Sven H Giese

List of Publications by Year
in descending order

15 papers	466 citations	10 h-index	16 g-index
20 all docs	20 docs citations	20 times ranked	727 citing authors

#	Article	IF	Citations
1	An integrated workflow for crosslinking mass spectrometry. Molecular Systems Biology, 2019, 15, e8994.	7.2	120
2	A Study into the Collision-induced Dissociation (CID) Behavior of Cross-Linked Peptides. Molecular and Cellular Proteomics, 2016, 15, 1094-1104.	3.8	78
3	Specificity control for read alignments using an artificial reference genome-guided false discovery rate. Bioinformatics, 2014, 30, 9-16.	4.1	63
4	In-Search Assignment of Monoisotopic Peaks Improves the Identification of Cross-Linked Peptides. Journal of Proteome Research, 2018, 17, 3923-3931.	3.7	36
5	Optimized Fragmentation Regime for Diazirine Photo-Cross-Linked Peptides. Analytical Chemistry, 2016, 88, 8239-8247.	6.5	34
6	Complementary Benzophenone Cross-Linking/Mass Spectrometry Photochemistry. Analytical Chemistry, 2017, 89, 5319-5324.	6.5	22
7	Retention time prediction using neural networks increases identifications in crosslinking mass spectrometry. Nature Communications, 2021, 12, 3237.	12.8	22
8	Noncovalently Associated Peptides Observed during Liquid Chromatography-Mass Spectrometry and Their Effect on Cross-Link Analyses. Analytical Chemistry, 2019, 91, 2678-2685.	6.5	19
9	Phosphoproteomic Analysis of Aurora Kinase Inhibition in Monopolar Cytokinesis. Journal of Proteome Research, 2015, 14, 4087-4098.	3.7	14
10	Peptide Retention in Hydrophilic Strong Anion Exchange Chromatography Is Driven by Charged and Aromatic Residues. Analytical Chemistry, 2018, 90, 4635-4640.	6.5	13
11	Ad hoc learning of peptide fragmentation from mass spectra enables an interpretable detection of phosphorylated and cross-linked peptides. Nature Machine Intelligence, 2022, 4, 378-388.	16.0	10
12	Comparative phosphoproteomic analysis reveals signaling networks regulating monopolar and bipolar cytokinesis. Scientific Reports, 2018, 8, 2269.	3.3	9
13	Leveraging Parameter Dependencies in High-Field Asymmetric Waveform Ion-Mobility Spectrometry and Size Exclusion Chromatography for Proteome-wide Cross-Linking Mass Spectrometry. Analytical Chemistry, 2022, 94, 4627-4634.	6.5	6
14	CovRadar: continuously tracking and filtering SARS-CoV-2 mutations for genomic surveillance. Bioinformatics, 2022, 38, 4223-4225.	4.1	4
15	Detection of Unknown Amino Acid Substitutions Using Error-Tolerant Database Search. Methods in Molecular Biology, 2016, 1362, 247-264.	0.9	3