JUSTIN S. WILLIAMS

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EDUCATION

The Pennsylvania State University

• Ph.D. in Biochemistry, Microbiology and Molecular Biology

University Park, PA

December 2016

Indiana University of Pennsylvania

• B.S. in Biochemistry

Indiana, PA

May 2010

Memphis, TN 2017-Current

RESEARCH EXPERIENCE

St. Jude Children's Research Hospital

Postdoctoral Research Associate

- Inferring genome-wide histone enrichment and gene expression from DNA methylome in pediatric cancer.
- Single-cell CNV estimation by TPM.
- Genetic and epigenetic analysis of Wilm's Tumor.
- Machine learning approaches for CRISPR/Cas9 off-target prediction.

The Pennsylvania State University

Graduate student with Dr. Teh-hui Kao

University Park, PA

2010-2016

- Assembled (de novo) and analyzed the sub-centromeric S-locus of Petunia inflata; performed comparative genomics between solanaceous S-loci.
- Identified novel F-box genes by a *de novo* transcriptome analysis.
- Determined S-locus F-box protein interaction specificity by transgenic assays.
- Chimeric protein interaction specificity by transgenic assays.

Indiana University of Pennsylvania

Undergraduate Research Assistant with Dr. John Southard

Performed fluorophore targeted mutagenesis.

Indiana, PA

2009-2010

Undergraduate Research Assistant with Dr. Jana Villemain

Performed protein purification in the study of DNA helicase Srs2.

2007-2008

SKILLS and TECHNIQUES

Bioinformatics and related skills:

- Analysis of single-cell RNA-seq data
- Feature and response variable development of NGS data.
- Machine learning including traditional and deep-learning approaches.
- Illumina RNA-seq sample preparation; Transcriptome assembly (de novo) and quality analysis.
- Hybrid genome assembly (PacBio and Illumina- de novo) and quality analysis.
- Novel gene annotation and discovery; phylogenetic analysis.

Software:

Python, R, Bash and Linux OS.

Wet lab skills:

- Immunofluorescence labeling and cell-sorting.
- Mammalian and plant cell culture.
- Ti-vector design and construction; Agrobacterium tumefaciens-mediated plant tissue transformation.

- Chimeric protein design for interaction specificity assays.
- Genetic linkage analysis and transcript expression by qPCR and RNA-seq.

LEADERSHIP EXPERIENCE

St. Jude Children's Research Hospital

Memphis, TN

Department Representative - Postdoctoral Leadership Council

2017-18

2013-16

• Helped with PDLC sponsored department fundraisers, new department postdoctoral orientation, and events for children and patients of St. Jude.

Summer Intern Mentor

Summer 2018

• Helped undergraduate students design and perform CRISPR/Cas9 experiments, validation and results interpretation

The Pennsylvania State University

University Park, PA

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Thesis Mentor, Undergraduate Schreyer Honors College

• Helped undergraduate students design and perform molecular genetic experiments.

Teaching Assistant Microbiology 107

Summer 2016

• Prepared materials and guided laboratory section.

Mentor, Summer Experience in the Eberly College of Science

Summer 2014-15

• Guided high school students through molecular biology experiments.

Teaching Assistant Microbiology 412

Fall 2011

• Presented laboratory lectures and guided laboratory section.

Teaching Assistant Microbiology 202

Spring 2011

• Prepared materials and guided laboratory section; wrote and graded exams.

Indiana University of Pennsylvania

Indiana, PA

President, Professional Fraternity of Chemists (Alpha Chi Sigma)

2009-2010

• Planned and executed educational outreach for underprivileged students, K-12 and provided fund-raising for local charities.

CONFERENCE, POSTER PRESENTATIONS

- Williams JS, Xu B, Putnam D, Thrasher A, and Chen X. DNA methylation reveals alternative promoter usage in genes critical to pediatric tumors. AACR, "Scholar-in-Training Award" Online, June 2020
- **Williams JS** and Xiang Chen. Methyl2Activity: A deep learning based model to predict epigenetic and transcriptional activities from DNA methylation. ISMB. Basel, Switzerland. July 2019.
- Williams JS and Xiang Chen. Methyl2Acetyl: Inferring Histone Enrichment and Gene Expression from WGBS. Poster presentation, ISMB. Chicago, Illinois. July 2018.
- **Williams JS**, Wu L, and Kao, T-h. Identification of 17 *S-locus F-box* genes of *Petunia inflata* by pollen transcriptome analysis and use of BAC clones containing pollen and pistil genes to characterize the *S*-locus. Abstract and oral presentation at World Petunia Conference. Murten, Switzerland. April 2015.
- **Williams JS**, Der JP, dePamphilis CW, and Kao, T-h. Identification of a complete suite of *Petunia S-locus F-box* genes involved in self-incompatibility by pollen transcriptome analysis. Poster and oral presentation in "Hot Topics by Emerging Scientists: Emerging Models", American Society of Plant Biologists. Portland, Oregon. July 2014.

