



# KELSI O. WEST, PHD, MPH

Bioinformatics Scientist II



Bryan, Texas



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in/kelsiwest-bin/f

## EDUCATION

### PhD, Genetics

#### Texas A&M University

Post-transcriptional  
Regulation of the Innate  
Immune Response  
2016 - 2020

### MPH, Epidemiology

#### East Tennessee State

2014 - 2016

### BS, Health Education

#### Salisbury University

Minors: Biology, Chemistry  
2010 - 2013

## EXPERTISE

### Technical

- R
- R Shiny
- Python
- Git
- Docker
- AWS

### Project Management

- Communication
- Problem-Solving
- Mentoring
- Planning
- Organization
- Leadership
- Quality Assurance

## PROFILE

Experienced Bioinformatics Scientist with a robust background in bioinformatic engineering, encompassing IT, and project management. Proficient in designing comprehensive solutions, from conceptualizing and constructing data processing pipelines to designing intuitive user interfaces. Skilled in R, Python, AWS, and Docker. Exceptionally adept in bridging software engineering and science through effective communication, mentoring, facilitating collaboration, and solving complex problems at the intersection of these fields.

## EXPERIENCE

### Catalytic Data Science

2020 - June 2024

#### Bioinformatics Scientist II (2022 - 2024)

#### Bioinformatics Scientist (2020 - 2022)

*Professional Highlight:* Led efforts in successfully implementing 25+ specialized analytics in diverse genomics research areas for agriculture and pharmaceutical customers

- Executing a vigorous infrastructure for fault-tolerant multi-omics analytics leveraging Docker, AWS, and a proprietary orchestrator
- Implementing containerization of genomic tools and Python API layers to deploy and maintain 60+ analytics modules and 90+ integrated pipelines
- Presenting and strategizing novel processes aimed at enhancing operational efficiency to executive leadership
- Mentoring team members in codebase and best practices, expediting high-quality analytics and pipeline delivery
- Analyzing molecular datasets for customers and team research needs using bioinformatics tools in diverse areas
- Developing internal documentation standards and biologically relevant QA test files to efficiently test and increase code maintainability

## EXPERTISE

### Analysis

- RNA-Seq
- scRNA-Seq
- WGS
- Quality Control
- Differential Isoforms
- Variant Detection
- Gene Fusions
- Annotation
- Gene-editing
- Cell Deconvolution
- Viral Integration
- Genome Assembly
- Metagenomics
- Gene Ontology
- Mass-Spectrometry
- Flow Cytometry
- ChIP-Seq
- ATAC-Seq
- File Conversion

### Laboratory

- Tissue culture
- Infection models
- BSL3 trained
- Lentiviral production
- Protein constructs
- Site-directed mutagenesis
- shRNA knockdown
- RT-qPCR
- Western blots
- ChIP
- CRISPR/Cas9
- Immunofluorescence
- Cellular fractionation
- Confocal microscopy
- BioID

## EXPERIENCE

### Texas A&M University

2016 - 2020

#### ***PhD Researcher; Microbial Pathogenesis and Immunology***

- Defined the function and regulation of phosphorylation of splicing factors and how differential phosphorylation affects host outcomes during *Salmonella* Typhimurium and *Mycobacterium tuberculosis* infection
- Aimed to understand the role of post-transcriptional gene regulation, specifically pre-mRNA splicing, in modulating the host responses to bacterial infection using bioinformatics and molecular techniques
- Utilized high throughput, unbiased approaches to identify alternatively spliced genes during *S. Typhimurium* and *M. tuberculosis* infection to host factors required for controlling and/or establishing infection

### East Tennessee State University

2015 - 2016

#### ***Research Assistant; Bill Gatton College of Pharmacy***

- Characterized side effects of nanoparticle drug formulation in commonly used in nonsteroidal anti-inflammatory drugs (NSAIDs), Diclofenac and Celecoxib
- Analyzed gastrointestinal, urinary and pharmacokinetic parameters utilizing different statistical programs such as SAS, SPSS, and R

#### ***Research Assistant; Department of Epidemiology***

- Collected epidemiological data through community surveys and interviews in Nueva Vida, Nicaragua
- Analyzed data using SAS and SPSS to conduct analysis about risk factors associated with many public health priorities around the world including type II diabetes, biosand water filters, HIV/AIDS, and pap smear utilization

## SELECTED PUBLICATIONS

*Global transcriptomics uncovers distinct contributions from splicing regulatory proteins to the macrophage innate immune responses.*  
Front. Immunol. 2021.

*LRRK2 regulates innate immune responses and neuroinflammation during Mycobacterium tuberculosis infection.*  
eLife. 2020.

*The splicing factor hnRNP M is a critical regulator of innate immune gene expression in macrophages.*  
Cell Reports. 2019.