

CURRICULUM VITAE
PETER WHITE, PhD

PRESENT TITLE & AFFILIATION

Chief Data Sciences Officer

The Abigail Wexner Research Institute at Nationwide Children's Hospital
Columbus, OH

Battelle Chair in Quantitative and Computational Biology

Nationwide Children's Hospital
Columbus, Ohio

Professor of Pediatrics with Tenure

Department of Pediatrics
The Ohio State University College of Medicine
Columbus, Ohio

OFFICE ADDRESS

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RESEARCH PROFILES

ORCID: [0000-0002-5218-5903](https://orcid.org/0000-0002-5218-5903)

Scopus Author ID: [57204282849](https://scopus.org/authid/57204282849); **SCOPUS H-INDEX: 37**

Research Gate: <https://www.researchgate.net/profile/Peter-White-33>

WOS Publons ResearcherID: [E-4301-2011](https://publons.com/researcher/E-4301-2011/); **Clarivate Web of Science H-INDEX: 37**

My NCBI: <https://www.ncbi.nlm.nih.gov/myncbi/peter.white.2/bibliography/public/>

EDUCATION

POST-GRADUATE EDUCATION & TRAINING

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

GRADUATE TRAINING

- 1998 **Ph.D. Molecular Biology**
University of Cambridge, Cambridge, UK
Thesis Title: “*Nutritional Regulation of Muscle Gene Expression*”

UNDERGRADUATE TRAINING

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

ACADEMIC APPOINTMENTS

- 2022 – Present **Battelle Chair in Quantitative and Computational Biology**
Endowed Chair
Nationwide Children’s Hospital
Columbus, Ohio
- 2023 – Present **Tenured Professor of Pediatrics**
Department of Pediatrics
The Ohio State University College of Medicine
Columbus, OH
- 2016 – 2023 **Tenured Associate Professor of Pediatrics**
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
- 2008 – 2011 **Research Assistant Professor of Pediatrics (Research Track)**
Department of Pediatrics
The Ohio State University College of Medicine
Columbus, OH

RESEARCH AND ADMINISTRATIVE APPOINTMENTS

2023 – Present	Chief Data Sciences Officer The Abigail Wexner Research Institute Nationwide Children's Hospital Columbus, OH
2016 – 2023	Senior Director, Computational Genomics Group The Institute for Genomic Medicine 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
2012 – 2016	Director of Molecular Bioinformatics The Research Institute at Nationwide Children's Hospital Columbus, OH
2008 – 2016	Director, Biomedical Genomics Core Facility The Research Institute at Nationwide Children's Hospital Columbus, OH

OTHER PROFESSIONAL EXPERIENCE

2016 – Present	Principal Investigator , The Institute for Genomic Medicine The Research Institute at Nationwide Children's Hospital Columbus, OH
2014 – 2020	Chief Scientific Officer , GenomeNext LLC, Columbus, OH
2008 – 2016	Principal Investigator , Center of Microbial Pathogenesis The Research Institute at Nationwide Children's Hospital Columbus, OH
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

SERVICE

ACADEMIC EDUCATIONAL PROGRAM RESPONSIBILITIES

2022 – Present	MSTP Admissions Subcommittee Member College of Medicine Medical Scientist Training Program (MSTP) The Ohio State University
2022 – Present	Discovery PREP Research Mentor College of Medicine Postbaccalaureate Research Education Program The Ohio State University
2017 – Present	Biomedical Sciences Graduate Program (BSGP) Mentor College of Medicine The Ohio State University
2016 - Present	Futures Matter Faculty Mentor Transformative Transdisciplinary Summer Research Program The Research Institute at Nationwide Children's Hospital
2018	Conference Organizing Committee Member 2018 Research Retreat The Research Institute at Nationwide Children's Hospital
2017	Conference Organizing Committee Member The Road to Collaboration: NCH/OSU Human Genetics Community Meeting The Research Institute at Nationwide Children's Hospital

ACADEMIC ADMINISTRATIVE RESPONSIBILITIES

2022	Faculty Search Committee Member The Institute for Genomic Medicine The Research Institute at Nationwide Children's Hospital
2022	Faculty Search Committee Member Center for Cardiovascular Research The Research Institute at Nationwide Children's Hospital
2021 - Present	Project Leadership Team Co-Chair National Cancer Institute (NCI) Clinical Trial Specimen Molecular Characterization Program (CTSMC)
2019 – Present	Advisory Board Member Research Cyberinfrastructure and Advanced Computing (RCAC) Advisory Council The Ohio State University
2018 – present	Executive Committee Member The IGM LIMS Executive Steering Committee (Project Sponsor) Nationwide Children's Hospital

2018 – present	Committee Chair The IGM Laboratory Information Management System (LIMS) Project Leadership Team Nationwide Children’s Hospital
2016 – Present	Executive Member The Institute for Genomic Medicine Senior Leadership Team Nationwide Children’s Hospital
2016 – Present	Executive Member The Institute for Genomic Medicine Senior Leadership Team Nationwide Children’s Hospital
2016 – 2017	Executive Committee Member The IGM Cloud Computing Executive Steering Committee Nationwide Children’s Hospital
2016 – 2017	Committee Chair The Institute for Genomic Medicine Cloud Computing Design Team Nationwide Children’s Hospital
2014 – 2017	Executive Committee Member Data & Analytics Strategy Committee Nationwide Children’s Hospital
2014 – 2016	Search Committee Member Director of the Institute for Genomic Medicine 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
2013 – present	Executive Committee Member Research Computing Steering Committee 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
2010 – 2014	Committee Member Research Information Technology Advisory Council The Research Institute at Nationwide Children’s Hospital
2010	Committee Chair Equipment Grant Advisory Committee The Research Institute at Nationwide Children’s Hospital

