

# Benjamin A Garcia

## List of Publications by Year in descending order

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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	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
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.	2.8	2
3	A Dynamic and Combinatorial Histone Code Drives Malaria Parasite Asexual and Sexual Development. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100199.	3.8	11
4	Structural visualization of de novo transcription initiation by <i>Saccharomyces cerevisiae</i> RNA polymerase II. <i>Molecular Cell</i> , 2022, 82, 660-676.e9.	9.7	9
5	Enzymatic transfer of acetate on histones from lysine reservoir sites to lysine activating sites. <i>Science Advances</i> , 2022, 8, eabj5688.	10.3	30
6	Data-Independent Acquisition for the Detection of Mononucleoside RNA Modifications by Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 885-893.	2.8	7
7	The Non-pregnant and Pregnant Human Cervix: a Systematic Proteomic Analysis. <i>Reproductive Sciences</i> , 2022, 29, 1542-1559.	2.5	4
8	The transcription factor PAX8 promotes angiogenesis in ovarian cancer through interaction with SOX17. <i>Science Signaling</i> , 2022, 15, eabm2496.	3.6	15
9	H3K36 dimethylation shapes the epigenetic interaction landscape by directing repressive chromatin modifications in embryonic stem cells. <i>Genome Research</i> , 2022, , gr.276383.121.	5.5	17
10	Chromatin profiling in human neurons reveals aberrant roles for histone acetylation and BET family proteins in schizophrenia. <i>Nature Communications</i> , 2022, 13, 2195.	12.8	13
11	Permethylated Ribonucleosides Provides Enhanced Mass Spectrometry Quantification of Post-Transcriptional RNA Modifications. <i>Analytical Chemistry</i> , 2022, 94, 7246-7254.	6.5	6
12	NSD1 mediates antagonism between SWI/SNF and polycomb complexes and is required for transcriptional activation upon EZH2 inhibition. <i>Molecular Cell</i> , 2022, 82, 2472-2489.e8.	9.7	18
13	TET2 chemically modifies tRNAs and regulates tRNA fragment levels. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 62-70.	8.2	42
14	Accelerating the Field of Epigenetic Histone Modification Through Mass Spectrometry-Based Approaches. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100006.	3.8	33
15	H1 histones control the epigenetic landscape by local chromatin compaction. <i>Nature</i> , 2021, 589, 293-298.	27.8	101
16	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
17	Comparative proteomics identifies Schlafen 5 (SLFN5) as a herpes simplex virus restriction factor that suppresses viral transcription. <i>Nature Microbiology</i> , 2021, 6, 234-245.	13.3	27
18	Enhancing Open Modification Searches via a Combined Approach Facilitated by Ursgal. <i>Journal of Proteome Research</i> , 2021, 20, 1986-1996.	3.7	8

