

# Paul Tempst

## List of Articles by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Deep Coverage of Global Protein Expression and Phosphorylation in Breast Tumor Cell Lines Using TMT 10-plex Isobaric Labeling. <i>Journal of Proteome Research</i> , 2017, 16, 1121-1132.	3.4	55
2	Unique Transcriptional Programs Identify Subtypes of AKI. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 1729-1740.	0.4	111
3	EGFR feedback-inhibition by Ran-binding protein 6 is disrupted in cancer. <i>Nature Communications</i> , 2017, 8, .	13.7	36
4	Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2357-2374.	3.0	173
5	Inhibition of Circulating Dipeptidyl Peptidase 4 Activity in Patients with Metastatic Prostate Cancer. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3082-3096.	3.0	29
6	The Histone Variant MacroH2A1 Regulates Target Gene Expression in Part by Recruiting the Transcriptional Coregulator PELP1. <i>Molecular and Cellular Biology</i> , 2014, 34, 2437-2449.	2.5	23
7	Aminopeptidase activities as prospective urinary biomarkers for bladder cancer. <i>Proteomics - Clinical Applications</i> , 2014, 8, 317-326.	2.3	15
8	PRMT4 Blocks Myeloid Differentiation by Assembling a Methyl-RUNX1-Dependent Repressor Complex. <i>Cell Reports</i> , 2013, 5, 1625-1638.	6.3	96
9	Proteasome-Mediated Processing of Def1, a Critical Step in the Cellular Response to Transcription Stress. <i>Cell</i> , 2013, 154, 983-995.	33.7	84
10	Design, Implementation and Multisite Evaluation of a System Suitability Protocol for the Quantitative Assessment of Instrument Performance in Liquid Chromatography-Multiple Reaction Monitoring-MS (LC-MRM-MS). <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2623-2639.	3.0	107
11	Mass-Encoded, Synthetic Biomarkers and Multiplexed Urinary Monitoring: New Frontiers in Disease Monitoring. <i>Clinical Chemistry</i> , 2013, 59, 1694-1695.	1.1	1
12	USP49 deubiquitinates histone H2B and regulates cotranscriptional pre-mRNA splicing. <i>Genes and Development</i> , 2013, 27, 1581-1595.	4.6	93
13	TRIM3, a tumor suppressor linked to regulation of p21Waf1/Cip1. <i>Oncogene</i> , 2013, 33, 308-315.	6.5	55
14	LRPPRC is necessary for polyadenylation and coordination of translation of mitochondrial mRNAs. <i>EMBO Journal</i> , 2012, 31, 443-456.	7.4	322
15	Architecture of the Mediator head module. <i>Nature</i> , 2011, 475, 240-243.	38.0	110
16	MTERF4 Regulates Translation by Targeting the Methyltransferase NSUN4 to the Mammalian Mitochondrial Ribosome. <i>Cell Metabolism</i> , 2011, 13, 527-539.	25.2	258
17	L3MBTL2 Protein Acts in Concert with PcG Protein-Mediated Monoubiquitination of H2A to Establish a Repressive Chromatin Structure. <i>Molecular Cell</i> , 2011, 42, 438-450.	13.3	138
18	TLR signalling augments macrophage bactericidal activity through mitochondrial ROS. <i>Nature</i> , 2011, 472, 476-480.	38.0	1,562

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19	PRC2 Complexes with JARID2, MTF2, and esPRC2p48 in ES Cells to Modulate ES Cell Pluripotency and Somatic Cell Reprogramming. <i>Stem Cells</i> , 2011, 29, 229-240.	3.2	149
20	Bromodomain protein 7 interacts with PRMT5 and PRC2, and is involved in transcriptional repression of their target genes. <i>Nucleic Acids Research</i> , 2011, 39, 5424-5438.	15.5	81
