

Michiel Vermeulen

List of Publications by Year in descending order

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151
papers

14,775
citations

28242

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22147

113
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179
all docs

179
docs citations

179
times ranked

21751
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	1.6	1,319
2	Dynamic Readers for 5-(Hydroxy)Methylcytosine and Its Oxidized Derivatives. <i>Cell</i> , 2013, 152, 1146-1159.	13.5	888
3	Selective Anchoring of TFIID to Nucleosomes by Trimethylation of Histone H3 Lysine 4. <i>Cell</i> , 2007, 131, 58-69.	13.5	769
4	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	13.5	710
5	Nucleosome-Interacting Proteins Regulated by DNA and Histone Methylation. <i>Cell</i> , 2010, 143, 470-484.	13.5	524
6	Proteome-wide identification of ubiquitin interactions using UbIA-MS. <i>Nature Protocols</i> , 2018, 13, 530-550.	5.5	454
7	N6-methyladenosine (m6A) recruits and repels proteins to regulate mRNA homeostasis. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 870-878.	3.6	432
8	Histone H2A monoubiquitination promotes histone H3 methylation in Polycomb repression. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 569-571.	3.6	376
9	Nuclear Pore Components Are Involved in the Transcriptional Regulation of Dosage Compensation in <i>Drosophila</i> . <i>Molecular Cell</i> , 2006, 21, 811-823.	4.5	368
10	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. <i>Nature</i> , 2014, 510, 283-287.	13.7	331
11	Arginine methylation at histone H3R2 controls deposition of H3K4 trimethylation. <i>Nature</i> , 2007, 449, 928-932.	13.7	322
12	MBD2/NuRD and MBD3/NuRD, Two Distinct Complexes with Different Biochemical and Functional Properties. <i>Molecular and Cellular Biology</i> , 2006, 26, 843-851.	1.1	290
13	Tet oxidizes thymine to 5-hydroxymethyluracil in mouse embryonic stem cell DNA. <i>Nature Chemical Biology</i> , 2014, 10, 574-581.	3.9	270
14	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. <i>Nature Methods</i> , 2008, 5, 459-460.	9.0	268
15	Stoichiometry of chromatin-associated protein complexes revealed by label-free quantitative mass spectrometry-based proteomics. <i>Nucleic Acids Research</i> , 2013, 41, e28-e28.	6.5	222
16	Regulation of the Histone H4 Monomethylase PR-Set7 by CRL4Cdt2-Mediated PCNA-Dependent Degradation during DNA Damage. <i>Molecular Cell</i> , 2010, 40, 364-376.	4.5	213
17	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016, 48, 417-426.	9.4	210
18	Quantitative Dissection and Stoichiometry Determination of the Human SET1/MLL Histone Methyltransferase Complexes. <i>Molecular and Cellular Biology</i> , 2013, 33, 2067-2077.	1.1	202

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19	MicroRNA Regulation of Cbx7 Mediates a Switch of Polycomb Orthologs during ESC Differentiation. <i>Cell Stem Cell</i> , 2012, 10, 33-46.	5.2	191
20	The Complexity of PRC2 Subcomplexes. <i>Trends in Cell Biology</i> , 2019, 29, 660-671.	3.6	178
21	The dynamic interactome and genomic targets of Polycomb complexes during stem-cell differentiation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 682-690.	3.6	171
22	The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. <i>Nature Genetics</i> , 2019, 51, 1645-1651.	9.4	171
23	A Map of General and Specialized Chromatin Readers in Mouse Tissues Generated by Label-free Interaction Proteomics. <i>Molecular Cell</i> , 2013, 49, 368-378.	4.5	170
24	High-throughput identification of human SNPs affecting regulatory element activity. <i>Nature Genetics</i> , 2019, 51, 1160-1169.	9.4	157
25	High confidence determination of specific protein-protein interactions using quantitative mass spectrometry. <i>Current Opinion in Biotechnology</i> , 2008, 19, 331-337.	3.3	156
26	Histone propionylation is a mark of active chromatin. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 1048-1056.	3.6	148
27	MTF2 recruits Polycomb Repressive Complex 2 by helical-shape-selective DNA binding. <i>Nature Genetics</i> , 2018, 50, 1002-1010.	9.4	147
28	Redox-Dependent Control of FOXO/DAF-16 by Transportin-1. <i>Molecular Cell</i> , 2013, 49, 730-742.	4.5	138
29	PRC2.1 and PRC2.2 Synergize to Coordinate H3K27 Trimethylation. <i>Molecular Cell</i> , 2019, 76, 437-452.e6.	4.5	137
30	Probing the Tumor Suppressor Function of BAP1 in CRISPR-Engineered Human Liver Organoids. <i>Cell Stem Cell</i> , 2019, 24, 927-943.e6.	5.2	136
31	Single-Cell DNA Methylation Profiling: Technologies and Biological Applications. <i>Trends in Biotechnology</i> , 2018, 36, 952-965.	4.9	133
32	Characterizing Protein-Protein Interactions Using Mass Spectrometry: Challenges and Opportunities. <i>Trends in Biotechnology</i> , 2016, 34, 825-834.	4.9	131
33	Targeted degradation of BRD9 reverses oncogenic gene expression in synovial sarcoma. <i>ELife</i> , 2018, 7, .	2.8	125
34	Single-Molecule Imaging Uncovers Rules Governing Nonsense-Mediated mRNA Decay. <i>Molecular Cell</i> , 2019, 75, 324-339.e11.	4.5	116
35	An Interaction Landscape of Ubiquitin Signaling. <i>Molecular Cell</i> , 2017, 65, 941-955.e8.	4.5	109
36	Integrative multi-omics analysis of intestinal organoid differentiation. <i>Molecular Systems Biology</i> , 2018, 14, e8227.	3.2	106

