Curriculum Vitae
Chiang-Ching Spencer Huang, Ph.D.

PERSONAL INFORMATION

Home Address: 4270 Peppercorn Circle
Brookfield, Wisconsin, 53005
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Milwaukee, Wisconsin, 53205
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EDUCATION

University of Michigan, Ann Arbor, MI August 2003
Ph.D. in Biostatistics
University of Iowa, Iowa City, IA June 1998
Master of Science in Statistics
National Chiao-Tung University, Hsinchu, Taiwan June 1987
Bachelor of Science in Applied Mathematics

POSITION and EXPERIENCE

Associate Professor of Biostatistics August 2013-Present
Joseph J. Zilber School of Public Health, University of Wisconsin, Milwaukee

Associate Professor
Department of Preventive Medicine, Feinberg School of Medicine, September 2012 – August 2013
Northwestern University

Director, Bioinformatics Research Collaboratory September 2012 –August 2013
Feinberg School of Medicine, Northwestern University Clinical and Translational Sciences Institute

Assistant Professor September 2003–August 2012
Department of Preventive Medicine, Feinberg School of Medicine,
Northwestern University

Director, Public Health Informatics July 2007– October 2010
Northwestern University Biomedical Informatics Center

Adjunct Associate Professor April 2017-Present
Medical College of Wisconsin

Scientific Advisory Board member, CereDx, Inc. May 2014-Present

COMMITTEE and PROFESSIONAL/SCIENTIFIC SERVICE

Biostatistics Program Lead April 2015-Present
Zilber School of Public Health, UWM
MPHCC subcommittee August 2017-Present
Zilber School of Public Health, UWM
Graduate Program Representative October 2014-June 2017
Zilber School of Public Health, UWM
Chair, PhDCC subcommittee September 2016-June 2017
Zilber School of Public Health, UWM
Executive Committee September 2013-Present
Zilber School of Public Health, UWM
Dean Search and Screen Committee October 2016-March 2107
Zilber School of Public Health, UWM
Biostatistics Visiting Assistant Professor Search and Screen Committee Dec 2016-March 2107
Zilber School of Public Health, UWM
Academic Planning Committee September 2014-May 2016
Zilber School of Public Health, UWM
Graduate Program Committee September 2013-May 2015
Zilber School of Public Health, UWM
Chair, Biostatistics Faculty Search and Screen Committee October 2013-May 2104
Zilber School of Public Health, UWM
Chair, Big Data Feasibility Working Group Committee January 2104-May 2014
Zilber School of Public Health, UWM

Genetics/Genomics Committee September 2007–May 2014
Multi-Ethnic Study of Atherosclerosis (MESA) (NIH/NHLBI)
Genetics Committee October 2008–October 2011
Longitudinal Studies of Coronary Artery Risk Development in Young Adults (CARDIA) (NIH/NHLBI)
Genomics Committee October 2007–October 2009
Hispanic Community Health Study (NIH/NHLBI)
Reviewer, NCI Program Project (P01) III Review February, 2018
Reviewer, NCI Clinical and Translational R21 and Omnibus R03 September, 2017
Reviewer, NCI SPORE Special Emphasis Panel (SEP) June, 2017
Reviewer, France AGreenSkill – Pathways for Inventive Researchers grant program May, 2017
Reviewer, Poland National Science Center PRELUDIUM grant program October, 2016
Reviewer, 2015 CTSI Pilot Award September 2014
Clinical and Translational Science Institute of Southeast Wisconsin
Reviewer, Taiwan National Health Research Institutes (NHRI) Extramural Grant Scientific Review 2013-14
Reviewer, NIH/NIGMS Special Emphasis Panel August, 2009
Grand Opportunities (GO) grant applications in response to the NIGMS topic:
"Leukocyte Gene Expression in Healthy Humans"

Scientific program committee June 2010
International Chinese Statistical Association
Scientific Conference Session Organizer
"Statistical Issues in Analyzing Emerging Genomic Data" June 2010
The 19th International Chinese Statistical Association Applied Statistics Symposium

"Coronary Artery Disease Risk Factors"
The 3rd Annual International Congress of Cardiology July 2011

Abstract Grader
American Heart Association Scientific Sessions, 2008, 2009, 2010, 2011, 2012, 2013, 2014

Journal Peer-Reviewer
Journal of the American Medical Association, Analytic Chemistry, Archives of Internal Medicine, Arthritis & Rheumatism, Bioinfomatics, BMC Medical Genomics, Cancer Informatics, Circulation, Circulation Research, Genomics, Oncotarget, Scientific Report, Trends in Biotechnology, PLoS ONE, Journal of Proteome Research, Journal of Vascular Research

AWARDS, HONORS, DISTINCTIONS

Best Poster in Population Science November 2008, Chicago
2008 American Heart Association Scientific Poster Competition: "A Genomic Signature of Atherosclerosis among Individuals with Low Framingham Risk Score: The Multi-Ethnic Study of Atherosclerosis (MESA)"

TEACHING

STAT 465: Statistical Methods for Computational Biology and Bioinformatics (Guest lecturer)
Department of Statistics, Northwestern University Fall term 2003–2005

EPI BIO 499: Statistical Consultation August–December, 2007
MS in Epidemiology and Biostatistics (MSEB) Program
Department of Preventive Medicine, Northwestern University

Summer Course: R in Bioinformatics July, 2008
National Taiwan University

MSCI 490: Independent Study in Genetic Epidemiology April–June 2009
MS in Clinical Investigation (MSCI) Program
Northwestern University Clinical and Translational Sciences (NUCATS) Institute

EPI BIO 502: Advanced Biostatistics September–December 2009
MS in Epidemiology and Biostatistics (MSEB) Program
Department of Preventive Medicine, Northwestern University

EPI BIO 428: Bioinformatics and Data Mining April–June 2011
MS in Epidemiology and Biostatistics (MSEB) Program
Department of Preventive Medicine, Northwestern University

