

Michiel Vermeulen

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

153
papers

10,698
citations

50
h-index

102
g-index

179
ext. papers

13,215
ext. citations

13.6
avg, IF

6.22
L-index

#	Paper	IF	Citations
153	UBE2O and USP7 co-regulate RECQL4 ubiquitylation and homologous recombination-mediated DNA repair.. <i>FASEB Journal</i> , 2022 , 36, e22112	0.9	0
152	Bifunctional protein PCBD2 operates as a co-factor for hepatocyte nuclear factor 1 α and modulates gene transcription. <i>FASEB Journal</i> , 2021 , 35, e21366	0.9	
151	Chromosomal instability by mutations in the novel minor spliceosome component CENATAC. <i>EMBO Journal</i> , 2021 , 40, e106536	13	4
150	PIWI proteomics identifies Atari and Pasilla as piRNA biogenesis factors in <i>Aedes</i> mosquitoes. <i>Cell Reports</i> , 2021 , 35, 109073	10.6	5
149	Androgen receptor signalling confers clonogenic and migratory advantages in urothelial cell carcinoma of the bladder. <i>Molecular Oncology</i> , 2021 , 15, 1882-1900	7.9	2
148	Chromatin Proteomics to Study Epigenetics - Challenges and Opportunities. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100056	7.6	5
147	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	5.7	2
146	Dysregulated RASGRP1 expression through RUNX1 mediated transcription promotes autoimmunity. <i>European Journal of Immunology</i> , 2021 , 51, 471-482	6.1	3
145	Identification of <i>Allobaculum mucolyticum</i> as a novel human intestinal mucin degrader. <i>Gut Microbes</i> , 2021 , 13, 1966278	8.8	7
144	Identifying Protein-(Hydroxy)Methylated DNA Interactions Using Quantitative Interaction Proteomics. <i>Methods in Molecular Biology</i> , 2021 , 2272, 209-224	1.4	
143	A CSB-PAF1C axis restores processive transcription elongation after DNA damage repair. <i>Nature Communications</i> , 2021 , 12, 1342	17.4	10
142	Predicting protein condensate formation using machine learning. <i>Cell Reports</i> , 2021 , 34, 108705	10.6	11
141	SALL4 controls cell fate in response to DNA base composition. <i>Molecular Cell</i> , 2021 , 81, 845-858.e8	17.6	5
140	BANP opens chromatin and activates CpG-island-regulated genes. <i>Nature</i> , 2021 , 596, 133-137	50.4	6
139	SNX27-driven membrane localisation of OTULIN antagonises linear ubiquitination and NF- κ B signalling activation. <i>Cell and Bioscience</i> , 2021 , 11, 146	9.8	1
138	Off-the-shelf proximity biotinylation for interaction proteomics. <i>Nature Communications</i> , 2021 , 12, 5015	17.4	4
137	RNA-Centric Methods: Toward the Interactome of Specific RNA Transcripts. <i>Trends in Biotechnology</i> , 2021 , 39, 890-900	15.1	3

