeding for nutritional quality and stress tolerance.

Jonathan Berlingeri, Abelina Fuentes, Earl Ranario, Heesup Yun, Ellen Y Rim, Oscar Garrett, **Alexander Howard**, Mary-Francis LaPorte, Sassoum Lo, Duke Pauli, Jenna Hershberger, Mason Earles, Allen Van Deynze, Edward Charles Brummer, Richard Michelmore, Christopher Y. S. Wong, Troy S. Magney, Pamela C. Ronald, Daniel E. Runcie, Brian N. Bailey, Christine H. Diepenbrock. Theoretical and Applied Genetics. August 8, 2025.

Combining Directed Evolution with Machine Learning Enables Accurate Genotype-to-Phenotype Predictions.

Alexander J. Howard, Ellen Y. Rim, Oscar D. Garrett, Yejin Shim, James H. Notwell, Pamela C. Ronald. Under review. January 29, 2025.

Directed evolution of a plant immune receptor for broad spectrum recognition of pathogen effectors.

Ellen Y. Rim, Oscar D. Garrett*, **Alexander J. Howard***, Yejin Shim, Yuanyuan Li, Jonathan E. Van Dyke, Ryan C. Packer, Nguyen Ho, Rashmi S. Jain, Valley J. Stewart, Savithramma P. Dinesh-Kumar, James H. Notwell, Pamela C. Ronald. Under review. October 01, 2024. (* = Authors contributed equally to the work)

PRESENTATIONS

Directed evolution and machine learning identifies rice immune receptor variants with enhanced recognition of a key pathogen ligand.
Genetic Engineering for a Sustainable Future, Keystone Symposia.
January 21, 2025

BLOGS

How Biotechnology is Reshaping Our Plates.

Oscar Garrett, Janessa Destremps, **Alexander Howard**, Rachel Foster. ScienceSays Blog. April 21, 2025.

COMMUNITY SERVICE

2024- 2026

Senior leadership officer at Science Says

<https://davissciencesays.ucdavis.edu/>

Wrote and recorded science content for social media outreach campaigns and ran public-facing events geared towards students, children, and lay-people for the purpose of demystifying the scientific process and combatting misinformation related to scientific research.

HOBBIES AND INTERESTS

OUTDOOR ACTIVITIES

Hiking and backpacking on trails at state and national parks
Growing vegetables and herbs in my home garden

ARTS & CRAFTS

Playing classical pieces on the piano
Sewing/altering clothing for myself and my friends
Restoring furniture around the house

FOOD CULTURE

Cooking new recipes from inherited cookbooks
Preserving garden-grown produce by canning and pickling
Visiting local bakeries and breweries when traveling