CURRICULUM VITAE

ALANNA C. MORRISON, PH.D., FAHA

The University of Texas Health Science
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Citizenship: United States Citizen
Updated: 2024

RESEARCH INTERESTS:

Genetic epidemiology, cardiovascular disease epidemiology, genomic statistical analyses, complex disease genetics, multi-omics

ACADEMIC POSITIONS:

January 2023-present	*Co-Director of the Human Genetics Center*; Department of Epidemiology, UTHealth Houston SPH
April 2022-present	*Faculty, Associate Member*; The University of Texas MD Anderson Cancer Center UTHealth Houston Graduate School of Biomedical Sciences (GSBS)
December 2021-present	Thomas Stull Matney, Ph.D. Endowed Professorship in Environmental and Genetic Sciences
January 2016-present	*Chair*; Department of Epidemiology, UTHealth Houston SPH
January 2016-December 2022	*Director of the Human Genetics Center*; Department of Epidemiology, UTHealth Houston SPH
September 2014-present	*Full Professor with Tenure*; Human Genetics Center, Department of Epidemiology, UTHealth Houston SPH
April 2004-March 2022	*Faculty, Regular Member*; GSBS
September 2011-August 2014	*Associate Professor with Tenure*; Human Genetics Center; Department of Epidemiology, UTHealth Houston SPH
October 2009-August 2011	*Associate Professor, Tenure Track*; Human Genetics Center, Department of Epidemiology, UTHealth Houston SPH
September 2008-September 2009	*Associate Professor, Non-tenure Track*; Human Genetics Center; Division of Epidemiology and Disease Control, UTHealth Houston SPH
June 2003-August 2008	*Assistant Professor, Non-tenure Track*; Human Genetics Center; Division of Epidemiology and Disease Control, UTHealth Houston SPH
August 2002-June 2003	*Research Fellow*; Human Genetics Center, UTHealth Houston SPH

May 2001-August 2002 *Post-doctoral Fellow*; Human Genetics Center, UTHealth Houston SPH

EDUCATION:

1996-2001 Degree Awarded: Ph.D., Human and Molecular Genetics
The University of Texas MD Anderson Cancer Center UTHealth Houston Graduate School of Biomedical Sciences (GSBS)
Dissertation: "Familial aggregation, candidate genes and genome scans: analyzing the role of genetics in stroke"
Advisor: Eric Boerwinkle, Ph.D.

1993-1996 Degree Awarded: B.S. High Honors
Department of Biology
University of Michigan Honors College
University of Michigan, Ann Arbor, MI
Honors Thesis: "Opthalmic sustained release cysteamine for cystinosis induced corneal opacities"
Advisor: Robert J. Levy, M.D., Department of Pediatric Cardiology

HONORS AND AWARDS:

2023 UTHealth Houston SPH Research Mentor-Mentee Award
2021 UTHealth Houston President's Scholar Award for Excellence in Research
2017 UTHealth Houston SPH Research Mentor-Mentee Award
2017 UTHealth Houston Presidential Collaborative Award
2013 UTHealth Houston SPH Front of the Envelope Award
2011 Fellow of the American Heart Association, affiliated with the Council on Functional Genomics and Translational Biology
2005 University of Texas Health Science Center Outstanding Young Investigator
2000-2001 University of Texas Health Science Center Presidents' Research Scholarship
1998-1999 Schissler Foundation Fellowship
1996 High Honors Distinction for Honors Thesis, University of Michigan
1993-1994 University of Michigan Alumni Scholarship

UNIVERSITY COMMITTEES AND ACTIVITIES:

UTHealth Houston School of Public Health

2022-present School of Public Health new building programming committee
2019-2021 Research Work Group Co-Lead, UTH-MDA Population Health Initiative
2018-2022 Member, Training in Precision Environmental Health Sciences (T32 ES027801) Executive Committee
2016-present Member, CPRIT UTHealth Innovation in Cancer Prevention Research Training Program Executive Committee
2016-present Member, SPH Executive Council
2016-present Member, SPH Research Council
2014-2016 Faculty Chair Elect
2011-2016 Epidemiology Curriculum Coordinator
2011-2016 Chair and Member, Epidemiology Curriculum Committee
2011-2016 Member, Academic Council
2011-2016 Member, Department of Epidemiology Faculty Search Committee

2009-2010 Member, Department of Epidemiology, Website Development Committee
2008 Annual Activity Report Peer Reviewer
2007-2008 Member, Division of Epidemiology and Disease Control Advisory Committee
2007-2008 Member, Peer Review Panel
2007 Member, Division of Epidemiology and Disease Control Retreat Planning Committee

The University of Texas MD Anderson Cancer Center UTHealth Houston Graduate School of Biomedical Sciences (GSBS)

2017-2020 Member, Quantitative Sciences Program Executive Committee
2013-2014 Alternate Member, Curriculum Committee
2012-2013 Member, GSBS Executive Committee
2012-2013 Chair, Student Affairs Committee
2011-2012 Co-chair, Student Affairs Committee
2010-2013 Regular Member, Student Affairs Committee
2009-2010 Alternate Member, Student Affairs Committee
2006-2011 Chair, Program in Human and Molecular Genetics Admissions Committee
2005-2008 Member, Curriculum Committee
2005 Member, Schissler Foundation Fellows Peer Review Committee
2004-2012 Member, Program in Human and Molecular Genetics Admissions Committee
1998-2003 Member, Outreach Program

NATIONAL, INTERNATIONAL, AND PEER REVIEW COMMITTEES:

National Memberships

American Heart Association, Council on Functional Genomics and Translational Biology

National Committees, Collaborative Studies, and Consortia

2020-present Executive Committee Member, Cohorts of Heart and Aging Genomic Epidemiology (CHARGE) Consortium
2019-2020 Host and Planning Committee, Cohorts of Heart and Aging Genomic Epidemiology (CHARGE) Consortium 2020 Meeting
2018 Co-Chair, Program Development Committee for the NHLBI Trans-Omics for Precision Medicine (TOPMed) Program 2018 Meeting
2016-2017 Standing Member, American Heart Association Institute for Precision Cardiovascular Medicine Data Science and Technology Committee
2016-present Investigator, NHLBI TOPMed Program
2016-2022 Blood Pressure Working Group Convener, NHLBI TOPMed Program
2014-present Research Steering Committee Member, Cohorts of Heart and Aging Genomic Epidemiology (CHARGE) Consortium
2009-2015 Investigator, NHLBI Exome Sequencing Project (ESP)
2008-present Investigator, Cohorts of Heart and Aging Genomic Epidemiology (CHARGE) Consortium
2006-2011 Investigator, NHLBI Candidate Gene Association Resource (CARe)
2005-2006 Member, NHLBI GENELINK Project for Collaborative Linkage Analysis
1999-2014 Investigator, NHLBI Family Blood Pressure Program (FBPP)
1996-present Investigator, Atherosclerosis Risk in Communities (ARIC) Study