21	Fas-associated Death Domain (FADD) and the E3 Ubiquitin-Protein Ligase TRIM21 Interact to Negatively Regulate Virus-induced Interferon Production. <i>Journal of Biological Chemistry</i> , 2011, 286, 6521-6531.	2.2	67
22	Superoxide dismutase 1 (SOD1) is a target for a small molecule identified in a screen for inhibitors of the growth of lung adenocarcinoma cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16375-16380.	7.5	154
23	SETDB1 Is Involved in Postembryonic DNA Methylation and Gene Silencing in <i>Drosophila</i> . <i>PLoS ONE</i> , 2010, 5, e10581.	2.3	22
24	Interlaboratory Study Characterizing a Yeast Performance Standard for Benchmarking LC-MS Platform Performance. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 242-254.	3.0	157
25	Merlin/NF2 Suppresses Tumorigenesis by Inhibiting the E3 Ubiquitin Ligase CRL4DCAF1 in the Nucleus. <i>Cell</i> , 2010, 140, 477-490.	33.7	314
26	Processing of autophagic protein LC3 by the 20S proteasome. <i>Autophagy</i> , 2010, 6, 126-137.	13.7	95
27	Repeatability and Reproducibility in Proteomic Identifications by Liquid Chromatography-Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 761-776.	3.4	556
28	Analytical Validation of Protein-Based Multiplex Assays: A Workshop Report by the NCI-FDA Interagency Oncology Task Force on Molecular Diagnostics. <i>Clinical Chemistry</i> , 2010, 56, 237-243.	1.1	60
29	Performance Metrics for Liquid Chromatography-Tandem Mass Spectrometry Systems in Proteomics Analyses. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 225-241.	3.0	183
30	Heterogeneous Nuclear Ribonucleoprotein L Is a Subunit of Human KMT3a/Set2 Complex Required for H3 Lys-36 Trimethylation Activity in Vivo. <i>Journal of Biological Chemistry</i> , 2009, 284, 15701-15707.	2.2	108
31	The H3K4 Demethylase Lid Associates with and Inhibits Histone Deacetylase Rpd3. <i>Molecular and Cellular Biology</i> , 2009, 29, 1401-1410.	2.5	71
32	MTERF2 is a nucleoid component in mammalian mitochondria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009, 1787, 296-302.	0.9	75
33	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. <i>Nature Biotechnology</i> , 2009, 27, 633-641.	29.9	1,000
34	Phosphorylation-dependent regulation of cytosolic localization and oncogenic function of Skp2 by Akt/PKB. <i>Nature Cell Biology</i> , 2009, 11, 420-432.	16.3	226
35	Pathway-Based Biomarker Search by High-Throughput Proteomics Profiling of Secretomes. <i>Journal of Proteome Research</i> , 2009, 8, 1489-1503.	3.4	79
36	Ubiquitin Ligase Nedd4L Targets Activated Smad2/3 to Limit TGF- $\beta$ Signaling. <i>Molecular Cell</i> , 2009, 36, 457-468.	13.3	363

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37	Induced ncRNAs allosterically modify RNA-binding proteins in cis to inhibit transcription. <i>Nature</i> , 2008, 454, 126-130.	38.0	941
38	PRDM16 controls a brown fat/skeletal muscle switch. <i>Nature</i> , 2008, 454, 961-967.	38.0	2,207
39	The HSA domain binds nuclear actin-related proteins to regulate chromatin-remodeling ATPases. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 469-476.	8.8	195
40	Reversal of RNA Polymerase II Ubiquitylation by the Ubiquitin Protease Ubp3. <i>Molecular Cell</i> , 2008, 30, 498-506.	13.3	63
41	Regulation of the brown and white fat gene programs through a PRDM16/CtBP transcriptional complex. <i>Genes and Development</i> , 2008, 22, 1397-1409.	4.6	438