NATIONAL ACTIVITIES

2023	Ad hoc reviewer: NIH CTSA Collaborative and Innovative Acceleration Award (UG3/UH3) National Center for Advancing Translational Sciences, NIH
2022	Ad hoc reviewer: NIH Undiagnosed Diseases Network Review National Institute of Neurological Disorders and Stroke (NINDS) Special Emphasis Panel
2022	Ad hoc reviewer: NIH Small Business: Health Informatics Small Business and Technology Transfer Study Section
2021 - Present	Executive Steering Committee Member National Cancer Institute (NCI) Molecular Characterization Initiative (MCI)
2019	Scientific Advisory Board Member St. Jude Children's Research Hospital, Memphis, TN
2018	Ad hoc reviewer: NIH Undiagnosed Disease Network Phase II Sequencing Core National Human Genome Research Institute (NHGRI)
2015	Ad hoc reviewer: NIH Center for Scientific Review Special Emphasis Panel Shared Instrumentation: Genomics Office of Research Infrastructure Programs (ORIP)
2014	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)
2012	Ad hoc reviewer: NIH Center for Scientific Review Special Emphasis Panel Shared Instrumentation: Genomics Office of Research Infrastructure Programs (ORIP)
2011 – 2012	Member, Batch Effects Committee The Cancer Genome Atlas (NCI)
2010	Ad hoc reviewer: NIH Center for Scientific Review Shared Instrumentation Study Section National Council for Research Resources (NCRR)

- 2009 – 2014 **Genomics Consultant**
Biospecimen Core Resource
The Cancer Genome Atlas (NCI)
Nationwide Children's Hospital
- 2009 **Ad hoc reviewer: NIH**
Population Genetics Analysis Program Special Emphasis Panel
National Institute of Allergy and Infectious Diseases (NIAID)
- 2009 **Ad hoc reviewer: NIH**
Center for Scientific Review Special Emphasis Panel
Genome Instrumentation
National Council for Research Resources (NCRR)

INTERNATIONAL ACTIVITIES

- 2021 - 2022 **Research partner, The MASThers Project**
A transatlantic consortium of scientists working to understand the
Molecular Mechanisms of Aortic Stenosis as a Basis of Prevention
and Therapy.
- 2021 **Ad hoc reviewer: Fondazione Cariplo, Italy**
Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico
- 2020 **Ad hoc reviewer: Medical Research Council, UK**
Molecular & Cellular Medicine Board
- 2017 **Ad hoc reviewer: Genome Quebec**
Genome Canada 2017 LSARP Competition
Expert Review Committee
- 2017 **Ad hoc reviewer: Canada Foundation for Innovation**
John R. Evans Leaders Fund
Expert Review Committee

HONORS AND AWARDS

- 2022 **The OSU Department of Pediatrics 2021 Outstanding Mentor Award**
This award is given in recognition of exemplary mentoring of undergraduate
students, graduate students, postdoctoral fellows, residents, fellows, or faculty
members in research, creative, clinical, and other scholarly activities.
- 2017 **Nationwide Children's Hospital Team of the Year 2017**
Led The Institute for Genomic Medicine Cloud Design Team, which received
the 2017 Outstanding Team of the Year award.
- 2015 **2015 College of Medicine Outstanding Faculty Achievement Award**
The Ohio State University
- 2015 **The CLARITY Undiagnosed Challenge (First place)**
Winner of a \$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

- 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
- 2013 **The CLARITY Challenge** (Finalist)
Boston Children's Hospital
- 2012 **Inventor of the Year** (Finalist)
TechColumbus Innovation Awards

RESEARCH SUPPORT

ONGOING RESEARCH

S21-121 **P White**, C Cottrell, R Wilson, E Mardis (Leadership Team) 7/1/21-6/30/2025
National Cancer Institute (NCI/NIH) / Leidos Biomedical Research Contract \$50,808,000
The Molecular Characterization Initiative (MCI)

The Childhood Cancer Data Initiative (CCDI) supports the critical need to collect, analyze, and share data to address the burden of cancer in children, adolescents, and young adults (AYAs). The initiative supports childhood cancer research and aims to make it easier for researchers to learn from the approximately 16,000 children and adolescents diagnosed with cancer in the United States each year. As part of this initiative, NCI's Molecular Characterization Initiative (MCI) program supports the Nationwide Children's Hospital (NCH) Institute for Genomics Medicine (IGM) in providing a comprehensive molecular characterization of pediatric cancer samples from the Project:EveryChild – a childhood cancer registry maintained by the Children's Oncology Group (COG). Under MCI, IGM receives specimens from the COG Biorepository (operated by the NCH Biopathology Center (BPC)). IGM characterizes the samples using genomics, transcriptomics, and epigenomics technologies and generates Clinical Reports and a comprehensive set of Molecular Data.

*Role: **Senior Computational Investigator / Co-Investigator***

R21 HL161823 **Peter White** and Vidu Garg (Co-PI): 1/1/22-12/31/2023
National Heart Lung and Blood Institute (NHLBI/NIH) \$230,000
A Multi-omic approach towards improving candidate gene identification and variant prioritization in patients with congenital heart disease

This exploratory grant aims to use a machine learning approach that utilizes transcriptomic datasets from mouse and iPSC models of congenital heart disease to prioritize pathogenic variants in patients with congenital heart disease.

*Role: **Co-Principal Investigator / Senior Computational Investigator***

U54 CA232561 Timothy P Cripe and Elaine R Mardis (Co-PI) 9/12/2019-8/31/2024
National Cancer Institute (NCI/NIH) \$10,242,127
Pediatric Ohio-New York Cancer (Peds-ONC) Immunotherapy Center

We seek to discover and validate strategies to leverage 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 CA223219 Paul J Goodfellow (PI) 7/1/2018-6/30/2023
National Cancer Institute (NCI/NIH) \$2,515,795
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. Studying DNA specimens prepared in clinically approved laboratories will make it possible to rapidly take research findings to clinical testing. Robust tumor-based testing applied to all endometrial cancer patients will translate to improved cancer prevention and treatment.

Role: ***Co-Investigator / Senior Computational Investigator***

R01 HL157491 Christopher Breuer (PI) 4/1/2021 – 3/31/2025
National Heart Lung and Blood Institute (NHLBI/NIH) \$2,979,312
Elucidating the Molecular Mechanisms Underlying LYST-mediated Tissue Engineered Vascular Graft Stenosis

In this project, we will elucidate the mechanism underlying LYST-mediated TEVG stenosis, the most common graft-related complication, and the critical barrier preventing its widespread clinical use.