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37	Characterization of Lysine 56 of Histone H3 as an Acetylation Site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 25949-25952.	1.6	105
38	ZMYND8 Co-localizes with NuRD on Target Genes and Regulates Poly(ADP-Ribose)-Dependent Recruitment of GATAD2A/NuRD to Sites of DNA Damage. <i>Cell Reports</i> , 2016, 17, 783-798.	2.9	100
39	Phosphorylation of Histone H3 Thr-45 Is Linked to Apoptosis. <i>Journal of Biological Chemistry</i> , 2009, 284, 16575-16583.	1.6	98
40	The rRNA m ⁶ A methyltransferase METTL5 is involved in pluripotency and developmental programs. <i>Genes and Development</i> , 2020, 34, 715-729.	2.7	93
41	Proteome-Wide Analysis of Disease-Associated SNPs That Show Allele-Specific Transcription Factor Binding. <i>PLoS Genetics</i> , 2012, 8, e1002982.	1.5	92
42	MBD5 and MBD6 interact with the human PR ² UB complex through their methyl ³ CpG ⁴ binding domain. <i>Proteomics</i> , 2014, 14, 2179-2189.	1.3	90
43	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. <i>Cell Stem Cell</i> , 2019, 24, 123-137.e8.	5.2	90
44	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020, 48, 830-846.	6.5	88
45	Towards elucidating the stability, dynamics and architecture of the nucleosome remodeling and deacetylase complex by using quantitative interaction proteomics. <i>FEBS Journal</i> , 2015, 282, 1774-1785.	2.2	86
46	The chromodomain helicase Chd4 is required for Polycomb-mediated inhibition of astroglial differentiation. <i>EMBO Journal</i> , 2013, 32, 1598-1612.	3.5	80
47	Cdyl, a New Partner of the Inactive X Chromosome and Potential Reader of H3K27me3 and H3K9me2. <i>Molecular and Cellular Biology</i> , 2013, 33, 5005-5020.	1.1	80
48	DNA methylation: old dog, new tricks?. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 949-954.	3.6	79
49	EZH1P constrains Polycomb Repressive Complex 2 activity in germ cells. <i>Nature Communications</i> , 2019, 10, 3858.	5.8	76
50	Insight into the Architecture of the NuRD Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 21844-21855.	1.6	75
51	Global absolute quantification reveals tight regulation of protein expression in single <i>Xenopus</i> eggs. <i>Nucleic Acids Research</i> , 2014, 42, 9880-9891.	6.5	71
52	Predicting protein condensate formation using machine learning. <i>Cell Reports</i> , 2021, 34, 108705.	2.9	70
53	Inactivation of Yeast Isw2 Chromatin Remodeling Enzyme Mimics Longevity Effect of Calorie Restriction via Induction of Genotoxic Stress Response. <i>Cell Metabolism</i> , 2014, 19, 952-966.	7.2	69
54	Grasping trimethylation of histone H3 at lysine 4. <i>Epigenomics</i> , 2010, 2, 395-406.	1.0	66

