

Mark A. Urich
619-277-7569
markurich@gmail.com
markurich.com

PERSONAL

I am a problem solver at heart; I enjoy spending hours fixing things and solving tough puzzles. After over 8 years of working in an academic research lab, generating mounds of genomic data, I decided to start over and pursue a field that allows me to make a living doing what I love. I began a career in research because I wanted to help expand the collective knowledge of humanity. With the amount of data being produced these days, I feel that I can accomplish that goal better through software development.

RECENT PROJECTS

Anno-JR: Anno-J on Rails

An app for creating and managing sequencing data browsers with Anno-J.

Source: <https://github.com/maalur/anno-jr>

Schmitz Lab Website

A website template, built with Rails, designed and developed for a former colleague's research lab.

<http://schmitzlab.genetics.uga.edu/> Source: https://github.com/maalur/schmitz_app

Twitter Clone

A Twitter clone, built with Ruby on Rails and Bootstrap.

<https://afternoon-savannah-4285.herokuapp.com/> Source: https://github.com/maalur/sample_app

SKILLS

Ruby, Ruby on Rails, Javascript, Coffeescript, Backbone.js, jQuery, SQL, HTML, CSS, Sass

EDUCATION

2009-2011, AS, Grossmont College, Mathematics

Emphasis in biotechnology; Relevant coursework: linear algebra and differential equations.

2005-2010, AS, Cuyamaca College, Biology

Emphasis in biotechnology; Relevant coursework: C++ and Java programming.

EMPLOYMENT

2013-present, SEQUENCING CONSULTANT

DNA, RNA, and MethylC-seq library preparation services, training, and consulting.

2010-2013, LAB TECHNICIAN, The Salk Institute for Biological Studies, Ecker Lab, La Jolla, CA

Performed key sequencing experiments for a number of research projects, including:

- **1001 Genomes/Epigenomes:** Identification and characterization of naturally-occurring epialleles as an extension of the 1001 Genomes project. <http://www.1001genomes.org/>

- **NIH Roadmap Epigenomics Mapping Consortium:** Producing a public resource of human epigenomic data to catalyze basic biology and disease-oriented research using next-generation sequencing technologies to map DNA methylation, histone modifications, chromatin accessibility and RNA transcripts in stem cells and primary ex vivo tissues. roadmapepigenomics.org

- **Mouse ENCODE:** Enhancing the value of the human ENCODE Project through relevant comparative studies with access to cell types, tissues, and developmental time points that are not addressable by the human project. Providing a general resource to inform and accelerate ongoing efforts in mouse genomics and disease modeling with human translational potential. <http://mouseencode.org/>

2009, TUTOR, Grossmont Union High School District, La Mesa, CA

Tutored students in Chemistry and Physics as part of the after school ASPIRE program.

2005-2010, LAB ASSISTANT, The Salk Institute for Biological Studies, Ecker Lab, La Jolla, CA

Studied ETHYLENE-INSENSITIVE5 and its role as a 5' to 3' exoribonuclease.

A list of my current publications can be found at: <http://scholar.google.com/citations?user=ZxwExtQAAAAJ>