

# Richard Scheltema

## 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.

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	Notch-Jagged signaling complex defined by an interaction mosaic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	3
35	Quantifying Positional Isomers (QPI) by Top-Down Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 20, 100070	7.6	
34	How paired PSII-LHCII supercomplexes mediate the stacking of plant thylakoid membranes unveiled by structural mass-spectrometry. <i>Nature Communications</i> , <b>2020</b> , 11, 1361	17.4	32
33	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> , <b>2020</b> , 117, 1976-1987	11.5	14
32	To Cleave or Not To Cleave in XL-MS?. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2020</b> , 31, 196-206	3.5	28
31	Benefits of Collisional Cross Section Assisted Precursor Selection (caps-PASEF) for Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2020</b> , 19, 1677-1687	7.6	14
30	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 6953-6961	7.8	57
29	Life history shapes variation in egg composition in the blue tit. <i>Communications Biology</i> , <b>2019</b> , 2, 6	6.7	11
28	PhoX: An IMAC-Enrichable Cross-Linking Reagent. <i>ACS Central Science</i> , <b>2019</b> , 5, 1514-1522	16.8	55
27	Cross-ID: Analysis and Visualization of Complex XL-MS-Driven Protein Interaction Networks. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 642-651	5.6	10
26	Histone Interaction Landscapes Visualized by Crosslinking Mass Spectrometry in Intact Cell Nuclei. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 2018-2033	7.6	56
25	Efficient and robust proteome-wide approaches for cross-linking mass spectrometry. <i>Nature Protocols</i> , <b>2018</b> , 13, 2964-2990	18.8	77
24	Symmetry of Charge Partitioning in Collisional and UV Photon-Induced Dissociation of Protein Assemblies. <i>Journal of the American Chemical Society</i> , <b>2016</b> , 138, 10860-8	16.4	37
23	Implementation of Ultraviolet Photodissociation on a Benchtop Q Exactive Mass Spectrometer and Its Application to Phosphoproteomics. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 2303-10	7.8	56
22	A Double-Barrel Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) System to Quantify 96 Interactomes per Day. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 2030-41	7.6	31
21	Time- and compartment-resolved proteome profiling of the extracellular niche in lung injury and repair. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 819	12.2	139
20	Structural model of a CRISPR RNA-silencing complex reveals the RNA-target cleavage activity in Cmr4. <i>Molecular Cell</i> , <b>2014</b> , 56, 43-54	17.6	112

19	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> , <b>2014</b> , 13, 3698-708	7.6	229
18	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1905-13	7.6	36
17	Direct proteomic quantification of the secretome of activated immune cells. <i>Science</i> , <b>2013</b> , 340, 475-8	33.3	147
16	SprayQc: a real-time LC-MS/MS quality monitoring system to maximize uptime using off the shelf components. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 3458-66	5.6	51
15	A framework for intelligent data acquisition and real-time database searching for shotgun proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, M111.013185	7.6	40
14	PeakML/mzMatch: a file format, Java library, R library, and tool-chain for mass spectrometry data analysis. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 2786-93	7.8	210
13	Andromeda: a peptide search engine integrated into the MaxQuant environment. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 1794-805	5.6	3402
12	Metabolomic characterization of the salt stress response in <i>Streptomyces coelicolor</i> . <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 2574-81	4.8	62
11	Two time-point assessment of bile acid kinetics in humans using stable isotopes. <i>Isotopes in Environmental and Health Studies</i> , <b>2010</b> , 46, 325-36	1.5	3
10	The potential of metabolomics for Leishmania research in the post-genomics era. <i>Parasitology</i> , <b>2010</b> , 137, 1291-302	2.7	35
9	Metabolomics to unveil and understand phenotypic diversity between pathogen populations. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e904	4.8	85
8	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. <i>Genome Biology</i> , <b>2010</b> , 11, R27	18.3	16
7	Towards an unbiased metabolic profiling of protozoan parasites: optimisation of a Leishmania sampling protocol for HILIC-orbitrap analysis. <i>Analytical and Bioanalytical Chemistry</i> , <b>2010</b> , 398, 2059-69	4.4	47
6	Use of reconstituted metabolic networks to assist in metabolomic data visualization and mining. <i>Metabolomics</i> , <b>2010</b> , 6, 312-321	4.7	27
5	Simple data-reduction method for high-resolution LC-MS data in metabolomics. <i>Bioanalysis</i> , <b>2009</b> , 1, 1551-7	2.1	46
4	Probabilistic assignment of formulas to mass peaks in metabolomics experiments. <i>Bioinformatics</i> , <b>2009</b> , 25, 512-8	7.2	75
3	System-wide molecular evidence for phenotypic buffering in Arabidopsis. <i>Nature Genetics</i> , <b>2009</b> , 41, 1663-3	36.3	205
2	Increasing the mass accuracy of high-resolution LC-MS data using background ions: a case study on the LTQ-Orbitrap. <i>Proteomics</i> , <b>2008</b> , 8, 4647-56	4.8	51

- 1 Metabolomic profiling using Orbitrap Fourier transform mass spectrometry with hydrophilic interaction chromatography: a method with wide applicability to analysis of biomolecules. *Rapid Communications in Mass Spectrometry*, **2008**, 22, 1912-8 2.2 89