Sharon Y R Dent

List of Publications by Year
in descending order

121 papers	15,030 citations	28274 55 h-index	21540 114 g-index
126 all docs	126 docs citations	126 times ranked	16635 citing authors

#	Article	IF	Citations
1	Histone Acetyltransferases. Annual Review of Biochemistry, 2001, 70, 81-120.	11.1	1,751
2	Tetrahymena Histone Acetyltransferase A: A Homolog to Yeast Gcn5p Linking Histone Acetylation to Gene Activation. Cell, 1996, 84, 843-851.	28.9	1,465
3	New Nomenclature for Chromatin-Modifying Enzymes. Cell, 2007, 131, 633-636.	28.9	849
4	Distinct roles of GCN5/PCAF-mediated H3K9ac and CBP/p300-mediated H3K18/27ac in nuclear receptor transactivation. EMBO Journal, 2011, 30, 249-262.	7.8	655
5	HDAC6 Modulates Cell Motility by Altering the Acetylation Level of Cortactin. Molecular Cell, 2007, 27, 197-213.	9.7	626
6	Chromatin modifiers and remodellers: regulators of cellular differentiation. Nature Reviews Genetics, 2014, 15, 93-106.	16.3	566
7	Transcription-linked acetylation by Gcn5p of histones H3 and H4 at specific lysines. Nature, 1996, 383, 269-272.	27.8	563
8	Histone H3 lysine 4 methylation is mediated by Set1 and required for cell growth and rDNA silencing in Saccharomyces cerevisiae. Genes and Development, 2001, 15, 3286-3295.	5.9	536
9	Cross-regulation of histone modifications. Nature Structural and Molecular Biology, 2007, 14, 1017-1024.	8.2	354
10	Histone acetyltransferases: function, structure, and catalysis. Current Opinion in Genetics and Development, 2001, 11, 155-161.	3.3	351
11	DANPOS: Dynamic analysis of nucleosome position and occupancy by sequencing. Genome Research, 2013, 23, 341-351.	5.5	331
12	AF9 YEATS Domain Links Histone Acetylation to DOT1L-Mediated H3K79 Methylation. Cell, 2014, 159, 558-571.	28.9	311
13	Essential and redundant functions of histone acetylation revealed by mutation of target lysines and loss of the Gcn5p acetyltransferase. EMBO Journal, 1998, 17, 3155-3167.	7.8	292
14	Histone Acetylation and Chromatin Assembly: A Single Escort, Multiple Dances?. Cell, 1996, 87, 5-8.	28.9	252
15	Chromatin condensation: does histone H1 dephosphorylation play a role?. Trends in Biochemical Sciences, 1992, 17, 93-98.	7.5	232
16	Loss of Gcn5l2 leads to increased apoptosis and mesodermal defects during mouse development. Nature Genetics, 2000, 26, 229-232.	21.4	231
17	Multiple faces of the SAGA complex. Current Opinion in Cell Biology, 2010, 22, 374-382.	5.4	225
18	The HP1Î±â€“CAF1â€“SetDB1â€containing complex provides H3K9me1 for Suv39â€mediated K9me3 in pericentric heterochromatin. EMBO Reports, 2009, 10, 769-775.	4.5	201

