

# Af Maarten Altelaar

## List of Publications by Year in descending order

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123  
papers

7,437  
citations

57758

44  
h-index

64796

79  
g-index

137  
all docs

137  
docs citations

137  
times ranked

10963  
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated High-Throughput Method for the Fast, Robust, and Reproducible Enrichment of Newly Synthesized Proteins. <i>Journal of Proteome Research</i> , 2022, 21, 189-199.	3.7	8
2	Combined Quantitative (Phospho)proteomics and Mass Spectrometry Imaging Reveal Temporal and Spatial Protein Changes in Human Intestinal Ischemiaâ€“Reperfusion. <i>Journal of Proteome Research</i> , 2022, 21, 49-66.	3.7	11
3	Angiotensin isoform 2 promotes binding of PALS1 to KIF13B at primary cilia and regulates ciliary length and signaling. <i>Journal of Cell Science</i> , 2022, 135, .	2.0	6
4	The encephalomyocarditis virus Leader promotes the release of virions inside extracellular vesicles via the induction of secretory autophagy. <i>Nature Communications</i> , 2022, 13, .	12.8	11
5	Drug-Induced Epigenomic Plasticity Reprograms Circadian Rhythm Regulation to Drive Prostate Cancer toward Androgen Independence. <i>Cancer Discovery</i> , 2022, 12, 2074-2097.	9.4	22
6	Anti-tumour immunity induces aberrant peptide presentation in melanoma. <i>Nature</i> , 2021, 590, 332-337.	27.8	81
7	Neuroproteomics of the Synapse: Subcellular Quantification of Protein Networks and Signaling Dynamics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100087.	3.8	7
8	The Role of Pseudo-Orthocaspase (SyOC) of <i>Synechocystis</i> sp. PCC 6803 in Attenuating the Effect of Oxidative Stress. <i>Frontiers in Microbiology</i> , 2021, 12, 634366.	3.5	4
9	Centrosomeâ€“mediated microtubule remodeling during axon formation in human iPSCâ€“derived neurons. <i>EMBO Journal</i> , 2021, 40, e106798.	7.8	8
10	MAPK-ERK is a central pathway in T-cell acute lymphoblastic leukemia that drives steroid resistance. <i>Leukemia</i> , 2021, 35, 3394-3405.	7.2	28
11	Cysteamineâ€“bicalutamide combination therapy corrects proximal tubule phenotype in cystinosis. <i>EMBO Molecular Medicine</i> , 2021, 13, e13067.	6.9	23
12	Proteomics and Phosphoproteomics Profiling of Drug-Addicted BRAFi-Resistant Melanoma Cells. <i>Journal of Proteome Research</i> , 2021, 20, 4381-4392.	3.7	3
13	Multistep mechanism of G-quadruplex resolution during DNA replication. <i>Science Advances</i> , 2021, 7, eabf8653.	10.3	29
14	Quantifying Positional Isomers (QPI) by Top-Down Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100070.	3.8	1
15	Smooth muscle-specific MMP17 (MT4-MMP) regulates the intestinal stem cell niche and regeneration after damage. <i>Nature Communications</i> , 2021, 12, 6741.	12.8	26
16	Elucidation of the pre-nucleation phase directing metal-organic framework formation. <i>Cell Reports Physical Science</i> , 2021, 2, 100680.	5.6	11
17	Spinal Muscular Atrophy Patient iPSC-Derived Motor Neurons Display Altered Proteomes at Early Stages of Differentiation. <i>ACS Omega</i> , 2021, 6, 35375-35388.	3.5	9
18	Combined EGFR and ROCK Inhibition in Triple-negative Breast Cancer Leads to Cell Death Via Impaired Autophagic Flux. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 261-277.	3.8	14

