

CURRICULUM VITAE
PETER WHITE, PHD

PRESENT TITLE & AFFILIATION

Senior Director, Computational Genomics Group, The Institute for Genomic Medicine
Principal Investigator, Abigail Wexner Research Institute
Nationwide Children's Hospital
Columbus, Ohio

Associate Professor of Pediatrics with Tenure
Department of Pediatrics
College of Medicine
The Ohio State University
Columbus, Ohio

OFFICE ADDRESS

The Institute for Genomic Medicine
Nationwide Children's Hospital
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Columbus, Ohio 43215

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EDUCATION

UNDERGRADUATE TRAINING

1994 **B.S. Applied Biology**
Brunel University, London, UK

GRADUATE TRAINING

1998 **PhD Molecular Biology**
University of Cambridge, Cambridge, UK
Thesis Title: "*Nutritional Regulation of Muscle Gene Expression*"

POST-GRADUATE EDUCATION & TRAINING

- 1998 – 2000 **Postdoctoral Fellow**
Howard Hughes Medical Institute
Department of Genetics
University of Pennsylvania School of Medicine
- 2000 – 2002 **Postdoctoral Scientist**
Rohm & Haas Company
Spring House, PA

PROFESSIONAL EXPERIENCE

- 2003 – 2008 **Technical Director**, Functional Genomics Core Facility
Institute of Diabetes, Obesity and Metabolism (IDOM)
Departments of Genetics and Endocrinology
University of Pennsylvania School of Medicine
Philadelphia, PA
- 2008 – 2016 **Principal Investigator**, Center of Microbial Pathogenesis
The Research Institute at Nationwide Children’s Hospital
Columbus, OH
- 2014 – Present **Chief Scientific Officer**, GenomeNext LLC,
Columbus, OH
- 2016 – Present **Principal Investigator**, The Institute for Genomic Medicine
The Research Institute at Nationwide Children’s Hospital
Columbus, OH

ACADEMIC APPOINTMENTS

- 2008 – 2011 **Research Assistant Professor of Pediatrics** (Research Track)
Department of Pediatrics
The Ohio State University College of Medicine
Columbus, OH
- 2011 – 2016 **Assistant Professor of Pediatrics** (Tenure Track)
Department of Pediatrics
The Ohio State University College of Medicine
Columbus, OH

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2016 – Present **Tenured Associate Professor of Pediatrics**
Department of Pediatrics
The Ohio State University College of Medicine
Columbus, OH

HOSPITAL AND ADMINISTRATIVE APPOINTMENTS

2008 – 2016 **Director, Biomedical Genomics Core Facility**
The Research Institute at Nationwide Children’s Hospital
Columbus, OH

2012 – 2016 **Director of Molecular Bioinformatics**
The Research Institute at Nationwide Children’s Hospital
Columbus, OH

2013 – 2016 **Clinical Genomics Consultant**
Cytogenetics and Molecular Genetics Laboratories
Department of Pathology and Laboratory Medicine
Nationwide Children’s Hospital
Columbus, OH

2016 – Present **Senior Director, Computational Genomics Group**
The Institute for Genomic Medicine
Nationwide Children’s Hospital
Columbus, OH

SERVICE

ACADEMIC ADMINISTRATIVE RESPONSIBILITIES

2010 **Committee Chair**
Equipment Grant Advisory Committee
The Research Institute at Nationwide Children’s Hospital

2010 – 2014 **Committee Member**
Research Information Technology Advisory Council
The Research Institute at Nationwide Children’s Hospital

2010 – 2011 **Search Committee Member**
Center for Molecular and Human Genetics
The Research Institute at Nationwide Children’s Hospital

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|----------------|--|
| 2013 – present | Executive Committee Member Research Computing Steering Committee The Research Institute at Nationwide Children’s Hospital |
| 2013 – 2014 | Search Committee Member Chief Research Information Officer The Research Institute at Nationwide Children’s Hospital |
| 2014 – 2016 | Search Committee Member Director of the Institute for Genomic Medicine The Research Institute at Nationwide Children’s Hospital |
| 2014 – 2017 | Executive Committee Member Data & Analytics Strategy Committee Nationwide Children’s Hospital |
| 2017 | Organizing Committee Member The Road to Collaboration: NCH/OSU Human Genetics Community Meeting The Research Institute at Nationwide Children’s Hospital |
| 2016 – 2017 | Committee Chair The Institute for Genomic Medicine Cloud Computing Design Team Nationwide Children’s Hospital |
| 2016 – 2017 | Executive Committee Member The IGM Cloud Computing Executive Steering Committee Nationwide Children’s Hospital |
| 2018 | Organizing Committee Member 2018 Research Retreat The Research Institute at Nationwide Children’s Hospital |
| 2016 – Present | Executive Member The Institute for Genomic Medicine Senior Leadership Team Nationwide Children’s Hospital |
| 2018 – present | Committee Chair The IGM Laboratory Information Management System (LIMS) Project Leadership Team Nationwide Children’s Hospital |
| 2018 – present | Executive Committee Member The IGM LIMS Executive Steering Committee (Project Sponsor) Nationwide Children’s Hospital |

NATIONAL ACTIVITIES

- 2009 **Ad hoc reviewer: NIH**
Center for Scientific Review Special Emphasis Panel
Genome Instrumentation
National Council for Research Resources (NCRR)
- 2009 **Ad hoc reviewer: NIH**
Population Genetics Analysis Program Special Emphasis Panel
National Institute of Allergy and Infectious Diseases (NIAID)
- 2009 – 2014 **Genomics Consultant**
Biospecimen Core Resource
The Cancer Genome Atlas (NCI)
Nationwide Children’s Hospital
- 2010 **Ad hoc reviewer: NIH**
Center for Scientific Review
Shared Instrumentation Study Section
National Council for Research Resources (NCRR)
- 2011 – 2012 **Member, Batch Effects Committee**
The Cancer Genome Atlas (NCI)
- 2012 **Ad hoc reviewer: NIH**
Center for Scientific Review Special Emphasis Panel
Shared Instrumentation: Genomics
Office of Research Infrastructure Programs (ORIP)
- 2013 **Ad hoc reviewer: NIH**
Understanding the Functions of Uncharacterized Genes in Infectious
Disease Pathogens (U19)
Special Emphasis Panel
National Institute of Allergy and Infectious Diseases (NIAID)
- 2014 **Ad hoc reviewer: NIH**
Center for Scientific Review Special Emphasis Panel
Shared Instrumentation: Genomics
Office of Research Infrastructure Programs (ORIP)
- 2015 **Ad hoc reviewer: NIH**
Center for Scientific Review Special Emphasis Panel
Shared Instrumentation: Genomics
Office of Research Infrastructure Programs (ORIP)

- 2018 **Ad hoc reviewer: NIH**
Undiagnosed Disease Network Phase II Sequencing Core
National Human Genome Research Institute (NHGRI)
- 2019 **Scientific Advisory Board Member**
St. Jude Children's Research Hospital, Memphis, TN

INTERNATIONAL ACTIVITIES

- 2017 **Ad hoc reviewer: Canada Foundation for Innovation**
John R. Evans Leaders Fund
Expert Review Committee
- 2017 **Ad hoc reviewer: Genome Quebec**
Genome Canada 2017 LSARP Competition
Expert Review Committee

HONORS AND AWARDS

- 2012 **Inventor of the Year** (Finalist)
TechColumbus Innovation Awards
- 2013 **The CLARITY Challenge** (Finalist)
Boston Children's Hospital
- 2014 **The INTEL Head in the Clouds Challenge on AWS POC**
Winner of \$80,000 award to perform population scale genomic analysis on the AWS Cloud using Intel processors
- 2015 **The CLARITY *Undiagnosed* Challenge** (First place)
Winner of \$25,000 award in an international competition to apply genomic information to diagnoses, and set clinical standards for analysis and reporting.
Boston Children's Hospital
- 2015 **2015 College of Medicine Faculty Achievement Award**
The Ohio State University
- 2017 **AWS Cloud Credits**
Winner of \$30,000 award from Amazon Web Services for AWS cloud credits to establish a genomics cloud computing environment for the Institute of Genomic Medicine.
- 2017 **Nationwide Children's Hospital Team of the Year 2017**
Lead The Institute for Genomic Medicine Cloud Design Team, which received the 2017 Outstanding Team of the Year award.

RESEARCH SUPPORT

ONGOING RESEARCH

U54 CA232561 Timothy P Cripe and Elaine R Mardis (Co-PI) 9/12/2019-8/31/2024
National Cancer Institute (NCI) / NIH

Pediatric Ohio-New York Cancer (Peds-ONC) Immunotherapy Center

We seek to discover and validate strategies to leverage both innate and adaptive immunity to devise and test novel immunotherapies for cancer. We also explore ways to enhance the effectiveness of cellular and virus derived immunotherapies by combining them with other biologics or small molecule drugs that modulate the tumor immune microenvironment. Our collective projects, supported by two shared resource cores, will reduce the burden of cancer by providing the nonclinical data needed to launch combination immunotherapy clinical trials and ultimately this project will lead to new and more effective treatment options for patients with childhood cancers.

Role: ***Co-Investigator***

R01 AR073311 Chack-Yung Yu, PhD (PI) 7/8/2018-5/31/2023
National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS) / NIH

Complement in Human Lupus: Deficiencies, Profiles and Complications

The complement system is an important effector arm of the immune response. This proposal seeks to study thoroughly the genes and proteins of the complement system on the cause and modifications of disease profiles and outcomes in human lupus and lupus nephritis.

Role: ***Co-Investigator as the senior Q/C Specialist***

R01 CA223219 Paul J Goodfellow, PhD (PI) 7/1/2018-6/30/2023
The Ohio State University / National Cancer Institute (NCI) / NIH

Combined NGS tumor-based detection of germline Lynch syndrome mutations and prognostic classification of endometrial cancers

The work proposed is to develop reliable, low-cost, and highly sensitive tumor-based DNA methods to identify women with inherited forms of endometrial cancer, and at the same time, test for genetic changes useful for treatment planning. By studying DNA specimens prepared in clinically approved laboratories, it will be possible to rapidly take research findings to clinical testing. Robust tumor-based testing that can be applied to all endometrial cancer patients will translate to improved cancer prevention and treatment.

Role: ***Co-Investigator as the senior Q/C Specialist***

R21 DC016709 Kenneth L Brockman, PhD (PI) 3/1/2019-8/31/2020
Medical College of Wisconsin / National Institute on Deafness & other Communication Disorders
Role of epigenetic regulation in the persistence of NTHI during colonization, ascension of the Eustachian tube and chronic otitis media

Otitis media, or middle ear infection, is the most predominant bacterial disease of childhood and is the most common cause of hearing loss in young children. Several of the bacteria that cause this disease have developed a novel mechanism (the phasevarion) to avoid immune system defenses and resist treatment. The overall focus our research and the goal of this project is to better understand the role of this novel mechanism during disease in order to enable the development of improved methods to prevent and treat otitis media and other upper respiratory infections.

Role: ***Co-Investigator as the senior Q/C Specialist***

COMPLETED RESEARCH

KOPP1610 Benjamin Kopp, MD (PI) 10/31/2016-04/30/2019
Cystic Fibrosis Foundation (CFF)
CFTR modulator impact on macrophage function and inflammatory networks

Cystic fibrosis (CF) is an under-recognized immunodeficiency. Although advances in CF knowledge and care (i.e., CFTR modulators) have improved clinical outcomes, patients with CF remain burdened by chronic, multi-drug-resistant bacterial infections. There is a clear need for NEW therapeutics approaches to infection in CF.