MSCI 428: Introduction to Bioinformatics January–April 2013
MS in Clinical Investigation (MSCI) Program
Northwestern University Clinical and Translational Sciences (NUCATS) Institute

PH711: Intermediate Biostatistics January-May 2015/2016

Master of Public Health (MPH) Program, Zilber School of Public Heath
University of Wisconsin, Milwaukee

PH721: Introduction to Translational Bioinformatics January-May 2016/17
Master of Public Health (MPH) Program, Zilber School of Public Heath
University of Wisconsin, Milwaukee

PH720: Seminar in Biostatistics and Bioinformatics September-December 2016
Master of Public Health (MPH) Program, Zilber School of Public Heath
University of Wisconsin, Milwaukee

PH813: Practice of Biostatistical Consulting September-December 2017
PhD Program, Zilber School of Public Heath
University of Wisconsin, Milwaukee

Fellow, Northwestern Searle Center for Teaching Excellence August 2009–June 2010

Mentoring Experience:

Xuexia Wang, PhD Mentor, 2013 September-December 2015
Assistant professor of Biostatistics
Joseph J Zilber School of Public Health
University of Wisconsin, Milwaukee

Cheng Zheng, PhD Mentor, 2014-Present
Assistant professor of Biostatistics
Joseph J Zilber School of Public Health
University of Wisconsin, Milwaukee

Simone Treiger Sredni, MD, PhD Mentor, 2007-2103
Assistant Professor
Department of Surgery, Division of Neurosurgery
Falk Brain Tumor Center
Ann & Robert H. Lurie Children's Hospital of Chicago

Monique Hinchcliff, MD July 2008 – Aug 2013
Assistant Professor of Medicine
Division of Rheumatology, Department of Medicine
Feinberg School of Medicine, Northwestern University

Rosemary Braun, PhD
Assistant Professor Mentor, 2012-2013
Department of Preventive Medicine
Feinberg School of Medicine, Northwestern University

Yinan Zhang, MS Academic Advisor, 2012-2013
PhD student in Walter S. and Lucienne Driskill
Graduate Training Program in Life Sciences

Feinberg School of Medicine, Northwestern University

Xingwang Zhao Academic Advisor, August 2014
MPH Student in Biostatistics, Zilber School of Public Health, University of Wisconsin, Milwaukee

Joseph Chase Academic Advisor, August 2015
MPH Student in Biostatistics, Zilber School of Public Health, University of Wisconsin, Milwaukee

Hua Huang, MS Academic Advisor, August 2016
PhD student in Biostatistics, Zilber School of Public Health, University of Wisconsin

RESEARCH INTERESTS

Human genome/epigenome variations and cancers, focusing on biomarker discovery for precision medicine through large scale RNA/DNA sequencing analysis

1. Genetic susceptibility of human cancers including prostate, esophagus and lung cancers using eQTL-based gene mapping, systems biology-based network analysis and large scale case-control association study.
2. RNA/DNA biomarkers for risk stratification, early diagnosis, treatment response and outcome prediction in cancer, cardiovascular diseases, and autoimmune diseases by testing blood/tissue DNA/RNAs in well-characterized patient populations using omics data and bioinformatics approaches.

RESEARCH GRANTS/CONTRACTS

Active

1R01 CA212097-01A1 (Wang, MCW) 8/01/2017-7/31/2022
NIH/NCI
Cell Free Nucleic Acid-based Biomarkers in Advanced Prostate Cancer
This study is to identify and validate blood- based nucleic acid biomarkers for predicting treatment response and clinical outcomes in metastatic hormone-sensitive prostate cancer patients. The study will functionally characterize the potential of the key candidate miRNAs in promoting growth and resistance of prostate cancer cells to androgen deprivation therapy or chemotherapy in vitro and in vivo.
Role: Co-Investigator

Cure JM Foundation (Pachman, Northwestern) 9/1/2017-8/31/2018
The purpose of this project is to perform linkage analysis from a large clinical cohort to identify shared genetic markers between juvenile dermatomyositis (JDM) and cancers. This study will survey family history of cancer among JDM patients and use statistical genetics and sequencing approach to identify associated risk variants.
Role: Key biostatistician

1UL1TR001436 (Shaker, MCW) 8/18/2015 – 3/31/2018
NIH/NCATs via Medical College of Wisconsin
Clinical and Translational Science Award
The purpose of the CTSI of Southeast Wisconsin is to support and advance education, collaboration, and research in clinical and translational science. The CTSI is a collaboration between the Medical College of Wisconsin, University of Wisconsin-Milwaukee, Marquette University, Milwaukee School of Engineering, Blood Institute of Wisconsin, Children's Hospital and Health Systems, Froedtert Lutheran Memorial Hospital, and the VA Medical Center.

Role: Co-Investigator

Completed

1R21 EB021590-01A1 (Gosain, Northwestern) 4/01/2016 – 1/31/2018
NIH/NIBIB
Determining the Biomechanical and Biological Response of Stretched Skin
This proposal will determine the temporal evolution and regional variation over a full expanded patch of tissue, as well as the biological mechanisms that contribute to this growth. The proposal will further test the hypothesis that through tissue expansion in pigs, skin growth varies and is maximal in areas of maximum stretch, and this will be correlated with gene expression and activation of known mechanotransduction pathways.
Role: Subcontract PI

R44AR061920 (Fanger, Northwestern) 9/6/2011-6/30/2017
NIH/NIAMS
Gene expression signatures to predict treatment treatment response in systemic sclerosis
The goal of this proposal is to validate a next generation diagnostic tool, the ScleroType test, that uses nanoString based gene expression analyses of skin to subtype scleroderma patients, and to further assess its ability to predict disease course and clinical improvement during treatment. Identification of gene expression signatures that identify patients most likely to benefit from specific therapies would provide a vast improvement to patient management by reducing exposure to side effects, reducing costs and importantly, enabling identification and selection of effective therapies for appropriate patients.
Role: Bioinformatics Consultant

