

Michael P Washburn

List of Publications by Year in descending order

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Version: 2024-02-01

152
papers

19,365
citations

20036

63
h-index

14012

133
g-index

167
all docs

167
docs citations

167
times ranked

26784
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of stem cells from large cell populations with topological scoring. <i>Molecular Omics</i> , 2021, 17, 59-65.	1.4	3
2	Multiple roles for PARP1 in ALC1-dependent nucleosome remodeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	3
3	Harnessing Ionic Selectivity in Acetyltransferase Chemoproteomic Probes. <i>ACS Chemical Biology</i> , 2021, 16, 27-34.	1.6	5
4	Structural basis of the interaction between SETD2 methyltransferase and hnRNP L paralogs for governing co-transcriptional splicing. <i>Nature Communications</i> , 2021, 12, 6452.	5.8	12
5	Perturbation of BRMS1 interactome reveals pathways that impact metastasis. <i>PLoS ONE</i> , 2021, 16, e0259128.	1.1	0
6	Driving integrative structural modeling with serial capture affinity purification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31861-31870.	3.3	8
7	Differential Complex Formation via Paralogs in the Human Sin3 Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1468-1484.	2.5	26
8	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. <i>Nature</i> , 2020, 583, 638-643.	13.7	175
9	The role of Mediator and Little Elongation Complex in transcription termination. <i>Nature Communications</i> , 2020, 11, 1063.	5.8	21
10	Integrative Modeling of a Sin3/HDAC Complex Sub-structure. <i>Cell Reports</i> , 2020, 31, 107516.	2.9	29
11	Merkel cell polyomavirus activates LSD1-mediated blockade of non-canonical BAF to regulate transformation and tumorigenesis. <i>Nature Cell Biology</i> , 2020, 22, 603-615.	4.6	47
12	The chromatin bound proteome of the human malaria parasite. <i>Microbial Genomics</i> , 2020, 6, .	1.0	13
13	STRIPAK directs PP2A activity toward MAP4K4 to promote oncogenic transformation of human cells. <i>ELife</i> , 2020, 9, .	2.8	46
14	Yeast Nuak1 phosphorylates histone H3 threonine 11 in low glucose stress by the cooperation of AMPK and CK2 signaling. <i>ELife</i> , 2020, 9, .	2.8	7
15	Biochemical Reduction of the Topology of the Diverse WDR76 Protein Interactome. <i>Journal of Proteome Research</i> , 2019, 18, 3479-3491.	1.8	14
16	BRK phosphorylates SMAD4 for proteasomal degradation and inhibits tumor suppressor FRK to control SNAIL, SLUG, and metastatic potential. <i>Science Advances</i> , 2019, 5, eaaw3113.	4.7	16
17	Topological scoring of protein interaction networks. <i>Nature Communications</i> , 2019, 10, 1118.	5.8	32
18	RUNX proteins desensitize multiple myeloma to lenalidomide via protecting IKZFs from degradation. <i>Leukemia</i> , 2019, 33, 2006-2021.	3.3	36