Role: ***Co-Investigator as the senior Q/C Specialist***

R01 AI116917 John Gunn, PhD (PI) 06/01/2016-05/31/2019
The Ohio State University / National Institutes of Health (NIH)
Mechanisms of the development and maintenance of Salmonella gallbladder carriage

Typhoid Fever is a global human-specific illness. Approximately 5% of individuals that resolve an acute infection become chronic carriers, with the gallbladder being the primary site of carriage. Our goal is to better understand the environment that allows for asymptomatic chronic carriage and to develop therapies to reverse/prevent it.

Role: ***Co-Investigator as the senior Q/C Specialist***

R21 AR070509 Chack-Yung Yu, PhD (PI) 4/17/2017-3/31/2019
National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS) / NIH
MHC Complement Variants in Disease Susceptibility of Idiopathic Inflammatory Myopathies

The goal of this project is to study how genetic diversity of complement contributes to pathogenesis of different forms of muscle diseases with inflammation. The project may yield new knowledge relevant for future treatment of inflamed muscle diseases.

Role: ***Co-Investigator as the senior Q/C Specialist***

Amazon Web Services **Peter White, PhD (PI)** 9/16/2016-9/15/2017
\$30,000 total costs AWS Cloud Credits for Research program award to establish a genomics cloud computing environment for the Institute for Genomic Medicine.

Role: **Principal Investigator**

1R01HL109758 **Peter White, PhD (Co-PI)** 9/24/2012 – 7/31/2017
National Institutes of Health (NIH) / National Heart, Lung, and Blood Institute (NHLBI)

Exome Sequencing and Functional Studies in Familial CHD

The objectives of this project are to utilize cutting edge next-generation sequencing technologies, innovative bioinformatics and statistical approaches, and advanced molecular biological techniques to identify genetic etiologies for congenital heart defects in humans.

Role: **Co-Principal Investigator**

OSU CCTS Award **Peter White, PhD (Co-PI)** 6/26/2015 – 4/30/2016
Ohio State University Office of Sponsored Programs

Development of Novel Humans In Vitro Models of Granulomatous Disease

Provide support for the proposed genomic approaches and contribute to the interpretation, presentation, and design of the experiments and preparation of subsequent related grant applications.

Role: **Co-Principal Investigator**

FA8650-12-2-6359 Gail Herman, PhD (PI) 9/30/2012 – 9/29/2015
Air Force Medical Service / Department of Defense

A Collaborative Translational Autism Research Program for the Military

Develop a registry for autism spectrum disorders composed of families from central Ohio and those in the military stationed at Wright-Patterson Air Force Base (WPAFB) and result in the improved diagnosis and care of those enrolled and enhance biomedical research on the diagnosis, causes and treatment of autism in general.

Role: **Co-Investigator**

Sponsored Research Project **Peter White, PhD (PI)** 12/1/2014 – 11/30/2015
GenomeNext LLC

Churchill Development Plan: Online Software as a Service

NCHRI Internal Award Samantha King, PhD (PI) 2/1/2012 – 1/31/2014
Identification of Pneumococcal Sequence Variants that Correlate with Development of Hemolytic Uremic Syndrome

Completion of these proposed studies will be significant as the increased understanding of pHUS achieved will allow researchers to take, for the first time, a rational approach to development of treatments for this devastating disease. The proposed research is innovative as it uses cutting edge technology to take a genome wide approach to understanding pHUS.

Role: **Collaborator**

NCHRI Internal Award **Peter White, PhD (PI)** 5/1/2012 – 7/31/2013
Churchill on the Cloud

Development of a cloud computing prototype for the discovery of human genetic variation.

Office of Technology Commercialization

Role: **Principal Investigator**

1R21HL106549-01 Kim McBride, M.D. (PI) 12/1/2010 – 11/30/2012
National Institutes of Health (NIH) / National Heart, Lung, and Blood Institute (NHLBI)
Exome Sequencing in Familial Cardiovascular Malformations

Left ventricular outflow tract malformations are most often diagnosed in infancy or childhood. The investigation specifically targets this group. The research will be performed in large tertiary care centers for children by teams with extensive expertise in the medical and surgical care of critically ill children.

Role: **Co-Investigator**

NCHRI Internal Award **Peter White, PhD (PI)** 11/1/2010 – 10/31/12
Elucidation of the Genetic Basis for Prune Belly Syndrome

We propose that a gene with a critical role in mesenchymal development is mutated in individuals with prune belly syndrome, and the use of exome capture and DNA sequencing to identify this gene.

Role: **Principal Investigator**

FA7014-09-2-0004 Gail Herman, M.D., PhD (PI) 9/30/2009 – 9/29/2012
Air Force Medical Service
Comprehensive Clinical Phenotyping and Genetic Mapping for the Discovery of Autism Susceptibility Genes

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Develop a registry for autism spectrum disorders composed of families from central Ohio and those in the military stationed at Wright-Patterson Air Force Base (WPAFB) and result in the improved diagnosis and care of those enrolled and enhance biomedical research on the diagnosis, causes and treatment of autism in general.

Role: **Co-Investigator**

1S10RR026942 **Peter White, PhD (PI)** 3/18/2010 – 4/18/2011

National Institutes of Health (NIH) / National Council for Research Resources (NCRR)

Shared Instrumentation Grant Program (S10)

Acquisition of an Illumina Genome Analyzer for the Research Institute

The major goal of this project is to establish the next generation sequencing technology at the Research Institute at Nationwide Children’s Hospital.

Role: **Principal Investigator**

N01-CM-91001-03 Peter Houghton, PhD (PI) 11/01/2009 -- 11/30/2011

National Institutes of Health (NIH) / National Cancer Institute (NCI)

Pediatric Preclinical Testing Program

Evaluate new agents in comprehensive models of childhood cancer xenografts and identify those having either broad spectrum or tumor-specific activity.

Role: **Co-Investigator**

29XS073ST Julie Gastier-Foster, PhD (PI) 10/31/2009 – 5/22/2012

National Institutes of Health (NIH) / National Cancer Institute (NCI)

Biospecimen Core Resource for The Cancer Genome Atlas Project

The Contractor shall function as a fundamental resource and play a key role in TCGA. Key goals shall include ensuring that standards are developed, implemented and maintained for all aspects of cancer-related biospecimen management and processing to support genomic characterization.

Role: **Co-Investigator**

PATENTS AND TECHNOLOGY LICENSES

PUBLISHED PATENTS

US Patent 9,552,458 B2 “Comprehensive Analysis Pipeline for Discovery of Human Genetic Variation” **White, Peter**. Newsom, David. Yangqiu Hu. Filed March 16, 2012. Licensed to GenomeNext LLC June 14, 2014. Published January 24, 2017.

PCT/US2015/061924 “Parallel-Processing Systems and Methods for Highly Scalable Analysis of Biological Sequence Data” Fitch, James. **White, Peter**. Kelly, Ben. Filed November 20, 2015. Patent Application (US 2017/0316154 A1) Published November 2, 2017.

PENDING PATENTS

US Provisional Patent Application 62/083,000 “Systems and Methods for Highly Scalable Analysis of Genome Sequence Data” **White, Peter**. Kelly, Benjamin. Fitch, James. Filed on November 11, 2014. Licensed to GenomeNext LLC November 11, 2014

PCT Patent Application No. PCT/US2015/061924 “Systems and Methods for Highly Scalable Analysis of Genome Sequence Data” **White, Peter**. Fitch, James. Kelly, Ben. Filed 11/20/2015. Published as WO 2016/081866 on 05/26/2016.

US Continuation Patent Application 15/412,503 “Comprehensive Analysis Pipeline for Discovery of Human Genetic Variation” **White, Peter**. Newsom, David. Yangqiu Hu. Filed on January 24, 2017. Licensed to GenomeNext LLC November 11, 2014

INVENTION DISCLOSURES

Ahmer, Brian. Ali, Mohamed. Gonzalez, Juan. Berman, Edward. Newsom, David. **White, Peter**. (2013) A Critical Nutrient Source and Drug Target During Salmonella-Mediated Inflammation. *Invention Disclosure* April 18, 2013. Technology Commercialization & Knowledge Transfer, The Ohio State University.

Ahmer, Brian. Ali, Mohamed. Newsom, David. **White, Peter**. (2012) Salmonella Genetic Locus Required for Colonization of the Inflamed Intestine. *Invention Disclosure* May 10, 2012. Technology Commercialization & Knowledge Transfer, The Ohio State University.

White, Peter. Newsom, David. Yangqiu Hu. (2013) Churchill: A Comprehensive Analysis Pipeline for Discovery of Human Genetic Variation. *Invention Disclosure* February 24, 2012. Office of Technology Commercialization, The Research Institute at Nationwide Children's Hospital.

White, Peter. Kelly, Benjamin. Fitch, James. (2014) Solutions for Highly Scalable Analysis of Genome Sequence Data: New Methods to Parallelize Secondary Data Analysis. *Invention Disclosure* November 3, 2014. Office of Technology Commercialization, The Research Institute at Nationwide Children's Hospital.

White, Peter. Fitch, James. (2014) "Listener" Designed to Provision AWS Resources and Execute Analysis Pipelines. *Invention Disclosure* November 3, 2014. Office of Technology Commercialization, The Research Institute at Nationwide Children's Hospital.

White, Peter. Kuck, Harkness. Kelly, Benjamin. Fitch, James. (2014) Tertiary Data Analysis and a Database Framework for Large Genomic Datasets. *Invention Disclosure* November 3, 2014. Office of Technology Commercialization, The Research Institute at Nationwide Children's Hospital.

Koboldt, Daniel. **White, Peter.** Gastier-Foster, Julie. Zmuda, Erik. (2016) Improved variant prioritization for clinical sequencing. *Invention Disclosure* October 3, 2016. Office of Technology Commercialization, The Research Institute at Nationwide Children's Hospital.

