

# John Didion | PhD

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## Education

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- 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

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- 2014.09 to Present **National Human Genome Research Institute** Bethesda, MD  
*Postdoctoral Fellow, Laboratory of Dr. Francis S Collins*
- Leveraging a large, multi-'omics dataset to investigate epigenetic mechanisms underlying regulatory variants implicated in type 2 diabetes.
  - Developing machine-learning approaches to imputation for multi-'omics data.
  - Designed and currently optimizing a novel sequencing assay for single-molecule resolution transcriptome analysis.
  - Using single-cell gene expression and chromatin accessibility data to understand cell-to-cell variability in pancreatic islets, including responses to glucose perturbation.
  - Developed user-friendly software tools for QC and pre-processing of NGS reads.
  - Applied for and awarded six grants, including an American Diabetes Association fellowship and an NIH K22.
- 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 transmission distortion in the Collaborative Cross.
  - 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

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

## Teaching Experience

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2016.10 to present	<b>NIH</b> <i>Software Carpentry, Instructor</i>
2016.10 to present	<b>FAES (NIH)</b> <i>American Academy of Bioinformatics, Instructor (paid)</i>
2016.06 to present	<b>NHGRI</b> <i>Post-baccalaureate project, Mentor</i>
2015.06 to 2015.09	<b>NHGRI</b> <i>Summer student research project, Mentor</i>
2013.09 to 2014.05	<b>University of North Carolina at Chapel Hill</b> <i>Undergraduate senior research project, Mentor</i>
2013.09 to 2013.12	<b>University of North Carolina at Chapel Hill</b> <i>Genetic Analysis 2, Teaching Assistant</i>

## Publications

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### Journal Articles.....

- [19] **Didion JP**, Martin M, and Collins FS, "Atropos: specific, sensitive, and speedy trimming of sequencing reads," *Preprint, submitted*, 2017. DOI: 10.7287/peerj.preprints.2452v3.
- [18] Varshneya A, Scott LJ, Welch R, Erdos MR, Chines PS, Narisu N, D'Oliveira RA, Orchard P, Wolford BN, Kursawee R, Vadlamudi S, Cannon ME, **Didion JP**, et al. "Genetic regulatory signatures underlying islet gene expression and type 2 diabetes," *Proc Nat Acad Sci USA*, 2017. DOI: 10.1073/pnas.1621192114.
- [17] Morgan AP, **Didion JP**, et al. "Genome report: whole genome sequence of two wild-derived *Mus musculus domesticus* inbred strains, LEWES/EiJ and ZALLENDE/EiJ, with different diploid numbers," *G3*, 2016. DOI: 10.1534/g3.116.034751.
- [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

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2017.04	<b>NIAID Genomics and Immunology Speaker Series</b>	Bethesda, MD
2017.01	<b>NIH Data Science Interest Group</b>	Bethesda, MD
2015.1	<b>NIH Digital Summit</b>	Bethesda, MD
2013.09	<b>27th Intl. Mammalian Genome Conference</b>	Salamanca, Spain
2013.05	<b>12th Annual Meeting of the Complex Traits Community</b>	Madison, WI
2012.09	<b>16th EBM Conference</b>	Marseille, France
2012.09	<b>UNC Genetics Department Retreat</b>	Myrtle Beach, SC
2010.10	<b>24th Intl. Mammalian Genome Conference</b>	Heraklion, Greece
2010.05	<b>9th Annual Meeting of the Complex Traits Community</b>	Chicago, IL
2009.09	<b>23rd Intl. Mammalian Genome Conference</b>	San Diego, CA

## Poster Presentations

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

## Funding

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2017.04 to 2021.04	<b>NIH 1 K22 ES028024-01 BD2K Career Transition Award</b> <i>A Big Data Approach to Learning the Type 2 Diabetes Regulome</i> Career transition award with 3 years tenure-track funding
2017.01 to 2019.12	<b>American Diabetes Association Postdoctoral Fellowship</b> <i>The Type 2 Diabetes Epigenome: A Multi-Tissue and Multi-Omics Investigation of a Complex Disease</i> Postdoctoral fellowship with up to 3 years salary and research support
2016.09	<b>NIH Intramural Sequencing Center Pilot Grant</b> <i>Transcriptome analysis at single-molecule resolution</i> Institutional award with funding for sequencing services
2015.11	<b>NIH Intramural Sequencing Center Pilot Grant</b> <i>Extending ATAC-Seq to archival frozen and fixed tissue samples</i> Institutional award with funding for sequencing services
2015.05	<b>NIH Intramural Sequencing Center Pilot Grant</b> <i>Identifying functional variants in T2D GWAS loci using CATCh-PET</i> Institutional award with funding for sequencing services
2014.12	<b>NIH Intramural Sequencing Center Pilot Grant</b> <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	<b>Department of Health and Human Services Ignite</b> <i>LabGenius: The Smart Lab Notebook for Scientists</i> Incubator program with USD 5000 funding
2009.09 to 2010.08	<b>Bioinformatics and Computational Biology Training Grant</b> <i>NIH GM067553-04</i> Institution-awarded fellowship
2009.09	<b>International Mammalian Genome Society Fellowship</b> <i>Travel grant</i>

## Honors & Awards

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

## Professional Memberships & Service

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2016.10	<b>CSHL Biological Data Science Hackathon</b> <i>Team Lead</i>
2016.08 to present	<b>Software Carpentry</b> <i>Certified Instructor</i>
2016.01 to present	<b>NHGRI Preprint Journal Club</b> <i>Organizer</i>
2016.01, 2016.08	<b>NCBI Hackathon</b> <i>Team Lead</i>
2013.09 to 2015.09	<b>International Mammalian Genome Society</b> <i>Secretariat member (honorary)</i>
2013.08	<b>UNC Genetics Department Retreat</b> <i>Abstract Review Committee</i>