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19	A chemoproteomic portrait of the oncometabolite fumarate. <i>Nature Chemical Biology</i> , 2019, 15, 391-400.	3.9	77
20	Ataxin-7 and Non-stop coordinate SCAR protein levels, subcellular localization, and actin cytoskeleton organization. <i>ELife</i> , 2019, 8, .	2.8	13
21	Loss of KLHL6 promotes diffuse large B-cell lymphoma growth and survival by stabilizing the mRNA decay factor roquin2. <i>Nature Cell Biology</i> , 2018, 20, 586-596.	4.6	35
22	A Structured Workflow for Mapping Human Sin3 Histone Deacetylase Complex Interactions Using Halo-MudPIT Affinity-Purification Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1432-1447.	2.5	27
23	Differential HDAC1/2 network analysis reveals a role for prefoldin/CCT in HDAC1/2 complex assembly. <i>Scientific Reports</i> , 2018, 8, 13712.	1.6	32
24	The ULK1-FBXW5-SEC23B nexus controls autophagy. <i>ELife</i> , 2018, 7, .	2.8	63
25	Chromatin remodeller Fun30/Ft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. <i>Nature Communications</i> , 2017, 8, 14527.	5.8	41
26	The TDH/ GCN5L1/ Fbxo15/ KBP axis limits mitochondrial biogenesis in mouse embryonic stem cells. <i>Nature Cell Biology</i> , 2017, 19, 341-351.	4.6	41
27	The WHHERE coactivator complex is required for retinoic acid-dependent regulation of embryonic symmetry. <i>Nature Communications</i> , 2017, 8, 728.	5.8	27
28	The human cytoplasmic dynein interactome reveals novel activators of motility. <i>ELife</i> , 2017, 6, .	2.8	120
29	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016, 11, e0155492.	1.1	27
30	The Spliceosomal Protein SF3B5 is a Novel Component of Drosophila SAGA that Functions in Gene Expression Independent of Splicing. <i>Journal of Molecular Biology</i> , 2016, 428, 3632-3649.	2.0	29
31	The Enok acetyltransferase complex interacts with Elg1 and negatively regulates PCNA unloading to promote the G1/S transition. <i>Genes and Development</i> , 2016, 30, 1198-210.	2.7	11
32	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. <i>Molecular Cell</i> , 2016, 62, 558-571.	4.5	106
33	TNIP2 is a Hub Protein in the NF- κ B Network with Both Protein and RNA Mediated Interactions. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3435-3449.	2.5	27
34	HIV-1 and HIV-2 exhibit divergent interactions with HLTf and UNG2 DNA repair proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3921-30.	3.3	58
35	There is no human interactome. <i>Genome Biology</i> , 2016, 17, 48.	3.8	17
36	Dynamic and Combinatorial Landscape of Histone Modifications during the Intraerythrocytic Developmental Cycle of the Malaria Parasite. <i>Journal of Proteome Research</i> , 2016, 15, 2787-2801.	1.8	49

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37	Proteomic and Genomic Analyses of the Rvb1 and Rvb2 Interaction Network upon Deletion of R2TP Complex Components. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 960-974.	2.5	11
38	Moco biosynthesis and the ATAC acetyltransferase engage translation initiation by inhibiting latent PKR activity. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 44-50.	1.5	11
39	CyclinA2-Cyclin-dependent Kinase Regulates SAMHD1 Protein Phosphohydrolase Domain. <i>Journal of Biological Chemistry</i> , 2015, 290, 13279-13292.	1.6	84
40	Characterization of Human Cyclin-Dependent Kinase 12 (CDK12) and CDK13 Complexes in C-Terminal Domain Phosphorylation, Gene Transcription, and RNA Processing. <i>Molecular and Cellular Biology</i> , 2015, 35, 928-938.	1.1	153
41	Conserved abundance and topological features in chromatin remodeling protein interaction networks. <i>EMBO Reports</i> , 2015, 16, 116-126.	2.0	17
42	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. <i>Molecular Cell</i> , 2015, 57, 685-694.	4.5	92
43	The Integrator complex controls the termination of transcription at diverse classes of gene targets. <i>Cell Research</i> , 2015, 25, 288-305.	5.7	113
44	Assembly of the Elongin A Ubiquitin Ligase Is Regulated by Genotoxic and Other Stresses. <i>Journal of Biological Chemistry</i> , 2015, 290, 15030-15041.	1.6	24
45	Structural analyses of the chromatin remodelling enzymes INO80-C and SWR-C. <i>Nature Communications</i> , 2015, 6, 7108.	5.8	61
46	Improving Label-Free Quantitative Proteomics Strategies by Distributing Shared Peptides and Stabilizing Variance. <i>Analytical Chemistry</i> , 2015, 87, 4749-4756.	3.2	36
47	Serine and SAM Responsive Complex SESAME Regulates Histone Modification Crosstalk by Sensing Cellular Metabolism. <i>Molecular Cell</i> , 2015, 60, 408-421.	4.5	136
48	The H-Index of $\hat{\alpha}$ An Approach to Correlate Tandem Mass Spectral Data of Peptides with Amino Acid Sequences in a Protein Database $\hat{\alpha}$ ™. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1799-1803.	1.2	10
49	Cyclin-dependent Kinase-mediated Sox2 Phosphorylation Enhances the Ability of Sox2 to Establish the Pluripotent State. <i>Journal of Biological Chemistry</i> , 2015, 290, 22782-22794.	1.6	40
50	Degradation of Cep68 and PCNT cleavage mediate Cep215 removal from the PCM to allow centriole separation, disengagement and licensing. <i>Nature Cell Biology</i> , 2015, 17, 31-43.	4.6	69
51	Loss of <i>Drosophila</i> Ataxin-7, a SAGA subunit, reduces H2B ubiquitination and leads to neural and retinal degeneration. <i>Genes and Development</i> , 2014, 28, 259-272.	2.7	51
52	Suberoylanilide Hydroxamic Acid (SAHA)-Induced Dynamics of a Human Histone Deacetylase Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3114-3125.	2.5	26
53	Gene duplication and neofunctionalization: POLR3G and POLR3GL. <i>Genome Research</i> , 2014, 24, 37-51.	2.4	47
54	Swi/Snf dynamics on stress-responsive genes is governed by competitive bromodomain interactions. <i>Genes and Development</i> , 2014, 28, 2314-2330.	2.7	41

