

Johannes P C Vissers

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

4,548
citations

201674

27
h-index

144013

57
g-index

60
all docs

60
docs citations

60
times ranked

6255
citing authors

#	ARTICLE	IF	CITATIONS
1	Absolute Quantification of Proteins by LCMSE. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 144-156.	3.8	1,349
2	Database searching and accounting of multiplexed precursor and product ion spectra from the data independent analysis of simple and complex peptide mixtures. <i>Proteomics</i> , 2009, 9, 1696-1719.	2.2	521
3	The detection, correlation, and comparison of peptide precursor and product ions from data independent LC-MS with data dependant LC-MS/MS. <i>Proteomics</i> , 2009, 9, 1683-1695.	2.2	460
4	Microcolumn liquid chromatography: instrumentation, detection and applications. <i>Journal of Chromatography A</i> , 1997, 779, 1-28.	3.7	199
5	Recent developments in microcolumn liquid chromatography. <i>Journal of Chromatography A</i> , 1999, 856, 117-143.	3.7	175
6	Analysis and Quantification of Diagnostic Serum Markers and Protein Signatures for Gaucher Disease. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 755-766.	3.8	123
7	Mass spectrometry proteomic analysis of stress adaptation reveals both common and distinct response pathways in <i>Propionibacterium freudenreichii</i> . <i>Archives of Microbiology</i> , 2004, 181, 215-230.	2.2	100
8	Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3709-3715.	3.8	98
9	A proteome approach defines protective functions of tobacco leaf trichomes. <i>Proteomics</i> , 2005, 5, 2508-2518.	2.2	85
10	Binding of the AVR4 Elicitor of <i>Cladosporium fulvum</i> to Chitotriose Units Is Facilitated by Positive Allosteric Protein-Protein Interactions. <i>Journal of Biological Chemistry</i> , 2004, 279, 16786-16796.	3.4	83
11	Alignment and statistical difference analysis of complex peptide data sets generated by multidimensional LC-MS. <i>Proteomics</i> , 2006, 6, 641-653.	2.2	81
12	Survey of bacterial proteins released in cheese: a proteomic approach. <i>International Journal of Food Microbiology</i> , 2004, 94, 185-201.	4.7	80
13	Scanning Quadrupole Data-Independent Acquisition, Part A: Qualitative and Quantitative Characterization. <i>Journal of Proteome Research</i> , 2018, 17, 770-779.	3.7	62
14	Using ion purity scores for enhancing quantitative accuracy and precision in complex proteomics samples. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1127-1139.	3.7	59
15	Elevation of glycoprotein nonmetastatic melanoma protein B in type 1 Gaucher disease patients and mouse models. <i>FEBS Open Bio</i> , 2016, 6, 902-913.	2.3	59
16	Colloid Chemical Aspects of Slurry Packing Techniques in Microcolumn Liquid Chromatography. <i>Analytical Chemistry</i> , 1995, 67, 2103-2109.	6.5	52
17	Screening for anabolic steroids and related compounds in illegal cocktails by liquid chromatography/time-of-flight mass spectrometry and liquid chromatography/quadrupole time-of-flight tandem mass spectrometry with accurate mass measurement. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1577-1585.	1.5	52
18	Optimised injection techniques for micro and capillary liquid chromatography. <i>Journal of Chromatography A</i> , 1996, 746, 1-7.	3.7	47

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19	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
20	Label-free mass spectrometric profiling of urinary proteins and metabolites from paediatric idiopathic nephrotic syndrome. <i>Biochemical and Biophysical Research Communications</i> , 2014, 452, 21-26.	2.1	36
21	Nonionic detergent phase extraction for the proteomic analysis of heart membrane proteins using label-free LC-MS. <i>Proteomics</i> , 2008, 8, 3895-3905.	2.2	34
22	Simulating and validating proteomics data and search results. <i>Proteomics</i> , 2011, 11, 1189-1211.	2.2	34
23	A comparison of collision cross section values obtained via travelling wave ion mobility-mass spectrometry and ultra high performance liquid chromatography-ion mobility-mass spectrometry: Application to the characterisation of metabolites in rat urine. <i>Journal of Chromatography A</i> , 2019, 1602, 386-396.	3.7	34
24	Protein Markers for Insulin-Producing Beta Cells with Higher Glucose Sensitivity. <i>PLoS ONE</i> , 2010, 5, e14214.	2.5	33
25	Calculation of retention factors in capillary electrochromatography from chromatographic and electrophoretic data. <i>Journal of High Resolution Chromatography</i> , 1995, 18, 540-544.	1.4	31
26	Sodium Dodecyl Sulphate Removal from Tryptic Digest Samples for On-line Capillary Liquid Chromatography/Electrospray Mass Spectrometry. , 1996, 31, 1021-1027.		31
27	Towards a proteome signature for invasive ductal breast carcinoma derived from label-free nanoscale LC-MS protein expression profiling of tumorous and glandular tissue. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 395, 2443-2456.	3.7	31
28	Gaucher disease: a model disorder for biomarker discovery. <i>Expert Review of Proteomics</i> , 2009, 6, 411-419.	3.0	31
29	Quantitative Proteome Analysis of Mouse Liver Lysosomes Provides Evidence for Mannose 6-phosphate-independent Targeting Mechanisms of Acid Hydrolases in Mucopolipidosis II. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 438-450.	3.8	30
30	Cov-MS: A Community-Based Template Assay for Mass-Spectrometry-Based Protein Detection in SARS-CoV-2 Patients. <i>Jacs Au</i> , 2021, 1, 750-765.	7.9	29
31	A novel Interface for variable flow nanoscale LC/MS/MS for improved proteome coverage. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 760-771.	2.8	28
32	An Ion Mobility Assisted Data Independent LC-MS Strategy for the Analysis of Complex Biological Samples. <i>Current Analytical Chemistry</i> , 2013, 9, 199-211.	1.2	27
33	Asymmetric Proteome Equalization of the Skeletal Muscle Proteome Using a Combinatorial Hexapeptide Library. <i>PLoS ONE</i> , 2011, 6, e28902.	2.5	25
34	Two-dimensional capillary liquid chromatography based on microfractionation. <i>Journal of Separation Science</i> , 1999, 11, 277-286.	1.0	23
35	Application of Predicted Collisional Cross Section to Metabolome Databases to Probabilistically Describe the Current and Future Ion Mobility Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 661-669.	2.8	23
36	The use of proteome similarity for the qualitative and quantitative profiling of reperfused myocardium. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 1317-1326.	2.3	22

