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

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A. GENERAL INFORMATION

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

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B. EDUCATIONAL BACKGROUND:

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

C. PROFESSIONAL POSITIONS AND EMPLOYMENT:

Academics Positions

Assistant Member, Memorial Sloan Kettering Cancer Center 2007-Present

Graduate Student Research Assistant, University of Michigan 2002–2007

Graduate Student Research Assistant, University of Michigan1999-2002

Hospital Positions

Assistant Attending Biostatistician, Memorial Hospital for Cancer and Allied Diseases 2007-Present

D. LICENSURE, BOARD CERTIFICATION, MALPRACTICE

E. PROFESSIONAL MEMBERSHIP

Member	American Statistical Association
Member	International Biometric Society

Member	International Society for Computational Biology

F. HONORS AND AWARDS:

Byar Young Investigator Travel Award, Biometrics Section, American Statistical Association, 2008
Rackham Predoctoral Fellowship, University of Michigan, 2006-2007
International Biometric Society (ENAR) Distinguished Student Paper Award, 2005 Spring Meeting.
Rackham Travel Grant, University of Michigan, December 2004 and January 2006.
Genetics Study Fellowship, University of Michigan, May 2000 - August 2000.
People's Fellowship, Fudan University, Shanghai, China, 1995.

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

J. RESEARCH SUPPORT:

ACTIVE

Starr Award I3-A137 (PI: Shen) 40% effort 8/1/09 – 7/31/11
Starr Cancer Consortium $200,000
An Integrative Paradigm for the Discovery of Novel Tumor Subtypes and Associated Cancer Genes
The major goals of the project: 1) Development of an integrative paradigm for tumor subtype discovery that allows simultaneous statistical inference from multiple "omic" data sets. 2) Implementation of the integrative methods and software development. 3) Functional validation of key cancer genes that characterize newly identified tumor subtypes.

U24 CA143840 (PIs: Sander and Ladanyi) 20% effort 9/28/09 – 7/31/14
NIH/NCI $760,456
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.

PO1 CA129243 (PI: Kris) 15% effort 7/23/07 – 6/30/12
NIH/NCI $1,014,527

New Targets for Therapy for Adenocarcinoma of the Lung
The major goals of the program projects are to link mutations in tumors to improved outcomes in patients.

U24 CA126543 (PI: Ladanyi) 15% effort 9/28/06 – 8/31/10
NIH/NCI $745,955
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.

P01 CA047179 (PI: Singer) 10% effort 7/17/06 – 6/30/11
NIH/NCI $972,626
Soft Tissue Sarcoma Program Project (Project 4)
The goal of the project is to integrate synovial sarcoma data from Affymetrix expression profiling data with RNA interference (RNAi), chromatin immunoprecipitation (ChrIP), bioinformatics, and re-sequencing to gain insights into pathogenesis and to identify new methods for prognostication and targeted therapy.

K. EXTRAMURAL PROFESSIONAL RESPONSIBILITIES

Posters/Presentations

- “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
- “Integrative Clustering of Multiple Genomic Data Types for the Discovery of Novel Tumor Subtypes”, Lighting session presentation, TCGA Steering Committee Meeting, 2009, Bethesda, Maryland
- “Integrative Clustering of Multiple Genomic Data Types for the Discovery of Novel Tumor Subtypes”, Contributed paper, Joint Statistical Meeting, 2009, Washington DC
- “Reconstructing Tumor-wise Protein Expression in Tissue Microarray Studies using a Bayesian Cell Mixture Model”, Contributed paper, JSM meeting, 2008, Denver, Colorado
- “Analysis of Tissue Microarray Data using Measurement Error Models”, Contributed paper, ENAR Spring Meeting, 2007, Atlanta, Georgia
- “Eigengene based Linear Discriminant Model for Gene Expression Data Analysis.”, Contributed paper, ENAR Spring Meeting, 2006, Tampa, Florida
- “A two-stage Mixture Model for Meta-Analysis of Microarray Data”, Distinguished Student Paper Winner, ENAR Spring Meeting, 2005, Austin, Texas
- “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.

