Devin K Schweppe

List of Publications by Year
in descending order

38 papers	5,073 citations	218677 26 h-index	315739 38 g-index
44 all docs	44 docs citations	44 times ranked	8072 citing authors

#	Article	IF	Citations
1	Architecture of the human interactome defines protein communities and disease networks. Nature, 2017, 545, 505-509.	27.8	1,190
2	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. Cell, 2020, 180, 387-402.e16.	28.9	596
3	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. Cell, 2021, 184, 3022-3040.e28.	28.9	455
4	Quantitative Phosphoproteomics Identifies Substrates and Functional Modules of Aurora and Polo-Like Kinase Activities in Mitotic Cells. Science Signaling, 2011, 4, rs5.	3.6	447
5	TMTpro reagents: a set of isobaric labeling mass tags enables simultaneous proteome-wide measurements across 16 samples. Nature Methods, 2020, 17, 399-404.	19.0	276
6	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. Cell, 2020, 180, 968-983.e24.	28.9	220
7	Full-Featured, Real-Time Database Searching Platform Enables Fast and Accurate Multiplexed Quantitative Proteomics. Journal of Proteome Research, 2020, 19, 2026-2034.	3.7	171
8	Mitochondrial protein interactome elucidated by chemical cross-linking mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1732-1737.	7.1	165
9	Characterization and Optimization of Multiplexed Quantitative Analyses Using High-Field Asymmetric-Waveform Ion Mobility Mass Spectrometry. Analytical Chemistry, 2019, 91, 4010-4016.	6.5	155
10	Reimagining high-throughput profiling of reactive cysteines for cell-based screening of large electrophile libraries. Nature Biotechnology, 2021, 39, 630-641.	17.5	142
11	Active Instrument Engagement Combined with a Real-Time Database Search for Improved Performance of Sample Multiplexing Workflows. Journal of Proteome Research, 2019, 18, 1299-1306.	3.7	109
12	Host-Microbe Protein Interactions during Bacterial Infection. Chemistry and Biology, 2015, 22, 1521-1530.	6.0	103
13	Quantitative phosphoproteomic profiling of human non-small cell lung cancer tumors. Journal of Proteomics, 2013, 91, 286-296.	2.4	92
14	In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in Acinetobacter baumannii strain AB5075. Nature Communications, 2016, 7, 13414.	12.8	81
15	Quantitative interactome analysis reveals a chemoresistant edgotype. Nature Communications, 2015, 6, 7928.	12.8	77
16	In Vivo Conformational Dynamics of Hsp90 and Its Interactors. Cell Chemical Biology, 2016, 23, 716-726.	5.2	73
17	Sample multiplexing for targeted pathway proteomics in aging mice. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9723-9732.	7.1	73
18	BioPlex Display: An Interactive Suite for Large-Scale AP–MS Protein–Protein Interaction Data. Journal of Proteome Research, 2018, 17, 722-726.	3.7	59

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19	Optimized Workflow for Multiplexed Phosphorylation Analysis of TMT-Labeled Peptides Using High-Field Asymmetric Waveform Ion Mobility Spectrometry. Journal of Proteome Research, 2020, 19, 554-560.	3.7	56
20	XLinkDB 2.0: integrated, large-scale structural analysis of protein crosslinking data. Bioinformatics, 2016, 32, 2716-2718.	4.1	54
21	Improved Monoisotopic Mass Estimation for Deeper Proteome Coverage. Journal of Proteome Research, 2021, 20, 591-598.	3.7	52
22	A General Method for Targeted Quantitative Cross-Linking Mass Spectrometry. PLoS ONE, 2016, 11, e0167547.	2.5	46
23	Benchmarking the Orbitrap Tribrid Eclipse for Next Generation Multiplexed Proteomics. Analytical Chemistry, 2020, 92, 6478-6485.	6.5	44
24	Large-Scale and Targeted Quantitative Cross-Linking MS Using Isotope-Labeled Protein Interaction Reporter (PIR) Cross-Linkers. Journal of Proteome Research, 2017, 16, 720-727.	3.7	38
25	A Nondesensitizing Kainate Receptor Point Mutant. Molecular Pharmacology, 2009, 76, 534-542.	2.3	33
26	Homogeneous Oligomers of Pro-apoptotic BAX Reveal Structural Determinants of Mitochondrial Membrane Permeabilization. Molecular Cell, 2020, 79, 68-83.e7.	9.7	32
27	Facultative protein selenation regulates redox sensitivity, adipose tissue thermogenesis, and obesity. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10789-10796.	7.1	30
28	Integrating Cross-Linking Experiments with Ab Initio Protein–Protein Docking. Journal of Molecular Biology, 2018, 430, 1814-1828.	4.2	22
29	Advances in quantitative high-throughput phosphoproteomics with sample multiplexing. Proteomics, 2021, 21, e2000140.	2.2	22
30	XLmap: an R package to visualize and score protein structure models based on sites of protein cross-linking. Bioinformatics, 2016, 32, 306-308.	4.1	17
31	Stress granules and RNA processing bodies are novel autoantibody targets in systemic sclerosis. Arthritis Research and Therapy, 2016, 18, 27.	3.5	16
32	TomahaqCompanion: A Tool for the Creation and Analysis of Isobaric Label Based Multiplexed Targeted Assays. Journal of Proteome Research, 2019, 18, 594-605.	3.7	14
33	In Vivo Cross-Linking MS Reveals Conservation in OmpA Linkage to Different Classes of β-Lactamase Enzymes. Journal of the American Society for Mass Spectrometry, 2020, 31, 190-195.	2.8	13
34	Spectral Library Searching To Identify Cross-Linked Peptides. Journal of Proteome Research, 2016, 15, 1725-1731.	3.7	12
35	The skeletal phenotype of Achondrogenesis type 1A is caused exclusively by cartilage defects. Development (Cambridge), 2018, 145, .	2.5	12
36	Strategies for mass spectrometry-based phosphoproteomics using isobaric tagging. Expert Review of Proteomics, 2021, 18, 795-807.	3.0	6

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37	Parallel Notched Gas-Phase Enrichment for Improved Proteome Identification and Quantification with Fast Spectral Acquisition Rates. Journal of Proteome Research, 2020, 19, 2750-2757.	3.7	4
38	Suboptimal Comparison of Partitions. Journal of Classification, 2020, 37, 435-461.	2.2	1