

Benjamin A Garcia

List of Publications by Year in descending order

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Version: 2024-02-01

254
papers

25,939
citations

12330

69
h-index

8630

146
g-index

268
all docs

268
docs citations

268
times ranked

37117
citing authors

#	ARTICLE	IF	CITATIONS
1	Tumour exosome integrins determine organotropic metastasis. <i>Nature</i> , 2015, 527, 329-335.	27.8	3,688
2	Inhibition of PRC2 Activity by a Gain-of-Function H3 Mutation Found in Pediatric Glioblastoma. <i>Science</i> , 2013, 340, 857-861.	12.6	1,074
3	Cytoplasmic chromatin triggers inflammation in senescence and cancer. <i>Nature</i> , 2017, 550, 402-406.	27.8	851
4	Regulation of HP1â€‘chromatin binding by histone H3 methylation and phosphorylation. <i>Nature</i> , 2005, 438, 1116-1122.	27.8	834
5	Human chimeric antigen receptor macrophages for cancer immunotherapy. <i>Nature Biotechnology</i> , 2020, 38, 947-953.	17.5	692
6	Extracellular Vesicle and Particle Biomarkers Define Multiple Human Cancers. <i>Cell</i> , 2020, 182, 1044-1061.e18.	28.9	691
7	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
8	Akt-Dependent Metabolic Reprogramming Regulates Tumor Cell Histone Acetylation. <i>Cell Metabolism</i> , 2014, 20, 306-319.	16.2	473
9	SnapShot: Histone Modifications. <i>Cell</i> , 2014, 159, 458-458.e1.	28.9	362
10	The histone lysine methyltransferase KMT2D sustains a gene expression program that represses B cell lymphoma development. <i>Nature Medicine</i> , 2015, 21, 1199-1208.	30.7	359
11	The histone mark H3K36me2 recruits DNMT3A and shapes the intergenic DNA methylation landscape. <i>Nature</i> , 2019, 573, 281-286.	27.8	338
12	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. <i>Nature</i> , 2014, 510, 283-287.	27.8	331
13	Histone H3K36 mutations promote sarcomagenesis through altered histone methylation landscape. <i>Science</i> , 2016, 352, 844-849.	12.6	327
14	Chemical derivatization of histones for facilitated analysis by mass spectrometry. <i>Nature Protocols</i> , 2007, 2, 933-938.	12.0	324
15	Mll3 and Mll4 Facilitate Enhancer RNA Synthesis and Transcription from Promoters Independently of H3K4 Monomethylation. <i>Molecular Cell</i> , 2017, 66, 568-576.e4.	9.7	322
16	Comprehensive Catalog of Currently Documented Histone Modifications. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a025064.	5.5	320
17	Quantitative Proteomic Analysis of Histone Modifications. <i>Chemical Reviews</i> , 2015, 115, 2376-2418.	47.7	306
18	Histone serotonylation is a permissive modification that enhances TFIIID binding to H3K4me3. <i>Nature</i> , 2019, 567, 535-539.	27.8	292

