

# Simone Sidoli

## List of Publications by Year in descending order

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Version: 2024-02-01

138  
papers

6,056  
citations

81434

41  
h-index

111975

67  
g-index

163  
all docs

163  
docs citations

163  
times ranked

10077  
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative subcellular acyl-CoA analysis reveals distinct nuclear metabolism and isoleucine-dependent histone propionylation. <i>Molecular Cell</i> , 2022, 82, 447-462.e6.	4.5	45
2	Multi-omic profiling of histone variant H3.3 lysine 27 methylation reveals a distinct role from canonical H3 in stem cell differentiation. <i>Molecular Omics</i> , 2022, 18, 296-314.	1.4	2
3	A Dynamic and Combinatorial Histone Code Drives Malaria Parasite Asexual and Sexual Development. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100199.	2.5	11
4	Enzymatic transfer of acetate on histones from lysine reservoir sites to lysine activating sites. <i>Science Advances</i> , 2022, 8, eabj5688.	4.7	30
5	Type I and II PRMTs inversely regulate post-transcriptional intron detention through Sm and CHTOP methylation. <i>ELife</i> , 2022, 11, .	2.8	20
6	Genotype-specific features reduce the susceptibility of South American yellow fever virus strains to vaccine-induced antibodies. <i>Cell Host and Microbe</i> , 2022, 30, 248-259.e6.	5.1	11
7	Synthesis and Characterization of Transition-State Analogue Inhibitors against Human DNA Methyltransferase 1. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 5462-5494.	2.9	2
8	CpG island reconfiguration for the establishment and synchronization of polycomb functions upon exit from naive pluripotency. <i>Molecular Cell</i> , 2022, 82, 1169-1185.e7.	4.5	10
9	Macrophages use apoptotic cell-derived methionine and DNMT3A during efferocytosis to promote tissue resolution. <i>Nature Metabolism</i> , 2022, 4, 444-457.	5.1	56
10	The transcription factor PAX8 promotes angiogenesis in ovarian cancer through interaction with SOX17. <i>Science Signaling</i> , 2022, 15, eabm2496.	1.6	15
11	Pipecolic Acid, a Putative Mediator of the Encephalopathy of Cerebral Malaria and the Experimental Model of Cerebral Malaria. <i>Journal of Infectious Diseases</i> , 2022, 225, 705-714.	1.9	3
12	Altered abundances of human immunoglobulin M and immunoglobulin G subclasses in Alzheimer's disease frontal cortex. <i>Scientific Reports</i> , 2022, 12, 6934.	1.6	1
13	Methamphetamine Dysregulates Macrophage Functions and Autophagy to Mediate HIV Neuropathogenesis. <i>Biomedicine</i> , 2022, 10, 1257.	1.4	2
14	Dense Granule Protein GRA64 Interacts with Host Cell ESCRT Proteins during <i>Toxoplasma gondii</i> Infection. <i>MBio</i> , 2022, 13, .	1.8	14
15	CRISPR screening uncovers a central requirement for HHEX in pancreatic lineage commitment and plasticity restriction. <i>Nature Cell Biology</i> , 2022, 24, 1064-1076.	4.6	15
16	White adipose remodeling during browning in mice involves YBX1 to drive thermogenic commitment. <i>Molecular Metabolism</i> , 2021, 44, 101137.	3.0	13
17	H1 histones control the epigenetic landscape by local chromatin compaction. <i>Nature</i> , 2021, 589, 293-298.	13.7	101
18	One-shot analysis of translated mammalian lncRNAs with AHARIBO. <i>ELife</i> , 2021, 10, .	2.8	15