42	JAMP Optimizes ERAD to Protect Cells from Unfolded Proteins. <i>Molecular Biology of the Cell</i> , 2008, 19, 5019-5028.	2.5	15
43	Methylation of RUNX1 by PRMT1 abrogates SIN3A binding and potentiates its transcriptional activity. <i>Genes and Development</i> , 2008, 22, 640-653.	4.6	174
44	HDAC6 is a specific deacetylase of peroxiredoxins and is involved in redox regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9633-9638.	7.5	311
45	Role of hPHF1 in H3K27 Methylation and Hox Gene Silencing. <i>Molecular and Cellular Biology</i> , 2008, 28, 1862-1872.	2.5	162
46	A Sequence-specific Exopeptidase Activity Test (SSEAT) for $\alpha$ -Functional Biomarker Discovery. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 509-518.	3.0	81
47	WSTF regulates the H2A.X DNA damage response via a novel tyrosine kinase activity. <i>Nature</i> , 2008, 457, 57-62.	38.0	389
48	Demethylation of Histone H3K36 and H3K9 by Rph1: a Vestige of an H3K9 Methylation System in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2007, 27, 3951-3961.	2.5	83
49	Ubiquitylation of histone H2B controls RNA polymerase II transcription elongation independently of histone H3 methylation. <i>Genes and Development</i> , 2007, 21, 835-847.	4.6	148
50	Myoferlin Regulates Vascular Endothelial Growth Factor Receptor-2 Stability and Function. <i>Journal of Biological Chemistry</i> , 2007, 282, 30745-30753.	2.2	113
51	Phosphorylation of Thyroid Hormone Receptor-associated Nuclear Receptor Corepressor Holocomplex by the DNA-dependent Protein Kinase Enhances Its Histone Deacetylase Activity. <i>Journal of Biological Chemistry</i> , 2007, 282, 9312-9322.	2.2	37
52	Genome-Wide Dynamics of SAPHIRE, an Essential Complex for Gene Activation and Chromatin Boundaries. <i>Molecular and Cellular Biology</i> , 2007, 27, 4058-4069.	2.5	25
53	NEDD4-1 Is a Proto-Oncogenic Ubiquitin Ligase for PTEN. <i>Cell</i> , 2007, 128, 129-139.	33.7	676
54	Ubiquitination Regulates PTEN Nuclear Import and Tumor Suppression. <i>Cell</i> , 2007, 128, 141-156.	33.7	698

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55	Communication between Distant Sites in RNA Polymerase II through Ubiquitylation Factors and the Polymerase CTD. <i>Cell</i> , 2007, 129, 57-68.	33.7	66
56	The Retinoblastoma Binding Protein RBP2 Is an H3K4 Demethylase. <i>Cell</i> , 2007, 128, 889-900.	33.7	418
57	L3MBTL1, a Histone-Methylation-Dependent Chromatin Lock. <i>Cell</i> , 2007, 129, 915-928.	33.7	339
58	MTERF3 Is a Negative Regulator of Mammalian mtDNA Transcription. <i>Cell</i> , 2007, 130, 273-285.	33.7	232
59	PLU-1 Is an H3K4 Demethylase Involved in Transcriptional Repression and Breast Cancer Cell Proliferation. <i>Molecular Cell</i> , 2007, 25, 801-812.	13.3	456
60	A Histone H2A Deubiquitinase Complex Coordinating Histone Acetylation and H1 Dissociation in Transcriptional Regulation. <i>Molecular Cell</i> , 2007, 27, 609-621.	13.3	294
61	Recognition of Trimethylated Histone H3 Lysine 4 Facilitates the Recruitment of Transcription Postinitiation Factors and Pre-mRNA Splicing. <i>Molecular Cell</i> , 2007, 28, 665-676.	13.3	518
62	The trithorax-group protein Lid is a histone H3 trimethyl-Lys4 demethylase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 341-343.	8.8	103
63	DNMT3L connects unmethylated lysine 4 of histone H3 to de novo methylation of DNA. <i>Nature</i> , 2007, 448, 714-717.	38.0	1,476
