

Richard Scheltema

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36
papers

5,588
citations

27
h-index

36
g-index

36
ext. papers

7,100
ext. citations

9.5
avg, IF

5.6
L-index

#	Paper	IF	Citations
36	Andromeda: a peptide search engine integrated into the MaxQuant environment. <i>Journal of Proteome Research</i> , 2011 , 10, 1794-805	5.6	3402
35	The Q Exactive HF, a Benchtop mass spectrometer with a pre-filter, high-performance quadrupole and an ultra-high-field Orbitrap analyzer. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3698-708	7.6	229
34	PeakML/mzMatch: a file format, Java library, R library, and tool-chain for mass spectrometry data analysis. <i>Analytical Chemistry</i> , 2011 , 83, 2786-93	7.8	210
33	System-wide molecular evidence for phenotypic buffering in Arabidopsis. <i>Nature Genetics</i> , 2009 , 41, 1663-3	36.3	205
32	Direct proteomic quantification of the secretome of activated immune cells. <i>Science</i> , 2013 , 340, 475-8	33.3	147
31	Time- and compartment-resolved proteome profiling of the extracellular niche in lung injury and repair. <i>Molecular Systems Biology</i> , 2015 , 11, 819	12.2	139
30	Structural model of a CRISPR RNA-silencing complex reveals the RNA-target cleavage activity in Cmr4. <i>Molecular Cell</i> , 2014 , 56, 43-54	17.6	112
29	Metabolomic profiling using Orbitrap Fourier transform mass spectrometry with hydrophilic interaction chromatography: a method with wide applicability to analysis of biomolecules. <i>Rapid Communications in Mass Spectrometry</i> , 2008 , 22, 1912-8	2.2	89
28	Metabolomics to unveil and understand phenotypic diversity between pathogen populations. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e904	4.8	85
27	Efficient and robust proteome-wide approaches for cross-linking mass spectrometry. <i>Nature Protocols</i> , 2018 , 13, 2964-2990	18.8	77
26	Probabilistic assignment of formulas to mass peaks in metabolomics experiments. <i>Bioinformatics</i> , 2009 , 25, 512-8	7.2	75
25	Metabolomic characterization of the salt stress response in <i>Streptomyces coelicolor</i> . <i>Applied and Environmental Microbiology</i> , 2010 , 76, 2574-81	4.8	62
24	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
23	Implementation of Ultraviolet Photodissociation on a Benchtop Q Exactive Mass Spectrometer and Its Application to Phosphoproteomics. <i>Analytical Chemistry</i> , 2016 , 88, 2303-10	7.8	56
22	Histone Interaction Landscapes Visualized by Crosslinking Mass Spectrometry in Intact Cell Nuclei. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2018-2033	7.6	56
21	PhoX: An IMAC-Enrichable Cross-Linking Reagent. <i>ACS Central Science</i> , 2019 , 5, 1514-1522	16.8	55
20	SprayQc: a real-time LC-MS/MS quality monitoring system to maximize uptime using off the shelf components. <i>Journal of Proteome Research</i> , 2012 , 11, 3458-66	5.6	51

19	Increasing the mass accuracy of high-resolution LC-MS data using background ions: a case study on the LTQ-Orbitrap. <i>Proteomics</i> , 2008 , 8, 4647-56	4.8	51
18	Towards an unbiased metabolic profiling of protozoan parasites: optimisation of a Leishmania sampling protocol for HILIC-orbitrap analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2010 , 398, 2059-69	4.4	47
17	Simple data-reduction method for high-resolution LC-MS data in metabolomics. <i>Bioanalysis</i> , 2009 , 1, 1551-7	2.1	46
16	A framework for intelligent data acquisition and real-time database searching for shotgun proteomics. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.013185	7.6	40
15	Symmetry of Charge Partitioning in Collisional and UV Photon-Induced Dissociation of Protein Assemblies. <i>Journal of the American Chemical Society</i> , 2016 , 138, 10860-8	16.4	37
14	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1905-13	7.6	36
13	The potential of metabolomics for Leishmania research in the post-genomics era. <i>Parasitology</i> , 2010 , 137, 1291-302	2.7	35
12	How paired PSII-LHCII supercomplexes mediate the stacking of plant thylakoid membranes unveiled by structural mass-spectrometry. <i>Nature Communications</i> , 2020 , 11, 1361	17.4	32
11	A Double-Barrel Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) System to Quantify 96 Interactomes per Day. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2030-41	7.6	31
10	To Cleave or Not To Cleave in XL-MS?. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 196-206	3.5	28
9	Use of reconstituted metabolic networks to assist in metabolomic data visualization and mining. <i>Metabolomics</i> , 2010 , 6, 312-321	4.7	27
8	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. <i>Genome Biology</i> , 2010 , 11, R27	18.3	16
7	Missing regions within the molecular architecture of human fibrin clots structurally resolved by XL-MS and integrative structural modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 1976-1987	11.5	14
6	Benefits of Collisional Cross Section Assisted Precursor Selection (caps-PASEF) for Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1677-1687	7.6	14
5	Life history shapes variation in egg composition in the blue tit. <i>Communications Biology</i> , 2019 , 2, 6	6.7	11
4	Cross-ID: Analysis and Visualization of Complex XL-MS-Driven Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2019 , 18, 642-651	5.6	10
3	Two time-point assessment of bile acid kinetics in humans using stable isotopes. <i>Isotopes in Environmental and Health Studies</i> , 2010 , 46, 325-36	1.5	3
2	Notch-Jagged signaling complex defined by an interaction mosaic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3

1 Quantifying Positional Isomers (QPI) by Top-Down Mass Spectrometry. *Molecular and Cellular Proteomics*, **2021**, 20, 100070

7.6