

# Af Maarten Altelaar

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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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.

123  
papers

5,557  
citations

39  
h-index

72  
g-index

137  
ext. papers

6,726  
ext. citations

8.6  
avg, IF

5.58  
L-index

#	Paper	IF	Citations
123	Elucidation of the pre-nucleation phase directing metal-organic framework formation. <i>Cell Reports Physical Science</i> , <b>2021</b> , 2, 100680	6.1	2
122	Smooth muscle-specific MMP17 (MT4-MMP) regulates the intestinal stem cell niche and regeneration after damage. <i>Nature Communications</i> , <b>2021</b> , 12, 6741	17.4	4
121	Automated High-Throughput Method for the Fast, Robust, and Reproducible Enrichment of Newly Synthesized Proteins. <i>Journal of Proteome Research</i> , <b>2021</b> ,	5.6	1
120	Centrosome-mediated microtubule remodeling during axon formation in human iPSC-derived neurons. <i>EMBO Journal</i> , <b>2021</b> , 40, e106798	13	4
119	MAPK-ERK is a central pathway in T-cell acute lymphoblastic leukemia that drives steroid resistance. <i>Leukemia</i> , <b>2021</b> , 35, 3394-3405	10.7	5
118	Cysteamine-bicalutamide combination therapy corrects proximal tubule phenotype in cystinosis. <i>EMBO Molecular Medicine</i> , <b>2021</b> , 13, e13067	12	7
117	Anti-tumour immunity induces aberrant peptide presentation in melanoma. <i>Nature</i> , <b>2021</b> , 590, 332-337	50.4	28
116	Neuroproteomics of the Synapse: Subcellular Quantification of Protein Networks and Signaling Dynamics. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 20, 100087	7.6	2
115	The Role of Pseudo-Orthocaspase (SyOC) of sp. PCC 6803 in Attenuating the Effect of Oxidative Stress. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 634366	5.7	3
114	Proteomics and Phosphoproteomics Profiling of Drug-Addicted BRAFi-Resistant Melanoma Cells. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 4381-4392	5.6	1
113	Multistep mechanism of G-quadruplex resolution during DNA replication. <i>Science Advances</i> , <b>2021</b> , 7, eabf8653	18.5	4
112	Quantifying Positional Isomers (QPI) by Top-Down Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 20, 100070	7.6	
111	Combined Quantitative (Phospho)proteomics and Mass Spectrometry Imaging Reveal Temporal and Spatial Protein Changes in Human Intestinal Ischemia-Reperfusion. <i>Journal of Proteome Research</i> , <b>2021</b> ,	5.6	3
110	Spinal Muscular Atrophy Patient iPSC-Derived Motor Neurons Display Altered Proteomes at Early Stages of Differentiation.. <i>ACS Omega</i> , <b>2021</b> , 6, 35375-35388	3.9	0
109	Quantitative proteomic analysis of Rett iPSC-derived neuronal progenitors. <i>Molecular Autism</i> , <b>2020</b> , 11, 38	6.5	5
108	Deciphering the Proteome Dynamics during Development of Neurons Derived from Induced Pluripotent Stem Cells. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 2391-2403	5.6	6
107	Quantitative mapping of transcriptome and proteome dynamics during polarization of human iPSC-derived neurons. <i>ELife</i> , <b>2020</b> , 9,	8.9	5

