BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2.

NAME Rahmatpanah, Farah	POSITION TITLE Post-doctoral Scholar
eRA Commons user name FRAHMATPANAH	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
University of Missouri, Columbia	M.S.	May 1997	Biochemistry
University of Missouri, Columbia	Ph.D.	May 2008	Area of Pathobiology
University of California, Irvine	Post doc	2008	Breast and Prostate Cancer

A. Personal Statement

I am a postdoctoral fellow at the University of California at Irvine. During my post-doctoral training, I was the lead investigator responsible for the experimental design, analysis and preparation of two completed projects relating to ERBB2 breast cancer; 1) ChIP-Chip analysis of mechanism of action of HER2 in breast cancer (manuscript in progress) 2) Identification of the new targets of HER2 signaling in breast cancer.

Additionally, I have participated in a project conducted by other members of our laboratory in an attempt to identify new diagnostic and prognostic biomarkers of prostate cancer. This study identified a set of diagnostic genes that are differentially expressed in stroma near a prostate tumor when compared to normal prostate stroma. For my efforts during my fellowship, I have been rewarded with the following: 1) Obtained a two year postdoctoral fellowship (3/2009-3/2011) NCI training grant 2) Received a competitive award from the NIH Loan Repayment Program 3) Chao Family Comprehensive Cancer Center, UC Irvine Seed Grant, April 2012.

B. Research and Professional Experience

2008-present: Post-doctoral scholar, University of California, Irvine (UCI)
2003-2008: Sr. research specialist, University of Missouri, Columbia
2000-2003: Research specialist, University of Missouri, Columbia
1997-1998: Analytical Chemist, ConAgra, Columbia, Missouri
1992-1997: Research Assistant, University of Missouri, Columbia

C. Selected Peer Reviewed Publications

1. Yan PS, Chen C-M, Shi H, ***Rahmatpanah F,*** Wei SH, Caldwell CW. Huang TH-M. Dissecting complex epigenetic alterations in breast cancer using CpG island microarrays. *Cancer Research* 2001: 61:8375-8380. PMID: 11731411.
2. Shi H, Yan PS, Chen C-M, ***Rahmatpanah F***, Lofton- Day C, Caldwell CW, Huang TH-M. Expressed CpG island sequence tag microarray for dual screening of DNA hypermethylation and gene silencing in cancer cells. *Cancer Research* 2002; 62:3214-3220. PMID: 12036936.
3. Yan PS, Shi H***, Rahmatpanah F***, Hsiau TH, Hsiau AH, Leu YW, Liu JC, Huang TH. Differential distribution of DNA Methylation within RASSF1A CpG island in breast cancer. *Cancer Research* 2003 Oct 1; 63(19): 6178-86. PMID: 14559801.
4. Shi H, Wei SH, Leu YW, ***Rahmatpanah F***, Liu JC, Yan PS, Nephew KP, Huang TH-M. An integrated microarray system for analyzing Gene Expression, DNA Methylation and histone acetylation. *Cancer Research*. 2003; May 1; 63 99):2164-71. PMID: 12727835
5. Leu YW, ***Rahmatpanah F***, Shi H, Wei SH, Liu JC, Yan PS, Huang TH. Double RNA interference of DNMT3b and DNMT1 enhances DNA demethylation and gene reactivation. *Cancer Research* 2003; Oct1; 63 (19):6110-5. PMID: 14559786.
6. ***Rahmatpanah FB,*** Carstens S, Guo J, Sjahputera O, Taylor KH, Duff D, Shi H, Davis JW, Hooshmand SI, Chitma- Matsiga R, Caldwell CW. Differential DNA Methylation patterns of small B cell Lymphoma subclasses with differential clinical behavior. *Leukemia.* 2006 Oct; 20(10): 1855-62. doi: 10.2217/epi.09.10.PMID: 16900213. ***Editorial Comments in Leukemia. 2006 Oct; 20(10):1658-60.***
7. Taylor KH, ***Rahmatpanah F*****, Davis J W, Caldwell CW. Chromosomal location of DNA methylation in small B- cell lymphoma. Leukemia. 2008 Mar; 22 (3): 638-41 (** Equal contributions). PMID: 17728784.
8. ***Farahnaz B. Rahmatpanah,*** Stephenie Carstens, Elise C. Welsh, Ozy Sjahputera, Kristen H. Taylor, Huidong Shi, Wade J. Davis, Sam H. Hooshmand, Gerald Arthur, Tait Shanafelt, Neil Kay, James E. Wooldridge and Charles W. Caldwell. Large –scale analysis of DNA Methylation in chronic lymphocytic leukemia, *Epigenomics* (2009) I (1), 39-61. PMID: 20495622.
9. Lynda B. Bennett, Kristen H Taylor, Gerald A Arthur, ***Farahnaz Rahmatpanah***, Sam I Hooshmand, Charles W. Caldwell. Epigenetic regulation of WNT signaling in chronic lymphocytic leukemia. *Epigenomics,* Feb 2010, Vol.2, No1, 53-70. PMID: 20473358.
10. Jia, Z.[1], Wang, Y.[1], Sawyers, A., Yao, H., ***Rahmatpanah, F.***, Xia, X., Xu, Q., Pio, R., Turan, T., Koziol, J., Goodison, S., Carpenter, P., Wang-Rodriquez, J., Simoneau, A., Meyskens, F., Sutton, M., Lernhardt, W., Beach, T., Monforte, J., McClelland, M., Mercola, D. (2011) Diagnosis of Prostate Cancer Using Differentially Expressed Genes in Stroma. *Cancer Researc**h***, 71:2476-2487. AACR Press Release. doi: 10.1158/0008-5472.CAN-10-2585.PMID: 21459804.
11. Jia, Z., **Rahmatpanah, F**., Chen, X., Lernhardt, W., Wang, Y., Xia, X., Sawyers, A., Sutton, M., McClelland, M.*, Mercola, D.* (2012) Expression changes in the stroma of prostate cancer predict subsequent relapse. ***PLoS ONE***, 7(8): e41371. PMID: 22984381.

