# Seungjin Na

## List of Publications by Year
in descending order

| 26 | 799 | 623734 | 552781 |
|---|---|---|---|
| papers | citations | 14 | 26 |
|  |  | h-index | g-index |

| 27 | 27 | 27 | 1296 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Fast Multi-blind Modification Search through Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2012, 11, M111.010199. | 3.8 | 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. | 3.7 | 79 |
| 3 | Novel Oxidative Modifications in Redox-Active Cysteine Residues. Molecular and Cellular Proteomics, 2011, 10, M110.000513. | 3.8 | 79 |
| 4 | Proteogenomic strategies for identification of aberrant cancer peptides using large‐scale next‐generation sequencing data. Proteomics, 2014, 14, 2719-2730. | 2.2 | 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. | 14.5 | 55 |
| 6 | Software eyes for protein post‐translational modifications. Mass Spectrometry Reviews, 2015, 34, 133-147. | 5.4 | 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. | 3.8 | 48 |
| 8 | Quality Assessment of Tandem Mass Spectra Based on Cumulative Intensity Normalization. Journal of Proteome Research, 2006, 5, 3241-3248. | 3.7 | 45 |
| 9 | 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 |
| 10 | Prediction of Novel Modifications by Unrestrictive Search of Tandem Mass Spectra. Journal of Proteome Research, 2009, 8, 4418-4427. | 3.7 | 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. | 3.7 | 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. | 6.5 | 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. | 2.5 | 18 |
| 15 | MODplus: Robust and Unrestrictive Identification of Post-Translational Modifications Using Mass Spectrometry. Analytical Chemistry, 2019, 91, 11324-11333. | 6.5 | 17 |
| 16 | High-throughput peptide quantification using mTRAQ reagent triplex. BMC Bioinformatics, 2011, 12, S46. | 2.6 | 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. | 4.1 | 14 |
| 18 | Proteogenomic Approach to UTR Peptide Identification. Journal of Proteome Research, 2020, 19, 212-220. | 3.7 | 11 |

| # | 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. | 3.7 | 10 |
| 20 | deMix: Decoding Deuterated Distributions from Heterogeneous Protein States via HDX-MS. Scientific Reports, 2019, 9, 3176. | 3.3 | 10 |
| 21 | The Antibody Repertoire of Colorectal Cancer. Molecular and Cellular Proteomics, 2017, 16, 2111-2124. | 3.8 | 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. | 3.7 | 7 |
| 23 | Multi-species Identification of Polymorphic Peptide Variants via Propagation in Spectral Networks. Molecular and Cellular Proteomics, 2016, 15, 3501-3512. | 3.8 | 6 |
| 24 | Cataract-Associated New Mutants S175G/H181Q of βγ2-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 |
| 25 | Deephos: predicted spectral database search for TMT-labeled phosphopeptides and its false discovery rate estimation. Bioinformatics, 2022, 38, 2980-2987. | 4.1 | 3 |
| 26 | TIDD: tool-independent and data-dependent machine learning for peptide identification. BMC Bioinformatics, 2022, 23, 109. | 2.6 | 2 |