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.

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	The copper chaperone CCS facilitates copper binding to MEK1/2 to promote kinase activation. *Journal of Biological Chemistry*, **2021**, 297, 101314	5.4	2
89	N-alpha-acetylation of Huntingtin protein increases its propensity to aggregate. *Journal of Biological Chemistry*, **2021**, 297, 101363	5.4	0
88	Molecular mechanism of N-terminal acetylation by the ternary NatC complex. *Structure*, **2021**, 29, 1094-1104.e4	5.2	0
87	Discovery of spirohydantoins as selective, orally bioavailable inhibitors of p300/CBP histone acetyltransferases. *Bioorganic and Medicinal Chemistry Letters*, **2021**, 39, 127854	2.9	4
86	Novel Bisubstrate Inhibitors for Protein N-Terminal Acetyltransferase D. *Journal of Medicinal Chemistry*, **2021**, 64, 8263-8271	8.3	2
85	The MEK/ERK Network as a Therapeutic Target in Human Cancer. *Molecular Cancer Research*, **2021**, 19, 361-374	6.6	15
84	Remodelin Is a Cryptic Assay Interference Chemotype That Does Not Inhibit NAT10-Dependent Cytidine Acetylation. *ACS Medicinal Chemistry Letters*, **2021**, 12, 887-892	4.3	4
83	Protein N-Terminal Acetylation: Structural Basis, Mechanism, Versatility, and Regulation. *Trends in Biochemical Sciences*, **2021**, 46, 15-27	10.3	18
82	Reply to: Acetyl-CoA is produced by the citrate synthase homology module of ATP-citrate lyase. *Nature Structural and Molecular Biology*, **2021**, 28, 639-641	17.6	0
81	Unfolding Mechanisms and Conformational Stability of the Dimeric Endophilin N-BAR Domain. *ACS Omega*, **2021**, 6, 20790-20803	3.9	0
80	DAXX represents a new type of protein-folding enabler. *Nature*, **2021**, 597, 132-137	50.4	10
79	Drugging the "Undruggable" MYCN Oncogenic Transcription Factor: Overcoming Previous Obstacles to Impact Childhood Cancers. *Cancer Research*, **2021**, 81, 1627-1632	10.1	7
78	Molecular basis for N-terminal acetylation by human NatE and its modulation by HYPK. *Nature Communications*, **2020**, 11, 818	17.4	14
77	Molecular basis for N-terminal alpha-synuclein acetylation by human NatB. *ELife*, **2020**, 9,	8.9	7
76	Molecular Characterization of the HIRA Histone Chaperone Complex from Chaetomium thermophilum. *FASEB Journal*, **2020**, 34, 1-1	0.9	
75	Molecular basis for acetyl-CoA production by ATP-citrate lyase. *Nature Structural and Molecular Biology*, **2020**, 27, 33-41	17.6	8
74	Rap1-mediated nucleosome displacement can regulate gene expression in senescent cells without impacting the pace of senescence. *Aging Cell*, **2020**, 19, e13061	9.9	6

73	Identification and Characterization of a B-Raf Kinase αHelix Critical for the Activity of MEK Kinase in MAPK Signaling. *Biochemistry*, **2020**, 59, 4755-4765	3.2	3
72	Structure and Mechanism of Acetylation by the N-Terminal Dual Enzyme NatA/Naa50 Complex. *Structure*, **2019**, 27, 1057-1070.e4	5.2	21
71	Phenotypic and biochemical analysis of an international cohort of individuals with variants in NAA10 and NAA15. *Human Molecular Genetics*, **2019**, 28, 2900-2919	5.6	23
70	The HIRA histone chaperone complex subunit UBN1 harbors H3/H4- and DNA-binding activity. *Journal of Biological Chemistry*, **2019**, 294, 9239-9259	5.4	5
69	ATP-citrate lyase multimerization is required for coenzyme-A substrate binding and catalysis. *Journal of Biological Chemistry*, **2019**, 294, 7259-7268	5.4	10