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55	Histone H3 lysine-to-methionine mutants as a paradigm to study chromatin signaling. <i>Science</i> , 2014, 345, 1065-1070.	6.0	163
56	Controlling for Gene Expression Changes in Transcription Factor Protein Networks. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1510-1522.	2.5	23
57	The Little Elongation Complex Functions at Initiation and Elongation Phases of snRNA Gene Transcription. <i>Molecular Cell</i> , 2013, 51, 493-505.	4.5	54
58	FBH1 promotes DNA double-strand breakage and apoptosis in response to DNA replication stress. <i>Journal of Cell Biology</i> , 2013, 200, 141-149.	2.3	50
59	Regulation of the CRL4Cdt2 Ubiquitin Ligase and Cell-Cycle Exit by the SCFFbxo11 Ubiquitin Ligase. <i>Molecular Cell</i> , 2013, 49, 1159-1166.	4.5	67
60	Role for Human Mediator Subunit MED25 in Recruitment of Mediator to Promoters by Endoplasmic Reticulum Stress-responsive Transcription Factor ATF6 β . <i>Journal of Biological Chemistry</i> , 2013, 288, 26179-26187.	1.6	33
61	Quantitative Proteomics Demonstrates That the RNA Polymerase II Subunits Rpb4 and Rpb7 Dissociate during Transcriptional Elongation. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1530-1538.	2.5	45
62	FBXL2- and PTPL1-mediated degradation of p110-free p85 β regulatory subunit controls the PI(3)K signalling cascade. <i>Nature Cell Biology</i> , 2013, 15, 472-480.	4.6	98
63	Binding of <i>Drosophila</i> Polo kinase to its regulator Matrimony is noncanonical and involves two separate functional domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1222-31.	3.3	27
64	Polycomb Repressive Complex 2-Dependent and -Independent Functions of Jarid2 in Transcriptional Regulation in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2012, 32, 1683-1693.	1.1	66
65	Human Family with Sequence Similarity 60 Member A (FAM60A) Protein: a New Subunit of the Sin3 Deacetylase Complex. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1815-1828.	2.5	47
66	Shaggy/glycogen synthase kinase 3 β and phosphorylation of Sarah/regulator of calcineurin are essential for completion of <i>Drosophila</i> female meiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6382-6389.	3.3	44
67	Endoplasmic Reticulum Stress-responsive Transcription Factor ATF6 β Directs Recruitment of the Mediator of RNA Polymerase II Transcription and Multiple Histone Acetyltransferase Complexes. <i>Journal of Biological Chemistry</i> , 2012, 287, 23035-23045.	1.6	22
68	The Super Elongation Complex Family of RNA Polymerase II Elongation Factors: Gene Target Specificity and Transcriptional Output. <i>Molecular and Cellular Biology</i> , 2012, 32, 2608-2617.	1.1	150
69	Cyclin F-Mediated Degradation of Ribonucleotide Reductase M2 Controls Genome Integrity and DNA Repair. <i>Cell</i> , 2012, 149, 1023-1034.	13.5	313
70	Affinity purification of protein complexes for analysis by multidimensional protein identification technology. <i>Protein Expression and Purification</i> , 2012, 86, 105-119.	0.6	24
71	Chromatin remodelers Isw1 and Chd1 maintain chromatin structure during transcription by preventing histone exchange. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 884-892.	3.6	256
72	A Metazoan ATAC Acetyltransferase Subunit That Regulates Mitogen-activated Protein Kinase Signaling Is Related to an Ancient Molybdopterin Synthase Component. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 90-99.	2.5	6

