

# William S. Sanders

## Employment

Director, Research IT - Infrastructure & Data Services	Information Technology The Jackson Laboratory Farmington, CT	Nov-2021 to Present
Senior Manager - Research Cyberinfrastructure	Information Technology The Jackson Laboratory Farmington, CT	Jul-2021 to Nov-2021
Manager - Research Cyberinfrastructure	Information Technology The Jackson Laboratory Farmington, CT	Jan-2018 to Jul-2021
Systems Analyst - High Performance Computing	Information Technology The Jackson Laboratory Farmington, CT	Feb-2016 to Jan-2018
Section Editor (Bioinformatics)	Genomics, Proteomics, and Bioinformatics Beijing Institute of Genomics Chinese Academy of Sciences Beijing, China	Apr-2014 to Jun-2015
Postdoctoral Associate - Peterson Laboratory	Institute for Genomics, Biocomputing, and Biotechnology Mississippi State University Starkville, MS	Oct-2011 to Feb-2016
Programmer / Analyst	Institute for Genomics, Biocomputing, and Biotechnology Mississippi State University Starkville, MS	May-2011 to Oct-2011
Graduate Research Assistant	Department of Computer Science & Engineering Mississippi State University Starkville, MS	Jan-2007 to May-2011
Graduate Research Assistant	Department of Biochemistry & Molecular Biology Mississippi State University Starkville, MS	Jan-2004 to Dec-2006
Teaching Assistant	Department of Biochemistry & Molecular Biology Mississippi State University Starkville, MS	Jun-2002 to May-2003
Computer & Network Technician	Computers Plus Oxford, MS	Jul-1998 to Jun-1999

## Education

Ph.D.	Molecular Biology <i>Computational Biology &amp; Machine Learning</i> Advisor: Dr. Susan Bridges	Mississippi State University	2011
M.B.A.	Business Administration	University of Illinois at Urbana-Champaign	2023
M.S.	Computer Science	Mississippi State University	2020
B.S.	Computer Science	Mississippi State University	2003
B.S.	Biochemistry	Mississippi State University	2003

## Publications

NIH SenNet Consortium to map senescent cells throughout the human lifespan to understand physiological health	<b>Nature Aging</b>	2022
Performance Modeling of Scalable Resource Allocations with the Imperial PEPA Compiler	<b>IEEE 21st International Symposium on Parallel and Distributed Computing (ISPD)</b>	2022
Addressing the Robustness of Resource Allocation in the Presence of Application and System Irregularities via PEPA Based Modeling	<b>Lecture Notes in Computer Science (International Conference on Computational Science (ICCS))</b>	2020
Robustness Analysis of Scaled Resource Allocation Models Using the Imperial PEPA Compiler	<b>IEEE 19th International Symposium on Parallel and Distributed Computing (ISPD)</b>	2020
A Container-Based Framework to Facilitate Reproducibility in Employing Stochastic Process Algebra for Modeling Parallel Computing Systems	<b>IEEE International Parallel and Distributed Processing Symposium Workshops</b>	2019
A genomic resource for the sedentary semi-endoparasitic reniform nematode, <i>Rotylenchulus reniformis</i> Linford & Oliveira	<b>Journal of Nematology</b>	2019
Five life stage specific transcriptome assemblies for <i>Rotylenchulus reniformis</i>	<b>Journal of Nematology</b>	2018
Insights into the evolution of the New World diploid cottons ( <i>Gossypium</i> , subgenus <i>Houzingenia</i> ) based on genome sequencing	<b>Genome Biology and Evolution</b>	2018
Comparative genomics of an unusual biogeographic disjunction in the cotton tribe (Gossypieae) yields insights into genome downsizing	<b>Genome Biology and Evolution</b>	2017
Independent Domestication of Two Old World Cotton Species	<b>Genome Biology and Evolution</b>	2016
Comparative Analysis of Fresh and Cryopreserved Boar Spermatozoa Using RNA Sequencing	<b>Reproduction, Fertility, and Development</b>	2015
Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres	<b>Nature</b>	2012
Prediction of Cell Penetrating Peptides by Support Vector Machines	<b>PLoS Computational Biology</b>	2011