64	Regulation of cell cycle progression and gene expression by H2A deubiquitination. <i>Nature</i> , 2007, 449, 1068-1072.	38.0	294
65	SIRT1 regulates the histone methyl-transferase SUV39H1 during heterochromatin formation. <i>Nature</i> , 2007, 450, 440-444.	38.0	420
66	Differential exoprotease activities confer tumor-specific serum peptidome patterns. <i>Journal of Clinical Investigation</i> , 2006, 116, 271-284.	10.6	698
67	JHDM2A, a JmjC-Containing H3K9 Demethylase, Facilitates Transcription Activation by Androgen Receptor. <i>Cell</i> , 2006, 125, 483-495.	33.7	781
68	Hematopoiesis Controlled by Distinct TIF1 <sup>3</sup> and Smad4 Branches of the TGF <sup>2</sup> Pathway. <i>Cell</i> , 2006, 125, 929-941.	33.7	361
69	A CK2-Dependent Mechanism for Degradation of the PML Tumor Suppressor. <i>Cell</i> , 2006, 126, 269-283.	33.7	279
70	Histone H3 and H4 Ubiquitylation by the CUL4-DDB-ROC1 Ubiquitin Ligase Facilitates Cellular Response to DNA Damage. <i>Molecular Cell</i> , 2006, 22, 383-394.	13.3	480
71	The transcriptional repressor JHDM3A demethylates trimethyl histone H3 lysine <sup>9</sup> and lysine <sup>36</sup> . <i>Nature</i> , 2006, 442, 312-316.	38.0	591
72	Highly efficient selenomethionine labeling of recombinant proteins produced in mammalian cells. <i>Protein Science</i> , 2006, 15, 2008-2013.	5.9	42

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73	The RSC Chromatin Remodeling Complex Bears an Essential Fungal-Specific Protein Module With Broad Functional Roles. <i>Genetics</i> , 2006, 172, 795-809.	4.2	63
74	Serum Peptidome Patterns That Distinguish Metastatic Thyroid Carcinoma from Cancer-free Controls Are Unbiased by Gender and Age. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1840-1852.	3.0	164
75	Defects in energy homeostasis in Leigh syndrome French Canadian variant through PGC-1 $\alpha$ /LRP130 complex. <i>Genes and Development</i> , 2006, 20, 2996-3009.	4.6	94
76	Brd4 links chromatin targeting to HPV transcriptional silencing. <i>Genes and Development</i> , 2006, 20, 2383-2396.	4.6	204
77	BAFF controls B cell metabolic fitness through a PKC $\delta$ <sup>2</sup> - and Akt-dependent mechanism. <i>Journal of Experimental Medicine</i> , 2006, 203, 2551-2562.	9.3	190
78	CHMP5 is essential for late endosome function and down-regulation of receptor signaling during mouse embryogenesis. <i>Journal of Cell Biology</i> , 2006, 172, 1045-1056.	5.5	127
79	Metazoan Scc4 Homologs Link Sister Chromatid Cohesion to Cell and Axon Migration Guidance. <i>PLoS Biology</i> , 2006, 4, e242.	5.0	98
80	The human PAF complex coordinates transcription with events downstream of RNA synthesis. <i>Genes and Development</i> , 2005, 19, 1668-1673.	4.6	219
81	<i>Mycobacterium tuberculosis</i> appears to lack $\alpha$ -ketoglutarate dehydrogenase and encodes pyruvate dehydrogenase in widely separated genes. <i>Molecular Microbiology</i> , 2005, 57, 859-868.	2.6	110
82	Adhesion signaling by a novel mitotic substrate of src kinases. <i>Oncogene</i> , 2005, 24, 5333-5343.	6.5	130
83	Physical and Functional Interaction between Elongator and the Chromatin-associated Kti12 Protein. <i>Journal of Biological Chemistry</i> , 2005, 280, 19454-19460.	2.2	34
84	S-nitroso proteome of <i>Mycobacterium tuberculosis</i> : Enzymes of intermediary metabolism and antioxidant defense. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 467-472.	7.5	175