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19	The Platelet Microparticle Proteome. <i>Journal of Proteome Research</i> , 2005, 4, 1516-1521.	3.7	278
20	Expression Patterns and Post-translational Modifications Associated with Mammalian Histone H3 Variants. <i>Journal of Biological Chemistry</i> , 2006, 281, 559-568.	3.4	278
21	Acetate Production from Glucose and Coupling to Mitochondrial Metabolism in Mammals. <i>Cell</i> , 2018, 175, 502-513.e13.	28.9	269
22	Organismal Differences in Post-translational Modifications in Histones H3 and H4. <i>Journal of Biological Chemistry</i> , 2007, 282, 7641-7655.	3.4	267
23	Critical Role of Histone Turnover in Neuronal Transcription and Plasticity. <i>Neuron</i> , 2015, 87, 77-94.	8.1	257
24	BRD4 assists elongation of both coding and enhancer RNAs by interacting with acetylated histones. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1047-1057.	8.2	247
25	SIRT1 is downregulated by autophagy in senescence and ageing. <i>Nature Cell Biology</i> , 2020, 22, 1170-1179.	10.3	236
26	High-Resolution Mapping of RNA-Binding Regions in the Nuclear Proteome of Embryonic Stem Cells. <i>Molecular Cell</i> , 2016, 64, 416-430.	9.7	226
27	Capturing the Onset of PRC2-Mediated Repressive Domain Formation. <i>Molecular Cell</i> , 2018, 70, 1149-1162.e5.	9.7	222
28	A Specific LSD1/KDM1A Isoform Regulates Neuronal Differentiation through H3K9 Demethylation. <i>Molecular Cell</i> , 2015, 57, 957-970.	9.7	221
29	H3K27M induces defective chromatin spread of PRC2-mediated repressive H3K27me2/me3 and is essential for glioma tumorigenesis. <i>Nature Communications</i> , 2019, 10, 1262.	12.8	215
30	Impaired H3K36 methylation defines a subset of head and neck squamous cell carcinomas. <i>Nature Genetics</i> , 2017, 49, 180-185.	21.4	195
31	Detection of early pancreatic ductal adenocarcinoma with thrombospondin-2 and CA19-9 blood markers. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	193
32	An integrated multi-omics approach identifies epigenetic alterations associated with Alzheimer's disease. <i>Nature Genetics</i> , 2020, 52, 1024-1035.	21.4	191
33	Selective inhibition of EZH2 and EZH1 enzymatic activity by a small molecule suppresses MLL-rearranged leukemia. <i>Blood</i> , 2015, 125, 346-357.	1.4	188
34	Acetyl-CoA Metabolism Supports Multistep Pancreatic Tumorigenesis. <i>Cancer Discovery</i> , 2019, 9, 416-435.	9.4	184
35	Targeting CDK9 Reactivates Epigenetically Silenced Genes in Cancer. <i>Cell</i> , 2018, 175, 1244-1258.e26.	28.9	182
36	Microbes vs. chemistry in the origin of the anaerobic gut lumen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4170-4175.	7.1	176

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37	MacroH2A histone variants act as a barrier upon reprogramming towards pluripotency. <i>Nature Communications</i> , 2013, 4, 1565.	12.8	169
38	Genomic and Proteomic Resolution of Heterochromatin and Its Restriction of Alternate Fate Genes. <i>Molecular Cell</i> , 2017, 68, 1023-1037.e15.	9.7	159
39	Inhibition of DHHC20-Mediated EGFR Palmitoylation Creates a Dependence on EGFR Signaling. <i>Molecular Cell</i> , 2016, 62, 385-396.	9.7	147
40	The Neuropeptide Corazonin Controls Social Behavior and Caste Identity in Ants. <i>Cell</i> , 2017, 170, 748-759.e12.	28.9	146
41	Characterization of histone acylations links chromatin modifications with metabolism. <i>Nature Communications</i> , 2017, 8, 1141.	12.8	145
42	Lowered H3K27me3 and DNA hypomethylation define poorly prognostic pediatric posterior fossa ependymomas. <i>Science Translational Medicine</i> , 2016, 8, 366ra161.	12.4	144
43	Pervasive H3K27 Acetylation Leads to ERV Expression and a Therapeutic Vulnerability in H3K27M Gliomas. <i>Cancer Cell</i> , 2019, 35, 782-797.e8.	16.8	143
44	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, , .	0.3	138
45	The Cerebral Cavemous Malformation Pathway Controls Cardiac Development via Regulation of Endocardial MEKK3 Signaling and KLF Expression. <i>Developmental Cell</i> , 2015, 32, 168-180.	7.0	137
46	PFA ependymoma-associated protein EZHIP inhibits PRC2 activity through a H3 K27M-like mechanism. <i>Nature Communications</i> , 2019, 10, 2146.	12.8	136
47	Resetting the Epigenetic Histone Code in the MRL-lpr/lpr Mouse Model of Lupus by Histone Deacetylase Inhibition. <i>Journal of Proteome Research</i> , 2005, 4, 2032-2042.	3.7	135
48	Large-scale global identification of protein lysine methylation in vivo. <i>Epigenetics</i> , 2013, 8, 477-485.	2.7	125
49	Reproductive tract extracellular vesicles are sufficient to transmit intergenerational stress and program neurodevelopment. <i>Nature Communications</i> , 2020, 11, 1499.	12.8	125
50	Characterization of Phosphorylation Sites on Histone H1 Isoforms by Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 1219-1227.	3.7	119
51	Analysis of protein phosphorylation by mass spectrometry. <i>Methods</i> , 2005, 35, 256-264.	3.8	116
52	Comprehensive analysis of histone post-translational modifications in mouse and human male germ cells. <i>Epigenetics and Chromatin</i> , 2016, 9, 24.	3.9	113
53	EpiProfile 2.0: A Computational Platform for Processing Epi-Proteomics Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2018, 17, 2533-2541.	3.7	113
54	Breaking the histone code with quantitative mass spectrometry. <i>Expert Review of Proteomics</i> , 2011, 8, 631-643.	3.0	105

