

# Steve M M Sweet

## List of Publications by Year in descending order

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27  
papers

2,093  
citations

394421

19  
h-index

526287

27  
g-index

27  
all docs

27  
docs citations

27  
times ranked

3695  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Extraction from Parallel Reaction Monitoring to Quantify Background Peptides for Improved Normalization and Quality Control in Targeted Proteomics. <i>Analytical Chemistry</i> , 2021, 93, 13434-13440.	6.5	7
2	Identifying the Cellular Interactome of Epstein-Barr Virus Lytic Regulator Zta Reveals Cellular Targets Contributing to Viral Replication. <i>Journal of Virology</i> , 2020, 94, .	3.4	9
3	Data-Independent Acquisition Mass Spectrometry To Quantify Protein Levels in FFPE Tumor Biopsies for Molecular Diagnostics. <i>Journal of Proteome Research</i> , 2018, 18, 426-435.	3.7	18
4	The helicase, DDX3X, interacts with poly(A)-binding protein 1 (PABP1) and caprin-1 at the leading edge of migrating fibroblasts and is required for efficient cell spreading. <i>Biochemical Journal</i> , 2017, 474, 3109-3120.	3.7	22
5	The amyloid architecture provides a scaffold for enzyme-like catalysts. <i>Nanoscale</i> , 2017, 9, 10773-10783.	5.6	89
6	PARP3 is a sensor of nicked nucleosomes and monoribosylates histone H2BGlu2. <i>Nature Communications</i> , 2016, 7, 12404.	12.8	60
7	Histone H2AX Y142 phosphorylation is a low abundance modification. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 139-145.	1.5	12
8	Identification of Epstein-Barr Virus Replication Proteins in Burkitt's Lymphoma Cells. <i>Pathogens</i> , 2015, 4, 739-751.	2.8	17
9	Site-specific human histone H3 methylation stability: fast K4me3 turnover. <i>Proteomics</i> , 2014, 14, 2190-2199.	2.2	30
10	Oncogene-induced cellular senescence elicits an anti-Warburg effect. <i>Proteomics</i> , 2013, 13, 2585-2596.	2.2	36
11	Novel Binding Partners and Differentially Regulated Phosphorylation Sites Clarify Eps8 as a Multi-Functional Adaptor. <i>PLoS ONE</i> , 2013, 8, e61513.	2.5	12
12	Total kinetic analysis reveals how combinatorial methylation patterns are established on lysines 27 and 36 of histone H3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13549-13554.	7.1	129
13	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.	27.8	587
14	The MMSET histone methyl transferase switches global histone methylation and alters gene expression in t(4;14) multiple myeloma cells. <i>Blood</i> , 2011, 117, 211-220.	1.4	300
15	Intact mass detection, interpretation, and visualization to automate Top-Down proteomics on a large scale. <i>Proteomics</i> , 2010, 10, 3589-3597.	2.2	48
16	Signal Transducers and Activators of Transcription-3 Binding to the Fibroblast Growth Factor Receptor Is Activated by Receptor Amplification. <i>Cancer Research</i> , 2010, 70, 3391-3401.	0.9	156
17	Kinetics of Re-establishing H3K79 Methylation Marks in Global Human Chromatin*. <i>Journal of Biological Chemistry</i> , 2010, 285, 32778-32786.	3.4	56
18	Differential Phosphoproteomics of Fibroblast Growth Factor Signaling: Identification of Src Family Kinase-Mediated Phosphorylation Events. <i>Journal of Proteome Research</i> , 2010, 9, 2317-2328.	3.7	46

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19	Size-Sorting Combined with Improved Nanocapillary Liquid Chromatography~Mass Spectrometry for Identification of Intact Proteins up to 80 kDa. <i>Analytical Chemistry</i> , 2010, 82, 1234-1244.	6.5	91
20	Large Scale Localization of Protein Phosphorylation by Use of Electron Capture Dissociation Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 904-912.	3.8	79
21	Database Search Strategies for Proteomic Data Sets Generated by Electron Capture Dissociation Mass Spectrometry. <i>Journal of Proteome Research</i> , 2009, 8, 5475-5484.	3.7	14
22	SLoMo: Automated Site Localization of Modifications from ETD/ECD Mass Spectra. <i>Journal of Proteome Research</i> , 2009, 8, 1965-1971.	3.7	92
23	On-Line Liquid Chromatography Electron Capture Dissociation for the Characterization of Phosphorylation Sites in Proteins. <i>Methods in Molecular Biology</i> , 2009, 527, 191-199.	0.9	2
24	Targeted Online Liquid Chromatography Electron Capture Dissociation Mass Spectrometry for the Localization of Sites of in Vivo Phosphorylation in Human Sprouty2. <i>Analytical Chemistry</i> , 2008, 80, 6650-6657.	6.5	30
25	The Deleted in Brachydactyly B Domain of ROR2 Is Required for Receptor Activation by Recruitment of Src. <i>PLoS ONE</i> , 2008, 3, e1873.	2.5	64
26	Electron capture dissociation in the analysis of protein phosphorylation. <i>Expert Review of Proteomics</i> , 2007, 4, 149-159.	3.0	31
27	Strategy for the Identification of Sites of Phosphorylation in Proteins:~Neutral Loss Triggered Electron Capture Dissociation. <i>Analytical Chemistry</i> , 2006, 78, 7563-7569.	6.5	56