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**RESEARCH EXPERIENCE (MAJOR PROJECTS)****08/2020 – Present****RNA-Seq Immune Analysis Pipeline****Advisor: X. Shirley Liu | Dana-Farber Cancer Institute**  
**Franziska Michor | Dana-Farber Cancer Institute**

- Integrated bulk-RNA-related computational tools into a snakemake pipeline.
- Developed visualization modules to facilitate comparison.
- Processed and analyzed bulk RNA-seq data from the CIMAC-CIDC immunotherapy clinical trial.

**CIMAC-CIDC:** <https://cimak-network.org>**Github:** [https://github.com/liulab-dfci/RIMA\\_pipeline](https://github.com/liulab-dfci/RIMA_pipeline)**Tutorial:** <https://liulab-dfci.github.io/RIMA>**06/2021 - Present****Association between EMT and Immune Evasion****Advisor: X. Shirley Liu | Dana-Farber Cancer Institute**  
**Kai Wucherpennig | Dana-Farber Cancer Institute**

- Conducted analysis of CRISPR screening data in collaboration with experimental researchers.
- Utilized public CRISPR data to help identify key genes related to EMT and immune evasion.

**08/2021 – 10/2021****Hippo Signaling Pathway Regulates Cancer Cell-intrinsic MHCII Expression****Advisor: X. Shirley Liu | Dana-Farber Cancer Institute**

- Elucidated a tumor-specific MHCII gene signature from single-cell RNA-seq data to support work related to MHCII expression.
- Applied and modified the model to predict tumor-specific MHCII levels from bulk RNA-seq.

**Status:** submitted to the Genome Medicine**03/2021 – 09/2021****Syngeneic Mouse Tumor Database (TISMO)****Advisor: X. Shirley Liu | Dana-Farber Cancer Institute**

- Collected and processed 605 *in vitro* and 1518 *in vivo* RNA-seq samples from 49 syngeneic cancer cell lines.
- Built TISMO website interface and developed visualization functions.

**TISMO website:** <http://tismo.cistrome.org>**08/2019 – 03/2020****Potential Epigenetic Factors Regulating Mouse ESC Development****Advisor: Wei Li | Children's National Hospital**  
**Jin Zhang | Zhejiang University, China**

- Analyzed Single-cell CRISPR screens to study epigenetic factors that regulates mouse ESC self-renewal.
- Applied trajectory analysis to study mouse ESC differentiation.

03/2019 – 01/2020

## Novel Bioinformatics Methodology for Single-Cell CRISPR Screening

Advisor: Wei Li | Children's National Hospital

- Applied and modified Robust Rank Aggregation (RRA) and the linear regression (LR) approach to detect gene expression regulatory relationship from cells with perturbations.
- Validated the methods using public CROP-seq data.
- Developed visualization functions.

Github: <https://github.com/weililab/scMAGeCK>

07/2016 – 07/2017

## Mechanisms of Bacterial Nitrogen-fixation

Advisor: Sanfeng Chen | China Agricultural University, China

- Reconstructed the pET-28b plasmid with the synthetic *nif* gene.
- Screened successfully introduced strains.
- Performed Nitrogen-fixing related protein induction, extraction, isolation, and western blot for protein validation.

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## EMPLOYMENT

08/2020 – Present

### Computational Biologist I

Department of Data Science  
Dana-Farber Cancer Institute  
450 Brookline Avenue, Boston, MA 02215

05/2019 – 08/2019

### Research Assistant

Center for Genetic Medicine Research  
Children's National Medical Center  
111 Michigan Ave NW, Washington, DC, 20010

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## EDUCATION

08/2018 – 05/2020

### George Washington University | Bioinformatics (Master)

**Major:** Bioinformatics, Next Generation Sequencing, Big data, Biochemistry, Medical Genome

**Tools:** Python, Linux, R, Seurat, Cell Ranger

09/2013 – 07/2017

### China Agricultural University | Biological Science (Bachelor)

**Major:** Biochemistry, Molecular Biology, Genetics

**Tools:** C Programming Languages

**Lab:** Biochemistry Laboratory, Cell Biology Laboratory

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**PUBLICATIONS (\* FIRST/CO-FIRST AUTHOR)**

- **TISMO: syngeneic mouse tumor database to model tumor immunity and immunotherapy response**

*Nucleic Acids Res.* 2021. Sep 17; PMID: 34534350; [doi.org/10.1093/nar/gkab804](https://doi.org/10.1093/nar/gkab804)  
Zeng Z\*, Wong CJ\*, **Yang L\***, et al.

- **scMAGeCK links genotypes with multiple phenotypes in single-cell CRISPR screens**

*Genome Biol* **21**, 19 (2020); PMID: 31980032; [10.1186/s13059-020-1928-4](https://doi.org/10.1186/s13059-020-1928-4)  
**Yang, L\***, Zhu, Y\*, Yu, H. *et al.*

- **CRISPR Screening “Big Data” Informs Novel Therapeutic Solutions**

*Cris. J.*, Jun 2, 2019; PMID: 31225758; [10.1089/crispr.2019.29062.sch](https://doi.org/10.1089/crispr.2019.29062.sch)  
Chen, S\*, **Yang, L\***. & Li, W.

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**SUBMITTED AND PREPRINT MANUSCRIPTS (\* FIRST/CO-FIRST AUTHOR)**

- **2021**

**Tutorial: integrative computational analysis of tumor immunity of bulk RNA-seq data using RIMA**

Submitted to *Nature protocols*

**Yang L\***, Wang J\*, Altreuter J\*, Jhaveri A\*, Wong CJ, et al.

**Machine learning on syngeneic mouse tumor profiles to model clinical immunotherapy response**

Submitted to *Science Advances*

Zeng Z, Gu S, Wong CJ, Ouardaoui N, **Yang L**, et al.

**Hippo signaling pathway regulates cancer cell-intrinsic MHCII expression**

Submitted to *ImmunoTherapy of Cancer*

Zeng Z, Gu S, Ouardaoui N, Tymms C, **Yang L**, et al.

**Durvalumab, tremelimumab alone or in combination with low-dose or hypofractionated targeted radiotherapy in metastatic non-small cell lung cancer refractory to prior PD(L)-1 therapy: a multicentre, open-label, randomized, phase 2 trial**

Accepted by *Lancet oncology*

Jonathan D Schoenfeld, Anita Giobbie-Hurder, Srinika Ranasinghe, Katrina Z Kao, Ana Lako, Junko Tsuji, Yang Liu, Ryan C Brennick, Ryan D Gentzler, Carrie Lee, Joleen Hubbard, Susanne M Arnold, James L Abbruzzese, Salma K Jabbour, Nataliya V. Uboha, Kevin Stephans, Jennifer M Johnson, Haesong Park, Liza C Villaruz, Elad Sharon, Howard Streicher, Mansoor Ahmed, Hayley Lyon, Carrie Cibuskis, Niall Lennon, Aashna Jhaveri, **Lin Yang**, Jennifer Altreuter, et al.

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**SKILLS**

**Languages:** R, Python

**Technologies:** Git, Snakemake

**Bioinformatics:** Bulk and Single-Cell RNA-seq, Spatial transcriptomics, CRISPR screening