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55	LLY-507, a Cell-active, Potent, and Selective Inhibitor of Protein-lysine Methyltransferase SMYD2. <i>Journal of Biological Chemistry</i> , 2015, 290, 13641-13653.	3.4	104
56	H1 histones control the epigenetic landscape by local chromatin compaction. <i>Nature</i> , 2021, 589, 293-298.	27.8	101
57	Analytical tools and current challenges in the modern era of neuroepigenomics. <i>Nature Neuroscience</i> , 2014, 17, 1476-1490.	14.8	100
58	Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. <i>Molecular Cell</i> , 2018, 70, 422-434.e6.	9.7	100
59	Histone Acetyltransferase p300 Induces De Novo Super-Enhancers to Drive Cellular Senescence. <i>Molecular Cell</i> , 2019, 73, 684-698.e8.	9.7	97
60	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.	5.5	96
61	Unique roles for histone H3K9me states in RNAi and heritable silencing of transcription. <i>Nature</i> , 2017, 547, 463-467.	27.8	96
62	Glucose Metabolism Drives Histone Acetylation Landscape Transitions that Dictate Muscle Stem Cell Function. <i>Cell Reports</i> , 2019, 27, 3939-3955.e6.	6.4	94
63	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. <i>Cell</i> , 2020, 183, 1617-1633.e22.	28.9	93
64	RNA exploits an exposed regulatory site to inhibit the enzymatic activity of PRC2. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 237-247.	8.2	88
65	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.	3.8	87
66	Recognition of Histone Crotonylation by Taf14 Links Metabolic State to Gene Expression. <i>Molecular Cell</i> , 2019, 76, 909-921.e3.	9.7	83
67	Taxane-Platin-Resistant Lung Cancers Co-develop Hypersensitivity to JumonjiC Demethylase Inhibitors. <i>Cell Reports</i> , 2017, 19, 1669-1684.	6.4	82
68	Modifications of Human Histone H3 Variants during Mitosis. <i>Biochemistry</i> , 2005, 44, 13202-13213.	2.5	81
69	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.	3.8	81
70	Origins and Formation of Histone Methylation across the Human Cell Cycle. <i>Molecular and Cellular Biology</i> , 2012, 32, 2503-2514.	2.3	79
71	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. <i>Cell</i> , 2020, 181, 1329-1345.e24.	28.9	79
72	The PZP Domain of AF10 Senses Unmodified H3K27 to Regulate DOT1L-Mediated Methylation of H3K79. <i>Molecular Cell</i> , 2015, 60, 319-327.	9.7	78