L. BIBLIOGRAPHY

Original Peer-Reviewed Articles

1. **Shen R**, Olshen AB, Ladanyi M. Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis. Bioinformatics. 2009 Sep 16. [Epub ahead of print]
2. Regales L, Gong Y, **Shen R**, Stanchina E, Vivanco I, Goel A, Koutcher JA, Spassova M, Ouerfelli O, Mellinghoff IK, Zakowski MF, Politi KA, Pao W. Novel dual targeting of EGFR can overcome a major drug resistance mutation in EGFR-mutant lung cancer. Journal of Clinical Investigation. 2009 Oct;119(10):3000-10. doi: 10.1172/JCI38746. Epub 2009 Sep 14.
3. Gong Y, Yao E, **Shen R**, Goel A, Arcila M, Teruya-Feldstein J, Zakowski MF, Frankel S, Peifer M, Thomas RK, Ladanyi M, Pao W. Expression levels of total IGF-1R and sensitivity of NSCLC cells in vitro to an anti-IGF-1R antibody (R1507). PLos ONE. 2009 Oct 6;4(10):e7273.
4. Varambally S, Laxman B, Mehra R, Cao Q, Dhanasekaran SM, Tomlins SA, Granger J, Vellaichamy A, Sreekumar A, Yu J, Gu W, **Shen R**, Ghosh D, Wright LM, Kladney RD, Kuefer R, Rubin MA, Fimmel CJ, Chinnaiyan AM. Golgi protein GOLM1 is a tissue and urine biomarker of prostate cancer. Neoplasia. 2008 Nov;10(11):1285-94. PMCID: PMC2570605
5. **Shen R**, Taylor JM, Ghosh D. Reconstructing tumor-wise protein expression in tissue microarray studies using a Bayesian cell mixture model. Bioinformatics. 2008 Dec 15; 24(24):2880-6.
6. **Shen R**, Chinnaiyan AM, Ghosh D. Pathway analysis reveals functional convergence of gene expression profiles in breast cancer. BMC Medical Genomics. 2008 Jun 27;1:28. PMCID: PMC2447843
7. **Shen R**, Ghosh D, Taylor JM. Modeling intra-tumor protein expression heterogeneity in tissue microarray experiments. Statistics in Medicine. 2008 May 20;27(11):1944-59. PMCID: PMC2753194
8. Yu J, Cao Q, Mehra R, Laxman B, Yu J, Tomlins SA, Creighton CJ, Dhanasekaran SM, **Shen R**, Chen G, Morris DS, Marquez VE, Shah RB, Ghosh D, Varambally S, Chinnaiyan AM. Integrative genomics analysis reveals silencing of beta-adrenergic signaling by polycomb in prostate cancer. Cancer Cell. 2007 Nov;12(5):419-31.
9. Choi H, **Shen R**, Chinnaiyan Am, Ghosh D. A latent variable approach for meta-analysis of gene expression data from multiple microarray experiements. BMC Bioinformatics 2007: 8: 364. PMCID: PMC2246152
10. Mehra R, Han B, Tomlins SA, Wang L, Menon A, Wasco MJ, **Shen R**, Montie JE, Chinnaiyan AM, Shah RB. Heterogeneity of TMPRSS2 gene rearrangements in multifocal prostate adenocarcinoma: molecular evidence for an independent group of diseases. Cancer Research 2007; 67: 7991-7995.
11. Mehra R, Tomlins SA, **Shen R**, Nadeem O, Wang L, Wei JT, Pienta KJ, Ghosh D, Rubin MA, Chinnaiyan AM, Shah RB. Comprehensive assessment of TMPRSS2 and ETS family gene aberrations in clinically localized prostate cancer. Modern Pathology 2007; 20: 538-544.

12. **Shen R**, Ghosh D, Chinnaiyan AM, Meng Z. Eigengene based linear discriminant model for gene expression data analysis. Bioinformatics 2006; 22: 2635-2642. software download: elda.zip.
13. Fu Z, Kitagawa Y, **Shen R**, Shah R, Mehra R, Rhodes D, Keller PJ, Mizokami A, Dunn R, Chinnaiyan AM, Yao Z, Keller ET. Metastasis suppressor gene raf kinase inhibitor protein (RKIP) is a novel prognostic marker in prostate cancer. Prostate 2006; 66:248-256.
14. Kim R, Demichelis F, Tang J, Riva A, **Shen R**, Gibbs DF, Mahavishno V, Chinnaiyan AM, Rubin MA. Internet-based profiler system as integrative framework to support translational research. BMC Bioinformatics 2005;6:304. PMCID: PMC1343596
15. Mehra R, Varambally S, Ding L, **Shen R**, Sabel MS, Ghosh D, Chinnaiyan AM, Kleer CG. Identification of GATA3 as a breast cancer prognostic marker by global gene expression meta-analysis. Cancer Research 2005;65:11259-11264.
16. Wang X, Yu J, Sreekumar A, Varambally S, **Shen R**, Giacherio D, Mehra R, Montie JE, Pienta KJ, Sanda MG, Kantoff PW, Rubin MA, Wei JT, Ghosh D, Chinnaiyan AM. Autoantibody signatures in prostate cancer. New England Journal of Medicine 2005;353:1224-1235.
17. Rubin MA, Bismar TA, Andrén O, Mucci L, Kim R, **Shen R**, Ghosh D, Wei JT, Chinnaiyan AM, Adami HO, Kantoff PW, Johansson JE. Decreased alpha-methylacyl CoA racemase expression in localized prostate cancer is associated with an increased rate of biochemical recurrence and cancer-specific death. Cancer Epidemiol Biomarkers Prev. 2005 Jun;14(6):1424-32.
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19. Kwak SH, **Shen R**, Schiefelbein J. Positional signaling mediated by a receptor-like kinase in Arabidopsis. Science. 2005 Feb 18;307(5712):1111-3. Epub 2004 Dec 23.
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aggressive breast cancer and promotes neoplastic transformation of breast epithelial cells. Proceedings of the National Academy of Sciences 2003;100:11606-11611. PMCID: PMC208805

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27. 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