1R21 AR066846-01 (Pachman) 9/16/2014-8/31/2017
NIH/NIAMS
iPS-Derived Myogenic Cells from Identical Twins, Discordant for Juvenile Dermatomyositis
The major goal of this project is to derive a signle cell population of myogenic presursor cells from iPSCs from monozygotic twins discordant for JDM and their controls in order to characterize the genetic contribution of muscle to disease pathophysiology. RNA-seq wll be used to identify the geentic indicator in the iPS.
Role: Co-Investigator/Subcontract PI

(Hinchcliff) 07/01/11 – 04/30/17
Scleroderma Foundation
Measuring Gene Expression in the Skin: Novel Biomarkers for Scleroderma
The experiments in this proposal will test whether DNA microarray analyses of skin can predict response to mycophenolate mofetil (MMF). The goal is to identify a subset of genes whose expression changes during MMF treatment and uncover the dysregulated molecular pathways that may be involved in scleroderma (SSc).
Role: Co-Investigator

5R01 NR012692 (Pachman) 09/29/10 – 07/31/14
NIH/NINR
Disease Chronicity in Juvenile Dermatomyositis (JDM): Epigenetic Clues
The purpose of this study is to identify epigenetic mechanisms - differences in global methylation and miRNA expression - critical in dissecting the impact of chronic inflammation and gender on JDM microvasculopathy. In this study, the quality of life of the children with JDM will be determined and

correlated with their epigenetic status - inherited changes in phenotype determined by genes and the environment - by testing diagnostic muscle biopsies from untreated children with JDM with long compared with short disease duration and age-, gender-matched healthy controls.
Role: Co-Investigator/Subcontract PI

P60 AR048098-09 (Pope/Chang) 08/01/07 – 07/31/13
NIH/NIAMS
Multidisciplinary Clinical Research Center in Rheumatology
The goals of the Northwestern University Multidisciplinary Clinical Research Center in Rheumatology are: 1) to conduct cutting-edge, nationally recognized and funded research aimed at the prevention or control of arthritis and musculoskeletal diseases; and 2) to provide the academic environment that supports and enhances the interdisciplinary research of the MCRC faculty.
Role: Co-Investigator

N01-HC-95164 (Liu) 01/15/10 – 07/31/13
NIH/NHLBI
Multi-Ethnic Study of Atherosclerosis (MESA)
The primary objective of this project is to conduct a longitudinal study in a representative population-based sample of 6,800 White, Black, Hispanic, and Asian men and women ages 45-84 at baseline to: a) evaluate various measures of subclinical cardiovascular disease (CVD); b) examine factors associated with progression of subclinical CVD to overt disease; and c) develop population-based methods for identifying high-risk asymptomatic persons for prevention and intervention.
Role: Co-Investigator

N01-HC-48049 (Liu) 12/20/07 – 07/31/13
NIH/NHLBI
Longitudinal Studies of Coronary Artery Risk Development in Young Adults (CARDIA)
CARDIA is a 4-center national collaborative longitudinal investigation of physiological, psychological, and other factors which may influence the evolution of coronary heart disease risk factors in young black and white men and women initially ages 18-30 in 1985-1986.
Role: Co-Investigator

5 P30 CA060553-17 (Rosen) 09/14/07 - 07/31/13
NIH/NCI
The Robert H. Lurie Comprehensive Cancer Center
The goals of this Cancer Center Support Grant are to conduct and support cancer research and to integrate cancer-related research throughout the university; to coordinate and integrate cancer-related activities of the University including community outreach initiatives; to develop and conduct cancer education programs; to promote and participate in state-of-the-are care of cancer patients at the affiliated hospitals of the McGaw Medical Center of Northwestern University and; to develop and implement the initiatives in cancer prevention and control research. These goals are accomplished through the activities of the 10 establish programs and 13 shared resources.
Role: Biostatistician

U10 CA98543 (Perlman/Huang) 09/01/09 – 10/31/12
NIH/NCI
The Therapeutically Applicable Research to Generate Effective Treatments (TARGET): Analysis of High Risk Wilms' Tumor

This project was to interrogate the genomic, transcriptomic, epigenomic, and mutational characteristics of high risk Wilms' tumors treated on NWTSG/COG protocols using microarray and next generation DNA sequencing technology. The goal is to 1) identify genetic mutations involved in the pathogenesis of Wilms' tumor, and in the development of relapse and anaplasia; 2) assess genomic gains and losses in relapse favorable histology Wilms tumor (RFHWT) and unfavorable histology Wilms' tumor (UFWT); 3) define transcription patterns within RFHWT and UFWT; 4) define activated pathways in RFHWT, UFWT, and favorable histology Wilms' tumor (FHWT).
Role: Subcontract PI

RC1 ES018461-02 (Hou) 09/27/09 – 07/31/11
NIH/NIEHS
DNA Methylation Alterations in Response to Pesticide Exposures
This project was to study whether Organophosphate Pesticides (OP) exposure alters gene promoter DNA methylation patterns in human subjects, and in OP-treated cell lines.
Role: Co-Investigator

R01 HL084228 (Stamler) 02/01/07 – 01/31/11
NIH/NHLBI
Metabolomics-Measured Urinary Metabolites, Diet & BP, 17 Population Samples: INTERMAP
The goal of this project is to investigate how nutrient intake influences metabolomic patterns and to identify urinary metabolite biomarkers in relation with blood pressure using H^1 NMR metabolomic profiles of 4,670 individuals in the INTERMAP cohort.
Role: Co-Investigator