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73	Improving Proteomics Mass Accuracy by Dynamic Offline Lock Mass. <i>Analytical Chemistry</i> , 2011, 83, 9344-9351.	3.2	46
74	Human Mediator Subunit MED26 Functions as a Docking Site for Transcription Elongation Factors. <i>Cell</i> , 2011, 146, 92-104.	13.5	293
75	The Little Elongation Complex Regulates Small Nuclear RNA Transcription. <i>Molecular Cell</i> , 2011, 44, 954-965.	4.5	75
76	Temporal Regulation of Gene Expression of the <i>Thermus thermophilus</i> Bacteriophage P23-45. <i>Journal of Molecular Biology</i> , 2011, 405, 125-142.	2.0	33
77	Unraveling the dynamics of protein interactions with quantitative mass spectrometry. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011, 46, 216-228.	2.3	25
78	Post-transcription initiation function of the ubiquitous SAGA complex in tissue-specific gene activation. <i>Genes and Development</i> , 2011, 25, 1499-1509.	2.7	60
79	Combinatorial depletion analysis to assemble the network architecture of the SAGA and ADA chromatin remodeling complexes. <i>Molecular Systems Biology</i> , 2011, 7, 503.	3.2	140
80	Driving biochemical discovery with quantitative proteomics. <i>Trends in Biochemical Sciences</i> , 2011, 36, 170-177.	3.7	11
81	Vpx relieves inhibition of HIV-1 infection of macrophages mediated by the SAMHD1 protein. <i>Nature</i> , 2011, 474, 658-661.	13.7	1,060
82	Unraveling the Ubiquitome of the Human Malaria Parasite. <i>Journal of Biological Chemistry</i> , 2011, 286, 40320-40330.	1.6	66
83	The COMPASS Family of H3K4 Methylases in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4310-4318.	1.1	195
84	Subunit Organization of the Human INO80 Chromatin Remodeling Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 11283-11289.	1.6	93
85	DYRK1A protein kinase promotes quiescence and senescence through DREAM complex assembly. <i>Genes and Development</i> , 2011, 25, 801-813.	2.7	231
86	Nuclear cGMP-Dependent Kinase Regulates Gene Expression via Activity-Dependent Recruitment of a Conserved Histone Deacetylase Complex. <i>PLoS Genetics</i> , 2011, 7, e1002065.	1.5	41
87	The tumour antigen PRAME is a subunit of a Cul2 ubiquitin ligase and associates with active NFY promoters. <i>EMBO Journal</i> , 2011, 30, 3786-3798.	3.5	59
88	Deacetylase Inhibitors Dissociate the Histone-Targeting ING2 Subunit from the Sin3 Complex. <i>Chemistry and Biology</i> , 2010, 17, 65-74.	6.2	79
89	SCFCyclin F controls centrosome homeostasis and mitotic fidelity through CP110 degradation. <i>Nature</i> , 2010, 466, 138-142.	13.7	235
90	Gcn5 regulates the dissociation of SWI/SNF from chromatin by acetylation of Swi2/Snf2. <i>Genes and Development</i> , 2010, 24, 2766-2771.	2.7	67