Role: ***Co-Investigator***

COMPLETED RESEARCH

AVIF Innovation Fund Peter White and Kim McBride (Co-PI) 7/1/2020-6/30/2022
Additional Ventures Innovation Fund (AVIF) \$351,962
Development of a protocol to risk stratify individuals with single ventricle CHD using deep phenotyping and genome sequencing

We will standardize a deep phenotyping protocol for evaluating patients with Congenital Heart Disease (CHD) and utilize genome sequencing and machine learning to identify novel genetic variants that contribute to Single Ventricle-CHD.

This award is funded at an equivalent level to an NIH R01.

Role: ***Co-Principal Investigator / Senior Computational Investigator***

CCTS Machine Learning Pilot Peter White (PI) 6/1/2021 – 5/31/2022
Ohio State University Center for Clinical and Translational Science (CCTS) \$75,736
Elucidation of the role of long non-coding RNAs in Congenital Heart Disease

In this CCTS-funded pilot project, we will utilize machine learning techniques to identify genetic variants that impact the function of long non-coding RNAs (lncRNAs) in congenital heart disease (CHD).

Role: ***Principal Investigator***

AVIF Innovation Funds 2020 Christopher Breuer (PI) 7/1/2020-6/30/2022
Additional Ventures Innovation Fund (AVIF) \$299,191
Unlocking our Regenerative Capacity: Elucidating the Role of LYST on Neotissue Formation in Tissue Engineered Constructs

The primary objective of this study is to determine the molecular mechanisms by which the lysosomal trafficking regulator gene (LYST) modulates neotissue formation in tissue-engineered vascular grafts (TEVG). Then based on our discoveries, the secondary objective of this study is to

rationally design a method for improving the performance of the TEVG by altering LYST expression.

This award is funded at an equivalent level to an NIH R01.

Role: ***Co-Investigator***

R21 DC016709 Kenneth L Brockman (PI) 3/1/2019-8/31/2020
National Institute on Deafness & other Communication Disorders (NIDCD/NIH) \$455,370
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 childhood's most predominant bacterial disease 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 of our research and the goal of this project is to better understand the role of this novel mechanism during disease to enable the development of improved methods to prevent and treat otitis media and other upper respiratory infections.

Role: ***Co-Investigator / Senior Computational Investigator***

R01 AR073311 Chack-Yung Yu (PI) 7/8/2018-5/31/2020
National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS/NIH) \$2,103,946
Complement in Human Lupus: Deficiencies, Profiles and Complications

The complement system is a critical effector arm of the immune response. This proposal thoroughly studies the complement system's genes and proteins on the cause and modifications of disease profiles and outcomes in human lupus and lupus nephritis.

Role: ***Co-Investigator***

KOPP16IO Benjamin Kopp (PI) 10/31/2016-04/30/2019
Cystic Fibrosis Foundation (CFF) \$108,000
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 / Senior Computational Investigator***

R01 AI116917 John Gunn (PI) 06/01/2015-05/31/2019
National Institute of Allergy and Infectious Diseases (NIAID/NIH) \$3,028,917
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 / Senior Computational Investigator***

R21 AR070509 Chack-Yung Yu (PI) 4/17/2017-3/31/2019
National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS/NIH) \$375,305
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***

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

R01 HL109758 **Peter White, Kim McBride & Vidu Garg (Co-PI)** 9/24/2012 – 7/31/2017
National Heart, Lung, and Blood Institute (NHLBI/NIH) \$2,681,237
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 (Co-PI)** 6/26/2015 – 4/30/2016
The OSU Center for Clinical and Translational Science \$50,000
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 (PI) 9/30/2012 – 9/29/2015
Air Force Medical Service / Department of Defense \$3,000,000
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 (PI)** 12/1/2014 – 11/30/2015
GenomeNext LLC \$250,000
Churchill Development Plan: Online Software as a Service
The White Lab at The Research Institute at Nationwide Children's will work with the GenomeNext development team to forklift the Churchill solution to GenomeNext AWS environment, assisting with the necessary optimization, testing and optimization of data upload and analysis modules.
Role: ***Principal Investigator***

R56 AI109002 John Gunn (PI) 8/8/2014 – 7/31/2015
National Institute of Allergy and Infectious Diseases (NIAID/NIH) \$617,221

Chronic Infection of the Gallbladder by Salmonella

The Ohio State University subcontract. Typhoid Fever is a global human-specific illness caused primarily by *Salmonella enterica* serovar Typhi (*S. Typhi*). Approximately 5% of those infected with *S. Typhi* that resolve an acute infection become chronic carriers, with the gallbladder (GB) being the primary site of carriage. We will use our chronic mouse model to characterize both host and bacterial responses associated with gallbladder colonization and establishment of chronic infection. 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**

HHSN261201000047C Julie Gastier-Foster (PI) 5/23/2012 - 7/31/2014
National Cancer Institute (NCI/NIH) \$11,542,415

Biospecimen Core Resource for The Cancer Genome Atlas Project

Review and process blood and tissue samples and their associated data using optimized standard operating procedures for the entire TCGA Research Network, as part of an effort to understand the molecular basis of cancer through the application of genome analysis technologies, including large-scale genome sequencing.

Role: **Consultant**

R01 AI073971 Brian Ahmer (PI) 3/1/2011 – 4/30/2014
National Institute of Allergy and Infectious Diseases (NIAID/NIH) \$2,842,316

Salmonella Polymicrobial Interactions

OSU subcontract with Brian Ahmer. This subcontract project will involve \$100,000 per year of direct costs, primarily for the manufacture of arrays, nucleic acid preparation, amplification, labeling, hybridization, image analysis, data preprocessing and normalization, and assistance with secondary analysis and statistical interpretation of the data. We will hybridize more than 200 arrays per year using samples from swine, and process this data for genes that contribute significantly to fitness.

