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Position: Ph.D student

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Education

2012.03-present	Ph.D student	Graduate School of Analytical Science and Technology, Chungnam National University
2010.03-2012.02	M.S.	Graduate School of Analytical Science and Technology, Chungnam National University
2001.03-2009.02	B.S.	Department of chemistry, Chungnam National University

Professional Experience

yyyy.mm-yyyy.mm	position	affiliation
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Academic Society

yyyy.mm-yyyy.mm	position	society
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Publications

- Ji, E. S., Hwang, H., Park, G. W., Lee, J. Y., Lee, H. K., Choi, N. Y., Kim, K. H., ... & Ahn, Y. H. (2016). Analysis of fucosylation in liver-secreted N-glycoproteins from human hepatocellular carcinoma plasma using liquid chromatography with tandem mass spectrometry. *Analytical and Bioanalytical Chemistry*, 408(27), 7761-7774.
- Lee, J. Y., Lee, H. K., Park, G. W., Hwang, H., Jeong, H. K., Yun, K. N., Kim, K. H., ... & Yun, S. H. (2016). Characterization of Site-Specific N-Glycopeptide Isoforms of α -1-Acid Glycoprotein from an Interlaboratory Study Using LC-MS/MS. *Journal of Proteome Research*, 15(12), 4146-4164.
- Park, G. W., Hwang, H., Kim, K. H., Lee, J. Y., Lee, H. K., Park, J. Y., ... & Park, Y. M. (2016). Integrated Proteomic Pipeline Using Multiple Search Engines for a Proteogenomic Study with a Controlled Protein False Discovery Rate. *Journal of Proteome Research*.
- Park, G. W., Kim, J. Y., Hwang, H., Lee, J. Y., Ahn, Y. H., Lee, H. K., Kim, K. H., & Kim, Y. S. (2016). Integrated GlycoProteome Analyzer (I-GPA) for Automated Identification and Quantitation of Site-Specific N-Glycosylation. *Scientific reports*, 6.
- Hwang, H., Park, G. W., Kim, K. H., Lee, J. Y., Lee, H. K., Ji, E. S., ... & Park, Y. M. (2015). Chromosome-based proteomic study for identifying novel protein variants from human hippocampal tissue using customized neXtProt and GENCODE databases. *Journal of proteome*

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Kim, K. H., Ahn, Y. H., Ji, E. S., Lee, J. Y., Kim, J. Y., An, H. J., & Yoo, J. S. (2015). Quantitative analysis of low-abundance serological proteins with peptide affinity-based enrichment and pseudo-multiple reaction monitoring by hybrid quadrupole time-of-flight mass spectrometry. *Analytica Chimica Acta*, 882, 38-48.

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Ahn, Y. H., Kim, K. H., Shin, P. M., Ji, E. S., Kim, H., & Yoo, J. S. (2012). Identification of low-abundance cancer biomarker candidate TIMP1 from serum with lectin fractionation and peptide affinity enrichment by ultrahigh-resolution mass spectrometry. *Analytical chemistry*, 84(3), 1425-1431.

Ahn, Y. H., Ji, E. S., Shin, P. M., Kim, K. H., Kim, Y. S., Ko, J. H., & Yoo, J. S. (2012). A multiplex lectin-channel monitoring method for human serum glycoproteins by quantitative mass spectrometry. *Analyst*, 137(3), 691-703.

Ahn, Y. H., Kim, K. H., Shin, P. M., Ji, E. S., & Yoo, J. S. (2011). Mass Spectrometry for Analysis of Cancer Biomarker from Human Plasma. *Journal of Analytical Science & Technology 2 (Suppl A)*, A135-A139.