PUBLICATIONS

ARTICLES IN PEER REVIEWED JOURNALS

1. Dauncey MJ, Burton KA, **White P**, Harrison AP, Gilmour RS, Duchamp C, Cattaneo D. (1994) Nutritional regulation of growth hormone receptor gene expression. *The FASEB Journal: Official Publication Of The Federation Of American Societies For Experimental Biology*. 8(1):81-8. doi: 10.1096/fasebj.8.1.7507871. PubMed PMID: 7507871.
2. **White P**, Dauncey MJ. (1999) Differential expression of thyroid hormone receptor isoforms is strikingly related to cardiac and skeletal muscle phenotype during postnatal development. *Journal Of Molecular Endocrinology*. 23(2):241-54. doi: DOI 10.1677/jme.0.0230241. PubMed PMID: WOS:000083437200011.
3. Katsumata M, Cattaneo D, **White P**, Burton KA, Dauncey MJ. (2000) Growth hormone receptor gene expression in porcine skeletal and cardiac muscles is selectively regulated by postnatal undernutrition. *The Journal Of Nutrition*. 130(10):2482-8. doi: 10.1093/jn/130.10.2482. PubMed PMID: 11015477.
4. **White P**, Cattaneo D, Dauncey MJ. (2000) Postnatal regulation of myosin heavy chain isoform expression and metabolic enzyme activity by nutrition. *The British Journal Of Nutrition*. 84(2):185-94. doi: S0007114500001410 [pii]. PubMed PMID: 11029969.
5. **White P**, Cooke N. (2000) The multifunctional properties and characteristics of vitamin D-binding protein. *Trends in Endocrinology and Metabolism*. 11(8):320-7. doi: Doi 10.1016/S1043-2760(00)00317-9. PubMed PMID: WOS:000089611300005.
6. Dauncey MJ, **White P**, Burton KA, Katsumata M. (2001) Nutrition-hormone receptor-gene interactions: implications for development and disease. *The Proceedings Of The Nutrition Society*. 60(1):63-72. PubMed PMID: 11310425.
7. **White P**, Burton KA, Fowden AL, Dauncey MJ. (2001) Developmental expression analysis of thyroid hormone receptor isoforms reveals new insights into their essential functions in cardiac and skeletal muscles. *The FASEB Journal : Official Publication Of The Federation Of American Societies For Experimental Biology*. 15(8):1367-76. doi: 10.1096/fj.00-0725com. PubMed PMID: 11387234.
8. **White P**, Liebhaber SA, Cooke NE. (2002) 129X1/SvJ mouse strain has a novel defect in inflammatory cell recruitment. *Journal Of Immunology*. 168(2):869-74. doi: DOI 10.4049/jimmunol.168.2.869. PubMed PMID: WOS:000173193700041.
9. **White P**, Brestelli JE, Kaestner KH, Greenbaum LE. (2005) Identification of transcriptional networks during liver regeneration. *The Journal Of Biological Chemistry*. 280(5):3715-22. doi: 10.1074/jbc.M410844200. PubMed PMID: 15546871.
10. Burkhardt BR, Greene SR, **White P**, Wong RK, Brestelli JE, Yang J, Robert CE, Brusko TM, Wasserfall CH, Wu J, Atkinson MA, Gao Z, Kaestner KH, Wolf BA. (2006) PANDER-induced cell-death genetic networks in islets reveal central role for caspase-3 and cyclin-dependent kinase inhibitor 1A (p21). *Gene*. 369:134-41. doi: 10.1016/j.gene.2005.10.040. PubMed PMID: 16412588.

11. Mazzarelli JM, **White P**, Gorski R, Brestelli J, Pinney DF, Arsenlis A, Katokhin A, Belova O, Bogdanova V, Elisafenko E, Gubina M, Nizolenko L, Perelman P, Puzakov M, Shilov A, Trifonoff V, Vorobjeva N, Kolchanov N, Kaestner KH, Stoeckert CJ, Jr. (2006) Novel genes identified by manual annotation and microarray expression analysis in the pancreas. *Genomics*. 88(6):752-61. doi: 10.1016/j.ygeno.2006.04.005. PubMed PMID: 16725306.
12. Gao N, **White P**, Doliba N, Golson ML, Matschinsky FM, Kaestner KH. (2007) Foxa2 controls vesicle docking and insulin secretion in mature Beta cells. *Cell Metabolism*. 6(4):267-79. doi: 10.1016/j.cmet.2007.08.015. PubMed PMID: 17908556.
13. Gupta RK, Gao N, Gorski RK, **White P**, Hardy OT, Rafiq K, Brestelli JE, Chen G, Stoeckert CJ, Jr., Kaestner KH. (2007) Expansion of adult beta-cell mass in response to increased metabolic demand is dependent on HNF-4alpha. *Genes & Development*. 21(7):756-69. doi: 10.1101/gad.1535507. PubMed PMID: 17403778; PubMed Central PMCID: PMC1838528.
14. Hardy OT, Hohmeier HE, Becker TC, Manduchi E, Doliba NM, Gupta RK, **White P**, Stoeckert CJ, Jr., Matschinsky FM, Newgard CB, Kaestner KH. (2007) Functional genomics of the beta-cell: short-chain 3-hydroxyacyl-coenzyme A dehydrogenase regulates insulin secretion independent of K⁺ currents. *Molecular Endocrinology* 21(3):765-73. doi: 10.1210/me.2006-0411. PubMed PMID: 17185391.
15. Keller DM, McWeeney S, Arsenlis A, Drouin J, Wright CV, Wang H, Wollheim CB, **White P**, Kaestner KH, Goodman RH. (2007) Characterization of pancreatic transcription factor Pdx-1 binding sites using promoter microarray and serial analysis of chromatin occupancy. *The Journal Of Biological Chemistry*. 282(44):32084-92. doi: 10.1074/jbc.M700899200. PubMed PMID: 17761679.
16. Ku HT, Chai J, Kim YJ, **White P**, Purohit-Ghelani S, Kaestner KH, Bromberg JS. (2007) Insulin-expressing colonies developed from murine embryonic stem cell-derived progenitors. *Diabetes*. 56(4):921-9. doi: 10.2337/db06-0468. PubMed PMID: 17395739.
17. Mazzarelli JM, Brestelli J, Gorski RK, Liu J, Manduchi E, Pinney DF, Schug J, **White P**, Kaestner KH, Stoeckert CJ, Jr. (2007) EPConDB: a web resource for gene expression related to pancreatic development, beta-cell function and diabetes. *Nucleic Acids Research*. 35(Database issue):D751-5. doi: 10.1093/nar/gkl748. PubMed PMID: 17071715; PubMed Central PMCID: PMC1781120.
18. Bochkis IM, Rubins NE, **White P**, Furth EE, Friedman JR, Kaestner KH. (2008) Hepatocyte-specific ablation of Foxa2 alters bile acid homeostasis and results in endoplasmic reticulum stress. *Nature Medicine*. 14(8):828-36. doi: 10.1038/nm.1853. PubMed PMID: 18660816; PubMed Central PMCID: PMC4095974.
19. Mullany LK, **White P**, Hanse EA, Nelsen CJ, Goggin MM, Mullany JE, Anttila CK, Greenbaum LE, Kaestner KH, Albrecht JH. (2008) Distinct proliferative and transcriptional effects of the D-type cyclins in vivo. *Cell Cycle*. 7(14):2215-24. doi: 10.4161/cc.7.14.6274. PubMed PMID: 18635970; PubMed Central PMCID: PMC4000162.
20. Tuteja G, Jensen ST, **White P**, Kaestner KH. (2008) Cis-regulatory modules in the mammalian liver: composition depends on strength of Foxa2 consensus site. *Nucleic Acids Research*. 36(12):4149-57. doi: 10.1093/nar/gkn366. PubMed PMID: 18556755; PubMed Central PMCID: PMC2475634.

21. **White P**, May CL, Lamounier RN, Brestelli JE, Kaestner KH. (2008) Defining pancreatic endocrine precursors and their descendants. *Diabetes*. 57(3):654-68. doi: 10.2337/db07-1362. PubMed PMID: 18071024.
22. Anderson KR, **White P**, Kaestner KH, Sussel L. (2009) Identification of known and novel pancreas genes expressed downstream of Nkx2.2 during development. *Bmc Developmental Biology*. 9:65. doi: 10.1186/1471-213X-9-65. PubMed PMID: 20003319; PubMed Central PMCID: PMC2799404.
23. Gao N, **White P**, Kaestner KH. (2009) Establishment of intestinal identity and epithelial-mesenchymal signaling by Cdx2. *Developmental Cell*. 16(4):588-99. doi: 10.1016/j.devcel.2009.02.010. PubMed PMID: 19386267; PubMed Central PMCID: PMC2673200.
24. Golson ML, Le Lay J, Gao N, Bramswig N, Loomes KM, Oakey R, May CL, **White P**, Kaestner KH. (2009) Jagged1 is a competitive inhibitor of Notch signaling in the embryonic pancreas. *Mechanisms Of Development*. 126(8-9):687-99. doi: 10.1016/j.mod.2009.05.005. PubMed PMID: 19501159; PubMed Central PMCID: PMC2728177.
25. Le Lay J, Tuteja G, **White P**, Dhir R, Ahima R, Kaestner KH. (2009) CRTC2 (TORC2) contributes to the transcriptional response to fasting in the liver but is not required for the maintenance of glucose homeostasis. *Cell Metabolism*. 10(1):55-62. doi: 10.1016/j.cmet.2009.06.006. PubMed PMID: 19583954; PubMed Central PMCID: PMC2748661.
26. Li Z, **White P**, Tuteja G, Rubins N, Sackett S, Kaestner KH. (2009) Foxa1 and Foxa2 regulate bile duct development in mice. *The Journal Of Clinical Investigation*. 119(6):1537-45. doi: 10.1172/JCI38201. PubMed PMID: 19436110; PubMed Central PMCID: PMC2689124.
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21. **White P**, Newsom D, Zhong H, McBride K. (2011) "Whole-exome sequencing identifies an autosomal recessive mutation in familial congenital heart disease." Advances in Genome Biology & Technology Conference, Marco Island, FL. **Abstract selected podium presentation.**
22. Sowby W, Nick E, Rudrarahu S, Zhong H, Newsom D, **White P**. (2011) "Elucidating the genomic and epigenomic mechanisms of nutritionally regulated development programming." The Annual Research Conference, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio
23. Hu Y, Newsom D, Zhong H, Casper T, Geier B, **White P**. (2011) "Exome Capture and sequencing using the HiSeq 2000." The Annual Research Conference, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio
24. Casper T, Hu Y, Geier B, Zhong H, Newsom D, **White P**. (2011) "Surfing the HiSeq 2000 data tsunami." The Annual Research Conference, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio
25. Newsom D, Sowby W, Zhong H, Hu Y, Geier B, Casper T, **White P**. (2011) "The Biomedical Genomics Core." The Annual Research Conference, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio
26. Banks W, Hanser E, Cunningham D, Varga E, Evans J, Butter E., **White P**, Geier B, McBride K, Zernzach R, Herman G. (2011) "Analysis of candidate genes for ASD's within the Central Ohio Registry." The Annual Research Conference, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio

27. Geier B, Kurmasheva R, **White P**, Houghton PJ. (2011) "Evaluating pediatric preclinical trial therapeutics." The Annual Research Conference, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio
28. Santana E, Hu Y, **White P**, Munson Jr. RS, Harrison A. (2011) "A whole transcriptome analysis of nontypeable *Haemophilus influenzae*" The Annual Research Conference, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio
29. Harrison A, Baker BD, Newsom D, **White P**, Munson Jr. RS. (2011) "The RpoE regulons in nontypeable *Haemophilus influenzae*." The Annual Research Conference, The Research Institute at Nationwide Children's Hospital, Columbus, Ohio
30. Harrison A, Baker BD, Newsom D, **White P**, Munson Jr. RS. (2011) "The RpoE regulons in nontypeable *Haemophilus influenzae*." The American Society for Microbiology, New Orleans, Louisiana
31. Santana EA, Harrison A, Hu P, **White P**, Munson Jr. RS. (2012) "Fur-regulated small RNAs in nontypeable *Haemophilus influenzae*." The Ohio Branch, American Society for Microbiology, Mason Ohio
32. Corsmeier D, Kelly B, Hu Y, Casper T, Newsom D, Zhong H, **White P**. (2012) "ROOSEVELT: An interactive tool for tertiary analysis and visualization of human genetics." The 2nd International Society for Computational Biology Great Lakes Bioinformatics Conference, Ann Arbor, Michigan
33. Casper T, Hu Y, Munson R, **White P**. (2012) "A hybrid approach to *de novo* assembly of microbial genomes using short read sequencing data." The 2nd International Society for Computational Biology Great Lakes Bioinformatics Conference, Ann Arbor, Michigan
34. Hu Y, Newsome D, Kelly B, Casper T, Zhong H, **White P**. (2012) "Churchill: A comprehensive analysis pipeline for discovery of human genetic variation." The 2nd International Society for Computational Biology Great Lakes Bioinformatics Conference, Ann Arbor, Michigan
35. Kelly B, Hu Y, Casper T, Newsom D, Zhong H, Banks W, Herman G, **White P**. (2012) "Assessment of alignment and variant calling approaches for analysis of human exome capture sequencing data." The 2nd International Society for Computational Biology Great Lakes Bioinformatics Conference, Ann Arbor, Michigan
36. Flanigan KM, Gastier-Foster J, Pyatt R, Quinter Rosales X, Thrush D, Kneile K, Sahenk Z, Mendell J, Kelly B, Newsom D, Hu P, **White P**. (2012) "Comparison of commercially available exome capture kits in the diagnosis of neuromuscular disorders." The 17th International Congress of the World Muscle Society, Perth, Australia
37. **White P**, Kelly B, Hu P, Corsmeier D, Harvey D, Zhong H, Newsom D. (2013) "Churchill: A comprehensive and ultra-fast computational approach for the discovery of human genetic variation." Advances in Genome Biology & Technology Conference, Marco Island, Florida

