

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	Chromatin Regulation through Ubiquitin and Ubiquitin-like Histone Modifications. Trends in Biochemical Sciences, 2021, 46, 258-269.	7.5	56
2	HDAC inhibition results in widespread alteration of the histone acetylation landscape and BRD4 targeting to gene bodies. Cell Reports, 2021, 34, 108638.	6.4	60
3	Distinguishing Active Versus Passive Using Illumina MethylationEPIC BeadChip Microarrays. Methods in Molecular Biology, 2021, 2272, 97-140.	0.9	1
4	Binding specificity and function of the SWI/SNF subunit SMARCA4 bromodomain interaction with acetylated histone H3K14. Journal of Biological Chemistry, 2021, 297, 101145.	3.4	3
5	A trivalent nucleosome interaction by PHIP/BRWD2 is disrupted in neurodevelopmental disorders and cancer. Genes and Development, 2021, 35, 1642-1656.	5.9	16
6	Histone H3.3 phosphorylation amplifies stimulation-induced transcription. Nature, 2020, 583, 852-857.	27.8	88
7	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. Epigenetics and Chromatin, 2020, 13, 44.	3.9	10
8	A Degenerate Peptide Library Approach to Reveal Sequence Determinants of Methyllysine-Driven Protein Interactions. Frontiers in Cell and Developmental Biology, 2020, 8, 241.	3.7	3
9	Epigenetic Therapy for Epithelioid Sarcoma. Cell, 2020, 181, 211.	28.9	47
10	A physical basis for quantitative CHIP-sequencing. Journal of Biological Chemistry, 2020, 295, 15826-15837.	3.4	14
11	In silico APC/C substrate discovery reveals cell cycle-dependent degradation of UHRF1 and other chromatin regulators. PLoS Biology, 2020, 18, e3000975.	5.6	7
12	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. Journal of Biological Chemistry, 2019, 294, 15724-15732.	3.4	12
13	Lysine Methylation Regulators Moonlighting outside the Epigenome. Molecular Cell, 2019, 75, 1092-1101.	9.7	73
14	Selective binding of the PHD6 finger of MLL4 to histone H4K16ac links MLL4 and MOF. Nature Communications, 2019, 10, 2314.	12.8	40
15	Defining UHRF1 Domains that Support Maintenance of Human Colon Cancer DNA Methylation and Oncogenic Properties. Cancer Cell, 2019, 35, 633-648.e7.	16.8	89
16	Trabectedin Inhibits EWS-FLI1 and Evicts SWI/SNF from Chromatin in a Schedule-dependent Manner. Clinical Cancer Research, 2019, 25, 3417-3429.	7.0	32
17	A Read/Write Mechanism Connects p300 Bromodomain Function to H2A.Z Acetylation. IScience, 2019, 21, 773-788.	4.1	16
18	Comparative biochemical analysis of UHRF proteins reveals molecular mechanisms that uncouple UHRF2 from DNA methylation maintenance. Nucleic Acids Research, 2018, 46, 4405-4416.	14.5	25

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19	Structural basis for DNMT3A-mediated de novo DNA methylation. <i>Nature</i> , 2018, 554, 387-391.	27.8	215
20	A DNA methylation reader complex that enhances gene transcription. <i>Science</i> , 2018, 362, 1182-1186.	12.6	181
21	A functional proteomics platform to reveal the sequence determinants of lysine methyltransferase substrate selectivity. <i>Science Advances</i> , 2018, 4, eaav2623.	10.3	25
22	Examining the Roles of H3K4 Methylation States with Systematically Characterized Antibodies. <i>Molecular Cell</i> , 2018, 72, 162-177.e7.	9.7	90
23	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
24	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
25	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
26	Analysis of Histone Antibody Specificity with Peptide Microarrays. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	18
27	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
28	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
29	Substrate Specificity Profiling of Histone-Modifying Enzymes by Peptide Microarray. <i>Methods in Enzymology</i> , 2016, 574, 31-52.	1.0	15
30	ArrayNinja. <i>Methods in Enzymology</i> , 2016, 574, 53-77.	1.0	18
31	Multivalent Chromatin Engagement and Inter-domain Crosstalk Regulate MORC3 ATPase. <i>Cell Reports</i> , 2016, 16, 3195-3207.	6.4	40
32	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
33	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
34	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. <i>ELife</i> , 2016, 5, .	6.0	111
35	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
36	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

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37	Structural Plasticity of Methyllysine Recognition by the Tandem Tudor Domain of 53BP1. <i>Structure</i> , 2015, 23, 312-321.	3.3	32
38	An Acetyl-Methyl Switch Drives a Conformational Change in p53. <i>Structure</i> , 2015, 23, 322-331.	3.3	21
39	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
40	From Histones to Ribosomes: A Chromatin Regulator Tangoes with Translation. <i>Cancer Discovery</i> , 2015, 5, 228-230.	9.4	3
41	An Interactive Database for the Assessment of Histone Antibody Specificity. <i>Molecular Cell</i> , 2015, 59, 502-511.	9.7	139
42	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
43	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
44	An Allosteric Interaction Links USP7 to Deubiquitination and Chromatin Targeting of UHRF1. <i>Cell Reports</i> , 2015, 12, 1400-1406.	6.4	78
45	Interpreting the language of histone and DNA modifications. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 627-643.	1.9	596
46	Chromatin biochemistry enters the next generation of code 'seq-ing'. <i>Nature Methods</i> , 2014, 11, 799-800.	19.0	0
47	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
48	A Histone Methylation Network Regulates Transgenerational Epigenetic Memory in <i>C.Âelegans</i> . <i>Cell Reports</i> , 2014, 7, 113-126.	6.4	146
49	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
50	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
51	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
52	Dido3 PHD Modulates Cell Differentiation and Division. <i>Cell Reports</i> , 2013, 4, 148-158.	6.4	54
53	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
54	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

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55	Peptide Microarrays to Interrogate the "Histone Code". <i>Methods in Enzymology</i> , 2012, 512, 107-135.	1.0	64
56	Poly-acetylated chromatin signatures are preferred epitopes for site-specific histone H4 acetyl antibodies. <i>Scientific Reports</i> , 2012, 2, 489.	3.3	34
57	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
58	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
59	Pemetrexed Indirectly Activates the Metabolic Kinase AMPK in Human Carcinomas. <i>Cancer Research</i> , 2010, 70, 10299-10309.	0.9	81
60	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