Role: **Co-Investigator**

NCHRI Internal Award Samantha King (PI) 2/1/2012 – 1/31/2014
Collaborative Science Award \$30,000

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**

29XS073ST	Julie Gastier-Foster (PI)	10/31/2009 – 5/22/2012
National Cancer Institute (NCI/NIH)		\$5,394,517
<i>Biospecimen Core Resource for The Cancer Genome Atlas Project</i>		
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: <i>Co-Investigator</i>		

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.

PROVISIONAL 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.

Skillman-Lawrence, Patrick; Gordon, David; McBride, Kim; **White, Peter.** (2020) WHAAP: Wound Healing Automated Analysis Pipeline. *Invention Disclosure* April 6, 2020. Office of Technology Commercialization, The Abigail Wexner Research Institute at Nationwide Children's Hospital.

White, Peter; Schuetz, Robert; Chaudhari, Bimal; Antoniou, Austin. (2020) Cavalri: A Clinical Decision Support Algorithm for Rapid Identification of Diagnostic. *Invention Disclosure* November 20, 2022 (Reference #: IDF-002179). Office of Technology Commercialization, The Abigail Wexner Research Institute at Nationwide Children's Hospital.

PUBLICATIONS

ARTICLES IN PEER REVIEWED JOURNALS

1994 - 2005

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: 10.1677/jme.0.0230241. PubMed PMID: 10514561
3. **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
4. 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
5. **White P**, Cooke N. (2000) The multifunctional properties and characteristics of vitamin D-binding protein. *Trends In Endocrinology And Metabolism: Tem*. 11(8):320-7. doi: 10.1016/s1043-2760(00)00317-9. PubMed PMID: 10996527
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. doi: 10.1079/pns200071. 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: 10.4049/jimmunol.168.2.869. PubMed PMID: 11777984
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

2006 - 2010

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19. Zheng M, Newsom D, Sowby W, **White P**. (2010) “IUGR results in delayed islet formation and a significantly reduced beta cell mass.” The Annual Research Conference, The Research Institute at Nationwide Children’s Hospital, Columbus, Ohio
20. Newsom D, **White P**. (2010) “The Biomedical Genomics Core.” The Annual Research Conference, The Research Institute at Nationwide Children’s Hospital, Columbus, Ohio
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 discover 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 casual 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 sever *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. Mackos AR, **White P**, Bailey MT. (2017) “The colonic epithelial transcriptome and intestinal microbiome are significantly changed by social stressor exposure.” Brain Behavior and Immunity. <https://doi.org/10.1016/j.bbi.2017.07.069>. PsychoNeuroImmunology Research Society's 24th Annual Scientific Meeting, Galveston, TX.

94. Kelly B, Fitch J, Cottrell CE, Gastier-Foster J, **White P**, Leonard J, Wilson RK, Mardis ER. (2017) “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.
95. 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.
96. Spencer A, Fitch J, **White P**. (2017) “Differential Gene Expression Analysis through RNA-Seq.” Nationwide Children’s Hospital Research Retreat 2017, Columbus, Oh.
97. 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.
98. 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.
99. 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.
100. Gnoma 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.
101. **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.*
102. Nelin L, Gnoma 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.
103. 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.
104. Frnts 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.
105. 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.
106. 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.
107. Gnoma 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.
108. Li J, **White P**. (2018). “Global local folding of the human transcriptome.” Denman Undergraduate Research Forum, The Ohio State University, Columbus OH.

109. Li J, **White P.** (2018). “Global local folding of the human transcriptome.” Brazilian Graduate Students Conference (BRASCON), Columbus, OH.
110. 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.
111. 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.
112. 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.
113. 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 *Myl2* Variant Identified Through Exome Sequencing of an Autosomal Recessive Form of Hypertrophic Cardiomyopathy.” American Heart Association 2018, Chicago, IL.
114. 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.*
115. 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.*
116. 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.
117. **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.
118. 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

119. 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.
120. 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.
121. 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.
122. 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.
123. 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.
124. 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.
125. 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.
126. 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.
127. 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.

128. 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.
129. **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.***
130. 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.
131. 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.
132. 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.***
133. Gaither J, Brennen 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.
134. 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.
135. 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.
136. 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.
137. 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.***
138. 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.
139. 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.
140. 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.

141. Gaither J, Brennen 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.
142. 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.
143. 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.
144. 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.*
145. Bir N, Brennan PJ, Rajkovic A, Gaither J, Kelly BJ, Wheeler G, McElroy J, **White P**, Cottrell CE, Magrini VJ, Wilson RK, Mardis ER, Goodfellow P. “Clinically Validating Automation of Library Preparation for NGS-based Detection of Cancer Susceptibility and MSI in Endometrial Cancer Patients.” (2020) AGBT General Meeting 2020, Marco Island, FL.
146. 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.
147. 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.
148. 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.
149. 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.

150. 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.
151. 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.
152. 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.
153. Kautto EA, Melas M, Mori M, McBride KL, Mosher TM, Pfau RB, Hernandez-Gonzalez ME, McGrath SD, Magrini VJ, **White P**, Balch Samora J, Koboldt DC, Wilson RK. (2020) Long-read Whole-Genome Sequencing Reveals HOXD13 Alterations in Synpolydactyly. NCH Research Retreat 2018, Columbus, OH. *Abstract of distinction.*
154. 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.
155. 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.
156. de Faria FW, Schieffer KM, Pierson C, Boué D, Zumberge N, Rusin J, LaHaye S, Miller KE, Koboldt DC, Lichtenberg T, Leraas K, Brennan P, Kelly B, **White P**, Magrini V, Wilson RK, Mardis ER, Osorio DS, Leonard J, Finlay JL (2020) “EPEN-17. Favorable Outcome to Intensive Chemotherapy Without Irradiation in Infantile Metastatic Ependymoma with a Novel Molecular Profile: A Case Report.” 19th International Symposium on Pediatric Neuro-Oncology (ISPNO 2020), Karuizawa, Nagano, Japan.
157. Yasuhara J, Manivannan S, Gordon D, Skillman-Lawrence P, Flichtner S, Myers K, Zender G, McBride K, **White P**, Garg V. (2020) “Refinement of a Variant Prioritization Pipeline for Use in Multiplex Congenital Heart Disease.” 2020 Weinstein Cardiovascular Development and Regeneration Conference, Montreal, QC, Canada.
158. Bhayana S, Agrawal S, Chanley MA, Waller AP, Wolfgang KJ, Wijeratne S, Fitch J, **White P**, Kerlin BA, Smoyer WE. (2020) “Glomerular Transcriptomic Analysis of Glucocorticoid- and Pioglitazone-Treated Nephrotic Syndrome.” American Society of Nephrology Kidney Week 2020 (Virtual).