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91	Delayed Correlation of mRNA and Protein Expression in Rapamycin-treated Cells and a Role for Ggc1 in Cellular Sensitivity to Rapamycin. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 271-284.	2.5	134
92	Subunit Composition and Substrate Specificity of a MOF-containing Histone Acetyltransferase Distinct from the Male-specific Lethal (MSL) Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 4268-4272.	1.6	211
93	Linking H3K79 trimethylation to Wnt signaling through a novel Dot1-containing complex (DotCom). <i>Genes and Development</i> , 2010, 24, 574-589.	2.7	272
94	Heterochromatin protein 1 (HP1) connects the FACT histone chaperone complex to the phosphorylated CTD of RNA polymerase II. <i>Genes and Development</i> , 2010, 24, 2133-2145.	2.7	90
95	AFF4, a Component of the ELL/P-TEFb Elongation Complex and a Shared Subunit of MLL Chimeras, Can Link Transcription Elongation to Leukemia. <i>Molecular Cell</i> , 2010, 37, 429-437.	4.5	504
96	The ATAC Acetyltransferase Complex Coordinates MAP Kinases to Regulate JNK Target Genes. <i>Cell</i> , 2010, 142, 726-736.	13.5	66
97	Refinements to Label Free Proteome Quantitation: How to Deal with Peptides Shared by Multiple Proteins. <i>Analytical Chemistry</i> , 2010, 82, 2272-2281.	3.2	366
98	Determining Protein Complex Connectivity Using a Probabilistic Deletion Network Derived from Quantitative Proteomics. <i>PLoS ONE</i> , 2009, 4, e7310.	1.1	35
99	Poly(ADP-ribosyl)ation directs recruitment and activation of an ATP-dependent chromatin remodeler. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13770-13774.	3.3	322
100	Proteomics Reveals a Physical and Functional Link between Hepatocyte Nuclear Factor 4 $\hat{\pm}$ and Transcription Factor IID. <i>Journal of Biological Chemistry</i> , 2009, 284, 32405-32412.	1.6	9
101	A novel histone fold domain-containing protein that replaces TAF6 in <i>Drosophila</i> SAGA is required for SAGA-dependent gene expression. <i>Genes and Development</i> , 2009, 23, 2818-2823.	2.7	34
102	INTS3 controls the hSSB1-mediated DNA damage response. <i>Journal of Cell Biology</i> , 2009, 187, 25-32.	2.3	80
103	Regulation of H3K4 Trimethylation via Cps40 (Spp1) of COMPASS Is Monoubiquitination Independent: Implication for a Phe/Tyr Switch by the Catalytic Domain of Set1. <i>Molecular and Cellular Biology</i> , 2009, 29, 3478-3486.	1.1	54
104	Rtr1 Is a CTD Phosphatase that Regulates RNA Polymerase II during the Transition from Serine 5 to Serine 2 Phosphorylation. <i>Molecular Cell</i> , 2009, 34, 168-178.	4.5	125
105	Evaluation of Clustering Algorithms for Protein Complex and Protein Interaction Network Assembly. <i>Journal of Proteome Research</i> , 2009, 8, 2944-2952.	1.8	44
106	Effect of Dynamic Exclusion Duration on Spectral Count Based Quantitative Proteomics. <i>Analytical Chemistry</i> , 2009, 81, 6317-6326.	3.2	167
107	ATAC is a double histone acetyltransferase complex that stimulates nucleosome sliding. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 364-372.	3.6	171
108	Genomic and Proteomic Analysis of phiEco32, a Novel Escherichia coli Bacteriophage. <i>Journal of Molecular Biology</i> , 2008, 377, 774-789.	2.0	61

