CURRICULUM VITAE **Ronglai Shen, Ph.D.**

A. GENERAL INFORMATION

Name: **Ronglai Shen, Ph.D.**

Office Address:
Department of Epidemiology and Biostatistics
Memorial Sloan-Kettering Cancer Center
485 Lexington Ave, 2rd Floor
New York, NY 10017
Telephone: (646) 888-8243
Fax: (646) 735-0010
E-mail: shenr@mskcc.org

B. EDUCATIONAL BACKGROUND:

B.S.	Biochemistry	Fudan University	1995-1999
M.S.	Biology	University of Michigan	1999-2002
M.S.	Biostatistics	University of Michigan	2002-2004
Ph.D.	Biostatistics	University of Michigan	2004-2007

C. PROFESSIONAL POSITIONS AND EMPLOYMENT:

Academics Positions		**Dates Held**
Graduate Student Research Assistant	University of Michigan	1999-2002
Graduate Student Research Assistant	University of Michigan	2002–2007
Assistant Member (Level I)	Memorial Sloan Kettering Cancer Center	2007-2010
Assistant Member	Memorial Sloan Kettering Cancer Center	2010-2016
Associate Member	Memorial Sloan Kettering Cancer Center	2016-Present

Hospital Positions		**Dates Held**
Assistant Attending Biostatistician	Memorial Hospital	2007-2016
Associate Attending Biostatistician	Memorial Hospital	2016-Present

D. LICENSURE, BOARD CERTIFICATION, MALPRACTICE

Not applicable

E. PROFESSIONAL MEMBERSHIP

Member (2002-Present)	American Statistical Association
Member (2004-Present)	International Biometric Society
Member (2010-Present)	International Chinese Statistical Association

F. HONORS AND AWARDS:

- People's Fellowship, Fudan University, Shanghai, China, 1995.
- Genetics Study Fellowship, University of Michigan, May 2000 - August 2000.
- Rackham Travel Grant, University of Michigan, December 2004 and January 2006.
- International Biometric Society (ENAR) Distinguished Student Paper Award, 2005 Spring Meeting.
- Rackham Predoctoral Fellowship, University of Michigan, 2006-2007
- Byar Young Investigator Award, Biometrics Section, American Statistical Association, 2008
- Boyer young investigator award for distinguished achievement in clinical research, Memorial Sloan-Kettering Cancer Center, 2014

G. INSTITUTIONAL /HOSPITAL AFFILIATION

Primary Hospital Affiliation:	Memorial Hospital for Cancer and Allied Diseases, NY
Other Hospital Affiliations:	None
Other Institutional Affiliations:	None

H. EMPLOYMENT STATUS

Memorial Sloan-Kettering Cancer Center	Full-time

I. CURRENT AND PAST INSTITUTIONAL RESPONSIBILITIES AND PERCENT EFFORT

Activity	**Current Percent Effort**	**Involve WMC or researches?**	**Involve MSK trainees or researchers?**
Teaching/Mentoring	5%	**N**	**Y**
Clinical Care	N/A	**N/A**	**N/A**
Administration	5%	**N**	**Y**
Research	90%	**N**	**Y**
Total	**100%**		

J. RESEARCH SUPPORT:

ACTIVE

R21-CA195365 (PI: Shen) 6/10/2015-5/31/2017
NCI
Defining a novel subtype of luminal-TP53 mutant breast cancer with poor prognosis
This proposal will characterize a novel luminal-TP53 subtype that is genetically similar to triple-negative breast cancer, shows critical pathway activity associated with endocrine therapy resistance, and displays poor prognosis.
Role: principal investigator

GC226463 (PI: Shen) 7/31/2015 - 7/31/2017
Movember
Integrative Genomics of Prostate Cancer Progression
This project will collect primary and metastatic prostate tumor pairs by leveraging the existing Stand Up 2 Cancer / Prostate Cancer Foundation funded clinical trial resources and to perform whole-exome sequencing, targeted RNA sequencing along with comprehensive pathological reviews to identify molecular predictors of progression to metastatic disease.
Role: subcontract PI

U24 CA143840-05 (PI: Sander) 9/28/2009 - 7/31/2016
NIH/NCI
MSKCC Center for Translational Cancer Genomic Analysis
A Genome Data Analysis Center type B (GDAC-B) aims to develop novel integrative analysis methods for studying cancer genomic data, thereby enabling the translation of genomic insights into new clinical applications.
Role: co-investigator

