Dean Sanders

1306 Vilas Ave, Madison, WI, 53715  
Telphone: 920-207-6953

Email: [dmsanders@wisc.edu](mailto:dmsanders@wisc.edu)

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

**Education: University of Wisconsin-Madison** Madison, WI

## Ph.D. Genetics Fall 2013 - Fall 2018

## **University of Wisconsin-Madison** Madison, WI

M.S. Bacteriology Fall 2011 - Spring 2013

## **University of Wisconsin-Oshkosh** Oshkosh, WI

B.S. Microbiology Fall 2008 - Spring 2011

**Skills:** **Computational experience:**

* **Designed** bioinformatic pipelines for:
  + Genotype By Sequencing
  + *de novo* genome assembly
  + Genome Wide Association Studies
  + mRNA, ChIP, Bisulfite Seq
* **Proficiency in Python and R** for program design and **HTML, CSS, Javascript** for interactive report generation:
  + Pandas, Numpy, Scipy, Multiprocessing, and Cython
  + dplyr, ggplot2, Bioconductor packages
  + Jupyter notebook (Python 3 and R)
  + Wrote automated HTML reporting for GBS analysis
* **Knowledge of** software reproducibility practices, container based and virtualized environments:
  + git
  + Conda
  + Docker and Singularity
* **Direct experience** using high throughput computing systems:
  + Sun Grid Engine
  + Condor
  + Amazon Web Services
* Eight years experience using Unix Shell

**Analytical techniques:** Direct 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:** PerformedEpifluorescence 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
* 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 (2020) *CMT2* mutation in a Tibetan *A. thaliana* accession reduces DNA methylation genomewide and increased tolerance to environmental stressors (In preparation)

Jiang J, **Sanders D**, Wang B, Zhong X (2019) Regulation of plant DNA methylation by UV-B (In submission at Mol. Cell)

Mayer K\*, Chen X \*, **Sanders D**, Nyugen P, Moreno G, Zhong X (2019) HOS15 acts with HISTONE DEACETYLASE 9 to modulate transcription and development. Plant Physiology. DOI: https://doi.org/10.1104/pp.18.0115

**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