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19	Structure and noncanonical Cdk8 activation mechanism within an Argonaute-containing Mediator kinase module. <i>Science Advances</i> , 2021, 7, .	10.3	26
20	Histone Modifications in Papillomavirus Virion Minichromosomes. <i>MBio</i> , 2021, 12, .	4.1	13
21	Cryo-EM structures of engineered active bc1-cbb3 type CIII2CIV super-complexes and electronic communication between the complexes. <i>Nature Communications</i> , 2021, 12, 929.	12.8	17
22	Chromatin dysregulation associated with NSD1 mutation in head and neck squamous cell carcinoma. <i>Cell Reports</i> , 2021, 34, 108769.	6.4	42
23	Sex-specific effects of in vitro fertilization on adult metabolic outcomes and hepatic transcriptome and proteome in mouse. <i>FASEB Journal</i> , 2021, 35, e21523.	0.5	13
24	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
25	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
26	Structure of TFIIK for phosphorylation of CTD of RNA polymerase II. <i>Science Advances</i> , 2021, 7, .	10.3	9
27	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.	2.8	11
28	Comprehensive glycoproteomics shines new light on the complexity and extent of glycosylation in archaea. <i>PLoS Biology</i> , 2021, 19, e3001277.	5.6	9
29	Structural insight on assembly-line catalysis in terpene biosynthesis. <i>Nature Communications</i> , 2021, 12, 3487.	12.8	22
30	Cryo-EM structure of TFIIH/Rad4-Rad23-Rad33 in damaged DNA opening in nucleotide excision repair. <i>Nature Communications</i> , 2021, 12, 3338.	12.8	24
31	Intrinsically disordered Meningioma-1 stabilizes the BAF complex to cause AML. <i>Molecular Cell</i> , 2021, 81, 2332-2348.e9.	9.7	14
32	Biochemical and functional characterization of mutant KRAS epitopes validates this oncoprotein for immunological targeting. <i>Nature Communications</i> , 2021, 12, 4365.	12.8	53
33	Global Microbiota-Dependent Histone Acetylation Patterns Are Irreversible and Independent of Short Chain Fatty Acids. <i>Hepatology</i> , 2021, 74, 3427-3440.	7.3	4
34	Interaction with the CCT chaperonin complex limits APOBEC3A cytidine deaminase cytotoxicity. <i>EMBO Reports</i> , 2021, 22, e52145.	4.5	7
35	Chromatin-mediated alternative splicing regulates cocaine-reward behavior. <i>Neuron</i> , 2021, 109, 2943-2966.e8.	8.1	38
36	A Key Silencing Histone Mark on Chromatin Is Lost When Colorectal Adenocarcinoma Cells Are Depleted of Methionine by Methionine <sup>13</sup> -Lyase. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 735303.	3.5	7

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37	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.	2.8	2
38	Binding Sites and the Mechanism of Action of Propofol and a Photoreactive Analogue in Prokaryotic Voltage-Gated Sodium Channels. <i>ACS Chemical Neuroscience</i> , 2021, 12, 3898-3914.	3.5	3
39	Synthesis and Characterization of a Diazirine-Based Photolabel of the Nonanesthetic Propofol. <i>ACS Chemical Neuroscience</i> , 2021, 12, 176-183.	3.5	4
40	Longitudinal Large-Scale Semiquantitative Proteomic Data Stability Across Multiple Instrument Platforms. <i>Journal of Proteome Research</i> , 2021, 20, 5203-5211.	3.7	1
41	FLT3 Inhibition Downregulates EZH2 in AML and Promotes Myeloid Differentiation. <i>Blood</i> , 2021, 138, 785-785.	1.4	1
42	Adenovirus Remodeling of the Host Proteome and Host Factors Associated with Viral Genomes. <i>MSystems</i> , 2021, 6, e0046821.	3.8	6
43	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
44	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
45	Histone H3.3 G34 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
46	SIRT1 is downregulated by autophagy in senescence and ageing. <i>Nature Cell Biology</i> , 2020, 22, 1170-1179.	10.3	236
47	An integrated multi-omics approach identifies epigenetic alterations associated with Alzheimer's disease. <i>Nature Genetics</i> , 2020, 52, 1024-1035.	21.4	191
48	T9. EPIGENETIC PROFILING IN SCHIZOPHRENIA DERIVED HUMAN INDUCED PLURIPOTENT STEM CELLS (HIPSCS) AND NEURONS. <i>Schizophrenia Bulletin</i> , 2020, 46, S234-S234.	4.3	0
49	Histone Purification Combined with High-Resolution Mass Spectrometry to Examine Histone Post-translational Modifications and Histone Variants in <i>Caenorhabditis elegans</i> . <i>Current Protocols in Protein Science</i> , 2020, 102, e114.	2.8	5
50	Plasma proteomic profiling suggests an association between antigen driven clonal B cell expansion and ME/CFS. <i>PLoS ONE</i> , 2020, 15, e0236148.	2.5	24
51	Adenovirus-mediated ubiquitination alters protein-RNA binding and aids viral RNA processing. <i>Nature Microbiology</i> , 2020, 5, 1217-1231.	13.3	22
52	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
53	Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. <i>Cell</i> , 2020, 183, 1617-1633.e22.	28.9	93
54	The catalytic domain of the histone methyltransferase NSD2/MMSET is required for the generation of B1 cells in mice. <i>FEBS Letters</i> , 2020, 594, 3324-3337.	2.8	5