Machine Learning and Mapping Algorithms Applied to Proteomics Problems	<b>ProQuest/UMI Dissertation Publishing</b>	2011
The Proteogenomic Mapping Tool	<b>BMC Bioinformatics</b>	2011
Prediction of peptides observable by mass spectrometry applied at the experimental set level	<b>BMC Bioinformatics</b>	2007

## Funding

Role	Title	Organization	Amount	Date	Status
Key	U24 - Cellular Senescence Network: Consortium Organization and Data Coordinating Center	NIH	-	2021-2026	<b>Funded</b>
Key	U54 - The KAPP-Sen Tissue Mapping Center Collaborative	NIH	-	2021-2026	<b>Funded</b>
PI	JAX Research Computing Community Assessment	JAX	\$77,185.56	2021	<b>Funded</b>
PI	Finishing the <i>Crotalus horridus</i> (Timber Rattlesnake) Draft Genome with the MidSouth Computational Biology and Bioinformatics Society	MSU-IGBB, MSU-CSE, MSU-CVM	\$10,224.28	2015	<b>Funded</b>
PI	Sequencing and Assembling a Draft Genome of <i>Kokia drynarioides</i> , a <i>Gossypium</i> Outgroup	MSU-IGBB, USDA-FAS-Borlaug	\$12,962.00	2015	<b>Funded</b>
Co-PI	Developing Resources and Tools to Facilitate Discovery of Disease-Associated microRNAs in Farm Animals	USDA-NIFA	\$448,158.00	2014	Not Funded
PostDoc	Genomic Analysis of Cultivated Cotton and Related Wild Species	USDA ARS	-	2011-2016	<b>Funded</b>
PostDoc	Increasing US Cotton Competitiveness Through Genomics	USDA ARS	-	2007-2012	<b>Funded</b>

## Service

Scientific Track Chair - Panels	<b>Practice and Experience in Advanced Research Computing (PEARC) Conference - 2023</b> Portland, OR	2023
Campus Champions Leadership Team (Elected Member)	<b>Campus Champions</b> <a href="https://campuschampions.cyberinfrastructure.org/">https://campuschampions.cyberinfrastructure.org/</a>	2021-2023
Scientific Track Chair - Advanced Research Computing Software and Applications	<b>Practice and Experience in Advanced Research Computing (PEARC) Conference - 2019</b> Chicago, IL	2019

Technical Committee Member	<b>Practice and Experience in Advanced Research Computing (PEARC) Conference - 2018</b> Pittsburgh, PA	2017-2019
Organizing Committee Member	<b>MidSouth Computational Biology and Bioinformatics Society Annual Conference - 2018</b> Starkville, MS	2017-2018
Campus Champion The Jackson Laboratory	<b>Campus Champions - Extreme Science and Engineering Discovery Environment (XSEDE)</b> National Science Foundation	2016-Present
Workshop Organizer - Evolution of Genome Size	<b>Plant and Animal Genome Conference</b> San Diego, CA	2016-2020
Project Leader - <i>Crotalus horridus</i> (Timber Rattlesnake) Genome Project	<b>MidSouth Computational Biology and Bioinformatics Society</b>	2012-2018
Session Chair - Proteomics Session	<b>MidSouth Computational Biology and Bioinformatics Society Annual Conference</b> Oxford, MS	2012

## Certifications, Trainings, & Licensures

Gies College of Business University of Illinois at Urbana-Champaign	Entrepreneurship and Strategic Innovation	2023
ROI Training	Google Cloud Platform - Professional Cloud Architect Training	2022
SeaChange Resources	MaritimeQuest / Executive Leadership Program	2022
Gies College of Business University of Illinois at Urbana-Champaign	Financial Management	2022
Gies College of Business University of Illinois at Urbana-Champaign	Strategic Leadership & Management	2022
Dr. Daylian M. Cain Negotiation Mind Games	Negotiating in Difficult Times	2021
KU Leuven / EdX	Beer: The Science of Brewing	2021
SeaChange Resources	Leadership@theHelm / Crisis Management	2021
The Jackson Laboratory & Johns Hopkins University	Human and Mammalian Genetics and Genomics: The 61st McKusick Short Course	2020
Scaled Agile	Certified SAFe 4 DevOps Practitioner	2018
Scaled Agile	Leading SAFe (Certified SAFe 4 Agilist)	2018
The Jackson Laboratory	Frontline Leadership Training	2018
Karrass	Effective Negotiating	2017
Karrass	Negotiating Effectively Within Your Own Organization	2017