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19	Effects of electron-transfer/higher-energy collisional dissociation (ETHcD) on phosphopeptide analysis by data-independent acquisition. <i>International Journal of Mass Spectrometry</i> , 2020, 452, 116336.	1.5	1
20	Temporal Quantitative Proteomics of mGluR-induced Protein Translation and Phosphorylation in Neurons. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1952-1968.	3.8	12
21	Quantitative proteomic analysis of Rett iPSC-derived neuronal progenitors. <i>Molecular Autism</i> , 2020, 11, 38.	4.9	14
22	Deciphering the Proteome Dynamics during Development of Neurons Derived from Induced Pluripotent Stem Cells. <i>Journal of Proteome Research</i> , 2020, 19, 2391-2403.	3.7	14
23	Tumour kinome re-wiring governs resistance to palbociclib in oestrogen receptor positive breast cancers, highlighting new therapeutic modalities. <i>Oncogene</i> , 2020, 39, 4781-4797.	5.9	52
24	Arginine Î€-stacking drives binding to fibrils of the Alzheimer protein Tau. <i>Nature Communications</i> , 2020, 11, 571.	12.8	28
25	Quantitative mapping of transcriptome and proteome dynamics during polarization of human iPSC-derived neurons. <i>ELife</i> , 2020, 9, .	6.0	14
26	Actin from the apicomplexan <i>Neospora caninum</i> (NcACT) has different isoforms in 2D electrophoresis. <i>Parasitology</i> , 2019, 146, 33-41.	1.5	2
27	Crystal structure of the tubulin tyrosine carboxypeptidase complex VASH1Î€SVBP. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 567-570.	8.2	28
28	VAPÎ€SCRN1 interaction regulates dynamic endoplasmic reticulum remodeling and presynaptic function. <i>EMBO Journal</i> , 2019, 38, e101345.	7.8	53
29	Feedback-Driven Assembly of the Axon Initial Segment. <i>Neuron</i> , 2019, 104, 305-321.e8.	8.1	54
30	High-Throughput Assessment of Kinome-wide Activation States. <i>Cell Systems</i> , 2019, 9, 366-374.e5.	6.2	33
31	Conserved crosstalk between histone deacetylation and H3K79 methylation generates DOT1LÎ€dose dependency in HDAC1Î€deficient thymic lymphoma. <i>EMBO Journal</i> , 2019, 38, e101564.	7.8	28
32	MAP7 family proteins regulate kinesin-1 recruitment and activation. <i>Journal of Cell Biology</i> , 2019, 218, 1298-1318.	5.2	114
33	Feedback-Driven Mechanisms between Microtubules and the Endoplasmic Reticulum Instruct Neuronal Polarity. <i>Neuron</i> , 2019, 102, 184-201.e8.	8.1	68
34	Identification of a tumor-specific allo-HLAÎ€restricted Î³Î€TCR. <i>Blood Advances</i> , 2019, 3, 2870-2882.	5.2	28
35	Feeding cycle alters the biophysics and molecular expression of voltageÎ€gated Na + currents in rat hippocampal CA1 neurones. <i>European Journal of Neuroscience</i> , 2019, 49, 1418-1435.	2.6	0
36	PaDuA: A Python Library for High-Throughput (Phospho)proteomics Data Analysis. <i>Journal of Proteome Research</i> , 2019, 18, 576-584.	3.7	15