85	The Histone Chaperone TAF-I/SET/INHAT Is Required for Transcription In Vitro of Chromatin Templates. <i>Molecular and Cellular Biology</i> , 2005, 25, 797-807.	2.5	65
86	PARP-1 Determines Specificity in a Retinoid Signaling Pathway via Direct Modulation of Mediator. <i>Molecular Cell</i> , 2005, 18, 83-96.	13.3	213
87	Monoubiquitination of Human Histone H2B: The Factors Involved and Their Roles in HOX Gene Regulation. <i>Molecular Cell</i> , 2005, 20, 601-611.	13.3	471
88	A Direct Interaction between the RAG2 C Terminus and the Core Histones Is Required for Efficient V(D)J Recombination. <i>Immunity</i> , 2005, 23, 203-212.	22.6	60
89	Phosphorylation and Functional Inactivation of TSC2 by Erk. <i>Cell</i> , 2005, 121, 179-193.	33.7	1,207
90	Multiple Mechanisms Confining RNA Polymerase II Ubiquitylation to Polymerases Undergoing Transcriptional Arrest. <i>Cell</i> , 2005, 121, 913-923.	33.7	209

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91	The Drosophila Fragile X Protein Functions as a Negative Regulator in the orb Autoregulatory Pathway. <i>Developmental Cell</i> , 2005, 8, 331-342.	7.7	100
92	Correcting Common Errors in Identifying Cancer-Specific Serum Peptide Signatures. <i>Journal of Proteome Research</i> , 2005, 4, 1060-1072.	3.4	214
93	Histone demethylation by a family of JmjC domain-containing proteins. <i>Nature</i> , 2005, 439, 811-816.	38.0	2,040
94	Regulation of 2-Oxoglutarate (±-Ketoglutarate) Dehydrogenase Stability by the RING Finger Ubiquitin Ligase Siah. <i>Journal of Biological Chemistry</i> , 2004, 279, 53782-53788.	2.2	52
95	PINdb: a database of nuclear protein complexes from human and yeast. <i>Bioinformatics</i> , 2004, 20, 1413-1415.	4.7	37
96	Mutual Targeting of Mediator and the TFIID Kinase Kin28. <i>Journal of Biological Chemistry</i> , 2004, 279, 29114-29120.	2.2	42
97	The Yaf9 Component of the SWR1 and NuA4 Complexes Is Required for Proper Gene Expression, Histone H4 Acetylation, and Htz1 Replacement near Telomeres. <i>Molecular and Cellular Biology</i> , 2004, 24, 9424-9436.	2.5	103
98	Human Mob Proteins Regulate the NDR1 and NDR2 Serine-Threonine Kinases. <i>Journal of Biological Chemistry</i> , 2004, 279, 24444-24451.	2.2	90
99	A Prototype Antibody Microarray Platform to Monitor Changes in Protein Tyrosine Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 1102-1118.	3.0	97
100	Human SWI/SNF-Associated PRMT5 Methylates Histone H3 Arginine 8 and Negatively Regulates Expression of ST7 and NM23 Tumor Suppressor Genes. <i>Molecular and Cellular Biology</i> , 2004, 24, 9630-9645.	2.5	565
101	A new role for Nogo as a regulator of vascular remodeling. <i>Nature Medicine</i> , 2004, 10, 382-388.	33.0	231
102	Tandem bromodomains in the chromatin remodeler RSC recognize acetylated histone H3 Lys14. <i>EMBO Journal</i> , 2004, 23, 1348-1359.	7.4	220
103	Cleavage and proteasome-mediated degradation of the basal transcription factor TFIID. <i>EMBO Journal</i> , 2004, 23, 3083-3091.	7.4	23
104	Role of histone H2A ubiquitination in Polycomb silencing. <i>Nature</i> , 2004, 431, 873-878.	38.0	1,645
105	Regulation of p53 activity through lysine methylation. <i>Nature</i> , 2004, 432, 353-360.	38.0	753
106	OvaCheck: let's not dismiss the concept. <i>Nature</i> , 2004, 430, 611-611.	38.0	13