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109	Genome Comparison and Proteomic Characterization of Thermus thermophilus Bacteriophages P23-45 and P74-26: Siphoviruses with Triplex-forming Sequences and the Longest Known Tails. <i>Journal of Molecular Biology</i> , 2008, 378, 468-480.	2.0	56
110	Structural Changes in TAF4b-TFIID Correlate with Promoter Selectivity. <i>Molecular Cell</i> , 2008, 29, 81-91.	4.5	55
111	Distinct Modes of Regulation of the Uch37 Deubiquitinating Enzyme in the Proteasome and in the Ino80 Chromatin-Remodeling Complex. <i>Molecular Cell</i> , 2008, 31, 909-917.	4.5	132
112	Heterochromatin Protein 1a Stimulates Histone H3 Lysine 36 Demethylation by the Drosophila KDM4A Demethylase. <i>Molecular Cell</i> , 2008, 32, 696-706.	4.5	97
113	Drosophila ELMO/CED-12 interacts with Myoblast city to direct myoblast fusion and ommatidial organization. <i>Developmental Biology</i> , 2008, 314, 137-149.	0.9	83
114	Probabilistic assembly of human protein interaction networks from label-free quantitative proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1454-1459.	3.3	220
115	Characterization of Cullin-box Sequences That Direct Recruitment of Cul2-Rbx1 and Cul5-Rbx2 Modules to Elongin BC-based Ubiquitin Ligases. <i>Journal of Biological Chemistry</i> , 2008, 283, 8005-8013.	1.6	147
116	Neuralized-like 1 (Neur1) Targeted to the Plasma Membrane by N-Myristoylation Regulates the Notch Ligand Jagged1. <i>Journal of Biological Chemistry</i> , 2008, 283, 3846-3853.	1.6	69
117	Molecular Regulation of H3K4 Trimethylation by Wdr82, a Component of Human Set1/COMPASS. <i>Molecular and Cellular Biology</i> , 2008, 28, 7337-7344.	1.1	281
118	Lentiviral Vpx Accessory Factor Targets VprBP/DCAF1 Substrate Adaptor for Cullin 4 E3 Ubiquitin Ligase to Enable Macrophage Infection. <i>PLoS Pathogens</i> , 2008, 4, e1000059.	2.1	192
119	Statistical Similarities between Transcriptomics and Quantitative Shotgun Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 631-644.	2.5	146
120	PARC and CUL7 Form Atypical Cullin RING Ligase Complexes. <i>Cancer Research</i> , 2007, 67, 2006-2014.	0.4	56
121	Lentiviral Vpr usurps Cul4/DDB1[VprBP] E3 ubiquitin ligase to modulate cell cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11778-11783.	3.3	209
122	CHD8 Associates with Human Staf and Contributes to Efficient U6 RNA Polymerase III Transcription. <i>Molecular and Cellular Biology</i> , 2007, 27, 8729-8738.	1.1	67
123	Identification and Characterization of a Schizosaccharomyces pombe RNA Polymerase II Elongation Factor with Similarity to the Metazoan Transcription Factor ELL. <i>Journal of Biological Chemistry</i> , 2007, 282, 5761-5769.	1.6	25
124	Ctk Complex-Mediated Regulation of Histone Methylation by COMPASS. <i>Molecular and Cellular Biology</i> , 2007, 27, 709-720.	1.1	59
125	Histone Crosstalk between H2B Monoubiquitination and H3 Methylation Mediated by COMPASS. <i>Cell</i> , 2007, 131, 1084-1096.	13.5	373
126	Evolutionarily Conserved Multisubunit RBL2/p130 and E2F4 Protein Complex Represses Human Cell Cycle-Dependent Genes in Quiescence. <i>Molecular Cell</i> , 2007, 26, 539-551.	4.5	347