U01 CA114757 (Perlman/Huang) 06/01/05 – 05/30/10
NIH/NCI
Strategic Partnering to Evaluate Cancer Signatures (SPECS): Diagnostic and Prognostic Sarcoma Signatures
This is a multi-institutional collaborative project. The goal of this project was to confirm and refine previously identified molecular signatures of pediatric sarcomas for treatment response or diagnosis using modern high throughput genomics technologies.
Role: Subcontract PI

R01 HL086678 (Huang) 03/15/07 – 02/28/10
NIH/NHLBI
Atherosclerosis Risk Refinement: A Multi-Marker Approach Using Microarrays
The goal of this project was to use gene expression profiles of peripheral blood to identify atherosclerosis-related pathways and gene signatures that can improve risk stratification among individuals with low CVD 10-year predicted risk.
Role: PI

U01 CA088131 (Perlman/Huang) 12/01/04-11/30/06
NIH/NCI
Categorization of Wilms' Tumor by Genetic Expression
This project was to 1) identify new molecular categories of Wilms' tumor (WT) based on the gene expression profiles of samples from patients with this disease; 2) Develop a classification system (classifier) that will predict a defined number of clinically relevant categories based on expression of an established set of genes.

Role: Subcontract PI

SCHOLARLY BIBLIOGRAPHY

Peer-Reviewed Research Papers (*corresponding author, †key bioinformatician/biostatistician)

1. Chen G, Gharib TG**, Huang CC†**, Taylor JM, Misek DE, Kardia SL, Giordano TJ, Iannettoni MD, Orringer MB, Hanash SM, and Beer DG. Discordant Protein and mRNA Expression in Lung Adenocarcinomas**.** *Mol Cell Proteomic.* 2002, 1:314-22.
2. Beer DG, Kardia SL, **Huang CC†**, Levin AM, Misek DE, Lin L, Chen G, Gharib TG, Thomas DG, Giordano TJ, Lizyness ML, Kuick R, Hayasaka S, Taylor JM, Iannettoni MD, Orringer MB, Hanash S. Gene Expression Profiles Predict Survival in Lung Adenocarcinomas. *Nat Med.* 2002, 8,816-24.
3. Gharib TG, Chen G, Wang H, **Huang CC**, Prescott MS, Shedden KA, Misek DE, Thomas DG, Giordano TJ, Taylor JM, Kardia S, Yee J, Orringer MB, Hanash S, Beer DG. Proteomic Analysis of Cytokeratin Isoforms Uncovers Association with Survival in Lung Adenocarcinoma. *Neoplasia.* 2002, 4(5),440-8.
4. Moran CJ, Arenberg DA, **Huang CC†,** Giordano TG, Thomas DG, Misek DE, Chen G, Iannettoni, MD, Orringer MB, Hanash S, Beer DG. RANTES Expression Is a Predictor of Survival in Stage I Lung Adenocarcinoma. *Clin Cancer Res*. 2002, 8:3803-12.
5. Chen G, Gharib TJ, **Huang CC†**, Thomas DG, Shedden KA, Taylor JM, Kardia SL, Misek DE, Giordano TJ, Iannettoni MD, Orringer MB, Hanash SM, and Beer DG. Proteomic Analysis of Lung Adenocarcinoma: Identification of a Highly Expressed Set of Proteins in Tumors. *Clin Cancer Res.* 2002, 8: 2298-305.
6. Chen G, Wang H, Gharib TG, **Huang CC**, Thomas DG, Shedden KA, Kuick R, Taylor JM, Kardia SL, Misek DE, Giordano TJ, Iannettoni MD, Orringer MB, Hanash SM, and Beer DG. Overexpression of Oncoprotein 18 Correlates with Poor Differentiation in Lung Adenocarcinomas. *Mol Cell Proteomics*. 2003, 2(2):107-16.
7. Chen G, Gharib TG, Thomas DG, **Huang CC**, Misek DE, Kuick RD, Giordano TJ, Iannettoni MD, Orringer MB, Hanash SM, and Beer DG. Proteomic Analysis of EIF-5A in Lung Adenocarcinomas. *Proteomics*. 2003, 3(4):496-504.
8. Schwartz DR, Wu R, Kardia SL, Levin AM, **Huang CC**, Shedden KA, Kuick R, Misek DE, Hanash SM, Taylor JM, Reed H, Hendrix N, Zhai Y, Fearon ER, Cho KR. Novel Candidate Targets of ß-catenin/TCF Signaling Identified by Gene Expression Profiling of Ovarian Endometrioid Adenocarcinomas. *Cancer Res.* 2003, 63(11):2913-22.
9. Chen G, Gharib TG, Wang H, **Huang CC†**, Kuick R, Thomas DG, Shedden KA, Misek DE, Taylor JM, Giordano TJ, Kardia SL, Iannettoni MD, Yee J, Hogg PJ, Orringer MB, Hanash SM, and Beer DG. Protein Profiles Associated with Survival in Lung Adenocarcinoma. *PNAS.* 2003, 100(23):13537-42.
10. Gharib TG, Chen G, **Huang CC†**, Misek DE, Iannettoni MD, Hanash SM, Orringer MB, Beer DG. Genomic and Protemic Analyses of Vascular Endothelial Growth Factor and Insulin-Like Growth Factor-Binding Protein 3 in Lung Adenocarcinomas. *Clin Lung Cancer*. 2004, 5(5):307-12.
11. Pasche B, Knobloch TJ, Bian Y, Liu J, Phukan S, Rosman D, Kaklamani V, Baddi L, Siddiqui FS, Frankel W, Prior TW, Schuller DE, Agrawal A, Lang J, Dolan ME, Vokes EE, Lane WS, **Huang CC,** Caldes T, Cristofano AD, Hampel H, Nilsson I, Gunnar von Heijne, Fodde R, Murty VVVS, Albert de la Chapelle, Weghorst CM. Somatic Acquisition and Signaling of *TGFBR1**6A in Cancer. *JAMA.* 2005, 294:1625-33.
12. Cutcliffe C, Kersey D, **Huang CC†**, Zeng Y, Walterhouse D, Perlman EJ for the Renal Tumor Committee of the Children's Oncology Group. Clear Cell Sarcoma of the Kidney: Up-regulation of Neural Markers with Activation of the Sonic Hedgehog and Akt Pathways. *Clin Cancer Res.* 2005, 11: 7986-94.
13. **Huang CC**, Cutcliffe C, Coffin C, Sorensen P, Beckwith JB, Perlman EJ for the Renal Tumor Committee of the Children's Oncology Group. Classification of Malignant Pediatric Renal Tumors by Gene expression. *Pediatr Blood Cancer.* 2006, 46:728-38.

