Akhilesh Pandey, M.D., Ph.D.

Position : Professor
Department : McKusick-Nathans Institute of Genetic Medicine
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Education

INSTITUTION AND LOCATION	DEGREE	Completion Date MM/YYYY	FIELD OF STUDY
Armed Forces Medical College, Pune, India	M.D.	12/1988	Medicine
Kilpauk Medical College, Madras, India	Intern	05/1990	Medicine
University Of Michigan, Ann Arbor, Michigan	Ph.D.	06/1995	Pathology
University of Michigan, Ann Arbor, Michigan	Postdoctoral Fellow	06/1996	Molecular Biology
Whitehead Institute/MIT, Cambridge, Massachusetts	Postdoctoral Fellow	01/1999	Molecular Biology
Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts	Resident	06/1999	Clinical Pathology
University of Southern Denmark, Odense, Denmark	Visiting Scientist	02/2002	Proteomics

Positions and Honors

Positions and Employment

1998 - 2002 Instructor, Harvard Medical School, Department of Pathology, Boston, MA
2002 - 2006 Assistant Professor, Johns Hopkins University School of Medicine, McKusick-Nathans Institute of Genetic Medicine and Departments of Biological Chemistry and Oncology, Baltimore, MD
2005 - 2006 Assistant Professor, Department of Pathology, Johns Hopkins University School of Medicine, Baltimore, MD
2006 - 2010 Associate Professor, Johns Hopkins University School of Medicine, McKusick-Nathans Institute of Genetic Medicine and Departments of Biological Chemistry, Pathology and Oncology, Baltimore, MD
2010 - Professor, Department of Molecular Microbiology and Immunology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD
2010 - Professor, Johns Hopkins University School of Medicine, McKusick-Nathans Institute of Genetic Medicine and Departments of Biological Chemistry, Pathology and Oncology, Baltimore, MD
2016 - Director, Center for Translational Proteomics, Johns Hopkins University School of Medicine, Baltimore, MD

Other Experience and Professional Memberships

2000 - Member, American Society for Mass Spectrometry
2002 - Founder, Institute of Bioinformatics, Bangalore, India
2002 - 2007 Chief Scientific Advisor, Institute of Bioinformatics, Bangalore, India
2003 - 2006 Editorial Board Member, Genome Research
2006 - 2010 Editorial Board Member, Journal of Proteome Research
2007 - Director, Institute of Bioinformatics, Bangalore, India
2007 - Editorial Board Member, Clinical Proteomics, DNA Research
2009 - Editorial Board Member, Molecular and Cellular Proteomics

2011-	Editorial Board Member, Journal of Translational Medicine
2009 - 2016	Associate Editor, Journal of Proteomics
2014 - 2016	Senior Editor, Proteomics
2016 -	Editorial Board Member, Cancer Research

Honors

1996	Experimental Pathologist-in-training Award, American Society for Investigative Pathology
1997	Howard Temin Award, National Cancer Institute
2003	Sidney Kimmel Scholar Award, Sidney Kimmel Foundation
2004	Beckman Young Investigator Award, Beckman Foundation
2006	DOD Era of Hope Scholar Award, Department of Defense
2014	High Impact Research Icon, University of Malaya, Malaysia
2015	Discovery in Proteomic Sciences Award, Human Proteome Organization (HUPO)
2015	Margdarshi Fellowship, Wellcome Trust/Department of Biotechnology, India Alliance

Contributions to Science

1. Mass spectrometry: From using bioinformatics to identifying a novel cytokine receptor to developing the stable isotope labeling by amino acids in cell culture (SILAC) method for quantitative proteomics, I have constantly sought to develop and establish new technologies to solve biological problems. The SILAC method developed by me has become a gold standard for quantitative proteomics. I was one of the first to describe a global phosphoproteomic analysis using antibodies to selectively enrich phosphoserine and phosphothreonine containing proteins. My group was the first to describe (alongside a paper by Don Hunt's group) in PNAS, the use of electron transfer dissociation (ETD) as a high-throughput method for global characterization of phosphorylation sites and showed the unique advantages over of ETD over the conventional collision-induced dissociation (CID) method for a global phosphorylation analysis. I was also the first to establish a method that permits quantitation of phosphorylation events on individual phosphorylation sites using the SILAC method – this approach is now an integral part of many phosphoproteomic approaches that are widely by the biomedical community.