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55	The Nucleosome Remodeling and Deacetylase Complex NuRD Is Built from Preformed Catalytically Active Sub-modules. <i>Journal of Molecular Biology</i> , 2016, 428, 2931-2942.	2.0	62
56	Analysis of the Histone H3.1 Interactome: A Suitable Chaperone for the Right Event. <i>Molecular Cell</i> , 2015, 60, 697-709.	4.5	61
57	Evolutionary Acquisition of Cysteines Determines FOXO Paralog-Specific Redox Signaling. <i>Antioxidants and Redox Signaling</i> , 2015, 22, 15-28.	2.5	61
58	Quantitative Proteomics for Epigenetics. <i>ChemBioChem</i> , 2011, 12, 224-234.	1.3	59
59	Ythdf is a N6-methyladenosine reader that modulates Fmr1 target mRNA selection and restricts axonal growth in <i>Drosophila</i> . <i>EMBO Journal</i> , 2021, 40, e104975.	3.5	56
60	CDK2AP1/DOC-1 is a bona fide subunit of the Mi-2/NuRD complex. <i>Molecular BioSystems</i> , 2010, 6, 1700.	2.9	54
61	Global profiling of protein-DNA and protein-nucleosome binding affinities using quantitative mass spectrometry. <i>Nature Communications</i> , 2018, 9, 1653.	5.8	54
62	A domesticated transposon mediates the effects of a single nucleotide polymorphism responsible for enhanced muscle growth. <i>EMBO Reports</i> , 2010, 11, 305-311.	2.0	53
63	Sall4 controls differentiation of pluripotent cells independently of the Nucleosome Remodelling and Deacetylation (NuRD) complex. <i>Development (Cambridge)</i> , 2016, 143, 3074-84.	1.2	53
64	Cross-linking immunoprecipitation-MS (xIP-MS): Topological Analysis of Chromatin-associated Protein Complexes Using Single Affinity Purification. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 854-865.	2.5	53
65	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. <i>Nature Communications</i> , 2020, 11, 2718.	5.8	53
66	The Mad1-Sin3B interaction involves a novel helical fold. <i>Nature Structural Biology</i> , 2000, 7, 1100-1104.	9.7	52
67	The interactome of a family of potential methyltransferases in HeLa cells. <i>Scientific Reports</i> , 2019, 9, 6584.	1.6	52
68	A common intronic variant of PARP1 confers melanoma risk and mediates melanocyte growth via regulation of MITF. <i>Nature Genetics</i> , 2017, 49, 1326-1335.	9.4	51
69	An interaction proteomics survey of transcription factor binding at recurrent TERT promoter mutations. <i>Proteomics</i> , 2016, 16, 417-426.	1.3	50
70	Quantification of Proteins and Histone Marks in <i>Drosophila</i> Embryos Reveals Stoichiometric Relationships Impacting Chromatin Regulation. <i>Developmental Cell</i> , 2019, 51, 632-644.e6.	3.1	50
71	BANP opens chromatin and activates CpG-island-regulated genes. <i>Nature</i> , 2021, 596, 133-137.	13.7	49
72	A SILAC-Based Screen for Methyl-CpG Binding Proteins Identifies RBP-J as a DNA Methylation and Sequence-Specific Binding Protein. <i>PLoS ONE</i> , 2011, 6, e25884.	1.1	49

