Seungjin Na

List of Publications by Year
in descending order

26 papers	799 citations	623734 14 h-index	552781 26 g-index
27 all docs	27 docs citations	27 times ranked	1296 citing authors

#	Article	IF	Citations
1	TIDD: tool-independent and data-dependent machine learning for peptide identification. BMC Bioinformatics, 2022, 23, 109.	2.6	2
2	Deephos: predicted spectral database search for TMT-labeled phosphopeptides and its false discovery rate estimation. Bioinformatics, 2022, 38, 2980-2987.	4.1	3
3	Proteogenomic Approach to UTR Peptide Identification. Journal of Proteome Research, 2020, 19, 212-220.	3.7	11
4	Cataract-Associated New Mutants S175G/H181Q of $\beta\beta$2-Crystallin and P24S/S31G of γD-Crystallin Are Involved in Protein Aggregation by Structural Changes. International Journal of Molecular Sciences, 2020, 21, 6504.	4.1	4
5	Computational methods in mass spectrometry-based structural proteomics for studying protein structure, dynamics, and interactions. Computational and Structural Biotechnology Journal, 2020, 18, 1391-1402.	4.1	14
6	MODplus: Robust and Unrestrictive Identification of Post-Translational Modifications Using Mass Spectrometry. Analytical Chemistry, 2019, 91, 11324-11333.	6.5	17
7	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.	3.7	20
8	deMix: Decoding Deuterated Distributions from Heterogeneous Protein States via HDX-MS. Scientific Reports, 2019, 9, 3176.	3.3	10
9	The Antibody Repertoire of Colorectal Cancer. Molecular and Cellular Proteomics, 2017, 16, 2111-2124.	3.8	8
10	Multi-species Identification of Polymorphic Peptide Variants via Propagation in Spectral Networks. Molecular and Cellular Proteomics, 2016, 15, 3501-3512.	3.8	6
11	Characterization of disulfide bonds by planned digestion and tandem mass spectrometry. Molecular BioSystems, 2015, 11, 1156-1164.	2.9	19
12	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. Journal of Proteome Research, 2015, 14, 3555-3567.	3.7	36
13	Software eyes for protein post-translational modifications. Mass Spectrometry Reviews, 2015, 34, 133-147.	5.4	49
14	Proteogenomic strategies for identification of aberrant cancer peptides using large-scale next-generation sequencing data. Proteomics, 2014, 14, 2719-2730.	2.2	62
15	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.	2.5	18
16	Fast Multi-blind Modification Search through Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2012, 11, M111.010199.	3.8	143
17	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.	3.7	7
18	Novel Oxidative Modifications in Redox-Active Cysteine Residues. Molecular and Cellular Proteomics, 2011, 10, M110.000513.	3.8	79

#	ARTICLE	IF	CITATIONS
19	High-throughput peptide quantification using mTRAQ reagent triplex. BMC Bioinformatics, 2011, 12, S46.	2.6	14
20	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.	3.7	79
21	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.	3.7	10
22	Prediction of Novel Modifications by Unrestrictive Search of Tandem Mass Spectra. Journal of Proteome Research, 2009, 8, 4418-4427.	3.7	21
23	CIFTER:â€‰ Automated Charge-State Determination for Peptide Tandem Mass Spectra. Analytical Chemistry, 2008, 80, 1520-1528.	6.5	18
24	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.	3.8	48
25	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.	14.5	55
26	Quality Assessment of Tandem Mass Spectra Based on Cumulative Intensity Normalization. Journal of Proteome Research, 2006, 5, 3241-3248.	3.7	45