Peer Review

2012-2015 Reviewer, NHLBI Exome Sequencing Project Publications Committee
2007-2013 Reviewer, Family Blood Pressure Program Ancillary Study Review Committee
2005-2016 Reviewer, ARIC Study Publications Committee

Grant Review

September 2023	Reviewer, TOPMed Fellowship Program
December 2021	Reviewer, NIH DP5 (ZRG1 PSE-H 70 Study Section)
October 2018	Ad hoc member, NIH Genetics of Health & Disease (GHD) Study Section
March 2018	Reviewer, American Heart Association, Uncovering New Patterns in Cardiovascular Disease and Stroke Grants and Fellowships
2017	Ad hoc reviewer, NIH Genetics of Health & Disease (GHD) Study Section
2014-2015	Chair, American Heart Association, Genomics & Translational Biology Epidemiology and Observational Epidemiology (GTOE) Study Section
June 2013	Co-chair, NIH Cardiovascular and Sleep Epidemiology (CASE) Study Section
2012-2016	Standing member, NIH CASE (ZRG1 PSEQ 90) Study Section newly named Cancer, Heart, and Sleep Epidemiology Panel B (CHSB)
Mar 2012-Oct 2013	Co-chair, American Heart Association, Genomics & Translational Biology Epidemiology and Observational Epidemiology (GTOE) Study Section
2010-2015	Reviewer, American Heart Association, GTOE Study Section for the April 2010, October 2010, April 2011, October 2011, March 2012, October 2012, April 2013, October 2013, March 2014, and April 2015 cycles
June 2011	Ad hoc member, NIH KNOD Study Section
2012	Reviewer, Slovenian Research Agency
2011	Reviewer, Shota Rustaveli National Science Foundation for the country of Georgia
November 2010	Reviewer, NIH GHD/GCAT Special Emphasis Panel
July 2010	Reviewer, NIH NCI Transdisciplinary Research in Energetics and Cancer Review Panel
June 2009	Reviewer, NIH NIDDK KNOD Special Emphasis Panel
March 2009	Reviewer, NIH NIDDK Special Emphasis Panel
2009	Reviewer, Italian Ministry of Science
2009	Reviewer, American Association for the Advancement of Science (AAAS)
2007	Reviewer, Austrian Science Fund
2005	Reviewer, European Science Foundation

TEACHING EXPERIENCE:

Convener, Genomics & Bioinformatics certificate program
Convener, Online MPH in Epidemiology degree program

Fall

2007-present	Course coordinator, PH 2740, Cardiovascular Disease Epidemiology and Prevention, 3 credits. This course is offered online beginning in 2014.
2010-2014	Lecturer, PH 2612, Epidemiology I, 3 credits
2007	Lecturer, PH 2998, Genetics and Infectious Diseases, 2 credits

Spring

2009-2014	Lecturer, PH 2612, Epidemiology I, 3 credits
2005-2013	Lecturer, PH 2820, Molecular and Cellular Approaches to Human Genetics, 3 credits
2006-2007	Co-instructor, PH 2710, Advanced Epidemiological Methods I, 4 credits

Summer

2004-2020	Course coordinator, PH 2780, Applied Genetic Methods in Public Health, 3 credits. This course is offered online beginning in 2019.

MENTORING EXPERIENCE:

Formal Faculty Mentor

Faculty	*Discipline*	*Current Rank*	*Mentorship Period*
Chloé Sarnowski, PhD	Epidemiology and Human Genetics	Assistant Professor, tenure track	2021-present
Zeynep Coban-Akdemir, PhD	Epidemiology and Human Genetics	Assistant Professor, tenure track	2020-present
Paul de Vries, PhD	Epidemiology and Human Genetics	Associate Professor, tenured	2016-present
Han Chen, PhD	Epidemiology and Human Genetics	Associate Professor, tenured	2016-present
Bing Yu, PhD	Epidemiology and Human Genetics	Professor, tenured	2011-2024

Current Student Advisory Roles

Student	*UTHealth School and Department*	*Degree Program*	*Advisory Role*
Amanda Crawford	SPH, EPI	MPH	Primary advisor
Manal Elhaj	SPH, EPI	MPH	Primary advisor
Anthony Xu	SPH, EPI	MPH	Primary advisor
Andy Yanez	SPH, EPI	MPH	Primary advisor
Gennel Ortiz	SPH, EPI	MPH	Primary advisor
Mollie van Boskirk	SPH, EPI	MPH	Primary advisor
Natalie Hasbani	SPH, EPI	PhD	Dissertation Commitee
Julie Hahn	SPH, EPI	PhD	Primary advisor

Past Student Advisory Roles

Student	*UTHealth School and Department*	*Degree Program*	*Advisory Role*	*Year of Graduation*
Rashida Ghadiali	SPH, EPI	MPH	Primary advisor	2024
Jane Curlee	SPH, EPI	MPH	Primary advisor	2024
Rachel Harris	SPH, EPI	PhD	Primary advisor	2024
Caitlyn Seabolt	SPH, EPI	MPH	Primary advisor	2023
Kendall Vela	SPH, EPI	MPH	Primary advisor	2023
Alison McLendon	SPH, EPI	MPH	Primary advisor	2023
Drewan Dore	SPH, EPI	MPH	Primary advisor	2023
Monica Keller	SPH, EPI	MPH	Primary advisor	2023
Sobia Maqsood	SPH, EPI	MPH	Primary advisor	2022
George Gonzales	SPH, EPI	MPH	Primary advisor	2022
Tesha Landry	SPH, EPI	MPH	Primary advisor	2022
Naomi Tamez	SPH, EPI	MPH	Primary advisor	2022
Saeed Shoar	SPH, EPI	MPH	Primary advisor	2022
Amna Mahmud	SPH, EPI	MPH	Primary advisor	2022
Kara Churovich	SPH, EPI	MPH	Primary advisor	2022
Claudia Luna-Meza	SPH, EPI	MPH	Primary advisor	2022
Jesus Duran Ramirez	SPH, EPI	MPH	Primary advisor	2022
Morgan Bily	SPH, EPI	MPH	Primary advisor	2022