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73	Systematic Epigenomic Analysis Reveals Chromatin States Associated with Melanoma Progression. <i>Cell Reports</i> , 2017, 19, 875-889.	6.4	78
74	KMT2D regulates p63 target enhancers to coordinate epithelial homeostasis. <i>Genes and Development</i> , 2018, 32, 181-193.	5.9	77
75	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.	3.8	76
76	Automethylation of PRC2 promotes H3K27 methylation and is impaired in H3K27M pediatric glioma. <i>Genes and Development</i> , 2019, 33, 1428-1440.	5.9	75
77	Native Chromatin Proteomics Reveals a Role for Specific Nucleoporins in Heterochromatin Organization and Maintenance. <i>Molecular Cell</i> , 2020, 77, 51-66.e8.	9.7	75
78	A Dual Inhibitory Mechanism Sufficient to Maintain Cell-Cycle-Restricted CENP-A Assembly. <i>Molecular Cell</i> , 2017, 65, 231-246.	9.7	71
79	Naked Mole Rat Cells Have a Stable Epigenome that Resists iPSC Reprogramming. <i>Stem Cell Reports</i> , 2017, 9, 1721-1734.	4.8	71
80	Bacterial colonization reprograms the neonatal gut metabolome. <i>Nature Microbiology</i> , 2020, 5, 838-847.	13.3	70
81	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.	5.5	68
82	Quantitative Profiling of the Activity of Protein Lysine Methyltransferase SMYD2 Using SILAC-Based Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 892-905.	3.8	68
83	Middle-down proteomics: a still unexploited resource for chromatin biology. <i>Expert Review of Proteomics</i> , 2017, 14, 617-626.	3.0	67
84	Roles of H3K27me2 and H3K27me3 Examined during Fate Specification of Embryonic Stem Cells. <i>Cell Reports</i> , 2016, 17, 1369-1382.	6.4	66
85	Mapping H4K20me3 onto the chromatin landscape of senescent cells indicates a function in control of cell senescence and tumor suppression through preservation of genetic and epigenetic stability. <i>Genome Biology</i> , 2016, 17, 158.	8.8	65
86	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.	14.8	64
87	A Novel Quantitative Mass Spectrometry Platform for Determining Protein O-GlcNAcylation Dynamics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2462-2475.	3.8	63
88	TDP-43 Promotes Neurodegeneration by Impairing Chromatin Remodeling. <i>Current Biology</i> , 2017, 27, 3579-3590.e6.	3.9	63
89	Identification and interrogation of combinatorial histone modifications. <i>Frontiers in Genetics</i> , 2013, 4, 264.	2.3	62
90	Identification of nuclear hormone receptor pathways causing insulin resistance by transcriptional and epigenomic analysis. <i>Nature Cell Biology</i> , 2015, 17, 44-56.	10.3	61

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91	Co-repressor CBFA2T2 regulates pluripotency and germline development. <i>Nature</i> , 2016, 534, 387-390.	27.8	61
92	Tet2 Catalyzes Stepwise 5-Methylcytosine Oxidation by an Iterative and <i>de novo</i> Mechanism. <i>Journal of the American Chemical Society</i> , 2016, 138, 730-733.	13.7	60
93	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.	3.3	60
94	HDAC inhibition results in widespread alteration of the histone acetylation landscape and BRD4 targeting to gene bodies. <i>Cell Reports</i> , 2021, 34, 108638.	6.4	60
95	Mutations along a TET2 active site scaffold stall oxidation at 5-hydroxymethylcytosine. <i>Nature Chemical Biology</i> , 2017, 13, 181-187.	8.0	59
96	Chromatin Kinases Act on Transcription Factors and Histone Tails in Regulation of Inducible Transcription. <i>Molecular Cell</i> , 2016, 64, 347-361.	9.7	58
97	PHF19 promotes multiple myeloma tumorigenicity through PRC2 activation and broad H3K27me3 domain formation. <i>Blood</i> , 2019, 134, 1176-1189.	1.4	57
98	Histone H3.3 C34 mutations promote aberrant PRC2 activity and drive tumor progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27354-27364.	7.1	57
99	Histone H3K23-specific acetylation by MORF is coupled to H3K14 acylation. <i>Nature Communications</i> , 2019, 10, 4724.	12.8	56
100	Comprehensive Phosphoprotein Analysis of Linker Histone H1 from <i>Tetrahymena thermophila</i> . <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1593-1609.	3.8	55
101	Mass Spectrometric Analysis of Histone Proteoforms. <i>Annual Review of Analytical Chemistry</i> , 2014, 7, 113-128.	5.4	55
102	Histone H4 acetylation and the epigenetic reader Brd4 are critical regulators of pluripotency in embryonic stem cells. <i>BMC Genomics</i> , 2016, 17, 95.	2.8	55
103	Vitamin C induces specific demethylation of H3K9me2 in mouse embryonic stem cells via Kdm3a/b. <i>Epigenetics and Chromatin</i> , 2017, 10, 36.	3.9	55
104	High-Quality Genome Assemblies Reveal Long Non-coding RNAs Expressed in Ant Brains. <i>Cell Reports</i> , 2018, 23, 3078-3090.	6.4	54
105	Global Regulation of the Histone Mark H3K36me2 Underlies Epithelial Plasticity and Metastatic Progression. <i>Cancer Discovery</i> , 2020, 10, 854-871.	9.4	54
106	A computational platform for high-throughput analysis of RNA sequences and modifications by mass spectrometry. <i>Nature Communications</i> , 2020, 11, 926.	12.8	54
107	Stable-isotope-labeled Histone Peptide Library for Histone Post-translational Modification and Variant Quantification by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2450-2466.	3.8	53
108	A Global View of RNA-Protein Interactions Identifies Post-transcriptional Regulators of Root Hair Cell Fate. <i>Developmental Cell</i> , 2017, 41, 204-220.e5.	7.0	53