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19	Long-term behavioral and cell-type-specific molecular effects of early life stress are mediated by H3K79me2 dynamics in medium spiny neurons. <i>Nature Neuroscience</i> , 2021, 24, 667-676.	7.1	64
20	Combinatorial Histone H3 Modifications Are Dynamically Altered in Distinct Cell Cycle Phases. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1300-1311.	1.2	11
21	QSER1 protects DNA methylation valleys from de novo methylation. <i>Science</i> , 2021, 372, .	6.0	69
22	Protective neutralizing antibodies from human survivors of Crimean-Congo hemorrhagic fever. <i>Cell</i> , 2021, 184, 3486-3501.e21.	13.5	39
23	VAL genes regulate vegetative phase change via miR156-dependent and independent mechanisms. <i>PLoS Genetics</i> , 2021, 17, e1009626.	1.5	18
24	The Polycomb protein RING1B enables estrogen-mediated gene expression by promoting enhancer-promoter interaction and R-loop formation. <i>Nucleic Acids Research</i> , 2021, 49, 9768-9782.	6.5	18
25	Independent transcriptomic and proteomic regulation by type I and II protein arginine methyltransferases. <i>Science</i> , 2021, 24, 102971.	1.9	20
26	A Key Silencing Histone Mark on Chromatin Is Lost When Colorectal Adenocarcinoma Cells Are Depleted of Methionine by Methionine S-Methyltransferase. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 735303.	1.6	7
27	High throughput and low bias DNA methylation and hydroxymethylation analysis by direct injection mass spectrometry. <i>Analytica Chimica Acta</i> , 2021, 1180, 338880.	2.6	10
28	FGF-2 induces a failure of cell cycle progression in cells harboring amplified K-Ras, revealing new insights into oncogene-induced senescence. <i>Molecular Omics</i> , 2021, 17, 725-739.	1.4	2
29	DNA methylation and hydroxymethylation analysis using a high throughput and low bias direct injection mass spectrometry platform. <i>MethodsX</i> , 2021, 8, 101585.	0.7	4
30	Cytoplasmic Labile Iron Accumulates in Aging Stem Cells Perturbing a Key Rheostat for Identity Control. <i>Blood</i> , 2021, 138, 3282-3282.	0.6	1
31	FLT3 Inhibition Downregulates EZH2 in AML and Promotes Myeloid Differentiation. <i>Blood</i> , 2021, 138, 785-785.	0.6	1
32	An integrated multi-omics approach identifies epigenetic alterations associated with Alzheimer's disease. <i>Nature Genetics</i> , 2020, 52, 1024-1035.	9.4	191
33	PR-DUB maintains the expression of critical genes through FOXK1/2- and ASXL1/2/3-dependent recruitment to chromatin and H2AK119ub1 deubiquitination. <i>Genome Research</i> , 2020, 30, 1119-1130.	2.4	36
34	Guide for protein fold change and p-value calculation for non-experts in proteomics. <i>Molecular Omics</i> , 2020, 16, 573-582.	1.4	84
35	Phosphoproteomic Analysis of Rat Neutrophils Shows the Effect of Intestinal Ischemia/Reperfusion and Preconditioning on Kinases and Phosphatases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5799.	1.8	6
36	Disruption of ATRX-RNA interactions uncovers roles in ATRX localization and PRC2 function. <i>Nature Communications</i> , 2020, 11, 2219.	5.8	18

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37	Lysine 4 of histone H3.3 is required for embryonic stem cell differentiation, histone enrichment at regulatory regions and transcription accuracy. <i>Nature Genetics</i> , 2020, 52, 273-282.	9.4	37
38	Mass Spectrometry to Study Chromatin Compaction. <i>Biology</i> , 2020, 9, 140.	1.3	2
39	Mutant FOXL2C134W Hijacks SMAD4 and SMAD2/3 to Drive Adult Granulosa Cell Tumors. <i>Cancer Research</i> , 2020, 80, 3466-3479.	0.4	29
40	Bullet points to evaluate the performance of the middle-down proteomics workflow for histone modification analysis. <i>Methods</i> , 2020, 184, 86-92.	1.9	14
41	Comprehensive Map of the <i>Artemisia annua</i> Proteome and Quantification of Differential Protein Expression in Chemotypes Producing High versus Low Content of Artemisinin. <i>Proteomics</i> , 2020, 20, e1900310.	1.3	6
42	Toxoplasma gondii PPM3C, a secreted protein phosphatase, affects parasitophorous vacuole effector export. <i>PLoS Pathogens</i> , 2020, 16, e1008771.	2.1	13
43	Caenorhabditis elegans nuclear RNAi factor SET-32 deposits the transgenerational histone modification, H3K23me3. <i>ELife</i> , 2020, 9, .	2.8	32
44	A Workflow for Ultra-rapid Analysis of Histone Post-translational Modifications with Direct-injection Mass Spectrometry. <i>Bio-protocol</i> , 2020, 10, e3756.	0.2	7
45	Title is missing!. , 2020, 16, e1008771.		0
46	Title is missing!. , 2020, 16, e1008771.		0
47	Title is missing!. , 2020, 16, e1008771.		0
48	Title is missing!. , 2020, 16, e1008771.		0
49	Title is missing!. , 2020, 16, e1008771.		0
50	Title is missing!. , 2020, 16, e1008771.		0
51	Histone H3K23-specific acetylation by MORF is coupled to H3K14 acylation. <i>Nature Communications</i> , 2019, 10, 4724.	5.8	56
52	Quantitation of Single and Combinatorial Histone Modifications by Integrated Chromatography of Bottom-up Peptides and Middle-down Polypeptide Tails. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2449-2459.	1.2	18
53	A mass spectrometry-based assay using metabolic labeling to rapidly monitor chromatin accessibility of modified histone proteins. <i>Scientific Reports</i> , 2019, 9, 13613.	1.6	32
54	One minute analysis of 200 histone posttranslational modifications by direct injection mass spectrometry. <i>Genome Research</i> , 2019, 29, 978-987.	2.4	37

