

Dean Sanders

1306 Vilas Ave, Madison, WI, 53715

Telephone: 920-207-6953

Email: dmsanders@wisc.edu

Github: [sandman2127.github.io](https://github.com/sandman2127)

Education:

University of Wisconsin-Madison

Ph.D. Genetics

Madison, WI

Fall 2013 - Fall 2018

University of Wisconsin-Madison

M.S. Bacteriology

Madison, WI

Fall 2011 - Spring 2013

University of Wisconsin-Oshkosh

B.S. Microbiology

Oshkosh, WI

Fall 2008 - Spring 2011

Skills:

Computational experience:

- **Designed** bioinformatic pipelines for:
 - Genotype By Sequencing
 - *de novo* genome Assembly
 - mRNA, ChIP, Bisulfite Seq
- **Proficiency in Python and R** for program design and plotting
 - Pandas, Numpy, Multiprocessing, and Cython
 - dplyr, ggplot2
 - Jupyter notebook (Python 3 and R)
- **Experience** with software reproducibility practices:
 - Versioning control (git)
 - Container environments (docker)
- Seven years experience using Bash:
 - Unix file system hierarchy
 - Awk and GNU Parallel for scripting, data preprocessing and pipeline automation

Analytical techniques: Personal experience with ESI-MS/MS orbi-trap mass spectrometry and HPLC, sample prep and MS/MS data analysis

General molecular biology: Site directed mutagenesis, plasmid Isolation, molecular cloning, PCR, Sanger sequencing

Microscopy: Performed Epifluorescence and Confocal Microscopy

Experience:

Computational Biologist at the University of Wisconsin Bioinformatics

Resource Center with Dr. Derek Pavelec and Dr. Mark Berres, University of Wisconsin, Madison. December 2018 - Present.

- ❖ Genotype by sequencing
- ❖ Genome prediction
- ❖ SNP imputation
- ❖ GWAS and QTL analysis
- ❖ *de novo* genome assembly
- ❖ mRNA and Bisulfite-seq analysis

Graduate research assistant investigating histone lysine to methionine mutations and loss of DNA methylation during plant development and stress in *Arabidopsis thaliana* with Dr. Xuehua Zhong, University of Wisconsin, Madison. December 2013 - November 2018.

- ❖ Bioinformatic analysis of mRNA, ChIP, SNP and Bisulfite sequencing data
- ❖ Mass spectrometry sample preparation, injection and customized MS/MS data analysis
- ❖ General molecular cloning, transgenic plant production

Graduate research assistant examining bacterial biofilm disruption and production of antimicrobial secondary metabolites by the social amoeba *Dictyostelium* with Dr. Marcin Filutowicz and Dr. Kalin Vetsigian. University of Wisconsin, September 2011- May 2013.

- ❖ Epifluorescence and confocal microscopy
- ❖ C-18 solid phase extraction, HPLC and LC/MS-TOF

Communication: Mentoring experience:

- Personally mentored two graduate and four undergraduate students (4/6 now pursuing higher education)

Teaching assistantship:

- 3 semesters TA experience (>20 hours lecture time)

Python study group leader:

- Member of combee python study group since Fall 2016, leader in Fall 2017

Scientific meeting presentations:

- 6 conference presentations, 9 public outreach in the Wisconsin Institute for Discovery

Publications:

Sanders D *, Jiang J*, Wang B, Liu F, Zhong X (2019) CMT2 mutation in a Tibetan *A. thaliana* accession reduces DNA methylation genomewide and increased tolerance to environmental stressors (In submission at Plant Cell)

Jiang J, **Sanders D**, Wang B, Zhong X (2019) Regulation of plant DNA methylation by UV-B (In preparation)

Mayer K*, Chen X *, **Sanders D**, Nyugen P, Moreno G, Zhong X (2018) *HOS15* binds and promotes the activity of a core histone deacetylase complex in *Arabidopsis thaliana*. (In review at Plant Physiology)

Sanders D, Fieweger R, Lu L, Qian S, Dowell J, Denu JM, Zhong X (2017) Histone lysine-to-methionine mutations reduce histone methylation and cause developmental pleiotropy. *Plant Physiology*.173, 2243-2252.

Sanders D, Katarzyna B, Fikrullah K, Rakowski S, Lozano M, Filutowicz M (2017) Multiple dictyostelid species destroy biofilms of *Klebsiella oxytoca* and other Gram negative species. *Protist*. 168, 311-325.

Lu L, Chen X, **Sanders D**, Qian S, Zhong X (2015) High-resolution mapping of H4K16 and H3K23 acetylation reveals conserved and unique distribution patterns in *Arabidopsis* and rice. *Epigenetics*. 10, 1044-1053.

Patent:

Marcin Filutowicz, Katarzyna Dorota Borys, **Dean Sanders** (2014). Dictyostelid amoeba and biocontrol uses thereof. US20140056850 A1. Amoebagone, LLC