38. Pfau R, Newsom D, **White P**, Reshmi S, Gastier-Foster J, Astbury C, Pyatt R. (2013) "Comparison of expected and observed coverage for total coding regions of genes in the RAS pathway using three commercially available whole-exome capture kits." ACMG Clinical Genetics Meeting, Phoenix, Arizona
39. Corsmeier D, Kelly B, **White P**. (2013) "The transition to clinical NGS: How well do you know your sequencing pipeline?" 2nd International Society for Computational Biology Great Lakes Bioinformatics Conference, Pittsburg, Pennsylvania
40. Kelly B, Fitch J, Corsmeier D, White P. (2013) "Churchill: A comprehensive and ultra-fast computational approach for the discovery of human genetic variation." 2nd International Society for Computational Biology Great Lakes Bioinformatics Conference, Pittsburg, Pennsylvania
41. Boncachea EM, Zender G, Corsmeier D, Fitzgerald-Butt S, Newsom D, **White P**, McBride KL, Garg V. (2013) "Use of a targeted next generation sequencing approach for the study of a cardiac valve malformation with complex polygenic heritability." American Academy of Pediatrics National Conference and Exhibition, Orlando, Florida
42. Patwardhan A, Lintner K, Rider LG, Miller FW, O'Hanlon T, Wu YL, Zhou B, Wang H, Newsom D, **White P**, Spencer CH, Yu CY. (2013) "Copy number variations of complement C4A and C4B genes are genetic risk factor and disease modification factor, respectively, for juvenile dermatomyositis." American College of Rheumatology Meeting, San Diego, California
43. Ali MM, Newsom D, Gonzalez J, Sabag-Daigle A, Stahl C, Steidley B, Dubena J, Dyszel JL, Smith JN, Dieye Y, Krakowa S, Romeo T, Behrman EJ, **White P**, Ahmer BMM. (2013) "A glycation product is a critical nutrient source for *Salmonella* in the inflamed intestine." 4th ASM Conference on Salmonella: The Bacterium, the Host and the Environment, Boston, Massachusetts
44. Corsmeier D, Kelly B, **White P**. (2013) "The transition to clinical NGS: How well do you know your sequencing pipeline?" The American Society of Human Genetics 63rd Annual Meeting, Boston, Massachusetts
45. Kelly B, Fitch J, Corsmeier D, Newsom D, **White P**. (2013) "Churchill: A cloud-enabled, ultra-fast computational approach for the discovery of human genetic variation." The American Society of Human Genetics 63rd Annual Meeting, Boston, Massachusetts
46. Fitch J, Kelly B, **White P**. (2013) "Ultrafast analysis of the 1,000 genomes project in the cloud with Churchill." Nationwide Children's Hospital Research Day, Columbus, Ohio
47. Wetzel A, Woodiga S, Kelly B, Fitch J, Singh A, King S, **White P**. (2013) "Hybrid isolation and differential expression sequencing (HIDEn-Seq): a new RNA-Seq strategy to elucidate host-pathogen transcriptome during infection from a single sample." Nationwide Children's Hospital Research Day, Columbus, Ohio
48. **White P**. (2014) "Population scale genomic analysis in the cloud." AWS Government, Education, and Nonprofits Symposium, Washington, DC

49. McBride KL, Nunez C, Soldatova L, Zender G, Fitzgerald-Butt SM, Corsmeier D, Askwith C, Kelly L, El-Hodiri H, **White P.** (2014) "Exome sequencing reveals possible role of SNN1D in syndrome of heart defects, intellectual disability, severe speech delay and brachydactyly." Nationwide Children's Hospital and OSU Human Genetics and Genomics Community Symposium, Columbus, Ohio
50. Kelly B, Fitch J, Corsmeier D, Newsom D, **White P.** (2014) "From single sample clinical analysis to population genomics, Churchill is an ultra-fast computational approach to human variant discovery no matter the scale." Nationwide Children's Hospital and OSU Human Genetics and Genomics Community Symposium, Columbus, Ohio
51. Fitch J, Kelly B, **White P.** (2014) "Ultrafast analysis of the 1,000 genomes project in the cloud with Churchill." Nationwide Children's Hospital and OSU Human Genetics and Genomics Community Symposium, Columbus, Ohio
52. Corsmeier D, Fitzgerald-Butt S, Zender G, Garg V, McBride K, **White P.** (2014) "High-throughput sequencing and bioinformatics analysis in familial congenital heart disease." Nationwide Children's Hospital and OSU Human Genetics and Genomics Community Symposium, Columbus, Ohio
53. **White P,** Vieland V, Greenberg D, Hodge S. (2014) "Combine and conquer: An integrated software suite for finding causal relationships between sequence variants and clinical phenotypes." The Nationwide Children's Hospital and OSU Human Genetics Community meeting, Columbus, Ohio. ***Invited podium presentation.***
54. **White P.** (2014) "Genomics in The Research Institute." GLBIO Annual Meeting, Cincinnati, Ohio
55. **White P.** (2014) "Churchill: An ultra-fast analysis pipeline for the discovery of human genetic variation in clinical and population scale genomics." Podium presentation at the GLBIO Annual Meeting, Cincinnati, Ohio. ***Abstract selected podium presentation.***
56. **White P.** Kelly B, Fitch J, Corsmeier D, Kuck H, Naik A. (2014) "Population scale genomic analysis in the cloud." Podium presentation at the AWS Government, Education and Nonprofits Symposium, Washington, DC. ***Invited podium presentation.***
57. Banks III W, Cunningham d, Hansen E, Ratliff-Schaub K, Butter E, Schulteis D, Boreman C, Kelly B, **White P,** Herman G. (2014) "Exome sequencing of 43 sporadic cases with an autism spectrum disorder in a local cohort of families identifies several *de novo* variants and implicates additional genes in ASD pathogenesis." The American Society of Human Genetics 64th Annual Meeting, San Diego, California
58. Corsmeier D, Fitzgerald-Butt S, Zender G, Mori M, Kelly L, Waters K, Vieland V, El Hodiri H, Garg V, McBride K, **White P.** (2014) "High throughput sequencing and bioinformatics analysis in familial congenital heart disease." The American Society of Human Genetics 64th Annual Meeting, San Diego, California

59. Kelly B, Fitch J, Corsmeier D, Kuck H, Naik A, **White P.** (2014) "Churchill: An ultra-fast analysis pipeline for the discovery of human genetic variation in clinical and population scale genomics." The American Society of Human Genetics 64th Annual Meeting, San Diego, California
60. Nadella V, Kelly B, Zhong H, Naik A, Wetzel A, **White P.** (2015) "Clinical performance of exome capture technology: impact of kits, coverage and analysis." 2015 Advances in Genome Biology & Technology Conference, Marco Island, Florida
61. Nadella V, Kelly B, Zhong H, Naik A, Wetzel A, **White P.** (2015) "Clinical performance of exome capture technology: impact of kits, coverage and analysis." 2015 Association for Biomolecular Resource Facilities Conference, St. Louis, Missouri
62. King SJ, Wetzel AN, Woodiga SA, Kelly B, Fitch J, Singh AK, **White P.** (2015) "Simultaneous definition of host and bacterial transcriptomes from a single sample: A system applicable to many disease states including otitis media." International Society for Otitis Media 18th International Symposia, National Harbor, Maryland
63. LaHaye S, Corsmeier D, Bowman JL, Fitzgerald-Butt S, Zender G, Boose K, McBride KL, **White P,** Garg V. (2015) "Utilization of whole-exome sequencing to identify causative mutations in familial congenital heart disease." American Heart Association: Scientific Sessions Council: Functional Genomics and Translational Biology Meeting, Orlando Florida
64. LaHaye S, Corsmeier D, Bowman JL, Fitzgerald-Butt S, Zender G, Boose K, McBride KL, **White P,** Garg V. (2015) "Utilization of whole-exome sequencing to identify causative mutations in familial congenital heart disease." American Society of Human Genetics Meeting, Baltimore, Maryland
65. Duncan FJ, Naughton BJ, Meadows AS, Wetzel A, **White P,** Hoffman R, Fu H. (2015) "Broad blood transcriptional abnormalities and complexity of pathophysiology in patients with Type I diabetes." International Society for Pediatric and Adolescent Diabetes (ISPAD) Annual Meeting, Brisbane, Australia
66. Naik A, Kelly B, **White P.** (2015) "Sequencing depth of coverage as a quality control metric in whole exome sequencing fails to identify multiple regions in which variant calling and genotyping cannot be accurately performed." The American Society of Human Genetics 65th Annual Meeting. Baltimore, Maryland
67. Fitch J, Kelly B, **White P.** (2015) "Population scale human genome analysis on the cloud." The American Society of Human Genetics 65th Annual Meeting. Baltimore, Maryland
68. Kelly B, Fitch J, Kuck H, **White P.** (2015) "Churchill 2.0: Making the Ultra-Fast Analysis Pipeline for Clinical and Population-Scale Genomics Faster, More Efficient, and More Comprehensive." The American Society of Human Genetics 65th Annual Meeting. Baltimore, Maryland

69. Corsmeier D, **White P.** (2015) "An automated, differences-based model for retrospectively applying dynamic annotation data to static whole exome sequencing result sets." The American Society of Human Genetics 65th Annual Meeting. Baltimore, Maryland
70. Naik A, Kelly B, **White P.** (2015) "Sequencing depth of coverage as a quality control metric in whole exome sequencing fails to identify multiple regions in which variant calling and genotyping cannot be accurately performed." 2015 Annual Research Institute Retreat, Columbus, OH
71. Kuck H, Kelly B, **White P.** (2015) "Accelerating pathogenic variant discovery through comprehensive and computationally efficient tertiary data analysis." 2015 Annual Research Institute Retreat, Columbus, OH
72. Kelly B, Fitch J, Kuck H, Naik A, **White P.** (2015) "Churchill 2.0: Making the Ultra-Fast Analysis Pipeline for Clinical and Population-Scale Genomics Faster, More Efficient, and More Comprehensive." 2015 Annual Research Institute Retreat, Columbus, OH
73. Fitch J, **White P.** (2015) "Next Generation Genomic Data Analysis." 2015 Annual Research Institute Retreat, Columbus, OH
74. Locker C, Imawalle S, Bir N, Nadella V, Kelly B, Kuck H, Fitch J, **White P.** (2016) "Validating INDELS in the Genome In A Bottle Reference Genome Standard." Summer Poster Day, Columbus, OH.
75. Li J, Kelly B, Kuck H, Fitch J, **White P.** (2016) "Genome-wide *in silico* mRNA Analysis of *de novo* SNPs in Patients with Congenital Heart Disease." Summer Poster Day, Columbus, OH.
76. Obeng T, Wetzel A, Zhong H, Bir N, Mihalic Mosher T, Kuck H, Kelly B, McBride K, Herman G, **White P.** (2016) "Sanger Sequencing Validation of *B4GALT7* Compound Heterozygous Variants in a Family with a Rare Skeletal Dysplasia Disorder." Summer Poster Day, Columbus, OH.
77. Imwalle S, Gordon D, Kuck H, Herman G, McBride K, **White P.** (2016) "Using the Human Phenotype Ontology (HPO) to Identify Disease-Causing Genes in Proband with Brittle Bone Phenotype." Summer Poster Day, Columbus, OH.
78. Kelly B, Mihalic Mosher T, Kuck H, Fitch J, Gordon D, Koboldt DC, McBride KL, Herman GE, **White P.** (2016) "Accelerating Discovery in the Undiagnosed: Nationwide Children's Hospital's Research Genomics Strategic Initiative." ASHG's 66th Annual Meeting, Vancouver, Canada.
79. Fitch J, Gordon D, Fitzgerald-Butt S, Garg V, McBride K, **White P.** (2016) "CHDbase: a genomic variation data warehouse for congenital heart disease." ASHG's 66th Annual Meeting, Vancouver, Canada.
80. Gordon D, Kuck H, Kelly B, Fitch J, **White P.** (2016) "Efficient Population-Scale Variant Annotation and Analysis Through Big Data." ASHG's 66th Annual Meeting, Vancouver, Canada.

