

Devin K Schweppe

List of Publications by Year in descending order

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38
papers

5,073
citations

218677

26
h-index

315739

38
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44
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44
docs citations

44
times ranked

8072
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved Monoisotopic Mass Estimation for Deeper Proteome Coverage. <i>Journal of Proteome Research</i> , 2021, 20, 591-598.	3.7	52
2	Advances in quantitative high-throughput phosphoproteomics with sample multiplexing. <i>Proteomics</i> , 2021, 21, e2000140.	2.2	22
3	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. <i>Cell</i> , 2021, 184, 3022-3040.e28.	28.9	455
4	Reimagining high-throughput profiling of reactive cysteines for cell-based screening of large electrophile libraries. <i>Nature Biotechnology</i> , 2021, 39, 630-641.	17.5	142
5	Strategies for mass spectrometry-based phosphoproteomics using isobaric tagging. <i>Expert Review of Proteomics</i> , 2021, 18, 795-807.	3.0	6
6	Suboptimal Comparison of Partitions. <i>Journal of Classification</i> , 2020, 37, 435-461.	2.2	1
7	In Vivo Cross-Linking MS Reveals Conservation in OmpA Linkage to Different Classes of β^2 -Lactamase Enzymes. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 190-195.	2.8	13
8	Optimized Workflow for Multiplexed Phosphorylation Analysis of TMT-Labeled Peptides Using High-Field Asymmetric Waveform Ion Mobility Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 554-560.	3.7	56
9	Facultative protein selenation regulates redox sensitivity, adipose tissue thermogenesis, and obesity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10789-10796.	7.1	30
10	Homogeneous Oligomers of Pro-apoptotic BAX Reveal Structural Determinants of Mitochondrial Membrane Permeabilization. <i>Molecular Cell</i> , 2020, 79, 68-83.e7.	9.7	32
11	TMTpro reagents: a set of isobaric labeling mass tags enables simultaneous proteome-wide measurements across 16 samples. <i>Nature Methods</i> , 2020, 17, 399-404.	19.0	276
12	Full-Featured, Real-Time Database Searching Platform Enables Fast and Accurate Multiplexed Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 2026-2034.	3.7	171
13	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. <i>Cell</i> , 2020, 180, 968-983.e24.	28.9	220
14	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. <i>Cell</i> , 2020, 180, 387-402.e16.	28.9	596
15	Parallel Notched Gas-Phase Enrichment for Improved Proteome Identification and Quantification with Fast Spectral Acquisition Rates. <i>Journal of Proteome Research</i> , 2020, 19, 2750-2757.	3.7	4
16	Benchmarking the Orbitrap Tribrid Eclipse for Next Generation Multiplexed Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 6478-6485.	6.5	44
17	Sample multiplexing for targeted pathway proteomics in aging mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9723-9732.	7.1	73
18	Characterization and Optimization of Multiplexed Quantitative Analyses Using High-Field Asymmetric-Waveform Ion Mobility Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 4010-4016.	6.5	155

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19	Active Instrument Engagement Combined with a Real-Time Database Search for Improved Performance of Sample Multiplexing Workflows. <i>Journal of Proteome Research</i> , 2019, 18, 1299-1306.	3.7	109
20	TomahaqCompanion: A Tool for the Creation and Analysis of Isobaric Label Based Multiplexed Targeted Assays. <i>Journal of Proteome Research</i> , 2019, 18, 594-605.	3.7	14
21	The skeletal phenotype of Achondrogenesis type 1A is caused exclusively by cartilage defects. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	12
22	Integrating Cross-Linking Experiments with Ab Initio Proteinâ€“Protein Docking. <i>Journal of Molecular Biology</i> , 2018, 430, 1814-1828.	4.2	22
23	BioPlex Display: An Interactive Suite for Large-Scale APâ€“MS Proteinâ€“Protein Interaction Data. <i>Journal of Proteome Research</i> , 2018, 17, 722-726.	3.7	59
24	Mitochondrial protein interactome elucidated by chemical cross-linking mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1732-1737.	7.1	165
25	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	27.8	1,190
26	Large-Scale and Targeted Quantitative Cross-Linking MS Using Isotope-Labeled Protein Interaction Reporter (PIR) Cross-Linkers. <i>Journal of Proteome Research</i> , 2017, 16, 720-727.	3.7	38
27	XLmap: an R package to visualize and score protein structure models based on sites of protein cross-linking. <i>Bioinformatics</i> , 2016, 32, 306-308.	4.1	17
28	XLinkDB 2.0: integrated, large-scale structural analysis of protein crosslinking data. <i>Bioinformatics</i> , 2016, 32, 2716-2718.	4.1	54
29	Spectral Library Searching To Identify Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2016, 15, 1725-1731.	3.7	12
30	In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in <i>Acinetobacter baumannii</i> strain AB5075. <i>Nature Communications</i> , 2016, 7, 13414.	12.8	81
31	InÂVivo Conformational Dynamics of Hsp90 and Its Interactors. <i>Cell Chemical Biology</i> , 2016, 23, 716-726.	5.2	73
32	Stress granules and RNA processing bodies are novel autoantibody targets in systemic sclerosis. <i>Arthritis Research and Therapy</i> , 2016, 18, 27.	3.5	16
33	A General Method for Targeted Quantitative Cross-Linking Mass Spectrometry. <i>PLoS ONE</i> , 2016, 11, e0167547.	2.5	46
34	Quantitative interactome analysis reveals a chemoresistant edgotype. <i>Nature Communications</i> , 2015, 6, 7928.	12.8	77
35	Host-Microbe Protein Interactions during Bacterial Infection. <i>Chemistry and Biology</i> , 2015, 22, 1521-1530.	6.0	103
36	Quantitative phosphoproteomic profiling of human non-small cell lung cancer tumors. <i>Journal of Proteomics</i> , 2013, 91, 286-296.	2.4	92

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37	Quantitative Phosphoproteomics Identifies Substrates and Functional Modules of Aurora and Polo-Like Kinase Activities in Mitotic Cells. <i>Science Signaling</i> , 2011, 4, rs5.	3.6	447
38	A Nondesensitizing Kainate Receptor Point Mutant. <i>Molecular Pharmacology</i> , 2009, 76, 534-542.	2.3	33