14. Amin SA, **Huang CC†**, Reierstad S, Lin Z, Arbieva Z, Wiley E, Saborian H, Haynes B, Cotterill H, Dowsett M, Bulun SE. Paracrine-Stimulated Gene Expression Profile Favors Estradiol Production in Breast Tumors. *Mol Cell Endocrinol.* 2006, 253(1-2):44-55.
15. **Huang CC***, Taylor JM, Beer DG, Kardia SL. Hidden Markov Model for Defining Genomic Changes in Lung Cancer Using Gene Expression Data. *OMICS. 2006*, 10(3):276-88.
16. Lin Z, Reierstad S, **Huang, CC†**, Bulun SE. Novel Estrogen Receptor-alpha Binding Sites and Estradiol Target Genes Identified by Chromatin Immunoprecipitation Cloning in Breast Cancer. *Cancer Res.* 2007, 67(10): 5017-24.
17. Wang J, Jarrett J, **Huang CC†**, Satcher RL Jr, Levenson AS. Identification of Estrogen-responsive Genes Involved in Breast Cancer Metastases to the Bone. *Clin Exp Metastasis*. 2007, 24(6):411-22.
18. Xue Q, Lin Z, Cheng YH, **Huang CC**, Yin P, Reierstad S, Marsh E, Milad MP, Confino E, Innes J, Bulun S. Promoter Methylation Regulates Estrogen Receptor 2 Expression in Endometrium. *Bio. Reprod.* 2007, 77(4):681-7.
19. Liu H, Shi B, **Huang CC†**, Eksarko P, Pope RM. Transcriptional Diversity during Monocyte to Macrophage Differentiation. *Immunol Lett*. 2008, 117(1):70-80.
20. Rosman D, Phukan S, **Huang CC†**, Pasche B. TGFBR1*6A Enhances the Migration and Invasion of MCF-7 Breast Cancer Cells through RhoA Activation. *Cancer Res.* 2008, 68(5), 1319-28.
21. Zeng Q, Phukan S, Xu Y, Sadim M, Rosman DS, Liao J, Zhang M, Yang G-Y, **Huang CC**, Valle L, Cristofano AD, Chapelle A, Pasche B. *Tgfbr1* Haploinsufficiency Enhances *Apc*-mediated Colon Cancer Development. *Cancer Res*. 2009, 69(2):678-86.
22. Brown IJ, Elliott P, Robertson CE, Chan Q, Daviglus ML, Dyer AR, **Huang CC**, Rodriguez BL, Sakata K, Ueshima H, Van Horn L, Zhao L, Stamler J, for the INTERMAP Research Group. Dietary Starch Intake of Individuals and Their Blood Pressure: the International Study of Macronutrients and Micronutrients and Blood Pressure. *J Hypertens.* 2009, 27:231-6.
23. **Huang CC**, Gadd S, Breslow N, Cutcliffe C, Sredni ST, Helenowski IB, Dome JS, Grundy PE, Green DM, Fritsch MK, Perlman EJ. Predicting Relapse in Favorable Histology Wilms Tumor Using Gene Expression Analysis: A Report from the Renal Tumor Committee of the Children's Oncology Group. *Clin Cancer Res*. 2009, 15(5):1770-8.
24. **Huang CC**, Fornage M, Lloyd-Jones DM, Wei GS, Boerwinkle E, Liu K. Longitudinal Association of PCSK9 Sequence Variations with LDL-Cholesterol Levels: The Coronary Artery Risk Development in Young Adults (CARDIA) Study. *Circ Cardiovasc Genet*. 2009, 2(4):354-361.
25. Sredni ST, Gadd S, **Huang CC†**, Breslow N, Grundy P, Green DM, Dome JS, Shamburge RC, Beckwith JB, and Perlman EJ. Subset of Very Low Risk Wilms Tumors Show Distinct Gene Expression, Histologic, and Clinical Features. *Clin Cancer Res*. 2009, 15(22): 6800-9.
26. Sredni ST, Bonaldo MD, Costa FF, **Huang CC**, Hamm CA, Rajaram V, Tomita T, Goldman S, Bischof JM, Soares MB. Brief communication - Upregulation of mir-221 and mir-222 in Atipical Teratoid/ Rhabdoid Tumors: Potental Therapeutic Targets. *Childs Nerv Syst.* 2010, 26(3):279-83.
27. Gadd S, Sredni ST, **Huang CC†**, Perlman EJ. Rhabdoid Tumor: Gene Expression Clues to Pathogenesis and Potential Therapeutic Targets. *Lab Invest.* 2010, 90(5):724-38.
28. Desai J, Flatow JM, Song J, Zhu LJ, Du P, **Huang CC**, Lu H, Lin SM, Kibbe WA. Visual Presentation as a Welcome Alternative to Textual Presentation of Gene Annotation Information. *Adv Exp Med Biol.* 2010, 680:709-15.
29. Chadeau-Hyam M, Ebbels TM, Brown IJ, Chan Q, Stamler J, **Huang CC**, Daviglus ML, Ueshima H, Zhao L, Holmes E, Nicholson JK, Elliott P, De Iorio M. Metabolic Profiling and the Metabolome-wide Association Study: Significance Level for Biomarker Identification. *J Proteome Res.* 2010, 9(9):4620-7.
30. Du P, Zhang X, **Huang CC**, Jafari N, Kibbe WA, Hou L, Lin SM. Comparison of Beta-value and M-value Methods for Quantifying Methylation Levels by Microarray Analysis. *BMC Bioinformatics*. 2010,