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109	Biochemical and functional characterization of mutant KRAS epitopes validates this oncoprotein for immunological targeting. <i>Nature Communications</i> , 2021, 12, 4365.	12.8	53
110	An HDAC3-PROX1 corepressor module acts on HNF4 β to control hepatic triglycerides. <i>Nature Communications</i> , 2017, 8, 549.	12.8	52
111	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. <i>Cell Reports</i> , 2019, 27, 400-415.e5.	6.4	52
112	Target identification reveals lanosterol synthase as a vulnerability in glioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7957-7962.	7.1	52
113	Progress in epigenetic histone modification analysis by mass spectrometry for clinical investigations. <i>Expert Review of Proteomics</i> , 2015, 12, 499-517.	3.0	51
114	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.	6.5	51
115	The HDAC3 β -SMARCA4 β -miR-27a axis promotes expression of the <i>PAX3:FOXO1</i> fusion oncogene in rhabdomyosarcoma. <i>Science Signaling</i> , 2018, 11, .	3.6	51
116	H3K27M in Gliomas Causes a One-Step Decrease in H3K27 Methylation and Reduced Spreading within the Constraints of H3K36 Methylation. <i>Cell Reports</i> , 2020, 33, 108390.	6.4	50
117	The NANC1 β -Nkx2.1 gene duplex buffers Nkx2.1 expression to maintain lung development and homeostasis. <i>Genes and Development</i> , 2017, 31, 889-903.	5.9	49
118	Identifying Host Factors Associated with DNA Replicated During Virus Infection. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2079-2097.	3.8	49
119	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.	6.5	47
120	Nitric Oxide Regulates Gene Expression in Cancers by Controlling Histone Posttranslational Modifications. <i>Cancer Research</i> , 2015, 75, 5299-5308.	0.9	47
121	PRDM16 Suppresses MLL1 β Leukemia via Intrinsic Histone Methyltransferase Activity. <i>Molecular Cell</i> , 2016, 62, 222-236.	9.7	46
122	Folate deficiency affects histone methylation. <i>Medical Hypotheses</i> , 2016, 88, 63-67.	1.5	43
123	Analyses of Histone Proteoforms Using Front-end Electron Transfer Dissociation-enabled Orbitrap Instruments. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 975-988.	3.8	43
124	Uncovering BRD4 hyperphosphorylation associated with cellular transformation in NUT midline carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5352-E5361.	7.1	43
125	Histone Methylation Has Dynamics Distinct from Those of Histone Acetylation in Cell Cycle Reentry from Quiescence. <i>Molecular and Cellular Biology</i> , 2014, 34, 3968-3980.	2.3	42
126	H4K44 Acetylation Facilitates Chromatin Accessibility during Meiosis. <i>Cell Reports</i> , 2015, 13, 1772-1780.	6.4	42