Brittany Liebhard	SPH, EPI	MPH	Primary advisor	2022
Lori Boies	SPH, EPI	MPH	Primary advisor	2021
Adriene Chestang	SPH, EPI	MPH	Primary advisor	2021
Sarah Chowdhury	SPH, EPI	MPH	Primary advisor	2020
Elysia Garcia	SPH, Biostatistics	PhD	Dissertation committee	2020
Nader Zamani	SPH, EPI	MPH	Primary advisor	2019
Sofia Velazquez	SPH, EPI	MS	Primary advisor	2018
Zhe Wang	SPH, EPI	PhD	Dissertation committee	2018
Elizabeth Alore	SPH, EPI	MPH	Primary advisor	2018
Tianzhong Yang	SPH, Biostatistics	PhD	Dissertation committee	2018
Alem Belachew	GSBS, HMG**	PhD	Qualifying exam committee	2017
Michael Khayat	BCM†	PhD	Qualifying exam committee	2017
Upasana Banerjee	SPH, EPI	MPH	Primary advisor	2016
Gisele Moran	SPH, EPI	MPH	Primary advisor	2016
Yang Yang	SPH, Biostatistics	PhD	Dissertation committee	2015
Khanh Vu	SPH, EPI	PhD	Dissertation advisor	2015
Jie Yang	SPH, EPI	MS	Primary advisor	2015
Bethany Dawson	SPH, EPI	MPH	Primary advisor	2015
Unnati Shah	SPH, EPI	MPH	Primary advisor	2015
Monika Vishwakarma	SPH, EPI	MPH	Primary advisor	2014
E Lin	SPH, Biostatistics	PhD	Dissertation committee	2014
Wei Qiao	SPH, Biostatistics	PhD	Dissertation committee	2014
Taebeom Kim	SPH, Biostatistics	PhD	Dissertation committee	2014
Jorge Del-Aguila	GSBS, HMG**	PhD	Advisory, qualifying, and dissertation committee	2014
Jennifer Churchill	GSBS, HMG**	PhD	Advisory and dissertation committee	2013
Bing Yu	SPH, EPI	PhD	Dissertation committee	2013
Sepideh Nouri	GSBS, HMG**	MS	Advisory and thesis committee	2013
Surya Rednam	SPH, EPI	MS	Primary advisor	2013
Liang Chen	SPH, Biostatistics	MS	Thesis committee	2013
Abayomi Ogunwale	SPH, EPI	MPH	Primary advisor	2013
Aaya Nassar	SPH, EPI	PhD	Dissertation committee	2012
Suyu Liu	SPH, Biostatistics	PhD	Dissertation committee	2012
Ping Liu	SPH, Biostatistics	PhD	Dissertation committee	2012
Cecelia Ganduglia	SPH, MPACH††	DrPH	Dissertation committee	2012
Han Yang	SPH, Biostatistics	MS	Thesis committee	2012
Siddhartha Kar	SPH, EPI	MPH	Primary advisor	2012
Katie Jones	SPH, EPI	MPH	Primary advisor	2012
Chirag Bavishi	SPH, EPI	MPH	Primary advisor	2012
Wen-Ya Lee	SPH, Biostatistics	PhD	Dissertation committee	2011
Chung-Han Ho	SPH, Biostatistics	PhD	Dissertation committee	2011
Jiangong Niu	SPH, Biostatistics	MS	Thesis committee and research supervisor	2011
Wafa Taiym	SPH, EPI	MS	Thesis committee	2011
Myphuong Phan	SPH, EPI	MPH	Primary advisor	2011
Eva Parker	SPH, EDC*	MPH	Primary advisor	2010
Yi-Ping Fu	SPH, EDC*	PhD	Dissertation committee	2009
Catherine Spellicy	GSBS, HMG**	PhD	Dissertation committee	2009

Poonam Dhavan	SPH, EDC*	MPH	Primary advisor	2009
Ranjana Arora	SPH, EDC*	MPH	Primary advisor	2009
Tamra Meyer	SPH, EDC*	PhD	Dissertation committee	2008
Parvathy Nair	SPH, EDC*	PhD	Dissertation committee	2008
Laura Palmero	SPH, International and Family Health	MPH	Thesis supervisor	2007
Mala Pande	SPH, EDC*	PhD	Qualifying committee	2006
Christina Barroso	SPH, Health Promotion	DrPH	Dissertation committee	2005
Priya (Bhatia) Shetty	SPH, EDC*	MS	Primary advisor	2005
Amy Heck	GSBS, HMG**	MS	Thesis committee	2005

*Epidemiology and Disease Control (EDC)
**Program in Human and Molecular Genetics (HMG)
† Baylor College of Medicine (BCM)
††Management, Policy, and Community Health (MPACH)

Additional Past Advisory Roles

SPH MPH Secondary Advisor: Zizhuang Li (Graduated 2007), Satyam Nayak (Graduated 2008), Achilia Morrow (Graduated 2010), Charudatta Bavare (Graduated 2011), Hanoch Patt (Graduated 2012)

GSBS Tutorial Advisor: Selina Vattathil (Fall 2008), Alexander Li (Spring 2011), Andrea Ochoa (Fall 2011)

CPRIT Summer Undergraduate Internship Mentor: Jessica Bucio (2011), Mahmood Khan (2011), Huong Nguyen (2011), Nicholas Mahan (2012), David Wang (2012)

BUILDing Scholars Undergraduate Internship Mentor: Pablo Arenaz (2017)

PRESENTATIONS AND PUBLISHED ABSTRACTS:

Only invited presentations from the past five years are included. Not shown are numerous co-authored presentations and poster presentations.

Morrison A.C. State of CHARGE Address. Cohorts of Heart and Aging Genomic Epidemiology (CHARGE) Consortium Annual Meeting. San Antonio. October 2023

Morrison A.C. State of CHARGE Address. Cohorts of Heart and Aging Genomic Epidemiology (CHARGE) Consortium Annual Meeting. Philadelphia. April 2022

Morrison A.C. State of CHARGE Address. Cohorts of Heart and Aging Genomic Epidemiology (CHARGE) Consortium Annual Meeting. Virtual. October 2021

PEER REVIEWED PUBLICATIONS:

** represents joint lead/senior authorship*
 # represents trainee-led publications

1) **Morrison A.C.**, Brancati F., Folsom A.R., Smith L., Boerwinkle E. β3-adrenergic receptor Trp64Arg polymorphism does not predict incident CHD or carotid intima-media thickness in a community-based sample of whites: the ARIC study. Human Genetics (1999) 105(4):314-9

2) **Morrison A.C.**, Fornage M., Liao D., Boerwinkle E. Parental history of stroke predicts subclinical, but not clinical stroke. The Atherosclerosis Risk in Communities study. Stroke (2000) 31(9):2098-2102

3) Huang Q., **Morrison A.C.**, Boerwinkle E. Linkage disequilibrium structure and its impact on the localization of a candidate functional mutation. Genetic Epidemiology (2001) 21(Suppl 1):S620-S625

4) **Morrison A.C.**, Doris P.A., Folsom A.R., Nieto F.J., Boerwinkle E. G-protein β3 subunit and α-adducin polymorphisms and risk of subclinical and clinical stroke. The Atherosclerosis Risk in Communities study. Stroke (2001) 32(4):822-829

5) **Morrison A.C.**, Ballantyne C.M., Bray M.S., Chambless L.E., Sharrett A.R., Boerwinkle E. Lipoprotein lipase polymorphism predicts stroke risk in men. The Atherosclerosis Risk in Communities study. Genetic Epidemiology (2002) 22(3):233-242