P01 CA129243 (PI: Kris/Shen) 9/12/2012 - 8/31/2017
NIH/NCI
Targets for Therapy for Carcinomas of the Lung
This grant addresses the most critical roadblocks to improving the care and curability of persons with these illnesses: (1) understanding how cancers spread (metastasis) and (2) the lack of highly effective medicines to prevent spread or to eradicate cancers that have spread from the lung.
Role: Biostatistics and Bioinformatics core director

LC130190 (PI: Rudin) 8/1/2014 - 7/31/2016
Congressionally Directed Medical Research Programs
Genetic and Epigenetic Determinants of Lung Cancer Subtype: Adenocarcinoma to Small Cell Conversion
Our primary objectives are to use comprehensive genomic and epigenomic profiling of these closely related tumor pairs (1) to define key factors determining histologic subtype, and (2) to define biological pathways contributing to this exceptionally interesting mechanism of acquired resistance.
Role: co-investigator

U54 OD020355-01 (PI: Lowe/ Taylor) 8/1/2015 - 6/30/2020
OD
MSKCC Pilot Center for Precision Disease Modeling (Core-002 (101) The Bioinformatics Core)
MSKCC Pilot Center for Precision Disease modeling will coordinate & enhance the Institution's genomic, computational, and animal modeling efforts to facilitate the development of biologically accurate models of human disease. These models will then be used to study disease pathogenesis and to develop novel therapies for a variety of human diseases.
Role: co-investigator

Grant #291325 (PI: Grisham) 2/1/2014 - 1/31/2017
Ovarian Cancer Research Fund
Determining the molecular drivers of low-grade serous ovarian cancer
Role: co-investigator

P30 CA008748 (PI: Thompson/ Begg) 1/1/2014 - 12/31/2018
NCI
Cancer Center Support Grant (Biostatistics)
The CCSG funds support MSKCC's research infrastructure. These shared resources facilitate the research activities of the clinical, translational and laboratory programs at the Cancer Center.

Completed Research Support

Starr Award (PI: Shen) 8/1/09 – 7/31/12
Starr Cancer Consortium
An Integrative Paradigm for the Discovery of Novel Tumor Subtypes and Associated Cancer Genes
The major goal of the project is to implement integrative data analysis approaches for the identification of novel tumor subtypes and associated cancer genes in hepatocarcinomas and to functionally validate the findings using large-scale RNAi and cDNA screening platforms through collaboration with investigators at the Cold Spring Harbor Laboratory.
Role: principal investigator

GC218833 (PI: Paik) 8/1/2010 - 7/31/2013
Geoffrey Beene Cancer Research Center
Characterization of the Molecular Heterogeneity of EGFR Mutant Lung Adenocarcinoma: Baseline and Post-Treatment Tumor Analysis
Role: co-investigator

GC219084 (PI: Paik)
Geoffrey Beene Cancer Research Center 8/1/2011 - 7/31/2013

Squamous Cell Carcinoma of the Lung Mutation Analysis Program (SQ-MAP)
Role: co-investigator

P01 CA129243 (PI Kris) 7/23/07 – 6/30/12
NIH/NCI
New Targets for Therapy for Adenocarcinoma of the Lung
The major goals of the program projects are to link mutations in tumors to improve outcomes in patients.
Role: Biostatistics and bioinformatics core co-leader

US ARMY (W81XWH-10-1-0222) (PI Levine) 4/1/10 – 3/30/12
DOD/OCRP
Toward Personalized Ovarian Cancer Therapy through The Cancer Genome Atlas
The project objective is to identify proteins and corresponding signaling pathways that (1) correlate with the genomic alterations in ovarian carcinoma as determined by TCGA and (2) can be used as biomarkers for clinical outcome and/or chemotherapy response.
Role: Co-investigator

P01 CA047179 (PI Singer) 7/1/06 – 06/30/11
NIH/NCI
Soft Tissue Sarcoma Program Project
This program project investigates the biology, pathogenesis, progression and natural history of soft tissue sarcoma and then uses this knowledge to identify novel therapeutic targets that can be tested clinically.
Role: Co-Investigator

U24 CA126543 (PI: Ladanyi) 9/28/06 – 8/31/10
NIH/NCI
The TCGA Cancer Genome Characterization Center at MSKCC
The TCGA will provide comprehensive profiling of gene expression and of genomic gains and losses and will perform high level bioinformatic analyses to identify candidate genes for resequencing by the TCGA Genome Sequencing Centers and novel candidate intergenic rearrangements.