136	Reading ADP-ribosylation signaling using chemical biology and interaction proteomics. <i>Molecular Cell</i> , 2021 , 81, 4552-4567.e8	17.6	4
135	Characterization of a genomic region 8kb downstream of GFI1B associated with myeloproliferative neoplasms. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021 , 1867, 166259	6.9	
134	Ythdf is a N6-methyladenosine reader that modulates Fmr1 target mRNA selection and restricts axonal growth in Drosophila. <i>EMBO Journal</i> , 2021 , 40, e104975	13	19
133	Retinoic acid signaling drives differentiation toward the absorptive lineage in colorectal cancer. <i>IScience</i> , 2021 , 24, 103444	6.1	0
132	Massively parallel reporter assays of melanoma risk variants identify MX2 as a gene promoting melanoma. <i>Nature Communications</i> , 2020 , 11, 2718	17.4	24
131	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	1.6	3
130	Purification and enrichment of specific chromatin loci. <i>Nature Methods</i> , 2020 , 17, 380-389	21.6	15
129	Locus-specific chromatin isolation. <i>Nature Reviews Molecular Cell Biology</i> , 2020 , 21, 249-250	48.7	3
128	The translational landscape of ground state pluripotency. <i>Nature Communications</i> , 2020 , 11, 1617	17.4	10
127	The rRNA mA methyltransferase METTL5 is involved in pluripotency and developmental programs. <i>Genes and Development</i> , 2020 , 34, 715-729	12.6	45
126	RNF43 truncations trap CK1 to drive niche-independent self-renewal in cancer. <i>EMBO Journal</i> , 2020 , 39, e103932	13	17
125	The human methyltransferase ZCCHC4 catalyses N6-methyladenosine modification of 28S ribosomal RNA. <i>Nucleic Acids Research</i> , 2020 , 48, 830-846	20.1	38
124	PAQMAN: Protein-nucleic acid affinity quantification by MAss spectrometry in nuclear extracts. <i>Methods</i> , 2020 , 184, 70-77	4.6	4
123	Hydroxychloroquine Inhibits the Trained Innate Immune Response to Interferons. <i>Cell Reports Medicine</i> , 2020 , 1, 100146	18	13
122	EZHIP constrains Polycomb Repressive Complex 2 activity in germ cells. <i>Nature Communications</i> , 2019 , 10, 3858	17.4	42
121	PRC2.1 and PRC2.2 Synergize to Coordinate H3K27 Trimethylation. <i>Molecular Cell</i> , 2019 , 76, 437-452.e6	17.6	70
120	The Tudor protein Veneno assembles the ping-pong amplification complex that produces viral piRNAs in Aedes mosquitoes. <i>Nucleic Acids Research</i> , 2019 , 47, 2546-2559	20.1	18
119	The Complexity of PRC2 Subcomplexes. <i>Trends in Cell Biology</i> , 2019 , 29, 660-671	18.3	85

118	Single-Molecule Imaging Uncovers Rules Governing Nonsense-Mediated mRNA Decay. <i>Molecular Cell</i> , 2019 , 75, 324-339.e11	17.6	62
117	Probing the Tumor Suppressor Function of BAP1 in CRISPR-Engineered Human Liver Organoids. <i>Cell Stem Cell</i> , 2019 , 24, 927-943.e6	18	74
116	The Pluripotency Regulator PRDM14 Requires Hematopoietic Regulator CBFA2T3 to Initiate Leukemia in Mice. <i>Molecular Cancer Research</i> , 2019 , 17, 1468-1479	6.6	3
115	BRD9 binds cell type-specific chromatin regions regulating leukemic cell survival via STAT5 inhibition. <i>Cell Death and Disease</i> , 2019 , 10, 338	9.8	15
114	The interactome of a family of potential methyltransferases in HeLa cells. <i>Scientific Reports</i> , 2019 , 9, 6584	4.9	26
113	CBFMYH11 interferes with megakaryocyte differentiation via modulating a gene program that includes GATA2 and KLF1. <i>Blood Cancer Journal</i> , 2019 , 9, 33	7	3
112	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	11.5	26
111	Miniaturised interaction proteomics on a microfluidic platform with ultra-low input requirements. <i>Nature Communications</i> , 2019 , 10, 1525	17.4	22
110	Mass Spectrometry-Based Absolute Quantification of Single Embryo Proteomes. <i>Cold Spring Harbor Protocols</i> , 2019 , 2019,	1.2	3
109	High-throughput identification of human SNPs affecting regulatory element activity. <i>Nature Genetics</i> , 2019 , 51, 1160-1169	36.3	87
108	Quantification of Proteins and Histone Marks in Drosophila Embryos Reveals Stoichiometric Relationships Impacting Chromatin Regulation. <i>Developmental Cell</i> , 2019 , 51, 632-644.e6	10.2	24
107	The Nucleosome Remodelling and Deacetylation complex suppresses transcriptional noise during lineage commitment. <i>EMBO Journal</i> , 2019 , 38,	13	16
106	Identifying Readers for (hydroxy)methylated DNA Using Quantitative Interaction Proteomics: Advances and Challenges Ahead. <i>Journal of Molecular Biology</i> , 2019 ,	6.5	2
105	Maintenance of spatial gene expression by Polycomb-mediated repression after formation of a vertebrate body plan. <i>Development (Cambridge)</i> , 2019 , 146,	6.6	5
104	The impact of nonsense-mediated mRNA decay on genetic disease, gene editing and cancer immunotherapy. <i>Nature Genetics</i> , 2019 , 51, 1645-1651	36.3	77
103	Induction and Suppression of NF- κ B Signalling by a DNA Virus of. <i>Journal of Virology</i> , 2019 , 93,	6.6	21
102	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. <i>Cell Stem Cell</i> , 2019 , 24, 123-137.e8	18	50
101	Molecular mechanisms of bleeding disorder-associated GFI1B mutation and its affected pathways in megakaryocytes and platelets. <i>Haematologica</i> , 2019 , 104, 1460-1472	6.6	15

