

Ole Vorm

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/11098248/ole-vorm-publications-by-year.pdf>
Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
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	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
12	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
11	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
10	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
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	Mass spectrometric sequencing of proteins silver-stained polyacrylamide gels. <i>Analytical Chemistry</i> , 1996 , 68, 850-8	7.8	7831
7	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
6	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	3.2	15
5	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
4	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
3	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
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