

Ronen Marmorstein

List of Publications by Year in descending order

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96
papers

6,147
citations

81900

39
h-index

76900

74
g-index

107
all docs

107
docs citations

107
times ranked

9058
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Basis for Regulation of Mammalian Fatty Acid Synthase. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
2	Allosteric role of a structural NADP ⁺ molecule in glucose-6-phosphate dehydrogenase activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
3	The MEK/ERK Network as a Therapeutic Target in Human Cancer. <i>Molecular Cancer Research</i> , 2021, 19, 361-374.	3.4	95
4	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.	2.8	16
5	Protein N-Terminal Acetylation: Structural Basis, Mechanism, Versatility, and Regulation. <i>Trends in Biochemical Sciences</i> , 2021, 46, 15-27.	7.5	50
6	Identification and Characterization of a Bâ€Raf Kinase Alpha Helix Critical for the Activity of MEK Kinase in MAPK Signaling. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
7	Molecular mechanism of N-terminal acetylation by the ternary NatC complex. <i>Structure</i> , 2021, 29, 1094-1104.e4.	3.3	7
8	Discovery of spirohydantoin s as selective, orally bioavailable inhibitors of p300/CBP histone acetyltransferases. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021, 39, 127854.	2.2	9
9	Novel Bisubstrate Inhibitors for Protein N-Terminal Acetyltransferase D. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 8263-8271.	6.4	8
10	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.	8.2	1
11	Unfolding Mechanisms and Conformational Stability of the Dimeric Endophilin N-BAR Domain. <i>ACS Omega</i> , 2021, 6, 20790-20803.	3.5	3
12	DAXX represents a new type of protein-folding enabler. <i>Nature</i> , 2021, 597, 132-137.	27.8	54
13	Naa12 compensates for Naa10 in mice in the amino-terminal acetylation pathway. <i>ELife</i> , 2021, 10, .	6.0	6
14	Drugging the â€œUndruggableâ€•MYCN Oncogenic Transcription Factor: Overcoming Previous Obstacles to Impact Childhood Cancers. <i>Cancer Research</i> , 2021, 81, 1627-1632.	0.9	25
15	The copper chaperone CCS facilitates copper binding to MEK1/2 to promote kinase activation. <i>Journal of Biological Chemistry</i> , 2021, 297, 101314.	3.4	21
16	N-alpha-acetylation of Huntingtin protein increases its propensity to aggregate. <i>Journal of Biological Chemistry</i> , 2021, 297, 101363.	3.4	9
17	Molecular basis for acetyl-CoA production by ATP-citrate lyase. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 33-41.	8.2	31
18	Rap1â€mediated nucleosome displacement can regulate gene expression in senescent cells without impacting the pace of senescence. <i>Aging Cell</i> , 2020, 19, e13061.	6.7	13

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19	Identification and Characterization of a B-Raf Kinase $\hat{\pm}$ -Helix Critical for the Activity of MEK Kinase in MAPK Signaling. <i>Biochemistry</i> , 2020, 59, 4755-4765.	2.5	4
20	Molecular basis for N-terminal acetylation by human NatE and its modulation by HYPK. <i>Nature Communications</i> , 2020, 11, 818.	12.8	30
21	Molecular basis for N-terminal alpha-synuclein acetylation by human NatB. <i>ELife</i> , 2020, 9, .	6.0	25
22	Molecular Characterization of the HIRA Histone Chaperone Complex from <i>Chaetomium thermophilum</i> . <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	0
23	Biochemical and structural analysis of N-terminal acetyltransferases. <i>Methods in Enzymology</i> , 2019, 626, 271-299.	1.0	5
24	Structure and Mechanism of Acetylation by the N-Terminal Dual Enzyme NatA/Naa50 Complex. <i>Structure</i> , 2019, 27, 1057-1070.e4.	3.3	36
25	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.	2.9	46
26	The HIRA histone chaperone complex subunit UBN1 harbors H3/H4- and DNA-binding activity. <i>Journal of Biological Chemistry</i> , 2019, 294, 9239-9259.	3.4	10
27	ATP-citrate lyase multimerization is required for coenzyme-A substrate binding and catalysis. <i>Journal of Biological Chemistry</i> , 2019, 294, 7259-7268.	3.4	18
28	PPT1 Promotes Tumor Growth and Is the Molecular Target of Chloroquine Derivatives in Cancer. <i>Cancer Discovery</i> , 2019, 9, 220-229.	9.4	164
29	Molecular basis for chromatin assembly and modification by multiprotein complexes. <i>Protein Science</i> , 2019, 28, 329-343.	7.6	11
30	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.	3.4	19
31	CTCF-Induced Circular DNA Complexes Observed by Atomic Force Microscopy. <i>Journal of Molecular Biology</i> , 2018, 430, 759-776.	4.2	8
32	<i>N</i> -(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.	6.4	7
33	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.	7.1	67
34	Structure of Human NatA and Its Regulation by the Huntingtin Interacting Protein HYPK. <i>Structure</i> , 2018, 26, 925-935.e8.	3.3	49
35	Structural Basis for MARK1 Kinase Autoinhibition by Its KA1 Domain. <i>Structure</i> , 2018, 26, 1137-1143.e3.	3.3	15
36	Mechanism of BRAF Activation through Biochemical Characterization of the Recombinant Full-Length Protein. <i>ChemBioChem</i> , 2018, 19, 1988-1997.	2.6	32

