

# Scott B Rothbart

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

3,012

citations

29

h-index

54

g-index

65

ext. papers

3,758

ext. citations

12.5

avg, IF

5.35

L-index

#	Paper	IF	Citations
62	A trivalent nucleosome interaction by PHIP/BRWD2 is disrupted in neurodevelopmental disorders and cancer. <i>Genes and Development</i> , <b>2021</b> , 35, 1642-1656	12.6	3
61	Chromatin Regulation through Ubiquitin and Ubiquitin-like Histone Modifications. <i>Trends in Biochemical Sciences</i> , <b>2021</b> , 46, 258-269	10.3	12
60	HDAC inhibition results in widespread alteration of the histone acetylation landscape and BRD4 targeting to gene bodies. <i>Cell Reports</i> , <b>2021</b> , 34, 108638	10.6	15
59	Distinguishing Active Versus Passive DNA Demethylation Using Illumina MethylationEPIC BeadChip Microarrays. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2272, 97-140	1.4	
58	Binding specificity and function of the SWI/SNF subunit SMARCA4 bromodomain interaction with acetylated histone H3K14. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 297, 101145	5.4	0
57	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> , <b>2020</b> , 13, 44	5.8	2
56	A Degenerate Peptide Library Approach to Reveal Sequence Determinants of Methyllysine-Driven Protein Interactions. <i>Frontiers in Cell and Developmental Biology</i> , <b>2020</b> , 8, 241	5.7	0
55	Epigenetic Therapy for Epithelioid Sarcoma. <i>Cell</i> , <b>2020</b> , 181, 211	56.2	24
54	In silico APC/C substrate discovery reveals cell cycle-dependent degradation of UHRF1 and other chromatin regulators. <i>PLoS Biology</i> , <b>2020</b> , 18, e3000975	9.7	5
53	A physical basis for quantitative ChIP-sequencing. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 15826-15837	7.4	2
52	Histone H3.3 phosphorylation amplifies stimulation-induced transcription. <i>Nature</i> , <b>2020</b> , 583, 852-857	50.4	43
51	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> , <b>2019</b> , 294, 15724-15732	5.4	7
50	Lysine Methylation Regulators Moonlighting outside the Epigenome. <i>Molecular Cell</i> , <b>2019</b> , 75, 1092-1101	17.6	29
49	Selective binding of the PHD6 finger of MLL4 to histone H4K16ac links MLL4 and MOF. <i>Nature Communications</i> , <b>2019</b> , 10, 2314	17.4	19
48	Defining UHRF1 Domains that Support Maintenance of Human Colon Cancer DNA Methylation and Oncogenic Properties. <i>Cancer Cell</i> , <b>2019</b> , 35, 633-648.e7	24.3	45
47	Trabectedin Inhibits EWS-FLI1 and Evicts SWI/SNF from Chromatin in a Schedule-dependent Manner. <i>Clinical Cancer Research</i> , <b>2019</b> , 25, 3417-3429	12.9	19
46	A Read/Write Mechanism Connects p300 Bromodomain Function to H2A.Z Acetylation. <i>IScience</i> , <b>2019</b> , 21, 773-788	6.1	3

45	Comparative biochemical analysis of UHRF proteins reveals molecular mechanisms that uncouple UHRF2 from DNA methylation maintenance. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 4405-4416	20.1	19
44	Structural basis for DNMT3A-mediated de novo DNA methylation. <i>Nature</i> , <b>2018</b> , 554, 387-391	50.4	121
43	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> , <b>2018</b> , 115, 8775-8780	11.5	23
42	A DNA methylation reader complex that enhances gene transcription. <i>Science</i> , <b>2018</b> , 362, 1182-1186	33.3	103
41	A functional proteomics platform to reveal the sequence determinants of lysine methyltransferase substrate selectivity. <i>Science Advances</i> , <b>2018</b> , 4, eaav2623	14.3	18
40	Examining the Roles of H3K4 Methylation States with Systematically Characterized Antibodies. <i>Molecular Cell</i> , <b>2018</b> , 72, 162-177.e7	17.6	52
39	Study of mitotic chromatin supports a model of bookmarking by histone modifications and reveals nucleosome deposition patterns. <i>Genome Research</i> , <b>2018</b> , 28, 1455-1466	9.7	19
38	A D53 repression motif induces oligomerization of TOPLESS corepressors and promotes assembly of a corepressor-nucleosome complex. <i>Science Advances</i> , <b>2017</b> , 3, e1601217	14.3	40
37	Analysis of Histone Antibody Specificity with Peptide Microarrays. <i>Journal of Visualized Experiments</i> , <b>2017</b> ,	1.6	8
36	The Arginine Methyltransferase PRMT6 Regulates DNA Methylation and Contributes to Global DNA Hypomethylation in Cancer. <i>Cell Reports</i> , <b>2017</b> , 21, 3390-3397	10.6	43
35	Regulation of transcriptional elongation in pluripotency and cell differentiation by the PHD-finger protein Phf5a. <i>Nature Cell Biology</i> , <b>2016</b> , 18, 1127-1138	23.4	33
34	Systematic comparison of monoclonal versus polyclonal antibodies for mapping histone modifications by ChIP-seq. <i>Epigenetics and Chromatin</i> , <b>2016</b> , 9, 49	5.8	16
33	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. <i>ELife</i> , <b>2016</b> , 5,	8.9	80
32	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> , <b>2016</b> , 145, 154113	3.9	11
31	Substrate Specificity Profiling of Histone-Modifying Enzymes by Peptide Microarray. <i>Methods in Enzymology</i> , <b>2016</b> , 574, 31-52	1.7	10
30	ArrayNinja: An Open Source Platform for Unified Planning and Analysis of Microarray Experiments. <i>Methods in Enzymology</i> , <b>2016</b> , 574, 53-77	1.7	9
29	Multivalent Chromatin Engagement and Inter-domain Crosstalk Regulate MORC3 ATPase. <i>Cell Reports</i> , <b>2016</b> , 16, 3195-3207	10.6	32
28	From histones to ribosomes: a chromatin regulator tangoes with translation. <i>Cancer Discovery</i> , <b>2015</b> , 5, 228-30	24.4	1