American Red Cross	Adult CPR/AED, Infant CPR, and First Aid (GVCZ9G)	2017-2019
Software Carpentry Foundation	Software Carpentry Certified Instructor	2016
ROI Training	Google Cloud Platform Fundamentals Certificate (CP100A)	2016
Bagley College of Engineering Mississippi State University	Information Assurance Certificate (NSTISSI #4011 & NSTISSI #4014 Certified Program)	2010
Federal Communications Commission Amateur Radio Service	Amateur Radio Technician License (Callsign: KF5CZK)	2009
Bruker Daltonics	FLEX Series MALDI-TOF MS Operator Course	2006
Bagley College of Engineering Mississippi State University	Computational Biology Certificate	2007
Microsoft	Microsoft Certified Professional <i>Windows NT 4.0, Networking Essentials</i>	1998-2001
CompTIA	CompTIA A+ Certified Professional (COMP10072148)	1998

## Awards & Honors

JAX Champion - Excellence in Quality and Innovation Award	The Jackson Laboratory Bar Harbor, ME   Farmington, CT   Sacramento, CA	2018
1 <sup>st</sup> Place Postdoctoral Oral Presentation	MidSouth Computational Biology and Bioinformatics Society Annual Conference Little Rock, AR	Mar 13-14 2015
3 <sup>rd</sup> Place Student Oral Presentation	MidSouth Computational Biology and Bioinformatics Society Annual Conference Oklahoma City, OK	Feb 23-24 2008
1 <sup>st</sup> Place Student Poster Presentation	MidSouth Computational Biology and Bioinformatics Society Annual Conference New Orleans, LA	Feb 1-3 2007
University Honors Program - Phase I Scholar	Mississippi State University Starkville, MS	May 2000

## Teaching Experience

Instructor	Introduction to Application Containerization Using Singularity 12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics Chicago, IL	2021
Instructor	Python and R for Scientific Computing Software Carpentry Workshop The Jackson Laboratory	2019
Instructor	Introduction to High Performance Computing Workshop The Jackson Laboratory	2016-2019
Instructor	Excel, OpenRefine, Python Data Carpentry Workshop The Jackson Laboratory	2017
Instructor	Cloud Computing for Genomics Data Carpentry Workshop The Jackson Laboratory	2017
Instructor	R for Reproducible Scientific Analysis Software Carpentry Workshop The Jackson Laboratory	2016
Mentor	Day One Leadership Community Mississippi State University	2013-2015
Guest Lecturer	High Throughput Sequence Analysis ( <i>CSE 6990</i> ) Department of Computer Science & Engineering Mississippi State University	2015
Mentor	Norman E. Borlaug International Agricultural Science and Technology Fellowship Program Foreign Agricultural Service United States Department of Agriculture	2014-2015
Mentor	Research Experience for Undergraduates Undergraduate Research in Computational Biology Mississippi State University	2007-2015
Lecturer	Biochemistry Boot Camp Department of Chemistry Mississippi State University	2014-2015
Guest Lecturer	Genomes & Genomics ( <i>BCH 8653</i> ) Department of Biochemistry & Molecular Biology Mississippi State University	2012
Student	Tools for Teaching Introductory Computer Science ( <i>CSE 8990</i> ) Department of Computer Science & Engineering Mississippi State University	2010
Guest Lecturer	Essentials of Molecular Genetics ( <i>BCH 4113</i> ) Department of Biochemistry & Molecular Biology Mississippi State University	2009

Teaching Assistant	Protein Methods ( <i>BCH 4414/6414</i> ) Department of Biochemistry & Molecular Biology Mississippi State University	2004
Teaching Assistant	Biochemical Methods ( <i>BCH 4805/6805</i> ) Department of Biochemistry & Molecular Biology Mississippi State University	2002

## Reviewing Activities

Gene	Nucleic Acids Research	Bioinformatics
Interdisciplinary Sciences: Computational Life Sciences	Genomics, Proteomics, and Bioinformatics	BMC Genomics
PLoS One	BMC Bioinformatics	Journal of Translational Medicine
Journal of Biocomputing	BioSystems	

## Software Tools

<b>The Proteogenomic Mapping Tool.</b> <a href="http://www.agbase.msstate.edu/tools/pgm/">http://www.agbase.msstate.edu/tools/pgm/</a>	A Java-based implementation of the Aho-Corasick string searching algorithm which takes peptides observed by mass spectrometry and maps them onto a source genome.
<b>PepOut</b> – A Distance Based Peptide Validation Tool. <a href="http://www.agbase.msstate.edu/cgi-bin/tools/">http://www.agbase.msstate.edu/cgi-bin/tools/</a>	A Perl/MySQL-based program that uses the k-nearest neighbor algorithm combined with Bayesian probabilities to perform mass spectrometry peptide validation using target and decoy databases.