1. Steen H, **Pandey A,** Andersen JS, Mann M. (2002). Analysis of tyrosine phosphorylation sites in signaling molecules by a phosphotyrosine-specific immonium ion scanning method. Science's STKE 15, pl16. PMID: 12381836.

2. Molina H, Horn DM, Tang N, Mathivanan S, **Pandey A.** (2007). Global proteomic profiling of phosphopeptides using electron transfer dissociation tandem mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America.13, 2199-204. PMCID: PMC1794346.

3. Kandasamy, K., **Pandey, A.** and Molina, H. (2009). Evaluation of several MS/MS search algorithms for analysis of spectra derived from electron transfer dissociation experiments. Analytical Chemistry. 1, 7170-7180. PMID: 19639959.

4. Kim, M. S., Zhong, J., Kandasamy, K., Delanghe, B. and **Pandey, A.** (2011). Systematic evaluation of alternating CID and ETD fragmentation for phosphorylated peptides. Proteomics. 11, 2568-2572. PMID: 21598390. PMCID: PMC3664225.

2. Biomarker Discovery: My group is actively involved in applying proteomics technologies in identifying biomarkers in various cancers including pancreatic cancer, breast cancer, esophageal and gastric cancer. We are also investigating body fluids which includes urine, plasma, serum, cerebrospinal fluid and saliva for the discovery of biomarkers in disease conditions. We were the first to develop MRM assays to detect cancer-derived mutant peptides.

1. Harsha, H. C., Kandasamy, K., Ranganathan, P., Rani, S., Ramabadran, S., Gollapudi, S., Balakrishnan, L., Dwivedi, S. B., Telikicherla, D., Selvan, L. D. N., Goel, R., Mathivanan, S., Marimuthu, A., Kashyap, M. K., Vizza, R. F., Mayer, R. J., DeCaprio, J. A., Srivastava, S., Hanash, S. M., Hruban, R. H. and **Pandey, A.** (2009). A compendium of potential biomarkers of pancreatic cancer. PLoS Medicine. 6, e1000046. PMCID: PMC2661257

2. Wang, Q., Chaerkady, R., Wu, J., Hwang, H., J., Papadopoulos, N., Kopelovich, L., Maitra, A., Matthei, H., Eshleman, J., Hruban, R., Kinzler, K. W., Pandey, A. and Vogelstein, B. (2011). Mutant proteins as cancer-specific biomarkers. Proceedings of the National Academy of Sciences U.S.A. 108, 2444-2449. PMCID: PMC3038743

3. Marimuthu, A., O'Meally, R., Chaerkady, R., Subbannayya, Y., Nanjappa, V., Kumar, P., Kelkar, D., Pinto, S., Sharma, R., Renuse, S., Goel, R., Christopher, R., Delanghe, B., Cole, R. N., Harsha, H. C. and **Pandey, A.** (2011). A comprehensive map of the human urinary proteome. Journal of Proteome Research. 10, 2734-2743. PMCID: PMC4213861

4. Jhaveri, D. T., Kim, M. S., Thompson, E. D., Huang, L., Sharma, R., Klein, A. P., Zheng, L., Le, D. T., Laheru, D. A., Pandey, A., Jaffee, E. M. and Anders, R. A. (2016). Using quantitative seroproteomics to identify antibody biomarkers in pancreatic cancer. Cancer Immunology Research. 4, 225-233. PMCID: PMC4843125.