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19	Chromatin â€œPrepatternâ€•and Histone Modifiers in a Fate Choice for Liver and Pancreas. Science, 2011, 332, 963-966.	12.6	186
20	R loops stimulate genetic instability of CTGÂ·CAG repeats. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 692-697.	7.1	172
21	Gcn5 and SAGA Regulate Shelterin Protein Turnover and Telomere Maintenance. Molecular Cell, 2009, 35, 352-364.	9.7	156
22	Ssn6-Tup1 interacts with class I histone deacetylases required for repression. Genes and Development, 2000, 14, 2737-2744.	5.9	150
23	Regulation of the osteoblast-specific transcription factor Osterix by NO66, a Jumonji family histone demethylase. EMBO Journal, 2010, 29, 68-79.	7.8	143
24	Histone modifying enzymes and cancer: Going beyond histones. Journal of Cellular Biochemistry, 2005, 96, 1137-1148.	2.6	139
25	The Growth Suppressor PML Represses Transcription by Functionally and Physically Interacting with Histone Deacetylases. Molecular and Cellular Biology, 2001, 21, 2259-2268.	2.3	138
26	Enhancer transcription reveals subtype-specific gene expression programs controlling breast cancer pathogenesis. Genome Research, 2018, 28, 159-170.	5.5	137
27	The Set1 Methyltransferase Opposes Ipl1 Aurora Kinase Functions in Chromosome Segregation. Cell, 2005, 122, 723-734.	28.9	135
28	Transcriptional repression by Tup1â€“Ssn6This paper is one of a selection of papers published in this Special Issue, entitled 27th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2006, 84, 437-443.	2.0	124
29	USP22 regulates cell proliferation by deubiquitinating the transcriptional regulator FBP1. EMBO Reports, 2011, 12, 924-930.	4.5	120
30	c-Myc Transformation Domain Recruits the Human STAGA Complex and Requires TRRAP and GCN5 Acetylase Activity for Transcription Activation. Journal of Biological Chemistry, 2003, 278, 20405-20412.	3.4	118
31	Loss of Gcn5 Acetyltransferase Activity Leads to Neural Tube Closure Defects and Exencephaly in Mouse Embryos. Molecular and Cellular Biology, 2007, 27, 3405-3416.	2.3	118
32	Functions of SAGA in development andÂdisease. Epigenomics, 2014, 6, 329-339.	2.1	110
33	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. Molecular Cell, 2016, 62, 558-571.	9.7	106
34	KATs in cancer: functions and therapies. Oncogene, 2015, 34, 4901-4913.	5.9	102
35	YEATS2 links histone acetylation to tumorigenesis of non-small cell lung cancer. Nature Communications, 2017, 8, 1088.	12.8	102
36	Site-specific Loss of Acetylation upon Phosphorylation of Histone H3. Journal of Biological Chemistry, 2002, 277, 29496-29502.	3.4	98

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37	Tup1-Ssn6 Interacts with Multiple Class I Histone Deacetylases in Vivo. Journal of Biological Chemistry, 2003, 278, 50158-50162.	3.4	97
38	Chromatin-mediated transcription repression in yeast. Current Opinion in Genetics and Development, 1995, 5, 168-173.	3.3	95
39	Functions of histone-modifying enzymes in development. Current Opinion in Genetics and Development, 2006, 16, 137-142.	3.3	91
40	Histone-modifying enzymes: regulators of developmental decisions and drivers of human disease. Epigenomics, 2012, 4, 163-177.	2.1	89
41	Excision of Expanded GAA Repeats Alleviates the Molecular Phenotype of Friedreich's Ataxia. Molecular Therapy, 2015, 23, 1055-1065.	8.2	79
42	Long intronic GAAâ€¢TTC repeats induce epigenetic changes and reporter gene silencing in a molecular model of Friedreich ataxia. Nucleic Acids Research, 2008, 36, 6056-6065.	14.5	75
43	Myc and SAGA rewire an alternative splicing network during early somatic cell reprogramming. Genes and Development, 2015, 29, 803-816.	5.9	73
44	Glucagon regulates gluconeogenesis through KAT2B- and WDR5-mediated epigenetic effects. Journal of Clinical Investigation, 2013, 123, 4318-4328.	8.2	73
45	TGFÎ²-Activated USP27X Deubiquitinase Regulates Cell Migration and Chemoresistance via Stabilization of Snail1. Cancer Research, 2019, 79, 33-46.	0.9	70
46	Hyperexpansion of GAA repeats affects post-initiation steps of FXN transcription in Friedreich's ataxia. Nucleic Acids Research, 2011, 39, 8366-8377.	14.5	68
47	Histone-Dependent Association of Tup1-Ssn6 with Repressed Genes In Vivo. Molecular and Cellular Biology, 2002, 22, 693-703.	2.3	66
48	Reactivation of the silenced and imprinted alleles of ARHI is associated with increased histone H3 acetylation and decreased histone H3 lysine 9 methylation. Human Molecular Genetics, 2003, 12, 1791-1800.	2.9	64
49	The role of deubiquitinating enzymes in chromatin regulation. FEBS Letters, 2011, 585, 2016-2023.	2.8	62
50	Chromatin: Receiver and Quarterback for Cellular Signals. Cell, 2013, 152, 685-689.	28.9	62
51	Kâ€Łysine acetyltransferase 2a regulates a hippocampal gene expression network linked to memory formation. EMBO Journal, 2014, 33, 1912-1927.	7.8	62
52	Histone modification profiling in breast cancer cell lines highlights commonalities and differences among subtypes. BMC Genomics, 2018, 19, 150.	2.8	62
53	Unequal Access. Cell, 2000, 103, 699-702.	28.9	59
54	Proper expression of the Gcn5 histone acetyltransferase is required for neural tube closure in mouse embryos. Developmental Dynamics, 2008, 237, 928-940.	1.8	58