## Skills

<b>Software Skills</b>	Programming Languages: Python, C/C++, Perl, Java, MPI Statistical Analysis: R, SAS Other: MySQL, WEKA Machine Learning Toolkit, Apache, BioPerl, BioPython, ABySS Sequence Assembler, Velvet Sequence Assembler, Roche 454 GS De Novo Assembler, CLC Genomics Workbench
<b>Research Skills</b>	Genomics, Genome Sequence Assembly & Analysis, Proteomics, Mass Spectrometry, Artificial Intelligence, Machine Learning, Data mining, Algorithm Analysis & Design, Eukaryotic Tissue Culture, High Performance Computing, High Performance Liquid Chromatography, Gas Chromatography, Gel Electrophoresis
<b>Miscellaneous</b>	German (minimal professional proficiency), Grant Writing

## Presentations

Campus Champions: Connecting Community and Resources	Practice and Experience in Advanced Research Computing (PEARC) 2022 Boston, MA	Jul 11 2022
Words Matter! Promoting Inclusion through Language in Advanced Research Computing [Panelist]	Supercomputing 2021 St. Louis, MO	Nov 18 2021

Genomic Data Lakes: Research Data Storage at The Jackson Laboratory	2021 Bio-IT World Conference and Expo Boston, MA	Sep 9 2021
Bursts, Forecasting, and Storm Avoidance: Utilization of Cloud Platforms	Partly Cloudy 2019 Fred Hutchinson Cancer Research Center Seattle, WA	Oct 18 2019
Making It Work: Facilitating Collaboration Between IT and Researchers for Computation-Intensive Programs	University of Mississippi Medical Center (UMMC) Bioinformatics Collaborative Jackson, MS	Mar 28 2018
A Mitochondrial Genome of the Timber Rattlesnake ( <i>Crotalus horridus</i> ) and a Reptilian Mitochondrial Phylogeny	MidSouth Computational Biology and Bioinformatics Society Annual Conference Memphis, TN	Mar 3-5 2016
Genome size evolution among closely related species in <i>Gossypium</i>	Plant and Animal Genome Conference XXIV San Diego, CA	Jan 9-13 2016
Genome Assembly & Analysis – From “Gold-Standard” Assemblies to “Base Metals” <b>Kriton-Hatzio Symposium Keynote Address</b>	Southern Section of the American Society of Plant Biologists (SS-ASPB) Dauphin Island, AL	Mar 28-29 2015
Assembly and molecular characterization of a draft genome sequence and annotation of the plant-parasitic nematode <i>Rotylenchulus reniformis</i>	MidSouth Computational Biology and Bioinformatics Society Annual Conference Little Rock, AR	Mar 13-14 2015
Update on the Timber Rattlesnake Genome Collaborative Project	MidSouth Computational Biology and Bioinformatics Society Annual Conference Little Rock, AR	Mar 13-14 2015
Draft Genome Assembly and Comparative Genomic Analysis of the Plant-Parasitic Nematode <i>Rotylenchulus reniformis</i>	Plant and Animal Genome Conference XXIII San Diego, CA	Jan 10-14 2015
Molecular Insights into the <i>Rotylenchulus reniformis</i> transcriptome	Plant and Animal Genome Conference XXIII San Diego, CA	Jan 10-14 2015
MCBIOS Timber Rattlesnake Genome Project Collaboration	MidSouth Computational Biology and Bioinformatics Society Annual Conference Stillwater, OK	Mar 6-8 2014
Sequencing, Assembly, and Characterization of the Genome of <i>Rotylenchulus reniformis</i>	MidSouth Computational Biology and Bioinformatics Society Annual Conference Stillwater, OK	Mar 6-8 2014
SABRe – Sequence Assembly By Reference	MidSouth Computational Biology and Bioinformatics Society Annual Conference Stillwater, OK	Mar 6-8 2014
Assembly, Annotation and Proteogenomic Mapping of <i>Rotylenchulus reniformis</i>	Plant and Animal Genome Conference XXII San Diego, CA	Jan 11-15 2014
Unveiling the Molecular Arsenal within <i>Rotylenchulus reniformis</i> via <i>de novo</i> Transcriptome Assembly.	Annual Meeting of the Society of Nematologists Knoxville, TN	Jul 14-17 2013