UL1 RR024996 (PI Imperato-McGinley; Core PI Bajorin) 9/17/07–5/31/09
NIH/NCRR
Clinical and Translational Science Center (UL1)
Pilot Study of Biomarkers in Bladder Cancer
The purpose of this study is to evaluate whether RNA signatures from circulating mononuclear cells correlate with chemotherapy response in bladder cancer patients.

K. EXTRAMURAL PROFESSIONAL RESPONSIBILITIES

- Associate Editor, *BMC Bioinformatics,* 2010-Present

- Invited session organizer, Joint Statistical Meetings 2010, Vancouver, Canada, Session title: New Frontiers in Integrative Genomic Analysis

- Invited session organizer, Joint Statistical Meetings 2011, Miami Beach, FL, Session title: Statistical Challenges Arising from Next-Generation Sequencing Data

- Dissertation committee (outside member) 2011, Yi Su, Applied Mathematics and Statistics, State University of New York Stony Brook

- Invited Session organizer, Joint Statistical Meetings 2012, San Diego, CA, Session title: The Cancer Genome Atlas (TCGA): A Growing Data Resource

- Organizing Committee, Banff International Research Station Workshop 2013 (Banff, Canada): Statistical Data Integration Challenges in Computational Biology: Regulatory Networks and Personalized Medicine

- Doctoral dissertation co-advisor 2013-present, Esther Drill, Biostatistics, Columbia University

- Co-chair, the Statistical and Applied Mathematical Sciences Institute data integration working group (September 2014-present)

- Co-organizer, the Statistical and Applied Mathematical Sciences Institute workshop 2015: Bioinformatics: Statistical and Computational Challenges in Omics Data Integration

- Program committee, Eastern North American Region (ENAR) of the International Biometric 2015 Spring meeting, Miami, Florida

- Eastern North American Region (ENAR) of the International Biometric Society Regional Advisory Board 2015-2017

Posters/Presentations

- “Prognostic Meta-signature of Breast Cancer Developed by Two-stage Mixture Modeling of Microarray data”, Cancer Center Symposium, Poster Session, 2004, University of Michigan, Ann Arbor, Michigan.

- “A two-stage Mixture Model for Meta-Analysis of Microarray Data”, Distinguished Student Paper Winner, ENAR Spring Meeting, 2005, Austin, Texas

- “Eigengene based Linear Discriminant Model for Gene Expression Data Analysis.”, Contributed paper, ENAR Spring Meeting, 2006, Tampa, Florida

- “Analysis of Tissue Microarray Data using Measurement Error Models”, Contributed paper, ENAR Spring Meeting, 2007, Atlanta, Georgia
- “Reconstructing Tumor-wise Protein Expression in Tissue Microarray Studies using a Bayesian Cell Mixture Model”, Contributed paper, JSM meeting, 2008, Denver, Colorado
- “Integrative Clustering of Multiple Genomic Data Types for the Discovery of Novel Tumor Subtypes”, Contributed paper, Joint Statistical Meeting, 2009, Washington DC
- “Integrative Clustering of Multiple Genomic Data Types for the Discovery of Novel Tumor Subtypes”, Lightning session presentation, TCGA Steering Committee Meeting, 2009, Bethesda, Maryland
- “An Integrative Paradigm for the Discovery of Novel Tumor Subtypes and Associated Cancer Genes”, Invited poster presentation for Starr grant awardees, Starr Cancer Consortium Retreat, 2009, Cold Spring Harbor, New York, NY
- “An Integrative Paradigm for the Discovery of Novel Tumor Subtypes and Associated Cancer Genes”, Invited Platform Presentation, Starr Cancer Consortium, 2010, Cold Spring Harbor, New York, NY
- “Integrative Clustering of Multiple Omic Data Types”, Invited Talk, Joint Statistical Meetings, 2010, Vancouver, Canada
- “Sparse Integrative Clustering of Multiple Omic Data Sets with Application to Glioblastoma Subtype Analysis”, Invited Talk, 2010, University of California at San Francisco, San Francisco, CA
- “Sparse Integrative Clustering of Multiple Omic Data Sets”, Invited Talk, 2010, University of Wisconsin, Madison, Wisconsin
- “Sparse Integrative Clustering of Multiple Omic Data Sets”, Invited Talk, 2010, Institute for Computational Biomedicine, Weil Cornell Medical College, New York, NY
- “Sparse Integrative Clustering of Multiple Omic Data Sets”, Invited Talk, 2011, University of Medicine & Dentistry of New Jersey
- “An Integrative Genomics Paradigm for the Discovery of Novel Tumor Subtypes and Associated Cancer Genes”, Invited Talk, 2011, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, New York, NY
- “Pattern Discovery and Cancer Gene Identication in Integrated Cancer Genomic Data” , Invited Talk, 2012, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Boston, MA