6) **Morrison A.C.**, Bray M.S., Folsom A.R., Boerwinkle E. *ADD1 460W* allele associated with cardiovascular disease in hypertensive individuals. Hypertension (2002) 39(6):1053-1057

7) **Morrison A.C.**, Brown A., Kardia S.L.R., Turner S.T., Boerwinkle E. Evaluating the context-dependent effect of family history of stroke in a genome scan for hypertension. Stroke (2003) 34(5):1170-1175

8) **Morrison A.C.**, Cooper R., Hunt S., Lewis C.E., Luke A., Mosley T.H., Boerwinkle E. Genome scan for hypertension in non-obese African Americans. The National Heart, Lung and Blood Institute Family Blood Pressure Program. American Journal of Hypertension (2004) 17(9):834-838

9) **Morrison A.C.**, Boerwinkle E., Turner S.T., Ferrell R.E. Genome-wide linkage study of erythrocyte sodium-lithium countertransport. American Journal of Hypertension (2005) 18(5):653-656

10) Hoogeveen R.C., **Morrison A.**, Boerwinkle E., Miles J.S., Rhodes C.E., Sharrett A.R., Ballantyne C.M. Plasma MCP-1 level and risk for peripheral arterial disease and incident coronary heart disease: Atherosclerosis Risk in Communities study. Atherosclerosis (2005) 183(2):301-307

11) Chang Y.P., Kim J.D., Schwander K., Rao D.C., Miller M.B., Weder A.B., Cooper R.S., Schork N.J., Province M.A., **Morrison A.C.**, Kardia S.L., Quertermous T., Chakravarti A. The impact of data quality on the identification of complex disease genes: experience from the Family Blood Pressure Program. European Journal of Human Genetics (2006) 14(4):469-477

12) Greenwood T.A., Libiger O., Kardia S., Hanis C., **Morrison A.C.**, Gu C.C., Rice T., Miller M., Turner S.T., Myers R.H., Grove J., Hsiao C.F., Weder A.B., Schork N.J. Comprehensive linkage and linkage heterogeneity analysis of 4344 sibling pairs affected with hypertension from the Family Blood Pressure Program. Genetic Epidemiology (2007) 31(3):195-210

13) Grove M.L., **Morrison A.**, Folsom A.R., Boerwinkle E., Hoelscher D.M., Bray M.S. Gene-environment interaction and the *GNB3* gene in the Atherosclerosis Risk in Communities study. International Journal of Obesity (2007) 31(6):919-926

14) **Morrison A.C.**, Bare L.A., Chambless L.E., Ellis S.G., Malloy M., Kane J.P., Pankow J.S., Devlin J.J., Willerson J.T., Boerwinkle E. Prediction of coronary heart disease risk using a genetic risk score: the Atherosclerosis Risk in Communities (ARIC) study. American Journal of Epidemiology (2007) 166(1):28-35

15) Bare L.A., **Morrison A.C.**, Rowland C.M., Shiffman D., Luke M.M., Iakoubova O.A., Kane J.P., Malloy M.J., Ellis S.G., Pankow J.S., Willerson J.T., Devlin J.J., Boerwinkle E. Five common gene variants identify elevated genetic risk for coronary heart disease. Genetics in Medicine (2007) 9(10):682-689

16) **Morrison A.C.**, Boerwinkle E., Turner S.T., Ferrell R.E. Regional association-based fine-mapping for sodium-lithium countertransport on chromosome 10. American Journal of Hypertension (2008) 21(1):117-121. PMC2645713

17) Nambi V., **Morrison A.C.**, Hoogeveen R.C., Coresh J., Miles S., Rhodes C.E., Sharrett A.R., Boerwinkle E., Ballantyne C.M. Matrix metalloproteinase-1 and tissue inhibitors do not predict incident coronary artery disease in the Atherosclerosis Risk in Communities (ARIC) study. Texas Heart Institute Journal (2008) 35(4):388-394. PMC2607088

18) **Morrison A.C.**, Bare L.A., Luke M.M., Pankow J.S., Mosley T.H., Devlin J.J., Willerson J.T., Boerwinkle E. Single nucleotide polymorphisms associated with coronary heart disease predict incident ischemic stroke in the Atherosclerosis Risk in Communities (ARIC) study. Cerebrovascular Diseases (2008) 26(4):420-424. PMC2662496

19) Sherva R., Miller M.B., Pankow J.S., Hunt S.C., Boerwinkle E., Mosley T.H., Weder A.B., Curb J.D., Luke A., **Morrison A.C.**, Fornage M., Arnett D.K. A whole-genome scan for stroke or MI in Family Blood Pressure Program families. Stroke (2008) 39(4):1115-1120. PMID:18323513

20) Klos, K.L.E., Boerwinkle E., Ferrell R.E., Turner S.T., **Morrison A.C.** Estrogen receptor 1 (*ESR1*) polymorphism is associated with plasma lipid and apolipoprotein levels in Caucasians of the Rochester Family Heart Study. Journal of Lipid Research (2008) 49(8):1701-1706. PMC2637157

21) Au K.S., Tran P.X., Tsai C.C., O'Byrne M.R., Lin J-I., **Morrison A.C.**, Hampson A.W., Cirino P., Fletcher J.M., Ostermaier K.K., Tyerman G.H., Doebel S., Northrup H. Characteristics of a spina bifida population including North American Caucasian and Hispanic individuals. Birth Defects Research (Part A) (2008) 82(10):692-700. PMC2597629

22) Ehret G.B., **Morrison A.C.**, O'Connor A.A., Grove M.L., Baird L., Schwander K., Weder A., Cooper R.S., Rao D.C., Hunt S.C., Boerwinkle E., Chakravarti A. Replication of the Wellcome Trust genome-wide association study of essential hypertension: the Family Blood Pressure Program. European Journal of Human Genetics (2008) 16(12):1507-1511. PMC2585612

23) Meyer T.E.[#], Shiffman D., **Morrison A.C.**, Rowland C.M., Louie J.Z., Bare L.A., Ross D.A., Arellano A.R., Chasman D.I., Ridker P.M., Pankow J.S., Coresh J., Malloy M.J., Kane J.P., Ellis S.G., Devlin J.J., Boerwinkle E. *GOSR2* Lys67Arg is associated with hypertension in whites. American Journal of Hypertension (2009) 22(2):163-168. PMC4346180

24) Zheng X.[#], Kammerer C.M., Cox L.A., **Morrison A.**, Turner S.T., Ferrell R.E. Association of *SLC34A2* variation and sodium-lithium countertransport activity in humans and baboons. American Journal of Hypertension (2009) 22(3):288-293. PMC2652891