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37	The physiology of <i>Agaricus bisporus</i> in semi-commercial compost cultivation appears to be highly conserved among unrelated isolates. <i>Fungal Genetics and Biology</i> , 2018, 112, 12-20.	2.1	9
38	Nedd4-Binding Protein 1 and TNFAIP3-Interacting Protein 1 Control MHC-1 Display in Neuroblastoma. <i>Cancer Research</i> , 2018, 78, 6621-6631.	0.9	42
39	In vivo phosphoproteomics reveals kinase activity profiles that predict treatment outcome in triple-negative breast cancer. <i>Nature Communications</i> , 2018, 9, 3501.	12.8	45
40	A System-wide Approach to Monitor Responses to Synergistic BRAF and EGFR Inhibition in Colorectal Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1892-1908.	3.8	13
41	The HAUS Complex Is a Key Regulator of Non-centrosomal Microtubule Organization during Neuronal Development. <i>Cell Reports</i> , 2018, 24, 791-800.	6.4	75
42	Membrane-Depolarizing Channel Blockers Induce Selective Glioma Cell Death by Impairing Nutrient Transport and Unfolded Protein/Amino Acid Responses. <i>Cancer Research</i> , 2017, 77, 1741-1752.	0.9	21
43	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , 2017, 18, 1527-1542.	6.4	79
44	Robust, Sensitive, and Automated Phosphopeptide Enrichment Optimized for Low Sample Amounts Applied to Primary Hippocampal Neurons. <i>Journal of Proteome Research</i> , 2017, 16, 728-737.	3.7	117
45	Vasohibins encode tubulin detyrosinating activity. <i>Science</i> , 2017, 358, 1453-1456.	12.6	185
46	Opposite Electron-Transfer Dissociation and Higher-Energy Collisional Dissociation Fragmentation Characteristics of Proteolytic K/R(X) <sub>n</sub> and (X) <sub>n</sub> /K/R Peptides Provide Benefits for Peptide Sequencing in Proteomics and Phosphoproteomics. <i>Journal of Proteome Research</i> , 2017, 16, 852-861.	3.7	21
47	Association of Cell Adhesion Molecules Contactin-6 and Latrophilin-1 Regulates Neuronal Apoptosis. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 143.	2.9	28
48	Assessment of SRM, MRM <sup>3</sup> , and DIA for the targeted analysis of phosphorylation dynamics in non-small cell lung cancer. <i>Proteomics</i> , 2016, 16, 2193-2205.	2.2	53
49	BRAF V600E Kinase Domain Duplication Identified in Therapy-Refractory Melanoma Patient-Derived Xenografts. <i>Cell Reports</i> , 2016, 16, 263-277.	6.4	61
50	Monitoring light/dark association dynamics of multi-protein complexes in cyanobacteria using size exclusion chromatography-based proteomics. <i>Journal of Proteomics</i> , 2016, 142, 33-44.	2.4	12
51	Molecular Pathway of Microtubule Organization at the Golgi Apparatus. <i>Developmental Cell</i> , 2016, 39, 44-60.	7.0	114
52	Comprehensive Proteomic Analysis of Human Milk-derived Extracellular Vesicles Unveils a Novel Functional Proteome Distinct from Other Milk Components. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3412-3423.	3.8	129
53	Mast Cell Degranulation Is Accompanied by the Release of a Selective Subset of Extracellular Vesicles That Contain Mast Cell-Specific Proteases. <i>Journal of Immunology</i> , 2016, 197, 3382-3392.	0.8	49
54	Quantitative Proteomics Illuminates a Functional Interaction between mDia2 and the Proteasome. <i>Journal of Proteome Research</i> , 2016, 15, 4624-4637.	3.7	11