100	The HDAC inhibitor SAHA regulates CBX2 stability via a SUMO-triggered ubiquitin-mediated pathway in leukemia. <i>Oncogene</i> , 2018 , 37, 2559-2572	9.2	19
99	Global profiling of protein-DNA and protein-nucleosome binding affinities using quantitative mass spectrometry. <i>Nature Communications</i> , 2018 , 9, 1653	17.4	36
98	Proteome-wide identification of ubiquitin interactions using UbiA-MS. <i>Nature Protocols</i> , 2018 , 13, 530-558	10.8	151
97	Specific Labeling of Stem Cell Activity in Human Colorectal Organoids Using an ASCL2-Responsive Minigene. <i>Cell Reports</i> , 2018 , 22, 1600-1614	10.6	18
96	ZBTB2 reads unmethylated CpG island promoters and regulates embryonic stem cell differentiation. <i>EMBO Reports</i> , 2018 , 19,	6.5	15
95	Single-Cell DNA Methylation Profiling: Technologies and Biological Applications. <i>Trends in Biotechnology</i> , 2018 , 36, 952-965	15.1	83
94	TRiC controls transcription resumption after UV damage by regulating Cockayne syndrome protein A. <i>Nature Communications</i> , 2018 , 9, 1040	17.4	16
93	Immuno-detection by sequencing enables large-scale high-dimensional phenotyping in cells. <i>Nature Communications</i> , 2018 , 9, 2384	17.4	9
92	Targeted degradation of BRD9 reverses oncogenic gene expression in synovial sarcoma. <i>ELife</i> , 2018 , 7,	8.9	70
91	Author response: Targeted degradation of BRD9 reverses oncogenic gene expression in synovial sarcoma 2018 ,		4
90	NuRD-interacting protein ZFP296 regulates genome-wide NuRD localization and differentiation of mouse embryonic stem cells. <i>Nature Communications</i> , 2018 , 9, 4588	17.4	8
89	Splicing and Chromatin Factors Jointly Regulate Epidermal Differentiation. <i>Cell Reports</i> , 2018 , 25, 1292-1303.e50	10.5	50
88	MTF2 recruits Polycomb Repressive Complex 2 by helical-shape-selective DNA binding. <i>Nature Genetics</i> , 2018 , 50, 1002-1010	36.3	97
87	Integrative multi-omics analysis of intestinal organoid differentiation. <i>Molecular Systems Biology</i> , 2018 , 14, e8227	12.2	65
86	Promoter Mutations Ablate GABP Transcription Factor Binding in Melanoma. <i>Cancer Research</i> , 2017 , 77, 1649-1661	10.1	6
85	An Interaction Landscape of Ubiquitin Signaling. <i>Molecular Cell</i> , 2017 , 65, 941-955.e8	17.6	75
84	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. <i>Nature Communications</i> , 2017 , 8, 15034	17.4	26
83	Histone propionylation is a mark of active chromatin. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 1048-1056	17.6	90

