

**BIOGRAPHICAL SKETCH**

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NAME Samir M. Hanash, M.D., Ph.D.	POSITION TITLE Full Member
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EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)

INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
American University, Beirut, Lebanon	M.D.	1972	Medicine
University of Michigan, Ann Arbor, MI	Ph.D.	1976	Human Genetics

**A. Professional Experience**

7/73 - 6/76 Doctoral Candidate and post-doctoral fellow in Human Genetics, University of Michigan  
7/76 - 6/78 Residency in Pediatrics (levels 1 & 2), Children's Hospital of Michigan  
7/78 - 6/79 Instructor in Pediatric Hematology, University of Michigan  
7/79 - 8/84 Assistant Professor of Pediatrics, Dept. of Pediatric Hematology, University of Michigan  
8/84 - 8/89 Associate Professor of Pediatrics, University of Michigan  
1989-1990 Sabbatical Year-Max Planck Institute, Munich, W. Germany; California Institute of Technology  
9/89 - pres. Professor of Pediatrics, University of Michigan  
2004-pres. Full Member, Public Health Sciences Division, Program Head, Molecular Diagnostics  
Fred Hutchinson Cancer Research Center, Seattle, WA

**B. Selected publication (from a total of 273)**

- Hanash SM, Pitteri SJ, Faca VM. Mining the plasma proteome for cancer biomarkers. *Nature*. 2008 Apr 3;452(7187):571-9.
- Pitteri SJ, Faca VM, Kelly-Spratt KS, Kasarda AE, Wang H, Zhang Q, Newcomb L, Krasnoselsky A, Paczesny S, Choi G, Fitzgibbon M, McIntosh MW, Kemp CJ, Hanash SM. Plasma Proteome Profiling of a Mouse Model of Breast Cancer Identifies a Set of Up-Regulated Proteins in Common with Human Breast Cancer Cells *J Proteome Res*. 2008 Apr;7(4):1481-9.
- Pereira-Faca S, Kuick R, Puravs E, Zhang Q, Krasnoselsky A, Phanstiel D, Qiu J, Misek DE, Hinderer R, Tammemagi M, Pfeiffer R, Landi M, Caporaso N, Edelstein C, Goodman G, Barnett M, Thornquist M, Brenner DE, Hanash SM. Identification of 14-3-3 theta as an antigen that induces a humoral response in lung cancer. *Cancer Research* 2007 Dec 15;67(24):12000-6.
- Madoz-Gurpide J et al. Integral protein microarrays for the identification of lung cancer antigens in sera that induce a humoral immune response. *Molecular Cellular Proteomics* 2008 Feb;7(2):268-81.
- Pitteri S, Hanash S, Proteomic approaches for cancer biomarker discovery in plasma. *Expert Review Proteomics*. 2007 Oct;4(5):589-90.
- Faca V, Pitteri S, Newcomb L, Glukhova V, Phanstiel D, Krasnoselsky A, Zhang Q, Struthers J, Wang H, Eng J, Fitzgibbon M, McIntosh M, Hanash S. Contribution of protein fractionation to depth of analysis of the serum and plasma proteomes. *Journal of Proteome Research* 2007, 6, (9), 3558-65.
- Kuick R, Misek DE, Monsma DJ, Webb CP, Wang H, Peterson KJ, Pisano M, Omenn GS, Hanash SM. Discovery of cancer biomarkers through the use of mouse models. *Cancer Lett*. 2007 Apr 28;249(1):40-8.
- Wu R, Hendrix-Lucas N, Kuick R, Zhai Y, Schwartz DR, Akyol A, Hanash S, Misek DE, Katabuchi H, Williams BO, Fearon ER, Cho KR. Mouse model of human ovarian endometrioid adenocarcinoma based on somatic defects in the Wnt/beta-catenin and PI3K/Pten signaling pathways. *Cancer Cell*. 2007 Apr;11(4):321-33.
- Seliger B, Fedorushchenko A, Brenner W, Ackermann A, Atkins D, Hanash S, Lichtenfels R. Ubiquitin COOH-terminal hydrolase 1: a biomarker of renal cell carcinoma associated with enhanced tumor cell proliferation and migration. *Clin Cancer Res*. 2007 Jan 1;13(1):27-37.