81. Kuck H, Westmoreland P, Nadella V, Zhong H, McCarty D, **White P.** (2016) "Reducing Genotoxicity Risk in Gene Therapy – Identification of Tumor Insertion Sites Using NextGen Sequencing." ASHG's 66th Annual Meeting, Vancouver, Canada.
82. Kuck H, Westmoreland P, Nadella V, Zhong H, McCarty D, **White P.** (2016) "Reducing Genotoxicity Risk in Gene Therapy – Identification of Tumor Insertion Sites Using NextGen Sequencing." 2016 Annual Research Institute Retreat, Columbus, OH.
83. Kelly B, Mihalic Mosher T, Corsmeier D, Kuck H, Fitch J, Koboldt D, McBride KL, Herman GE, **White P.** (2016) "Accelerating Discovery in the Undiagnosed: Nationwide Children's Hospital's Research Genomics Strategic Initiative." 2016 Annual Research Institute Retreat, Columbus, OH.
84. Agrawal S, Chanley MA, Kitao T, Fitch J, **White P,** Smoyer WE. (2016) "Glucocorticoids and Mifepristone Provide Beneficial Effects against Nephrotic Syndrome via Similar and Different Glomerular Express." American Society of Nephrology meeting, Chicago, IL.
85. Westmoreland P, McCarty D, Kuck H, Nadella V, **White P.** (2016) "Role of Truncated Recombinant AAV Genomes in Tumor Formation." 2016 Annual Research Institute Retreat, Columbus, OH.
86. Swaminathan R, Huang Y, Yu E, Fitch J, Lintner K, **White P,** Lin S. (2016) "A Scalable and Secure Genome Archiving and Communication System for the Clinical Enterprise." The American Society for Human Genetics Annual Meeting, Vancouver, British Columbia, Canada. October 18-22, 2016.
87. Agrawal S, Chanley MA, Kitao T, Fitch J, **White P,** Smoyer WE. (2017) "Glucocorticoids and Mifepristone Provide Beneficial Effects against Nephrotic Syndrome via Similar and Different Glomerular Express." PAS meeting, San Francisco, CA.
88. Westmoreland P, McCarty D, Kuck H, Nadella V, **White P.** (2016) "Role of Truncated Recombinant AAV Genomes in Tumor Formation." 20th Annual Meeting of the American-Society-of-Gene-and-Cell-Therapy (ASGCT), Washington, DC. Published in: Molecular Therapy 25(5) Supplement 1:2-2.
89. Locke L, Julian M, **White P,** Papp A, Sadee W, Schlesinger L, Crouser E (2017) "Alternatively Activated (m2) Macrophage Polarization And The Sarcoidosis Immune Paradox." International Conference of the American-Thoracic-Society (ATS), Washington, DC. Published in" American Journal of Respiratory and Critical Care Medicine 195: A1060.
90. Gnona MK, Stewart WCL, **White P,** Klebanoff M, Nelin LD, Buhimschi IA (2017). "The SUPERBABY PROJECT: Genetic determinants of the favorable NICU course in premature newborns." ASHG, Orlando, FL.
91. **White, P.** Lammi G, Li J, Gaither J, Gordon D, Kuck H, Kelly B, Fitch J. (2017) "Global analysis of human mRNA folding disruptions in synonymous variants demonstrates significant population constraint." Cold Spring Harbor Genome Informatics Meeting, New York, NY.

92. Kelly B, Fitch J, Cottrell CE, Magrini V, Koboldt D, Gastier-Foster J, Leonard J, Wilson RK, Mardis ER, **White P.** (2017) "Utilization of linked-read, whole genome, whole exome and transcriptome sequencing in the comprehensive molecular profiling of pediatric brain tumors." Cold Spring Harbor Genome Informatics Meeting, New York, NY.
93. Kelly B, Fitch J, Cottrell CE, Gastier-Foster J, **White P,** Leonard J, Wilson RK, Mardis ER. "Comprehensive Genomic Profiling of Brain Cancers: Computationally Challenging Analyses with a Goal of Impacting on Patient Management." Cold Spring Harbor Genome Informatics Meeting, New York, NY.
94. Voytovich K, Spencer A, Fitch J, Mardis ER, **White P.** (2017) "Comparative study of fusion detection tools on RNA-Seq data." Nationwide Children's Hospital Research Retreat 2017, Columbus, Oh.
95. Spencer A, Fitch J, **White P.** (2017) "Differential Gene Expression Analysis through RNA-Seq." Nationwide Children's Hospital Research Retreat 2017, Columbus, Oh.
96. Gordon D, Kuck H, Kelly B, Fitch J, Lammi G, LaHaye S, Fitzgerald-Butt S, Garg V, McBride K, **White P.** (2017) "Accelerating Congenital Heart Defect Variant Analysis through Big Data." Nationwide Children's Hospital Research Retreat 2017, Columbus, Oh.
97. Brennan P, Kelly B, Magrini V, Mardis ER, Hampel H, Cohn D, Goodfellow P, **White P.** (2017) "Characterizing Endometrial Cancer through an Investigation of Microsatellite Instability and Variants in Mismatch Repair Genes." Nationwide Children's Hospital Research Retreat 2017, Columbus, Oh.
98. Mihalic Mosher T, Koboldt D, Hickey S, Kelly B, McBride K, **White P,** Wilson RK. (2017) "More Than Just X-Linked Intellectual Disability: Congenital Anomalies Associated with a Missense Variant in RLIM." Nationwide Children's Hospital Research Retreat 2017, Columbus, Oh.
99. Gnona KM, Stewart WCL, **White P,** Klebanoff M, Nelin LD, Buhimschi IA. (2017) "The SUPERBABY PROJECT: Genetic determinants of the favorable NICU course in premature newborns." American Society of Human Genetics Annual Meeting, Orlando, FL.
100. **White, P.** (2018) "Global analysis of human mRNA folding disruptions demonstrates significant population constraint." 2018 Advances in Genome Biology and Technology (AGBT) General Meeting, Orlando, FL. **Abstract selected podium presentation.**
101. Nelin L, Gnona K, Stewart W, **White P,** Klebanoff M, Buhimschi I. (2018). "Potential genetic determinants of resilience to the morbidities of prematurity." Pediatric Academic Societies (PAS) 2018 Meeting, Toronto, Canada.
102. Warren L, Antonara S, Gordon D, Erdem G, **White P.** (2018) "Characterization of an Invasive Group A Streptococcus Outbreak in Columbus, Ohio." Pediatric Academic Societies (PAS) 2018 Meeting, Toronto, Canada.
103. Frints S, **White P.** (2018). "Pathogenic Variants in E3 ubiquitin Ligase RLIM/RNF12 cause a variable X-Linked Congenital Malformation Syndrome with Intellectual Disability." 22nd International Conference on Prenatal Diagnosis and Therapy (ISPD), Antwerp, Belgium.

104. Westmoreland P, Kuck H, Nadella V, **White P**, Zaraspe K, Murakami N, Meadows A, Fu H, McCarty M. (2018) "Recombinant AAV Vector Design Influences its Genotoxic Potential." American Society of Gene & Cell Therapy Annual Meeting, Chicago, IL.
105. Kubatko A, **White P**, Grossman T, Hobby J, Brenneman J, Mooney W, Harms, D. (2018) "A Novel Web-Based Interface for Management of a Clinical Bioinformatics Pipeline." AGBT Precision Health 2018, La Jolla, CA.
106. Gnona M, Stewart W, **White P**, Klebanoff M, Nelin L, Buhimschi I. (2018). "Effects of Genetic Mutations on the Risk for Neonatal Complications". Annual Midwest Society for Pediatric Research Scientific Meeting 2018, Royal Oak, MI.
107. Li J, **White P**. (2018). "Global local folding of the human transcriptome." Denman Undergraduate Research Forum, The Ohio State University, Columbus OH.
108. Li J, **White P**. (2018). "Global local folding of the human transcriptome." Brazilian Graduate Students Conference (BRASCON), Columbus, OH.
109. Mihalic Mosher T, Koboldt D, Hickey S, Kelly B, McBride K, **White P**, Wilson RK. (2018). "More Than Just X-Linked Intellectual Disability: Congenital Anomalies Associated with a Missense Variant in RLIM." American College of Medical Genetics Annual Clinical Genetics Meeting, Charlotte, NC.
110. Miller KE, Koboldt DC, Kelly B, Brennan P, Magrini V, Gastier-Foster JM, **White P**, Varga E, Cottrell CE, Wilson RK, Mardis ER. (2018) "Pathogenic germline variants in a pediatric cancer cohort and identification of new candidate cancer predisposition genes." Annual American Society of Human Genetics Conference 2018, San Diego, CA.
111. Abdel-Rahman MH, Sample KM, Kelly B, Gordon D, Johansson P, Pilarski R, Boru G, Grosel T, Massengill JB, Kinnamon D, Davidorf FH, Hayward N, **White P**, Cebulla CM. (2018) "Whole exome sequencing identify potential candidate genes associated with hereditary predisposition to UM." Annual American Society of Human Genetics Conference 2018, San Diego, CA.
112. Manivannan S, Darouich S, Masmoudi A, Gordon D, Zender G, Fitzgerald-Butt S, Lariani I, McBride K, **White P**, Kharrat M, Garg V. (2018) "Novel *My/2* Variant Identified Through Exome Sequencing of an Autosomal Recessive Form of Hypertrophic Cardiomyopathy." American Heart Association 2018, Chicago, IL.
113. Brennan P, Kelly B, Wheeler G, Fitch J, Voytovich K, Spencer A, Varga E, Leraas K, Lichtenberg T, Magrini V, Koboldt D, Gastier-Foster J, Wilson R, Mardis E, Cottrell C, **White P**. (2018) "Integration of whole genome, whole exome, and transcriptome sequencing pipelines for comprehensive genomic profiling of 55 pediatric cancer subjects." Genome Informatics 2018, Wellcome Genome Campus Conference Centre, Hinxton, Cambridge, UK. **Abstract selected podium presentation.**