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55	Extracellular Vesicle and Particle Biomarkers Define Multiple Human Cancers. <i>Cell</i> , 2020, 182, 1044-1061.e18.	28.9	691
56	Lysine and Arginine Protein Post-translational Modifications by Enhanced DIA Libraries: Quantification in Murine Liver Disease. <i>Journal of Proteome Research</i> , 2020, 19, 4163-4178.	3.7	18
57	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
58	The Viral Polymerase Complex Mediates the Interaction of Viral Ribonucleoprotein Complexes with Recycling Endosomes during Sendai Virus Assembly. <i>MBio</i> , 2020, 11, .	4.1	10
59	N <sup>6</sup> -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
60	Improvements on the quantitative analysis of <i>Trypanosoma cruzi</i> histone post translational modifications: Study of changes in epigenetic marks through the parasite's metacyclogenesis and life cycle. <i>Journal of Proteomics</i> , 2020, 225, 103847.	2.4	22
61	Global Regulation of the Histone Mark H3K36me2 Underlies Epithelial Plasticity and Metastatic Progression. <i>Cancer Discovery</i> , 2020, 10, 854-871.	9.4	54
62	Reproductive tract extracellular vesicles are sufficient to transmit intergenerational stress and program neurodevelopment. <i>Nature Communications</i> , 2020, 11, 1499.	12.8	125
63	Human chimeric antigen receptor macrophages for cancer immunotherapy. <i>Nature Biotechnology</i> , 2020, 38, 947-953.	17.5	692
64	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
65	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
66	Bullet points to evaluate the performance of the middle-down proteomics workflow for histone modification analysis. <i>Methods</i> , 2020, 184, 86-92.	3.8	14
67	HYPERSol: High-Quality Data from Archival FFPE Tissue for Clinical Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 973-983.	3.7	33
68	Bacterial colonization reprograms the neonatal gut metabolome. <i>Nature Microbiology</i> , 2020, 5, 838-847.	13.3	70
69	Disruption of the <i>Plasmodium falciparum</i> Life Cycle through Transcriptional Reprogramming by Inhibitors of Jumonji Demethylases. <i>ACS Infectious Diseases</i> , 2020, 6, 1058-1075.	3.8	20
70	Metabolic Regulation of the Epigenome Drives Lethal Infantile Ependymoma. <i>Cell</i> , 2020, 181, 1329-1345.e24.	28.9	79
71	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
72	SIRT6 mono-ADP ribosylates KDM2A to locally increase H3K36me2 at DNA damage sites to inhibit transcription and promote repair. <i>Aging</i> , 2020, 12, 11165-11184.	3.1	29

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73	Mechanistic insights into volatile anesthetic modulation of K2P channels. <i>ELife</i> , 2020, 9, .	6.0	10
74	A Workflow for Ultra-rapid Analysis of Histone Post-translational Modifications with Direct-injection Mass Spectrometry. <i>Bio-protocol</i> , 2020, 10, e3756.	0.4	7
75	PHF19 promotes multiple myeloma tumorigenicity through PRC2 activation and broad H3K27me3 domain formation. <i>Blood</i> , 2019, 134, 1176-1189.	1.4	57
76	Histone H3K23-specific acetylation by MORF is coupled to H3K14 acylation. <i>Nature Communications</i> , 2019, 10, 4724.	12.8	56
77	Azi-medetomidine: Synthesis and Characterization of a Novel $\pm$ 2 Adrenergic Photoaffinity Ligand. <i>ACS Chemical Neuroscience</i> , 2019, 10, 4716-4728.	3.5	5
78	Recognition of Histone Crotonylation by Taf14 Links Metabolic State to Gene Expression. <i>Molecular Cell</i> , 2019, 76, 909-921.e3.	9.7	83
79	Preface. <i>Methods in Enzymology</i> , 2019, 626, xix-xx.	1.0	0
80	Quantitative analysis of global protein lysine methylation by mass spectrometry. <i>Methods in Enzymology</i> , 2019, 626, 475-498.	1.0	14
81	The histone mark H3K36me2 recruits DNMT3A and shapes the intergenic DNA methylation landscape. <i>Nature</i> , 2019, 573, 281-286.	27.8	338
82	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
83	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.	2.8	18
84	A mass spectrometry-based assay using metabolic labeling to rapidly monitor chromatin accessibility of modified histone proteins. <i>Scientific Reports</i> , 2019, 9, 13613.	3.3	32
85	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
86	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
87	One minute analysis of 200 histone posttranslational modifications by direct injection mass spectrometry. <i>Genome Research</i> , 2019, 29, 978-987.	5.5	37
88	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
89	PFA ependymoma-associated protein EZHIP inhibits PRC2 activity through a H3 K27M-like mechanism. <i>Nature Communications</i> , 2019, 10, 2146.	12.8	136
90	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