12. Chen, X., Xu, S., McClelland, M., **Rahmatpanah, F**., Sawyers, A., Jia, Z.*, Mercola, D*. (2012) An Accurate Prostate Cancer Prognosticator Using a Seven-Gene Signature Plus Gleason Score and Taking Cell Type Heterogeneity into Account. PLoS One. 2012;7(9):e45178. doi: 10.1371/journal.pone.0045178. Epub 2012 Sep 28. PMID: 23028830
13. **Rahmatpanah F**, Jia Z, Chen X, Jones FE, McClelland M, Dan Mercola. (2012) Expression of HER2 in Breast Cancer Promotes a Massive Reorganization of Gene Activity and Suggests a Role for Epigenetic Regulation. J Data Mining Genomics Proteomics 3:e102. doi:10.4172/2153-0602.1000e102.
14. Matthew A. Kinseth, Zhenyu Jia, **Farahnaz Rahmatpanah**, Anne Sawyers, Manuel Sutton, Jessica Wang-Rodriguez, Dan Mercola* and Kathleen L. McGuire*(2013) Expression between African American and Caucasian Prostate Cancer Tissue Reveals that Stroma is the Site of Aggressive Changes. International Journal of Cancer (in press).
15. Lee C, Zhang Q, Zi X, Dash A, Soares MB, ***Rahmatpanah F***, Jia Z, McClelland M, Mercola D. TGF-βmediated DNA methylation in prostate cancer. Transl Androl Urol 2012;1(2):78-88. DOI: 10.3978/j.issn.2223-4683

D. Research Support

Ongoing

UO1 CA152738-01 (Mercola/Lee – PI) 7/1/10 – 6/30/15
NIH/NCI Early Detection Research Network (EDRN) , NCI - $4.5 million
Role: Post doctoral scholar
"Evaluation of Predictive Signatures of Prostate Cancer"
A multi-disciplinary, multi-institutional consortium assembled to develop a predictive signature of prostate cancer and to validate the signature in a prospective trial.
"**The Prostate Cancer Tumor Microenvironment Exhibits Differentially Expressed Genes Useful for Diagnosis**"
The goal of this project is to develop a tissue resource and apply the tissue resource to a prospective clinical trial of the UCI SPECS Diagnostic Classifier for the diagnosis of prostate cancer using patient fresh frozen biopsy material for suspected prostate cancer cases where the initial biopsy used in the prospective study is ambiguous and a second biopsy is scheduled. The study will be evaluated by comparison of the prediction made for the first biopsy to the clinical results observed for the second biopsy. Early detection will be evaluated by comparison of the time of the first biopsy to the average time of second biopsies, usually 3 – 12 months. The functional role of the genes of the Diagnostic Classifier will be investigated by testing the hypothesis that paracrine factors of the tumor alter gene expression of tumor-adjacent but not distant stroma via the wnt and TGFberta1 regulated pathways.

DOD CDMRP PC120465 (Mercola- PI) 04/01/13- 03/30/16
Validation of Biomarkers of the Tumor Microenvironment
Role: Post doctoral scholar
This is a translation project the migrate previous identified RNA biomarkers for the diagnosis of prostate cancer using stroma tissue to a PCR-based assay using the stroma clinical biopsies in order to make a clinical applicable test for the diagnosis of prostate cancer for ambiguous cases.