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55	Chromatin Signaling to Kinetochores: Transregulation of Dam1 Methylation by Histone H2B Ubiquitination. Cell, 2011, 146, 709-719.	28.9	58
56	Gcn5 and PCAF Regulate <i>PPAR</i>Î³ and <i>Prdm16</i> Expression To Facilitate Brown Adipogenesis. Molecular and Cellular Biology, 2014, 34, 3746-3753.	2.3	58
57	Developmental potential ofGcn5â^'/â^' embryonic stem cells in vivo and in vitro. Developmental Dynamics, 2007, 236, 1547-1557.	1.8	55
58	REV7 is essential for DNA damage tolerance via two REV3L binding sites in mammalian DNA polymerase Î¶. Nucleic Acids Research, 2015, 43, 1000-1011.	14.5	55
59	N-Myc and GCN5 Regulate Significantly Overlapping Transcriptional Programs in Neural Stem Cells. PLoS ONE, 2012, 7, e39456.	2.5	55
60	Resetting the histone code at CDKN2A in HNSCC by inhibition of DNA methylation. Oncogene, 2003, 22, 8902-8911.	5.9	53
61	Gcn5 loss-of-function accelerates cerebellar and retinal degeneration in a SCA7 mouse model. Human Molecular Genetics, 2012, 21, 394-405.	2.9	49
62	TRIM28 interacts with EZH2 and SWI/SNF to activate genes that promote mammosphere formation. Oncogene, 2017, 36, 2991-3001.	5.9	48
63	Recruitment of the Yeast Tup1p-Ssn6p Repressor Is Associated with Localized Decreases in Histone Acetylation. Journal of Biological Chemistry, 2001, 276, 1808-1813.	3.4	44
64	Reelin is a target of polyglutamine expanded ataxin-7 in human spinocerebellar ataxia type 7 (SCA7) astrocytes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21319-21324.	7.1	42
65	USP44 Is an Integral Component of N-CoR that Contributes to Gene Repression by Deubiquitinating Histone H2B. Cell Reports, 2016, 17, 2382-2393.	6.4	41
66	The role of chromatin modifiers in normal and malignant hematopoiesis. Blood, 2013, 121, 3076-3084.	1.4	39
67	Global alterations in chromatin accessibility associated with loss of SIN4 function. Nucleic Acids Research, 1997, 25, 1240-1247.	14.5	38
68	Ubp8 and SAGA Regulate Snf1 AMP Kinase Activity. Molecular and Cellular Biology, 2011, 31, 3126-3135.	2.3	36
69	Leucine-rich repeat containing 8A (LRRC8A) â€"dependent volume-regulated anion channel activity is dispensable for T-cell development and function. Journal of Allergy and Clinical Immunology, 2017, 140, 1651-1659.e1.	2.9	36
70	GCN5 and p300 share essential functions during early embryogenesis. Developmental Dynamics, 2005, 233, 1337-1347.	1.8	34
71	Stabilization of the promoter nucleosomes in nucleosome-free regions by the yeast Cyc8â€"Tup1 corepressor. Genome Research, 2013, 23, 312-322.	5.5	33
72	The Histone Acetyltransferase Gcn5 Positively Regulates T Cell Activation. Journal of Immunology, 2017, 198, 3927-3938.	0.8	32