114. Gaither J, Li J, Gordon D, Lammi G, Kelly B, **White P.** (2018). "Constraint for mRNA structure in human synonymous mutations." Genome Informatics 2018, Wellcome Genome Campus Conference Centre, Hinxton, Cambridge, UK. **Abstract selected podium presentation.**
115. Kelly B, Brennan P, Kuck H, Gordon D, Lammi G, Wheeler G, Gaither J, Fitch J, **White P.** (2018). "Serverless cloud technologies for variant discovery and interpretation of human genetic disease." Genome Informatics 2018, Wellcome Genome Campus Conference Centre, Hinxton, Cambridge, UK.
116. **White P,** Kelly B, Brennan P, Mihalic Mosher T, Hickey S, McBride K, Koboldt D, Wilson R. (2018). "Diagnosing the undiagnosed: expanding the genetic etiology and phenotypic spectrum of rare pediatric conditions." Genome Informatics 2018, Wellcome Genome Campus Conference Centre, Hinxton, Cambridge, UK.
117. Zajo K, Mihalic-Mosher T, Sandberg K, Koboldt D, Wilson R, **White P,** Kelly B, Brennan P, Hickey S, McBride K, Erdman S. "Pedunculated Adenomas Presenting with Anemia in a Patient with a Novel Somatic APC Mosaicism." (2018) Collaborative Group of the Americas on Inherited Gastrointestinal Cancer Annual Meeting 2018, San Diego, CA
118. Cottrell C, Varga E, Vear S, Lichtenberg T, Leraas K, Schieffer K, Miller K, Magrini V, Wetzel A, Koboldt D, Kelly B, Fitch J, Brennan P, Wheeler G, **White P,** Dave-Wala A, Dishman D, Shoemaker L, Pfau R, Finlay J, Leonard J, Osorio D, AbdelBaki M, Yeager N, Setty B, Drapeau A, Shah N, Koo S, Boue D, Pierson C, Gastier-Foster J, Wilson RK, Mardis ER. (2018) "Design and Implementation of a Comprehensive Genomic Profiling Protocol for Rare and Refractory Pediatric Cancer and Hematologic Disease." NCH Research Retreat 2018, Columbus, OH.
119. Schieffer K, Miller K, Brennan P, Koboldt D, Pierson C, Leonard J, Pindrik J, Ostendorf A, Patel A, Varga E, Boczar A, Leraas K, Crist E, Magrini V, **White P,** Gastier-Foster J, Cottrell C, Zmuda E, Mardis E, Wilson R. "Somatic mosaicism of SLC35A2 p.Ser212fs*9 in brain tissue in a case of intractable epileptic spasms." NCH Research Retreat 2018, Columbus, OH.
120. Cottrell C, Varga E, Vear S, Lichtenberg T, Leraas K, Schieffer K, Miller K, Magrini V, Wetzel A, Koboldt D, Kelly B, Fitch J, Brennan P, Wheeler G, **White P,** McGrath S, Bir N, Zhong H, Miller A, Dave-Wala A, Dishman D, Shoemaker L, Pfau R, Finlay J, Leonard J, Osorio D, AbdelBaki M, Yeager N, Setty B, Drapeau A, Shah N, Koo S, Boué D, Pierson C, Gastier-Foster J, Wilson R, Mardis E. (2019) "Design and Implementation of a Comprehensive Genomic Profiling Protocol for Rare and Refractory Pediatric Cancer and Hematologic Disease" AGBT General Meeting 2019, Marco Island, FL.
121. Lahaye S, Voytovich K, Fitch J, Bir N, McGrath S, Miller A, Wetzel A, Magrini V, **White P,** Cottrell C, Mardis ER, Wilson RK. (2019) "Utilization of an ensemble approach for identification of driver fusions in pediatric cancer." OSUCCC – James 2019 Annual Scientific Meeting, Columbus, OH.

122. Miller K, Schieffer K, Fitch J, Magrini V, Wetzel A, Miller A, Boué D, Leonard J, Finlay J, Osorio D, AbdelBaki M, Pierson C, Drapeau A, Pindrik J, Leraas K, Varga E, Dishman D, Shoemaker L, Ross N, Pitts J, Gastier-Foster J, **White P**, Cottrell C, Wilson R, Mardis E. (2019) “Expression profiling-based characterization of immune cell populations in pediatric brain cancers” AACR Annual Meeting 2019, Atlanta, GA.
123. Schieffer K, Miller K, Boue DR, Koboldt D, Brennan P, Kelly BJ, Wheeler G, Magrini V, Wetzel A, Varga EA, Dishman D, Leraas K, Miller A, Agarwal V, AbdelBaki MS, Finlay J, Leonard JR, **White P**, Gastier-Foster J, Cottrell C, Mardis E, Wilson R. (2019). “Molecular profiling identifies a second malignancy in a patient with medulloblastoma.” AACR Annual Meeting 2019, Atlanta, GA.
124. Lahaye S, Voytovich K, Fitch J, Bir N, McGrath S, Miller A, Wetzel A, Magrini V, Mardis ER, Wilson RK, **White P**, Cottrell C. (2019) “Utilization of an ensemble approach for identification of driver fusions in pediatric cancer.” AACR Annual Meeting 2019, Atlanta, GA.
125. Locke LW, **White P**, Julian MW, Bicer S, Papp AC, Sadee W, Schlesinger LS, Crouser ED. (2019). “Human Sarcoidosis Vs TB: All Granulomas Are Not Created Equally.” American Thoracic Society 2019 International Conference, Dallas, TX.
126. Lichtenberg T, Cottrell C, Magrini V, Schieffer K, Varga E, Vear S, Leraas K, Miller K, LaHaye S, Wetzel A, Koboldt D, Kelly B, Fitch J, Brennan P, Wheeler G, **White P**, Pfau R, Koo S, Gastier-Foster J, Wilson R, Mardis E. (2019) “Clinical and Translational Data Processes and Workflows for a Pediatric Genomic Profiling Protocol” Childhood Cancer Data Initiative Symposium 2019, Washington, DC.
127. Gordon D, Kuck H, Lammi G, Bosley E, Kelly B, **White P**. (2019) “Varhouse: Translating Scalable and Secure Variant Interpretation from Research to the Clinic” ISMB/ECCB 2019, Basel, Switzerland.
128. **White P**, Gaither J, Gordon D, Lammi G, Moreland B. (2019) “Global analysis of human mRNA folding demonstrates significant population constraint of disruptive synonymous variants” ISMB/ECCB 2019, Basel, Switzerland. **Abstract selected podium presentation.**
129. Moreland B, Gaither J, **White P**. (2019) “Third nucleotide position content of nearby codons is highly predictive of synonymous codon usage” ISMB/ECCB 2019, Basel, Switzerland.
130. Cunningham D, Fitzgerald Butt S, Neinast R, Zender G, Corsmeier D, Gordon D, Kelly B, Garg V, **White P**, McBride KL. (2019) “A CASZ1 Transcription Factor Missense Variant in Family with Congenital Heart Disease Causes Protein Mislocalization and Reduced Activity” NCH Research Retreat 2019, Columbus, OH.

131. LaHaye S, Fitch J, Voytovich K, Schieffer K, Miller K, Bir N, McGrath SD, Miller A, Wetzel A, Leraas K, Varga E, AbdelBaki MS, Finlay JL, Leonard JR, Boue DR, Osorio D, Magrini V, Cottrell CE, Mardis ER, Wilson RK, **White P.** (2019) "Accurate identification of driver fusions in pediatric cancer" NCH Research Retreat 2019, Columbus, OH. **Abstract selected podium presentation.**
132. Gaither J, Brenneman J, Lammi G, Herman A, Kuck H, Gordon D, Kelly B, **White P.** (2019) "SNPDogg: Transparent pathogenicity assessment for missense variants" Genome Informatics 2019, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
133. Brennen P, Rajkovic A, Gaither J, Kelly B, Wheeler G, Bir N, Cottrell C, Magrini V, McElroy J, Goodfellow P, Mardis E, **White P.** (2019) "Tumor-only detection of MSI using machine learning in endometrial cancer patients" Genome Informatics 2019, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
134. Kuck H, Gordon D, Lammi G, Bosley E, **White P.** (2019) "Varhouse: A scalable, serverless warehouse for variant interpretation" Genome Informatics 2019, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
135. Moreland B, Gordon D, Lammi G, Bosley E, **White P.** (2019) "Determining the contribution of codon usage and RNA stability to predicting synonymous and intronic variant pathogenicity and impact on splicing" Genome Informatics 2019, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
136. Rajkovic A, Ceyhan D, Wheeler G, Lichtenberg T, Kelly B, **White P.** (2019) "Sub-continental ancestry inference based on the gnomAD dataset accurately classifies patients at NCH" Genome Informatics 2019, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY. **Abstract selected podium presentation.**
137. Wheeler G, Kelly B, Brennan P, **White P.** (2019) "Clonality-aware somatic analysis for improved diagnosis and treatment of complex and recurrent cancers" Genome Informatics 2019, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.
138. Bennett J, Gordon D, Skillman-Lawrence P, McBride K, **White P,** Garg V. (2019) "Use of Machine Learning to Identify High Risk Variants of Uncertain Significance in Lamin A/C Cardiomyopathy." CCTS 2019 Annual Scientific Meeting, Columbus, OH.
139. Lawrence P, Zender G, **White P,** McBride K. (2019) "Reducing the Burden of Genetic Functional Analysis: The Use of Image Recognition to Automate the Analysis of Wound Healing Assays." CCTS 2019 Annual Scientific Meeting, Columbus, OH.
140. Gaither J, Brenneman J, Lammi G, Herman A, Kuck H, Gordon D, Kelly B, **White P.** (2019) "SNPDogg: Identification and Explanation of Disease-Causing Genetic Variants." CCTS 2019 Annual Scientific Meeting, Columbus, OH.
141. Moreland B, Lammi G, Gordon D, Gaither J, White P. (2019) "Determining the contribution of RNA stability to predicting variant pathogenicity and impact on splicing." CCTS 2019 Annual Scientific Meeting, Columbus, OH.
142. Cottrell C, Schieffer K, LaHaye S, Magrini V, Varga E, Lichtenberg T, Leraas K, Vear S, Miller K, Wetzel A, Koboldt D, Bedrosian T, Kelly B, Fitch J, Brennan P, Wheeler G, **White P,** Setty B, Finlay J, Leonard J, Osorio DS, AbdelBaki M, Koo S, Boué D, Pierson CR, Wilson R, Mardis E. (2020) "Enrichment of Targetable Gene Fusion Events and their Associated Impact in a Pediatric Cancer Population." AGBT General Meeting 2020, Marco Island, FL.