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55	Differential proteomics reveals the hallmarks of seed development in common bean ( <i>Phaseolus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.4	23
56	Talin-KANK1 interaction controls the recruitment of cortical microtubule stabilizing complexes to focal adhesions. <i>ELife</i> , 2016, 5, .	6.0	150
57	Direct screening for chromatin status on DNA barcodes in yeast delineates the regulome of H3K79 methylation by Dot1. <i>ELife</i> , 2016, 5, .	6.0	22
58	Myc coordinates transcription and translation to enhance transformation and suppress invasiveness. <i>EMBO Reports</i> , 2015, 16, 1723-1736.	4.5	42
59	Uncovering the abilities of <i>Agaricus bisporus</i> to degrade plant biomass throughout its life cycle. <i>Environmental Microbiology</i> , 2015, 17, 3098-3109.	3.8	49
60	Cooperative induction of apoptosis in <i>NRAS</i> mutant melanoma by inhibition of <i>MEK</i> and <i>ROCK</i> . <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 307-317.	3.3	41
61	Signal Transduction Reaction Monitoring Deciphers Site-Specific PI3K-mTOR/MAPK Pathway Dynamics in Oncogene-Induced Senescence. <i>Journal of Proteome Research</i> , 2015, 14, 2906-2914.	3.7	33
62	<i>N</i> -lactoyl-amino acids are ubiquitous metabolites that originate from CNDP2-mediated reverse proteolysis of lactate and amino acids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6601-6606.	7.1	63
63	Dot1 histone methyltransferases share a distributive mechanism but have highly diverged catalytic properties. <i>Scientific Reports</i> , 2015, 5, 9824.	3.3	15
64	TRIM46 Controls Neuronal Polarity and Axon Specification by Driving the Formation of Parallel Microtubule Arrays. <i>Neuron</i> , 2015, 88, 1208-1226.	8.1	170
65	Proteomic Analyses Uncover a New Function and Mode of Action for Mouse Homolog of Diaphanous 2 (mDia2)*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1064-1078.	3.8	20
66	Identification of Putative Substrates for the Periplasmic Chaperone YfgM in <i>Escherichia coli</i> Using Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 216-226.	3.8	14
67	<i>De novo</i> discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , 2015, 235, 3-13.	4.5	116
68	Benchmarking Multiple Fragmentation Methods on an Orbitrap Fusion for Top-down Phospho-Proteoform Characterization. <i>Analytical Chemistry</i> , 2015, 87, 4152-4158.	6.5	99
69	PhosphoPath: Visualization of Phosphosite-centric Dynamics in Temporal Molecular Networks. <i>Journal of Proteome Research</i> , 2015, 14, 4332-4341.	3.7	56
70	Diet-Induced Neuropeptide Expression: Feasibility of Quantifying Extended and Highly Charged Endogenous Peptide Sequences by Selected Reaction Monitoring. <i>Analytical Chemistry</i> , 2015, 87, 9966-9973.	6.5	8
71	Coordination of peptidoglycan synthesis and outer membrane constriction during <i>Escherichia coli</i> cell division. <i>ELife</i> , 2015, 4, .	6.0	154
72	Daily Rhythms in the Cyanobacterium <i>Synechococcus elongatus</i> Probed by High-resolution Mass Spectrometry-based Proteomics Reveals a Small Defined Set of Cyclic Proteins. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2042-2055.	3.8	83