159. Cottrell CE, Setty BA, Lillis AP, Khansa I, Pearson GD, Fernandez-Faith E, Whitaker A, Kirschner RE, Jatana KR, Braswell L, Smith S, Lewis R, Truxal KV, Savage SK, Shenoy A, Jalkanen A, Lee K, Koo SC, Choi S, Leraas K, Cearlock S, Koboldt DC, LaHaye S, Brennan P, Kelly B, Wheeler G, Schieffer KM, **White P**, Magrini V, Wilson RK, Mardis ER. (2021) “Clinical Utility of Genomic Profiling in Vascular Malformation and Somatic Overgrowth.” AGBT Virtual General Meeting, March 1-3, 2021.
160. Hickey SE, Koboldt DC, Garner S, Choi S, Pfau R, McBride KL, **White P**, Wilson RK. “Research Genomic Testing Corrects Inaccurate Variant Segregation in Family With Hypohidrotic Ectodermal Dysplasia.” 2nd Annual Southern California Rare Disorders Symposium; March 19, 2021.
161. Melas M, Hickey SE, Bartholomew D, Truxal KV, McBride KL, Murugu M, Mori M, Corsmeier D, Jayaraman V, Dave-Wala A, McKinney A, Wetzel A, Wijeratne S, Caceres V, Garner S, Hashimoto S, Matthews T, Mouhlas D, Humphrey M, Grossman T, Kelly BJ, Koboldt DC, Magrini VJ, **White P**, Wilson RK, Cottrell CE, Lee K, Mathew MT. (2021) “Evaluating the Mutational Spectrum of SIN3A Alterations: A Case Series of Patients Profiled by Next Generation Sequencing.” ACMG 2021 Annual Clinical Genetics Meeting (Virtual); April 13-16, 2021.
162. Cottrell CE, Setty BA, Lillis AP, Khansa I, Pearson GD, Fernández-Faith E, Whitaker AT, Kirschner RE, Halsey JN, Jatana KR, Braswell LE, Smith S, Lewis R, Truxal KV, Savage SK, Shenoy A, Jalkanen AL, Lee K, Koo SC, Choi S, Leraas K, Cearlock S, Koboldt DC, LaHaye S, Brennan PJ, Kelly BJ, Wheeler G, Schieffer KM, **White P**, Magrini VJ, Wilson RK, Mardis ER. (2021) “Robust diagnostic yield and candidate gene discovery through paired exome analysis in vascular malformation and overgrowth.” ACMG 2021 Annual Clinical Genetics Meeting (Virtual); April 13-16, 2021.
163. Chaudhari BP, Cottrell CE, Magrini VJ, **White P**, Antoniou A, Choi S, Kelly BJ, Crist E, Brennan PJ, Wheeler G, Rajkovic A, Franklin SJ, Lammi GE, Kuck H, Gordon DL, Bosley E, Herman AC, Brenneman J, Voytovich KJ, Koboldt DC, Lee K, Leung MS, Hunter J, Schultz M, Chen I, Corsmeier D, Grubbs C, Jalkanen AL, Jayaraman V, Lehman AR, Bartholomew D, Hickey SE, Manickam K, McBride KL, Mori M, Truxal KV, Caceres V, Carroll J, Garner S, Gosselin R, Martin CC, Pastore MT, Savage SK, Schmalz B, Siemon A, Sites E, Zapanta B, Bir N, Woodiga SA, McKinney A, Zhong H, Mardis ER, & Wilson RK. (2021) “Outcomes of in-house rapid genome sequencing at a Children’s Hospital.” ACMG 2021 Annual Clinical Genetics Meeting (Virtual); April 13-16, 2021
164. Hickey SE, Bartholomew D, Truxal KV, McBride KL, Manickam K, Mori M, Corsmeier D, Jayaraman V, Dave-Wala A, McKinney A, Wetzel A, Wijeratne S, Caceres V, Garner S, Hashimoto S, Matthews T, Mouhlas D, Humphrey M, Grossman T, Kelly BJ, Koboldt DC, Magrini VJ, **White P**, Wilson RK, Cottrell CE, Lee K, Mathew M, & Melas M. (2021) “Evaluating the mutational spectrum of SIN3A alterations, a case series of patients profiled by next generation sequencing.” ACMG 2021 Annual Clinical Genetics Meeting (Virtual); April 13-16, 2021