3. Signal Transduction in Cancer: Understanding the signaling mechanisms in cancer is vital for design of targeted therapies for precision medicine. We have successfully elucidated significant changes in signaling and and miRNA targets within a variety of cancerous conditions including pancreatic cancer and breast cancer. Our study on pancreatic cancer have revealed heterogeneity and enabled personalized therapy by helping select those patients who are likely to benefit from therapy with EGFR kinase inhibitors. Using isogenic systems, we have elucidated the pathways downstream of *PIK3CA*, one of the most frequently mutated genes in cancer.

1. **Pandey A,** Podtelejnikov AV, Blagoev B, Bustelo XR, Mann M, Lodish HF. (2000). Analysis of receptor signaling pathways by mass spectrometry: identification of vav-2 as a substrate of the epidermal and platelet-derived growth factor receptors. Proceedings of the National Academy of Sciences of the United States of America. 4, 179-84 PMCID: PMC26636.

2. Wang, Q., Chaerkady, R., Wu, J., Hwang, H., J., Papadopoulos, N., Kopelovich, L., Maitra, A., Matthei, H., Eshleman, J., Hruban, R., Kinzler, K. W., **Pandey, A.** and Vogelstein, B. (2011). Mutant proteins as cancer-specific biomarkers. Proceedings of the National Academy of Sciences U.S.A. 108, 2444-2449. PMCID: PMC3038743

3. Wu X, Renuse S, Sahasrabuddhe NA, Zahari MS, Chaerkady R, Kim MS, Nirujogi RS, Mohseni M, Kumar P, Raju R, Zhong J, Yang J, Neiswinger J, Jeong JS, Newman R, Powers MA, Somani BL, Gabrielson E, Sukumar S, Stearns V, Qian J, Zhu H, Vogelstein B, Park BH and **Pandey A**. (2014). Activation of diverse signalling pathways by oncogenic PIK3CA mutations. Nature Communications. 23, 4961. PMCID: PMC4210192.

4. Wu, X., Zahari, M. S., Ma, B., Liu, R., Renuse, S., Sahasrabuddhe N. A., Chen, L., Chaerkady, R., Kim, M. S., Zhong, J., Jelinek, C., Bharbuiya, M. A., Leal-Rojas, P., Yang, Yi., Kashyap, M. K., Marimuthu, A., Ling, M., Fackler, M. J., Merino, V., Zhang, Z., Zahnow, C. A., Gabrielson, E., Stearns, V., Roa, J. C., Sukumar, S., Gill, P. S. and **Pandey, A.** (2015). Global phosphotyrosine survey in triple-negative breast cancer reveals activation of multiple tyrosine kinase signaling pathways. Oncotarget. 6, 29143-29160. PMCID: PMC4745717.

4. Proteogenomics: The first broad and systematic survey of the normal human proteome using mass spectrometry was carried out by my group. As part of this study and many other studies in the past, we have successfully integrated the mass spectrometry-based proteomic data to define and annotate genomes. This has played a crucial role in the improvement of genome annotation of several species including relatively well annotated human genome and others such as Zebrafish, *Mycobacterium tuberculosis*, *Anopheles gambiae* and *Anopheles stephensi*. Through this integrative systems biology approach, we have identified several novel coding regions in many genomes and refined many of the other previously known coding and non-coding regions.

1. Renuse S, Chaerkady R, **Pandey A.** (2011). Proteogenomics. Proteomics. 11, 620-30. PMID: 21246734.

2. Chaerkady R, Kelkar DS, Muthusamy B, Kandasamy K, Dwivedi SB, Sahasrabuddhe NA, Kim MS, Renuse S, Pinto SM, Sharma R, Pawar H, Sekhar NR, Mohanty AK, Getnet D, Yang Y, Zhong J, Dash AP, MacCallum RM, Delanghe B, Mlambo G, Kumar A, Keshava Prasad TS, Okulate M, Kumar N, **Pandey A.** (2011). A proteogenomic analysis of *Anopheles gambiae* using high-resolution Fourier transform mass spectrometry. Genome Research. 21, 1872-81. PMCID: PMC3205572.