25) Levy D., Ehret G.B., Rice K., Verwoert G.C., Launer L.J., Dehghan A., Glazer N.L., **Morrison A.C.**, Johnson A.D., Aspelund T., Aulchenko Y., Lumley T., Köttgen A., Vasan R.S., Rivadeneira F., Eiriksdottir G., Guo X., Arking D.E., Mitchell G.F., Mattace-Raso F.U., Smith A.V., Taylor K., Scharpf R.B., Hwang S.J., Sijbrands E.J., Bis J., Harris T.B., Ganesh S.K., O'Donnell C.J., Hofman A., Rotter J.I., Coresh J., Benjamin E.J., Uitterlinden A.G., Heiss G., Fox C.S., Witteman J.C., Boerwinkle E., Wang T.J., Gudnason

V., Larson M.G., Chakravarti A., Psaty B.M., van Duijn C.M. Genome-wide association study of blood pressure and hypertension. Nature Genetics (2009) 41(6):667-687. PMC2998712

26) Martinez C.A., Northrup H., Lin J.-I., **Morrison A.C.**, Fletcher J.M., Tyerman G.H., Au K.S. Genetic association study of putative functional single nucleotide polymorphisms of genes in folate metabolism and spina bifida. American Journal of Obstetrics and Gynecology (2009) 201(4):394.e1-11. PMC2790326

27) Rodin A.S., Litvinenko A., Klos K., **Morrison A.C.**, Woodage T., Coresh J., Boerwinkle E. Use of wrapper algorithms coupled with a random forests classifier for variable selection in large-scale genomic association studies. Journal of Computational Biology (2009) 16(12):1705-1718. PMC2980837

28) Hancock D.B., Eijgelsheim M., Wilk J.B., Gharib S.A., Loehr L.R., Marciante K.D., Franceschini N., van Durme Y.M., Chen T., Barr R.G., Schabath M.B., Couper D.J., Brusselle G.G., Psaty B.M., van Duijn C.M., Rotter J.I., Uitterlinden A.G., Hofman A., Punjabi M.N., Rivadeneira F., **Morrison A.C.**, Enright P.L., North K.E., Heckbert S.R., Lumley T., Stricker B.H., O'Connor G.T., London S.J. Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. Nature Genetics (2010) 42(1):45-52. PMC2832852

29) Kingah P.L.[#], Luu H.N., Volcik K.A., **Morrison A.C.**, Nettleton J.A., Boerwinkle E. Association of *NOS3* Glu298Asp SNP with hypertension and possible effect modification of dietary fat intake in the ARIC study. Hypertension Research (2010) 33(2):165-169. PMC2828038

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Redline S., Noordam R., Wang H. A large-scale genome-wide study of gene-sleep duration interactions for blood pressure in 811,405 individuals from diverse populations. medRxiv (2024)

ACTIVE RESEARCH SUPPORT:

NIH: R01 HL139553 (Morrison/de Vries/Smith) 02/05/18-03/31/27
Analysis of Whole Genome Sequence and Hemostasis Phenotypes
In the renewal of this project, we will expand our knowledge of the genetics of coagulation factor VIII (FVIII) and its carrier protein von Willebrand factor (VWF) in multi-ethnic populations, and explore complex regulatory mechanisms influencing FVIII and VWF levels such as epistasis and epigenetics. Results from this study will lead to a better understanding of the genomic and epigenetic regulation of FVIII and VWF levels and whether they play an independent or coordinated role in the pathology of thrombotic disease, thereby informing the targeted use of existing and novel therapies.
Role: Principal Investigator

NIH/NHLBI: R01 HL141291 (Morrison/Wolberg) 02/01/19-01/31/25 (2nd NCE)
Using Genomics and Functional Biology to Understand Fibrinogen and its ffect on Thrombotic and Atherosclerotic Outcomes
Through this interdisciplinary collaboration between genetic epidemiologists and functional biologists, we will investigate fibrinogen-associated loci to characterize the genomic regulation of fibrinogen, assess epigenetic association with fibrinogen levels, and translate results of genomic studies into a clear understanding of fibrinogen's role in thrombotic and atherosclerotic disease.
Role: Principal Investigator

NIH/NHLBI: R01 HL145025 (Chen/Manning) 07/15/19-06/30/25 (NCE)
Methods and Software for Large-Scale Gene-Environment Interaction Studies
The overall objectives of this project are to develop efficient statistical methods and computational algorithms for large-scale gene-environment interaction studies, and to implement them in open-source software programs and cloud-based analysis pipelines.
Role: Co-investigator

NIH/NHLBI: R01 HL146860 (de Vries) 03/17/20-02/28/25
Whole-genome sequencing analysis of coronary atherosclerosis and related traits
This project aims to integrate whole-genome sequence information to study subclinical atherosclerosis and coronary heart disease (CHD). Aims include discovering novel associated genetic variants, studying the underlying genetic architecture, determining the genetic correlation among the phenotypes, and exploring the use of rare variants in genetic risk prediction.
Role: Co-Investigator

NIH/NHLBI: R01 HL151855 (Meigs) 07/01/20-06/30/25 (NCE)
TOPMed Omics of Cardiovascular Disease in Diabetes
We will contribute expertise in diabetes and genetics in this effort to utilize large-scale whole genome sequence variation, whole blood DNA methylation, transcription, proteomics, and metabolomics to elucidate pathways that contribute to the increased risk of cardiovascular disease in people with type 2 diabetes.
Role: Co-investigator (subcontract)

NIH/NHLBI: R01 HL154385 (Smith) 08/15/20-06/30/25 (NCE)
Structural and Nucleotide Variation as Genomic Risks for Venous Thrombosis: TOPMed and INVENT Collaboration

We will assist with use of the Analysis Commons, conduct analyses, and provide validation of structural variations using DNA from several TOPMed studies in order to better understand genomic risks for venous thrombosis.
Role: Principal Investigator (subcontract)

NIH/NIDDK: UM1 DK078616 (Manning) 01/01/21-12/31/25
TOPMed Omics of Type 2 Diabetes and Quantitative Traits
We will investigate type 2 diabetes and quantitative traits by leveraging (1) the biracial Atherosclerosis Risk in Communities Study (ARIC) phenotype, omics, and genetic data; (2) strong TOPMed analytic expertise and leadership, and (3) an ongoing track record of successful collaboration with all investigators that are a part of this competing renewal.
Role: Principal Investigator (subcontract)

NIH/NHLBI: R01 HL156991 (Rao) 04/27/21-03/31/25
A Multi-Ancestry Study of Gene-Lifestyle Interactions and Multi-Omics in Cardiometabolic Traits
The primary goal of the proposed research is to leverage existing genomic and –omic data from large multi-ethnic cohorts to discover additional genetic loci for cardiovascular traits by modeling gene-lifestyle interactions.
Role: Principal Investigator (subcontract)

NIH R01 AA028263 (Liu) 05/01/21-04/30/26
Trans-omic Analysis of Alcohol Consumption and its Relation to Cardiovascular Disease
The objective of the proposed research is to harness understanding of the molecular targets of alcohol consumption as a mean to identify preventive and therapeutic targets to correct the adverse health effects of alcohol drinking.
Role: Co-Investigator (subcontract)