- “The Cancer Genome Atlas (TCGA): A Growing Data Resource”, Invited Talk, 2012, Joint Statistical Meetings, San Diego, CA

- “Pattern Discovery and Cancer Gene Identification in Integrated Cancer Genomic Data”, Invited Talk, 2013, Banff International Research Station Workshop “Statistical Data Integration Challenges in Computational Biology: Regulatory Networks and Personalized Medicine.” Banff, Canada.

- “Pattern Discovery and Cancer Gene Identification in Integrated Cancer Genomic Data”, Invited Seminar, 2013, Columbia University Statistical Genetics Seminar.

- “Pattern Discovery and Cancer Gene Identification in Integrated Cancer Genomic Data”, Invited Talk, 2014, Society for Industrial and Applied Mathematics (SIAM) annual meeting.

- “The Cancer Genome Atlas (TCGA): A Growing Data Resource and Open Challenges”, Invited Talk, 2014, the Statistical and Applied Mathematical Sciences Institute (SAMSI) workshop on Beyond Bioinformatics: Statistical and Mathematical Challenges (Bioinformatics), Research Triangle Part, NC

- “Statistical Models to Discover Principles of Biological Systems”, Invited Discussant, 2014, Joint Statistical Meetings, Boston, MA

- “A Latent Variable Approach for Integrative Clustering of Multiple Genomic Data Types”, Invited Talk, 2015, Eastern North American Region (ENAR) of the International Biometric Society (IBS) meeting, Miami, FL

- “Intratumor Genetic Heterogeneity Analysis and its Implications in Personalized Medicine”, Invited Talk, 2015, International Chinese Statistical Association (ICSA) Applied Statistics Symposium, Fort Collins, CO

- “Multiplatform Analysis of Molecular Heterogeneity in Cancer”, Invited Speaker, 2015, iBRIGHT: Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine, Houston, TX

- “Multiplatform Analysis of Molecular Heterogeneity in Cancer”, Invited Speaker 2015, Institute for computational biomedicine, Weill Cornell Medical College, New york, NY

- “Multiplatform Analysis of Molecular Heterogeneity in Cancer”, Invited Speaker 2015, University of North Carolina, Chapel Hill, NC

L. BIBLIOGRAPHY

1. Dash A, Maine IP, Varambally S, **Shen R**, Chinnaiyan AM, Rubin MA. Changes in differential gene expression because of warm ischemia time of radical prostatectomy specimens. *American Journal of Pathology* 2002; 161:1743-1748. PMCID: PMC1850797.
2. Zhou M, Shah R, **Shen R**, Rubin MA. Basal cell cocktail (34betaE12 + p63) improves the detection of prostate basal cells. *American Journal of Clinical Pathology* 2003; 27(3):365-71.
3. Kleer CG, Cao Q, Varambally S, **Shen R**, Ota I, Tomlins SA, Ghosh D, Sewalt RG, Otte AP, Hayes DF, Sabel MS, Livant D, Weiss SJ, Rubin MA, Chinnaiyan AM. EZH2 is a marker of aggressive breast cancer and promotes neoplastic transformation of breast epithelial cells. *Proceedings of the National Academy of Sciences* 2003; 100:11606-11611. PMCID: PMC208805.
4. Hofer MD, Fecko A, **Shen R**, Setlur SR, Pienta KG, Tomlins SA, Chinnaiyan AM, Rubin MA. Expression of the platelet-derived growth factor receptor in prostate cancer and treatment implications with tyrosine kinase inhibitors. *Neoplasia* 2004; 6(5):503-12.
5. Shah RB, Kunju LP, **Shen R**, LeBlanc M, Zhou M, Rubin MA. Usefulness of basal cell cocktail (34betaE12 + p63) in the diagnosis of atypical prostate glandular proliferations. *American Journal of Clinical Pathology* 2004;122(4):517-23.
6. **Shen R**, Ghosh D, Chinnaiyan A. Prognostic meta-signature of breast cancer developed by two-stage mixture modeling of microarray data. *BMC Genomics* 2004; 5:94. PMCID: PMC544889.
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EGFR can overcome a major drug resistance mutation in EGFR-mutant lung cancer. *Journal of Clinical Investigation* 2009; 119(10):3000-10.

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