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55	Single Cell Proteomics by Data-Independent Acquisition To Study Embryonic Asymmetry in <i>Xenopus laevis</i> . <i>Analytical Chemistry</i> , 2019, 91, 8891-8899.	3.2	38
56	Epigenomic Reordering Induced by Polycomb Loss Drives Oncogenesis but Leads to Therapeutic Vulnerabilities in Malignant Peripheral Nerve Sheath Tumors. <i>Cancer Research</i> , 2019, 79, 3205-3219.	0.4	38
57	Regulation of proline-directed kinases and the trans-histone code H3K9me3/H4K20me3 during human myogenesis. <i>Journal of Biological Chemistry</i> , 2019, 294, 8296-8308.	1.6	11
58	Isotopic Labeling and Quantitative Proteomics of Acetylation on Histones and Beyond. <i>Methods in Molecular Biology</i> , 2019, 1977, 43-70.	0.4	12
59	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. <i>Cell Reports</i> , 2019, 27, 400-415.e5.	2.9	52
60	Integrated Analysis of Acetyl-CoA and Histone Modification via Mass Spectrometry to Investigate Metabolically Driven Acetylation. <i>Methods in Molecular Biology</i> , 2019, 1928, 125-147.	0.4	25
61	Coordination between TGF- $\beta$ 2 cellular signaling and epigenetic regulation during epithelial to mesenchymal transition. <i>Epigenetics and Chromatin</i> , 2019, 12, 11.	1.8	21
62	Histone Acetyltransferase p300 Induces De Novo Super-Enhancers to Drive Cellular Senescence. <i>Molecular Cell</i> , 2019, 73, 684-698.e8.	4.5	97
63	Deep profiling and custom databases improve detection of proteoforms generated by alternative splicing. <i>Genome Research</i> , 2019, 29, 2046-2055.	2.4	23
64	Alcohol metabolism contributes to brain histone acetylation. <i>Nature</i> , 2019, 574, 717-721.	18.7	161
65	H3K9me3-heterochromatin loss at protein-coding genes enables developmental lineage specification. <i>Science</i> , 2019, 363, 294-297.	6.0	161
66	Impaired cocaine-induced behavioral plasticity in the male offspring of cocaine-experienced sires. <i>European Journal of Neuroscience</i> , 2019, 49, 1115-1126.	1.2	24
67	Acetyl-CoA Metabolism Supports Multistep Pancreatic Tumorigenesis. <i>Cancer Discovery</i> , 2019, 9, 416-435.	7.7	184
68	Integrating Proteomics and Targeted Metabolomics to Understand Global Changes in Histone Modifications. <i>Proteomics</i> , 2018, 18, e1700309.	1.3	18
69	Assessment of Quantification Precision of Histone Post-Translational Modifications by Using an Ion Trap and down To 50,000 Cells as Starting Material. <i>Journal of Proteome Research</i> , 2018, 17, 234-242.	1.8	10
70	Graphical Interpretation and Analysis of Proteins and their Ontologies (GiaPronto): A One-Click Graph Visualization Software for Proteomics Data Sets. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1426-1431.	2.5	14
71	Protein Kinase C Epsilon Is a Key Regulator of Mitochondrial Redox Homeostasis in Acute Myeloid Leukemia. <i>Clinical Cancer Research</i> , 2018, 24, 608-618.	3.2	20
72	Distinct Roles of Two Histone Methyltransferases in Transmitting H3K36me3-Based Epigenetic Memory Across Generations in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2018, 210, 969-982.	1.2	38