NIH/Fogarty: D43 (Mandalakas) 07/12/21-03/31/26
Siyakhula: Growing HIV/TB Research Knowledge for Growing Healthy Kids in Eswatini
This training program is a part of the Fogarty HIV research training program for low-and middle-income country institutions. It represents a partnership among Eswatini, Baylor College of Medicine, and UTHealth School of Public Health investigators with the goal of strengthening operational, clinical and translational research capacity in Eswatini, while simultaneously producing high-quality researchers who will successfully transition to independence and lead national efforts to end the dual HIV/TB epidemic.
Role: Principal Investigator (subcontract)

NIH/NHLBI R01 HL150186 (Lu) 08/01/21-07/31/25
Genetic study of coronary artery disease in individuals of African ancestry
The goals of this project are to 1) identify genetic variants associated with coronary artery disease (CAD) in African Americans, 2) characterize identified CAD loci with detailed cross-trait associations and integrative genomic information, and 3) create a CAD polygenic risk score specific to individuals of African ancestry and identify possibLe P.athogenic rare variants of large effect in CAD Mendelian genes.
Role: Principal Investigator (subcontract)

NIH/NHLBI: R01 HL105756 (Psaty) 08/01/22-06/30/25
CHARGE Consortium: Omics Discovery for CVD and Aging Phenotypes
The aims of this competing renewal application are: 1) to provide coordinating-center-like administrative support; 2) to organize two major meetings per year; 3) to provide travel awards to CHARGE meetings for new investigators; 4) to provide support for fellowship exchanges; 5) to provide modest support for cohort participation.
Role: Principal Investigator (subcontract)

NIH/NHLBI: R01 HL160793 (Yu) 08/01/22-06/30/26
Genetic Architecture of Cardiac Structure and Function and its Implication in Heart Failure
The major goal of this project is to identify specific genomic variants, captured by whole genome sequencing, associated with cardiac structure and function, as well as heart failure, to provide insights into the biological pathways underlying progressive cardiac dysfunction and heart failure.
Role: Co-investigator

NIH/NHLBI R01 HL168683 (Yu) 04/01/23-03/31/27
Molecular Determinants of Atherosclerotic Cardiovascular Disease in Multi-ethnic Populations
The major goal of this project is to use multi-omics technologies to identify novel genetic determinants and metabolites associated with atherosclerosis so that more efficacious intervention strategies can be appropriately administered.
Role: Co-investigator

NIH/NHLBI R01 HL162928 (Malhotra/de Vries) 04/01/23-03/31/27
The Role of Arylsulfatase in Vascular Calcification
This proposal aims to enhance our mechanistic insights of vascular disease by focusing on a novel biological pathway, the sulfatase family, that contributes to the development of calcified arteries and plaque development in the blood vessels of humans. Status of Support: Pending
Role: Co-investigator (subcontract)

NIH R01 AG080598 (Sofer) 09/20/23-05/31/28
Using polygenic Risk Scores and Omics to Study how Suboptimal Sleep Accelerates Cognitive Aging in Diverse Populations
The goal of the proposed study is to identify sleep phenotypes that are genetically associated with cognitive aging by developing polygenic risk scores (PRS) in three population-based cohort studies that include individuals from diverse U.S. populations. Integration of metabolomics and proteomics data that are available in all three cohorts will allow the characterization of biological pathways that underlie these relationships and enable the detection of biomarkers that mediate the effect of sleep phenotypes on cognitive decline and dementia risk.
Role: Co-investigator (subcontract)

NIH R01 HL148218 (Shah/Yu) 07/01/23-06/30/27
Proteomic Signatures to Identify Pathways Underlying the Progression to Heart Failure
The major goal of this project is to define the contributions of inflammatory pathways and identify novel causal pathways for the development of cardiac dysfunction and overt heart failure in the elderly.
Role: Co-investigator (subcontract)

COMPLETED RESEARCH SUPPORT:

Celera Contract (Boerwinkle) 09/29/04-03/31/08
Service Agreement
Novel Genes Influencing Cardiovascular Disease in the Population-at-large
Identification of single nucleotide polymorphisms associated with cardiovascular disease.
Role: Co-Investigator

NIH/NHLBI: R01 HL077491 (Morrison) 04/01/05-03/31/09
Genetic Etiology of Sodium-Lithium Countertransport
This research program involves follow-up of linkage peaks from genome-wide scans for sodium-lithium countertransport (SLC) in replication samples of pedigrees. These studies involve association mapping to refine

genomic regions of interest and identification of allelic variation influencing SLC as well as the risk of developing essential hypertension in cases and controls from 3 ethnic groups.
Role: Principal Investigator

NIH/NHLBI: R37 HL051021 (Boerwinkle) 08/15/94-06/30/09
Molecular Epidemiology of Essential Hypertension
Characterize the role of specific candidate genes on inter-individual blood pressure variation using linkage and association analyses. In those genes determined to have a significant impact, use detailed association and cladistic analyses to identify candidate functional mutations. Finally, we will test the ability of those functional mutations to predict hypertension and coronary heart disease.
Role: Co-Investigator

NIH: P01 HD035946 (Fletcher) 11/01/07-01/31/10
Spina Bifida: Cognitive and Neurobiological Variability
Investigate the etiology of spina bifida through genetic studies focused on candidate genes in the metabolic pathways of folate/homocysteine and glucose metabolism. Analyses in families and case-cohort samples will investigate the role of candidate genes in causing the cognitive and structural brain features observed in spina bifida.
Role: Principal Investigator (subcontract)

NIH/NHLBI: U01 HG004729 (Fornage) 07/01/08-06/30/10
GWAS of Longitudinal Blood Pressure Profiles from Young Adulthood to Middle-Age
The proposed research represents a collaborative effort to use existing specimens, high-quality phenotypic data on cardiovascular disease risk factors, and state-of-the-art analytical methods to identify and replicate genetic effects influencing longitudinal cardiovascular disease risk factor profiles, with a special emphasis on blood pressure.
Role: Co-Investigator

NIH/NINR: R01 NR010235 (Frazier) 09/29/07-05/31/12
Interactions among Depressive Symptoms and Genetic Influences on Cardiac Outcomes
The major goals of this project are to identify a well-defined, high-risk subgroup of patients with ACS in whom genetic factors influence inflammatory protein levels, the inflammatory protein response to depression, and the risk of future MACE. This study will determine whether a subgroup of ACS patients exists in which genetic factors interact with depression, resulting in even greater increases in inflammatory protein levels than those caused by either genetic variation or depression alone.
Role: Co-Investigator

NIH/NHLBI: RC2 HL102419 (Boerwinkle) 10/01/09-09/30/12
Building on GWAS for NHLBI-diseases: the CHARGE Consortium
In the context of a large consortium (CHARGE), the proposed research will follow-up specific statistically significant GWAS regions using targeted medical resequencing and follow-up GWAS for a specific clinically significant phenotype (i.e. HDL-cholesterol) using whole genome resequencing.
Role: Co-Investigator