10. Davis MA, Hanash S. High-throughput genomic technology in research and clinical management of breast cancer. Plasma-based proteomics in early detection and therapy. *Breast Cancer Res.* 2006 Dec 18;8(6):217.
11. M Mannova P, Fang R, Wang H, Deng B, McIntosh MW, Hanash SM, Beretta L. Modification of host lipid raft proteome upon hepatitis C virus replication. *Mol Cell Proteomics.* 2006 Dec; 5(12):2319-25.
12. Song K, Hanash S. Unraveling the complex proteome for biomarker discovery in gastrointestinal and liver diseases. *Gastroenterology.* 2006 Nov;131(5):1375-8.
13. Faca V, Coram M, Phanstiel D, Glukhova V, Zhang Q, Fitzgibbon M, McIntosh M, Hanash S,. Quantitative Analysis of Acrylamide Labeled Serum Proteins by LC-MS/MS *J Proteome Res.* 2006 Aug;5(8): 2009-18.
14. Gupta A, Williams BR, Hanash SM, Rawwas J. Cellular Retinoic Acid-Binding Protein II Is a Direct Transcriptional Target of MycN in Neuroblastoma. *Cancer Res.* 2006 Aug 15;66(16):8100-8.
15. Giordano TJ, Au AY, Kuick R, Thomas DG, Rhodes DR, Wilhelm KG Jr, Vinco M, Misek DE, Sanders D, Zhu Z, Ciampi R, Hanash S, Chinnaiyan A, Clifton-Bligh RJ, Robinson BG, Nikiforov YE, Koenig RJ. Delineation, functional validation, and bioinformatic evaluation of gene expression in thyroid follicular carcinomas with the PAX8-PPARG translocation. *Clin Cancer Res.* 2006 Apr 1;12(7 Pt 1):1983-93.
16. Murdoch S, Djuric U, Mazhar B, Seoud M, Khan R, Kuick R, Bagga R, Kircheisen R, Ao A, Ratti B, Hanash S, Rouleau GA, Slim R. Mutations in NALP7 cause recurrent hydatidiform moles and reproductive wastage in humans. *Nat Genet.* 2006 Mar;38(3):300-2.
17. States DJ, Omenn GS, Blackwell TW, Fermin D, Eng J, Speicher DW, Hanash SM. Challenges in deriving high-confidence protein identifications from data gathered by a HUPO plasma proteome collaborative study. *Nat Biotechnol.* 2006 Mar;24(3):333-8.
18. Rauch A, Bellew M, Eng J, Fitzgibbon M, Holzman T, Hussey P, Igra M, Maclean B, Lin CW, Detter A, Fang R, Faca V, Gafken P, Zhang H, Whitaker J, States D, Hanash S, Paulovich A, McIntosh MW., Computational Proteomics Analysis System (CPAS): an extensible, open-source analytic system for evaluating and publishing proteomic data and high throughput biological experiments. *J Proteome Res.* 2006 Jan;5(1):112-21.
19. Gao, WM, Kuick R, Orchekowski RP, Misek DE, Qiu J, Greenberg AK, Rom WN, Brenner DE, Omenn GS, Haab BB, Hanash SM. Distinctive serum protein profiles involving abundant proteins in lung cancer patients based upon antibody microarray analysis. *BMC Cancer.* 2005 Aug 23;5:110.
20. Omenn, G. S., D. J. States,...Hanash, S. (2005). "Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database." *Proteomics* Aug 16;5(13): 3226-3245.
21. Misek, D. E., R. Kuick, et al. "A wide range of protein isoforms in serum and plasma uncovered by a quantitative Intact Protein Analysis System (IPAS)." *Proteomics* 2005, Aug 5(13): 3343-52.
22. Wang, H, Clouthier SG, Galchev V, Misek DE, Duffner U, Min CK, Zhao R, Tra J, Omenn GS, Ferrara JL, Hanash SM. Intact-protein-based high-resolution three-dimensional quantitative analysis system for proteome profiling of biological fluids. *Mol Cell Proteomics.* 2005 May;4(5):618-25.
23. Hanash, S and Wang, H: Intact-protein based sample preparation strategies for proteome analysis in combination with mass spectrometry. *Mass Spectrom Rev.* May-June; 24(3):413-26, 2005.
24. Qiu, J, Madoz-Gurpide, SM: Development of natural protein microarrays for diagnosing cancer based on an antibody response to tumor antigens. *J Proteome Res.* Mar-Apr;3(2):261-267, 2004.
25. Bouwman, K, Qiu, J, Zhou, H, Schotanus, M, Mangold, L, Vogt, R, Erlandson, E, Trenkle, J, Partin, AW, Misek, DE, Omenn, GS, Haab, BB and Hanash, S: Microarrays of tumor cell derived proteins uncover a distinct pattern of prostate cancer serum immunoreactivity. *Proteomics.* Nov;3(11):2200-2207, 2003.
26. Nam, MJ, Madoz-Gurpide, J, Wang, H, Lescure, P, Schmalbach, CE, Zhao, R, Misek, DE, Kuick, R, Brenner, DE and Hanash, SM: Molecular profiling of the immune response in colon cancer using protein microarrays: Occurrence of autoantibodies to ubiquitin C-terminal hydrolase L3. *Proteomics.* Nov;3(11):2108-2115, 2003.
27. Shin, BK, Wang, H and Hanash, S: Proteomics approaches to uncover the repertoire of circulating biomarkers for breast cancer. *J Mammary Gland Biol Neoplasia,* Oct;7(4):407-413, 2003.