82	Proteomic landscape of the primary somatosensory cortex upon sensory deprivation. <i>GigaScience</i> , 2017 , 6, 1-10	7.6	6
81	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	36.3	36
80	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	17.6	16
79	N-methyladenosine (m ^A) recruits and repels proteins to regulate mRNA homeostasis. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 870-878	17.6	261
78	Click-MS: Tagless Protein Enrichment Using Bioorthogonal Chemistry for Quantitative Proteomics. <i>ACS Chemical Biology</i> , 2016 , 11, 3245-3250	4.9	10
77	The Nucleosome Remodeling and Deacetylase Complex NuRD Is Built from Preformed Catalytically Active Sub-modules. <i>Journal of Molecular Biology</i> , 2016 , 428, 2931-42	6.5	44
76	The dynamic interactome and genomic targets of Polycomb complexes during stem-cell differentiation. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 682-690	17.6	131
75	Characterizing Protein-Protein Interactions Using Mass Spectrometry: Challenges and Opportunities. <i>Trends in Biotechnology</i> , 2016 , 34, 825-834	15.1	99
74	Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , 2016 , 48, 417-26	36.3	157
73	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, 854-657.6	7.6	42
72	An interaction proteomics survey of transcription factor binding at recurrent TERT promoter mutations. <i>Proteomics</i> , 2016 , 16, 417-26	4.8	34
71	Recruitment of the Mammalian Histone-modifying EMSY Complex to Target Genes Is Regulated by ZNF131. <i>Journal of Biological Chemistry</i> , 2016 , 291, 7313-24	5.4	22
70	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	10.6	67
69	Sall4 controls differentiation of pluripotent cells independently of the Nucleosome Remodelling and Deacetylation (NuRD) complex. <i>Development (Cambridge)</i> , 2016 , 143, 3074-84	6.6	40
68	Perspective on unraveling the versatility of ζ -repressor complexes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015 , 1849, 1051-6	6	15
67	Analysis of the Histone H3.1 Interactome: A Suitable Chaperone for the Right Event. <i>Molecular Cell</i> , 2015 , 60, 697-709	17.6	45
66	Evolutionary acquisition of cysteines determines FOXO paralog-specific redox signaling. <i>Antioxidants and Redox Signaling</i> , 2015 , 22, 15-28	8.4	44
65	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, 1774-85	5.7	64

64	Developmental biology. A Me6Age for pluripotency. <i>Science</i> , 2015 , 347, 614-5	33.3	5
63	A novel microscopy-based high-throughput screening method to identify proteins that regulate global histone modification levels. <i>Journal of Biomolecular Screening</i> , 2014 , 19, 287-96		5
62	Tet oxidizes thymine to 5-hydroxymethyluracil in mouse embryonic stem cell DNA. <i>Nature Chemical Biology</i> , 2014 , 10, 574-81	11.7	215
61	Histone H2A monoubiquitination promotes histone H3 methylation in Polycomb repression. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 569-71	17.6	298
60	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, 952-66	24.6	59
59	DNA methylation: old dog, new tricks?. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 949-54	17.6	62
58	In vivo proximity labeling for the detection of protein-protein and protein-RNA interactions. <i>Journal of Proteome Research</i> , 2014 , 13, 6135-43	5.6	17
57	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. <i>Nature</i> , 2014 , 510, 283-7	50.4	259
56	Identifying nuclear protein-protein interactions using GFP affinity purification and SILAC-based quantitative mass spectrometry. <i>Methods in Molecular Biology</i> , 2014 , 1188, 207-26	1.4	21
55	MBD5 and MBD6 interact with the human PR-DUB complex through their methyl-CpG-binding domain. <i>Proteomics</i> , 2014 , 14, 2179-89	4.8	61
54	Global absolute quantification reveals tight regulation of protein expression in single <i>Xenopus</i> eggs. <i>Nucleic Acids Research</i> , 2014 , 42, 9880-91	20.1	47
53	Insight into the architecture of the NuRD complex: structure of the RbAp48-MTA1 subcomplex. <i>Journal of Biological Chemistry</i> , 2014 , 289, 21844-55	5.4	60
52	Exploring Chromatin Readers Using High-Accuracy Quantitative Mass Spectrometry-Based Proteomics 2014 , 133-148		2
51	A map of general and specialized chromatin readers in mouse tissues generated by label-free interaction proteomics. <i>Molecular Cell</i> , 2013 , 49, 368-78	17.6	128
50	Redox-dependent control of FOXO/DAF-16 by transportin-1. <i>Molecular Cell</i> , 2013 , 49, 730-42	17.6	113
49	Dynamic readers for 5-(hydroxy)methylcytosine and its oxidized derivatives. <i>Cell</i> , 2013 , 152, 1146-59	56.2	748
48	Identifying specific protein-DNA interactions using SILAC-based quantitative proteomics. <i>Methods in Molecular Biology</i> , 2013 , 977, 137-57	1.4	15
47	The chromodomain helicase Chd4 is required for Polycomb-mediated inhibition of astroglial differentiation. <i>EMBO Journal</i> , 2013 , 32, 1598-612	13	61

