

Ole Vorm

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

13
papers

8,957
citations

9
h-index

13
g-index

13
ext. papers

9,472
ext. citations

5
avg, IF

5.5
L-index

#	Paper	IF	Citations
13	Mass spectrometric sequencing of proteins silver-stained polyacrylamide gels. <i>Analytical Chemistry</i> , 1996 , 68, 850-8	7.8	7831
12	Improved Resolution and Very High Sensitivity in MALDI TOF of Matrix Surfaces Made by Fast Evaporation. <i>Analytical Chemistry</i> , 1994 , 66, 3281-3287	7.8	624
11	A Novel LC System Embeds Analytes in Pre-formed Gradients for Rapid, Ultra-robust Proteomics. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2284-2296	7.6	133
10	Improved mass accuracy in matrix-assisted laser desorption/ionization time-of-flight mass spectrometry of peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 1994 , 5, 955-8	3.5	127
9	Automation of matrix-assisted laser desorption/ionization mass spectrometry using fuzzy logic feedback control. <i>Analytical Chemistry</i> , 1997 , 69, 1706-14	7.8	86
8	Sequence patterns produced by incomplete enzymatic digestion or one-step Edman degradation of peptide mixtures as probes for protein database searches. <i>Electrophoresis</i> , 1996 , 17, 938-44	3.6	52
7	Peptide sequence information derived by partial acid hydrolysis and matrix-assisted laser desorption/ionization mass spectrometry. <i>Biological Mass Spectrometry</i> , 1994 , 23, 734-40		49
6	Integrated solid-phase extraction-capillary liquid chromatography (speLC) interfaced to ESI-MS/MS for fast characterization and quantification of protein and proteomes. <i>Journal of Proteome Research</i> , 2014 , 13, 6169-75	5.6	18
5	Detector Bias Gating for Improved Detector Response and Calibration in Matrix-assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry. <i>Journal of Mass Spectrometry</i> , 1996 , 31, 351-356 ²		15
4	Solid phase extraction-liquid chromatography (SPE-LC) interface for automated peptide separation and identification by tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2007 , 268, 147-157	1.9	9
3	Isocratic solid phase extraction-liquid chromatography (SPE-LC) interfaced to high-performance tandem mass spectrometry for rapid protein identification. <i>Journal of Proteome Research</i> , 2008 , 7, 3159-67 ^{5,6}		7
2	Synthesis and characterization of a 25-residue rubredoxin(II)-like metalloprotein and its valine-leucine mutant. <i>FEBS Letters</i> , 1992 , 312, 219-22	3.8	4
1	A novel LC system embeds analytes in pre-formed gradients for rapid, ultra-robust proteomics		2