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73	Analysis of the Effect of Intestinal Ischemia and Reperfusion on the Rat Neutrophils Proteome. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 89.	1.6	18
74	EpiProfile 2.0: A Computational Platform for Processing Epi-Proteomics Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2018, 17, 2533-2541.	1.8	113
75	The Tumor Suppressor CIC Directly Regulates MAPK Pathway Genes via Histone Deacetylation. <i>Cancer Research</i> , 2018, 78, 4114-4125.	0.4	56
76	Extensive Characterization of Heavily Modified Histone Tails by 193 nm Ultraviolet Photodissociation Mass Spectrometry via a Middle-Down Strategy. <i>Analytical Chemistry</i> , 2018, 90, 10425-10433.	3.2	26
77	Domain-focused CRISPR screen identifies HRI as a fetal hemoglobin regulator in human erythroid cells. <i>Science</i> , 2018, 361, 285-290.	6.0	119
78	Middle-Down MS is Ready to Answer Complex Questions in Chromatin Biology. <i>Proteomics</i> , 2018, 18, 1800131.	1.3	2
79	Abstract 5416: Isolation of the PAX8 transcriptional complex to identify novel therapeutic vulnerabilities for ovarian cancer. , 2018, , .		0
80	Neutrophil proteomic analysis reveals the participation of antioxidant enzymes, motility and ribosomal proteins in the prevention of ischemic effects by preconditioning. <i>Journal of Proteomics</i> , 2017, 151, 162-173.	1.2	10
81	Why proteomics is not the new genomics and the future of mass spectrometry in cell biology. <i>Journal of Cell Biology</i> , 2017, 216, 21-24.	2.3	28
82	Paternal cocaine taking elicits epigenetic remodeling and memory deficits in male progeny. <i>Molecular Psychiatry</i> , 2017, 22, 1641-1650.	4.1	53
83	Multicellular Tumor Spheroids Combined with Mass Spectrometric Histone Analysis To Evaluate Epigenetic Drugs. <i>Analytical Chemistry</i> , 2017, 89, 2773-2781.	3.2	27
84	Time-resolved Global and Chromatin Proteomics during Herpes Simplex Virus Type 1 (HSV-1) Infection. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S92-S107.	2.5	76
85	Quantitative chromatin proteomics reveals a dynamic histone post-translational modification landscape that defines asexual and sexual <i>Plasmodium falciparum</i> parasites. <i>Scientific Reports</i> , 2017, 7, 607.	1.6	60
86	Abnormal levels of histone methylation in the retinas of diabetic rats are reversed by minocycline treatment. <i>Scientific Reports</i> , 2017, 7, 45103.	1.6	18
87	Sample Preparation for Mass Spectrometry-based Identification of RNA-binding Regions. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	1
88	Identification of Nidogen 1 as a lung metastasis protein through secretome analysis. <i>Genes and Development</i> , 2017, 31, 1439-1455.	2.7	41
89	An HDAC3-PROX1 corepressor module acts on HNF4 $\beta$ to control hepatic triglycerides. <i>Nature Communications</i> , 2017, 8, 549.	5.8	52
90	Phosphoproteomics reveals that glycogen synthase kinase-3 phosphorylates multiple splicing factors and is associated with alternative splicing. <i>Journal of Biological Chemistry</i> , 2017, 292, 18240-18255.	1.6	52

