

Emma Pearce

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EDUCATION

MS in Biology, Focus in Bioinformatics & Genomics Anticipated Dec 2026
University of Oregon, Eugene, OR

BS in Biochemistry and Molecular Biology, Minor in Chemistry June 2022
Oregon State University, Corvallis, OR

SKILLS

Programming Languages: Python, R, Bash, C++

Wet lab: DNA/RNA purification and quantification, PCR, NGS library prep

Software/Tools: Git/GitHub, Slurm, NumPy, conda/mamba, Matplotlib, BLAST, Tidyverse, Tidymodels, DESeq2, STAR, ggplot2

RESEARCH EXPERIENCE

Graduate Student Researcher Oct 2025 – Current
KCGIP, University of Oregon in collaboration with InVivo Biosystems, Eugene, OR

Pipeline development for evaluation of CRISPR-Cas9 editing efficacy in zebrafish disease models, enabling precise and reproducible quantification of gene-editing outcomes.

- Accelerated company transition to next-generation sequencing, collaborated in a 3-member team to design and implement an NGS pipeline using Snakemake, Docker, R, and bash, that replaced Sanger sequencing validation for CRISPR mutation analysis.
- Increased accuracy and reproducibility of gene knockout evaluation, creating a scalable analysis tool integrated into existing workflows, to quantify gene knockout percentage, insertion/deletion frequencies, and editing efficiency with the tool AmpliCan in R.
- Enhanced cross-team data communication by designing a user-friendly website with React that presents CRISPR mutation statistics and visual summaries for research and industry stakeholders.

Research Associate 2 (Zinter Lab) Sep 2022 – June 2025
Pediatrics, UC San Francisco, San Francisco, CA

Cross-disciplinary study on pediatric lung disease following bone marrow transplants, showing that bronchial alveolar lavage (BAL) transcriptomics outperformed blood gene expression profiles in capturing lung-specific pathology.

- Demonstrated the clinical value of BAL sampling by showing that gene expression profiles from BAL, but not corresponding blood samples, captured lung-specific disease signatures in 210 pediatric patients, based on PCA, differential gene expression, and pathway analysis.
- Developed ML models that showed single-sample predictors lacked sufficient predictive ability (AUC < 0.65) of survival in pediatric lung disease patients using genomic data, imputed cell fractions, and clinical metadata.
- Established the lab's first standardized pipeline for bulk RNA-seq analysis in R, enabling reproducible and scalable workflows across multiple projects by integrating quality control, normalization, filtering, clinical metadata, and downstream statistical analyses.
- Facilitated cross-disciplinary understanding and shaped future analytical approaches by presenting research findings semiannually to interdisciplinary teams of clinicians, researchers, and data scientists through lab meetings and formal presentations.

Undergraduate Research Assistant (Chang Lab)

Oct 2019 – June 2022

Botany and Plant Pathology, Oregon State University, Corvallis, OR

Statistical and genomic analyses for common potato disease (scab), focusing on plasmid inheritance, pathogenicity, and horizontal gene transfer in *Streptomyces*.

- Investigated bacterial pathogenicity by sequencing and analyzing 166 strains of *Streptomyces* and identifying virulence islands and gene homologs across genomes.
- Provided evidence that control measures for common potato scab have curtailed pathogen dispersal by determining the inheritance of pathogenicity genes and mobile genetic elements.
- Characterized the evolutionary relationships of *Streptomyces* and related bacteria through phylogenetic analysis of genomic and plasmid data across 45 species, revealing clade-specific distributions of pathogenicity traits.
- Identified horizontal gene transfer events in *Streptomyces* evolution by analyzing phylogenetic incongruence across 100+ genes, plasmids, and genomic islands relative to species trees, revealing historical genomic mobility shaped pathogenicity.

PUBLICATIONS & PRESENTATIONS

Presenter. Jan 29-30, 2026. NGS Pipeline for Evaluating CRISPR Efficacy in Creating Models of Human Disease. Genomics in Action.

Presenter. May 20, 2025. *Comparative Transcriptome Analysis of BAL and Blood in Pediatric HCT Recipients*. ATS 2025 International Conference.

Pearce, E., DeRisi, J., Zinter, M., *et al.* July 2025. *Integrating pulmonary and systemic transcriptomes to characterize lung injury after pediatric hematopoietic stem cell transplant*. JCI Insight. 10(17):e194440

Zinter, M., Dvorak, C., Mayday, M., Reyes, G., Simon, R., Pearce, E., *et al.* Preprint. *Pulmonary microbiome and transcriptome signatures reveal distinct pathobiologic states associated with mortality in two cohorts of pediatric stem cell transplant patients*.

Zinter, M., Dvorak, C., Mayday, M., Reyes, G., Simon, R., Pearce, E., *et al.* May 2024 *Pathobiological signatures of dysbiotic lung injury in pediatric patients undergoing stem cell transplantation*. Nature Medicine, 30:1982–1993.

Weisberg, A., Pearce, E., Kramer, G., Chang, J., Clarke, C.. Nov 2023. *Diverse mobile genetic elements shaped the evolution of Streptomyces virulence*. Microbial Genomics. 9(11)

Savory, E., Weisberg, A., Stevens, D., Creason, A., Fuller, S., Pearce, E., Chang, J.. May 2020. *Phytopathogenic Rhodococcus have diverse plasmids with few conserved virulence functions*. Frontiers in Microbiology. 11:1022

SCHOLARSHIPS

KCGIP Inclusion and Diversity Scholarship, \$3000 <i>Awarded based on essay describing commitment to inclusion</i>	June 2025
KCGIP General Scholarship, \$5000 <i>Based on overall strength of program application</i>	June 2025