Identification of Protein Coding Genes in the Plant-parasitic Nematode <i>Rotylenchulus reniformis</i> through Comparative Proteogenomic Mapping with <i>Caenorhabditis elegans</i>	MidSouth Computational Biology and Bioinformatics Society Annual Conference Columbia, MO	Apr 5-6 2013
The Genome of Reniform Nematode, <i>Rotylenchulus reniformis</i>	MidSouth Computational Biology and Bioinformatics Society Annual Conference Columbia, MO	Apr 5-6 2013
<i>De Novo</i> Transcriptome Assembly of the Plant-Parasitic Nematode <i>Rotylenchulus reniformis</i>	MidSouth Computational Biology and Bioinformatics Society Annual Conference Columbia, MO	Apr 5-6 2013
Genome Size Evolution In <i>Gossypium</i> (Cotton): Progress and Prospects	Plant and Animal Genome Conference XXI San Diego, CA	Jan 12-16 2013
Assembling and Annotating the Genome of a Plant Parasitic Nematode, <i>Rotylenchulus reniformis</i> , with Sequences Obtained Using 2 <sup>nd</sup> Generation Sequencing Technologies	MidSouth Computational Biology and Bioinformatics Society Annual Conference Oxford, MS	Feb 17-18 2012
The <i>Rotylenchulus reniformis</i> Genome: Sequencing, Assembly, and Annotation	Plant and Animal Genome Conference XX San Diego, CA	Jan 14-18 2012
Sequencing and Analysis of the <i>Rotylenchulus reniformis</i> Transcriptome	Plant and Animal Genome Conference XX San Diego, CA	Jan 14-18 2012
Proteogenomic Mapping of <i>Gallus gallus</i> Serum	MidSouth Computational Biology and Bioinformatics Society Annual Conference College Station, TX	Apr 1-2 2011
Experimental genome annotation by proteogenomic mapping: experimental evidence for predicted proteins, novel proteins and protein structure	Workshop on Nanotechnology, Proteogenomics and Visual Analytic Applications for Schistosomiasis Control Abuja, Nigeria	Dec 14-18 2010
Metrics for Mass Spectrometry Dataset Quality Validation	MidSouth Computational Biology and Bioinformatics Society Annual Conference Jonesboro, AR	Feb 19-20 2010
A Staged Search Strategy for Proteomics Based Structural Annotation in Chicken	Plant and Animal Genome Conference XVIII San Diego, CA	Jan 9-13 2010
Proteomics Based Genome Annotation in <i>Gallus gallus</i>	Mississippi State University Digital Biology Learning Community Starkville, MS	Oct 21 2009
Features Predictive of Cell Penetrating Peptides Validated by Machine Learning Classifiers	Research in Computational Molecular Biology (RECOMB) 2009 Tucson, AZ	May 18-21 2009
Prediction of Cell Penetrating Peptides by Machine Learning Classifiers	Intelligent Systems for Molecular Biology (ISMB) 2008 Toronto, ON	Jul 19-23 2008
Proteomics Based Structural Genome Annotation in Chicken	Avian Genomics and Gene Ontology Annotation Workshop Starkville, MS	May 19-20 2008
Prospecting for new genes in the chicken genome using proteomics	Cold Spring Harbor Laboratory - Genome Informatics Meeting Cold Spring Harbor, NY	Nov 1-5 2007

## Miscellaneous

- OrCID: <https://orcid.org/my-orcid?orcid=0000-0001-9368-3004>
- Google Scholar: <https://scholar.google.com/citations?user=WIEDiZYAAAAJ&hl=en>
- GitHub: <https://github.com/williamssanders/public>
- LinkedIn: <https://www.linkedin.com/in/williamssanders/>
- JAX: <https://www.jax.org/people/shane-sanders>