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Academic Positions

2013– Assistant Professor, Department of Genetics, Perelman School of Medicine, University of Pennsylvania
2008 – 2012 Lilly-Life Sciences Research Foundation Postdoctoral Fellow, The University of Chicago, Department of Human Genetics, Laboratory of Kevin White

Education

2007 Ph.D. in Genetics, Stanford University. Advisor: Arend Sidow. Committee: Richard Myers, Gregory Barsh, Dmitri Petrov
2002 B.S. with High Honors in Biochemistry, University of Nebraska-Lincoln. Graduate of the University Honors Program

Awards and Fellowships

2008 – 2011 Lilly Fellowship, Life Sciences Research Foundation
2007 SMBE Graduate Student Travel Award
2005 – 2007 Stanford Genome Training Grant
2002 – 2005 National Science Foundation Graduate Research Fellowship
2001 Phi Beta Kappa
1997 – 2001 University of Nebraska Regent's, Robert C. Byrd Scholarships

Funding History

2013 – 2016 Identification and validation of cell specific eQTLs by Bayesian modeling, 1R01MH101822-01

Teaching and Professional Experience

2012– Academic Editor, PeerJ
2010 Instructor, ISTP30440: Systems Biology & Disease, The University of Chicago
2007– Journal referee: Genome Research, PLoS Genetics, PLoS Computational Biology, Nature Methods, Genome Biology, Human Molecular Genetics, Genetics, Physiological Genomics, Journal of Biomedical Informatics, PLoS One
2003 Teaching Assistant, Gene202: Human Genetics, Stanford University
2002 Teaching Assistant, Gene201: Human Genetics, Stanford University
2001 Teaching Assistant, Bioc433: Biochemistry Laboratory, University of Nebraska
1999 Teaching Assistant, Chem109: General Chemistry Laboratory, University of Nebraska

Publications

1. Mangravite LM*, Engelhardt BE*, Medina MW, Smith JD, **Brown CD**, Chasman DI, Mecham BH, Howie B, Shim H, Naidoo D, Feng Q, Rieder MJ, Chen YDI, Rotter JI, Ridker PM, Hopewell JC, Parish S, Armitage J, Collins R, Wilke RA, Nickerson DA, Stephens M, Krauss RM. A statin-dependent QTL for GATM expression is associated with statin-induced myopathy. *Nature*. 2013 Aug 28. doi: 10.1038/nature12508. PMID: 23995691.
2. **Brown CD**†, Mangravite LM, Engelhardt BE†. Integrative modeling of eQTLs and cis-regulatory elements suggests mechanisms underlying cell type specificity of eQTLs. *PLoS Genet*. 2013 Aug;9(8):e1003649. doi: 10.1371/journal.pgen.1003649. Epub 2013 Aug 1. PMID: 23935528; PMCID: PMC3731231.
3. Brägelmann J, Dagogo-Jack I, El Dinali M, Stricker T, **Brown CD**, Zuo Z, Khattri A, Keck M, McNerney ME, Longnecker R, Biegling K, Kocherginsky M, Alexander K, Salgia R, Lingen MW, Vokes EE, White KP, Cohen EE, Seiwert TY. Oral cavity tumors in younger patients show a poor prognosis and do not contain viral RNA. *Oral Oncology*. 2013 Mar 9. PMID: 23490885

