

Bing Li

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

9,555
citations

196777

29
h-index

214428

50
g-index

56
all docs

56
docs citations

56
times ranked

12997
citing authors

#	ARTICLE	IF	CITATIONS
1	SIRT2 regulates proliferation and chemotherapy response of MLL-ENL-driven acute myeloid leukemia. <i>Biochemical and Biophysical Research Communications</i> , 2022, 596, 36-42.	1.0	5
2	TOX4 facilitates promoter-proximal pausing and C-terminal domain dephosphorylation of RNA polymerase II in human cells. <i>Communications Biology</i> , 2022, 5, 300.	2.0	6
3	Phase separation of RNA-binding protein promotes polymerase binding and transcription. <i>Nature Chemical Biology</i> , 2022, 18, 70-80.	3.9	57
4	Muscle regeneration controlled by a designated DNA dioxygenase. <i>Cell Death and Disease</i> , 2021, 12, 535.	2.7	11
5	Integrative Epigenome Map of the Normal Human Prostate Provides Insights Into Prostate Cancer Predisposition. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 723676.	1.8	5
6	The TFIID pivot of preinitiation complex. <i>Science China Life Sciences</i> , 2021, , 1.	2.3	0
7	setd2 knockout zebrafish is viable and fertile: differential and developmental stress-related requirements for Setd2 and histone H3K36 trimethylation in different vertebrate animals. <i>Cell Discovery</i> , 2020, 6, 72.	3.1	8
8	HRP2â€“DPF3aâ€“BAF complex coordinates histone modification and chromatin remodeling to regulate myogenic gene transcription. <i>Nucleic Acids Research</i> , 2020, 48, 6563-6582.	6.5	25
9	Unique and Shared Roles for Histone H3K36 Methylation States in Transcription Regulation Functions. <i>Cell Reports</i> , 2020, 31, 107751.	2.9	35
10	Molecular basis of chromatin remodeling by Rhp26, a yeast CSB ortholog. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6120-6129.	3.3	10
11	Nuclear actin switch of the INO80 remodeler. <i>Journal of Molecular Cell Biology</i> , 2019, 11, 343-344.	1.5	1
12	Ubiquitin specific peptidase 5 promotes ovarian cancer cell proliferation through deubiquitinating HDAC2. <i>Aging</i> , 2019, 11, 9778-9793.	1.4	24
13	A Method for SUMO Modification of Proteins in vitro. <i>Bio-protocol</i> , 2018, 8, .	0.2	4
14	Sumoylation promotes optimal APC/C activation and timely anaphase. <i>ELife</i> , 2018, 7, .	2.8	26
15	Mechanistic insight into TRIP13-catalyzed Mad2 structural transition and spindle checkpoint silencing. <i>Nature Communications</i> , 2017, 8, 1956.	5.8	38
16	A sequential multi-target Mps1 phosphorylation cascade promotes spindle checkpoint signaling. <i>ELife</i> , 2017, 6, .	2.8	134
17	The Bub1â€“Plk1 kinase complex promotes spindle checkpoint signalling through Cdc20 phosphorylation. <i>Nature Communications</i> , 2016, 7, 10818.	5.8	100
18	Physical and functional interactions between nucleosomes and Rad27, a critical component of <sc>DNA</sc> processing during <sc>DNA</sc> metabolism. <i>FEBS Journal</i> , 2016, 283, 4247-4262.	2.2	3