28. Wang, H and Hanash, S: Multi-dimensional liquid based separations in proteomics. *J Chromatogr B.* April 5;787(1):11-18, 2003.
29. Hanash, S: Disease proteomes. *Nature.* March 13;422(6928):226-232, 2003.
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40. Wang, YK, Liao, PC, Allison, J, Gage, DA, Andrews, PC, Lubman, DM, Hanash, SM and Strahler, JR: Phorbol 12-myristate 13-acetate-induced phosphorylation of Op18 in Jurkat T cells: Identification of phosphorylation sites by matrix-assisted laser desorption ionization mass spectrometry. *J. Biol. Chem.* 268: 14269-14277, 1993.
41. Hanash, S, Strahler, J, Chan, Y, Kuick, R, Teichrow, D, Neel, JV, Hailat, N, Keim, D, Gratiot-Deans, J, Ungar, D, Melhem, R, Zhu, XX, Andrews, P, Lottspeich, F, Eckerskorn, C, Chu, E, Ali, I, Fox, D, Richardson, BC and Turka, L: Database analysis of protein expression patterns during T cell ontogeny and activation. *Proc. Natl. Acad. Sci., USA* 90: 3314-3318, 1993.
42. Hanash, SM, Strahler, JR, Neel, JV, Hailat, N, Melhem, R, Keim, D, Zhu, XX, Wagner, D, Gage, DA and Watson, JT: Highly resolving two-dimensional gels for protein microsequencing. *Proc. Natl. Acad. Sci., USA* 88: 5709-5713, 1991.

## C. RESEARCH SUPPORT

### Ongoing Research Support

CA039542

NIH/NCI

Cellular and Molecular Studies of Bone Marrow Transplant

7/1/04 – 6/30/09

The overall goal of this project is to explore the cellular and molecular mechanisms of allogeneic bone marrow transplantation (BMT) and to serve as a translational research platform for novel therapeutic strategies for patients with hematologic malignancies.

U01 CA84982 (Hanash)

NIH/NCI

9/24/04 – 8/31/09

Proteomics Biomarker Development Laboratory

The major goal of this project is the identification of novel cancer biomarkers using serum from cancer patients.

U54 (Gambhir/Agus)

5/1/06 – 4/30/10

NIH/NCI

Center of Cancer Nanotechnology Excellence – Therapy Monitoring (Project 4)

The objective of Project 4 is to test potential markers uncovered using proteomic profiling technologies and others that target proteins known to be associated with cancer.

N01-WH-74313; Contract #HHSN268200764313C (Li)

01/15/07 - 01/14/09

NHLBI

Identification and Validation of Circulating Biomarkers of the Early Detection of Breast Cancer in Pre-clinical Specimens

The specific aims of this proposal are: 1. To use three proteomic platforms to identify protein biomarkers in preclinical sera that could potentially be used for the early detection of breast cancer; 2. To validate the utility of the potential protein biomarkers identified in this study with respect to their specificity and sensitivity as markers of early detection; and 3. To enhance the predictive power of our set of protein biomarkers by including known risk factors for breast cancer in our models.

N01-WH-74315; Contract #HHSN268200764315C (Prentice)

01/15/07 – 01/14/09

NHLBI

Title: Proteomics and the Health Effects of Postmenopausal Hormone Therapy

The specific aims of this proposal are: 1. To use three proteomic platforms to identify protein biomarkers in preclinical sera to determine the health effects of postmenopausal hormone therapy; 2. To validate the utility of the potential protein biomarkers identified in this study with respect to their specificity and sensitivity as markers of early detection; and 3. To enhance the predictive power of our set of protein biomarkers by including potential risk factors of postmenopausal hormone therapy in our models.

U01 CA128427 (Hancock)

NIH/NCI

09/04/2007-06/30/2012

Glycan Markers for the Early Detection of Breast Cancer

A tumor glycome laboratory team with multi-disciplinary expertise in glycomics, proteomics, informatics and cancer markers is proposing to implement a new paradigm in the use of glycan biomarkers for early detection of cancer. Specific aim 1 is focused on the analysis of glycans and glycoproteins in plasma to identify differences in plasma between newly diagnosed breast cancer subjects and controls. Specific Aim 2 is focused on the analysis of breast cancer tissue obtained at the time of surgery to identify glycan and glycoprotein differences between tumor containing and tumor free tissue. The translational aspect of this study is achieved in specific aim 3 by the development of a high throughput and sensitive glycan assay platform (GAP) which will be used to pre-validate markers in a large sample set and thus facilitate subsequent clinical studies.

Avon Foundation (Hanash)

01/01/08-12/31/10

Title: Validation of an Autoantibody Signature for Breast Cancer

This proposal aims to define and validate a set of tumor antigens that induce an autoantibody response in breast cancer detectable in blood that would be particularly suited for early detection.