46	Quantitative dissection and stoichiometry determination of the human SET1/MLL histone methyltransferase complexes. <i>Molecular and Cellular Biology</i> , 2013 , 33, 2067-77	4.8	145
45	Stoichiometry of chromatin-associated protein complexes revealed by label-free quantitative mass spectrometry-based proteomics. <i>Nucleic Acids Research</i> , 2013 , 41, e28	20.1	183
44	Cdyl, a new partner of the inactive X chromosome and potential reader of H3K27me3 and H3K9me2. <i>Molecular and Cellular Biology</i> , 2013 , 33, 5005-20	4.8	57
43	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	3.7	32
42	Multivalent engagement of TFIID to nucleosomes. <i>PLoS ONE</i> , 2013 , 8, e73495	3.7	14
41	Making the most of methylation. <i>ELife</i> , 2013 , 2, e01387	8.9	2
40	MicroRNA regulation of Cbx7 mediates a switch of Polycomb orthologs during ESC differentiation. <i>Cell Stem Cell</i> , 2012 , 10, 33-46	18	163
39	Identifying chromatin readers using a SILAC-based histone peptide pull-down approach. <i>Methods in Enzymology</i> , 2012 , 512, 137-60	1.7	9
38	Proteome-wide analysis of disease-associated SNPs that show allele-specific transcription factor binding. <i>PLoS Genetics</i> , 2012 , 8, e1002982	6	74
37	Differential epigenetic regulation of GATA4 in gastric adenocarcinomas. <i>Epigenomics</i> , 2012 , 4, 367	4.4	2
36	Yeast Aging Proteome Unveiled a Novel Aging Regulation Pathway Mediated by the Chromatin Remodeling Complex ISW2. <i>FASEB Journal</i> , 2012 , 26, 965.2	0.9	
35	Towards cracking the epigenetic code using a combination of high-throughput epigenomics and quantitative mass spectrometry-based proteomics. <i>BioEssays</i> , 2011 , 33, 547-51	4.1	16
34	Quantitative proteomics for epigenetics. <i>ChemBioChem</i> , 2011 , 12, 224-34	3.8	54
33	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	3.7	38
32	A domesticated transposon mediates the effects of a single-nucleotide polymorphism responsible for enhanced muscle growth. <i>EMBO Reports</i> , 2010 , 11, 305-11	6.5	46
31	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <i>Science Signaling</i> , 2010 , 3, ra3	8.8	1106
30	Regulation of the histone H4 monomethylase PR-Set7 by CRL4(Cdt2)-mediated PCNA-dependent degradation during DNA damage. <i>Molecular Cell</i> , 2010 , 40, 364-76	17.6	187
29	Quantitative interaction proteomics and genome-wide profiling of epigenetic histone marks and their readers. <i>Cell</i> , 2010 , 142, 967-80	56.2	579

