

Scott B Rothbart

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

4,321
citations

126907

33
h-index

138484

58
g-index

65
all docs

65
docs citations

65
times ranked

6885
citing authors

#	ARTICLE	IF	CITATIONS
1	Interpreting the language of histone and DNA modifications. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 627-643.	1.9	596
2	Association of UHRF1 with methylated H3K9 directs the maintenance of DNA methylation. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1155-1160.	8.2	313
3	An H3K36 Methylation-Engaging Tudor Motif of Polycomb-like Proteins Mediates PRC2 Complex Targeting. <i>Molecular Cell</i> , 2013, 49, 571-582.	9.7	221
4	Structural basis for DNMT3A-mediated de novo DNA methylation. <i>Nature</i> , 2018, 554, 387-391.	27.8	215
5	A DNA methylation reader complex that enhances gene transcription. <i>Science</i> , 2018, 362, 1182-1186.	12.6	181
6	Multivalent histone engagement by the linked tandem Tudor and PHD domains of UHRF1 is required for the epigenetic inheritance of DNA methylation. <i>Genes and Development</i> , 2013, 27, 1288-1298.	5.9	155
7	A Histone Methylation Network Regulates Transgenerational Epigenetic Memory in <i>C.Âlegans</i> . <i>Cell Reports</i> , 2014, 7, 113-126.	6.4	146
8	The Histone-H3K4-Specific Demethylase KDM5B Binds to Its Substrate and Product through Distinct PHD Fingers. <i>Cell Reports</i> , 2014, 6, 325-335.	6.4	145
9	An Interactive Database for the Assessment of Histone Antibody Specificity. <i>Molecular Cell</i> , 2015, 59, 502-511.	9.7	139
10	Therapeutics by Cytotoxic Metabolite Accumulation: Pemetrexed Causes ZMP Accumulation, AMPK Activation, and Mammalian Target of Rapamycin Inhibition. <i>Cancer Research</i> , 2009, 69, 5467-5474.	0.9	136
11	Neuronal Stress Pathway Mediating a Histone Methyl/Phospho Switch Is Required for Herpes Simplex Virus Reactivation. <i>Cell Host and Microbe</i> , 2015, 18, 649-658.	11.0	121
12	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. <i>ELife</i> , 2016, 5, .	6.0	111
13	Examining the Roles of H3K4 Methylation States with Systematically Characterized Antibodies. <i>Molecular Cell</i> , 2018, 72, 162-177.e7.	9.7	90
14	Defining UHRF1 Domains that Support Maintenance of Human Colon Cancer DNA Methylation and Oncogenic Properties. <i>Cancer Cell</i> , 2019, 35, 633-648.e7.	16.8	89
15	Histone H3.3 phosphorylation amplifies stimulation-induced transcription. <i>Nature</i> , 2020, 583, 852-857.	27.8	88
16	Pemetrexed Indirectly Activates the Metabolic Kinase AMPK in Human Carcinomas. <i>Cancer Research</i> , 2010, 70, 10299-10309.	0.9	81
17	An Allosteric Interaction Links USP7 to Deubiquitination and Chromatin Targeting of UHRF1. <i>Cell Reports</i> , 2015, 12, 1400-1406.	6.4	78
18	Tandem PHD Fingers of MORF/MOZ Acetyltransferases Display Selectivity for Acetylated Histone H3 and Are Required for the Association with Chromatin. <i>Journal of Molecular Biology</i> , 2012, 424, 328-338.	4.2	75

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19	Lysine Methylation Regulators Moonlighting outside the Epigenome. <i>Molecular Cell</i> , 2019, 75, 1092-1101.	9.7	73
20	Molecular basis for chromatin binding and regulation of MLL5. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11296-11301.	7.1	72
21	AMP-activated Protein Kinase (AMPK) Control of mTORC1 Is p53- and TSC2-independent in Pemetrexed-treated Carcinoma Cells. <i>Journal of Biological Chemistry</i> , 2015, 290, 27473-27486.	3.4	66
22	Peptide Microarrays to Interrogate the "Histone Code". <i>Methods in Enzymology</i> , 2012, 512, 107-135.	1.0	64
23	A D53 repression motif induces oligomerization of TOPLESS corepressors and promotes assembly of a corepressor-nucleosome complex. <i>Science Advances</i> , 2017, 3, e1601217.	10.3	64
24	The Arginine Methyltransferase PRMT6 Regulates DNA Methylation and Contributes to Global DNA Hypomethylation in Cancer. <i>Cell Reports</i> , 2017, 21, 3390-3397.	6.4	60
25	HDAC inhibition results in widespread alteration of the histone acetylation landscape and BRD4 targeting to gene bodies. <i>Cell Reports</i> , 2021, 34, 108638.	6.4	60
26	Regulation of transcriptional elongation in pluripotency and cell differentiation by the PHD-finger protein Phf5a. <i>Nature Cell Biology</i> , 2016, 18, 1127-1138.	10.3	57
27	Identification of a Fragment-like Small Molecule Ligand for the Methyl-lysine Binding Protein, 53BP1. <i>ACS Chemical Biology</i> , 2015, 10, 1072-1081.	3.4	56
28	Chromatin Regulation through Ubiquitin and Ubiquitin-like Histone Modifications. <i>Trends in Biochemical Sciences</i> , 2021, 46, 258-269.	7.5	56
29	Dido3 PHD Modulates Cell Differentiation and Division. <i>Cell Reports</i> , 2013, 4, 148-158.	6.4	54
30	Epigenetic Therapy for Epithelioid Sarcoma. <i>Cell</i> , 2020, 181, 211.	28.9	47
31	Multivalent Chromatin Engagement and Inter-domain Crosstalk Regulate MORC3 ATPase. <i>Cell Reports</i> , 2016, 16, 3195-3207.	6.4	40
32	Selective binding of the PHD6 finger of MLL4 to histone H4K16ac links MLL4 and MOF. <i>Nature Communications</i> , 2019, 10, 2314.	12.8	40
33	Chromatin structure and its chemical modifications regulate the ubiquitin ligase substrate selectivity of UHRF1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8775-8780.	7.1	39
34	Structures of RNA polymerase II complexes with Bye1, a chromatin-binding PHF3/DIDO homologue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15277-15282.	7.1	38
35	Study of mitotic chromatin supports a model of bookmarking by histone modifications and reveals nucleosome deposition patterns. <i>Genome Research</i> , 2018, 28, 1455-1466.	5.5	35
36	Poly-acetylated chromatin signatures are preferred epitopes for site-specific histone H4 acetyl antibodies. <i>Scientific Reports</i> , 2012, 2, 489.	3.3	34

