

## SKILLS

### Data Science & Programming

- Python (Numpy, Pandas, Scikit-learn), SQL, Linux, R, Data Visualization, Git
- Machine Learning (Natural Language Processing, Time Series), Spark (Mapreduce, ML)
- Deep Learning (Tensorflow, Keras, Neural Network)

### Bio Expertise

- **Next Generation Sequencing (NGS) and transcriptomic proficiency**
  - RNA seq SRA meta-analysis on NCBI breast cancer cell datasets
  - Nanostring analysis for p53 target mRNA expression level in breast cancer cells
  - Target validation with nucleic acid isolation, qPCR, RT-PCR
- **Bioassay Development**
  - High-throughput screening platform for mutant p53 reactivating compounds
  - CRISPR-mediated gene editing: Gene knockout and Gene knock-in
- **Proteomic Analysis:** Western Blot, Stable Isotope Labeling (SILAC) LC-Mass Spectrometry
- **Biomarker Analysis:** Multicolor flow cytometry (BD FACSDIVA), ELISA
- **Mice handling, PBMC, and Stem Cell** culture experience
- **Regulatory Affairs Certificate:** UCSD, in progress

### Management, Troubleshooting, and Communication

- Mentored 6+ graduate students and research associates to help them achieve their project goals
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## EXPERIENCE

### Data Science Fellowship

#### The Data Incubator

June 2019 - Present

- Used Beautiful Soup, **Pandas**, Regex, Web-scraping, and NetworkX to identify degree of connection, page rank, and best friends in "New York Social Diary" archive
- Used **SQL** to query, aggregate, and analyze New York restaurant inspection data
- Used **Machine Learning** models to predict Yelp star ratings
- Used Count and Tfidf Vectorizer for **Natural Language Processing** on Yelp reviews for star ratings
- Used **Spark** to compute and predict user question tags from body texts on Stack Exchange
- Used Fully Connected **Neural Network**, CNN, RNN, and Learning Transfer to predict image classes in CIFAR-10 image dataset

### Postdoctoral Researcher

#### UC Irvine

Jan 2014 - Present

- Used CRISPR gene editing (gene tagging and knockout) and viral derived vectors to investigate PP2A L309 methylation during SAM-checkpoint activation
- Purified HBTH-tagged PP2A (SILAC) for LC-MS and used Python for proteomic analysis. Resulted in identifying PP2A interaction map during methionine stress
- Characterized spliceosome activity with reporter and minigene assay in cells under methionine stress

#### Actavalon Inc.

Jan 2014 - Jan 2015

- Developed bio-screening platform in mammalian cells for p53 reactivating compounds, resulted in a publication in **Nature**
  - Characterized, optimized, and increased efficacy of lead compounds for mutant p53 activation
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## EDUCATION

University of California, Irvine

Sep 2007 - Jan 2014

## Ph.D. Biological Sciences

- Identified metabolic checkpoint responses with virus-mediated gene expression and knockdown, resulted in discovery of p38 and MK2 induced cell cycle arrest during methionine stress
- Measured and quantified S-adenosylmethionine in mammalian cells with HPLC

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## AWARDS & PUBLICATIONS

<b>Data Science Fellowship</b>   The Data Incubator - San Francisco	2019
<b>Journal of Biological Chemistry</b>   Microhomology based CRISPR tagging tools for protein tracking, purification, and depletion	2019
<b>Methionine Dependence of Cancer and Aging</b>   Isolation and characterization of methionine-independent clones from methionine-dependent cancer cells	2019
<b>U.S. Patent</b>   Chembridge Small Molecules that could enhance p53 activity	2015
<b>Journal of Cell Science</b>   SAM limitation induces p38 mitogen-activated protein kinase and triggers cell cycle arrest in G1	2014
<b>Nature Communication</b>   Computational identification of a transiently open L1/S3 pocket for reactivation of mutant p53	2013
<b>Cell Cycle</b>   Downregulation of Cdc6 and pre-replication complexes in response to methionine stress in breast cancer cells	2012
<b>Predoctoral Fellowship</b>   California Institute for Regenerative Medicine	2012
<b>Journal of Biological Chemistry</b>   Transforming growth factor $\beta$ up-regulates cysteine-rich protein 2 in vascular smooth muscle cells via activating transcription factor 2	2008
<b>Genes to Cells</b>   Identification of a putative human mitochondrial thymidine monophosphate kinase associated with monocytic/macrophage terminal differentiation	2008

## REFERENCES

### Dr. Peter Kaiser

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### Dr. Richard Lathrope

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### Dr. Peter Donovan

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### Dr. Robert Schroll

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