106	Arginine Estacking drives binding to fibrils of the Alzheimer protein Tau. <i>Nature Communications</i> , <b>2020</b> , 11, 571	17.4	13
105	Combined EGFR and ROCK Inhibition in Triple-negative Breast Cancer Leads to Cell Death Via Impaired Autophagic Flux. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 19, 261-277	7.6	5
104	Effects of electron-transfer/higher-energy collisional dissociation (ET <sub>h</sub> CD) on phosphopeptide analysis by data-independent acquisition. <i>International Journal of Mass Spectrometry</i> , <b>2020</b> , 452, 116336	1.9	1
103	Temporal Quantitative Proteomics of mGluR-induced Protein Translation and Phosphorylation in Neurons. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 19, 1952-1968	7.6	5
102	Tumour kinome re-wiring governs resistance to palbociclib in oestrogen receptor positive breast cancers, highlighting new therapeutic modalities. <i>Oncogene</i> , <b>2020</b> , 39, 4781-4797	9.2	22
101	Feedback-Driven Assembly of the Axon Initial Segment. <i>Neuron</i> , <b>2019</b> , 104, 305-321.e8	13.9	25
100	High-Throughput Assessment of Kinome-wide Activation States. <i>Cell Systems</i> , <b>2019</b> , 9, 366-374.e5	10.6	12
99	Conserved crosstalk between histone deacetylation and H3K79 methylation generates DOT1L-dose dependency in HDAC1-deficient thymic lymphoma. <i>EMBO Journal</i> , <b>2019</b> , 38, e101564	13	17
98	MAP7 family proteins regulate kinesin-1 recruitment and activation. <i>Journal of Cell Biology</i> , <b>2019</b> , 218, 1298-1318	7.3	62
97	Actin from the apicomplexan <i>Neospora caninum</i> (NcACT) has different isoforms in 2D electrophoresis. <i>Parasitology</i> , <b>2019</b> , 146, 33-41	2.7	0
96	Crystal structure of the tubulin tyrosine carboxypeptidase complex VASH1-SVBP. <i>Nature Structural and Molecular Biology</i> , <b>2019</b> , 26, 567-570	17.6	16
95	VAP-SCRN1 interaction regulates dynamic endoplasmic reticulum remodeling and presynaptic function. <i>EMBO Journal</i> , <b>2019</b> , 38, e101345	13	26
94	Feedback-Driven Mechanisms between Microtubules and the Endoplasmic Reticulum Instruct Neuronal Polarity. <i>Neuron</i> , <b>2019</b> , 102, 184-201.e8	13.9	34
93	Identification of a tumor-specific allo-HLA-restricted $\alpha$ CR. <i>Blood Advances</i> , <b>2019</b> , 3, 2870-2882	7.8	18
92	Feeding cycle alters the biophysics and molecular expression of voltage-gated Na currents in rat hippocampal CA1 neurones. <i>European Journal of Neuroscience</i> , <b>2019</b> , 49, 1418-1435	3.5	
91	PaDuA: A Python Library for High-Throughput (Phospho)proteomics Data Analysis. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 576-584	5.6	7
90	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> , <b>2018</b> , 112, 12-20	3.9	7
89	The HAUS Complex Is a Key Regulator of Non-centrosomal Microtubule Organization during Neuronal Development. <i>Cell Reports</i> , <b>2018</b> , 24, 791-800	10.6	49