165. Schieffer KM, Miller AJ, Hernandez-Gonzalez ME, McGrath SD, Stonerock E, Choi S, Leraas K, Jalkanen AL, Fitch JR, LaHaye S, Kelly BJ, Koboldt DC, Koo SC, Savage SK, Kaler SG, Leonard JR, Pearson GD, Faith EF, Conces MR, Shukri A, Fung B, Pierson CR, **White P**, Magrini VJ, Wilson RK, Mardis ER, Cottrell CE, & Lee K (2021) “Expanding the phenotypic spectrum of internal tandem duplications in somatic disease.” ACMG 2021 Annual Clinical Genetics Meeting (Virtual); April 13-16, 2021
166. Chaudhari BP, Pitts J, Ravagnani S, Leraas K, **White P**, Magrini VJ, Cottrell CE, Kelly BJ, Brennan PJ, Wheeler G, Rajkovic A, Franklin SJ, Lammi GE, Kuck H, Gordon DL, Bosley E, Herman AC, Brenneman J, Voytovich KJ, Bir N, Woodiga SA, Mckinney A, Zhong H, Hunter J, Lee K, Leung MS, Schultz M, Chen I, Corsmeier D, Grubbs C, Jalkanen AL, Jayaraman V, Crist E, Mardis ER, & Wilson RK. (2021) “Determinants of turnaround time in a rapid genome sequencing program.” ACMG 2021 Annual Clinical Genetics Meeting (Virtual); April 13-16, 2021
167. Schultz M, Fitch JR, Lammi GE, Crist E, Cottrell CE, Magrini VJ, Chaudhari BP, & **White P**. (2021) “Application of constitutional rapid genome sequencing to detect infectious disease in a critically ill neonate.” ACMG 2021 Annual Clinical Genetics Meeting (Virtual); April 13-16, 2021
168. Melas M, Shatara M, Schieffer K, Lee K, Boue DR, Varga EA, Leraas KM, Rodriguez DP, Abdelbaki MS, Osorio DS, Finlay JL, **White P**, Magrini VJ, Wilson RK, Mardis ER, Cottrell CE. (2021) “Co-occurrence of Rosette-forming Glioneuronal Tumors with Noonan Syndrome.” Cancer Genomics Consortium, 12th Annual Meeting (Virtual); August 1-4, 2021. *Abstract selected podium presentation.*
169. Cottrell CE, Setty BA, Lillis AP, Khansa I, Pearson GD, Fernández-Faith E, Witman PM, Matarneh BA, Harfmann KL, Whitaker AT, Kirschner RE, Bjorklund KA, Grischkan JM, Jatana KR, Walz PC, Lind MN, Braswell LE, Smith S, Lewis R, Ho ML, Halsey J, Shenoy A, Aldrink JH, Mori M, Wojtowicz AA, Jacobson-Kelly AE, Jalkanen AL, Mathew M, Lee K, Varga E, Choi S, Patel B, Leraas K, Brennan PJ, Kelly BJ, Schieffer KM, **White P**, Magrini VJ, Wilson RK, Mardis ER. (2021) “Use of Paired Exome Analysis in Vascular Anomalies Expands the Associated Genetic Spectrum.” International Scientific Meeting for PIK3CA Related Conditions; October 28-29, 2021. *Abstract selected podium presentation.*
170. Wheeler G, Moreland B, Rajkovic A, Brenneman J, Kelly B, **White P**. (2021) “A combined ensemble and machine learning method for improved accuracy of structural variant detection.” CSHL Genome Informatics, Cold Spring Harbor, NY; November 3-5, 2021 (Virtual).
171. Moreland B, Lammi G, Gordon D, Gaither J, **White P**. (2021) “Information theoretic analysis of synonymous codon usage offers metrics to assess constraint on synonymous variants.” CSHL Genome Informatics 2021, Cold Spring Harbor, NY; November 3-5, 2021 (Virtual).
172. Schuetz R, Antoniou A, Chaudhari B, **White P**. (2021) “Evaluation and optimization of a clinical decision support algorithm for rapid identification of pathogenic variants.” CSHL Genome Informatics, Cold Spring Harbor, NY; November 3-5, 2021 (Virtual).

173. LaHaye S, Fitch J, Voytovich K, Herman AC, Kelly BJ, Lammi GE, Arbesfeld J, Wijeratne S, Franklin SJ, Schieffer KM, McGrath SD, Miller A, Wetzell A, Magrini V, Cottrell CE, Mardis ER, Wilson RK, **White P.** (2021) "Discovery of Clinically Relevant Fusions in Pediatric Cancer." CSHL Genome Informatics, Cold Spring Harbor, NY; November 3-5, 2021 (Virtual).
174. Franklin SJ, Mori M, Kelly BJ, Brant I, Chang P, Chaudhari B, Pfau R, Mihalic Mosher M, Crist E, Choi S, Williamson R, McBride K, Hickey SE, Koboldt DC, Wilson RK, **White P.** (2021) "Short tandem repeat characterization in a cohort of rare disease families." CSHL Genome Informatics, Cold Spring Harbor, NY; November 3-5, 2021 (Virtual).
175. Penalzoza J, Landis B, McBride K, and **White P.** (2021) "Analysis of Copy Number Variants in more than 1,300 patients with Congenital Heart Disease". CSHL Genome Informatics, Cold Spring Harbor, NY; November 3-5, 2021 (Virtual).
176. Bollas, A, Mardis, E, **White, P.** (2021) "A machine learning approach to detect somatic variants in tumor RNA-Seq." CSHL Genome Informatics, Cold Spring Harbor, NY; November 3-5, 2021 (Virtual).
177. Otero-Bravo A, Kelly B, Mardis E, White P. (2021) "Additional filtering for somatic variants derived from FFPE tumor samples." CSHL Genome Informatics, Cold Spring Harbor, NY; November 3-5, 2021 (Virtual).
178. Notestine R, Choi S, Varga E, Williamson R, Gosselin R, Mori M, Cottrell C, Magrini V, **White P**, Wilson RK, Chaudhari BP. (2021) "Rapid Genome Sequencing identifies ALDH7A1 variant causative of pyridoxine-dependent epilepsy (PDE)." Nationwide Children's Hospital Research Retreat 2021, Columbus, OH; November 16-17, 2021.
179. Choi S, Chaudhari BP, Varga E, Williamson R, McBride KL, Hickey SE, **White P**, Koboldt DC, Wilson RK. (2021) "Compound heterozygous variants in TTN identified in a deceased fetus with severe hydrops fetalis." Nationwide Children's Hospital Research Retreat 2021, Columbus, OH; November 16-17, 2021.
180. LaHaye S, Fitch J, Voytovich K, Herman AC, Kelly BJ, Lammi GE, Arbesfeld J, Wijeratne S, Franklin SJ, Schieffer KM, McGrath SD, Miller A, Wetzell A, Magrini V, Cottrell CE, Mardis ER, Wilson RK, **White P.** (2021) "Discovery of Clinically Relevant Fusions in Pediatric Cancer." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021.
181. Gaither J, Brenneman J, Lammi G, Herman H, Kuck H, Gordon D, Kelly B, **White P.** (2021) "SNPDogg: Single Nucleotide Polymorphism Deleteriousness Observation in Genomes using Gradient boosted trees." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021.
182. Schuetz R, Antoniou A, Chaudhari B, **White P.** (2021) "Evaluation and optimization of a clinical decision support algorithm for rapid identification of pathogenic variants." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021. *Research poster of distinction.*
183. Wheeler G, Moreland B, Rajkovic A, Brenneman J, Kelly B, **White P.** (2021) "A combined ensemble and machine learning method for improved accuracy of structural variant detection." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021. *Research poster of distinction.*