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91	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
92	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.	3.4	11
93	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
94	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
95	Novel functions of the ubiquitin-independent proteasome system in regulating <i>Xenopus</i> germline development. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	7
96	Histone serotonylation is a permissive modification that enhances TFIID binding to H3K4me3. <i>Nature</i> , 2019, 567, 535-539.	27.8	292
97	Isotopic Labeling and Quantitative Proteomics of Acetylation on Histones and Beyond. <i>Methods in Molecular Biology</i> , 2019, 1977, 43-70.	0.9	12
98	Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. <i>Cell Reports</i> , 2019, 27, 400-415.e5.	6.4	52
99	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
100	The long noncoding RNA Falcor regulates Foxa2 expression to maintain lung epithelial homeostasis and promote regeneration. <i>Genes and Development</i> , 2019, 33, 656-668.	5.9	30
101	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.	0.9	25
102	Coordination between TGF- $\beta$ 2 cellular signaling and epigenetic regulation during epithelial to mesenchymal transition. <i>Epigenetics and Chromatin</i> , 2019, 12, 11.	3.9	21
103	Histone Acetyltransferase p300 Induces De Novo Super-Enhancers to Drive Cellular Senescence. <i>Molecular Cell</i> , 2019, 73, 684-698.e8.	9.7	97
104	Deep profiling and custom databases improve detection of proteoforms generated by alternative splicing. <i>Genome Research</i> , 2019, 29, 2046-2055.	5.5	23
105	Impaired cocaine-induced behavioral plasticity in the male offspring of cocaine-experienced sires. <i>European Journal of Neuroscience</i> , 2019, 49, 1115-1126.	2.6	24
106	Histone modification signatures in human sperm distinguish clinical abnormalities. <i>Journal of Assisted Reproduction and Genetics</i> , 2019, 36, 267-275.	2.5	38
107	Acetyl-CoA Metabolism Supports Multistep Pancreatic Tumorigenesis. <i>Cancer Discovery</i> , 2019, 9, 416-435.	9.4	184
108	Proteomic approaches for cancer epigenetics research. <i>Expert Review of Proteomics</i> , 2019, 16, 33-47.	3.0	5

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109	Phosphorylation of TIP60 Suppresses 53BP1 Localization at DNA Damage Sites. <i>Molecular and Cellular Biology</i> , 2019, 39, .	2.3	11
110	SWI/SNF Dysregulation through a Prion-like Domain Causes AML. <i>Blood</i> , 2019, 134, 2512-2512.	1.4	3
111	Genomic and Proteomic Signatures of Replication Fork Collapse. <i>FASEB Journal</i> , 2019, 33, 345.2.	0.5	0
112	Integrating Proteomics and Targeted Metabolomics to Understand Global Changes in Histone Modifications. <i>Proteomics</i> , 2018, 18, e1700309.	2.2	18
113	Allosteric Activation Dictates PRC2 Activity Independent of Its Recruitment to Chromatin. <i>Molecular Cell</i> , 2018, 70, 422-434.e6.	9.7	100
114	KMT2D regulates p63 target enhancers to coordinate epithelial homeostasis. <i>Genes and Development</i> , 2018, 32, 181-193.	5.9	77
115	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
116	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
117	Assessment of Quantification Precision of Histone Post-Translational Modifications by Using an Ion Trap and down To 50â€000 Cells as Starting Material. <i>Journal of Proteome Research</i> , 2018, 17, 234-242.	3.7	10
118	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.	3.8	14
119	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.	7.0	20
120	Target site specificity and in vivo complexity of the mammalian arginylome. <i>Scientific Reports</i> , 2018, 8, 16177.	3.3	25
121	The HDAC3â€SMARCA4â€miR-27a axis promotes expression of the <i>PAX3:FOXO1</i> fusion oncogene in rhabdomyosarcoma. <i>Science Signaling</i> , 2018, 11, .	3.6	51
122	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
123	Hydrogen-Deuterium Exchange Coupled to Top- and Middle-Down Mass Spectrometry Reveals Histone Tail Dynamics before and after Nucleosome Assembly. <i>Structure</i> , 2018, 26, 1651-1663.e3.	3.3	30
124	Targeting CDK9 Reactivates Epigenetically Silenced Genes in Cancer. <i>Cell</i> , 2018, 175, 1244-1258.e26.	28.9	182
125	Acetate Production from Glucose and Coupling to Mitochondrial Metabolism in Mammals. <i>Cell</i> , 2018, 175, 502-513.e13.	28.9	269
126	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