NIH/NHLBI: RC2 HL103010 (Rich) 10/01/09-09/30/12
University of Virginia (Boerwinkle, Consortium PI)
Human Exome Sequencing in Six Well-Phenotyped NHLBI Cohorts
This consortium includes participants from NHLBI cohorts with DNA and extensive phenotype information across the spectrum of cardiovascular, lung and blood diseases. The proposed research will yield sequence data from all exons in the human genome.
Role: Co-Investigator

NIH/NHLBI: R01 HL091988 (Hixson) 07/01/08-06/30/13
Genes of Oxidative Stress and Atherosclerotic Complications of Hypertension
Evaluate oxidative stress genes and their role in sub-clinical coronary atherosclerosis in diverse populations.
Role: Co-Investigator

NIH/NHLBI: R01HL086694 (Chakravarti) 08/05/11-05/31/14
Johns Hopkins (Fornage, Consortium PI)
A Genome Wide Association Study in Essential Hypertension (FEHGAS2)
This project comprehensively explores the contribution of rare and common genomic variation to blood pressure levels and hypertension risk in individuals of European and African American ancestry.
Role: Co-Investigator

NIH/NHLBI: R01 HL090969 (Morrison) 07/01/09-06/30/14
Role of the Solute Carrier Gene Family in Hypertension
Evaluate two kidney-expressed SLC genes for an association with blood pressure phenotypes in individuals from the ARIC study and in sibships from the GENOA study. Cellular model systems will be used in order to better understand the transport properties of the SLC genes in which they reside and how these mechanisms are affected by genetic variation in the gene.
Role: Principal Investigator

NIH/NIAAA: R03 AA021272 (Morrison) 09/15/12-08/31/15
Epidemiology of Gene-Alcohol Interactions & Lipids
This project involves a genome-wide association study (GWAS) to identify gene-alcohol interactions influencing lipid levels in the Atherosclerosis Risk in Communities (ARIC) study.
Role: Principal Investigator

NIH/NHGRI: 2U54 HG003273-09 (Gibbs) 11/01/11-10/31/15
The Human Genome Sequencing Center
The University of Texas at Houston will lead the design and analysis team, and will be involved in all aspects of the human genetics research within the Baylor College of Medicine Human Genome Sequencing Center.
Role: Co-Investigator

AHA: 17POST33350042 (de Vries) 01/01/17-8/31/17
Genomic Discovery for Improved Risk Prediction of Coronary Heart Disease
This fellowship provides the opportunity to learn methods for analysis of sequencing data, gain exposure to other types of -omics data, and obtain experience in translational research related to cardiovascular disease.
Role: Mentor

NIH/NHLBI: R01 HL120393 (Psaty/Rich) 04/01/14-03/31/18
Rare Variants and NHLBI Traits in Deeply Phenotyped Cohorts
Using the available exome chip genotype data from 9 well-phenotyped cohorts, the primary aim is to discover novel candidate genes and putative functional variants for high-priority heart, lung and blood phenotypes in multi-ethnic cohorts.
Role: Co-Investigator

NIH/NHLBI: **R21 HL126032 (Morrison/Wei)** 12/15/14-11/30/17
Genome-wide Gene-by-Smoking Interaction Analysis of Pulmonary Function
We aim to understand how smoking modifies the association between genetic factors and lung function by using state-of-the-art statistical methods and analysis strategies that leverage available data resources (e.g., rare variation in protein coding regions of the genome and longitudinal measures of lung function and smoking

history). Results from this study may disclose novel genetic susceptibilities to smoking exposure or a greater understanding of the role of smoking in the development, progression, and severity of declining lung function.
Role: Principal Investigator

UTHealth Gift Account (Northrup/Hixson) 12/01/16-11/30/18
Presidential Collaborative Award
This project aims to investigate folate deficiency in relation to neural tube defects using multi-omics approaches in human cell models.
Role: Investigator

NIH/NHLBI: R01 HL118305 (Rao) 01/15/14-12/31/18
A Multi-Ethnic Study of Gene-Lifestyle Interactions in Cardiovascular Traits
The primary goal of the proposed research is to leverage existing GWAS and exome chip data in 25 large multi-ethnic cohorts to discover additional genetic loci for cardiovascular traits by modeling gene-lifestyle interactions, using pleiotropy analysis of correlated traits, and pathway analysis. The investigation will be carried out in samples of European Americans, African Americans, Hispanic Americans, and Asians.
Role: Principal Investigator (subcontract)

NIH/NICHD: R01 HD073434 (Au) 05/01/14-04/30/19
Creating a Myelomeningocele Exome Variant Map
This project proposes to use whole exome sequencing to identify novel and de novo variants in the exomes of 500 subjects affected with myelomeningocele and evaluate to evaluate these variants for their contribution to risk of myelomeningocele development using various statistical methods.
Role: Co-Investigator

NIH/NHLBI: R01 HL122684 (Ganesh) 08/15/15-04/30/20
Genetic Studies of the Impact of Hematologic Traits on Cardiovascular Disease
This project will evaluate the extent to which red blood cell traits influence blood pressure. This study involves statistical analyses in population cohorts as well as functional experiments.
Role: Co-Investigator (subcontract)

AHA: 17SDG33661228 (Yu) 07/01/17-12/31/19
The Application of Genomics and Metabolomics on Coronary Heart Disease Risk Prediction
The objective of the proposed research is to integrate multi-omics data to better understand the role of the metabolome in relation to coronary heart disease.
Role: Co-investigator

NIH/NHLBI: R01 HL131136-02S1 (Boerwinkle) 09/05/18-11/30/20
Epigenetics of Successful Aging - Administrative Supplement
This supplement will make available and analyze TOPMed and related data in an “Analysis Commons” where harmonized phenotype, genome sequence and other-omics data from multiple studies are brought together, analyzed and interpreted to promote novel gene and variant discovery.
Role: Co-investigator

NIH/NHLBI: R01 HL139553 (Morrison/Smith) 02/05/18-01/31/21
Analysis of Whole Genome Sequence and Hemostasis Phenotypes
To expand our knowledge of the genetic factors contributing to the plasma levels of 7 hemostasis phenotypes, we aim to use whole genome sequence data and imputed genotypes to facilitate new genomic discovery for these measured traits and to determine how genetic variation influencing these traits affects susceptibility to clinical outcomes such as venous thromboembolism and cardiovascular events.
Role: Principal Investigator

NIH/NIDDK: U01 DK105554 (Florez) 05/01/17-04/30/21
TOPMed Whole Genome Sequence Analysis of Type 2 Diabetes and Related Traits
This project aims to utilize TOPMed whole genome sequence data for discovery of genomic variation influencing type 2 diabetes and related traits.
Role: Principal Investigator (subcontract)