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73	Protein acetylation affects acetate metabolism, motility and acid stress response in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2014, 10, 762.	7.2	159
74	ROCK1 is a potential combinatorial drug target for BRAF mutant melanoma. <i>Molecular Systems Biology</i> , 2014, 10, 772.	7.2	48
75	Microtubule Minus-End Stabilization by Polymerization-Driven CAMSAP Deposition. <i>Developmental Cell</i> , 2014, 28, 295-309.	7.0	235
76	Phosphoproteome Dynamics in Onset and Maintenance of Oncogene-induced Senescence. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2089-2100.	3.8	11
77	Similar is not the same: Differences in the function of the (hemi-)cellulolytic regulator XlnR (Xlr1/Xyr1) in filamentous fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 73-81.	2.1	80
78	Flexibility in crosstalk between H2B ubiquitination and H3 methylation <i>in vivo</i> . <i>EMBO Reports</i> , 2014, 15, 1077-1084.	4.5	34
79	Single-step Enrichment by Ti4+-IMAC and Label-free Quantitation Enables In-depth Monitoring of Phosphorylation Dynamics with High Reproducibility and Temporal Resolution. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2426-2434.	3.8	89
80	Flexibility in crosstalk between H2B ubiquitination and H3 methylation <i>in vivo</i> . <i>EMBO Reports</i> , 2014, 15, 1220-1221.	4.5	4
81	Deletion of <i>flbA</i> Results in Increased Secretome Complexity and Reduced Secretion Heterogeneity in Colonies of <i>Aspergillus niger</i> . <i>Journal of Proteome Research</i> , 2013, 12, 1808-1819.	3.7	49
82	Profiling of Diet-Induced Neuropeptide Changes in Rat Brain by Quantitative Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 4594-4604.	6.5	24
83	Next-generation proteomics: towards an integrative view of proteome dynamics. <i>Nature Reviews Genetics</i> , 2013, 14, 35-48.	16.3	656
84	Deep proteome profiling of <i>Trichoplax adhaerens</i> reveals remarkable features at the origin of metazoan multicellularity. <i>Nature Communications</i> , 2013, 4, 1408.	12.8	50
85	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , 2013, 88, 14-26.	2.4	112
86	A central role for TFIID in the pluripotent transcription circuitry. <i>Nature</i> , 2013, 495, 516-519.	27.8	73
87	Unambiguous Phosphosite Localization using Electron-Transfer/Higher-Energy Collision Dissociation (EThcD). <i>Journal of Proteome Research</i> , 2013, 12, 1520-1525.	3.7	145
88	Imaging Mass Spectrometry-based Molecular Histology Differentiates Microscopically Identical and Heterogeneous Tumors. <i>Journal of Proteome Research</i> , 2013, 12, 1847-1855.	3.7	24
89	Quantitative global phosphoproteomics of human umbilical vein endothelial cells after activation of the Rap signaling pathway. <i>Molecular BioSystems</i> , 2013, 9, 732.	2.9	8
90	Characterization of Electron Transfer Dissociation in the Orbitrap Velos HCD Cell. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1663-1670.	2.8	5

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91	Spatio-temporal Analysis of Molecular Determinants of Neuronal Degeneration in the Aging Mouse Cerebellum. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1350-1362.	3.8	28
92	Unravelling the <i>Neospora caninum</i> secretome through the secreted fraction (ESA) and quantification of the discharged tachyzoite using high-resolution mass spectrometry-based proteomics. <i>Parasites and Vectors</i> , 2013, 6, 335.	2.5	15
93	Database independent proteomics analysis of the ostrich and human proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 407-412.	7.1	13
94	Toward Full Peptide Sequence Coverage by Dual Fragmentation Combining Electron-Transfer and Higher-Energy Collision Dissociation Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 9668-9673.	6.5	246
95	Spatially Resolving the Secretome within the Mycelium of the Cell Factory <i>Aspergillus niger</i> . <i>Journal of Proteome Research</i> , 2012, 11, 2807-2818.	3.7	41
96	Trends in ultrasensitive proteomics. <i>Current Opinion in Chemical Biology</i> , 2012, 16, 206-213.	6.1	134
97	Probing the Proteome Response to Toluene Exposure in the Solvent Tolerant <i>Pseudomonas putida</i> S12. <i>Journal of Proteome Research</i> , 2011, 10, 394-403.	3.7	44
98	Improved Peptide Identification by Targeted Fragmentation Using CID, HCD and ETD on an LTQ-Orbitrap Velos. <i>Journal of Proteome Research</i> , 2011, 10, 2377-2388.	3.7	277
99	Progressive methylation of ageing histones by Dot1 functions as a timer. <i>EMBO Reports</i> , 2011, 12, 956-962.	4.5	56
100	Improving SRM Assay Development: A Global Comparison between Triple Quadrupole, Ion Trap, and Higher Energy CID Peptide Fragmentation Spectra. <i>Journal of Proteome Research</i> , 2011, 10, 4334-4341.	3.7	90
101	Protein signatures associated with tumor cell dissemination in head and neck cancer. <i>Journal of Proteomics</i> , 2011, 74, 558-566.	2.4	21
102	Comparative Assessment of Site Assignments in CID and Electron Transfer Dissociation Spectra of Phosphopeptides Discloses Limited Relocation of Phosphate Groups. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2140-2148.	3.8	42
103	Dimethyl isotope labeling assisted de novo peptide sequencing. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1957-1965.	2.8	25
104	Gaining efficiency by parallel quantification and identification of iTRAQ-labeled peptides using HCD and decision tree guided CID/ETD on an LTQ Orbitrap. <i>Analyst</i> , 2010, 135, 2643.	3.5	12
105	Cellular Imaging Using Matrix-Enhanced and Metal-Assisted SIMS. <i>Methods in Molecular Biology</i> , 2010, 656, 197-208.	0.9	15
106	Strong Cation Exchange-based Fractionation of Lys-N-generated Peptides Facilitates the Targeted Analysis of Post-translational Modifications. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 190-200.	3.8	69
107	Fast and automated large-area imaging MALDI mass spectrometry in microprobe and microscope mode. <i>International Journal of Mass Spectrometry</i> , 2009, 285, 19-25.	1.5	37
108	Improved Identification of Endogenous Peptides from Murine Nervous Tissue by Multiplexed Peptide Extraction Methods and Multiplexed Mass Spectrometric Analysis. <i>Journal of Proteome Research</i> , 2009, 8, 870-876.	3.7	25