107	Suppression of mitochondrial respiration through recruitment of p160 myb binding protein to PGC-1 $\alpha$ : modulation by p38 MAPK. <i>Genes and Development</i> , 2004, 18, 278-289.	4.6	280
108	Serum Peptide Profiling by Magnetic Particle-Assisted, Automated Sample Processing and MALDI-TOF Mass Spectrometry. <i>Analytical Chemistry</i> , 2004, 76, 1560-1570.	6.5	459

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109	Siah2 Regulates Stability of Prolyl-Hydroxylases, Controls HIF1 $\alpha$ Abundance, and Modulates Physiological Responses to Hypoxia. <i>Cell</i> , 2004, 117, 941-952.	33.7	397
110	Histone Deimination Antagonizes Arginine Methylation. <i>Cell</i> , 2004, 118, 545-553.	33.7	785
111	Cytosol-derived proteins are sufficient for Arp2/3 recruitment and ARF/coatamer-dependent actin polymerization on Golgi membranes. <i>FEBS Letters</i> , 2004, 566, 281-286.	2.7	55
112	Human SirT1 Interacts with Histone H1 and Promotes Formation of Facultative Heterochromatin. <i>Molecular Cell</i> , 2004, 16, 93-105.	13.3	865
113	Different Ezh2-Containing Complexes Target Methylation of Histone H1 or Nucleosomal Histone H3. <i>Molecular Cell</i> , 2004, 14, 183-193.	13.3	399
114	Delayed-late activation of a myeloid defensin minimal promoter by retinoids and inflammatory mediators. <i>Leukemia Research</i> , 2004, 28, 879-889.	0.7	5
115	The budding yeast Rad9 checkpoint complex: chaperone proteins are required for its function. <i>EMBO Reports</i> , 2003, 4, 953-958.	5.2	25
116	mAM Facilitates Conversion by ESET of Dimethyl to Trimethyl Lysine 9 of Histone H3 to Cause Transcriptional Repression. <i>Molecular Cell</i> , 2003, 12, 475-487.	13.3	320
117	Nab2p and the Thp1p-Sac3p Complex Functionally Interact at the Interface between Transcription and mRNA Metabolism. <i>Journal of Biological Chemistry</i> , 2003, 278, 24225-24232.	2.2	93
118	G $\beta$ L, a Positive Regulator of the Rapamycin-Sensitive Pathway Required for the Nutrient-Sensitive Interaction between Raptor and mTOR. <i>Molecular Cell</i> , 2003, 11, 895-904.	13.3	932
119	Affinity Capture of Specific DNA-Binding Proteins for Mass Spectrometric Identification. <i>Analytical Chemistry</i> , 2003, 75, 6437-6448.	6.5	43
120	ASAP, a Novel Protein Complex Involved in RNA Processing and Apoptosis. <i>Molecular and Cellular Biology</i> , 2003, 23, 2981-2990.	2.5	149
121	Catalytic Properties of ADAM19. <i>Journal of Biological Chemistry</i> , 2003, 278, 22331-22340.	2.2	118
122	The laminin receptor modulates granulocyte-macrophage colony-stimulating factor receptor complex formation and modulates its signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14000-14005.	7.5	27
123	Proteolytic Cleavage of MLL Generates a Complex of N- and C-Terminal Fragments That Confers Protein Stability and Subnuclear Localization. <i>Molecular and Cellular Biology</i> , 2003, 23, 186-194.	2.5	213
124	Parkinson's Disease-associated $\alpha$ -Synuclein Is a Calmodulin Substrate. <i>Journal of Biological Chemistry</i> , 2003, 278, 17379-17387.	2.2	92
125	Revised Subunit Structure of Yeast Transcription Factor IIH (TFIIH) and Reconciliation with Human TFIIH. <i>Journal of Biological Chemistry</i> , 2003, 278, 43897-43900.	2.2	35
126	mSin3A/Histone Deacetylase 2- and PRMT5-Containing Brg1 Complex Is Involved in Transcriptional Repression of the Myc Target Gene <i>cad</i> . <i>Molecular and Cellular Biology</i> , 2003, 23, 7475-7487.	2.5	225