68	Biochemical and structural analysis of N-terminal acetyltransferases. *Methods in Enzymology*, **2019**, 626, 271-299	1.7	1
67	PPT1 Promotes Tumor Growth and Is the Molecular Target of Chloroquine Derivatives in Cancer. *Cancer Discovery*, **2019**, 9, 220-229	24.4	92
66	Molecular basis for chromatin assembly and modification by multiprotein complexes. *Protein Science*, **2019**, 28, 329-343	6.3	7
65	The scaffolding protein JADE1 physically links the acetyltransferase subunit HBO1 with its histone H3-H4 substrate. *Journal of Biological Chemistry*, **2018**, 293, 4498-4509	5.4	10
64	CTCF-Induced Circular DNA Complexes Observed by Atomic Force Microscopy. *Journal of Molecular Biology*, **2018**, 430, 759-776	6.5	5
63	N-(7-Cyano-6-(4-fluoro-3-(2-(3-(trifluoromethyl)phenyl)acetamido)phenoxy)benzo[d]thiazol-2-yl)cyclopropanecarboxami (TAK632) Promotes Inhibition of BRAF through the Induction of Inhibited Dimers. *Journal of Medicinal Chemistry*, **2018**, 61, 5034-5046	8.3	6
62	Structural determinants and cellular environment define processed actin as the sole substrate of the N-terminal acetyltransferase NAA80. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 4405-4410	11.5	38
61	Mechanism of BRAF Activation through Biochemical Characterization of the Recombinant Full-Length Protein. *ChemBioChem*, **2018**, 19, 1988-1997	3.8	13
60	Actin's N-terminal acetyltransferase uncovered. *Cytoskeleton*, **2018**, 75, 318-322	2.4	7
59	Functional activity of the H3.3 histone chaperone complex HIRA requires trimerization of the HIRA subunit. *Nature Communications*, **2018**, 9, 3103	17.4	23
58	Structure of Human NatA and Its Regulation by the Huntingtin Interacting Protein HYPK. *Structure*, **2018**, 26, 925-935.e8	5.2	33
57	Structural Basis for MARK1 Kinase Autoinhibition by Its KA1 Domain. *Structure*, **2018**, 26, 1137-1143.e3	5.2	9
56	Intramolecular autoinhibition of checkpoint kinase 1 is mediated by conserved basic motifs of the C-terminal kinase-associated 1 domain. *Journal of Biological Chemistry*, **2017**, 292, 19024-19033	5.4	9

55	Discovery of a selective catalytic p300/CBP inhibitor that targets lineage-specific tumours. *Nature*, **2017**, 550, 128-132	50.4	303
54	A Unified Approach to Targeting the Lysosome's Degradative and Growth Signaling Roles. *Cancer Discovery*, **2017**, 7, 1266-1283	24.4	114
53	Characterization of histone acylations links chromatin modifications with metabolism. *Nature Communications*, **2017**, 8, 1141	17.4	95
52	A Molecular Prospective for HIRA Complex Assembly and H3.3-Specific Histone Chaperone Function. *Journal of Molecular Biology*, **2017**, 429, 1924-1933	6.5	24
51	Probing the interaction between NatA and the ribosome for co-translational protein acetylation. *PLoS ONE*, **2017**, 12, e0186278	3.7	19
50	Opposing Functions of the N-terminal Acetyltransferases Naa50 and NatA in Sister-chromatid Cohesion. *Journal of Biological Chemistry*, **2016**, 291, 19079-91	5.4	7
49	Molecular Basis for Cohesin Acetylation by Establishment of Sister Chromatid Cohesion N-Acetyltransferase ESCO1. *Journal of Biological Chemistry*, **2016**, 291, 26468-26477	5.4	12
48	Crystal Structure of the Golgi-Associated Human N□Acetyltransferase 60 Reveals the Molecular Determinants for Substrate-Specific Acetylation. *Structure*, **2016**, 24, 1044-56	5.2	33
