

Ronen Marmorstein

List of Publications by Citations

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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.

90
papers

4,400
citations

35
h-index

65
g-index

107
ext. papers

5,365
ext. citations

10.3
avg, IF

5.72
L-index

#	Paper	IF	Citations
90	Autophagy mediates degradation of nuclear lamina. <i>Nature</i> , 2015 , 527, 105-9	50.4	365
89	Discovery of a selective catalytic p300/CBP inhibitor that targets lineage-specific tumours. <i>Nature</i> , 2017 , 550, 128-132	50.4	303
88	Writers and readers of histone acetylation: structure, mechanism, and inhibition. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014 , 6, a018762	10.2	287
87	Structure of Tetrahymena GCN5 bound to coenzyme A and a histone H3 peptide. <i>Nature</i> , 1999 , 401, 93-8	50.4	244
86	Histone modifying enzymes: structures, mechanisms, and specificities. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009 , 1789, 58-68	6	231
85	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
84	Protein modules that manipulate histone tails for chromatin regulation. <i>Nature Reviews Molecular Cell Biology</i> , 2001 , 2, 422-32	48.7	161
83	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
82	Structure of a human ASF1a-HIRA complex and insights into specificity of histone chaperone complex assembly. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 921-9	17.6	135
81	A Unified Approach to Targeting the Lysosome's Degradative and Growth Signaling Roles. <i>Cancer Discovery</i> , 2017 , 7, 1266-1283	24.4	114
80	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
79	Characterization of histone acylations links chromatin modifications with metabolism. <i>Nature Communications</i> , 2017 , 8, 1141	17.4	95
78	The catalytic mechanism of the ESA1 histone acetyltransferase involves a self-acetylated intermediate. <i>Nature Structural Biology</i> , 2002 , 9, 862-9		93
77	PPT1 Promotes Tumor Growth and Is the Molecular Target of Chloroquine Derivatives in Cancer. <i>Cancer Discovery</i> , 2019 , 9, 220-229	24.4	92
76	Human UBN1 is an ortholog of yeast Hpc2p and has an essential role in the HIRA/ASF1a chromatin-remodeling pathway in senescent cells. <i>Molecular and Cellular Biology</i> , 2009 , 29, 758-70	4.8	89
75	MYST protein acetyltransferase activity requires active site lysine autoacetylation. <i>EMBO Journal</i> , 2012 , 31, 58-70	13	87
74	Structure of SET domain proteins: a new twist on histone methylation. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 59-62	10.3	84

73	Ubinuclein-1 confers histone H3.3-specific-binding by the HIRA histone chaperone complex. <i>Nature Communications</i> , 2015 , 6, 7711	17.4	76
72	Crystal structure of a PUT3-DNA complex reveals a novel mechanism for DNA recognition by a protein containing a Zn ₂ Cys ₆ binuclear cluster. <i>Nature Structural Biology</i> , 1997 , 4, 751-9		76
71	Structure of a HAP1-DNA complex reveals dramatically asymmetric DNA binding by a homodimeric protein. <i>Nature Structural Biology</i> , 1999 , 6, 64-71		73
70	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
69	Biochemical and cellular analysis of Ogden syndrome reveals downstream Nt-acetylation defects. <i>Human Molecular Genetics</i> , 2015 , 24, 1956-76	5.6	65
68	Crystal structure of the stress-inducible human heat shock protein 70 substrate-binding domain in complex with peptide substrate. <i>PLoS ONE</i> , 2014 , 9, e103518	3.7	59
67	Human CABIN1 is a functional member of the human HIRA/UBN1/ASF1a histone H3.3 chaperone complex. <i>Molecular and Cellular Biology</i> , 2011 , 31, 4107-18	4.8	58
66	Design of Selective PAK1 Inhibitor G-5555: Improving Properties by Employing an Unorthodox Low-pK a Polar Moiety. <i>ACS Medicinal Chemistry Letters</i> , 2015 , 6, 1241-6	4.3	49
65	Molecular basis for oligomeric-DNA binding and episome maintenance by KSHV LANA. <i>PLoS Pathogens</i> , 2013 , 9, e1003672	7.6	49
64	Structure and mechanism of non-histone protein acetyltransferase enzymes. <i>FEBS Journal</i> , 2013 , 280, 5570-81	5.7	49
63	Architectural organization of the metabolic regulatory enzyme ghrelin O-acyltransferase. <i>Journal of Biological Chemistry</i> , 2013 , 288, 32211-32228	5.4	48
62	Identification of a novel family of BRAF(V600E) inhibitors. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 5220830		47
61	The molecular basis for histone H4- and H2A-specific amino-terminal acetylation by NatD. <i>Structure</i> , 2015 , 23, 332-41	5.2	46
60	Structure of Vps75 and implications for histone chaperone function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 12206-11	11.5	45
59	Salicylate, diflunisal and their metabolites inhibit CBP/p300 and exhibit anticancer activity. <i>ELife</i> , 2016 , 5,	8.9	45
58	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
57	Nonenzymatic Protein Acetylation Detected by NAPPA Protein Arrays. <i>ACS Chemical Biology</i> , 2015 , 10, 2034-47	4.9	36
56	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