4. Jiang Z, Xia F, Johnson K, **Brown CD**, Bartom E, Tuteja JH, Stevens R, Grossman R, Brumin M, White KP, Ghanim M. Comparative genome sequences of the primary endosymbiont *Candidatus Portiera aleyrodidarum* from the whitefly *Bemisia tabaci* B and Q biotypes. *Applied and Environmental Microbiology*. 2013 Jan 11. PMID: 23315735; PMCID: PMC3591977.
5. McNerney ME, **Brown CD**, Wang X, Bartom ET, Karmakar S, Bandlamudi C, Yu S, Ko J, Sandall BP, Stricker T, Anastasi J, Grossman RL, Cunningham JM, Le Beau MM, White KP. CUX1 is a haploinsufficient tumor suppressor gene on chromosome 7 frequently inactivated in acute myeloid leukemia. *Blood*. 2012 Dec 13. PMID: 23212519; PMCID: PMC3567344.
6. Gao W, Grossman R, Yu P, **Brown CD**, Slattery M, Ma L, White KP. Discovering Geometric Patterns in Genomic Data. *ACM-BCB 2012*.
7. Hekman KE, Yu G*, **Brown CD***, Zhu H, Du X, Gervin K, Undlien DE, Peterson A, Stevanin G, Clark HB, Pulst S, Bird T, White KP, Gomez CM. A Conserved eEF2 Coding Variant in SCA26 Leads to Loss of Translational Fidelity and Increased Susceptibility to Proteostatic Insult. *Human Molecular Genetics*. 2012 Sep 21. PMID:23001565. PMCID: PMC3516132.
8. Doré LC, Chlon TM, **Brown CD**, White KP, Crispino JD. Chromatin occupancy analysis reveals genome-wide GATA factor switching during hematopoiesis. *Blood*. 2012. Apr 19;119(16):3724-33. PMID: 22383799; PMCID: PMC3335379.
9. Tao Y*, Ruan J*, Yeh SH*, Lu X*, Wang Y*, Zhai W*, Cai J*, Ling S, Gong Q, Chong Z, Qu Z, Li Q, Liu J, Yang J, Zheng C, Zeng C, Wang HY, Zhang J, Wang SH, Hao L, Dong L, Li W, Sun M, Zou W, Yu C, Li C, Liu G, Jiang L, Xu J, Huang H, Li C, Mi S, Zhang B, Chen B, Zhao W, Hu S, Zhuang SM, Shen Y, Shi S, **Brown CD**, White KP, Chen DS, Chen PJ, Wu CI. Rapid growth of a hepatocellular carcinoma and the driving mutations revealed by cell-population genetic analysis of whole-genome data. *Proc Natl Acad Sci U S A*. 2011 Jul 19;108(29):12042-7. PMID:21730188
10. Innocenti F*, Cooper GM*, Stanaway IB, Gamazon ER, Smith JD, Mirkov S, Ramirez J, Liu W, Lin YS, Maloney C, Force Aldred S, Trinklein ND, Schuetz E, Nickerson DA, Thummel KE, Rieder MJ, Rettie AE, Ratain MJ, Cox NJ, **Brown CD**†. Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. *PLoS Genetics* 2011 7(5): e1002078. PMID: 21637794; PMCID: PMC3102751.
11. Nègre N*, **Brown CD***, Ma L*, Bristow CA*, Miller SW*, Wagner U*, Kheradpour P, Eaton ML, Loriaux P, Sealfon R, Li Z, Ishii H, Spokony RF, Chen J, Hwang L, Cheng C, Auburn RP, Davis MB, Domanus M, Shah PK, Morrison CA, Zieba J, Suchy S, Senderowicz L, Victorsen A, Bild NA, Grundstad AJ, Hanley D, MacAlpine DM, Mannervik M, Venken K, Bellen H, White R, Gerstein M, Russell S, Grossman RL, Ren B, Posakony JW, Kellis M, White KP. A cis-regulatory map for the *Drosophila* genome. *Nature* 2011 Mar 24; 471(7339):527-31. PMID: 21430782; PMCID: PMC3179250.
12. modENCODE Consortium, Roy S, Ernst J, Kharchenko PV, Kheradpour P, Negre N, Eaton ML, Landolin JM, Bristow CA, Ma L, Lin MF, Washietl S, Arshinoff BI, Ay F, Meyer PE, Robine N, Washington NL, Di Stefano L, Berezikov E, **Brown CD**, Candeias R, Carlson JW, Carr A, Jungreis I, Marbach D, Sealfon R, Tolstorukov MY, Will S, Alekseyenko AA, Artieri C, Booth BW, Brooks AN, Dai Q, Davis CA, Duff MO, Feng X, Gorchakov AA, Gu T, Henikoff JG, Kapranov P, Li R, MacAlpine HK, Malone J, Minoda A, Nordman J, Okamura K, Perry M, Powell SK, Riddle NC, Sakai A, Samsonova A, Sandler JE, Schwartz YB, Sher N, Spokony R, Sturgill D, van Baren M, Wan KH, Yang L, Yu C, Feingold E, Good P, Guyer M, Lowdon R, Ahmad K, Andrews J, Berger B, Brenner SE, Brent MR, Cherbas L, Elgin SC, Gingeras TR, Grossman R, Hoskins RA, Kaufman TC, Kent W, Kuroda MI, Orr-Weaver T, Perrimon N, Pirrotta V, Posakony JW, Ren B, Russell S, Cherbas P, Graveley BR, Lewis S, Micklem G, Oliver B, Park PJ, Celniker SE, Henikoff S, Karpen GH, Lai EC, MacAlpine DM, Stein LD, White KP, Kellis M. Identification of functional elements and regulatory circuits by *Drosophila* modENCODE. *Science*. 2010 Dec 24;330(6012):1787-97. doi: 10.1126/science.1198374. Epub 2010 Dec 22. PMID: 21177974; PMCID: PMC3192495.
13. Nègre N*, **Brown CD***, Shah PK, Kheradpour P, Morrison CA, Henikoff JG, Feng X, Ahmad K, Russell S, White RAH, Stein L, Henikoff S, Kellis M, White KP. A comprehensive map of insulator elements for the *Drosophila* genome. *PLoS Genetics* 2010 Jan 15;6(1):e1000814. PMID: 20084099; PMCID: PMC2797089.
14. Celniker SE, Dillon LAL, Gerstein MB, Gunsalus KC, Henikoff S, Karpen GH, Kellis M, Lai EC, Lieb JD, MacAlpine DM, Micklem G, Piano F, Snyder M, Stein L, White KP, Waterston RH, modENCODE Consortium. (2009). Unlocking the Secrets of the Genome. *Nature* 459 (7249): 927-930. PMID: 19536255

15. Liu J, Ghanim M, Xue L, **Brown CD**, Iossifov I, Angeletti C, Hua S, Nègre N, Ludwig M, Stricker T, Al-Ahmadie HA, Tretiakova M, Camp RL, Perera-Alberto M, Rimm DL, Xu T, Rzhetsky A, White KP.(2009). Analysis of Drosophila Segmentation Network Identifies a JNK Pathway Factor Overexpressed in Kidney Cancer. *Science* 323: 1218-1222. PMID: 19164706; PMCID: PMC2756524.
16. Cooper GM*, **Brown CD***. (2008). Qualifying the relationship between sequence conservation and molecular function. *Genome Research*. 18: 201-205. PMID: 18245453
17. **Brown CD**, Johnson DS, Sidow A. (2007). Functional architecture and evolution of transcriptional elements that drive gene coexpression. *Science*. 317: 1557-1560. PMID: 17872446
18. Johnson DS, Davidson B, **Brown CD**, Smith W, Sidow A. (2004). Noncoding regulatory sequences of Ciona exhibit strong correspondence between evolutionary constraint and functional importance. *Genome Research* 14: 2448-2456. PMID: 15545496; PMCID: PMC534669.

*Denotes equal contributions.

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