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37	Actin's N-terminal acetyltransferase uncovered. <i>Cytoskeleton</i> , 2018, 75, 318-322.	2.0	18
38	Functional activity of the H3.3 histone chaperone complex HIRA requires trimerization of the HIRA subunit. <i>Nature Communications</i> , 2018, 9, 3103.	12.8	41
39	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.	3.4	15
40	Discovery of a selective catalytic p300/CBP inhibitor that targets lineage-specific tumours. <i>Nature</i> , 2017, 550, 128-132.	27.8	498
41	A Unified Approach to Targeting the Lysosome's Degradative and Growth Signaling Roles. <i>Cancer Discovery</i> , 2017, 7, 1266-1283.	9.4	159
42	Characterization of histone acylations links chromatin modifications with metabolism. <i>Nature Communications</i> , 2017, 8, 1141.	12.8	145
43	A Molecular Prospective for HIRA Complex Assembly and H3.3-Specific Histone Chaperone Function. <i>Journal of Molecular Biology</i> , 2017, 429, 1924-1933.	4.2	31
44	Epigenetics meets metabolism through PHB-mediated histone H3.3 deposition by HIRA. <i>Stem Cell Investigation</i> , 2017, 4, 46-46.	3.0	0
45	Probing the interaction between NatA and the ribosome for co-translational protein acetylation. <i>PLoS ONE</i> , 2017, 12, e0186278.	2.5	30
46	Salicylate, diflunisal and their metabolites inhibit CBP/p300 and exhibit anticancer activity. <i>ELife</i> , 2016, 5, .	6.0	55
47	Chemically Linked Vemurafenib Inhibitors Promote an Inactive BRAF ^{V600E} Conformation. <i>ACS Chemical Biology</i> , 2016, 11, 2876-2888.	3.4	26
48	Structural and Functional Role of Acetyltransferase hMOF K274 Autoacetylation. <i>Journal of Biological Chemistry</i> , 2016, 291, 18190-18198.	3.4	15
49	Preface. <i>Methods in Enzymology</i> , 2016, 573, xvii-xix.	1.0	0
50	Opposing Functions of the N-terminal Acetyltransferases Naa50 and NatA in Sister-chromatid Cohesion. <i>Journal of Biological Chemistry</i> , 2016, 291, 19079-19091.	3.4	12
51	Preface. <i>Methods in Enzymology</i> , 2016, 574, xv-xvii.	1.0	0
52	Molecular Basis for Cohesin Acetylation by Establishment of Sister Chromatid Cohesion N-Acetyltransferase ESCO1. <i>Journal of Biological Chemistry</i> , 2016, 291, 26468-26477.	3.4	18
53	Crystal Structure of the Golgi-Associated Human N ¹ -Acetyltransferase 60 Reveals the Molecular Determinants for Substrate-Specific Acetylation. <i>Structure</i> , 2016, 24, 1044-1056.	3.3	45
54	The N-terminal Acetyltransferase Naa10/ARD1 Does Not Acetylate Lysine Residues. <i>Journal of Biological Chemistry</i> , 2016, 291, 5270-5277.	3.4	44