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73	Two Chromatin Remodeling Activities Cooperate during Activation of Hormone Responsive Promoters. <i>PLoS Genetics</i> , 2009, 5, e1000567.	1.5	47
74	The Nucleosome Remodelling and Deacetylation complex suppresses transcriptional noise during lineage commitment. <i>EMBO Journal</i> , 2019, 38, .	3.5	45
75	In Vitro Targeting Reveals Intrinsic Histone Tail Specificity of the Sin3/Histone Deacetylase and N-CoR/SMRT Corepressor Complexes. <i>Molecular and Cellular Biology</i> , 2004, 24, 2364-2372.	1.1	43
76	A Dual Role for SAGA-Associated Factor 29 (SGF29) in ER Stress Survival by Coordination of Both Histone H3 Acetylation and Histone H3 Lysine-4 Trimethylation. <i>PLoS ONE</i> , 2013, 8, e70035.	1.1	43
77	EZH1/2 function mostly within canonical PRC2 and exhibit proliferation-dependent redundancy that shapes mutational signatures in cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6075-6080.	3.3	42
78	Identification of <i>Allobaculum mucolyticum</i> as a novel human intestinal mucin degrader. <i>Gut Microbes</i> , 2021, 13, 1966278.	4.3	42
79	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. <i>Nature Communications</i> , 2017, 8, 15034.	5.8	40
80	Molecular characterization of Sin3 PAH-domain interactor specificity and identification of PAH partners. <i>Nucleic Acids Research</i> , 2006, 34, 3929-3937.	6.5	37
81	Recruitment of the Mammalian Histone-modifying EMSY Complex to Target Genes Is Regulated by ZNF131. <i>Journal of Biological Chemistry</i> , 2016, 291, 7313-7324.	1.6	35
82	The Tudor protein Veneno assembles the ping-pong amplification complex that produces viral piRNAs in <i>Aedes</i> mosquitoes. <i>Nucleic Acids Research</i> , 2019, 47, 2546-2559.	6.5	35
83	Induction and Suppression of NF- κ B Signalling by a DNA Virus of <i>Drosophila</i> . <i>Journal of Virology</i> , 2019, 93, .	1.5	35
84	The HDAC inhibitor SAHA regulates CBX2 stability via a SUMO-triggered ubiquitin-mediated pathway in leukemia. <i>Oncogene</i> , 2018, 37, 2559-2572.	2.6	32
85	BRD9 binds cell type-specific chromatin regions regulating leukemic cell survival via STAT5 inhibition. <i>Cell Death and Disease</i> , 2019, 10, 338.	2.7	31
86	A CSB-PAF1C axis restores processive transcription elongation after DNA damage repair. <i>Nature Communications</i> , 2021, 12, 1342.	5.8	31
87	Off-the-shelf proximity biotinylation for interaction proteomics. <i>Nature Communications</i> , 2021, 12, 5015.	5.8	31
88	RNF43 truncations trap CK1 to drive niche-independent self-renewal in cancer. <i>EMBO Journal</i> , 2020, 39, e103932.	3.5	31
89	Integrated multi-omics reveal polycomb repressive complex 2 restricts human trophoblast induction. <i>Nature Cell Biology</i> , 2022, 24, 858-871.	4.6	30
90	Identifying Nuclear Protein-Protein Interactions Using GFP Affinity Purification and SILAC-Based Quantitative Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2014, 1188, 207-226.	0.4	29

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91	Miniaturised interaction proteomics on a microfluidic platform with ultra-low input requirements. <i>Nature Communications</i> , 2019, 10, 1525.	5.8	29
92	SALL4 controls cell fate in response to DNA base composition. <i>Molecular Cell</i> , 2021, 81, 845-858.e8.	4.5	29
93	Specific Labeling of Stem Cell Activity in Human Colorectal Organoids Using an ASCL2-Responsive Minigene. <i>Cell Reports</i> , 2018, 22, 1600-1614.	2.9	28
94	Reading ADP-ribosylation signaling using chemical biology and interaction proteomics. <i>Molecular Cell</i> , 2021, 81, 4552-4567.e8.	4.5	28
95	TRiC controls transcription resumption after UV damage by regulating Cockayne syndrome protein A. <i>Nature Communications</i> , 2018, 9, 1040.	5.8	27
96	A Feed-Forward Repression Mechanism Anchors the Sin3/Histone Deacetylase and N-CoR/SMRT Corepressors on Chromatin. <i>Molecular and Cellular Biology</i> , 2006, 26, 5226-5236.	1.1	26
97	Chromosomal instability by mutations in the novel minor spliceosome component <i>CENATAC</i> . <i>EMBO Journal</i> , 2021, 40, e106536.	3.5	26
98	Purification and enrichment of specific chromatin loci. <i>Nature Methods</i> , 2020, 17, 380-389.	9.0	25
99	Hydroxychloroquine Inhibits the Trained Innate Immune Response to Interferons. <i>Cell Reports Medicine</i> , 2020, 1, 100146.	3.3	24
100	Quantitative proteomics: a tool to assess cell differentiation. <i>Current Opinion in Cell Biology</i> , 2009, 21, 761-766.	2.6	23
101	In Vivo Proximity Labeling for the Detection of Protein-Protein and Protein-RNA Interactions. <i>Journal of Proteome Research</i> , 2014, 13, 6135-6143.	1.8	22
102	<i>ZBTB2</i> reads unmethylated CpG island promoters and regulates embryonic stem cell differentiation. <i>EMBO Reports</i> , 2018, 19, .	2.0	22
103	NuRD-interacting protein ZFP296 regulates genome-wide NuRD localization and differentiation of mouse embryonic stem cells. <i>Nature Communications</i> , 2018, 9, 4588.	5.8	22
104	Myeloid Transforming Protein Evi1 Interacts with Methyl-CpG Binding Domain Protein 3 and Inhibits in Vitro Histone Deacetylation by Mbd3/Mi-2/NuRD. <i>Biochemistry</i> , 2008, 47, 6418-6426.	1.2	21
105	Identifying Specific Protein-DNA Interactions Using SILAC-Based Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2013, 977, 137-157.	0.4	21
106	Splicing and Chromatin Factors Jointly Regulate Epidermal Differentiation. <i>Cell Reports</i> , 2018, 25, 1292-1303.e5.	2.9	21
107	Molecular mechanisms of bleeding disorder-associated <i>GFI1B</i> ^{Q287*} mutation and its affected pathways in megakaryocytes and platelets. <i>Haematologica</i> , 2019, 104, 1460-1472.	1.7	21
108	Perspective on unraveling the versatility of co-repressor complexes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 1051-1056.	0.9	20

