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Education

1985.04-1990.03	B. Engn.	Kyoto University
1990.04-1992.03	M. Engn.	Kyoto University
1998.05	Ph. D.	Kyoto University

Professional Experience

1992-2006	Researcher \rightarrow Senior Scientist	Eisai Co., Ltd.
	\rightarrow Semon Scientist	
2001-2003	Guest Researcher	University of Southern Denmark (M. Mann lab)
2006-2010	Associate Professor	Institute for Advanced Biosciences, Keio University
2010-current	Professor	Graduate School of Pharmaceutical Sciences,
		Kyoto University

Academic Society

2018.01-current	President	Japanese Proteomics Society
2017.01-current	Council member	Human Proteome Organization
2017.01-current 2011.01-current	Council member Council member	Asia Oceania Human Proteome Organization The Society for Chromatographic Sciences, Japan

Publications

- Imamura H, Wagih O, Niinae T, Sugiyama N, Beltrao P, <u>Ishihama Y.</u> Identifications of Putative PKA Substrates with Quantitative Phosphoproteomics and Primary-Sequence-Based Scoring. J Proteome Res. 16(4):1825-1830, 2017.
- Okuda S, Watanabe Y, Moriya Y, Kawano S, Yamamoto T, Matsumoto M, Takami T, Kobayashi D, Araki N, Yoshizawa AC, Tabata T, Sugiyama N, Goto S, <u>Ishihama Y.</u> jPOSTrepo: an international standard data repository for proteomes, **Nucleic Acids Res.**, 45(D1):D1107-D1111,2017.
- Miki T, Awa M, Nishikawa Y, Kiyonaka S, Wakabayashi M, <u>Ishihama Y</u>, Hamachi I. A conditional proteomics approach to identify proteins involved in zinc homeostasis. **Nat Methods**, 13(11):931-7, 2016.
- Tsai CF, Wang YT, Yen HY, Tsou CC, Ku WC, Lin PY, Chen HY, Nesvizhskii AI, <u>Ishihama Y</u>, Chen YJ. Large-scale determination of absolute phosphorylation stoichiometries in human cells by motif-targeting quantitative proteomics. **Nat. Commun.**, 6: 6622, 2015.
- Lin MH, Sugiyama N, <u>Ishihama Y.</u> Systematic profiling of the bacterial phosphoproteome reveals bacterium-specific features of phosphorylation. **Sci. Signal.**, 58(394): rs10, 2015.