184. Moreland B, Lammi G, Gordon D, Gaither J, **White P.** (2021) "Information-theoretic analysis of "silent" genetic variation reveals sources of constraint." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021.
185. Franklin SJ, Mori M, Kelly BJ, Brant I, Chang P, Chaudhari B, Pfau R, Mihalic Mosher T, Crist E, Choi S, Williamson R, McBride KL, Hickey SE, Koboldt DC, Wilson RK, **White P.** (2021) "Short tandem repeat characterization in a cohort of rare disease families." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021.
186. Brant, I, Brennan, P, Franklin, SJ, Kelly, B, Koboldt, DC, Otero-Bravo, A, **White, P.** (2021) "Reducing Cloud Computing Costs through Compression of Genome Sequencing Data." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021.
187. Bollas, A, Mardis, E, **White, P.** (2021) "RNA-Seq as a proxy for DNA methylation-based CNS tumor classification." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021.
188. Otero-Bravo A, Kelly B, Mardis E, **White P.** (2021) "Additional filtering for somatic variants derived from FFPE tumor samples." Nationwide Children's Hospital Research Retreat, Columbus, OH; November 16-17, 2021.
189. Choi SS, **White P**, Chaudhari B. (2022). "The Importance of Parental Sequencing Depth in the Setting of Rapid Genome Sequencing." Annual Clinical Genetics Meeting, Nashville, TN; March 23-26, 2022. ***Awarded 2022 ACMG Top-Rated Abstract***
190. Schuetz R, Antoniou A, Chaudhari B, **White P.** (2022). "Development and optimization of a clinical support algorithm for rapid identification of diagnostic germline variants." Annual Clinical Genetics Meeting, Nashville, TN; March 23-26, 2022. ***Awarded 2022 ACMG Top-Rated Abstract***
191. Yasuhara J, Manivannan S, Majumdar U, Gordon D, Myers K, Zender G, McBride K, **White P**, Garg V. (2022) "A Novel Pathogenic *GATA6* Variant Identified in a Family with Persistent Truncus Arteriosus, Childhood-onset Diabetes Mellitus and Spontaneous Intestinal Perforation." Weinstein Cardiovascular Development & Regeneration Conference, Marseille, France; May 12-14, 2022.
192. Bollas A, **White P**, Mardis E. (2022). "A machine learning approach to detect somatic variants in tumor RNA-Seq." Intelligent Systems for Molecular Biology, Madison, WI; July 10-14, 2022.
193. Penaloza J, Moreland B, McBride K, **White P**, (2022). "Multiclass Classifier for Predicting Congenital Heart Disease Subgroups using data from Copy Number Variants." Intelligent Systems for Molecular Biology, Madison, WI; July 10-14, 2022.
194. Arbesfeld J, Stevenson J, Kuzma K, O'Sullivan C, LaHaye S, Fitch J, Sboner A, Myrand S, Viachos I, **White P**, Wagner A. (2022). "FUSOR and the VICC Fusion Curation Interface: Tools for the Structured Representation of Gene Fusions." Intelligent Systems for Molecular Biology, Madison, WI; July 10-14, 2022. ***Abstract selected podium presentation.***
195. Gordon DM, Bennett JS, Majumdar U, Lawrence PJ, Matos-Nieves A, Myers K, Kamp AN, Leonard JC, McBride KL, **White P**, Garg V. (2022). "Use of machine learning to classify high-risk variants of uncertain significance in lamin A/C cardiac disease." Intelligent Systems for Molecular Biology, Madison, WI; July 10-14, 2022. ***Abstract selected podium presentation.***

196. Moreland B, Gaither J, **White P.** (2022). “Information theoretic analysis of synonymous codon usage offers context-dependent metric to assess constraint on synonymous variants.” Intelligent Systems for Molecular Biology, Madison, WI; July 10-14, 2022. ***Abstract selected podium presentation.***
197. **White P.** (2022). “Solving the Puzzle of Genetic Disease with Bits and Bytes.” Intelligent Systems for Molecular Biology, Madison, WI; July 10-14, 2022. ***Abstract selected podium presentation.***
198. Yasuhara J, Manivannan S, Majumdar U, Gordon D, Myers K, Zender G, McBride K, **White P**, Garg V. (2022) “A Novel Pathogenic *GATA6* Variant Identified in a Family with Persistent Truncus Arteriosus, Childhood-onset Diabetes Mellitus and Spontaneous Intestinal Perforation.” American Heart Association Scientific Sessions, Chicago, IL; November 5-7, 2022.

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
Clinical and Translational Medicine
Cold Spring Harbor Molecular Case Studies
Diagnostics
European Journal of Medical Genetics
Experimental and Molecular Pathology
Genes
Genome Biology
Genome Medicine
Human Genetics
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

NOTE: 94th percentile for review activity as assessed by Publons

TEACHING

LECTURES/PRESENTATIONS

National/International

- October 1, 1998 “Postnatal undernutrition markedly upregulates cardiac $\alpha 1$ and $\alpha 2$ 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
- June 7, 2021 “When doctors don’t know what’s wrong”
Featured TED Talk Podcast TEDx SHORTS
<https://podcasts.apple.com/us/podcast/tedx-shorts/id1509561884?i=1000512213690>
- June 16, 2021 “Leading the Journey to Best Outcomes through Partnership”
Invited Lecture Zero Childhood Cancer Collaboration Meeting (*virtual*)
Children’s Cancer Institute, Australia
- July 12, 2022 “Solving the Puzzle of Genetic Disease with Bits and Bytes”
Podium Presentation Translational Medicine COSI, Intelligent Systems for Molecular Biology (ISMB) 2022
Madison, WI