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37	Molecular Insights into Inhibition of the Methylated Histone-Plant Homeodomain Complexes by Calixarenes. <i>Journal of Biological Chemistry</i> , 2015, 290, 22919-22930.	3.4	33
38	Structural Plasticity of Methyllysine Recognition by the Tandem Tudor Domain of 53BP1. <i>Structure</i> , 2015, 23, 312-321.	3.3	32
39	Trabectedin Inhibits EWS-FLI1 and Evicts SWI/SNF from Chromatin in a Schedule-dependent Manner. <i>Clinical Cancer Research</i> , 2019, 25, 3417-3429.	7.0	32
40	A Role for Widely Interspaced Zinc Finger (WIZ) in Retention of the G9a Methyltransferase on Chromatin. <i>Journal of Biological Chemistry</i> , 2015, 290, 26088-26102.	3.4	29
41	Systematic comparison of monoclonal versus polyclonal antibodies for mapping histone modifications by ChIP-seq. <i>Epigenetics and Chromatin</i> , 2016, 9, 49.	3.9	25
42	Comparative biochemical analysis of UHRF proteins reveals molecular mechanisms that uncouple UHRF2 from DNA methylation maintenance. <i>Nucleic Acids Research</i> , 2018, 46, 4405-4416.	14.5	25
43	A functional proteomics platform to reveal the sequence determinants of lysine methyltransferase substrate selectivity. <i>Science Advances</i> , 2018, 4, eaav2623.	10.3	25
44	An Acetyl-Methyl Switch Drives a Conformational Change in p53. <i>Structure</i> , 2015, 23, 322-331.	3.3	21
45	ArrayNinja. <i>Methods in Enzymology</i> , 2016, 574, 53-77.	1.0	18
46	Analysis of Histone Antibody Specificity with Peptide Microarrays. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	18
47	A Read/Write Mechanism Connects p300 Bromodomain Function to H2A.Z Acetylation. <i>IScience</i> , 2019, 21, 773-788.	4.1	16
48	A trivalent nucleosome interaction by PHIP/BRWD2 is disrupted in neurodevelopmental disorders and cancer. <i>Genes and Development</i> , 2021, 35, 1642-1656.	5.9	16
49	Substrate Specificity Profiling of Histone-Modifying Enzymes by Peptide Microarray. <i>Methods in Enzymology</i> , 2016, 574, 31-52.	1.0	15
50	A physical basis for quantitative ChIP-sequencing. <i>Journal of Biological Chemistry</i> , 2020, 295, 15826-15837.	3.4	14
51	A fast, open source implementation of adaptive biasing potentials uncovers a ligand design strategy for the chromatin regulator BRD4. <i>Journal of Chemical Physics</i> , 2016, 145, 154113.	3.0	13
52	The finger loop of the SRA domain in the E3 ligase UHRF1 is a regulator of ubiquitin targeting and is required for the maintenance of DNA methylation. <i>Journal of Biological Chemistry</i> , 2019, 294, 15724-15732.	3.4	12
53	Identification of a BET Family Bromodomain/Casein Kinase II/TAF-Containing Complex as a Regulator of Mitotic Condensin Function. <i>Cell Reports</i> , 2014, 6, 892-905.	6.4	11
54	The histone and non-histone methyllysine reader activities of the UHRF1 tandem Tudor domain are dispensable for the propagation of aberrant DNA methylation patterning in cancer cells. <i>Epigenetics and Chromatin</i> , 2020, 13, 44.	3.9	10

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55	In silico APC/C substrate discovery reveals cell cycle-dependent degradation of UHRF1 and other chromatin regulators. <i>PLoS Biology</i> , 2020, 18, e3000975.	5.6	7
56	From Histones to Ribosomes: A Chromatin Regulator Tangoes with Translation. <i>Cancer Discovery</i> , 2015, 5, 228-230.	9.4	3
57	A Degenerate Peptide Library Approach to Reveal Sequence Determinants of Methyllysine-Driven Protein Interactions. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 241.	3.7	3
58	Binding specificity and function of the SWI/SNF subunit SMARCA4 bromodomain interaction with acetylated histone H3K14. <i>Journal of Biological Chemistry</i> , 2021, 297, 101145.	3.4	3
59	Distinguishing Active Versus Passive Using Illumina MethylationEPIC BeadChip Microarrays. <i>Methods in Molecular Biology</i> , 2021, 2272, 97-140.	0.9	1
60	Chromatin biochemistry enters the next generation of code 'seq-ing'. <i>Nature Methods</i> , 2014, 11, 799-800.	19.0	0