BIOGRAPHICAL SKETCH

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NAME: Sungyong You

eRA COMMONS USER NAME (credential, e.g., agency login): yousung1

POSITION TITLE: Instructor

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

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Seoul National University, Seoul, Korea	B.S.	02/2001	Agriculture and Life Sciences
Seoul National University, Seoul, Korea	M.S.	02/2005	Pharmacy
Pohang University of Science and Technology, Pohang, Korea	Ph.D.	02/2012	Systems Biology
Cedars-Sinai Medical Center, Los Angeles	Postdoc	12/2013	Cancer Biology

A. Personal Statement

I am an Assistant Professor in the Departments of Surgery and Biomedical Sciences at Cedars-Sinai Medical Center. I have a strong background in computational biology, with specific training and expertise in statistical analysis of large-scale genomics, transcriptomics, and proteomics data. I also have extensive experience in the selection and evaluation of potential candidates of molecular biomarker in urologic oncologic disease. I recently developed a novel prostate cancer classification system using an advanced clustering approach in combination with an integrative computational framework. The major theme areas of my research are: 1) disease-relevant studies directed toward identifying the drivers of pathogenesis, 2) discovery and assessment of biomarkers with the goal of classifying disease entities, prognosis and response to therapeutic interventions, and 3) potential association of specific signal transduction and metabolic networks with disease phenotypes as an approach to identifying novel therapeutic targets.

B. Positions and Honors

Positions and Employment

2005-2008 Database Administrator of Bioinformatics Core, National Core Research Center for Systems Bio-Dynamics, Pohang University of Science and Technology (POSTECH), Pohang, Korea.
2012-2013 Postdoctoral Fellow, Department of Surgery, Cedars-Sinai Medical Center, Los Angeles, CA
2014-2016 Instructor, Department of Surgery, Cedars-Sinai Medical Center, Los Angeles, CA

Honors and Special Awards

2011 Graduate Student Fellowship Award of Boryung pharmaceutical Co., Korea.
2013 Best Poster Award, The American Urological Association Annual Meeting, USA
2014 Prostate Cancer Research Program (PCRP) Postdoctoral Training Award, Dept. of Defense
2014 Postdoctoral Scholarship Award, Urology Care Foundation (UCF)

Patents

1. Kim WU, Cho CS, Hwang D, **You S**, and Yoon HY., Compositions comprising NFAT5 inhibitor as an active ingredient for preventing or treating of angiogenesis-related diseases., Application Number: 10-2010-0037515.

2. Hwang D, Kim WU, Cho CS, **You S**, and Yoon HY, Markers for diagnosing angiogenesis-related diseases and use thereof., Registration Number: 10-1204620.

3. Kim HK, Rho S, Hwang D, Park KU, Lee YM, Yoon SJ, **You S**., Systems Biological Method of Biomarker Selection For Diagnosis of Lung Cancer, Subtype of Lung Cancer, And Biomarker Selected By The Same., Registration Number: 10-1378919.

4. Kim WU, Hwang D, Yi CE, Kang MJ, Park YJ, and **You S**., Biomarkers for assessing rheumatoid arthritis disease activity., Application Number: 10-2014-0076050.

5. **You S**, Freeman MR, Kim J, Knudsen B, Method of Diagnosing and Treating Prostate Cancer., Reference Number: 065472-000582PR00.

6. Rotinen M, **You S**, Murali R, Freeman MR., Agent for Treating Castration Resistant Prostate Cancer., Reference Number: 065472-000593PR00.

C. Contribution to Science

My research has focused on disease-relevant studies directed toward identifying the drivers in pathogenesis. Using the transcriptomic and proteomic analysis of preclinical models, we showed 1) that microtubule instability arising from perturbations in the DIAPH3 network potentially reports taxane sensitivity in human tumors; 2) that MYC is a novel target for pharmacological intervention in fibroproliferative expansion of bladder smooth muscle, and potentially in cancers in which PDGFR-dependent signaling or MYC activation promote tumor progression; and 3) novel roles of TWIST1, POSTN, and GREM1 in rheumatoid arthritis pathogenesis.

Morley S, **You S**, Pollan S, Choi J, Zhou B, Hager MH, Steadman K, Spinelli C, Rajendran K, Gertych A, Kim J, Adam RM, Yang W, Krishnan R, Knudsen B, Di Vizio D, Freeman MR, (2015). Regulation of microtubule dynamics by DIAPH3 influences amoeboid tumor cell mechanics and sensitivity to taxanes. *Scientific Report*. July. 5(12136):1-16. DOI:10.1038/srep12136. PMID: 26179371.