88	Nedd4-Binding Protein 1 and TNFAIP3-Interacting Protein 1 Control MHC-1 Display in Neuroblastoma. <i>Cancer Research</i> , <b>2018</b> , 78, 6621-6631	10.1	23
87	In vivo phosphoproteomics reveals kinase activity profiles that predict treatment outcome in triple-negative breast cancer. <i>Nature Communications</i> , <b>2018</b> , 9, 3501	17.4	26
86	A System-wide Approach to Monitor Responses to Synergistic BRAF and EGFR Inhibition in Colorectal Cancer Cells. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 1892-1908	7.6	7
85	Membrane-Depolarizing Channel Blockers Induce Selective Glioma Cell Death by Impairing Nutrient Transport and Unfolded Protein/Amino Acid Responses. <i>Cancer Research</i> , <b>2017</b> , 77, 1741-1752	10.1	15
84	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , <b>2017</b> , 18, 1527-1542	16.7	47
83	Robust, Sensitive, and Automated Phosphopeptide Enrichment Optimized for Low Sample Amounts Applied to Primary Hippocampal Neurons. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 728-737	5.6	64
82	Vasohibins encode tubulin detyrosinating activity. <i>Science</i> , <b>2017</b> , 358, 1453-1456	33.3	109
81	Opposite Electron-Transfer Dissociation and Higher-Energy Collisional Dissociation Fragmentation Characteristics of Proteolytic K/R(X) and (X)K/R Peptides Provide Benefits for Peptide Sequencing in Proteomics and Phosphoproteomics. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 852-861	5.6	15
80	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> , <b>2016</b> , 197, 3382-3392	5.3	36
79	Quantitative Proteomics Illuminates a Functional Interaction between mDia2 and the Proteasome. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 4624-4637	5.6	8
78	Differential proteomics reveals the hallmarks of seed development in common bean ( <i>Phaseolus vulgaris</i> L.). <i>Journal of Proteomics</i> , <b>2016</b> , 143, 188-198	3.9	19
77	Talin-KANK1 interaction controls the recruitment of cortical microtubule stabilizing complexes to focal adhesions. <i>ELife</i> , <b>2016</b> , 5,	8.9	100
76	Direct screening for chromatin status on DNA barcodes in yeast delineates the regulome of H3K79 methylation by Dot1. <i>ELife</i> , <b>2016</b> , 5,	8.9	18
75	Association of Cell Adhesion Molecules Contactin-6 and Latrophilin-1 Regulates Neuronal Apoptosis. <i>Frontiers in Molecular Neuroscience</i> , <b>2016</b> , 9, 143	6.1	17
74	Assessment of SRM, MRM(3) , and DIA for the targeted analysis of phosphorylation dynamics in non-small cell lung cancer. <i>Proteomics</i> , <b>2016</b> , 16, 2193-205	4.8	38
73	BRAF(V600E) Kinase Domain Duplication Identified in Therapy-Refractory Melanoma Patient-Derived Xenografts. <i>Cell Reports</i> , <b>2016</b> , 16, 263-277	10.6	40
72	Monitoring light/dark association dynamics of multi-protein complexes in cyanobacteria using size exclusion chromatography-based proteomics. <i>Journal of Proteomics</i> , <b>2016</b> , 142, 33-44	3.9	8
71	Molecular Pathway of Microtubule Organization at the Golgi Apparatus. <i>Developmental Cell</i> , <b>2016</b> , 39, 44-60	10.2	74

70	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> , <b>2016</b> , 15, 3412-3423	7.6	77
69	De novo discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , <b>2015</b> , 235, 3-13	9.4	95
68	Benchmarking multiple fragmentation methods on an orbitrap fusion for top-down phospho-proteoform characterization. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 4152-8	7.8	87
67	PhosphoPath: Visualization of Phosphosite-centric Dynamics in Temporal Molecular Networks. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 4332-41	5.6	48
66	Diet-induced neuropeptide expression: feasibility of quantifying extended and highly charged endogenous peptide sequences by selected reaction monitoring. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 9966-73	7.8	4
65	Myc coordinates transcription and translation to enhance transformation and suppress invasiveness. <i>EMBO Reports</i> , <b>2015</b> , 16, 1723-36	6.5	28
64	Uncovering the abilities of <i>Agaricus bisporus</i> to degrade plant biomass throughout its life cycle. <i>Environmental Microbiology</i> , <b>2015</b> , 17, 3098-109	5.2	37
63	Cooperative induction of apoptosis in NRAS mutant melanoma by inhibition of MEK and ROCK. <i>Pigment Cell and Melanoma Research</i> , <b>2015</b> , 28, 307-17	4.5	32
62	Signal Transduction Reaction Monitoring Deciphers Site-Specific PI3K-mTOR/MAPK Pathway Dynamics in Oncogene-Induced Senescence. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 2906-14	5.6	27
61	N-lactoyl-amino acids are ubiquitous metabolites that originate from CNBP2-mediated reverse proteolysis of lactate and amino acids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 6601-6	11.5	32
60	Dot1 histone methyltransferases share a distributive mechanism but have highly diverged catalytic properties. <i>Scientific Reports</i> , <b>2015</b> , 5, 9824	4.9	12
59	TRIM46 Controls Neuronal Polarity and Axon Specification by Driving the Formation of Parallel Microtubule Arrays. <i>Neuron</i> , <b>2015</b> , 88, 1208-1226	13.9	125
58	Proteomic analyses uncover a new function and mode of action for mouse homolog of Diaphanous 2 (mDia2). <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 1064-78	7.6	14
57	Identification of putative substrates for the periplasmic chaperone YfgM in <i>Escherichia coli</i> using quantitative proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 216-26	7.6	12
56	Coordination of peptidoglycan synthesis and outer membrane constriction during <i>Escherichia coli</i> cell division. <i>ELife</i> , <b>2015</b> , 4,	8.9	127
55	Microtubule minus-end stabilization by polymerization-driven CAMSAP deposition. <i>Developmental Cell</i> , <b>2014</b> , 28, 295-309	10.2	175
54	Phosphoproteome dynamics in onset and maintenance of oncogene-induced senescence. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2089-100	7.6	8
53	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> , <b>2014</b> , 72, 73-81	3.9	58