143. Kelly B, Bir N, Brennen P, Rajkovic A, Gaither J, Wheeler G, Cottrell C, Magrini V, Cohn D, Hampel H, Goodfellow P, Mardis E, **White P**. (2020) "A tumor-only NGS assay and analysis techniques for the assessment of treatment options and future cancer risks for women with endometrial cancer." AGBT General Meeting 2020, Marco Island, FL. **Abstract selected podium presentation.**
144. Marilena M, Varga E, Schieffer K, Leraas K, Lichtenberg T, Colace S, Pfau R, Jayaraman V, LaHaye S, Miller K, Wetzel A, Koboldt D, Kelly B, Brennan P, Wheeler G, **White P**, Koo S, Aldrink J, Setty B, Lehman A, Magrini V, Wilson R, Mardis E, Cottrell C. (2020) "Comprehensive Tumor Profiling Reveals Unexpected Constitutional Diagnoses of Tuberous Sclerosis and Insulin-like Growth Factor 1 Resistance." ACMG Annual Clinical Genetics Meeting 2020, San Antonio, TX.
145. Leraas K, Shatara M, Rodriguez D, Magrini V, Varga E, Colace S, Lichtenberg T, Schieffer K, Miller K, LaHaye S, Brunson A, Blakey B, Wetzel A, Koboldt D, Kelly B, Fitch J, Brennan P, Wheeler G, **White P**, Pfau R, Finlay J, Leonard J, Osorio D, AbdelBaki M, Koo S, Boue D, Pierson C, Wilson R, Mardis E, Cottrell C. (2020) "Comprehensive Molecular Profiling of Synchronous Tumors in Individuals with *SMARCB1* Germline Alteration Reveals Unique Molecular Signatures." AACR Annual Meeting 2020, San Diego, CA.
146. Schieffer K, Miller K, Varga E, Magrini V, Koboldt D, Leraas K, Lichtenberg T, Colace S, Brennan P, Kelly B, Wheeler G, Bedrosian T, LaHaye S, Fitch J, **White P**, Shatara M, Gupta A, Setty B, Olshefski R, AbdelBaki M, Leonard J, Finlay J, Koo S, Boue D, Pierson C, Wilson R, Mardis E, Cottrell C. (2020) "Comprehensive Genomic Profiling in a Pediatric Cohort: Novel Co-Occurrence of Cancer and Constitutional Disease." AMP Europe 2020, Milan, Italy.
147. Lichtenberg T, Schieffer K, Varga E, Colace S, Leraas K, Franklin S, Kelly B, **White P**, Magrini V, Wilson R, Mardis M, Cottrell C. (2020) "Putting the Meaning in Metadata: How to Collect, Harmonize and Share Non-Genomic Patient Data Used During Genomic Analysis." AACR Meeting 2020, San Diego, CA.
148. Cottrell C, Schieffer K, LaHaye S, Magrini V, Varga E, Lichtenberg T, Leraas K, Vear S, Miller K, Wetzel A, Koboldt D, Bedrosian T, Kelly B, Fitch J, Brennan P, Wheeler G, Voytovich K, **White P**, Gupta A, Setty B, Finlay J, Leonard J, Osorio D, AbdelBaki M, Koo S, Boue D, Pierson C, Wilson R, Mardis E. (2020) "Comprehensive Genomic Characterization of Congenital and Infantile Cancers Reveals High Yield of Medically Meaningful Findings." AMP Europe 2020, Milan, Italy.
149. Akhavanfard S, Ranalli M, Varga E, Schieffer K, Magrini M, Leraas K, Lichtenberg T, Colace S, Pfau R, Jayaraman V, LaHaye S, Miller K, Wetzel A, Koboldt D, Kelly B, Brennan P, Wheeler G, Feldman A, **White P**, Sribnick E, Koo S, Boue D, Wilson R, Mardis E, Cottrell C. (2020) "The Clinical Utility of An N-of-1 Patient Study, Exemplified In A Patient With Primary Meningeal Melanoma." ACMG Annual Clinical Genetics Meeting 2020, San Antonio, TX.
150. Koo S, Schieffer K, LaHaye S, Wheeler G, Kelly B, Magrini V, **White P**, Wilson R, Mardis E, Cottrell C. (2020) "Comparison of Different Methods of Tumor Cellularity Assessment in a Pediatric Cancer Cohort." AMP Europe 2020, Milan, Italy.
151. Locke L, Julian M, Bicer S, **White P**, Schlesinger L, Crouser E. (2020) "Phagosome-regulated mTOR Signaling during Sarcoidosis Granulomagenesis." ATS International Conference 2020, Philadelphia, PA.

152. Bhayana S, Chanley M, Waller A, Wolfgang K, Wijeratne S, Fitch J, **White P**, Kerlin B, Smoyer W. (2020) "Comparative Transcriptomic Analysis of Methylprednisolone and Pioglitazone treated Glomeruli in a Rat Nephrotic Syndrome model." PAS Meeting, Philadelphia, PA.

WHITE PAPERS

1. Corsmeier D, Herman G, McBride K, Flanigan K, Pyatt R, Varga E, Hashimoto S, Fitzgerald-Butt S, Kelly B, Fitch J, Kuck H, Moosavinasab S, Huang Y, Lin S, **White P**. (2015) NCHRI CLARITY Undiagnosed Challenge Final Report. White Paper: CLARITY Undiagnosed, Boston Children's Hospital, Boston, MA.
2. Fitch J, Navarro E, Kelly B, Kuck H, Frege T, Hirmas J, **White, P**. (2015). Population-Scale Genomic Analysis Of 2,500 Human Genome Sequences In The Amazon Cloud. White Paper: Intel Head In The Clouds Challenge On AWS POC
3. Corsmeier D, Fitzgerald-Butt S, Herman G, Kelly B, Lamb Thrush D, McBride K, Newsom D, Pierson C, Rakowsky A, and **White P**. (2012) NCHRI CLARITY Challenge Final Report. White Paper: The CLARITY Challenge, Boston Children's Hospital, Boston, MA.
4. Manduchi E and **White P**. (2004). Issues Related to Microarray Experimental Design and Normalization. White Paper: University of Pennsylvania School of Medicine, Philadelphia, PA

EDITORIALS AND REVIEW ACTIVITIES

JOURNAL REVIEWER

American Journal of Medical Genetics
Bioinformatics
Biotechniques
BMC Bioinformatics
BMC Medical Genomics
Cancers
European Journal of Medical Genetics
Genes
Genome Biology
Genome Medicine
International Journal of Molecular Sciences
iScience
Journal of Medical Genetics
Maternal Health, Neonatology and Perinatology
Molecular Psychiatry
Nature Biotechnology
Oncotarget
PLOS One
Scientific Reports, Nature Publishing Group

TEACHING

LECTURES/PRESENTATIONS

National/International

- October 1, 1998 “Postnatal undernutrition markedly upregulates cardiac α 1 and α 2 thyroid hormone receptor gene expression”.
Podium Presentation at the Nutrition Society meeting
Newcastle, UK
- November 5, 2006 The BCBC Functional Genomics Core.
Podium Presentation at the Beta Cell Biology Consortium Investigator
Retreat
Boston, MA
- February 4, 2011 “Whole-exome sequencing identifies an autosomal recessive mutation in
familial congenital heart disease”
Podium Presentation at the 2011 Advances in Genome Biology &
Technology Conference (AGBT)
Marco Island, FL
- May 17, 2014 “Churchill: A cloud-enabled, ultra-fast computational approach for the
discovery of human genetic variation”
Invited Lecture at the Great Lakes Bioinformatics Conference 2014
Cincinnati, OH
- May 17, 2014 “Genomics in the Research Institute: Data, Data, DATA”
Panel Discussion at the Great Lakes Bioinformatics Conference 2014
Cincinnati, OH
- June 24, 2014 “Population scale genomic analysis in the cloud”
Invited Lecture at the Amazon Web Services Government, Education and
Nonprofits Symposium
Washington, DC
- May 13, 2015 “Population scale human genome analysis on the cloud”
Invited Lecture at the BioConference Live Genetics & Genomics 2015
Virtual Conference

- June 25, 2015 “Intel head in the clouds challenge on AWS POC: Population scale human genome analysis on the cloud”
Invited Lecture at the Amazon Web Services Government, Education and Nonprofits Symposium
Washington, DC
- April 28, 2016 “The post-genomic era: accelerating biological discovery through sequencing technology and population scale genomic analysis.”
Invited Lecture International *Burkholderia cepacia* Working Group (IBCWG 2016) 20th Annual Meeting
Columbus, OH
- June 16, 2016 “Next Generation Sequencing Analysis and Clinical Applications”
Invited Lecture Sanford Imagenetics & Medical Genetics Conference
Sioux Falls, SD
- June 29, 2016 “An armory of methods for diagnosis: our CLARITY Undiagnosed Experience”
Invited Lecture Festival of Genomics: Practical Clinical Techniques
Boston, MA
- November 3, 2017 “Global analysis of human mRNA folding disruptions in synonymous variants demonstrates significant population constraint”
Podium Presentation Genome Informatics 2017
Cold Spring Harbor, NY
- February 13, 2018 “Global analysis of human mRNA folding disruptions demonstrates significant population constraint”
Podium Presentation 2018 Advances in Genome Biology and Technology (AGBT) General Meeting
Orlando, FL
- July 24, 2019 “Global analysis of human mRNA folding demonstrates significant population constraint of disruptive synonymous variants”
Podium Presentation Integrative RNA Biology COSI, Intelligent Systems for Molecular Biology (ISMB) and European Conference on Computational Biology (ECCB) 2019
Basel, Switzerland

Local/Regional

- September 27, 2010 “The Biomedical Genomic Core”
OSU CCC 2010 Biomedical Resources Workshop
Columbus, OH
- November 4, 2010 “Genomics at Nationwide Children’s Hospital”
OSU CCC Genomics Consortium Meeting
Columbus, OH
- November 4, 2010 “Next generation sequencing at Nationwide Children’s Hospital”
Battelle Whole Genome Sequencing Collaborative Group
Columbus, OH
- January 20, 2011 “Needle in a haystack: Finding casual variants in whole-exome and whole-genome sequencing data”
Invited Lecture at the Department of Pharmacology, The Ohio State University
Columbus, OH
- May 6, 2011 “Genomics at NCH” at the Nationwide Children’s Hospital and Battelle
Collaboration Workshop
Columbus, OH
- June 16, 2011 “Next-generation sequencing technology”
U.S. Air Force Meeting, Central Ohio Registry for Autism, Nationwide
Children’s Hospital
Columbus, OH
- October 5, 2012 “Introduction to genome and exome sequencing”
DoD 24 Month Interim Progress Meeting, Central Ohio Registry for
Autism, Nationwide Children’s Hospital
Columbus, OH
- December 5, 2012 “Ultra-fast analysis of human genome resequencing data in autism
spectrum disorders”
DoD Interim Progress & Kick-Off Meeting, Central Ohio Registry for
Autism, Nationwide Children’s Hospital,
Columbus, OH

- March 13, 2013 "Churchill: Ultra-fast analysis of the human genome"
Invited Lecture
2013 Technology Showcase, Nationwide Children's Hospital
Columbus, OH
- September 20, 2013 "Next generation sequencing and the search for causal variants in genetic disease"
Invited Lecture at the 2013 Annual Ohio Genetic Counselor Meeting
Columbus, OH
- February 25, 2014 "The genomics era"
Invited Lecture at the Ohio University Bioinformatics Journal Club
Athens, OH
- February 25, 2014 "Churchill: A cloud-enabled, ultra-fast computational approach for the discovery of human genetic variation"
Invited Lecture at the Ohio University Bioinformatics Distinguished Lecture Series
Athens, OH
- March 31, 2014 "Genomics at Nationwide Children's"
Intelligent Communities Site Visit, Nationwide Children's Hospital
Columbus, OH
- May 20, 2014 "Combine and conquer: An integrated software suite for finding causal relationships between sequence variants and clinical phenotypes"
Invited Lecture at the Road to Collaboration: NCH and OSU Human Genetics Community Meeting, The Research Institute at Nationwide Children's Hospital
Columbus, OH
- August 28, 2014 "Genomics at Nationwide Children's Hospital"
Nationwide Insurance Executive Board Meeting, Nationwide Children's Hospital
Columbus, OH
- December 8, 2014 "Genomics: Helping kids everywhere"
Keynote Lecture at the Annual Nationwide Insurance Board of Trustees Meeting, Nationwide Children's Hospital
Columbus, OH