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127	Scm3 Is Essential to Recruit the Histone H3 Variant Cse4 to Centromeres and to Maintain a Functional Kinetochore. <i>Molecular Cell</i> , 2007, 26, 853-865.	4.5	222
128	Quantitative shotgun proteomics using a protease with broad specificity and normalized spectral abundance factors. <i>Molecular BioSystems</i> , 2007, 3, 354.	2.9	144
129	The Inhibition of Polo Kinase by Matrimony Maintains G2 Arrest in the Meiotic Cell Cycle. <i>PLoS Biology</i> , 2007, 5, e323.	2.6	68
130	YY1 functions with INO80 to activate transcription. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 872-874.	3.6	178
131	Statistical Analysis of Membrane Proteome Expression Changes in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2006, 5, 2339-2347.	1.8	1,042
132	A role for Yin Yang-1 (YY1) in the assembly of snRNA transcription complexes. <i>Gene</i> , 2006, 377, 96-108.	1.0	10
133	<i>Thermus thermophilus</i> Bacteriophage ϕ YS40 Genome and Proteomic Characterization of Virions. <i>Journal of Molecular Biology</i> , 2006, 364, 667-677.	2.0	60
134	Proteasome recruitment and activation of the Uch37 deubiquitinating enzyme by Adrm1. <i>Nature Cell Biology</i> , 2006, 8, 994-1002.	4.6	282
135	Host Cell Factor and an Uncharacterized SANT Domain Protein Are Stable Components of ATAC, a Novel dAda2A/dGcn5-Containing Histone Acetyltransferase Complex in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2006, 26, 871-882.	1.1	107
136	Quantitative proteomic analysis of distinct mammalian Mediator complexes using normalized spectral abundance factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18928-18933.	3.3	495
137	Mnd1/Hop2 Facilitates Dmc1-Dependent Interhomolog Crossover Formation in Meiosis of Budding Yeast. <i>Molecular and Cellular Biology</i> , 2006, 26, 2913-2923.	1.1	49
138	The Essential Gene <i>wda</i> Encodes a WD40 Repeat Subunit of <i>Drosophila</i> SAGA Required for Histone H3 Acetylation. <i>Molecular and Cellular Biology</i> , 2006, 26, 7178-7189.	1.1	30
139	The Deubiquitylation Activity of Ubp8 Is Dependent upon Sgf11 and Its Association with the SAGA Complex. <i>Molecular and Cellular Biology</i> , 2005, 25, 1173-1182.	1.1	143
140	A Mammalian Chromatin Remodeling Complex with Similarities to the Yeast INO80 Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 41207-41212.	1.6	211
141	Characterization of the Yeast Trimeric-SAS Acetyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 11987-11994.	1.6	76
142	The Mammalian YL1 Protein Is a Shared Subunit of the TRRAP/TIP60 Histone Acetyltransferase and SRCAP Complexes. <i>Journal of Biological Chemistry</i> , 2005, 280, 13665-13670.	1.6	185
143	The HIR corepressor complex binds to nucleosomes generating a distinct protein/DNA complex resistant to remodeling by SWI/SNF. <i>Genes and Development</i> , 2005, 19, 2534-2539.	2.7	89
144	Molecular Regulation of Histone H3 Trimethylation by COMPASS and the Regulation of Gene Expression. <i>Molecular Cell</i> , 2005, 19, 849-856.	4.5	263

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145	Histone H3 Methylation by Set2 Directs Deacetylation of Coding Regions by Rpd3S to Suppress Spurious Intragenic Transcription. <i>Cell</i> , 2005, 123, 581-592.	13.5	1,154
146	The mammalian Mediator complex. <i>FEBS Letters</i> , 2005, 579, 904-908.	1.3	43
147	Correlation of Relative Abundance Ratios Derived from Peptide Ion Chromatograms and Spectrum Counting for Quantitative Proteomic Analysis Using Stable Isotope Labeling. <i>Analytical Chemistry</i> , 2005, 77, 6218-6224.	3.2	324
148	A Mammalian Mediator Subunit that Shares Properties with <i>Saccharomyces cerevisiae</i> Mediator Subunit Cse2. <i>Journal of Biological Chemistry</i> , 2004, 279, 5846-5851.	1.6	24
149	Acetylation by Tip60 Is Required for Selective Histone Variant Exchange at DNA Lesions. <i>Science</i> , 2004, 306, 2084-2087.	6.0	602
150	A Set of Consensus Mammalian Mediator Subunits Identified by Multidimensional Protein Identification Technology. <i>Molecular Cell</i> , 2004, 14, 685-691.	4.5	270
151	Proteomic analysis of chromatin-modifying complexes in <i>Saccharomyces cerevisiae</i> identifies novel subunits. <i>Biochemical Society Transactions</i> , 2004, 32, 899-903.	1.6	33
152	A proteomic view of the <i>Plasmodium falciparum</i> life cycle. <i>Nature</i> , 2002, 419, 520-526.	13.7	1,184