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109	Phospho-H1 Decorates the Inter-chromatid Axis and Is Evicted along with Shugoshin by SET during Mitosis. <i>Molecular Cell</i> , 2017, 67, 579-593.e6.	4.5	20
110	Multivalent Engagement of TFIID to Nucleosomes. <i>PLoS ONE</i> , 2013, 8, e73495.	1.1	19
111	RNA-Centric Methods: Toward the Interactome of Specific RNA Transcripts. <i>Trends in Biotechnology</i> , 2021, 39, 890-900.	4.9	19
112	The translational landscape of ground state pluripotency. <i>Nature Communications</i> , 2020, 11, 1617.	5.8	18
113	Towards cracking the epigenetic code using a combination of high-throughput epigenomics and quantitative mass spectrometry-based proteomics. <i>BioEssays</i> , 2011, 33, 547-551.	1.2	17
114	Immuno-detection by sequencing enables large-scale high-dimensional phenotyping in cells. <i>Nature Communications</i> , 2018, 9, 2384.	5.8	17
115	There is another: H3K27me3-mediated genomic imprinting. <i>Trends in Genetics</i> , 2022, 38, 82-96.	2.9	16
116	Cross-linking mass spectrometry reveals the structural topology of peripheral NuRD subunits relative to the core complex. <i>FEBS Journal</i> , 2021, 288, 3231-3245.	2.2	15
117	Identifying Chromatin Readers Using a SILAC-Based Histone Peptide Pull-Down Approach. <i>Methods in Enzymology</i> , 2012, 512, 137-160.	0.4	14
118	Chromatin Proteomics to Study Epigenetics – Challenges and Opportunities. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100056.	2.5	14
119	PIWI proteomics identifies Atari and Pasilla as piRNA biogenesis factors in <i>Aedes</i> mosquitoes. <i>Cell Reports</i> , 2021, 35, 109073.	2.9	14
120	Maintenance of spatial gene expression by Polycomb-mediated repression after formation of a vertebrate body plan. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	13
121	Locus-specific chromatin isolation. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 249-250.	16.1	13
122	Click-MS: Tagless Protein Enrichment Using Bioorthogonal Chemistry for Quantitative Proteomics. <i>ACS Chemical Biology</i> , 2016, 11, 3245-3250.	1.6	12
123	Differential regulation of lineage commitment in human and mouse primed pluripotent stem cells by the nucleosome remodelling and deacetylation complex. <i>Stem Cell Research</i> , 2020, 46, 101867.	0.3	11
124	Proteomic landscape of the primary somatosensory cortex upon sensory deprivation. <i>GigaScience</i> , 2017, 6, 1-10.	3.3	10
125	Retinoic acid signaling drives differentiation toward the absorptive lineage in colorectal cancer. <i>IScience</i> , 2021, 24, 103444.	1.9	10
126	SMYD3 Impedes Small Cell Lung Cancer Sensitivity to Alkylation Damage through RNF113A Methylation-Phosphorylation Cross-talk. <i>Cancer Discovery</i> , 2022, 12, 2158-2179.	7.7	10

