

Ronen Marmorstein

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.

79
papers

8,644
citations

47
h-index

80
g-index

80
ext. papers

9,487
ext. citations

10.8
avg. IF

5.99
L-index

#	Paper	IF	Citations
79	Discovery of spirohydantoin as selective, orally bioavailable inhibitors of p300/CBP histone acetyltransferases. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021 , 39, 127854	2.9	4
78	Molecular basis for acetyl-CoA production by ATP-citrate lyase. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 33-41	17.6	8
77	Molecular basis for chromatin assembly and modification by multiprotein complexes. <i>Protein Science</i> , 2019 , 28, 329-343	6.3	7
76	The scaffolding protein JADE1 physically links the acetyltransferase subunit HBO1 with its histone H3-H4 substrate. <i>Journal of Biological Chemistry</i> , 2018 , 293, 4498-4509	5.4	10
75	Structural determinants and cellular environment define processed actin as the sole substrate of the N-terminal acetyltransferase NAA80. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 4405-4410	11.5	38
74	Discovery of Spiro Oxazolidinediones as Selective, Orally Bioavailable Inhibitors of p300/CBP Histone Acetyltransferases. <i>ACS Medicinal Chemistry Letters</i> , 2018 , 9, 28-33	4.3	40
73	Structure of Human NatA and Its Regulation by the Huntingtin Interacting Protein HYPK. <i>Structure</i> , 2018 , 26, 925-935.e8	5.2	33
72	Discovery of a selective catalytic p300/CBP inhibitor that targets lineage-specific tumours. <i>Nature</i> , 2017 , 550, 128-132	50.4	303
71	Characterization of histone acylations links chromatin modifications with metabolism. <i>Nature Communications</i> , 2017 , 8, 1141	17.4	95
70	Probing the interaction between NatA and the ribosome for co-translational protein acetylation. <i>PLoS ONE</i> , 2017 , 12, e0186278	3.7	19
69	Molecular Basis for Cohesin Acetylation by Establishment of Sister Chromatid Cohesion N-Acetyltransferase ESCO1. <i>Journal of Biological Chemistry</i> , 2016 , 291, 26468-26477	5.4	12
68	Crystal Structure of the Golgi-Associated Human NEAcetyltransferase 60 Reveals the Molecular Determinants for Substrate-Specific Acetylation. <i>Structure</i> , 2016 , 24, 1044-56	5.2	33
67	The N-terminal Acetyltransferase Naa10/ARD1 Does Not Acetylate Lysine Residues. <i>Journal of Biological Chemistry</i> , 2016 , 291, 5270-7	5.4	31
66	Molecular Basis for Histone Acetyltransferase Regulation by Binding Partners, Associated Domains, and Autoacetylation. <i>ACS Chemical Biology</i> , 2016 , 11, 632-42	4.9	35
65	Structural and Functional Role of Acetyltransferase hMOF K274 Autoacetylation. <i>Journal of Biological Chemistry</i> , 2016 , 291, 18190-8	5.4	14
64	Nonenzymatic Protein Acetylation Detected by NAPPA Protein Arrays. <i>ACS Chemical Biology</i> , 2015 , 10, 2034-47	4.9	36
63	The molecular basis for histone H4- and H2A-specific amino-terminal acetylation by NatD. <i>Structure</i> , 2015 , 23, 332-41	5.2	46

