

# Michael P Washburn

## List of Publications by Year in descending order

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152  
papers

19,365  
citations

16451

64  
h-index

12272

133  
g-index

167  
all docs

167  
docs citations

167  
times ranked

24143  
citing authors

#	ARTICLE	IF	CITATIONS
1	A proteomic view of the Plasmodium falciparum life cycle. Nature, 2002, 419, 520-526.	27.8	1,184
2	Histone H3 Methylation by Set2 Directs Deacetylation of Coding Regions by Rpd3S to Suppress Spurious Intragenic Transcription. Cell, 2005, 123, 581-592.	28.9	1,154
3	Vpx relieves inhibition of HIV-1 infection of macrophages mediated by the SAMHD1 protein. Nature, 2011, 474, 658-661.	27.8	1,060
4	Statistical Analysis of Membrane Proteome Expression Changes in Saccharomyces cerevisiae. Journal of Proteome Research, 2006, 5, 2339-2347.	3.7	1,042
5	Acetylation by Tip60 Is Required for Selective Histone Variant Exchange at DNA Lesions. Science, 2004, 306, 2084-2087.	12.6	602
6	AFF4, a Component of the ELL/P-TEFb Elongation Complex and a Shared Subunit of MLL Chimeras, Can Link Transcription Elongation to Leukemia. Molecular Cell, 2010, 37, 429-437.	9.7	504
7	Quantitative proteomic analysis of distinct mammalian Mediator complexes using normalized spectral abundance factors. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18928-18933.	7.1	495
8	Histone Crosstalk between H2B Monoubiquitination and H3 Methylation Mediated by COMPASS. Cell, 2007, 131, 1084-1096.	28.9	373
9	Refinements to Label Free Proteome Quantitation: How to Deal with Peptides Shared by Multiple Proteins. Analytical Chemistry, 2010, 82, 2272-2281.	6.5	366
10	Evolutionarily Conserved Multisubunit RBL2/p130 and E2F4 Protein Complex Represses Human Cell Cycle-Dependent Genes in Quiescence. Molecular Cell, 2007, 26, 539-551.	9.7	347
11	Correlation of Relative Abundance Ratios Derived from Peptide Ion Chromatograms and Spectrum Counting for Quantitative Proteomic Analysis Using Stable Isotope Labeling. Analytical Chemistry, 2005, 77, 6218-6224.	6.5	324
12	Poly(ADP-ribosyl)ation directs recruitment and activation of an ATP-dependent chromatin remodeler. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13770-13774.	7.1	322
13	Cyclin F-Mediated Degradation of Ribonucleotide Reductase M2 Controls Genome Integrity and DNA Repair. Cell, 2012, 149, 1023-1034.	28.9	313
14	Human Mediator Subunit MED26 Functions as a Docking Site for Transcription Elongation Factors. Cell, 2011, 146, 92-104.	28.9	293
15	Proteasome recruitment and activation of the Uch37 deubiquitinating enzyme by Adrm1. Nature Cell Biology, 2006, 8, 994-1002.	10.3	282
16	Molecular Regulation of H3K4 Trimethylation by Wdr82, a Component of Human Set1/COMPASS. Molecular and Cellular Biology, 2008, 28, 7337-7344.	2.3	281
17	Linking H3K79 trimethylation to Wnt signaling through a novel Dot1-containing complex (DotCom). Genes and Development, 2010, 24, 574-589.	5.9	272
18	A Set of Consensus Mammalian Mediator Subunits Identified by Multidimensional Protein Identification Technology. Molecular Cell, 2004, 14, 685-691.	9.7	270