55	Viral reprogramming of the Daxx histone H3.3 chaperone during early Epstein-Barr virus infection. <i>Journal of Virology</i> , 2014 , 88, 14350-63	6.6	34
54	Crystal Structure of the Golgi-Associated Human N ^ε Acetyltransferase 60 Reveals the Molecular Determinants for Substrate-Specific Acetylation. <i>Structure</i> , 2016 , 24, 1044-56	5.2	33
53	Structure of Human NatA and Its Regulation by the Huntingtin Interacting Protein HYPK. <i>Structure</i> , 2018 , 26, 925-935.e8	5.2	33
52	The N-terminal Acetyltransferase Naa10/ARD1 Does Not Acetylate Lysine Residues. <i>Journal of Biological Chemistry</i> , 2016 , 291, 5270-7	5.4	31
51	Implications for the evolution of eukaryotic amino-terminal acetyltransferase (NAT) enzymes from the structure of an archaeal ortholog. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 14652-7	11.5	30
50	A Molecular Prospective for HIRA Complex Assembly and H3.3-Specific Histone Chaperone Function. <i>Journal of Molecular Biology</i> , 2017 , 429, 1924-1933	6.5	24
49	Identification of an ubinuclein 1 region required for stability and function of the human HIRA/UBN1/CABIN1/ASF1a histone H3.3 chaperone complex. <i>Biochemistry</i> , 2012 , 51, 2366-77	3.2	24
48	Phenotypic and biochemical analysis of an international cohort of individuals with variants in NAA10 and NAA15. <i>Human Molecular Genetics</i> , 2019 , 28, 2900-2919	5.6	23
47	Functional activity of the H3.3 histone chaperone complex HIRA requires trimerization of the HIRA subunit. <i>Nature Communications</i> , 2018 , 9, 3103	17.4	23
46	Structure of HAP1-18-DNA implicates direct allosteric effect of protein-DNA interactions on transcriptional activation. <i>Nature Structural Biology</i> , 1999 , 6, 22-7		23
45	Modulation of DNA-binding domains for sequence-specific DNA recognition. <i>Gene</i> , 2003 , 304, 1-12	3.8	22
44	Structure and Mechanism of Acetylation by the N-Terminal Dual Enzyme NatA/Naa50 Complex. <i>Structure</i> , 2019 , 27, 1057-1070.e4	5.2	21
43	Probing the interaction between NatA and the ribosome for co-translational protein acetylation. <i>PLoS ONE</i> , 2017 , 12, e0186278	3.7	19
42	Protein N-Terminal Acetylation: Structural Basis, Mechanism, Versatility, and Regulation. <i>Trends in Biochemical Sciences</i> , 2021 , 46, 15-27	10.3	18
41	Dissecting the Molecular Roles of Histone Chaperones in Histone Acetylation by Type B Histone Acetyltransferases (HAT-B). <i>Journal of Biological Chemistry</i> , 2015 , 290, 30648-57	5.4	17
40	Chemically Linked Vemurafenib Inhibitors Promote an Inactive BRAF Conformation. <i>ACS Chemical Biology</i> , 2016 , 11, 2876-2888	4.9	16
39	The MEK/ERK Network as a Therapeutic Target in Human Cancer. <i>Molecular Cancer Research</i> , 2021 , 19, 361-374	6.6	15
38	Molecular basis for N-terminal acetylation by human NatE and its modulation by HYPK. <i>Nature Communications</i> , 2020 , 11, 818	17.4	14