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73	Transcriptional Control: An Activating Role for Arginine Methylation. Current Biology, 2002, 12, R59-R61.	3.9	31
74	Gcn5 and <scp>PCAF</scp> negatively regulate interferonâ€Î² production through <scp>HAT</scp>â€independent inhibition of <scp>TBK</scp>1. EMBO Reports, 2014, 15, 1192-1201.	4.5	31
75	Poly(Q) Expansions in ATXN7 Affect Solubility but Not Activity of the SAGA Deubiquitinating Module. Molecular and Cellular Biology, 2015, 35, 1777-1787.	2.3	31
76	DNA-protein interactions at theS.cerevisiaeÎ±2 operatorin vivo. Nucleic Acids Research, 1993, 21, 3295-3300.	14.5	30
77	The Lysine Acetyltransferase GCN5 Is Required for iNKT Cell Development through EGR2 Acetylation. Cell Reports, 2017, 20, 600-612.	6.4	30
78	Usp22 controls multiple signaling pathways that are essential for vasculature formation in the mouse placenta. Development (Cambridge), 2019, 146, .	2.5	30
79	Deficient LRRC8A-dependent volume-regulated anion channel activity is associated with male infertility in mice. JCI Insight, 2018, 3, .	5.0	29
80	Now open: Evolving insights to the roles of lysine acetylation in chromatin organization and function. Molecular Cell, 2022, 82, 716-727.	9.7	29
81	Proper Gcn5 histone acetyltransferase expression is required for normal anteroposterior patterning of the mouse skeleton. Development Growth and Differentiation, 2008, 50, 321-330.	1.5	28
82	GCN5 Regulates FGF Signaling and Activates Selective MYC Target Genes during Early Embryoid Body Differentiation. Stem Cell Reports, 2018, 10, 287-299.	4.8	27
83	Cross-talk between chromatin acetylation and SUMOylation of tripartite motifâ€“containing protein 24 (TRIM24) impacts cell adhesion. Journal of Biological Chemistry, 2018, 293, 7476-7485.	3.4	27
84	Protein-arginine Methyltransferase 1 (PRMT1) Methylates Ash2L, a Shared Component of Mammalian Histone H3K4 Methyltransferase Complexes. Journal of Biological Chemistry, 2011, 286, 12234-12244.	3.4	25
85	The complete amino acid sequence of an HMG-like protein isolated from the macronucleus ofTetrahymena. Nucleic Acids Research, 1987, 15, 8112-8112.	14.5	24
86	Low expression of ASH2L protein correlates with a favorable outcome in acute myeloid leukemia. Leukemia and Lymphoma, 2017, 58, 1207-1218.	1.3	24
87	Complex functions of Gcn5 and Pcaf in development and disease. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194609.	1.9	23
88	Increased Susceptibility to Skin Carcinogenesis Associated with a Spontaneous Mouse Mutation in the Palmitoyl Transferase Zdhhc13 Gene. Journal of Investigative Dermatology, 2015, 135, 3133-3143.	0.7	22
89	GCN5 HAT inhibition reduces human Burkitt lymphoma cell survival through reduction of MYC target gene expression and impeding BCR signaling pathways. Oncotarget, 2019, 10, 5847-5858.	1.8	22
90	Histone H3K4 methylation regulates deactivation of the spindle assembly checkpoint through direct binding of Mad2. Genes and Development, 2016, 30, 1187-1197.	5.9	21