NIH/NHLBI: R01 HL142003 (Yu) 05/01/18-04/30/21
Trans-omics Analysis to Unravel Molecular Underpinnings of Heart, Lung and Blood Disease Risk Factors
The overall goal of this application is to identify genetic variants that influence circulating metabolites (metabQTL) in multi-ethnic populations and utilize metabQTL findings to identify molecular pathways that regulate heart, lung and blood disease risk factors.
Role: Co-investigator

Harris County: Contract (Boerwinkle) 09/01/20-04/30/21
UTH/BCM COVID-19 SARS-CoV-2 Surveillance Testing Program for Harris County
We propose to plan and accomplish a SARS-CoV-2 surveillance program designed to guide policy and communication strategies, advise the need for augmented virus testing, and better understand the mechanism and venues of virus.
Role: Co-Investigator

NIH/NIDDK: U01 DK78616 (Meigs) 06/01/15-05/31/21
Rare Sequencing Variation and Diabetes Quantitative Traits
Genome-wide rare variant scans of whole genome sequence data will be used to define genetic variant architecture of type 2 diabetes and related quantitative traits.
Role: Co-investigator (subcontract)

NIH/NHLBI: R01 HL134894 (Smith) 08/19/17-07/31/21
Population Genomic Variation, Functional Biology, and the Risk of Venous Thrombosis
The goals of this project are a) to coordinate and advance new genetic discovery in the setting of 2 international consortia on hemostasis and venous thrombosis (VT), and b) to integrate population work with functional biology work.
Role: Principal Investigator (subcontract)

NIH/NHLBI: R56 HL150186 (Lu) 09/17/20- 08/31/21
Genetic Study of Coronary Artery Disease in Individuals of African Ancestry
The goals of this project are to 1) identify genetic variants associated with coronary artery disease (CAD) in African Americans, 2) characterize identified CAD loci with detailed cross-trait associations and integrative genomic information, and 3) create a CAD polygenic risk score specific to individuals of African ancestry and identify possible Pathogenic rare variants of large effect in CAD Mendelian genes.
Role: Principal Investigator (subcontract)

NIH/NHLBI: R01 HL086694 (Chakravarti) 08/03/18-01/31/22
From GWAS Loci to Blood Pressure Genes, Variants & Mechanisms (FEHGAS3)
This project uses functional genomics inspired reverse genetics strategy to identify the transcription factors (TF), cis-regulatory elements (CRE), DNA variants and blood pressure genes in target tissues. Newly developed experimental and computational tools are used to discover the functional genetic modules, at identified BP loci and genome-wide, affecting inter-individual BP variation.
Role: Principal Investigator (subcontract)

CPRIT: RP180166 (Hildebrandt/Morrison) 03/01/18-02/28/22

Molecular Mechanisms of Anthracycline Response in Cardiomyocytes and Link to Genetic Susceptibility to Cardiotoxicity in Long-term Childhood Cancer Survivors
This proposal will test the hypothesis that functional changes occur in the human cardiomyocyte following exposure to anthracyclines and that identification of the key mediators of these molecular mechanisms can provide a biological link to genetic susceptibility to cardiotoxicity in long-term childhood cancer survivors previously treated with anthracyclines.
Role: Principal Investigator (subcontract)

NIH/NHLBI: R01 HL141824 (Yu) 04/01/18-03/31/22
Metabolic Signatures Underlying Cardiac Function for Heart Failure in Multi-Ethnic Populations
The goal of this project is to use multi-omics technologies to identify novel genetic determinants and metabolic signatures associated with cardiac dysfunction and heart failure risk so that more efficacious intervention strategies can be appropriately administered. The results of this research will enable continued scientific progress toward an understanding of heart failure etiology.
Role: Co-investigator

NIH/NHLBI: R01 HL105756 (Psaty) 07/15/18-06/30/22
CHARGE Consortium: Gene Discovery for CVD and Aging Phenotypes
The aims of this competing renewal application are: 1) to provide coordinating-center-like administrative support; 2) to organize two major meetings per year; 3) to provide travel awards to CHARGE meetings for new investigators; 4) to provide support for fellowship exchanges; 5) to provide modest support for cohort participation.
Role: Principal Investigator (subcontract)

NIH: 3UL1TR003167-02S1 (Fernandez) 09/01/20-08/31/22
RADx: Understanding and Addressing COVID-19 Testing Disparities in VulnerabLe P.opulations: A Multilevel and Multi-method Approach
Building on the partnerships and resources of the Center for Clinical and Translational Science (CCTS), the goal of the study is to partner with our community and stakeholder colleagues to identify dynamic disease hotspots and testing deserts in racially diverse neighborhoods of the target regions; and, to use that information to inform the rapid adaptation and deployment of multilevel level just-in-time adaptive intervention strategies to reach vulnerabLe Populations.
Role: Co-Investigator

NIH/NIEHS: P30 ES030285 (Walker) 05/15/19-03/31/23
Gulf Coast Center for Precision Environmental Health
The Gulf Coast Center for Precision Environmental Health (GC-CPEH) is a multi-institutional Center supporting academic and research partnerships between Baylor College of Medicine (BCM), The University of Texas Health Science Center at Houston School of Public Health (UTHealth) School of Public Health, and UTMB. The GC-CEPH will be the focal point and catalyst for impactful EHS research, bi-directional communication with local communities and stakeholders, and the engine driving translation of precision environmental health research advances to improve human health.
Role: Principal Investigator (subcontract)

Harris County Contract (Otto) 10/17/22-09/30/23
Harris Cares: Embrace HOPE (Healing, Opportunity, Prosperity, Equity)
The goal of the COVID-19 surveillance/analytics core is to support science-based public health action to address COVID-19-related health disparities and advance health equity in Harris County. The surveillance core will work in collaboration with HCPH experts to advance COVID-19 analytics and strengthen infrastructure to address future outbreaks in Harris County. Procedures and metrics developed will be used to monitor disease indicators in real or near real time, allowing continuous identification of population subgroups with

disproportionate burden of COVID-19 infection, severe illness and death, as well as inequalities in vaccine distribution and access. In particular, we will develop, leverage, and expand existing methods, procedures and metrics.
Role: Co-investigator

NIH/NHLBI: R01 HL148218 (Shah/Yu) 07/15/20-06/30/23
Proteomic Signatures to Identify Pathways Underlying the Progression to Heart Failure
The goal of this application is to define the contributions of inflammatory pathways and identify novel causal pathways for the development of cardiac dysfunction and overt heart failure in the elderly.
Role: Co-Investigator (subcontract)

NIH/NCI: R01 CA233719 (Scheurer) 08/01/21-07/31/24
Molecular Epidemiology of Langerhans Cell Histiocytosis: Evaluating the Impact of SMAD6 and Genetic Ancestry on Disease Risk
The research team at The University of Texas Health Science Center at Houston will implement a genome-wide analysis pipeline and perform admixture mapping of local genetic ancestries on somatic mutational profiles of Langerhans Cell Histiocytosis patients, as well as follow-up fine-mapping of admixture mapping association signals.
Role: Co-investigator (subcontract)