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19	Combinatorial Histone Readout by the Dual Plant Homeodomain (PHD) Fingers of Rco1 Mediates Rpd3S Chromatin Recruitment and the Maintenance of Transcriptional Fidelity. <i>Journal of Biological Chemistry</i> , 2016, 291, 14796-14802.	1.6	26
20	Histone H3K4 methylation regulates deactivation of the spindle assembly checkpoint through direct binding of Mad2. <i>Genes and Development</i> , 2016, 30, 1187-1197.	2.7	21
21	Homodimeric PHD Domain-containing Rco1 Subunit Constitutes a Critical Interaction Hub within the Rpd3S Histone Deacetylase Complex. <i>Journal of Biological Chemistry</i> , 2016, 291, 5428-5438.	1.6	20
22	Balancing acts of SRI and an auto-inhibitory domain specify Set2 function at transcribed chromatin. <i>Nucleic Acids Research</i> , 2015, 43, 4881-4892.	6.5	28
23	Chemical Tools To Decipher Regulation of Phosphatases by Proline Isomerization on Eukaryotic RNA Polymerase II. <i>ACS Chemical Biology</i> , 2015, 10, 2405-2414.	1.6	22
24	Nucleosome Contact Triggers Conformational Changes of Rpd3S Driving High-Affinity H3K36me Nucleosome Engagement. <i>Cell Reports</i> , 2015, 10, 204-215.	2.9	46
25	The Cdc20-binding Phe Box of the Spindle Checkpoint Protein BubR1 Maintains the Mitotic Checkpoint Complex During Mitosis. <i>Journal of Biological Chemistry</i> , 2015, 290, 2431-2443.	1.6	56
26	NuA4 Links Methylation of Histone H3 Lysines 4 and 36 to Acetylation of Histones H4 and H3. <i>Journal of Biological Chemistry</i> , 2014, 289, 32656-32670.	1.6	30
27	Reading Histone Modifications. , 2014, , 355-373.		0
28	ZMYND11 links histone H3.3K36me3 to transcription elongation and tumour suppression. <i>Nature</i> , 2014, 508, 263-268.	13.7	276
29	Genome-wide si RNA screen reveals coupling between mitotic apoptosis and adaptation. <i>EMBO Journal</i> , 2014, 33, 1960-1976.	3.5	39
30	Chromatin Remodelers Fine-Tune H3K36me-Directed Deacetylation of Neighbor Nucleosomes by Rpd3S. <i>Molecular Cell</i> , 2013, 52, 255-263.	4.5	52
31	Multivalent di-nucleosome recognition enables the Rpd3S histone deacetylase complex to tolerate decreased H3K36 methylation levels. <i>EMBO Journal</i> , 2012, 31, 3564-3574.	3.5	49
32	Functional redundancy between Cdc20 ubiquitination and p31 comet. <i>FASEB Journal</i> , 2012, 26, .	0.2	0
33	Readers of histone modifications. <i>Cell Research</i> , 2011, 21, 564-578.	5.7	478
34	Acetyl-CoA Induces Cell Growth and Proliferation by Promoting the Acetylation of Histones at Growth Genes. <i>Molecular Cell</i> , 2011, 42, 426-437.	4.5	583
35	SIRT2 Maintains Genome Integrity and Suppresses Tumorigenesis through Regulating APC/C Activity. <i>Cancer Cell</i> , 2011, 20, 487-499.	7.7	460
36	PICH and BLM limit histone association with anaphase centromeric DNA threads and promote their resolution. <i>EMBO Journal</i> , 2011, 30, 3309-3321.	3.5	82

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37	Phosphorylated Pol II CTD Recruits Multiple HDACs, Including Rpd3C(S), for Methylation-Dependent Deacetylation of ORF Nucleosomes. <i>Molecular Cell</i> , 2010, 39, 234-246.	4.5	208
38	Histone H3 Lysine 36 Dimethylation (H3K36me2) Is Sufficient to Recruit the Rpd3s Histone Deacetylase Complex and to Repress Spurious Transcription. <i>Journal of Biological Chemistry</i> , 2009, 284, 7970-7976.	1.6	135
39	Heterochromatin Protein 1a stimulates histone H3 lysine 36 demethylation by the <i>Drosophila</i> KDM4A demethylase. <i>FASEB Journal</i> , 2009, 23, 325.3.	0.2	0
40	The MSL3 chromodomain directs a key targeting step for dosage compensation of the <i>Drosophila melanogaster</i> X chromosome. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1318-1325.	3.6	110
41	Infrequently transcribed long genes depend on the Set2/Rpd3S pathway for accurate transcription. <i>Genes and Development</i> , 2007, 21, 1422-1430.	2.7	177
42	The Role of Chromatin during Transcription. <i>Cell</i> , 2007, 128, 707-719.	13.5	3,062
43	MSL Complex Is Attracted to Genes Marked by H3K36 Trimethylation Using a Sequence-Independent Mechanism. <i>Molecular Cell</i> , 2007, 28, 121-133.	4.5	195
44	Combined Action of PHD and Chromo Domains Directs the Rpd3S HDAC to Transcribed Chromatin. <i>Science</i> , 2007, 316, 1050-1054.	6.0	294
45	RSC Exploits Histone Acetylation to Abrogate the Nucleosomal Block to RNA Polymerase II Elongation. <i>Molecular Cell</i> , 2006, 24, 481-487.	4.5	171
46	In and out: histone variant exchange in chromatin. <i>Trends in Biochemical Sciences</i> , 2005, 30, 680-687.	3.7	134
47	Preferential occupancy of histone variant H2AZ at inactive promoters influences local histone modifications and chromatin remodeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18385-18390.	3.3	287
48	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
49	SWI/SNF-dependent chromatin remodeling of RNR3 requires TAFII and the general transcription machinery. <i>Genes and Development</i> , 2003, 17, 502-515.	2.7	74
50	The Set2 Histone Methyltransferase Functions through the Phosphorylated Carboxyl-terminal Domain of RNA Polymerase II. <i>Journal of Biological Chemistry</i> , 2003, 278, 8897-8903.	1.6	307
51	Mad2-Independent Inhibition of APCCdc20 by the Mitotic Checkpoint Protein BubR1. <i>Developmental Cell</i> , 2001, 1, 227-237.	3.1	383
52	Ssn6-Tup1 Regulates RNR3 by Positioning Nucleosomes and Affecting the Chromatin Structure at the Upstream Repression Sequence. <i>Journal of Biological Chemistry</i> , 2001, 276, 33788-33797.	1.6	67
53	Derepression of DNA damage-regulated genes requires yeast TAFII. <i>EMBO Journal</i> , 2000, 19, 4091-4100.	3.5	30