

John Didion | PhD

☎ (919) 536 9924 • ✉ john.didion@nih.gov • 🌐 john.didion.net
📄 jdidion • 🐦 jdidion • 🌐 jdidion • ORCID 0000-0002-8111-6261

Education

- 2008.08 to 2014.05 **Doctor of Philosophy, Bioinformatics and Computational Biology**
University of North Carolina, Chapel Hill, NC
- 1996.09 to 2001.06 **Bachelor of Science, Computer Science**
Northwestern University, Evanston, IL

Research Experience

- 2014.09 to Present **National Human Genome Research Institute** Bethesda, MD
Postdoctoral Fellow, Laboratory of Dr. Francis S Collins
Investigating the role of epigenetics in common complex disease, especially type 2 diabetes.
- 2009.05 to 2014.08 **University of North Carolina at Chapel Hill** Chapel Hill, NC
Research Assistant, Laboratory of Dr. Fernando Pardo-Manuel de Villena
Characterized the genetic determinants of two meiotic drive systems in the mouse. First, conducted a GWAS of wild mice to identify genes associated with the accumulation of Robertsonian translocations. Second, mapped a novel meiotic drive locus, R2d2, and multiple modifier loci responsible for extreme TRD in the Collaborative Cross. Also developed CLASP, a software tool for validation of cell lines used in research.
- 2007.08 to 2008.08 **Institute for Systems Biology** Seattle, WA
Computational Biology Software Engineer, Laboratory of Dr. Ruedi Aebersold
Developed informatics software to support proteomics research. Created TIQAM, a work flow management system for MRM (Multiple Reaction Monitoring) experiments.

Industry Experience

- 2004.09 to 2007.08 **Muze, Inc.** Seattle, WA
Software Development Engineer
- 2003.09 to 2004.09 **Encyclopaedia Britannica, Online Services** Chicago, IL
Software Developer
- 2001.05 to 2003.08 **ThoughtWorks, LLC** Chicago, IL
Software Developer/Consultant

Teaching Experience

- 2015.06 to 2015.09 **NHGRI**
Summer student research project, Mentor
- 2013.09 to 2014.05 **University of North Carolina at Chapel Hill**
Undergraduate senior research project, Mentor
- 2013.09 to 2013.12 **University of North Carolina at Chapel Hill**
Genetic Analysis 2, Teaching Assistant

Publications

Journal Articles.....

- [16] **Didion JP**, Morgan AP, et al. “*R2d2* drives selfish sweeps in the house mouse,” *Molecular Biology and Evolution*, vol. 33, no. 6, pp. 1381–1395, 2016. DOI: 10.1093/molbev/msw036.
- [15] Morgan AP, Holt JM, McMullan RC, Bell TA, Clayshulte AM-F, **Didion JP**, et al. “The many evolutionary fates of a large segmental duplication in mouse,” *Genetics*, 2016. DOI: 10.1534/genetics.116.191007.
- [14] Scott LJ, Erdos MR, Huyghe JR, Welch RP, Beck AT, Wolford BN, Chines PS, **Didion JP**, et al. “The genetic regulatory signature of type 2 diabetes in human skeletal muscle,” *Nature Communications*, vol. 7, p. 11764, 2016. DOI: 10.1038/ncomms11764.
- [13] Chandler RL, Damrauer JS, Raab JR, Schisler JC, Wilkerson MD, **Didion JP**, et al. “Coexistent ARID1A–PIK3CA mutations promote ovarian clear-cell tumorigenesis through pro-tumorigenic inflammatory cytokine signaling,” *Nature Communications*, vol. 6, p. 6118, 2015. DOI: 10.1038/ncomms7118.
- [12] Crowley JJ, ...13 others..., **Didion JP**, et al. “Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance,” *Nature Genetics*, vol. 47, no. 4, pp. 353–360, 2015. DOI: 10.1038/ng.3222.
- [11] **Didion JP**, Morgan AP, Clayshulte AMF, et al. “A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2,” *PLoS Genetics*, vol. 11, no. 2, e1004850, 2015. DOI: 10.1371/journal.pgen.1004850.
- [10] Morgan AP, Fu C-P, Kao C-Y, Welsh CE, **Didion JP**, et al. “The Mouse Universal Genotyping Array: from substrains to subspecies,” *G3*, vol. 6, no. 2, pp. 263–279, 2015. DOI: 10.1534/g3.115.022087.
- [9] **Didion JP**, Buus RJ, Naghashfar Z, et al. “SNP array profiling of mouse cell lines identifies their strains of origin and reveals cross-contamination and widespread aneuploidy,” *BMC Genomics*, vol. 15, p. 847, 2014. DOI: 10.1186/1471-2164-15-847.
- [8] **Didion JP** and Pardo-Manuel de Villena F, “Deconstructing *Mus gemischus*: advances in understanding ancestry, structure, and variation in the genome of the laboratory mouse,” *Mammalian Genome*, vol. 24, no. 1–2, pp. 1–20, 2013. DOI: 10.1007/s00335-012-9441-z.
- [7] Calaway JD, Lenarcic AB, **Didion JP**, et al. “Genetic architecture of skewed X inactivation in the laboratory mouse,” *PLoS Genetics*, vol. 9, no. 10, e1003853, 2013. DOI: 10.1371/journal.pgen.1003853.
- [6] Collaborative Cross Consortium, “The genome architecture of the Collaborative Cross mouse genetic reference population,” *Genetics*, vol. 190, no. 2, pp. 389–401, 2012. DOI: 10.1534/genetics.111.132639.
- [5] **Didion JP**, Yang H, Sheppard K, et al. “Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias,” *BMC Genomics*, vol. 13, p. 34, 2012. DOI: 10.1186/1471-2164-13-34.