27	An Interactive Database for the Assessment of Histone Antibody Specificity. <i>Molecular Cell</i> , <b>2015</b> , 59, 502-11	17.6	109
26	AMP-activated Protein Kinase (AMPK) Control of mTORC1 Is p53- and TSC2-independent in Pemetrexed-treated Carcinoma Cells. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 27473-86	5.4	37
25	Molecular Insights into Inhibition of the Methylated Histone-Plant Homeodomain Complexes by Calixarenes. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 22919-30	5.4	24
24	An Allosteric Interaction Links USP7 to Deubiquitination and Chromatin Targeting of UHRF1. <i>Cell Reports</i> , <b>2015</b> , 12, 1400-6	10.6	55
23	Neuronal Stress Pathway Mediating a Histone Methyl/Phospho Switch Is Required for Herpes Simplex Virus Reactivation. <i>Cell Host and Microbe</i> , <b>2015</b> , 18, 649-58	23.4	90
22	A Role for Widely Interspaced Zinc Finger (WIZ) in Retention of the G9a Methyltransferase on Chromatin. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 26088-102	5.4	22
21	Structural plasticity of methyllysine recognition by the tandem tudor domain of 53BP1. <i>Structure</i> , <b>2015</b> , 23, 312-21	5.2	24
20	An acetyl-methyl switch drives a conformational change in p53. <i>Structure</i> , <b>2015</b> , 23, 322-31	5.2	16
19	Identification of a fragment-like small molecule ligand for the methyl-lysine binding protein, 53BP1. <i>ACS Chemical Biology</i> , <b>2015</b> , 10, 1072-81	4.9	44
18	Interpreting the language of histone and DNA modifications. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2014</b> , 1839, 627-43	6	459
17	Chromatin biochemistry enters the next generation of code decoding. <i>Nature Methods</i> , <b>2014</b> , 11, 799-800	21.6	
16	The histone-H3K4-specific demethylase KDM5B binds to its substrate and product through distinct PHD fingers. <i>Cell Reports</i> , <b>2014</b> , 6, 325-35	10.6	113
15	A histone methylation network regulates transgenerational epigenetic memory in <i>C. elegans</i> . <i>Cell Reports</i> , <b>2014</b> , 7, 113-26	10.6	121
14	Identification of a BET family bromodomain/casein kinase II/TAF-containing complex as a regulator of mitotic condensin function. <i>Cell Reports</i> , <b>2014</b> , 6, 892-905	10.6	9
13	Molecular basis for chromatin binding and regulation of MLL5. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 11296-301	11.5	61
12	An H3K36 methylation-engaging Tudor motif of polycomb-like proteins mediates PRC2 complex targeting. <i>Molecular Cell</i> , <b>2013</b> , 49, 571-82	17.6	165
11	Dido3 PHD modulates cell differentiation and division. <i>Cell Reports</i> , <b>2013</b> , 4, 148-58	10.6	40
10	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> , <b>2013</b> , 110, 15277-82	11.5	25

9	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> , <b>2013</b> , 27, 1288-98	12.6	129
8	Poly-acetylated chromatin signatures are preferred epitopes for site-specific histone H4 acetyl antibodies. <i>Scientific Reports</i> , <b>2012</b> , 2, 489	4.9	33
7	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> , <b>2012</b> , 424, 328-38	6.5	59
6	Association of UHRF1 with methylated H3K9 directs the maintenance of DNA methylation. <i>Nature Structural and Molecular Biology</i> , <b>2012</b> , 19, 1155-60	17.6	253
5	Peptide microarrays to interrogate the "histone code". <i>Methods in Enzymology</i> , <b>2012</b> , 512, 107-35	1.7	53
4	Pemetrexed indirectly activates the metabolic kinase AMPK in human carcinomas. <i>Cancer Research</i> , <b>2010</b> , 70, 10299-309	10.1	76
3	Therapeutics by cytotoxic metabolite accumulation: pemetrexed causes ZMP accumulation, AMPK activation, and mammalian target of rapamycin inhibition. <i>Cancer Research</i> , <b>2009</b> , 69, 5467-74	10.1	125
2	Systematic comparison of monoclonal versus polyclonal antibodies for mapping histone modifications by ChIP-seq		1
1	Study of mitotic chromatin supports a model of bookmarking by histone modifications and reveals nucleosome deposition patterns		2