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37	Hydrodynamic aspects of slurry packing processes in microcolumn liquid chromatography. <i>Journal of Chromatography A</i> , 2000, 883, 11-25.	3.7	20
38	Characterisation of glycoproteins using a quadrupole time-of-flight mass spectrometer configured for electron transfer dissociation. <i>Rapid Communications in Mass Spectrometry</i> , 2013, 27, 2383-2390.	1.5	20
39	Accuracy and Reproducibility in Quantification of Plasma Protein Concentrations by Mass Spectrometry without the Use of Isotopic Standards. <i>PLoS ONE</i> , 2015, 10, e0140097.	2.5	20
40	Rapid and sensitive detection of SARS-CoV-2 infection using quantitative peptide enrichment LC-MS analysis. <i>ELife</i> , 2021, 10, .	6.0	20
41	Qualitative and Quantitative Proteomic Profiling of Cripto ⁺ Embryonic Stem Cells by Means of Accurate Mass LC-MS Analysis. <i>Journal of Proteome Research</i> , 2009, 8, 1047-1058.	3.7	19
42	Proteomic Profiling of Proliferating and Differentiated Neural mes-c-myc A1 Cell Line from Mouse Embryonic Mesencephalon by LC-MS. <i>Journal of Proteome Research</i> , 2009, 8, 227-238.	3.7	19
43	Determination of Protein Haptenation by Chemical Sensitizers Within the Complexity of the Human Skin Proteome. <i>Toxicological Sciences</i> , 2018, 162, 429-438.	3.1	19
44	Lipid profiling of complex biological mixtures by liquid chromatography/mass spectrometry using a novel scanning quadrupole data-independent acquisition strategy. <i>Rapid Communications in Mass Spectrometry</i> , 2017, 31, 1599-1606.	1.5	18
45	Verification of a Parkinson's Disease Protein Signature in T-Lymphocytes by Multiple Reaction Monitoring. <i>Journal of Proteome Research</i> , 2014, 13, 3554-3561.	3.7	17
46	Scanning Quadrupole Data-Independent Acquisition, Part B: Application to the Analysis of the Calcineurin-Interacting Proteins during Treatment of <i>Aspergillus fumigatus</i> with Azole and Echinocandin Antifungal Drugs. <i>Journal of Proteome Research</i> , 2018, 17, 780-793.	3.7	17
47	Advances in quadrupole and time-of-flight mass spectrometry for peptide MRM based translational research analysis. <i>Proteomics</i> , 2016, 16, 2206-2220.	2.2	16
48	A Probabilistic Framework for Peptide and Protein Quantification from Data-Dependent and Data-Independent LC-MS Proteomics Experiments. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 468-482.	2.0	13
49	Design and Application of a Data-Independent Precursor and Product Ion Repository. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1808-1820.	2.8	13
50	Use of Cyclic Ion Mobility Spectrometry (cIM)-Mass Spectrometry to Study the Intramolecular Transacylation of Diclofenac Acyl Glucuronide. <i>Analytical Chemistry</i> , 2021, 93, 7413-7421.	6.5	13
51	Multi-mode acquisition (MMA): An MS/MS acquisition strategy for maximizing selectivity, specificity and sensitivity of DIA product ion spectra. <i>Proteomics</i> , 2016, 16, 2284-2301.	2.2	12
52	Profiling of the known-unknown <i>Passiflora</i> variant complement by liquid chromatography - ion mobility - Mass spectrometry. <i>Talanta</i> , 2021, 221, 121311.	5.5	12
53	Sedimentation behaviour and colloidal properties of porous, chemically modified silicas in non-aqueous solvents. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 1997, 126, 33-44.	4.7	11
54	Investigation into Small Molecule Isomeric Glucuronide Metabolite Differentiation Using In Silico and Experimental Collision Cross-Section Values. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1976-1986.	2.8	11

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55	Comparison of spherically and irregularly shaped stationary phase packings in microcolumn liquid chromatography. <i>Journal of Separation Science</i> , 1995, 7, 239-245.	1.0	9
56	An Ion Mobility Assisted Data Independent LC-MS Strategy for the Analysis of Complex Biological Samples. <i>Current Analytical Chemistry</i> , 2013, 9, 199-211.	1.2	5
57	Plasma biomarker identification in <i>S</i> -adenosylhomocysteine hydrolase deficiency. <i>Electrophoresis</i> , 2011, 32, 1970-1975.	2.4	3
58	Evaluation of acquisition modes for semi-quantitative analysis by targeted and untargeted mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2022, 36, e9308.	1.5	3