52	Flexibility in crosstalk between H2B ubiquitination and H3 methylation in vivo. <i>EMBO Reports</i> , <b>2014</b> , 15, 1077-84	6.5	26
51	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> , <b>2014</b> , 13, 2426-34	7.6	80
50	Flexibility in crosstalk between H2B ubiquitination and H3 methylation in vivo. <i>EMBO Reports</i> , <b>2014</b> , 15, 1220-1221	6.5	4
49	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> , <b>2014</b> , 13, 2042-55	7.6	55
48	Protein acetylation affects acetate metabolism, motility and acid stress response in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 762	12.2	98
47	ROCK1 is a potential combinatorial drug target for BRAF mutant melanoma. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 772	12.2	38
46	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> , <b>2013</b> , 12, 1808-19	5.6	36
45	Profiling of diet-induced neuropeptide changes in rat brain by quantitative mass spectrometry. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 4594-604	7.8	21
44	Next-generation proteomics: towards an integrative view of proteome dynamics. <i>Nature Reviews Genetics</i> , <b>2013</b> , 14, 35-48	30.1	530
43	Deep proteome profiling of <i>Trichoplax adhaerens</i> reveals remarkable features at the origin of metazoan multicellularity. <i>Nature Communications</i> , <b>2013</b> , 4, 1408	17.4	40
42	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , <b>2013</b> , 88, 14-26	3.9	100
41	A central role for TFIID in the pluripotent transcription circuitry. <i>Nature</i> , <b>2013</b> , 495, 516-9	50.4	62
40	Unambiguous phosphosite localization using electron-transfer/higher-energy collision dissociation (EThcD). <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 1520-5	5.6	125
39	Imaging mass spectrometry-based molecular histology differentiates microscopically identical and heterogeneous tumors. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 1847-55	5.6	18
38	Quantitative global phosphoproteomics of human umbilical vein endothelial cells after activation of the Rap signaling pathway. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 732-49		8
37	Characterization of electron transfer dissociation in the Orbitrap Velos HCD cell. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2013</b> , 24, 1663-70	3.5	3
36	Spatio-temporal analysis of molecular determinants of neuronal degeneration in the aging mouse cerebellum. <i>Molecular and Cellular Proteomics</i> , <b>2013</b> , 12, 1350-62	7.6	21
35	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> , <b>2013</b> , 6, 335	4	12