Yang W*, Ramachandran A*, **You S***, Jeong HB, Morley S, Logvinenko T, Kim J, Hwang D, Freeman MR, and Adam RM, (2014). Integration of proteomic and transcriptomic profiles identifies a novel PDGF-MYC network in human smooth muscle cells. *Cell Communication and Signaling*. Aug 1;12(1):44. PMID: 25080971 *** co-first author**

You S*, Yoo SA, Choi S, Kim JY, Park SJ, Ji DJ, Kim TH, Kim KJ, Cho CS, Hwang D, and Kim WU. (2014). Identification of key regulators for the migration and invasion of rheumatoid synoviocytes through a systems approach, *Proceedings of the National Academy of Sciences of the United States of America*, 111:550-555. doi: 10.1073/pnas.1311239111. PMID: 24374632 *** first author**

Han EJ, Yoo SA, Kim GM, Hwang, D, Cho CS, **You S***, Kim WU. (2016). GREM1 is a key regulator of synovial hyperplasia in rheumatoid arthritis, *Journal of Rheumatology*. Mar;43(3):474-85. PMID: 26834210 *** co-corresponding author**

Other studies have focused on discovery and assessment of biomarkers with the goal of classifying disease entities, prognosis and response to therapeutic interventions. We performed large scale quantitative proteomic analysis to identify disease specific proteins, and explored important cellular functions associated with disease pathogenesis and resistance to therapeutic interventions.

Choi DY*, **You S***, Jung JH, Lee JC, Rho JK, Lee KY, Freeman MR, Kim KP, and Kim J. (2014). Extracellular vesicles shed from gefitinib-resistant non-small cell lung cancer regulate the tumor microenvironment. *Proteomics*. Jun 19 doi: 10.1002/pmic.201400008. PMID: 24946052 *** co-first author**

Kang MJ*, Park YJ*, **You S***, Yoo SA, Choi S, Kim DH, Cho CS, Yi EC, Hwang D, Kim WU. (2014). A urinary proteome profile predictive of disease activity in rheumatoid arthritis. *Journal of Proteome Research*. Nov 7;13(11):5206-17. doi: 10.1021/pr500467d. PMID: 25222917 *** co-first author**

Minciacchi VR*, **You S***, Cristiana S, Morley S, Zandian M, Paul-Joseph A, Lorenzo C, Chiara C, Reis-Sobreiro M, Morello M, Geetanjali K, Jang S, Kim. DK, Elhan HB, Emma TG, Martin G, Gho YS, Surech M, Yang J, Yang W, Freeman MR, Di Vizio D, (2015). Large Oncosomes Contain Distinct Protein Cargo and Represent a Separate Functional Class of Tumor-Derived Extracellular Vesicles. *Oncotarget*. Mar 14. PMID:25857301 *** co-first author**

I also have extensive experience in the development of computational infrastructure for integrative data analysis. I have developed a database to provide comprehensive resources of molecular profiles and network analysis tools in 12 cancer types. In addition, I recently constructed the "Prostate Cancer Transcriptome Atlas (PCTA)" database containing 50 human PC transcriptome data sets with clinical information from public databases and the literature. The PCTA provides the following advantages in prostate cancer research: 1) to overcome limitations from low statitical power arising from limited sample number per individual study cohort; 2) to evaluate the clinical significance of consistent gene expression changes; and 3) to focus narrowly on specific patient subpopulations.

Lee JH*, **You S***, Hyeon DY, Kang B, Kim H, Park KM, Han B, Hwang D, Kim S. (2015). Comprehensive data resources and analytical tools for pathological association of aminoacyl tRNA synthetases with cancer. *Database (Oxford)*. Mar 29;2015. doi: 10.1093/database/bav022. PMID: 25824651 *** co-first author**

You S, Kim J, Freeman MR, (2014). Prostate cancer classification using a transcriptome atlas. *Annual PCF Scientific Retreat*.

You S, Knudsen BS, Erho N, Alshalalfa M, Takhar M, Ashab HA, Davicioni E, Karnes RJ, Klein EA, Den RB, Ross AE, Schaeffer EM, Garraway IP, Kim J, Freeman MR. (2016). Integrated classification of prostate cancer reveals a novel luminal subtype with poor outcome. *Cancer Research*. Jun 14:2016. doi: 10.1158/0008-5472.CAN-16-0902. PMID: 27302169. ***This study has been highlighted in Research Highlights section of *Nature Reviews Urology* entitled "Prostate cancer: Novel subtyping could aid stratification and therapy" (2016) July 5. doi:10.1038/nrurol.2016.130**

Complete List of Published Work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/sungyong.you.1/bibliography/40981105/public/?sort=date&direction=ascending

D. Research Support

Ongoing research project

The Urology Care Foundation Research Scholar Program (You S) 7/1/14-6/30/17
An Epigenomic Pathway From Cholesterol to Intracrine Androgen
Goal: To identify the SAFB1 loss-induced transcriptional program in prostate cancer progression
Role: PI

NIH/NCI (Chung) 3/3/15-2/29/20
Prostate Cancer Bone Metastasis Biology and Targeting
Role: Bioinformatician

Department of Defense (Freeman) 9/1/16 – 8/31/19
Large Oncosomes: A Master Regulator of Aggressive Prostate Cancer Variants
Role: Bioinformatician