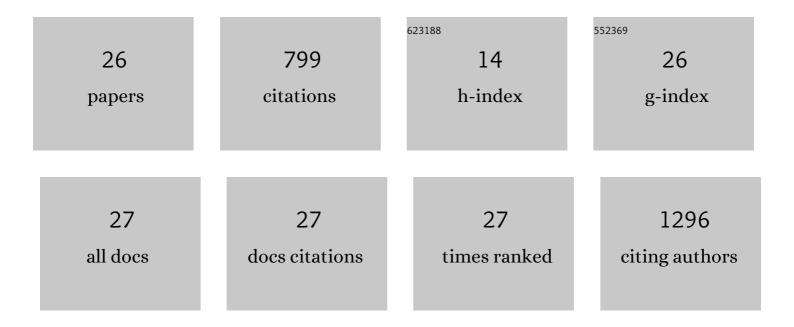
Seungjin Na

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Fast Multi-blind Modification Search through Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2012, 11, M111.010199.	2.5	143
2	New Algorithm for the Identification of Intact Disulfide Linkages Based on Fragmentation Characteristics in Tandem Mass Spectra. Journal of Proteome Research, 2010, 9, 626-635.	1.8	79
3	Novel Oxidative Modifications in Redox-Active Cysteine Residues. Molecular and Cellular Proteomics, 2011, 10, M110.000513.	2.5	79
4	Proteogenomic strategies for identification of aberrant cancer peptides using largeâ€scale nextâ€generation sequencing data. Proteomics, 2014, 14, 2719-2730.	1.3	62
5	MODi : a powerful and convenient web server for identifying multiple post-translational peptide modifications from tandem mass spectra. Nucleic Acids Research, 2006, 34, W258-W263.	6.5	55
6	Software eyes for protein postâ€ŧranslational modifications. Mass Spectrometry Reviews, 2015, 34, 133-147.	2.8	49
7	Unrestrictive Identification of Multiple Post-translational Modifications from Tandem Mass Spectrometry Using an Error-tolerant Algorithm Based on an Extended Sequence Tag Approach. Molecular and Cellular Proteomics, 2008, 7, 2452-2463.	2.5	48
8	Quality Assessment of Tandem Mass Spectra Based on Cumulative Intensity Normalization. Journal of Proteome Research, 2006, 5, 3241-3248.	1.8	45
9	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. Journal of Proteome Research, 2015, 14, 3555-3567.	1.8	36
10	Prediction of Novel Modifications by Unrestrictive Search of Tandem Mass Spectra. Journal of Proteome Research, 2009, 8, 4418-4427.	1.8	21
11	Common Repository of FBS Proteins (cRFP) To Be Added to a Search Database for Mass Spectrometric Analysis of Cell Secretome. Journal of Proteome Research, 2019, 18, 3800-3806.	1.8	20
12	Characterization of disulfide bonds by planned digestion and tandem mass spectrometry. Molecular BioSystems, 2015, 11, 1156-1164.	2.9	19
13	CIFTER:  Automated Charge-State Determination for Peptide Tandem Mass Spectra. Analytical Chemistry, 2008, 80, 1520-1528.	3.2	18
14	Reinvestigation of Aminoacyl-TRNA Synthetase Core Complex by Affinity Purification-Mass Spectrometry Reveals TARSL2 as a Potential Member of the Complex. PLoS ONE, 2013, 8, e81734.	1.1	18
15	MODplus: Robust and Unrestrictive Identification of Post-Translational Modifications Using Mass Spectrometry. Analytical Chemistry, 2019, 91, 11324-11333.	3.2	17
16	High-throughput peptide quantification using mTRAQ reagent triplex. BMC Bioinformatics, 2011, 12, S46.	1.2	14
17	Computational methods in mass spectrometry-based structural proteomics for studying protein structure, dynamics, and interactions. Computational and Structural Biotechnology Journal, 2020, 18, 1391-1402.	1.9	14
18	Proteogenomic Approach to UTR Peptide Identification. Journal of Proteome Research, 2020, 19, 212-220.	1.8	11

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#	Article	IF	CITATIONS
19	Target-Decoy with Mass Binning: A Simple and Effective Validation Method for Shotgun Proteomics Using High Resolution Mass Spectrometry. Journal of Proteome Research, 2010, 9, 1150-1156.	1.8	10
20	deMix: Decoding Deuterated Distributions from Heterogeneous Protein States via HDX-MS. Scientific Reports, 2019, 9, 3176.	1.6	10
21	The Antibody Repertoire of Colorectal Cancer. Molecular and Cellular Proteomics, 2017, 16, 2111-2124.	2.5	8
22	Monoisotopic Mass Determination Algorithm for Selenocysteine-Containing Polypeptides from Mass Spectrometric Data Based on Theoretical Modeling of Isotopic Peak Intensity Ratios. Journal of Proteome Research, 2012, 11, 4488-4498.	1.8	7
23	Multi-species Identification of Polymorphic Peptide Variants via Propagation in Spectral Networks. Molecular and Cellular Proteomics, 2016, 15, 3501-3512.	2.5	6
24	Cataract-Associated New Mutants S175G/H181Q of βΒ2-Crystallin and P24S/S31G of γD-Crystallin Are Involved in Protein Aggregation by Structural Changes. International Journal of Molecular Sciences, 2020, 21, 6504.	1.8	4
25	Deephos: predicted spectral database search for TMT-labeled phosphopeptides and its false discovery rate estimation. Bioinformatics, 2022, 38, 2980-2987.	1.8	3
26	TIDD: tool-independent and data-dependent machine learning for peptide identification. BMC Bioinformatics, 2022, 23, 109.	1.2	2