47	The N-terminal Acetyltransferase Naa10/ARD1 Does Not Acetylate Lysine Residues. *Journal of Biological Chemistry*, **2016**, 291, 5270-7	5.4	31
46	Molecular Basis for Histone Acetyltransferase Regulation by Binding Partners, Associated Domains, and Autoacetylation. *ACS Chemical Biology*, **2016**, 11, 632-42	4.9	35
45	Conserved Lysine Acetylation within the Microtubule-Binding Domain Regulates MAP2/Tau Family Members. *PLoS ONE*, **2016**, 11, e0168913	3.7	10
44	Salicylate, diflunisal and their metabolites inhibit CBP/p300 and exhibit anticancer activity. *ELife*, **2016**, 5,	8.9	45
43	Chemically Linked Vemurafenib Inhibitors Promote an Inactive BRAF Conformation. *ACS Chemical Biology*, **2016**, 11, 2876-2888	4.9	16
42	Structural and Functional Role of Acetyltransferase hMOF K274 Autoacetylation. *Journal of Biological Chemistry*, **2016**, 291, 18190-8	5.4	14
41	Structural biology: Hypoxia response becomes crystal clear. *Nature*, **2015**, 524, 298-300	50.4	1
40	Design of Selective PAK1 Inhibitor G-5555: Improving Properties by Employing an Unorthodox Low-pK a Polar Moiety. *ACS Medicinal Chemistry Letters*, **2015**, 6, 1241-6	4.3	49
39	Autophagy mediates degradation of nuclear lamina. *Nature*, **2015**, 527, 105-9	50.4	365
38	Nonenzymatic Protein Acetylation Detected by NAPPA Protein Arrays. *ACS Chemical Biology*, **2015**, 10, 2034-47	4.9	36

37	Biochemical and cellular analysis of Ogden syndrome reveals downstream Nt-acetylation defects. *Human Molecular Genetics*, **2015**, 24, 1956-76	5.6	65
36	Dissecting the Molecular Roles of Histone Chaperones in Histone Acetylation by Type B Histone Acetyltransferases (HAT-B). *Journal of Biological Chemistry*, **2015**, 290, 30648-57	5.4	17
35	Ubinuclein-1 confers histone H3.3-specific-binding by the HIRA histone chaperone complex. *Nature Communications*, **2015**, 6, 7711	17.4	76
34	The molecular basis for histone H4- and H2A-specific amino-terminal acetylation by NatD. *Structure*, **2015**, 23, 332-41	5.2	46
33	Writers and readers of histone acetylation: structure, mechanism, and inhibition. *Cold Spring Harbor Perspectives in Biology*, **2014**, 6, a018762	10.2	287
32	Crystal structure of the stress-inducible human heat shock protein 70 substrate-binding domain in complex with peptide substrate. *PLoS ONE*, **2014**, 9, e103518	3.7	59
31	Viral reprogramming of the Daxx histone H3.3 chaperone during early Epstein-Barr virus infection. *Journal of Virology*, **2014**, 88, 14350-63	6.6	34
30	Molecular basis for N-terminal acetylation by the heterodimeric NatA complex. *Nature Structural and Molecular Biology*, **2013**, 20, 1098-105	17.6	107
29	Molecular basis for oligomeric-DNA binding and episome maintenance by KSHV LANA. *PLoS Pathogens*, **2013**, 9, e1003672	7.6	49
28	Architectural organization of the metabolic regulatory enzyme ghrelin O-acyltransferase. *Journal of Biological Chemistry*, **2013**, 288, 32211-32228	5.4	48
27	Structure and mechanism of non-histone protein acetyltransferase enzymes. *FEBS Journal*, **2013**, 280, 5570-81	5.7	49
26	Implications for the evolution of eukaryotic amino-terminal acetyltransferase (NAT) enzymes from the structure of an archaeal ortholog. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 14652-7	11.5	30
25	Identification of a novel family of BRAF(V600E) inhibitors. *Journal of Medicinal Chemistry*, **2012**, 55, 5220-30	8.9	47