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91	Proteome-wide acetylation dynamics in human cells. <i>Scientific Reports</i> , 2017, 7, 10296.	1.6	42
92	Characterization of histone acylations links chromatin modifications with metabolism. <i>Nature Communications</i> , 2017, 8, 1141.	5.8	145
93	Recent Achievements in Characterizing the Histone Code and Approaches to Integrating Epigenomics and Systems Biology. <i>Methods in Enzymology</i> , 2017, 586, 359-378.	0.4	44
94	Middle-down proteomics: a still unexploited resource for chromatin biology. <i>Expert Review of Proteomics</i> , 2017, 14, 617-626.	1.3	67
95	Characterization of Individual Histone Posttranslational Modifications and Their Combinatorial Patterns by Mass Spectrometry-Based Proteomics Strategies. <i>Methods in Molecular Biology</i> , 2017, 1528, 121-148.	0.4	38
96	High performance mass spectrometry based proteomics reveals enzyme and signaling pathway regulation in neutrophils during the early stage of surgical trauma. <i>Proteomics - Clinical Applications</i> , 2017, 11, 1600001.	0.8	10
97	Nuclear phosphoproteome analysis of 3T3L1 preadipocyte differentiation reveals system-wide phosphorylation of transcriptional regulators. <i>Proteomics</i> , 2017, 17, 1600248.	1.3	10
98	Genomic and Proteomic Resolution of Heterochromatin and Its Restriction of Alternate Fate Genes. <i>Molecular Cell</i> , 2017, 68, 1023-1037.e15.	4.5	159
99	Metabolic labeling in middle-down proteomics allows for investigation of the dynamics of the histone code. <i>Epigenetics and Chromatin</i> , 2017, 10, 34.	1.8	32
100	Abstract 684: Integrative proteomics and transcriptomics to define the cell surface landscape of neuroblastoma. , 2017, , .		0
101	Dynamic changes of histone H3 marks during <i>Caenorhabditis elegans</i> lifecycle revealed by middle-down proteomics. <i>Proteomics</i> , 2016, 16, 459-464.	1.3	18
102	Multiplexed data independent acquisition (MSX-DIA) applied by high resolution mass spectrometry improves quantification quality for the analysis of histone peptides. <i>Proteomics</i> , 2016, 16, 2095-2105.	1.3	21
103	Identification and Quantification of Histone PTMs Using High-Resolution Mass Spectrometry. <i>Methods in Enzymology</i> , 2016, 574, 3-29.	0.4	34
104	Roles of H3K27me2 and H3K27me3 Examined during Fate Specification of Embryonic Stem Cells. <i>Cell Reports</i> , 2016, 17, 1369-1382.	2.9	66
105	High-Resolution Mapping of RNA-Binding Regions in the Nuclear Proteome of Embryonic Stem Cells. <i>Molecular Cell</i> , 2016, 64, 416-430.	4.5	226
106	Complete Workflow for Analysis of Histone Post-translational Modifications Using Bottom-up Mass Spectrometry: From Histone Extraction to Data Analysis. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	138
107	Histone modification profiling reveals differential signatures associated with human embryonic stem cell self-renewal and differentiation. <i>Proteomics</i> , 2016, 16, 448-458.	1.3	29
108	Differential quantification of isobaric phosphopeptides using data-independent acquisition mass spectrometry. <i>Molecular BioSystems</i> , 2016, 12, 2385-2388.	2.9	11

