

John P. Didion, PhD

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Education

Doctor of Philosophy, Bioinformatics, University of North Carolina, Chapel Hill, NC, 2008-2014.

Bachelor of Science, Computer Science, Northwestern University, Evanston, IL, 2001.

Positions Held

2014-Present	Collins Group, National Human Genome Research Institute <i>Postdoctoral Fellow</i> Investigating the role of epigenetics in common complex disease, especially type 2 diabetes.	Bethesda, MD
2009-2014	Pardo-Manuel de Villena Laboratory, Univ. of North Carolina <i>Research Assistant</i> 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, <i>R2d2</i> , 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.	Chapel Hill, NC
2007-2008	Aebersold Laboratory, Institute for Systems Biology <i>Computational Biology Software Engineer</i> Developed informatics software to support proteomics research. Created TIQAM, a workflow management system for MRM (Multiple Reaction Monitoring) experiments.	Seattle, WA
2004-2007	Muze, Inc. <i>Software Development Engineer</i>	Seattle, WA
2003-2004	Encyclopaedia Britannica, Online Services <i>Software Developer</i>	Chicago, IL
2001-2003	ThoughtWorks, LLC <i>Software Developer/Consultant</i>	Chicago, IL

Publications

11. **Didion JP**, et al. A multi-megabase copy number gain causes maternal transmission ratio distortion on mouse Chromosome 2. Accepted, *PLoS Genetics*.
10. Chandler RL, Damrauer JS, Raab J, **Didion JP**, et al. Concurrent ARID1A loss and PIK3CA activation leads to aggressive ovarian tumorigenesis in the mouse. Accepted, *Nature Comm.*
9. Crowley JJ, ...13 others..., **Didion JP**, et al. Pervasive allelic imbalance revealed by allele-specific gene expression in highly divergent mouse crosses. Accepted, *Nature Genetics*.

8. **Didion JP**, et al. High-throughput SNP profiling of mouse cell lines identifies their strain origin and reveals cross-contamination and widespread aneuploidy. *BMC Genomics* 2014, 15:847.
7. Calaway JD, Lenarcic AB, **Didion JP**, Wang JR, Searle JB, McMillan L, Valdar W, Pardo-Manuel de Villena F. Genetic architecture of skewed X inactivation in the laboratory mouse. *PLoS Genetics* 2013, e1003853.
6. **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* 2013 24:1-2.
Cover article
5. **Didion JP***, Yang H*, et al. Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. *BMC Genomics* 2012, 13:34.
** Co-first author*
4. Collaborative Cross Consortium. The genome architecture of the Collaborative Cross mouse genetic reference population. *Genetics* 2012, 190:389-401.
Cover article
3. Yang H, Wang J, **Didion JP**, et al. Subspecific Origin and Haplotype Diversity in the Laboratory Mouse. *Nature Genetics* 2011, 43:648-655.
2. Aylor D, ...11 others..., **Didion JP**, et al. Genetic Analysis of Complex Traits in the Emerging Collaborative Cross. *Genome Research* 2011, 21:1213-1222.
1. Eisener-Dorman A*, **Didion JP***, Santos C*, Calaway JD*. The 23rd International Mammalian Genome Conference meeting report. *Mammalian Genome* 2010, 21:217-223.
** Co-first author*
- o. Lange V, Malmstrom JA, **Didion JP**, et al. Targeted Quantitative Analysis of *Streptococcus pyogenes* Virulence Factors by Multiple Reaction Monitoring. *Molecular & Cellular Proteomics* 2008, 7:1489-1500.

Submitted and In Prep

Didion JP, et al. Genetic loci associated with preferential segregation of Robertsonian translocations identified by genome-wide association study of wild mice. In prep.

Calabrese JM, Starmer J, Yee D, Fedoriw AM, Smith K, Safi A, **Didion JP**, et al. Defining principles of gene and regulatory element imprinting in mouse trophoblast stem cells. Under review.

Honors and Awards

2014	HHS Ignite Selected Team Incubator program with \$5,000 funding	LabGenius: The Smart Lab Notebook for Scientists
2014	Nominated for Dean's Distinguished Dissertation Award in Bioinformatics and Computational Biology Institutional award	
2009-2010	Bioinformatics and Computational Biology Training Grant (GM067553-04) Institution-awarded fellowship	
2009/9	International Mammalian Genome Society Fellowship Travel grant	

Invited Presentations

2012/2	High-throughput mammalian genetics University of North Carolina
2011/1	High-throughput epigenetics: a methylation assay for the mouse Center for Genome Dynamics (Bar Harbor, ME)

Other Presentations, Meetings and Posters

2013/9	27th Intl. Mammalian Genome Conference (Salamanca, Spain) <i>Verne Chapman Young Scientist Award</i>	oral presentation
2013/5	12th Annual Meeting of the Complex Traits Community (Madison, WI) <i>Chicago Prize for Best Graduate Student Presentation</i>	oral presentation
2012/9	16th EBM Conference (Marseille, France)	oral presentation, poster
2012/9	UNC Genetics Department Retreat (Myrtle Beach, SC)	oral presentation
2011/9	UNC Genetics Department Retreat (Myrtle Beach, SC)	poster
2011/6	Genetics Society of America Mouse Genetics (Washington D.C.)	poster
2011/6	National Centers for Systems Biology Annual Meeting (Duke University)	poster
2010/10	24th Intl. Mammalian Genome Conference (Heraklion, Greece) <i>Genome Research Award for Outstanding Poster</i>	oral presentation, poster
2010/9	UNC Genetics Department Retreat (Myrtle Beach, SC)	poster
2010/5	9th Annual Meeting of the Complex Traits Community (Chicago, IL)	oral presentation
2009/9	23rd Intl. Mammalian Genome Conference (San Diego, CA)	oral presentation, poster
2009/9	UNC Genetics Department Retreat (Asheville, NC)	poster

Teaching

2013-14	Undergraduate senior research project Mentor
2013	Genetic Analysis 2 Teaching Assistant

Professional Memberships and Service

2013-2015	Secretariat, International Mammalian Genome Society Honorary Member
2013/9	Abstract Review Committee, UNC Genetics Department Retreat

Last updated: January 11, 2015
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