- **Williams JS**, Xu B, Putnam D, Thrasher A, and Chen X (2020). MethylationToActivity: a deep-learning framework that reveals promoter activity landscapes from DNA methylomes in individual tumors. *In Review*. BioRxiv doi: 10.1101/2020.06.09.143172
- Chen W, Zhang S, Williams JS, Ju B, Shaner B, Easton J, Wu G, and Chen X (2020). A comparison of methods accounting for batch effects in differential expression analysis of UMI count based single cell RNA sequencing. *Comp. Struct. Biotech. J.* doi: 10.1016/j.csbj.2020.03.026
- Murphy A, Chen X, Pinto E, **Williams JS**, et al., (2019). Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. *Nat. Med.* doi: 10.1038/s41467-019-13646-9
- Cheng C, Easton J, Rosencrance C, Li Y, Ju B, **Williams JS**, Mulder HL, Chen W, and Chen X (2019). LCA robustly reveals subtle diversity in large-scale single-cell RNA-seq data. *Nucleic Acids Res.* doi: 10.1093/nar/gkz826
- Sun L, Williams JS, Li S, Wu L, Khatri WA, Stone PG, Keebaugh MD and Kao T-h (2018). S-Locus F-Box Proteins Are Solely Responsible for Pollen Function in S-RNase-Based Self-Incompatibility of Petunia. *Plant Cell.* doi: 10.1105/tpc.18.00615
- Wu L, Williams JS, Wang N, Khatri WA, San Román D, and Kao T-h (2017). Use of Domain-Swapping to Identify Candidate Amino Acids Involved in Differential Interactions between Two Allelic Variants of Type-1 S-Locus F-Box Protein and S3-RNase in *Petunia inflata*. *Plant Cell and Phys*. doi: 10.1093/pcp/pcx176
- Li S, **Williams JS**, Sun P, and Kao T-h (2016). All 17 types of S-locus F-box proteins of *S*₂- and *S*₃- haplotypes of *Petunia inflata* are assembled into similar SCF complexes with specific function in self-incompatibility. *Plant Journal* doi:10.1111/tpj.13222
- **Williams JS**, Wu L, Shu L, Sun P, and Kao T-h (2015). Insight into S-RNase-based self-incompatibility in *Petunia*: recent findings and future direction. *Front. Plant Sci.* doi: 10.3389/fpls.2015.00041
- Sun P, Li S, Lu D, **Williams JS**, and Kao T-h (2015). Pollen S-locus F-box proteins of *Petunia* involved in S-RNase-based self-incompatibility are themselves subject to ubiquitin-mediated degradation. *Plant J*. 83:213–223.
- **Williams JS,** Der JP, dePamphilis CW, and Kao T-h (2014). Transcriptome analysis reveals the same 17 *S-locus F-box* genes in two haplotypes of the self-incompatibility locus of *Petunia inflata*. *Plant Cell* 26:2873–2888.
- Sun P, **Williams JS**, Li S, and Kao, T-h (2014). S-RNase-based self-incompatibility in *Petunia*: a complex non-self-recognition system between pollen and pistil. In "Sexual Reproduction in Animals and Plants (Sawada H, Inoue N, Iwano M eds), 289–303, *Springer*, Tokyo Heidelberg New York Dordrecht London.
- Li S*, Sun P*, **Williams JS**, and Kao T-h (2014). Identification of the self-incompatibility-locus F-box protein-containing complex in *Petunia inflata*. *Plant Reprod*. 27:31–45, *Co-first authors.
- **Williams JS**, Natale CA, Wang N, Li S, Brubaker TR, Sun P, and Kao T-h (2014). Four previously identified *S-locus F-box* genes of *Petunia inflata* are involved in pollen specificity in self-incompatibility. *Mol. Plant* 7:567–569.