28	Nucleosome-interacting proteins regulated by DNA and histone methylation. <i>Cell</i> , 2010 , 143, 470-84	56.2	448
27	Grasping trimethylation of histone H3 at lysine 4. <i>Epigenomics</i> , 2010 , 2, 395-406	4.4	59
26	CDK2AP1/DOC-1 is a bona fide subunit of the Mi-2/NuRD complex. <i>Molecular BioSystems</i> , 2010 , 6, 1700-6		43
25	Phosphorylation of histone H3 Thr-45 is linked to apoptosis. <i>Journal of Biological Chemistry</i> , 2009 , 284, 16575-16583	5.4	85
24	Quantitative proteomics: a tool to assess cell differentiation. <i>Current Opinion in Cell Biology</i> , 2009 , 21, 761-6	9	21
23	Two chromatin remodeling activities cooperate during activation of hormone responsive promoters. <i>PLoS Genetics</i> , 2009 , 5, e1000567	6	42
22	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. <i>Nature Methods</i> , 2008 , 5, 459-60	21.6	237
21	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, 6418-26	3.2	18
20	High confidence determination of specific protein-protein interactions using quantitative mass spectrometry. <i>Current Opinion in Biotechnology</i> , 2008 , 19, 331-7	11.4	139
19	Arginine methylation at histone H3R2 controls deposition of H3K4 trimethylation. <i>Nature</i> , 2007 , 449, 928-32	50.4	282
18	Selective anchoring of TFIID to nucleosomes by trimethylation of histone H3 lysine 4. <i>Cell</i> , 2007 , 131, 58-69	56.2	643
17	Molecular characterization of Sin3 PAH-domain interactor specificity and identification of PAH partners. <i>Nucleic Acids Research</i> , 2006 , 34, 3929-37	20.1	31
16	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, 5226-36	4.8	25
15	MBD2/NuRD and MBD3/NuRD, two distinct complexes with different biochemical and functional properties. <i>Molecular and Cellular Biology</i> , 2006 , 26, 843-51	4.8	257
14	Nuclear pore components are involved in the transcriptional regulation of dosage compensation in <i>Drosophila</i> . <i>Molecular Cell</i> , 2006 , 21, 811-23	17.6	331
13	Targeted discovery tools: proteomics and chromatin immunoprecipitation-on-chip. <i>BJU International</i> , 2005 , 96 Suppl 2, 16-22	5.6	8
12	Characterization of lysine 56 of histone H3 as an acetylation site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005 , 280, 25949-52	5.4	97
11	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, 2364-72	4.8	39

10	An in vitro assay to study the recruitment and substrate specificity of chromatin modifying enzymes. <i>Biological Procedures Online</i> , 2004 , 6, 157-162	8.3	3
9	The Mad1-Sin3B interaction involves a novel helical fold. <i>Nature Structural Biology</i> , 2000 , 7, 1100-4		48
8	The Tudor protein Veneno assembles the ping-pong amplification complex that 1 produces viral piRNAs in <i>Aedes</i> mosquitoes		1
7	Massively parallel reporter assays combined with cell-type specific eQTL informed multiple melanoma loci and identified a pleiotropic function of HIV-1 restriction gene, MX2, in melanoma promotion		2
6	A CSB-PAF1C axis restores processive transcription elongation after DNA damage repair		2
5	Chromosomal instability by mutations in a novel specificity factor of the minor spliceosome		1
4	Induction and suppression of NF-kB signalling by a DNA virus of <i>Drosophila</i>		3
3	Subunit redundancy within the NuRD complex ensures fidelity of ES cell lineage commitment		1
2	The GBAF chromatin remodeling complex binds H3K27ac and mediates enhancer transcription		2
1	Systematic identification of human SNPs affecting regulatory element activity		4