

Seungjin Na

List of Publications by Year in descending order

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26
papers

799
citations

623188

14
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552369

26
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27
all docs

27
docs citations

27
times ranked

1296
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast Multi-blind Modification Search through Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 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. <i>Journal of Proteome Research</i> , 2010, 9, 626-635.	1.8	79
3	Novel Oxidative Modifications in Redox-Active Cysteine Residues. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.000513.	2.5	79
4	Proteogenomic strategies for identification of aberrant cancer peptides using large-scale next-generation sequencing data. <i>Proteomics</i> , 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. <i>Nucleic Acids Research</i> , 2006, 34, W258-W263.	6.5	55
6	Software eyes for protein post-translational modifications. <i>Mass Spectrometry Reviews</i> , 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. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2452-2463.	2.5	48
8	Quality Assessment of Tandem Mass Spectra Based on Cumulative Intensity Normalization. <i>Journal of Proteome Research</i> , 2006, 5, 3241-3248.	1.8	45
9	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. <i>Journal of Proteome Research</i> , 2015, 14, 3555-3567.	1.8	36
10	Prediction of Novel Modifications by Unrestrictive Search of Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 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. <i>Journal of Proteome Research</i> , 2019, 18, 3800-3806.	1.8	20
12	Characterization of disulfide bonds by planned digestion and tandem mass spectrometry. <i>Molecular BioSystems</i> , 2015, 11, 1156-1164.	2.9	19
13	CIFTER: Automated Charge-State Determination for Peptide Tandem Mass Spectra. <i>Analytical Chemistry</i> , 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. <i>PLoS ONE</i> , 2013, 8, e81734.	1.1	18
15	MODplus: Robust and Unrestrictive Identification of Post-Translational Modifications Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 11324-11333.	3.2	17
16	High-throughput peptide quantification using mTRAQ reagent triplex. <i>BMC Bioinformatics</i> , 2011, 12, S46.	1.2	14
17	Computational methods in mass spectrometry-based structural proteomics for studying protein structure, dynamics, and interactions. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1391-1402.	1.9	14
18	Proteogenomic Approach to UTR Peptide Identification. <i>Journal of Proteome Research</i> , 2020, 19, 212-220.	1.8	11

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19	Target-Decoy with Mass Binning: A Simple and Effective Validation Method for Shotgun Proteomics Using High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 1150-1156.	1.8	10
20	deMix: Decoding Deuterated Distributions from Heterogeneous Protein States via HDX-MS. <i>Scientific Reports</i> , 2019, 9, 3176.	1.6	10
21	The Antibody Repertoire of Colorectal Cancer. <i>Molecular and Cellular Proteomics</i> , 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. <i>Journal of Proteome Research</i> , 2012, 11, 4488-4498.	1.8	7
23	Multi-species Identification of Polymorphic Peptide Variants via Propagation in Spectral Networks. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3501-3512.	2.5	6
24	Cataract-Associated New Mutants S175G/H181Q of α 2-Crystallin and P24S/S31G of β 3D-Crystallin Are Involved in Protein Aggregation by Structural Changes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6504.	1.8	4
25	DeepPhos: predicted spectral database search for TMT-labeled phosphopeptides and its false discovery rate estimation. <i>Bioinformatics</i> , 2022, 38, 2980-2987.	1.8	3
26	TIDD: tool-independent and data-dependent machine learning for peptide identification. <i>BMC Bioinformatics</i> , 2022, 23, 109.	1.2	2