11:587.
31. Katz BZ, Salimi B, Gadd SL, **Huang CC†**, Kabat WJ, Kersey D, McCabe C, Heald-Sargent T, Katz ED, Yogev R. Differential Gene Expression of Soluble CD8+ T-cell Mediated Suppression of HIV Replication in Three Older Children. *J Med Virol.* 2011, 83(1):24-32.
32. Brown IJ, Stamler J, Van Horn L, Robertson CE, Chan Q, Dyer AR, **Huang CC**, Rodriguez BL, Zhao L, Daviglus ML, Ueshima H, Elliott P; for the International Study of Macro/Micronutrients and Blood Pressure Research Group. Sugar-Sweetened Beverage, Sugar Intake of Individuals, and Their Blood Pressure: International Study of Macro/Micronutrients and Blood Pressure. *Hypertension*. 2011, 57(4):695-701.
33. Sredni ST, **Huang CC†**, Bonaldo MD, Tomita T. MicroRNA Expression Profiling for Molecular Classification of Pediatric Brain Tumors. *Pediatr Blood Cancer.* 2011, 57(1):183-4.
34. **Huang CC***, Liu K, Pope RM, Du P, Lin S, Rajamannan NM, Huang Q, Jafari N, Burke GL, Post W, Watson KE, Johnson C, Daviglus, M, Lloyd-Jones DM. Activated Toll-like Receptor Signaling in Atherosclerosis Among Women with Lower Framingham Risk Score: the Multi-Ethnic Study of Atherosclerosis. *PLoS ONE*. 2011, 6(6):e21067.
35. **Huang CC***, Lloyd-Jones DM, Guo X, Rajamannan NM, Lin S, Du P, Huang Q, Hou L, Liu K. Gene Expression Variation Between African Americans and Whites Is Associated with Coronary Artery Calcification: the Multi-Ethnic Study of Atherosclerosis. *Physiol Genomics.* 2011, 43(13): 836-43.
36. Sredni ST, Gadd S, Jafari N, **Huang CC*.** A Parallel Comparison of mRNA and microRNA Profiling of Peripheral Blood in Young Adult Women. *Frontiers in Genetics*. 2:49. doi: 10.3389/fgene.2011. 00049, July 2011.
37. Kuo CH, Wang KC, Tian TF, Tsai MH, Chiung YM, Hsiech CM, Tsai SJ, Wang SY, Tsai DM, **Huang CC**, Tseng YJ. Metabolomic Characterization of Laborers Exposed to Welding Fumes. *Chem Res Toxicol.* 2012, 25(3): 276-86.
38. Gadd S, Beezhold P, Jennings L, George D, Leuer K, **Huang CC**, Huff V, Tognon C, Sorensen PH, Triche T, Coffin CM, Perlman EJ. Mediators of Receptor Tyrosine Kinase activation in infantile fibrosarcoma: a Children's Oncology Group study. *J Pathol.* 2012, 228(1): 119-30. Feb 28.
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65. Du M, Giridhar KV, Tian Y, Tschannen MR, Zhu J, **Huang CC**, Kilari D, Kohli M, Wang L. Plasma exosomal miRNAs-based prognosis in metastatic kidney cancer. *Oncotarget.* 2017 Jul 22;8(38):63703-63714

Under review

1. **Huang CC**, Lin YC, Du M, Huang H, Hillman D, Wang L, Sicotte H, Wang L, Wang L, Kohli M. Comparative analysis of metastatic tumor tissue and matched plasma cell free DNA copy number alterations in castration-resistant prostate cancer (CRPC).
2. Pachman LM, Curran ML, Morgan GA, Targoff IN, Huang H, Xu D, **Huang CC**. 101 Juvenile Myositis Patients: Disease Activity and Damage over 60 months.

Editorials

Huang CC, Bredel M. Use of Gene Signatures to Improve Risk Estimation in Human Cancer. *JAMA.* 2008, 299(13), 1605-7.

Book Chapters

Jennings L and **Huang CC**. "Expression Profiling in Pediatric Acute Leukemias". *Diagnostic Pediatric Hematopathology*, 2011, Cambridge.

Huang CC and Gadd S. "Gene Expression". *Cardiovascular Genetics and Genomics in Clinical Practice*, 2014, demosMEDICAL, New York.