37	Structural and Functional Role of Acetyltransferase hMOF K274 Autoacetylation. <i>Journal of Biological Chemistry</i> , 2016 , 291, 18190-8	5.4	14
36	Mechanism of BRAF Activation through Biochemical Characterization of the Recombinant Full-Length Protein. <i>ChemBioChem</i> , 2018 , 19, 1988-1997	3.8	13
35	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
34	ATP-citrate lyase multimerization is required for coenzyme-A substrate binding and catalysis. <i>Journal of Biological Chemistry</i> , 2019 , 294, 7259-7268	5.4	10
33	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
32	Conserved Lysine Acetylation within the Microtubule-Binding Domain Regulates MAP2/Tau Family Members. <i>PLoS ONE</i> , 2016 , 11, e0168913	3.7	10
31	DAXX represents a new type of protein-folding enabler. <i>Nature</i> , 2021 , 597, 132-137	50.4	10
30	Intramolecular autoinhibition of checkpoint kinase 1 is mediated by conserved basic motifs of the C-terminal kinase-associated 1 domain. <i>Journal of Biological Chemistry</i> , 2017 , 292, 19024-19033	5.4	9
29	Structural Basis for MARK1 Kinase Autoinhibition by Its KA1 Domain. <i>Structure</i> , 2018 , 26, 1137-1143.e3	5.2	9
28	Dehydrogenases, NAD, and transcription--what's the connection?. <i>Structure</i> , 2002 , 10, 1465-6	5.2	8
27	Molecular basis for acetyl-CoA production by ATP-citrate lyase. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 33-41	17.6	8
26	Structural and chemical basis of histone acetylation. <i>Novartis Foundation Symposium</i> , 2004 , 259, 78-98; discussion 98-101, 163-9		8
25	Opposing Functions of the N-terminal Acetyltransferases Naa50 and NatA in Sister-chromatid Cohesion. <i>Journal of Biological Chemistry</i> , 2016 , 291, 19079-91	5.4	7
24	Actin's N-terminal acetyltransferase uncovered. <i>Cytoskeleton</i> , 2018 , 75, 318-322	2.4	7
23	Molecular basis for N-terminal alpha-synuclein acetylation by human NatB. <i>ELife</i> , 2020 , 9,	8.9	7
22	Molecular basis for chromatin assembly and modification by multiprotein complexes. <i>Protein Science</i> , 2019 , 28, 329-343	6.3	7
21	Drugging the "Undruggable" MYCN Oncogenic Transcription Factor: Overcoming Previous Obstacles to Impact Childhood Cancers. <i>Cancer Research</i> , 2021 , 81, 1627-1632	10.1	7
20	N-(7-Cyano-6-(4-fluoro-3-(2-(3-(trifluoromethyl)phenyl)acetamido)phenoxy)benzo[d]thiazol-2-yl)cyclopropanecarboxamide (TAK632) Promotes Inhibition of BRAF through the Induction of Inhibited Dimers. <i>Journal of Medicinal Chemistry</i> , 2018 , 61, 5034-5046	8.3	6

19	Rap1-mediated nucleosome displacement can regulate gene expression in senescent cells without impacting the pace of senescence. <i>Aging Cell</i> , 2020 , 19, e13061	9.9	6
18	The HIRA histone chaperone complex subunit UBN1 harbors H3/H4- and DNA-binding activity. <i>Journal of Biological Chemistry</i> , 2019 , 294, 9239-9259	5.4	5
17	CTCF-Induced Circular DNA Complexes Observed by Atomic Force Microscopy. <i>Journal of Molecular Biology</i> , 2018 , 430, 759-776	6.5	5
16	Discovery of spirohydantoin s as selective, orally bioavailable inhibitors of p300/CBP histone acetyltransferases. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021 , 39, 127854	2.9	4
15	Remodelin Is a Cryptic Assay Interference Chemotype That Does Not Inhibit NAT10-Dependent Cytidine Acetylation. <i>ACS Medicinal Chemistry Letters</i> , 2021 , 12, 887-892	4.3	4
14	Transcription initiation at its most basic level. <i>Cell</i> , 2003 , 115, 370-2	56.2	3
13	Identification and Characterization of a B-Raf Kinase Helix Critical for the Activity of MEK Kinase in MAPK Signaling. <i>Biochemistry</i> , 2020 , 59, 4755-4765	3.2	3
12	The copper chaperone CCS facilitates copper binding to MEK1/2 to promote kinase activation. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101314	5.4	2
11	Novel Bisubstrate Inhibitors for Protein N-Terminal Acetyltransferase D. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 8263-8271	8.3	2
10	Structural biology: Hypoxia response becomes crystal clear. <i>Nature</i> , 2015 , 524, 298-300	50.4	1
9	Biochemical and structural analysis of N-terminal acetyltransferases. <i>Methods in Enzymology</i> , 2019 , 626, 271-299	1.7	1
8	Novel bisubstrate inhibitors for protein N-terminal acetyltransferase D		1
7	N-alpha-acetylation of Huntingtin protein increases its propensity to aggregate. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101363	5.4	0
6	Molecular mechanism of N-terminal acetylation by the ternary NatC complex. <i>Structure</i> , 2021 , 29, 1094-1104.e4	11.4	0
5	Reply to: Acetyl-CoA is produced by the citrate synthase homology module of ATP-citrate lyase. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 639-641	17.6	0
4	Unfolding Mechanisms and Conformational Stability of the Dimeric Endophilin N-BAR Domain. <i>ACS Omega</i> , 2021 , 6, 20790-20803	3.9	0
3	Structure and function of the SWIRM domain, a conserved protein module found in chromatin regulatory complexes. <i>FASEB Journal</i> , 2006 , 20, A34	0.9	0
2	Molecular Characterization of the HIRA Histone Chaperone Complex from <i>Chaetomium thermophilum</i> . <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	0

- 1 Structure and chemistry of the human p300/CBP and yeast Rtt109 histone acetyltransferase. *FASEB Journal*, **2009**, 23, 89.2 0.9