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109	In-Depth Profiling of Post-Translational Modifications on the Related Transcription Factor Complexes TFIIID and SAGA. <i>Journal of Proteome Research</i> , 2009, 8, 5020-5030.	3.7	28
110	Straightforward and de Novo Peptide Sequencing by MALDI-MS/MS Using a Lys-N Metalloendopeptidase. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 650-660.	3.8	42
111	Tissue Analysis with High-Resolution Imaging Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2009, 492, 295-308.	0.9	3
112	Automated, feature-based image alignment for high-resolution imaging mass spectrometry of large biological samples. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 823-832.	2.8	34
113	Cooperative action of NC2 and Mot1p to regulate TATA-binding protein function across the genome. <i>Genes and Development</i> , 2008, 22, 2359-2369.	5.9	66
114	Imaging mass spectrometry at cellular length scales. <i>Nature Protocols</i> , 2007, 2, 1185-1196.	12.0	108
115	High-resolution MALDI imaging mass spectrometry allows localization of peptide distributions at cellular length scales in pituitary tissue sections. <i>International Journal of Mass Spectrometry</i> , 2007, 260, 203-211.	1.5	107
116	Imaging of peptides in the rat brain using MALDI-FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 145-151.	2.8	144
117	Gold-Enhanced Biomolecular Surface Imaging of Cells and Tissue by SIMS and MALDI Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 734-742.	6.5	273
118	High Resolution Mass Spectrometric Imaging of Cells and Tissue: MALDI and Surface Enhanced SIMS Put to Work. <i>Microscopy and Microanalysis</i> , 2006, 12, 1210-1211.	0.4	0
119	Why don't biologists use SIMS?. <i>Applied Surface Science</i> , 2006, 252, 6827-6835.	6.1	104
120	The influence of the cholesterol microenvironment in tissue sections on molecular ionization efficiencies and distributions in ToF-SIMS. <i>Applied Surface Science</i> , 2006, 252, 6702-6705.	6.1	13
121	Subcellular imaging mass spectrometry of brain tissue. <i>Journal of Mass Spectrometry</i> , 2005, 40, 160-168.	1.6	173
122	Direct Molecular Imaging of <i>Lymnaea stagnalis</i> Nervous Tissue at Subcellular Spatial Resolution by Mass Spectrometry. <i>Analytical Chemistry</i> , 2005, 77, 735-741.	6.5	182
123	Determination of polycyclic aromatic hydrocarbons and polycyclic aromatic sulfur heterocycles by high-performance liquid chromatography with fluorescence and atmospheric pressure chemical ionization mass spectrometry detection in seawater and sediment samples. <i>Journal of Chromatography A</i> , 2002, 958, 141-148.	3.7	47