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127	<i><i>SDHD</i> Promoter Mutations Ablate GABP Transcription Factor Binding in Melanoma. Cancer Research, 2017, 77, 1649-1661.</i>	0.4	9
128	Dysregulated RASGRP1 expression through RUNX1 mediated transcription promotes autoimmunity. European Journal of Immunology, 2021, 51, 471-482.	1.6	9
129	Targeted discovery tools: proteomics and chromatin immunoprecipitation-on-chip. BJU International, 2005, 96, 16-22.	1.3	8
130	CBFÎ ² -MYH11 interferes with megakaryocyte differentiation via modulating a gene program that includes GATA2 and KLF1. Blood Cancer Journal, 2019, 9, 33.	2.8	7
131	Identifying Readers for (hydroxy)methylated DNA Using Quantitative Interaction Proteomics: Advances and Challenges Ahead. Journal of Molecular Biology, 2020, 432, 1792-1800.	2.0	7
132	IRF8 is a transcriptional activator of CD37 expression in diffuse large B-cell lymphoma. Blood Advances, 2022, 6, 2254-2266.	2.5	7
133	UBE2O and USP7 coâ€regulate RECQL4 ubiquitinylation and homologous recombinationâ€mediated DNA repair. FASEB Journal, 2022, 36, e22112.	0.2	7
134	A Me6Age for pluripotency. Science, 2015, 347, 614-615.	6.0	6
135	PAQMAN: Protein-nucleic acid affinity quantification by MAss spectrometry in nuclear extracts. Methods, 2020, 184, 70-77.	1.9	6
136	A Novel Microscopy-Based High-Throughput Screening Method to Identify Proteins That Regulate Global Histone Modification Levels. Journal of Biomolecular Screening, 2014, 19, 287-296.	2.6	5
137	Mass Spectrometry-Based Absolute Quantification of Single Xenopus Embryo Proteomes. Cold Spring Harbor Protocols, 2019, 2019, pdb.prot098376.	0.2	5
138	The Pluripotency Regulator PRDM14 Requires Hematopoietic Regulator CBFA2T3 to Initiate Leukemia in Mice. Molecular Cancer Research, 2019, 17, 1468-1479.	1.5	5
139	Androgen receptor signalling confers clonogenic and migratory advantages in urothelial cell carcinoma of the bladder. Molecular Oncology, 2021, 15, 1882-1900.	2.1	5
140	SNX27-driven membrane localisation of OTULIN antagonises linear ubiquitination and NF-ÎB signalling activation. Cell and Bioscience, 2021, 11, 146.	2.1	4
141	An in vitro assay to study the recruitment and substrate specificity of chromatin modifying enzymes. Biological Procedures Online, 2004, 6, 157-162.	1.4	3
142	Research Highlights: Highlights from the latest articles on epigenetics in tumorigenesis. Epigenomics, 2012, 4, 367-368.	1.0	2
143	OUP accepted manuscript. Human Molecular Genetics, 2021, , .	1.4	2
144	Exploring Chromatin Readers Using High-Accuracy Quantitative Mass Spectrometry-Based Proteomics. , 2014, , 133-148.		2

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145	Making the most of methylation. <i>ELife</i> , 2013, 2, e01387.	2.8	2
146	In need of good neighbours: transcription factors require local <scp>DNA</scp> hypomethylation for target binding. <i>EMBO Journal</i> , 2016, 35, 374-375.	3.5	1
147	Bifunctional protein PCBD2 operates as a co-factor for hepatocyte nuclear factor 1 ² and modulates gene transcription. <i>FASEB Journal</i> , 2021, 35, e21366.	0.2	1
148	CBFB-MYH11/RUNX1 together with a compendium of hematopoietic regulators, chromatin modifiers and basal transcription factors occupies self-renewal genes in inv(16) acute myeloid leukemia. <i>Experimental Hematology</i> , 2013, 41, S50.	0.2	0
149	Identifying Proteinâ€“(Hydroxy)Methylated DNA Using Quantitative Interaction Proteomics. <i>Methods in Molecular Biology</i> , 2021, 2272, 209-224.	0.4	0
150	Characterization of a genomic region 8Åkb downstream of GFI1B associated with myeloproliferative neoplasms. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166259.	1.8	0
151	Yeast Aging Proteome Unveiled a Novel Aging Regulation Pathway Mediated by the Chromatin Remodeling Complex ISW2. <i>FASEB Journal</i> , 2012, 26, 965.2.	0.2	0