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127	The C-terminal domain phosphatase and transcription elongation activities of FCP1 are regulated by phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2328-2333.	7.5	31
128	Identification and Functional Characterization of the p66/p68 Components of the MeCP1 Complex. <i>Molecular and Cellular Biology</i> , 2002, 22, 536-546.	2.5	71
129	Purification and Characterization of the Human Elongator Complex. <i>Journal of Biological Chemistry</i> , 2002, 277, 3047-3052.	2.2	237
130	A Complex of the Srb8, -9, -10, and -11 Transcriptional Regulatory Proteins from Yeast. <i>Journal of Biological Chemistry</i> , 2002, 277, 44202-44207.	2.2	143
131	Elongator is a histone H3 and H4 acetyltransferase important for normal histone acetylation levels in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 3517-3522.	7.5	521
132	Lysine methylation within the globular domain of histone H3 by Dot1 is important for telomeric silencing and Sir protein association. <i>Genes and Development</i> , 2002, 16, 1518-1527.	4.6	494
133	Role of the Sin3-Histone Deacetylase Complex in Growth Regulation by the Candidate Tumor Suppressor p33ING1. <i>Molecular and Cellular Biology</i> , 2002, 22, 835-848.	2.5	214
134	Histone methyltransferase activity associated with a human multiprotein complex containing the Enhancer of Zeste protein. <i>Genes and Development</i> , 2002, 16, 2893-2905.	4.6	1,523
135	Set9, a novel histone H3 methyltransferase that facilitates transcription by precluding histone tail modifications required for heterochromatin formation. <i>Genes and Development</i> , 2002, 16, 479-489.	4.6	499
136	The Core of the Polycomb Repressive Complex Is Compositionally and Functionally Conserved in Flies and Humans. <i>Molecular and Cellular Biology</i> , 2002, 22, 6070-6078.	2.5	379
137	P-Rex1, a PtdIns(3,4,5)P <sub>3</sub> - and G $\beta$ <sup>13</sup> -Regulated Guanine-Nucleotide Exchange Factor for Rac. <i>Cell</i> , 2002, 108, 809-821.	33.7	516
138	mTOR Interacts with Raptor to Form a Nutrient-Sensitive Complex that Signals to the Cell Growth Machinery. <i>Cell</i> , 2002, 110, 163-175.	33.7	2,847
139	Conversion of Proepithelin to Epithelins. <i>Cell</i> , 2002, 111, 867-878.	33.7	639
140	Isolation and mass spectrometry of transcription factor complexes. <i>Methods</i> , 2002, 26, 260-269.	3.5	81
141	Identification of ARAP3, a Novel PI3K Effector Regulating Both Arf and Rho GTPases, by Selective Capture on Phosphoinositide Affinity Matrices. <i>Molecular Cell</i> , 2002, 9, 95-108.	13.3	299
142	The Genome-Wide Localization of Rsc9, a Component of the RSC Chromatin-Remodeling Complex, Changes in Response to Stress. <i>Molecular Cell</i> , 2002, 9, 563-573.	13.3	137
143	PR-Set7 Is a Nucleosome-Specific Methyltransferase that Modifies Lysine 20 of Histone H4 and Is Associated with Silent Chromatin. <i>Molecular Cell</i> , 2002, 9, 1201-1213.	13.3	553
144	The Yeast Capping Enzyme Represses RNA Polymerase II Transcription. <i>Molecular Cell</i> , 2002, 10, 883-894.	13.3	40

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146	Methylation of H3-Lysine 79 Is Mediated by a New Family of HMTases without a SET Domain. <i>Current Biology</i> , 2002, 12, 1052-1058.	3.6	804
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