62	Structure of the p300 histone acetyltransferase bound to acetyl-coenzyme A and its analogues. <i>Biochemistry</i> , 2014 , 53, 3415-22	3.2	47
61	Catalytic mechanism of histone acetyltransferase p300: from the proton transfer to acetylation reaction. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 2009-19	3.4	25
60	Writers and readers of histone acetylation: structure, mechanism, and inhibition. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014 , 6, a018762	10.2	287
59	Molecular basis for N-terminal acetylation by the heterodimeric NatA complex. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1098-105	17.6	107
58	Chaperone-mediated acetylation of histones by Rtt109 identified by quantitative proteomics. <i>Journal of Proteomics</i> , 2013 , 81, 80-90	3.9	17
57	Histone acetyltransferases: Rising ancient counterparts to protein kinases. <i>Biopolymers</i> , 2013 , 99, 98-111	1.2	54
56	Structure and mechanism of non-histone protein acetyltransferase enzymes. <i>FEBS Journal</i> , 2013 , 280, 5570-81	5.7	49
55	Structure of the β -tubulin acetyltransferase, β TAT1, and implications for tubulin-specific acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 19655-60	11.5	59
54	Different regions of the HPV-E7 and Ad-E1A viral oncoproteins bind competitively but through distinct mechanisms to the CH1 transactivation domain of p300. <i>Biochemistry</i> , 2012 , 51, 9524-34	3.2	11
53	Identification and characterization of small molecule antagonists of pRb inactivation by viral oncoproteins. <i>Chemistry and Biology</i> , 2012 , 19, 518-28		22
52	MYST protein acetyltransferase activity requires active site lysine autoacetylation. <i>EMBO Journal</i> , 2012 , 31, 58-70	13	87
51	Structure of the Rtt109-AcCoA/Vps75 complex and implications for chaperone-mediated histone acetylation. <i>Structure</i> , 2011 , 19, 221-31	5.2	40
50	Structure of a ternary Naa50p (NAT5/SAN) N-terminal acetyltransferase complex reveals the molecular basis for substrate-specific acetylation. <i>Journal of Biological Chemistry</i> , 2011 , 286, 37002-10	5.4	68
49	Virtual ligand screening of the p300/CBP histone acetyltransferase: identification of a selective small molecule inhibitor. <i>Chemistry and Biology</i> , 2010 , 17, 471-82		463
48	Structure and biochemical characterization of protein acetyltransferase from <i>Sulfolobus solfataricus</i> . <i>Journal of Biological Chemistry</i> , 2009 , 284, 19412-9	5.4	17
47	Identification and characterization of novel sirtuin inhibitor scaffolds. <i>Bioorganic and Medicinal Chemistry</i> , 2009 , 17, 7031-41	3.4	30
46	Histone modifying enzymes: structures, mechanisms, and specificities. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009 , 1789, 58-68	6	231
45	The structural basis of protein acetylation by the p300/CBP transcriptional coactivator. <i>Nature</i> , 2008 , 451, 846-50	50.4	323

44	Fungal Rtt109 histone acetyltransferase is an unexpected structural homolog of metazoan p300/CBP. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 738-45	17.6	93
43	Structure and chemistry of the p300/CBP and Rtt109 histone acetyltransferases: implications for histone acetyltransferase evolution and function. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 741-7	8.1	130
42	Structural basis for dimerization in DNA recognition by Gal4. <i>Structure</i> , 2008 , 16, 1019-26	5.2	55
41	14-3-3 interaction with histone H3 involves a dual modification pattern of phosphoacetylation. <i>Molecular and Cellular Biology</i> , 2008 , 28, 2840-9	4.8	72
40	Structural and Chemical Basis of Histone Acetylation. <i>Novartis Foundation Symposium</i> , 2008 , 78-101		11
39	Multiple roles for acetylation in the interaction of p300 HAT with ATF-2. <i>Biochemistry</i> , 2007 , 46, 8207-16	3.2	36
38	The human monocytic leukemia zinc finger histone acetyltransferase domain contains DNA-binding activity implicated in chromatin targeting. <i>Journal of Biological Chemistry</i> , 2007 , 282, 36603-13	5.4	37
37	Structure of the retinoblastoma protein bound to adenovirus E1A reveals the molecular basis for viral oncoprotein inactivation of a tumor suppressor. <i>Genes and Development</i> , 2007 , 21, 2711-6	12.6	65
36	Structure of a Leu3-DNA complex: recognition of everted CGG half-sites by a Zn ₂ Cys ₆ binuclear cluster protein. <i>Structure</i> , 2006 , 14, 725-35	5.2	14
35	Structure of the human Papillomavirus E7 oncoprotein and its mechanism for inactivation of the retinoblastoma tumor suppressor. <i>Journal of Biological Chemistry</i> , 2006 , 281, 578-86	5.4	154
34	When viral oncoprotein meets tumor suppressor: a structural view. <i>Genes and Development</i> , 2006 , 20, 2332-7	12.6	16
33	Acetylation of the p53 DNA-binding domain regulates apoptosis induction. <i>Molecular Cell</i> , 2006 , 24, 841-51	5.6	562
32	Structure and activity of enzymes that remove histone modifications. <i>Current Opinion in Structural Biology</i> , 2005 , 15, 673-80	8.1	97
31	Biochemical and structural characterization of recombinant histone acetyltransferase proteins. <i>Methods in Enzymology</i> , 2004 , 376, 106-19	1.7	16
30	Structure and substrate binding properties of cobB, a Sir2 homolog protein deacetylase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2004 , 337, 731-41	6.5	111
29	Structural basis for nicotinamide cleavage and ADP-ribose transfer by NAD(+)-dependent Sir2 histone/protein deacetylases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 8563-8	11.5	148
28	Crystal structure of the retinoblastoma tumor suppressor protein bound to E2F and the molecular basis of its regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 2363-8	11.5	109
27	Structure of SET domain proteins: a new twist on histone methylation. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 59-62	10.3	84