PETER WHITE, PHD

- January 14, 2015 “Working with data on the genomic scale”
Invited Lecture at the NCH and OSU Human Genetics Community Meeting, Ohio State University
Columbus, OH
- April 16, 2015 “Genomics: Helping kids everywhere”
Keynote Lecture at the Nationwide Children’s Foundation Professional Advisors Dinner, Smith & Wollensky
Easton, OH
- June 11, 2015 “Discovery of Human Genetic Variation in Clinical and Population Scale Genomics” **Invited Lecture** at Lerner Research Institute, Cleveland Clinic Foundation
Cleveland, OH
- March 1, 2016 “Genomic Medicine: accelerating discovery through sequencing discovery through technology and data analytics” **Invited Lecture** at P&C Legal Office
Columbus, OH
- August 31, 2016 “Genomic Medicine: accelerating discovery through sequencing technology and data analytics” **Invited Lecture** at Signet Accel Genomics 101
Columbus, OH
- August 25, 2016 “Genomic Medicine: Helping Kids Everywhere” **Invited Lecture** at Nationwide Insurance and Farm Bureau Leadership Meeting
Columbus, OH
- March 1, 2017 “Genomic Medicine: accelerating discovery through sequencing technology and data analytics” **Invited Lecture** at Nationwide Insurance P & C Legal Offsite Meeting
Columbus, OH
- May 22, 2017 “Using Genomic Medicine to Accelerate Discovery and Diagnoses” **Invited Lecture** at The Columbus Rotary and televised on the Columbus Television Network
Columbus, OH
- November 15, 2019 “When doctors don’t know what’s wrong”
Invited TED Talk TEDx Columbus 2019: SPARK
Davidson Theatre at the Rife Center, Columbus, OH

December 18, 2019 “Genomic Medicine at Nationwide Children’s” **Invited Lecture** at Wright Patterson Airforce Base
Dayton, OH

Institutional

February 1, 2011 “Needle in a haystack: Finding casual variants in whole-exome and whole-genome sequencing data”
Epigenetics Group Meeting, The Research Institute at Nationwide Children’s Hospital
Columbus, OH

April 27, 2011 “Needle in a haystack: Finding casual variants in whole-exome and whole-genome sequencing data”
Cytogenetics/Molecular Genetics Lab Meeting, The Research Institute at Nationwide Children’s Hospital
Columbus, OH

July 26, 2011 “Biomedical Genomics Core
Center Directors Meeting, The Research Institute at Nationwide Children’s Hospital
Columbus, OH

September 14, 2011 “Living the pseudo-dream”
Center for Microbial Pathogenesis: Work in Progress, The Research Institute at Nationwide Children’s Hospital
Columbus, OH

November 7, 2011 “Using next generation sequencing to discover causes of unique familial disease”
Bench to Outcomes Seminar Series, The Research Institute at Nationwide Children’s Hospital
Columbus, OH

March 1, 2012 “The White Lab”
Center for Microbial Pathogenesis, Nationwide Children’s Hospital
Columbus, OH

December 6, 2012 “Churchill: Ultra-fast analysis of human genome resequencing data”
Molecular Genetics Group, Nationwide Children’s Hospital
Columbus, OH

PETER WHITE, PHD

- December 13, 2012 “Churchill: Ultra-fast analysis of human genome resequencing data”
Battelle Center for Mathematical Medicine, The Research Institute at
Nationwide Children’s Hospital
Columbus, OH
- December 18, 2012 “Molecular bioinformatics of human genome resequencing analysis”
CHD Research Affinity Group, The Research Institute at Nationwide
Children’s Hospital
Columbus, OH
- December 21, 2012 “Exome sequencing and analysis in diffuse pontine glioma”
The Research Institute at Nationwide Children’s Hospital
Columbus, OH
- February 12, 2013 “Genomics research in 2013”
Clinical Fellows Prospective Research Training, The Research Institute at
Nationwide Children’s Hospital
Columbus, OH
- March 6, 2013 “Secondary analysis of human genomic resequencing data”
The Molecular Cytogenetics Group Meeting, The Research Institute at
Nationwide Children’s Hospital
Columbus, OH
- March 13, 2013 “Churchill: Faster, cheaper, better”
The Center for Microbial Pathogenesis Work in Progress, The Research
Institute at Nationwide Children’s Hospital
Columbus, OH
- November 13, 2013 "Genomics and the Strategic Plan"
All Admin Meeting, The Research Institute at Nationwide Children's
Hospital
Columbus, OH
- January 24, 2014 “Genomics at Nationwide Children’s”
Board of Directors Meeting. Nationwide Children’s Hospital
Columbus, OH
- April 14, 2014 “Biomedical Genomics Core: 2014 update”
Research Leadership Meeting, The Research Institute at Nationwide
Children’s Hospital
Columbus, OH

PETER WHITE, PHD

- May 6, 2014 “Genomics at Nationwide Children’s”
Management Committee Meeting, Nationwide Children’s Hospital
Columbus, OH
- August 21, 2014 “NCH & GenomeNext partnership: Development of a solution for clinical
NGS variant analysis”
Clinical Group Meeting, Nationwide Children’s Hospital
Columbus, OH
- September 14, 2014 “The White Lab”
Nationwide Children’s Hospital CMP Faculty Meeting
Columbus, OH
- March 18, 2015 “Genomics: The road to best outcomes”
Coffee Connections, Nationwide Children’s Hospital Foundation,
Nationwide Children’s Hospital
Columbus, OH
- May 13, 2015 “Genomic medicine”
Nationwide Direct & Member Solutions Team Meeting, Nationwide
Children’s Hospital
Columbus, OH
- August 21, 2015 “Genomic Medicine: Helping Kids Everywhere”
Nationwide Insurance Foundation Meeting, Nationwide Children’s
Hospital
Columbus, OH
- October 21, 2015 “Genomic Medicine: Helping Kids Everywhere”
Nationwide Insurance Executive Meeting, Nationwide Children’s Hospital
Columbus, OH
- April 12, 2016 “Biomedical Genomics Core Update”
The Research Institute at Nationwide Children’s Hospital, Research Town
Hall Meeting
Columbus, OH
- April 21, 2016 “Genomic Medicine: Helping Kids Everywhere”
Nationwide Children’s Hospital, Foundation Board of Trustees Meeting
Columbus, OH
- September 15, 2016 “Genomic Medicine: accelerating discovery through sequencing
technology”
Nationwide Children’s Hospital, BCR Informatics Lunch and Learn

PETER WHITE, PHD

- September 29, 2016 “Genomic Medicine: accelerating discovery through sequencing technology”
Nationwide Children’s Hospital, Lounge and Learn
Columbus, OH
- January 20, 2017 “Acute lymphoblastic leukemia Tumor / Normal Analysis”
The Institute for Genomic Medicine at Nationwide Children’s Hospital
Columbus, OH
- May 30, 2017 “IGM Computational Genomics Strategy”
The Institute for Genomic Medicine at Nationwide Children’s Hospital,
Leadership Strategy and Planning Meeting
Columbus, OH
- November 29, 2017 “RNA Folding and Population Constraint”
The Institute for Genomic Medicine at Nationwide Children’s Hospital,
Computational Genomics Group Meeting
Columbus, OH
- June 11, 2019 “Captain Ahab and the Search for Zebras”
Invited Lecture DISCOVERYx, Nationwide Children’s Hospital
Columbus, OH
- June 14, 2019 “Computational Genomics: Who, Why, What & How”
Computational Genomics Group Retreat
Columbus, OH
- October 15, 2019 “Genomic Medicine at Nationwide Children’s: Genome Analysis and Rare Disease”
Education Module Lecture, Nationwide Children’s Hospital
Columbus, OH
- January 9, 2020 “Giving a TED Talk”
The Institute for Genomic Medicine at Nationwide Children’s Hospital
Townhall Meeting
Columbus, OH
- May 30, 2017 “IGM Computational Genomics Group Strategic Plan”
The Institute for Genomic Medicine at Nationwide Children’s Hospital
Leadership Strategy and Planning Meeting
Columbus, OH

TEACHING AND MENTORSHIP - DIRECT SUPERVISION

Postdoctoral Fellows

| | |
|--------------|------------------------|
| 2018-Present | Blythe Moreland, PhD |
| 2018-Present | Stephanie LaHaye, PhD |
| 2012-2016 | Donald Corsmeier, DVM. |
| 2014 | Mari Mori, MD |
| 2012-2013 | William Harvey, PhD |

Graduate Students

| | |
|------|--|
| 2020 | Jacqueline Penaloza (Rotation Student), The Ohio State University College of Medicine Biomedical Sciences Graduate Program |
| 2019 | Emily Hoskins (Rotation Student), The Ohio State University College of Medicine Biomedical Sciences Graduate Program |
| 2018 | Audrey Bollas (Rotation Student), The Ohio State University College of Medicine Biomedical Sciences Graduate Program |
| 2015 | Nevin Britto M.D. Candidate (Class of 2018) The Ohio State University College of Medicine |
| 2014 | Dan Wang Purdue University, Indiana |
| 2012 | Donald Corsmeier DVM, School of Veterinary Medicine |
| 2009 | Meng Wang The Ohio State University, Bioinformatics/Biostatistics |

Undergraduate Students

| | |
|-----------|--|
| 2017-2019 | Patrick Skillman, Washington and Lee University, Virginia |
| 2016-2019 | James Li The Ohio State University |
| 2014-2016 | Cameron Locker Purdue University, Indiana |
| 2012-2014 | Logan Griffith Wittenberg University, Pre-Med |
| 2010 | Zhi (Meredith) Zheng The Ohio State University- Engineering |

PETER WHITE, PHD

2010-2011 Elizabeth Nick
Northwestern University, Education and Social Policy

High School Students

2019-Present Isaiah Brant
Fort Hayes High School
2019 Defne Ceyhan
Upper Arlington High School
2019 Kaya Ceyhan
Upper Arlington High School
2018-2019 Elizabeth White
Bexley High School
2016 Sara Imwalle
Bexley High School
2016 Tarma Obeng
Fort Hayes Career Center
2009- 2011 Sachin Rudraraju
Worthington High School

CONFERENCES AND SYMPOSIA

May 20, 2014 **Organizing Committee Co-Chair:** *The Road to Collaboration: NCH and OSU Human Genetics Community Meeting*
The Research Institute at Nationwide Children's Hospital
Columbus, OH

January 14, 2015 **Organizing Committee Member:** *The Road to Collaboration: NCH and OSU Human Genetics Community Meeting*
The Ohio State University
Columbus, OH


2015 – Present **Organizer:** *Annual David Newsom Memorial Lectureship*
The Research Institute at Nationwide Children's Hospital
Columbus, OH

October 15, 2018 **Organizing Committee Co-Chair:** *The Annual Research Retreat*
The Research Institute at Nationwide Children's Hospital
Columbus, OH

PROFESSIONAL MEMBERSHIPS AND ACTIVITIES

| | |
|----------------|--|
| 2003 – 2008 | Beta Cell Biology Consortium (BCBC) Vanderbilt University, Nashville, TN |
| 2009 – 2011 | International Society for Developmental Origins of Health and Disease Southampton, UK |
| 2009 – 2017 | Association of Biomolecular Resource Facilities (ABRF) Bethesda, MD |
| 2010 – present | American Society of Human Genetics (ASHG) Bethesda, MD |
| 2011 – present | International Society for Computational Biology (ISCB) La Jolla, CA |

I have reviewed the curriculum vitae for completeness and accuracy and agree with its content.

Signature: 
Date: January 21, 2020