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19	Molecular Regulation of Histone H3 Trimethylation by COMPASS and the Regulation of Gene Expression. <i>Molecular Cell</i> , 2005, 19, 849-856.	9.7	263
20	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.	8.2	256
21	SCFCyclin F controls centrosome homeostasis and mitotic fidelity through CP110 degradation. <i>Nature</i> , 2010, 466, 138-142.	27.8	235
22	DYRK1A protein kinase promotes quiescence and senescence through DREAM complex assembly. <i>Genes and Development</i> , 2011, 25, 801-813.	5.9	231
23	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.	9.7	222
24	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.	7.1	220
25	A Mammalian Chromatin Remodeling Complex with Similarities to the Yeast INO80 Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 41207-41212.	3.4	211
26	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.	3.4	211
27	Lentiviral Vpr usurps Cul4 $\hat{=}$ 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.	7.1	209
28	The COMPASS Family of H3K4 Methylases in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4310-4318.	2.3	195
29	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.	4.7	192
30	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.	3.4	185
31	YY1 functions with INO80 to activate transcription. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 872-874.	8.2	178
32	Dynamic RNA acetylation revealed by quantitative cross-evolutionary mapping. <i>Nature</i> , 2020, 583, 638-643.	27.8	175
33	ATAC is a double histone acetyltransferase complex that stimulates nucleosome sliding. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 364-372.	8.2	171
34	Effect of Dynamic Exclusion Duration on Spectral Count Based Quantitative Proteomics. <i>Analytical Chemistry</i> , 2009, 81, 6317-6326.	6.5	167
35	Histone H3 lysine-to-methionine mutants as a paradigm to study chromatin signaling. <i>Science</i> , 2014, 345, 1065-1070.	12.6	163
36	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.	2.3	153

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37	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.	2.3	150
38	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.	3.4	147
39	Statistical Similarities between Transcriptomics and Quantitative Shotgun Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 631-644.	3.8	146
40	Quantitative shotgun proteomics using a protease with broad specificity and normalized spectral abundance factors. <i>Molecular BioSystems</i> , 2007, 3, 354.	2.9	144
41	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.	2.3	143
42	Combinatorial depletion analysis to assemble the network architecture of the SAGA and ADA chromatin remodeling complexes. <i>Molecular Systems Biology</i> , 2011, 7, 503.	7.2	140
43	Serine and SAM Responsive Complex SESAME Regulates Histone Modification Crosstalk by Sensing Cellular Metabolism. <i>Molecular Cell</i> , 2015, 60, 408-421.	9.7	136
44	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.	3.8	134
45	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.	9.7	132
46	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.	9.7	125
47	The human cytoplasmic dynein interactome reveals novel activators of motility. <i>ELife</i> , 2017, 6, .	6.0	120
48	The Integrator complex controls the termination of transcription at diverse classes of gene targets. <i>Cell Research</i> , 2015, 25, 288-305.	12.0	113
49	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.	2.3	107
50	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. <i>Molecular Cell</i> , 2016, 62, 558-571.	9.7	106
51	FBXL2- and PTPL1-mediated degradation of p110-free p85 <sup>12</sup> regulatory subunit controls the PI(3)K signalling cascade. <i>Nature Cell Biology</i> , 2013, 15, 472-480.	10.3	98
52	Heterochromatin Protein 1a Stimulates Histone H3 Lysine 36 Demethylation by the <i>Drosophila</i> KDM4A Demethylase. <i>Molecular Cell</i> , 2008, 32, 696-706.	9.7	97
53	Subunit Organization of the Human INO80 Chromatin Remodeling Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 11283-11289.	3.4	93
54	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. <i>Molecular Cell</i> , 2015, 57, 685-694.	9.7	92

