

# Stephen Holman

## List of Publications by Year in descending order

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29  
papers

1,335  
citations

759233

12  
h-index

501196

28  
g-index

30  
all docs

30  
docs citations

30  
times ranked

2413  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies. <i>Nature Communications</i> , 2022, 13, 801.	12.8	47
2	Advancements in the characterisation of oligonucleotides by high performance liquid chromatography-mass spectrometry in 2021: A short review. <i>Analytical Science Advances</i> , 2022, 3, 90-102.	2.8	8
3	Application of open port sampling interface mass spectrometry (OPSI-MS) to deuterium exchange as an aid for structural elucidation. <i>Rapid Communications in Mass Spectrometry</i> , 2021, 35, e8536.	1.5	3
4	Advances in high-resolution mass spectrometry applied to pharmaceuticals in 2020: A whole new age of information. <i>Analytical Science Advances</i> , 2021, 2, 142-156.	2.8	16
5	Response to "In defense of the quasimolecular ion". <i>Journal of Mass Spectrometry</i> , 2021, 56, e4724.	1.6	0
6	Quantitative Proteomics of Enriched Esophageal and Gut Tissues from the Human Blood Fluke <i>Schistosoma mansoni</i> Pinpoints Secreted Proteins for Vaccine Development. <i>Journal of Proteome Research</i> , 2020, 19, 314-326.	3.7	17
7	A proteome-integrated, carbon source dependent genetic regulatory network in <i>Saccharomyces cerevisiae</i> . <i>Molecular Omics</i> , 2020, 16, 59-72.	2.8	11
8	Towards a generic method for ion chromatography/mass spectrometry of low-molecular-weight amines in pharmaceutical drug discovery and development. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34 Suppl 4, e8680.	1.5	4
9	Response to "Molecular ion: A more contemporary definition". <i>Journal of Mass Spectrometry</i> , 2020, 55, e4649.	1.6	2
10	Glycolytic flux in <i>Saccharomyces cerevisiae</i> is dependent on RNA polymerase III and its negative regulator Maf1. <i>Biochemical Journal</i> , 2019, 476, 1053-1082.	3.7	9
11	Meet the Associate Editors: Stephen Holman. <i>Rapid Communications in Mass Spectrometry</i> , 2019, 33, 11-13.	1.5	5
12	DOSCATs: Double standards for protein quantification. <i>Scientific Reports</i> , 2017, 7, 45570.	3.3	8
13	Absolute protein quantification of the yeast chaperome under conditions of heat shock. <i>Proteomics</i> , 2016, 16, 2128-2140.	2.2	18
14	Direct and Absolute Quantification of over 1800 Yeast Proteins via Selected Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1309-1322.	3.8	80
15	Analysis of Intrinsic Peptide Detectability via Integrated Label-Free and SRM-Based Absolute Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 2945-2959.	3.7	46
16	Dynamic phosphorylation of RelA on Ser42 and Ser45 in response to TNF $\alpha$ stimulation regulates DNA binding and transcription. <i>Open Biology</i> , 2016, 6, 160055.	3.6	19
17	Protein turnover measurement using selected reaction monitoring-mass spectrometry (SRM-MS). <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2016, 374, 20150362.	3.4	10
18	RePLiCal: A QconCAT Protein for Retention Time Standardization in Proteomics Studies. <i>Journal of Proteome Research</i> , 2016, 15, 1090-1102.	3.7	16

#	ARTICLE	IF	CITATIONS
19	Representation of selected reaction monitoring data in the mzQuantML data standard. <i>Proteomics</i> , 2015, 15, 2592-2596.	2.2	7
20	Evaluation of dimethyl sulfoxide (DMSO) as a mobile phase additive during top 3 label-free quantitative proteomics. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 157-160.	1.5	15
21	The power of ion mobility-mass spectrometry for structural characterization and the study of conformational dynamics. <i>Nature Chemistry</i> , 2014, 6, 281-294.	13.6	753
22	Peptide Scrambling During Collision-Induced Dissociation is Influenced by N-terminal Residue Basicity. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 1927-1938.	2.8	10
23	Quantitative analysis of chaperone network throughput in budding yeast. <i>Proteomics</i> , 2013, 13, 1276-1291.	2.2	33
24	A quantitative assessment of the chemical variation in food grade polyethylene cling film, a common wrapping material for illicit drugs, using attenuated total reflection-Fourier transform infrared spectroscopy. <i>Analytical Methods</i> , 2012, 4, 1667.	2.7	8
25	The use of selected reaction monitoring in quantitative proteomics. <i>Bioanalysis</i> , 2012, 4, 1763-1786.	1.5	66
26	Global absolute quantification of a proteome: Challenges in the deployment of a QconCAT strategy. <i>Proteomics</i> , 2011, 11, 2957-2970.	2.2	103
27	The low-energy collision-induced dissociation product ion spectra of protonated beta-blockers reveal an analogy to fragmentation behaviour under electron ionisation conditions. <i>Journal of Mass Spectrometry</i> , 2011, 46, 1182-1185.	1.6	3
28	Evidence for site-specific intra-ionic hydrogen/deuterium exchange in the low-energy collision-induced dissociation product ion spectra of protonated small molecules generated by electrospray ionisation. <i>Journal of Mass Spectrometry</i> , 2010, 45, 347-357.	1.6	6
29	A Rapid Methodology for the Characterization of Dialkyl Tertiary Amine-N-Oxide Metabolites Using Structurally Dependent Dissociation Pathways and Reconstructed Ion Current Chromatograms. <i>Analytical Chemistry</i> , 2010, 82, 2347-2354.	6.5	8