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List of Publications by Year in descending order

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42
papers

8,073
citations

201385

27
h-index

264894

42
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47
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docs citations

47
times ranked

11017
citing authors

#	ARTICLE	IF	CITATIONS
1	PARK7/DJ-1 promotes pyruvate dehydrogenase activity and maintains Treg homeostasis during ageing. <i>Nature Metabolism</i> , 2022, 4, 589-607.	5.1	18
2	Chromatin-Associated Protein Complexes Link DNA Base J and Transcription Termination in <i>Leishmania</i> . <i>MSphere</i> , 2021, 6, .	1.3	12
3	Proteomic/transcriptomic analysis of erythropoiesis. <i>Current Opinion in Hematology</i> , 2021, 28, 150-157.	1.2	5
4	TAF8 regions important for TFIID lobe B assembly or for TAF2 interactions are required for embryonic stem cell survival. <i>Journal of Biological Chemistry</i> , 2021, 297, 101288.	1.6	4
5	A Structural Model of the Endogenous Human BAF Complex Informs Disease Mechanisms. <i>Cell</i> , 2020, 183, 802-817.e24.	13.5	100
6	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. <i>Molecular Cell</i> , 2020, 78, 960-974.e11.	4.5	83
7	Assembly of SNAPc, Bdp1, and TBP on the U6 snRNA Gene Promoter in <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Biology</i> , 2020, 40, .	1.1	6
8	Loss of the neural-specific BAF subunit ACTL6B relieves repression of early response genes and causes recessive autism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10055-10066.	3.3	34
9	Absolute quantification of transcription factors in human erythropoiesis using selected reaction monitoring mass spectrometry. <i>STAR Protocols</i> , 2020, 1, 100216.	0.5	4
10	Histone Octamer Structure Is Altered Early in ISW2 ATP-Dependent Nucleosome Remodeling. <i>Cell Reports</i> , 2019, 28, 282-294.e6.	2.9	20
11	Identification of Cross-linked Peptides Using Isotopomeric Cross-linkers. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1643-1653.	1.2	2
12	Single-Cell Proteomics Reveal that Quantitative Changes in Co-expressed Lineage-Specific Transcription Factors Determine Cell Fate. <i>Cell Stem Cell</i> , 2019, 24, 812-820.e5.	5.2	99
13	Architecture of the chromatin remodeler RSC and insights into its nucleosome engagement. <i>ELife</i> , 2019, 8, .	2.8	68
14	Transcription Activation Domains of the Yeast Factors Met4 and Ino2: Tandem Activation Domains with Properties Similar to the Yeast Gcn4 Activator. <i>Molecular and Cellular Biology</i> , 2018, 38, .	1.1	19
15	Gcn4-Mediator Specificity Is Mediated by a Large and Dynamic Fuzzy Protein-Protein Complex. <i>Cell Reports</i> , 2018, 22, 3251-3264.	2.9	110
16	Molecular structure of promoter-bound yeast TFIID. <i>Nature Communications</i> , 2018, 9, 4666.	5.8	32
17	Structure of human TFIID and mechanism of TBP loading onto promoter DNA. <i>Science</i> , 2018, 362, .	6.0	123
18	Modular Organization and Assembly of SWI/SNF Family Chromatin Remodeling Complexes. <i>Cell</i> , 2018, 175, 1272-1288.e20.	13.5	460

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19	Loss of Snf5 Induces Formation of an Aberrant SWI/SNF Complex. <i>Cell Reports</i> , 2017, 18, 2135-2147.	2.9	75
20	Mechanism for microbial population collapse in a fluctuating resource environment. <i>Molecular Systems Biology</i> , 2017, 13, 919.	3.2	22
21	SMARCB1 is required for widespread BAF complex-mediated activation of enhancers and bivalent promoters. <i>Nature Genetics</i> , 2017, 49, 1613-1623.	9.4	207
22	Function of Conserved Topological Regions within the <i>Saccharomyces cerevisiae</i> Basal Transcription Factor TFIIH. <i>Molecular and Cellular Biology</i> , 2016, 36, 2464-2475.	1.1	12
23	An LXR-NCOA 5 gene regulatory complex directs inflammatory cross-talk-dependent repression of macrophage cholesterol efflux. <i>EMBO Journal</i> , 2015, 34, 1244-1258.	3.5	35
24	Regulation of Mec1 kinase activity by the SWI/SNF chromatin remodeling complex. <i>Genes and Development</i> , 2015, 29, 591-602.	2.7	20
25	Architecture of the Human and Yeast General Transcription and DNA Repair Factor TFIIH. <i>Molecular Cell</i> , 2015, 59, 794-806.	4.5	91
26	Architecture of the <i>S. cerevisiae</i> SAGA transcription coactivator complex. <i>EMBO Journal</i> , 2014, 33, 2534-2546.	3.5	100
27	Control of RecBCD Enzyme Activity by DNA Binding- and Chi Hotspot-Dependent Conformational Changes. <i>Journal of Molecular Biology</i> , 2014, 426, 3479-3499.	2.0	38
28	Architecture of the <i>Saccharomyces cerevisiae</i> RNA polymerase I Core Factor complex. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 810-816.	3.6	44
29	Proteomic and bioinformatic analysis of mammalian SWI/SNF complexes identifies extensive roles in human malignancy. <i>Nature Genetics</i> , 2013, 45, 592-601.	9.4	1,082
30	An Integrated Chemical Cross-linking and Mass Spectrometry Approach to Study Protein Complex Architecture and Function. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.008318.	2.5	35
31	An embryonic stem cell chromatin remodeling complex, esBAF, is essential for embryonic stem cell self-renewal and pluripotency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5181-5186.	3.3	515
32	CTCF physically links cohesin to chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8309-8314.	3.3	449
33	The transcription elongation factor TFIIIS is a component of RNA polymerase II preinitiation complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16068-16073.	3.3	97
34	An Essential Switch in Subunit Composition of a Chromatin Remodeling Complex during Neural Development. <i>Neuron</i> , 2007, 55, 201-215.	3.8	647
35	Activator-Mediated Recruitment of the MLL2 Methyltransferase Complex to the β -Globin Locus. <i>Molecular Cell</i> , 2007, 27, 573-584.	4.5	122
36	Using Stable Isotope Tagging and Mass Spectrometry to Characterize Protein Complexes and to Detect Changes in Their Composition. <i>Methods in Molecular Biology</i> , 2007, 359, 17-35.	0.4	12

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37	Identification of TFB5, a new component of general transcription and DNA repair factor IIF. Nature Genetics, 2004, 36, 707-713.	9.4	147
38	A new, tenth subunit of TFIIF is responsible for the DNA repair syndrome trichothiodystrophy group A. Nature Genetics, 2004, 36, 714-719.	9.4	307
39	Dynamic changes in transcription factor complexes during erythroid differentiation revealed by quantitative proteomics. Nature Structural and Molecular Biology, 2004, 11, 73-80.	3.6	199
40	The study of macromolecular complexes by quantitative proteomics. Nature Genetics, 2003, 33, 349-355.	9.4	350
41	Automated Statistical Analysis of Protein Abundance Ratios from Data Generated by Stable-Isotope Dilution and Tandem Mass Spectrometry. Analytical Chemistry, 2003, 75, 6648-6657.	3.2	343
42	Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network. Science, 2001, 292, 929-934.	6.0	1,921