PRESENTATIONS

Invited Presentations

1. "Omics: the Future for Personalized Medicine". *Utah ASA Chapter, Provo, UT, Feb. 2004.*
2. "Markov Model for Defining Genomic Changes in Cancer Using Microarray Data". *ENAR Statistical Meetings, Pittsburg, PA, March 2004.*
3. "Prognosis of Non-small Cell Lung Cancer Using Gene Expression Profiles". *Northwestern Bioinformatics Mini Symposium, Evanston, IL, July 2004.*
4. "Nutri-Metabolomics and Epidemiology – Personalized Nutrition". *Northwestern University, Chicago, IL, June 2006.*
5. "Robustness of cancer prognostic markers using gene expression microarrays". *Joint Statistical Meetings 2007, Salt Lake City, UT, July 2007.*
6. "Functional Genomics and Personalized Medicine". *Fuzhou Medical University, Fuzhou, China, Sept 2007.*
7. "Identification of Robust Genomic Signatures via Multiple Cross Validation". *Emerging Information and Technology Bioinformatics and Biomedical Research Symposium 2008, Princeton, NJ, June 2008.*
8. "Association of Aspartame and Aspartic Acid Intake with Body Mass Index: the INTREMAP Study". *Joint Conference - 49th Cardiovascular Disease Epidemiology and Prevention -and- Nutrition, Physical Activity and metabolism, Tampa, FL, March 2009.*
9. "Longitudinal Association of PCSK9 Sequence Variations with LDL-Cholesterol Levels: The Coronary Artery Risk Development in Young Adults (CARDIA) Study". *PCSK9 Conference, Nantes, France, March 2010.*
10. "Methylation Detection Call for Whole Genome Methylation Data". *ICSA 2010 Applied Statistics Symposium. Indianapolis, IN, June 2010.*
11. "Gene Expression Variation Between African Americans and Whites Is Associated with Coronary Artery Calcification: the Multi-Ethnic Study of Atherosclerosis." *Joint Conference – 51st Cardiovascular Disease Epidemiology and Prevention -and- Nutrition, Physical Activity and Metabolism, Atlanta, GA, March 2011.*
12. "Application of Bioinformatics to Human Diseases – Roadmap to Discovery." *Beigene Inc., Philadelphia, PA, September 2011.*
13. "Activated TLR Signaling in Atherosclerosis Among Women with Lower Framingham Risk Score." *BIT's 3rd Annual International Congress of Cardiology, Beijing, China, December 2011.*
14. "Meta analysis of transcriptomic profiling in vascular diseases reveals systemic immune dysregulation." *Department of Biostatistics & Medical Informatics, University of Wisconsin, Madison, November 2012*
15. "Prognostic and Diagnostic Values of Blood Transcriptomic and Metabolmic Profiling in Cardiovascular Diseases." *Aurora Research Institute, Aurora Sinai Medical Center, Milwaukee, July 2013*
16. "Meta analysis of immune transcriptomic networks reveals concordant immune dysregulation in vascular diseases". *Division of Biostatistics, Medical College of Wisconsin, Milwaukee, March 2015*.
17. "Utility of high throughput technologies in biomarker discovery for precision medicine". *The 4th International Symposium on Biopharmaceutical Statistics, Beijing, China, July 2015*.
18. "Genomic variations in plasma cell free DNA differentiate early stage lung cancers from normal control". *8th World Cancer Congress 2015, Busan, Korea, Dec 2015.*
19. "Plasma genetic and genomic abnormalities predict treatment response and clinical outcome in advanced prostate cancer". *9th World Cancer Congress 2016*, *Shanghai, China, May 2016*
20. "RNAseq detection of gene dysfunction in PBMCs from juvenile dermatomyositis, positive for P155/140 myositis specific antibody". *ACR/ARHP Annual Meeting, San Diego, Nov 2017*.

21. "Statistical Analysis of for comparison of genomic abnormalities between plasma cell free DNA and tumor tissue DNA". *Department of Preventive Medicine, Northwestern University. Feb 2018*.

Poster Presentations

1. Sturek JM, Hedrick CC, Mauldin JP, **Huang CC**, Carr J, Swords-Jenny N, Goodarzi MO, Taylor K, Rotter JI, Adar SD, Kao WHL, Post WR, Danniel KR, Rick SS. ABCG1 SNPs, Diabetes, and Variation in Lipid Levels in the Multi-Ethnic Study of Atherosclerosis (MESA). *Joint Conference - 48th Cardiovascular Disease Epidemiology and Prevention -and- Nutrition, Physical Activity and Metabolism, Colorado Springs, CO, March 2008.*
2. Brown IJ, Elliott P, Chan Q, Daviglus ML,Dyer AR, **Huang CC**, Robertson CE, Rodriguez BL, Sakata K, Ueshima H, Van Horn L, Stamler J. Dietary Carbohydrate Intake of Individuals (Total, Starch, Total Sugar) and Their Blood Pressure: INTERMAP Study. *Joint Conference - 48th Cardiovascular Disease Epidemiology and Prevention -and- Nutrition, Physical Activity and metabolism, Colorado Springs, CO, March 2008.*
3. Gadd SL, **Huang CC**, Perlman EJ. Defining Subsets of Favorable Histology Wilms Tumor Using Global Gene Expression Analysis. *6th International Conference on the Biology of Childhood Renal Tumors, Chamonix-Mont Blanc, March 2008.*
4. Sredni ST, Gadd SL, **Huang CC**, Perlman EJ. Rhabdoid Tumors: Gene Expression Patterns ProvideClues to the Cell of Origin, Pathogenesis, and Potential Therapeutic Targets. *Thirteenth International Symposium on Pediatric Neuro-Oncology. Chicago, IL, July 2008.*
5. Sredni ST, Costa FF, **Huang CC**, Bonaldo MDF, Bischof J, Tomita T, Goldman S, Rajaram V, Soares MB. Study of Expression Pattern from 365 MicroRNAs in Atypical Theratoid-rhabdoid Tumors. A Comparison With Medulloblastomas. *40th Meeting of the International Society of Pediatric Oncology. Berlin, Germany, Oct 2008.*
6. **Huang CC,** Liu K, Rajamannan N, Du P, Lin S, Burke G, Shea S, Szklo M, Watson K, Johnson C, Lloyd-Jones DM. A Genomic Signature of Atherosclerosis among Individuals with Low Framingham Risk Score: The Multi-Ethnic Study of Atherosclerosis (MESA). *AHA Scientific Sessions 2008, New Orleans, LA, Nov 2008.*
7. **Huang CC**, Fornage M, Lloyd-Jones DM, Wei GS, Boerwinkle E, Liu K. Association of PCSK9 Gene Variants with Longitudinal LDL-Cholesterol Levels: The Coronary Artery Risk Development in Young Adults (CARDIA) Study**.** *AHA Scientific Sessions 2008, New Orleans, LA, Nov 2008.*
8. Hinchcliff M, **Huang CC**, Sadim M, Raval D, Varga J, Pasche B. Genetic Variants in the Transforming Growth Factor-b (TGF-b) Signaling Axis in Patients with Scleroderma. *NIH Career Development in Women's Health, Building Interdisciplinary Research Careers in Women's Health, Bethesda, MD, November 2008.*
9. Gadd SL, **Huang CC**, Perlman EJ. Clear Cell Sarcoma of the Kidney: Diagnostic and Prognostic Markers. *Annual SPECS Meeting, Nashville, December 2008*.
10. Gadd SL, **Huang CC**, Perlman EJ. Potential Diagnostic Utility of MicroRNA Analysis for Nonrhabdomyosarcomatous Soft Tissue Sarcomas (NRSTS). *Annual SPECS Meeting, Nashville, TN, December 2008.*
11. Tseng YJ, **Huang CC**, Kuo C, Wang S, Tsai M, Chiung Y. Metabolomic Profiling on Labours Exposed to Welding Fume, *Proceedings of the 22nd International Symposium on Microscale bioseparations and methods for systems biology, Berlin, German, March, 2008.*
12. Sredni ST, Costa FF, Hamm C, **Huang CC**, Bonaldo MDF, Bischof J, Tomita T, Goldman S, Rajarma V, Soares MB. Regulation of the Cell-cycle Inhibitor P27Kip1 by Mir-221 and Mir-222 in Pediatric Brain Tumors. *Society for Pediatric Pathology Spring Meeting, Boston, MA, March 2009.*

