John Didion | PhD

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

Teaching Experience

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

[12] 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.

[11] 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*, online, 2015. DOI: 10.1038/ng.3222.

[10] **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.

[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 and **Didion JP** and Santos C and 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, Malmström JA, **Didion JP**, et al. "Targeted quantitative analysis of Streptococcus pyogenes virulence factors by multiple reaction monitoring," *Molecular & 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

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

2014.12	**NIH Intramural Sequencing Center Pilot Grant** *Epigenomic regulation of glucose response in a human pancreatic islet β cell line* Institutional award with funding for sequencing services
2014.12 to 2015.04	**Department of Health and Human Services Ignite** *LabGenius to The Smart Lab Notebook for Scientists* Incubator program with USD 5,000 funding
2009.09 to 2010.08	**Bioinformatics and Computational Biology Training Grant** *NIH GM067553-04* Institution-awarded fellowship
2009.09	**International Mammalian Genome Society Fellowship** *Travel grant*

Honors & Awards

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

Professional Memberships & Service

2013.09 to 2015.09	**International Mammalian Genome Society** *Secretariat member (honorary)*
2013.08	**UNC Genetics Department Retreat** *Abstract Review Committee*