24	Identification of an ubinuclein 1 region required for stability and function of the human HIRA/UBN1/CABIN1/ASF1a histone H3.3 chaperone complex. *Biochemistry*, **2012**, 51, 2366-77	3.2	24
23	MYST protein acetyltransferase activity requires active site lysine autoacetylation. *EMBO Journal*, **2012**, 31, 58-70	13	87
22	Structure of a ternary Naa50p (NAT5/SAN) N-terminal acetyltransferase complex reveals the molecular basis for substrate-specific acetylation. *Journal of Biological Chemistry*, **2011**, 286, 37002-10	5.4	68
21	Human CABIN1 is a functional member of the human HIRA/UBN1/ASF1a histone H3.3 chaperone complex. *Molecular and Cellular Biology*, **2011**, 31, 4107-18	4.8	58
20	Human UBN1 is an ortholog of yeast Hpc2p and has an essential role in the HIRA/ASF1a chromatin-remodeling pathway in senescent cells. *Molecular and Cellular Biology*, **2009**, 29, 758-70	4.8	89

19	Histone modifying enzymes: structures, mechanisms, and specificities. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2009**, 1789, 58-68	6	231
18	Structure and chemistry of the human p300/CBP and yeast Rtt109 histone acetyltransferase. *FASEB Journal*, **2009**, 23, 89.2	0.9	
17	Structure of Vps75 and implications for histone chaperone function. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 12206-11	11.5	45
16	Structure of a human ASF1a-HIRA complex and insights into specificity of histone chaperone complex assembly. *Nature Structural and Molecular Biology*, **2006**, 13, 921-9	17.6	135
15	Structure and function of the SWIRM domain, a conserved protein module found in chromatin regulatory complexes. *FASEB Journal*, **2006**, 20, A34	0.9	
14	Structural and chemical basis of histone acetylation. *Novartis Foundation Symposium*, **2004**, 259, 78-98; discussion 98-101, 163-9		8
13	Structure of SET domain proteins: a new twist on histone methylation. *Trends in Biochemical Sciences*, **2003**, 28, 59-62	10.3	84
12	Transcription initiation at its most basic level. *Cell*, **2003**, 115, 370-2	56.2	3
11	Modulation of DNA-binding domains for sequence-specific DNA recognition. *Gene*, **2003**, 304, 1-12	3.8	22
10	Dehydrogenases, NAD, and transcription--what's the connection?. *Structure*, **2002**, 10, 1465-6	5.2	8
9	The catalytic mechanism of the ESA1 histone acetyltransferase involves a self-acetylated intermediate. *Nature Structural Biology*, **2002**, 9, 862-9		93
8	Protein modules that manipulate histone tails for chromatin regulation. *Nature Reviews Molecular Cell Biology*, **2001**, 2, 422-32	48.7	161
7	Crystal structure of yeast Esa1 suggests a unified mechanism for catalysis and substrate binding by histone acetyltransferases. *Molecular Cell*, **2000**, 6, 1195-205	17.6	141
6	Catalytic mechanism and function of invariant glutamic acid 173 from the histone acetyltransferase GCN5 transcriptional coactivator. *Journal of Biological Chemistry*, **1999**, 274, 18157-60	5.4	181
5	Structure of Tetrahymena GCN5 bound to coenzyme A and a histone H3 peptide. *Nature*, **1999**, 401, 93-8	50.4	244
4	Structure of HAP1-18-DNA implicates direct allosteric effect of protein-DNA interactions on transcriptional activation. *Nature Structural Biology*, **1999**, 6, 22-7		23
3	Structure of a HAP1-DNA complex reveals dramatically asymmetric DNA binding by a homodimeric protein. *Nature Structural Biology*, **1999**, 6, 64-71		73
2	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

LIST OF PUBLICATIONS