34	Toward full peptide sequence coverage by dual fragmentation combining electron-transfer and higher-energy collision dissociation tandem mass spectrometry. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 9668-73	7.8	203
33	Spatially resolving the secretome within the mycelium of the cell factory <i>Aspergillus niger</i> . <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 2807-18	5.6	35
32	Trends in ultrasensitive proteomics. <i>Current Opinion in Chemical Biology</i> , <b>2012</b> , 16, 206-13	9.7	120
31	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> , <b>2012</b> , 109, 407-12	11.5	12
30	Improved peptide identification by targeted fragmentation using CID, HCD and ETD on an LTQ-Orbitrap Velos. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 2377-88	5.6	248
29	Progressive methylation of ageing histones by Dot1 functions as a timer. <i>EMBO Reports</i> , <b>2011</b> , 12, 956-62	6.5	39
28	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> , <b>2011</b> , 10, 4334-41	5.6	77
27	Probing the proteome response to toluene exposure in the solvent tolerant <i>Pseudomonas putida</i> S12. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 394-403	5.6	38
26	Protein signatures associated with tumor cell dissemination in head and neck cancer. <i>Journal of Proteomics</i> , <b>2011</b> , 74, 558-66	3.9	19
25	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, The</i> , <b>2010</b> , 135, 2643-52	5	12
24	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> , <b>2010</b> , 9, 2140-8	7.6	36
23	Dimethyl isotope labeling assisted de novo peptide sequencing. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2010</b> , 21, 1957-65	3.5	22
22	Cellular imaging using matrix-enhanced and metal-assisted SIMS. <i>Methods in Molecular Biology</i> , <b>2010</b> , 656, 197-208	1.4	11
21	Strong cation exchange-based fractionation of Lys-N-generated peptides facilitates the targeted analysis of post-translational modifications. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 190-200	7.6	64
20	Fast and automated large-area imaging MALDI mass spectrometry in microprobe and microscope mode. <i>International Journal of Mass Spectrometry</i> , <b>2009</b> , 285, 19-25	1.9	33
19	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> , <b>2009</b> , 8, 870-6	5.6	23
18	In-depth profiling of post-translational modifications on the related transcription factor complexes TFIID and SAGA. <i>Journal of Proteome Research</i> , <b>2009</b> , 8, 5020-30	5.6	24
17	Straightforward and de novo peptide sequencing by MALDI-MS/MS using a Lys-N metalloendopeptidase. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 650-60	7.6	39

16	Tissue analysis with high-resolution imaging mass spectrometry. <i>Methods in Molecular Biology</i> , <b>2009</b> , 492, 295-308	1.4	3
15	Cooperative action of NC2 and Mot1p to regulate TATA-binding protein function across the genome. <i>Genes and Development</i> , <b>2008</b> , 22, 2359-69	12.6	58
14	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> , <b>2008</b> , 19, 823-32	3.5	31
13	Imaging mass spectrometry at cellular length scales. <i>Nature Protocols</i> , <b>2007</b> , 2, 1185-96	18.8	98
12	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> , <b>2007</b> , 260, 203-211	1.9	96
11	Imaging of peptides in the rat brain using MALDI-FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2007</b> , 18, 145-51	3.5	135
10	Gold-enhanced biomolecular surface imaging of cells and tissue by SIMS and MALDI mass spectrometry. <i>Analytical Chemistry</i> , <b>2006</b> , 78, 734-42	7.8	256
9	High Resolution Mass Spectrometric Imaging of Cells and Tissue: MALDI and Surface Enhanced SIMS Put to Work. <i>Microscopy and Microanalysis</i> , <b>2006</b> , 12, 1210-1211	0.5	
8	Why don't biologists use SIMS?. <i>Applied Surface Science</i> , <b>2006</b> , 252, 6827-6835	6.7	94
7	The influence of the cholesterol microenvironment in tissue sections on molecular ionization efficiencies and distributions in ToF-SIMS. <i>Applied Surface Science</i> , <b>2006</b> , 252, 6702-6705	6.7	11
6	Direct molecular imaging of <i>Lymnaea stagnalis</i> nervous tissue at subcellular spatial resolution by mass spectrometry. <i>Analytical Chemistry</i> , <b>2005</b> , 77, 735-41	7.8	166
5	Subcellular imaging mass spectrometry of brain tissue. <i>Journal of Mass Spectrometry</i> , <b>2005</b> , 40, 160-8	2.2	163
4	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> , <b>2002</b> , 958, 141-8	4.5	40
3	Deciphering the protein dynamics and molecular determinants of iPSC-derived neurons		1
2	Quantitative proteomic alterations of human iPSC-based neuronal development indicate early onset of Rett syndrome		1
1	Glucocorticoids regulate cancer cell dormancy		3