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”
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 at the 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
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
https://www.ted.com/talks/peter_white_when_doctors_don_t_know_what_s_wrong
- December 18, 2019 “Genomic Medicine at Nationwide Children’s”
Invited Lecture at Wright Patterson Airforce Base
Dayton, OH
- February 22, 2022 “You Will Be Found: The Search for Answers in Rare Disease”
Invited Lecture at Nationwide Children’s Rare Disease Day 2022 Patient
and Family Symposium.
Columbus, OH
- March 30, 2023 “Heartfelt Courage: Advancing Pediatric Cardiology with Genomics”
Invited Lecture at The Heart Center Research Day
The Abigail Wexner Research Institute at Nationwide Children’s Hospital
Columbus, 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
- 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
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
Columbus, OH
- 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 Group Strategic Plan”
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
Columbus, OH
- September 10, 2020 “IGM Computational Genomics Group”
The Institute for Genomic Medicine at Nationwide Children’s Hospital
IGM Faculty Meeting
Columbus, OH
- February 1, 2021 “IGM Computational Genomics Group Vision Meeting”
The Institute for Genomic Medicine at Nationwide Children’s Hospital
Computational Genomics Group Strategy and Planning Meeting
Columbus, OH

March 23, 2021	<p>“IGM Strategic Plan” The Institute for Genomic Medicine at Nationwide Children’s Hospital Computational Genomics Research Group Meeting Columbus, OH</p>
May 20, 2021	<p>“Automating Cancer Analysis” The Institute for Genomic Medicine at Nationwide Children’s Hospital Cancer Genomics Meeting Columbus, OH</p>
June 16, 2021	<p>“Leading the Journey to Best Outcomes through Partnership” Nationwide Children’s Hospital Information Services Leadership Team Meeting Columbus, OH</p>
July 7, 2021	<p>“Leading the Journey to Best Outcomes: Our Role as the Computational Genomics Group” The Institute for Genomic Medicine at Nationwide Children’s Hospital Computational Genomics Group Meeting Columbus, OH</p>
December 2, 2021	<p>“NCI’s Clinical Trial Specimen Molecular Characterization (CTSMC) Program” The Institute for Genomic Medicine at Nationwide Children’s Hospital Cancer Genomics Meeting Columbus, OH</p>
January 10, 2022	<p>“The IGM Cardiovascular Translational Protocol” The Institute for Genomic Medicine at Nationwide Children’s Hospital Executive Governance Meeting Columbus, OH</p>
September 23, 2022	<p>“Single Ventricle Outcomes Progress Report” The Abigail Wexner Research Institute at Nationwide Children’s Hospital Columbus, OH</p>
April 18, 2023	<p>“Introducing the Office of Data Sciences” Spring Town Hall Meeting The Abigail Wexner Research Institute at Nationwide Children’s Hospital Columbus, OH</p>

TEACHING AND MENTORSHIP - DIRECT SUPERVISION

Postdoctoral Fellows

2021-Present	Kevin Ying, PhD
2018-Present	Blythe Moreland, PhD
2020-2021	Ezgi Karaesmen, PhD
2018-2020	Stephanie LaHaye, PhD
2012-2016	Donald Corsmeier, DVM.
2012-2013	William Harvey, PhD

Medical Fellows

2014	Mari Mori, MD
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Graduate Students

Dissertation Advisor

2022-Present	Jeremy Arbesfeld (Co-Mentor) The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2021-Present	Robert Schuetz The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2020-Present	Audrey Bollas The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2020-Present	Jacqueline Penaloza The Ohio State University College of Medicine Biomedical Sciences Graduate Program

Internship / Rotation Mentor

2021	Jeremy Arbesfeld (Rotation Student) The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2021	Mark Vater (Rotation Student) The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2021	Shinka Mori (Graduate Student Intern) University of California, Los Angeles
2020	Robert Schuetz (Rotation Student) The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2020	Jacqueline Penaloza (Rotation Student) The Ohio State University College of Medicine Biomedical Sciences Graduate Program

PETER WHITE, PHD

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 (Medical Student Research Internship) M.D. Candidate (Class of 2018) The Ohio State University College of Medicine
2014	Dan Wang (MS Student Research Internship) Purdue University, Indiana
2012	Donald Corsmeier (DVM Student Research Internship) The Ohio State University, School of Veterinary Medicine
2009	Meng Wang (MS Student Research Internship) The Ohio State University, Bioinformatics/Biostatistics

Dissertation Committee Membership

2019-2021	Elan Shatoff The Ohio State University College of Arts and Sciences Physics Graduate Program
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Candidacy Committee Membership

2022	Alexi “Lex” Tallan The Ohio State University College of Medicine Molecular, Cellular, and Developmental Biology (MCDB) Graduate Program
2022	Robert Schuetz (<i>Committee Chair</i>) The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2021	Audrey Bollas The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2021	Jacqueline Penaloza (<i>Committee Chair</i>) The Ohio State University College of Medicine Biomedical Sciences Graduate Program
2019	Elan Shatoff The Ohio State University College of Arts and Sciences Physics Graduate Program

Undergraduate Students

2022-Present	Lennon Anderson The Ohio State University
2022-Present	Lauren Griffith The Ohio State University
2022-Present	Anthony Petulla Miami University, Ohio
2021-Present	Isaiah Brant Ohio Wesleyan, Ohio
2020-2022	Defne Ceyhan The Ohio State University
2020	Patrick McBride Oberlin College and Conservatory, Ohio
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
2010-2011	Elizabeth Nick Northwestern University, Education and Social Policy

High School Students

2022	Anthony Preston Fort Hayes High School
2021-Present	Thomas Hohmann St. Charles Preparatory School
2019-2020	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
- 2022 – Present American Heart Association (AHA)
Dallas, TX
- 2023 – Present American Medical Informatics Association (AMIA)
Washington, DC

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

Signature: 

Date: January 10, 2024