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91	Transcriptional Activation of MYC-Induced Genes by GCN5 Promotes B-cell Lymphomagenesis. Cancer Research, 2020, 80, 5543-5553.	0.9	21
92	The subunit-exchange model of histone acetylation. Trends in Cell Biology, 1996, 6, 371-375.	7.9	20
93	Diencephalic Size Is Restricted by a Novel Interplay Between GCN5 Acetyltransferase Activity and Retinoic Acid Signaling. Journal of Neuroscience, 2017, 37, 2565-2579.	3.6	19
94	Something about silencing. Nature Genetics, 1996, 14, 3-4.	21.4	18
95	KATapulting toward Pluripotency and Cancer. Journal of Molecular Biology, 2017, 429, 1958-1977.	4.2	18
96	Expanded complexity of unstable repeat diseases. BioFactors, 2013, 39, 164-175.	5.4	17
97	Targeting the SAGA and ATAC Transcriptional Coactivator Complexes in MYC-Driven Cancers. Cancer Research, 2020, 80, 1905-1911.	0.9	17
98	Cytoplasmic ATXN7L3B Interferes with Nuclear Functions of the SAGA Deubiquitinase Module. Molecular and Cellular Biology, 2016, 36, 2855-2866.	2.3	16
99	Mutagenicity of the non-carcinogenic dibenzylnitrosamine and an alpha-acetoxy derivative. Cancer Letters, 1979, 6, 83-87.	7.2	15
100	Histone Modifications in Corepressor Functions. Current Topics in Developmental Biology, 2004, 59, 145-163.	2.2	14
101	A Two-Way Street: LSD1 Regulates Chromatin Boundary Formation in S. pombe and Drosophila. Molecular Cell, 2007, 26, 160-162.	9.7	13
102	Chromatin 'resetting' during transcription elongation: a central role for methylated H3K36. Nature Structural and Molecular Biology, 2012, 19, 863-864.	8.2	13
103	Conservation and diversity of the eukaryotic SAGA coactivator complex across kingdoms. Epigenetics and Chromatin, 2021, 14, 26.	3.9	12
104	Repression of GCN5 expression or activity attenuates c-MYC expression in non-small cell lung cancer. American Journal of Cancer Research, 2019, 9, 1830-1845.	1.4	11
105	Physical and Functional Interaction of the Yeast Corepressor Tup1 with mRNA 5â€²-Triphosphatase. Journal of Biological Chemistry, 2003, 278, 18895-18901.	3.4	10
106	Tousled-mediated Activation of Aurora B Kinase Does Not Require Tousled Kinase Activity in Vivo. Journal of Biological Chemistry, 2008, 283, 12763-12768.	3.4	10
107	Complementary Roles of GCN5 and PCAF in Foxp3+ T-Regulatory Cells. Cancers, 2019, 11, 554.	3.7	9
108	The lasting influence of LSD1 in the blood. ELife, 2013, 2, e00963.	6.0	9

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109	No Spt6, No Nucleosomes, No Activator Required. Molecular Cell, 2006, 21, 452-453.	9.7	8
110	Selecting and Isolating Colonies of Human Induced Pluripotent Stem Cells Reprogrammed from Adult Fibroblasts. Journal of Visualized Experiments, 2012, , .	0.3	8
111	The Set2 methyltransferase associates with Ssn6 yet Tup1-Ssn6 repression is independent of histone methylation. Biochemical and Biophysical Research Communications, 2006, 339, 905-914.	2.1	5
112	Usp22 Overexpression Leads to Aberrant Signal Transduction of Cancer-Related Pathways but Is Not Sufficient to Drive Tumor Formation in Mice. Cancers, 2021, 13, 4276.	3.7	4
113	Naked (N) mutant mice carry a nonsense mutation in the homeobox of <i>Hoxc13</i>. Experimental Dermatology, 2022, 31, 330-340.	2.9	1
114	Navigating EMT with COMPASS and PRC2. Nature Cell Biology, 2022, 24, 412-414.	10.3	1
115	Histone Acetyltransferases in Development. , 2004, , 105-113.		0
116	The H2BK123Rgument. Journal of Cell Biology, 2009, 186, 313-315.	5.2	0
117	Abstract IA07: New functions for histone modifying enzymes. , 2013, , .		0
118	Abstract SY24-01: A SAGA of GCN5 and USP22 in stem cells and cancer. , 2014, , .		0
119	Abstract PR06: Analysis of enhancer transcription reveals novel gene regulatory networks in breast cancer. , 2016, , .		0
120	Abstract 363: Role of the SAGA histone acetylation module in lung cancer. , 2018, , .		0
121	Abstract 4333: GCN5 positively correlates with c-MYC in non-small cell lung cancer. , 2019, , .		0