- [4] Aylor DL, ...11 others..., **Didion JP**, et al. "Genetic analysis of complex traits in the emerging Collaborative Cross," *Genome Research*, vol. 21, no. 8, pp. 1213–1222, 2011. DOI: 10.1101/gr.111310.110.
- [3] Yang H, Wang JR, **Didion JP**, et al. "Subspecific origin and haplotype diversity in the laboratory mouse," *Nature Genetics*, vol. 43, no. 7, pp. 648–655, 2011. DOI: 10.1038/ng.847.
- [2] Eisener-Dorman AF, **Didion JP**, Santos C, Calaway JD, "The 23rd International Mammalian Genome Conference meeting report," *Mammalian Genome*, vol. 21, no. 5–6, pp. 217–223, 2010. DOI: 10.1007/s00335-010-9265-7.
- [1] Lange V, Malmstrom JA, **Didion JP**, et al. "Targeted quantitative analysis of *Streptococcus pyogenes* virulence factors by multiple reaction monitoring," *Molecular and Cellular Proteomics*, vol. 7, no. 8, pp. 1489–1500, 2008. DOI: 10.1074/mcp.M800032-MCP200.

Oral Presentations

2013.09	27th Intl. Mammalian Genome Conference	Salamanca, Spain
2013.05	12th Annual Meeting of the Complex Traits Community	Madison, WI
2012.09	16th EBM Conference	Marseille, France
2012.09	UNC Genetics Department Retreat	Myrtle Beach, SC
2010.10	24th Intl. Mammalian Genome Conference	Heraklion, Greece
2010.05	9th Annual Meeting of the Complex Traits Community	Chicago, IL
2009.09	23rd Intl. Mammalian Genome Conference	San Diego, CA

Poster Presentations

2015.10	American Society of Human Genetics Conference	Baltimore, MD
2015.05	Biology of Genomes Conference	Cold Spring Harbor, NY
2014.10	28th Intl. Mammalian Genome Conference	Bar Harbor, ME
2011.09	UNC Genetics Department Retreat	Myrtle Beach, SC
2011.06	Genetics Society of America Mouse Genetics	Washington D.C.
2011.06	National Centers for Systems Biology Annual Meeting	Duke University
2010.09	UNC Genetics Department Retreat	Myrtle Beach, SC
2009.09	UNC Genetics Department Retreat	Asheville, NC

Funding

2015.11	NIH Intramural Sequencing Center Pilot Grant <i>Extending ATAC-Seq to archival frozen and fixed tissue samples</i>
2015.05	NIH Intramural Sequencing Center Pilot Grant <i>Identifying functional variants in T2D GWAS loci using CATCh-PET</i>
2014.12	NIH Intramural Sequencing Center Pilot Grant <i>Epigenomic regulation of glucose response in a human pancreatic islet Beta cell line</i> Institutional award with funding for sequencing services
2014.12 to 2015.04	Department of Health and Human Services Ignite <i>LabGenius: The Smart Lab Notebook for Scientists</i> Incubator program with USD 5000 funding
2009.09 to 2010.08	Bioinformatics and Computational Biology Training Grant <i>NIH GM067553-04</i> Institution-awarded fellowship
2009.09	International Mammalian Genome Society Fellowship <i>Travel grant</i>

Honors & Awards

2014.12	Dean's Distinguished Dissertation Award (Nominee) <i>University of North Carolina at Chapel Hill</i> Nominee from the Bioinformatics and Computational Biology program
2013.09	Verne Chapman Young Scientist Award <i>International Mammalian Genome Society</i> Best talk at the International Mammalian Genome Conference
2013.05	Chicago Prize <i>Complex Traits Consortium</i> Best graduate student talk at the Complex Traits Consortium meeting
2010.10	Genome Research Award for Outstanding Poster <i>International Mammalian Genome Society</i> Outstanding poster at the International Mammalian Genome Conference

Professional Memberships & Service

2016.01 to present	NHGRI Preprint Journal Club <i>Organizer</i>
2016.01	NCBI Hackathon <i>Team Lead</i>
2013.09 to 2015.09	International Mammalian Genome Society <i>Secretariat member (honorary)</i>
2013.08	UNC Genetics Department Retreat <i>Abstract Review Committee</i>