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55	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.	5.9	90
56	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.	5.9	89
57	CyclinA2-Cyclin-dependent Kinase Regulates SAMHD1 Protein Phosphohydrolase Domain. <i>Journal of Biological Chemistry</i> , 2015, 290, 13279-13292.	3.4	84
58	Drosophila ELMO/CED-12 interacts with Myoblast city to direct myoblast fusion and ommatidial organization. <i>Developmental Biology</i> , 2008, 314, 137-149.	2.0	83
59	INTS3 controls the hSSB1-mediated DNA damage response. <i>Journal of Cell Biology</i> , 2009, 187, 25-32.	5.2	80
60	Deacetylase Inhibitors Dissociate the Histone-Targeting ING2 Subunit from the Sin3 Complex. <i>Chemistry and Biology</i> , 2010, 17, 65-74.	6.0	79
61	A chemoproteomic portrait of the oncometabolite fumarate. <i>Nature Chemical Biology</i> , 2019, 15, 391-400.	8.0	77
62	Characterization of the Yeast Trimeric-SAS Acetyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 11987-11994.	3.4	76
63	The Little Elongation Complex Regulates Small Nuclear RNA Transcription. <i>Molecular Cell</i> , 2011, 44, 954-965.	9.7	75
64	Neuralized-like 1 (Neurl1) Targeted to the Plasma Membrane by N-Myristoylation Regulates the Notch Ligand Jagged1. <i>Journal of Biological Chemistry</i> , 2008, 283, 3846-3853.	3.4	69
65	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.	10.3	69
66	The Inhibition of Polo Kinase by Matrimony Maintains G2 Arrest in the Meiotic Cell Cycle. <i>PLoS Biology</i> , 2007, 5, e323.	5.6	68
67	CHD8 Associates with Human Staf and Contributes to Efficient U6 RNA Polymerase III Transcription. <i>Molecular and Cellular Biology</i> , 2007, 27, 8729-8738.	2.3	67
68	Gcn5 regulates the dissociation of SWI/SNF from chromatin by acetylation of Swi2/Snf2. <i>Genes and Development</i> , 2010, 24, 2766-2771.	5.9	67
69	Regulation of the CRL4Cdt2 Ubiquitin Ligase and Cell-Cycle Exit by the SCFFbxo11 Ubiquitin Ligase. <i>Molecular Cell</i> , 2013, 49, 1159-1166.	9.7	67
70	The ATAC Acetyltransferase Complex Coordinates MAP Kinases to Regulate JNK Target Genes. <i>Cell</i> , 2010, 142, 726-736.	28.9	66
71	Unraveling the Ubiquitome of the Human Malaria Parasite. <i>Journal of Biological Chemistry</i> , 2011, 286, 40320-40330.	3.4	66
72	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.	2.3	66

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73	The ULK1-FBXW5-SEC23B nexus controls autophagy. <i>ELife</i> , 2018, 7, .	6.0	63
74	Genomic and Proteomic Analysis of phiEco32, a Novel Escherichia coli Bacteriophage. <i>Journal of Molecular Biology</i> , 2008, 377, 774-789.	4.2	61
75	Structural analyses of the chromatin remodelling enzymes INO80-C and SWR-C. <i>Nature Communications</i> , 2015, 6, 7108.	12.8	61
76	Thermus thermophilus Bacteriophage $\phi$ YS40 Genome and Proteomic Characterization of Virions. <i>Journal of Molecular Biology</i> , 2006, 364, 667-677.	4.2	60
77	Post-transcription initiation function of the ubiquitous SAGA complex in tissue-specific gene activation. <i>Genes and Development</i> , 2011, 25, 1499-1509.	5.9	60
78	Ctk Complex-Mediated Regulation of Histone Methylation by COMPASS. <i>Molecular and Cellular Biology</i> , 2007, 27, 709-720.	2.3	59
79	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.	7.8	59
80	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.	7.1	58
81	PARC and CUL7 Form Atypical Cullin RING Ligase Complexes. <i>Cancer Research</i> , 2007, 67, 2006-2014.	0.9	56
82	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.	4.2	56
83	Structural Changes in TAF4b-TFIID Correlate with Promoter Selectivity. <i>Molecular Cell</i> , 2008, 29, 81-91.	9.7	55
84	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.	2.3	54
85	The Little Elongation Complex Functions at Initiation and Elongation Phases of snRNA Gene Transcription. <i>Molecular Cell</i> , 2013, 51, 493-505.	9.7	54
86	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.	5.9	51
87	FBH1 promotes DNA double-strand breakage and apoptosis in response to DNA replication stress. <i>Journal of Cell Biology</i> , 2013, 200, 141-149.	5.2	50
88	Mnd1/Hop2 Facilitates Dmc1-Dependent Interhomolog Crossover Formation in Meiosis of Budding Yeast. <i>Molecular and Cellular Biology</i> , 2006, 26, 2913-2923.	2.3	49
89	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.	3.7	49
90	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.	3.8	47