3. Kelkar DS, Provost E, Chaerkady R, Muthusamy B, Manda SS, Subbannayya T, Selvan LD, Wang CH, Datta KK, Woo S, Dwivedi SB, Renuse S, Getnet D, Huang TC, Kim MS, Pinto SM, Mitchell CJ, Madugundu AK, Kumar P, Sharma J, Advani J, Dey G, Balakrishnan L, Syed N, Nanjappa V, Subbannayya Y, Goel R, Prasad TS, Bafna V, Sirdeshmukh R, Gowda H, Wang C, Leach SD, **Pandey A.** (2014). Annotation of the zebrafish genome through an integrated transcriptomic and proteomic analysis. Molecular and Cellular Proteomics. 13, 3184-98. PMCID: PMC4223501.

4. Mitchell, C. J., Getnet, D., Kim, M. S., Manda, S. S., Kumar, P., Huang, T. C., Pinto, S., Nirujogi, R. S., Iwasaki, M., Shaw, P., Wu, X., Zhong, J., Chaerkady, R., Marimuthu, A., Muthusamy, B., Sahasrabuddhe, N. A., Raju, R., Bowman, C., Danilova, L., Cutler, J., Kelkar, D. S., Drake, C. G., Prasad, T. S. K., Marchionni, L., Marukami, P. N., Scott, A. F., Shi, L., Thierry-Mieg, J., Thierry-Mieg, T., Irizarry, R., Cope, L., Ishihama, Y., Wang, C., Gowda, H. and **Pandey, A.** (2015). A multi-omic analysis of human naive CD4+ T cells. BMC Systems Biology. 9, 75. PMCID: PMC4636073.

5. Development of resources for the scientific community: My group is actively involved in the development of resources that provides a comprehensive compilation of the existing data to the scientific community. These resources include Human protein reference database (HPRD), Oncomine, NetPath, Human Proteinpedia, Human Proteome Map, Plasma Proteome Database, Pancreatic Cancer Database and others. HPRD provides information on protein-protein interactions, post-translational modifications, localization and domain and motif information of human proteins, while NetPath is a curated resource for the signaling pathways in humans. In addition, I have been an active participant in other community initiatives such as HUPO's Proteomics Standards Initiative, Chromosome-Human Proteome Project, BioPAX, Sequencing Quality Control (SEQC) and Clinical Prteomics Tumor Analysis Consortium.

1. Amanchy, R, Periaswamy, B, Mathivanan, S, Reddy, R, Tattikota, SG. and **Pandey, A.** (2007). A compendium of curated phosphorylation-based substrate and binding motifs. Nature Biotechnology. 25, 285-286. PMID: 17344875

2. Mathivanan S, Ahmed M, 152 other authors, Yates JR, Zhong J, Zhou M, Zhu Y, Zurbig P, **Pandey A.** (2008) Human Proteinpedia enables sharing of human protein data. Nature Biotechnology 26, 164-7. PMID: 18259167.

3. Kandasamy K, Mohan SS, Raju R, Keerthikumar S, Kumar GS, Venugopal AK, Telikicherla D, Navarro JD, Mathivanan S, Pecquet C, Gollapudi SK, Tattikota SG, Mohan S, Padhukasahasram H, Subbannayya Y, Goel R, Jacob HK, Zhong J, Sekhar R, Nanjappa V, Balakrishnan L, Subbaiah R, Ramachandra YL, Rahiman BA, Prasad TS, Lin JX, Houtman JC, Desiderio S, Renauld JC, Constantinescu SN, Ohara O, Hirano T, Kubo M, Singh S, Khatri P, Draghici S, Bader GD, Sander C, Leonard WJ and **Pandey A.** (2010). NetPath: a public resource of curated signal transduction pathways. Genome Biology. 12; R3. PMCID: PMC2847715.

4. Wu, X., Zahari, M. S., Renuse, S., Sakamuri, S., Singal, M., Gabrielson, E., Sukumar, S. and **Pandey, A.** (2014). A breast cancer cell microarray (CMA) as a rapid method to characterize candidate biomarkers. Cancer Biology and Therapy. 15, 1593-9. PMCID: PMC4119079.