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127	Proteome-wide acetylation dynamics in human cells. <i>Scientific Reports</i> , 2017, 7, 10296.	3.3	42
128	Interrogation of nonconserved human adipose lincRNAs identifies a regulatory role of <i>linc-ADAL</i> in adipocyte metabolism. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	42
129	TET2 chemically modifies tRNAs and regulates tRNA fragment levels. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 62-70.	8.2	42
130	Chromatin dysregulation associated with NSD1 mutation in head and neck squamous cell carcinoma. <i>Cell Reports</i> , 2021, 34, 108769.	6.4	42
131	Recognition of Histone H3K14 Acylation by MORF. <i>Structure</i> , 2017, 25, 650-654.e2.	3.3	41
132	Identification of Nidogen 1 as a lung metastasis protein through secretome analysis. <i>Genes and Development</i> , 2017, 31, 1439-1455.	5.9	41
133	N ⁶ -methyladenosine and RNA secondary structure affect transcript stability and protein abundance during systemic salt stress in <i>Arabidopsis</i> . <i>Plant Direct</i> , 2020, 4, e00239.	1.9	41
134	H3.3 G34W Promotes Growth and Impedes Differentiation of Osteoblast-Like Mesenchymal Progenitors in Giant Cell Tumor of Bone. <i>Cancer Discovery</i> , 2020, 10, 1968-1987.	9.4	40
135	Multi-faceted quantitative proteomics analysis of histone H2B isoforms and their modifications. <i>Epigenetics and Chromatin</i> , 2015, 8, 15.	3.9	39
136	Characterization of BRD4 during Mammalian Postmeiotic Sperm Development. <i>Molecular and Cellular Biology</i> , 2015, 35, 1433-1448.	2.3	38
137	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.	0.9	38
138	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.	2.9	38
139	Single Cell Proteomics by Data-Independent Acquisition To Study Embryonic Asymmetry in <i>Xenopus laevis</i> . <i>Analytical Chemistry</i> , 2019, 91, 8891-8899.	6.5	38
140	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.	0.9	38
141	Histone modification signatures in human sperm distinguish clinical abnormalities. <i>Journal of Assisted Reproduction and Genetics</i> , 2019, 36, 267-275.	2.5	38
142	Chromatin-mediated alternative splicing regulates cocaine-reward behavior. <i>Neuron</i> , 2021, 109, 2943-2966.e8.	8.1	38
143	Protein profile of osteoarthritic human articular cartilage using tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 2999-3006.	1.5	37
144	One minute analysis of 200 histone posttranslational modifications by direct injection mass spectrometry. <i>Genome Research</i> , 2019, 29, 978-987.	5.5	37

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145	Quantitative live cell imaging reveals influenza virus manipulation of Rab11A transport through reduced dynein association. <i>Nature Communications</i> , 2020, 11, 23.	12.8	37
146	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.	21.4	37
147	Histone Acetyltransferase MOF Blocks Acquisition of Quiescence in Ground-State ESCs through Activating Fatty Acid Oxidation. <i>Cell Stem Cell</i> , 2020, 27, 441-458.e10.	11.1	37
148	Improved SILAC Quantification with Data-Independent Acquisition to Investigate Bortezomib-Induced Protein Degradation. <i>Journal of Proteome Research</i> , 2021, 20, 1918-1927.	3.7	36
149	Histone H3K27 dimethyl loss is highly specific for malignant peripheral nerve sheath tumor and distinguishes true PRC2 loss from isolated H3K27 trimethyl loss. <i>Modern Pathology</i> , 2019, 32, 1434-1446.	5.5	34
150	Drawbacks in the use of unconventional hydrophobic anhydrides for histone derivatization in bottom-up proteomics PTM analysis. <i>Proteomics</i> , 2015, 15, 1459-1469.	2.2	33
151	HYPERsol: High-Quality Data from Archival FFPE Tissue for Clinical Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 973-983.	3.7	33
152	Accelerating the Field of Epigenetic Histone Modification Through Mass Spectrometry-Based Approaches. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100006.	3.8	33
153	KAT6A and ENL Form an Epigenetic Transcriptional Control Module to Drive Critical Leukemogenic Gene-Expression Programs. <i>Cancer Discovery</i> , 2022, 12, 792-811.	9.4	33
154	Metabolic labeling in middle-down proteomics allows for investigation of the dynamics of the histone code. <i>Epigenetics and Chromatin</i> , 2017, 10, 34.	3.9	32
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