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127	An allosteric propofol-binding site in kinesin disrupts kinesin-mediated processive movement on microtubules. <i>Journal of Biological Chemistry</i> , 2018, 293, 11283-11295.	3.4	16
128	High-Quality Genome Assemblies Reveal Long Non-coding RNAs Expressed in Ant Brains. <i>Cell Reports</i> , 2018, 23, 3078-3090.	6.4	54
129	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.	6.5	26
130	Wnt5a signaling induced phosphorylation increases APT1 activity and promotes melanoma metastatic behavior. <i>ELife</i> , 2018, 7, .	6.0	29
131	Identification of binding sites contributing to volatile anesthetic effects on GABA type A receptors. <i>FASEB Journal</i> , 2018, 32, 4172-4189.	0.5	22
132	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
133	Rpp29 regulates histone H3.3 chromatin assembly through transcriptional mechanisms. <i>Journal of Biological Chemistry</i> , 2018, 293, 12360-12377.	3.4	14
134	Capturing the Onset of PRC2-Mediated Repressive Domain Formation. <i>Molecular Cell</i> , 2018, 70, 1149-1162.e5.	9.7	222
135	Epiproteomic Landscape and Histone Code of Cutaneous T-Cell Lymphoma/S�azary Syndrome. <i>Blood</i> , 2018, 132, 780-780.	1.4	1
136	Impaired H3K36 methylation defines a subset of head and neck squamous cell carcinomas. <i>Nature Genetics</i> , 2017, 49, 180-185.	21.4	195
137	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.	5.2	28
138	Recognition of Histone H3K14 Acylation by MORF. <i>Structure</i> , 2017, 25, 650-654.e2.	3.3	41
139	Multicellular Tumor Spheroids Combined with Mass Spectrometric Histone Analysis To Evaluate Epigenetic Drugs. <i>Analytical Chemistry</i> , 2017, 89, 2773-2781.	6.5	27
140	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
141	Monitoring proteolytic processing events by quantitative mass spectrometry. <i>Expert Review of Proteomics</i> , 2017, 14, 409-418.	3.0	10
142	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
143	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
144	Systematic Epigenomic Analysis Reveals Chromatin States Associated with Melanoma Progression. <i>Cell Reports</i> , 2017, 19, 875-889.	6.4	78

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145	Unique roles for histone H3K9me states in RNAi and heritable silencing of transcription. <i>Nature</i> , 2017, 547, 463-467.	27.8	96
146	Taxane-Platin-Resistant Lung Cancers Co-develop Hypersensitivity to JumonjiC Demethylase Inhibitors. <i>Cell Reports</i> , 2017, 19, 1669-1684.	6.4	82
147	The NANCIâ€“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
148	Photoaffinity Ligand for the Inhalational Anesthetic Sevoflurane Allows Mechanistic Insight into Potassium Channel Modulation. <i>ACS Chemical Biology</i> , 2017, 12, 1353-1362.	3.4	29
149	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
150	Mutations along a TET2 active site scaffold stall oxidation at 5-hydroxymethylcytosine. <i>Nature Chemical Biology</i> , 2017, 13, 181-187.	8.0	59
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