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91	Gene duplication and neofunctionalization: POLR3G and POLR3GL. <i>Genome Research</i> , 2014, 24, 37-51.	5.5	47
92	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.	10.3	47
93	Improving Proteomics Mass Accuracy by Dynamic Offline Lock Mass. <i>Analytical Chemistry</i> , 2011, 83, 9344-9351.	6.5	46
94	STRIPAK directs PP2A activity toward MAP4K4 to promote oncogenic transformation of human cells. <i>ELife</i> , 2020, 9, .	6.0	46
95	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.	3.8	45
96	Evaluation of Clustering Algorithms for Protein Complex and Protein Interaction Network Assembly. <i>Journal of Proteome Research</i> , 2009, 8, 2944-2952.	3.7	44
97	Shaggy/glycogen synthase kinase 3 <sup>Î²</sup> 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.	7.1	44
98	The mammalian Mediator complex. <i>FEBS Letters</i> , 2005, 579, 904-908.	2.8	43
99	Nuclear cGMP-Dependent Kinase Regulates Gene Expression via Activity-Dependent Recruitment of a Conserved Histone Deacetylase Complex. <i>PLoS Genetics</i> , 2011, 7, e1002065.	3.5	41
100	Swi/Snf dynamics on stress-responsive genes is governed by competitive bromodomain interactions. <i>Genes and Development</i> , 2014, 28, 2314-2330.	5.9	41
101	Chromatin remodeller Fun30Ft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. <i>Nature Communications</i> , 2017, 8, 14527.	12.8	41
102	The TDH <sup>Î</sup> GCN5L1 <sup>Î</sup> Fbxo15 <sup>Î</sup> KBP axis limits mitochondrial biogenesis in mouse embryonic stem cells. <i>Nature Cell Biology</i> , 2017, 19, 341-351.	10.3	41
103	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.	3.4	40
104	Improving Label-Free Quantitative Proteomics Strategies by Distributing Shared Peptides and Stabilizing Variance. <i>Analytical Chemistry</i> , 2015, 87, 4749-4756.	6.5	36
105	RUNX proteins desensitize multiple myeloma to lenalidomide via protecting IKZFs from degradation. <i>Leukemia</i> , 2019, 33, 2006-2021.	7.2	36
106	Determining Protein Complex Connectivity Using a Probabilistic Deletion Network Derived from Quantitative Proteomics. <i>PLoS ONE</i> , 2009, 4, e7310.	2.5	35
107	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.	10.3	35
108	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.	5.9	34