13. Statkute L, Carns M, **Huang CC**, Hinchcliff ME, Varga J. Autoantibody Profiles in Systemic Sclerosis More Predictive of Clinical Outcomes than Disease Subset Classification. *American College of Rheumatology Annual Scientific Meeting*, 2009.
14. **Huang CC**, McDermott M, Kuo CH, Liu K, Tseng J. Serum Metabolomic Profiles Reveal Distinct Glucose Metabolism, And Protein Breakdown Patterns Between PAD Patients Immediately Prior To Death And Those Without Acute Events. *Joint Conference - 50th Cardiovascular Disease Epidemiology and Prevention -and- Nutrition, Physical Activity and metabolism, San Francisco, CA, March 2010.*
15. Gadd SL, **Huang CC**, Kersey D, Beezhold P, Lu Y, Huff V, Perlman EJ. Comprehensive Genomic Analysis of Diffuse Hyperblastic Periloblar Nephroblastomatosis. *AACR Meeting Orlando, FL April 2011*.
16. Sredni ST, Hendrickson P, Morgan G, Shrestha S, **Huang CC**, Chen YW, Pachman LM. Pathophysiology of Untreated Juvenile Dermatomyositis Muscle: Hypoxia and Apoptosis are Regulated by MicroRNAs. *Clinical Immunology Society Annual Meeting, Chicago, IL, May 2011.*
17. **Huang CC**, Sredni ST, Gadd SL, Jafari N. A Parallel Study of mRNA and MicroRNA Profiling of Peripheral Blood in Young Adult Women. *12th International Congress of Human Genetics/ASHG 61st Annual Meeting, Montreal, Canada, October 2011.*
18. Hinchcliff M, Pennison MJ, Zimmerman JW, Bellam N, Zeng Q, **Huang CC**, Pope R, Sadim M, Wolf W, Edberg J, Kimberly R, Zhang K, Li KJ, Yi N, Mayes MD, Varga J, Pasche B. *A Hypomorphic TGFBR1 Variant is Associated with Risk for Systemic Sclerosis in Humans. American College of Rheumatology Annual Scientific Meeting, Chicago, IL, Nov 2011.*
19. Korman B, Skamra C, Wu P, Sandhu A, Huang QQ, **Huang CC**, Pope RM, Ramsey-Goldman R. Gene Expression Profiles in Monocytes and Macrophages from SLE Patients and Healthy Controls with and without an Atherosclerosis Phenotype. *American College of Rheumatology Annual Scientific Meeting, Chicago, IL, Nov 2011.*
20. Sredni ST, Hendrickson P, Kim E, Morgan G, Shrestha S, Chen Y-W, **Huang CC**, Pachman LM. MicroRNAs MiR-15b and MiR-206 are Key Factors in the Regulation of Impaired Angiogenesis in Muscle of Children with Untreated Juvenile Dermatomyositis**.** *American College of Rheumatology Annual Scientific Meeting, Chicago, IL, Nov 2011.*
21. **Huang CC**, Seiberg R, Zhang, Y, Feng G. Activation of TLR signaling in atherosclerosis and ischemic stroke. *ASHG 62nd Annual Meeting, San Francisco, CA, November 2012.*
22. Pachman LM, Linter KE, Wu YL, Ferguson LJ, Morgan GA, **Huang CC**, Yu CY. Decreased C4A gene copy numbers in children with Juvenile Dermatomyositis: association with decreased C4 protein and lower absolute number of CD 3 negative CD16/56+ Natural Killer cells. *American College of Rheumatology Annual Scientific Meeting, Washington DC, Nov 2012.*
23. Pachman LM, Ferguson LJ, Morgan GA, Benuck I, **Huang CC**. Increased Fasting lipids in children with Juvenile Dermatomyositis: associations with positive family history of hyperlipidemia, and clinical findings. *American College of Rheumatology Annual Scientific Meeting, Washington DC, Nov 2012.*
24. **Huang CC**, Chantler P, VanGilder R, Barr T Systemic Transcriptional Alterations of Innate-adaptive Immune Signaling Pathways in Atherosclerosis, Ischemia Stroke, And Myocardial Infarction. *Arteriosclerosis, Thrombosis and Vascular Biology. Scientific Sessions, Toronto, CA, May 2014*
25. **Huang CC**, Wang L, Du M, Lin YC, Huang H, Wang L, Wang L, Kohli M. Comparison of genomic abnormalities between plasma cell free DNA and metastatic tissue DNA in metastatic castrate resistant prostate cancer (mCRPC). *American Association for Cancer Research Annual Meeting, Washington DC. April 2017*