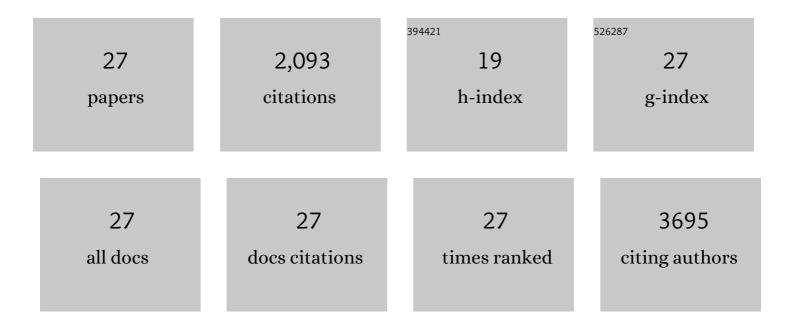
## Steve M M Sweet

List of Publications by Year in descending order

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STEVE M M SWEET

#	Article	IF	CITATIONS
1	Mapping intact protein isoforms in discovery mode using top-down proteomics. Nature, 2011, 480, 254-258.	27.8	587
2	The MMSET histone methyl transferase switches global histone methylation and alters gene expression in t(4;14) multiple myeloma cells. Blood, 2011, 117, 211-220.	1.4	300
3	Signal Transducers and Activators of Transcription-3 Binding to the Fibroblast Growth Factor Receptor Is Activated by Receptor Amplification. Cancer Research, 2010, 70, 3391-3401.	0.9	156
4	Total kinetic analysis reveals how combinatorial methylation patterns are established on lysines 27 and 36 of histone H3. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13549-13554.	7.1	129
5	SLoMo: Automated Site Localization of Modifications from ETD/ECD Mass Spectra. Journal of Proteome Research, 2009, 8, 1965-1971.	3.7	92
6	Size-Sorting Combined with Improved Nanocapillary Liquid Chromatographyâ~`Mass Spectrometry for Identification of Intact Proteins up to 80 kDa. Analytical Chemistry, 2010, 82, 1234-1244.	6.5	91
7	The amyloid architecture provides a scaffold for enzyme-like catalysts. Nanoscale, 2017, 9, 10773-10783.	5.6	89
8	Large Scale Localization of Protein Phosphorylation by Use of Electron Capture Dissociation Mass Spectrometry. Molecular and Cellular Proteomics, 2009, 8, 904-912.	3.8	79
9	The Deleted in Brachydactyly B Domain of ROR2 Is Required for Receptor Activation by Recruitment of Src. PLoS ONE, 2008, 3, e1873.	2.5	64
10	PARP3 is a sensor of nicked nucleosomes and monoribosylates histone H2BGlu2. Nature Communications, 2016, 7, 12404.	12.8	60
11	Strategy for the Identification of Sites of Phosphorylation in Proteins:  Neutral Loss Triggered Electron Capture Dissociation. Analytical Chemistry, 2006, 78, 7563-7569.	6.5	56
12	Kinetics of Re-establishing H3K79 Methylation Marks in Global Human Chromatin*. Journal of Biological Chemistry, 2010, 285, 32778-32786.	3.4	56
13	Intact mass detection, interpretation, and visualization to automate Topâ€Down proteomics on a large scale. Proteomics, 2010, 10, 3589-3597.	2.2	48
14	Differential Phosphoproteomics of Fibroblast Growth Factor Signaling: Identification of Src Family Kinase-Mediated Phosphorylation Events. Journal of Proteome Research, 2010, 9, 2317-2328.	3.7	46
15	Oncogene-induced cellular senescence elicits an anti-Warburg effect. Proteomics, 2013, 13, 2585-2596.	2.2	36
16	Electron capture dissociation in the analysis of protein phosphorylation. Expert Review of Proteomics, 2007, 4, 149-159.	3.0	31
17	Targeted Online Liquid Chromatography Electron Capture Dissociation Mass Spectrometry for the Localization of Sites of in Vivo Phosphorylation in Human Sprouty2. Analytical Chemistry, 2008, 80, 6650-6657.	6.5	30
18	Siteâ€specific human histone H3 methylation stability: fast K4me3 turnover. Proteomics, 2014, 14, 2190-2199.	2.2	30

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19	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. Biochemical Journal, 2017, 474, 3109-3120.	3.7	22
20	Data-Independent Acquisition Mass Spectrometry To Quantify Protein Levels in FFPE Tumor Biopsies for Molecular Diagnostics. Journal of Proteome Research, 2018, 18, 426-435.	3.7	18
21	Identification of Epstein-Barr Virus Replication Proteins in Burkitt's Lymphoma Cells. Pathogens, 2015, 4, 739-751.	2.8	17
22	Database Search Strategies for Proteomic Data Sets Generated by Electron Capture Dissociation Mass Spectrometry. Journal of Proteome Research, 2009, 8, 5475-5484.	3.7	14
23	Novel Binding Partners and Differentially Regulated Phosphorylation Sites Clarify Eps8 as a Multi-Functional Adaptor. PLoS ONE, 2013, 8, e61513.	2.5	12
24	Histone H2AX Y142 phosphorylation is a low abundance modification. International Journal of Mass Spectrometry, 2015, 391, 139-145.	1.5	12
25	Identifying the Cellular Interactome of Epstein-Barr Virus Lytic Regulator Zta Reveals Cellular Targets Contributing to Viral Replication. Journal of Virology, 2020, 94, .	3.4	9
26	Clobal Extraction from Parallel Reaction Monitoring to Quantify Background Peptides for Improved Normalization and Quality Control in Targeted Proteomics. Analytical Chemistry, 2021, 93, 13434-13440.	6.5	7
27	On-Line Liquid Chromatography Electron Capture Dissociation for the Characterization of Phosphorylation Sites in Proteins. Methods in Molecular Biology, 2009, 527, 191-199.	0.9	2