

BIOGRAPHICAL SKETCH

NAME <p style="text-align: center;">Kong-Joo Lee</p>	POSITION TITLE <p style="text-align: center;">Professor</p>		
CURRENT AFFILIATION College of Pharmacy / Division of Life & Pharmaceutical Sciences Ewha Womans University			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Ewha Womans University	Bachelor's degree	1973-1977	Pharmacy
Korea Advanced Institute of Science and Technology(KAIST)	Master's degree	1977-1979	Biotechnology(Biochemistry)
Stanford University	Doctor's degree	1980-1986	Chemistry (Biophysical chemistry)
Stanford Medical School Stanford University	Postdoctoral fellow	1986-1988	

List of five recent publications by the candidate:

- Jaeho Jeong, Yongsik Jung, Seungjin Na, Jihye Jeong, Eunsun Lee, Mi-Sun Kim, Sun Choi, Dong-Hae Shin, Eunok Paek, Hee-Yoon Lee, Kong-Joo Lee. Novel Oxidative modifications in Redox-active cysteine residues. *Mol Cell Proteomics* (2011)
- Seonhwa Choi, Jaeho Jeong, Seungjin Na, Hyo Sun Lee, Hwa-Young Kim, Kong-Joo Lee, Eunok Paek, A new algorithm for the identification of intact disulfide linkages based on fragmentation characteristics in tandem mass spectra. *J Proteome Res* (2010)
- Na Rae Hwang, Seung-Hee Yim, Young Mee Kim, Jaeho Jeong, Eun Joo Song, Yoonji Lee, Jin Hee Lee, Sun Choi, and Kong-Joo Lee. Oxidative Modifications of Glyceraldehyde-3-Phosphate Dehydrogenase Play a Key Role in Its Multiple Cellular Functions. *Biochem J.* (2009)
- Hyun Jung Kim, Young Mee Kim, Sangmi Lim, You Kyung Nam, Jaeho Jeong & Kong-Joo Lee, Ubiquitin C-terminal hydrolase-L1 is a key regulator of tumor cell invasion and metastasis. *Oncogene* (2009)
- Jawon Seo, Jaeho Jeong, Young Mee Kim, Narae Hwang, Eunok Paek and Kong-Joo Lee, **A Strategy for Comprehensive Identification of Post-Translational Modifications in Cellular Proteins, Including Low Abundance Modifications: Application to GAPDH.** *J. Proteome Res.* (2008)

Please indicate in 200 words or less the reason(s) why you would be a suitable candidate for the HUPO Council elections.

By employing cutting edge technologies for proteomics using mass spectrometry, bioinformatics and biological study, I have unveiled the functional regulations of proteins involved in stress- and angiogenesis-related signaling pathways from 1997. I am the first generation of proteomics using MALDI-TOF MS and ESI-q-TOF Tandem MS in combination with the previous experiences on biochemistry and analytical tools (LC, CE and GC/LC-MS), establishing the understanding of novel molecular changes occurring in response to various stresses, and developed the tools for detecting novel post-translational modifications (PTMs) and database for PTMs in signaling pathways. I was an editorial board member of *Mol. Cell. Proteomics* from 2001 to 2006 and got funded the National Core Research Center for Cell Signaling & Drug Discovery from KOSEF during 2006-2013, one of the biggest and competitive research projects in Korea. I clearly understand the direction of application strategy of proteomics which is important for proteomics society and for the progress of science. Based on my experiences and prospect on both analytical and biological, and both basic and application aspects, I believe that I can contribute the advancement of HUPO and scientific progress using proteomics.