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109	Systems Level Analysis of Histone H3 Post-translational Modifications (PTMs) Reveals Features of PTM Crosstalk in Chromatin Regulation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2715-2729.	2.5	76
110	Histone H4 acetylation and the epigenetic reader Brd4 are critical regulators of pluripotency in embryonic stem cells. <i>BMC Genomics</i> , 2016, 17, 95.	1.2	55
111	Analyses of Histone Proteoforms Using Front-end Electron Transfer Dissociation-enabled Orbitrap Instruments. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 975-988.	2.5	43
112	Loss of HP1 causes depletion of H3K27me3 from facultative heterochromatin and gain of H3K27me2 at constitutive heterochromatin. <i>Genome Research</i> , 2016, 26, 97-107.	2.4	96
113	Properly reading the histone code by MS-based proteomics. <i>Proteomics</i> , 2015, 15, 2901-2902.	1.3	12
114	EpiProfile Quantifies Histone Peptides With Modifications by Extracting Retention Time and Intensity in High-resolution Mass Spectra*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1696-1707.	2.5	81
115	Application of Mass Spectrometry in Translational Epigenetics. , 2015, , 55-78.		2
116	Optimization of calmodulin-affinity chromatography for brain and organelles. <i>EuPA Open Proteomics</i> , 2015, 8, 55-67.	2.5	1
117	Defining heterochromatin in <i>C. elegans</i> through genome-wide analysis of the heterochromatin protein 1 homolog HPL-2. <i>Genome Research</i> , 2015, 25, 76-88.	2.4	68
118	Proteogenomics analysis reveals specific genomic orientations of distal regulatory regions composed by non-canonical histone variants. <i>Epigenetics and Chromatin</i> , 2015, 8, 13.	1.8	10
119	Two distinct modes for propagation of histone PTMs across the cell cycle. <i>Genes and Development</i> , 2015, 29, 585-590.	2.7	334
120	Bottom-Up and Middle-Down Proteomics Have Comparable Accuracies in Defining Histone Post-Translational Modification Relative Abundance and Stoichiometry. <i>Analytical Chemistry</i> , 2015, 87, 3129-3133.	3.2	47
121	Quantitative proteomics analysis of platelet-derived microparticles reveals distinct protein signatures when stimulated by different physiological agonists. <i>Journal of Proteomics</i> , 2015, 121, 56-66.	1.2	81
122	Sequential Window Acquisition of all Theoretical Mass Spectra (SWATH) Analysis for Characterization and Quantification of Histone Post-translational Modifications. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2420-2428.	2.5	87
123	Progress in epigenetic histone modification analysis by mass spectrometry for clinical investigations. <i>Expert Review of Proteomics</i> , 2015, 12, 499-517.	1.3	51
124	Low Resolution Data-Independent Acquisition in an LTQ-Orbitrap Allows for Simplified and Fully Untargeted Analysis of Histone Modifications. <i>Analytical Chemistry</i> , 2015, 87, 11448-11454.	3.2	51
125	H3K23me2 is a new heterochromatic mark in <i>Caenorhabditis elegans</i> . <i>Nucleic Acids Research</i> , 2015, 43, gkv1063.	6.5	37
126	Drawbacks in the use of unconventional hydrophobic anhydrides for histone derivatization in bottom-up proteomics PTM analysis. <i>Proteomics</i> , 2015, 15, 1459-1469.	1.3	33



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127	Tumor suppressor ASXL1 is essential for the activation of INK4B expression in response to oncogene activity and anti-proliferative signals. <i>Cell Research</i> , 2015, 25, 1205-1218.	5.7	41
128	Top-down and Middle-down Protein Analysis Reveals that Intact and Clipped Human Histones Differ in Post-translational Modification Patterns*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3142-3153.	2.5	49
129	The PZP Domain of AF10 Senses Unmodified H3K27 to Regulate DOT1L-Mediated Methylation of H3K79. <i>Molecular Cell</i> , 2015, 60, 319-327.	4.5	78
130	Large Scale Analysis of Co-existing Post-translational Modifications in Histone Tails Reveals Global Fine Structure of Cross-talk. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1855-1865.	2.5	65
131	Comparative Proteomic Analysis of Histone Post-translational Modifications upon Ischemia/Reperfusion-Induced Retinal Injury. <i>Journal of Proteome Research</i> , 2014, 13, 2175-2186.	1.8	16
132	Middle-down hybrid chromatography/tandem mass spectrometry workflow for characterization of combinatorial post-translational modifications in histones. <i>Proteomics</i> , 2014, 14, 2200-2211.	1.3	76
133	KYSS: Mass spectrometry data quality assessment for protein analysis and large-scale proteomics. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 702-707.	1.0	3
134	Transcription Factor Cooperativity in Early Adipogenic Hotspots and Super-Enhancers. <i>Cell Reports</i> , 2014, 7, 1443-1455.	2.9	199
135	A Rapid Size-Exclusion Solid-Phase Extraction Step for Enhanced Sensitivity in Multi-Allergen Determination in Dark Chocolate and Biscuits by Liquid Chromatography-Tandem Mass Spectrometry. <i>Food Analytical Methods</i> , 2013, 6, 1144-1152.	1.3	35
136	Precision Mapping of Coexisting Modifications in Histone H3 Tails from Embryonic Stem Cells by ETD-MS/MS. <i>Analytical Chemistry</i> , 2013, 85, 8232-8239.	3.2	70
137	The <i>C. elegans</i> H3K27 Demethylase UTX-1 Is Essential for Normal Development, Independent of Its Enzymatic Activity. <i>PLoS Genetics</i> , 2012, 8, e1002647.	1.5	59
138	Proteomics in chromatin biology and epigenetics: Elucidation of post-translational modifications of histone proteins by mass spectrometry. <i>Journal of Proteomics</i> , 2012, 75, 3419-3433.	1.2	115