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109	Proteomic analysis of chromatin-modifying complexes in <i>Saccharomyces cerevisiae</i> identifies novel subunits. <i>Biochemical Society Transactions</i> , 2004, 32, 899-903.	3.4	33
110	Temporal Regulation of Gene Expression of the <i>Thermus thermophilus</i> Bacteriophage P23-45. <i>Journal of Molecular Biology</i> , 2011, 405, 125-142.	4.2	33
111	Role for Human Mediator Subunit MED25 in Recruitment of Mediator to Promoters by Endoplasmic Reticulum Stress-responsive Transcription Factor ATF6 $\beta$ . <i>Journal of Biological Chemistry</i> , 2013, 288, 26179-26187.	3.4	33
112	Differential HDAC1/2 network analysis reveals a role for prefoldin/CCT in HDAC1/2 complex assembly. <i>Scientific Reports</i> , 2018, 8, 13712.	3.3	32
113	Topological scoring of protein interaction networks. <i>Nature Communications</i> , 2019, 10, 1118.	12.8	32
114	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.	2.3	30
115	The Spliceosomal Protein SF3B5 is a Novel Component of <i>Drosophila</i> SAGA that Functions in Gene Expression Independent of Splicing. <i>Journal of Molecular Biology</i> , 2016, 428, 3632-3649.	4.2	29
116	Integrative Modeling of a Sin3/HDAC Complex Sub-structure. <i>Cell Reports</i> , 2020, 31, 107516.	6.4	29
117	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.	7.1	27
118	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016, 11, e0155492.	2.5	27
119	TNIP2 is a Hub Protein in the NF- $\kappa$ B Network with Both Protein and RNA Mediated Interactions. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3435-3449.	3.8	27
120	The WHHERE coactivator complex is required for retinoic acid-dependent regulation of embryonic symmetry. <i>Nature Communications</i> , 2017, 8, 728.	12.8	27
121	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.	3.8	27
122	Suberoylanilide Hydroxamic Acid (SAHA)-Induced Dynamics of a Human Histone Deacetylase Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3114-3125.	3.8	26
123	Differential Complex Formation via Paralogs in the Human Sin3 Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1468-1484.	3.8	26
124	Identification and Characterization of a <i>Schizosaccharomyces pombe</i> RNA Polymerase II Elongation Factor with Similarity to the Metazoan Transcription Factor ELL. <i>Journal of Biological Chemistry</i> , 2007, 282, 5761-5769.	3.4	25
125	Unraveling the dynamics of protein interactions with quantitative mass spectrometry. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011, 46, 216-228.	5.2	25
126	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.	3.4	24



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127	Affinity purification of protein complexes for analysis by multidimensional protein identification technology. <i>Protein Expression and Purification</i> , 2012, 86, 105-119.	1.3	24
128	Assembly of the Elongin A Ubiquitin Ligase Is Regulated by Genotoxic and Other Stresses. <i>Journal of Biological Chemistry</i> , 2015, 290, 15030-15041.	3.4	24
129	Controlling for Gene Expression Changes in Transcription Factor Protein Networks. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1510-1522.	3.8	23
130	Endoplasmic Reticulum Stress-responsive Transcription Factor ATF6 $\beta$ 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.	3.4	22
131	The role of Mediator and Little Elongation Complex in transcription termination. <i>Nature Communications</i> , 2020, 11, 1063.	12.8	21
132	Conserved abundance and topological features in chromatin remodeling protein interaction networks. <i>EMBO Reports</i> , 2015, 16, 116-126.	4.5	17
133	There is no human interactome. <i>Genome Biology</i> , 2016, 17, 48.	8.8	17
134	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.	10.3	16
135	Biochemical Reduction of the Topology of the Diverse WDR76 Protein Interactome. <i>Journal of Proteome Research</i> , 2019, 18, 3479-3491.	3.7	14
136	The chromatin bound proteome of the human malaria parasite. <i>Microbial Genomics</i> , 2020, 6, .	2.0	13
137	Ataxin-7 and Non-stop coordinate SCAR protein levels, subcellular localization, and actin cytoskeleton organization. <i>ELife</i> , 2019, 8, .	6.0	13
138	Structural basis of the interaction between SETD2 methyltransferase and hnRNP L paralogs for governing co-transcriptional splicing. <i>Nature Communications</i> , 2021, 12, 6452.	12.8	12
139	Driving biochemical discovery with quantitative proteomics. <i>Trends in Biochemical Sciences</i> , 2011, 36, 170-177.	7.5	11
140	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.	5.9	11
141	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.	3.8	11
142	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.	3.3	11
143	A role for Yin Yang-1 (YY1) in the assembly of snRNA transcription complexes. <i>Gene</i> , 2006, 377, 96-108.	2.2	10
144	The H-Index of $\delta$ -An Approach to Correlate Tandem Mass Spectral Data of Peptides with Amino Acid Sequences in a Protein Database $\delta$ <sup>TM</sup> . <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1799-1803.	2.8	10

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145	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.	3.4	9
146	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.	7.1	8
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152	Perturbation of BRMS1 interactome reveals pathways that impact metastasis. <i>PLoS ONE</i> , 2021, 16, e0259128.	2.5	0