26	Structure of the yeast Hst2 protein deacetylase in ternary complex with 2FO-acetyl ADP ribose and histone peptide. <i>Structure</i> , 2003 , 11, 1403-11	5.2	101
25	Structure and autoregulation of the yeast Hst2 homolog of Sir2. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 864-71	17.6	89
24	Modulation of DNA-binding domains for sequence-specific DNA recognition. <i>Gene</i> , 2003 , 304, 1-12	3.8	22
23	Structural basis for histone and phosphohistone binding by the GCN5 histone acetyltransferase. <i>Molecular Cell</i> , 2003 , 12, 461-73	17.6	123
22	Molecular basis for Gcn5/PCAF histone acetyltransferase selectivity for histone and nonhistone substrates. <i>Biochemistry</i> , 2003 , 42, 14366-74	3.2	61
21	Structure of a Sir2 substrate, Alba, reveals a mechanism for deacetylation-induced enhancement of DNA binding. <i>Journal of Biological Chemistry</i> , 2003 , 278, 26071-7	5.4	49
20	Insights into structure and function of GCN5/PCAF and yEsa 1 histone acetyltransferase domains. <i>Methods in Enzymology</i> , 2003 , 371, 545-64	1.7	9
19	The catalytic mechanism of the ESA1 histone acetyltransferase involves a self-acetylated intermediate. <i>Nature Structural Biology</i> , 2002 , 9, 862-9		93
18	Structure of the GCN5 histone acetyltransferase bound to a bisubstrate inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 14065-70	11.5	95
17	Protein modules that manipulate histone tails for chromatin regulation. <i>Nature Reviews Molecular Cell Biology</i> , 2001 , 2, 422-32	48.7	161
16	Crystal structure of the mouse p53 core DNA-binding domain at 2.7 Å resolution. <i>Journal of Biological Chemistry</i> , 2001 , 276, 12120-7	5.4	70
15	Structure of histone acetyltransferases. <i>Journal of Molecular Biology</i> , 2001 , 311, 433-44	6.5	132
14	Histone acetyltransferases: function, structure, and catalysis. <i>Current Opinion in Genetics and Development</i> , 2001 , 11, 155-61	4.9	304
13	Application of a fluorescent histone acetyltransferase assay to probe the substrate specificity of the human p300/CBP-associated factor. <i>Analytical Biochemistry</i> , 2000 , 287, 319-28	3.1	79
12	Crystal structure of yeast Esa1 suggests a unified mechanism for catalysis and substrate binding by histone acetyltransferases. <i>Molecular Cell</i> , 2000 , 6, 1195-205	17.6	141
11	Phosphorylation of serine 10 in histone H3 is functionally linked in vitro and in vivo to Gcn5-mediated acetylation at lysine 14. <i>Molecular Cell</i> , 2000 , 5, 917-26	17.6	455
10	Oligomerization properties of the viral oncoproteins adenovirus E1A and human papillomavirus E7 and their complexes with the retinoblastoma protein. <i>Biochemistry</i> , 2000 , 39, 16033-45	3.2	40
9	Catalytic mechanism and function of invariant glutamic acid 173 from the histone acetyltransferase GCN5 transcriptional coactivator. <i>Journal of Biological Chemistry</i> , 1999 , 274, 18157-60	5.4	181

- 8 Structure of Tetrahymena GCN5 bound to coenzyme A and a histone H3 peptide. *Nature*, **1999**, 401, 93-850.4 244
- 7 Structure of HAP1-18-DNA implicates direct allosteric effect of protein-DNA interactions on transcriptional activation. *Nature Structural Biology*, **1999**, 6, 22-7 23
- 6 Structure of a HAP1-DNA complex reveals dramatically asymmetric DNA binding by a homodimeric protein. *Nature Structural Biology*, **1999**, 6, 64-71 73
- 5 p53 sites acetylated in vitro by PCAF and p300 are acetylated in vivo in response to DNA damage. *Molecular and Cellular Biology*, **1999**, 19, 1202-9 4.8 660
- 4 Structures of SAP-1 bound to DNA targets from the E74 and c-fos promoters: insights into DNA sequence discrimination by Ets proteins. *Molecular Cell*, **1998**, 2, 201-12 17.6 94
- 3 Crystal structure of a PUT3-DNA complex reveals a novel mechanism for DNA recognition by a protein containing a Zn₂Cys₆ binuclear cluster. *Nature Structural Biology*, **1997**, 4, 751-9 76
- 2 DNA recognition by GAL4: structure of a protein-DNA complex. *Nature*, **1992**, 356, 408-14 50.4 617
- 1 Solution structure of the DNA-binding domain of Cd2-GAL4 from *S. cerevisiae*. *Nature*, **1992**, 356, 450-3 50.4 122