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55	Molecular Basis for Histone Acetyltransferase Regulation by Binding Partners, Associated Domains, and Autoacetylation. <i>ACS Chemical Biology</i> , 2016, 11, 632-642.	3.4	42
56	Conserved Lysine Acetylation within the Microtubule-Binding Domain Regulates MAP2/Tau Family Members. <i>PLoS ONE</i> , 2016, 11, e0168913.	2.5	16
57	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, 30648-30657.	3.4	24
58	Ubinuclein-1 confers histone H3.3-specific-binding by the HIRA histone chaperone complex. <i>Nature Communications</i> , 2015, 6, 7711.	12.8	99
59	The Molecular Basis for Histone H4- and H2A-Specific Amino-Terminal Acetylation by NatD. <i>Structure</i> , 2015, 23, 332-341.	3.3	68
60	Hypoxia response becomes crystal clear. <i>Nature</i> , 2015, 524, 298-299.	27.8	2
61	Design of Selective PAK1 Inhibitor G-5555: Improving Properties by Employing an Unorthodox Low-p <i>K_a</i> Polar Moiety. <i>ACS Medicinal Chemistry Letters</i> , 2015, 6, 1241-1246.	2.8	68
62	Autophagy mediates degradation of nuclear lamina. <i>Nature</i> , 2015, 527, 105-109.	27.8	510
63	Nonenzymatic Protein Acetylation Detected by NAPPA Protein Arrays. <i>ACS Chemical Biology</i> , 2015, 10, 2034-2047.	3.4	47
64	Biochemical and cellular analysis of Ogden syndrome reveals downstream Nt-acetylation defects. <i>Human Molecular Genetics</i> , 2015, 24, 1956-1976.	2.9	97
65	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.	2.5	78
66	Viral Reprogramming of the Daxx Histone H3.3 Chaperone during Early Epstein-Barr Virus Infection. <i>Journal of Virology</i> , 2014, 88, 14350-14363.	3.4	45
67	Writers and Readers of Histone Acetylation: Structure, Mechanism, and Inhibition. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a018762-a018762.	5.5	419
68	Molecular basis for N-terminal acetylation by the heterodimeric NatA complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1098-1105.	8.2	137
69	Molecular Basis for Oligomeric-DNA Binding and Episome Maintenance by KSHV LANA. <i>PLoS Pathogens</i> , 2013, 9, e1003672.	4.7	70
70	Architectural Organization of the Metabolic Regulatory Enzyme Ghrelin O-Acyltransferase. <i>Journal of Biological Chemistry</i> , 2013, 288, 32211-32228.	3.4	59
71	Structure and mechanism of non-histone protein acetyltransferase enzymes. <i>FEBS Journal</i> , 2013, 280, 5570-5581.	4.7	65
72	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, 14652-14657.	7.1	43

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73	MYST protein acetyltransferase activity requires active site lysine autoacetylation. EMBO Journal, 2012, 31, 58-70.	7.8	101
74	Identification of a Novel Family of BRAF ^{V600E} Inhibitors. Journal of Medicinal Chemistry, 2012, 55, 5220-5230.	6.4	66
75	Identification of an Ubiquitin 1 Region Required for Stability and Function of the Human HIRA/UBN1/CABIN1/ASF1a Histone H3.3 Chaperone Complex. Biochemistry, 2012, 51, 2366-2377.	2.5	26
76	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, 37002-37010.	3.4	86
77	Human CABIN1 Is a Functional Member of the Human HIRA/UBN1/ASF1a Histone H3.3 Chaperone Complex. Molecular and Cellular Biology, 2011, 31, 4107-4118.	2.3	87
78	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, 758-770.	2.3	109
79	Histone modifying enzymes: Structures, mechanisms, and specificities. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2009, 1789, 58-68.	1.9	272
80	Structure and chemistry of the human p300/CBP and yeast Rtt109 histone acetyltransferase. FASEB Journal, 2009, 23, 89.2.	0.5	0
81	Structure of Vps75 and implications for histone chaperone function. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12206-12211.	7.1	54
82	Structure of a human ASF1a-HIRA complex and insights into specificity of histone chaperone complex assembly. Nature Structural and Molecular Biology, 2006, 13, 921-929.	8.2	161
83	Structure and function of the SWIRM domain, a conserved protein module found in chromatin regulatory complexes. FASEB Journal, 2006, 20, A34.	0.5	0
84	Structural and chemical basis of histone acetylation. Novartis Foundation Symposium, 2004, 259, 78-98; discussion 98-101, 163-9.	1.1	8
85	Structure of SET domain proteins: a new twist on histone methylation. Trends in Biochemical Sciences, 2003, 28, 59-62.	7.5	99
86	Transcription Initiation at Its Most Basic Level. Cell, 2003, 115, 370-372.	28.9	3
87	Modulation of DNA-binding domains for sequence-specific DNA recognition. Gene, 2003, 304, 1-12.	2.2	24
88	Dehydrogenases, NAD, and Transcription—What's the Connection?. Structure, 2002, 10, 1465-1466.	3.3	8
89	The catalytic mechanism of the ESA1 histone acetyltransferase involves a self-acetylated intermediate. Nature Structural Biology, 2002, 9, 862-9.	9.7	98
90	Protein modules that manipulate histone tails for chromatin regulation. Nature Reviews Molecular Cell Biology, 2001, 2, 422-432.	37.0	180

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91	Crystal Structure of Yeast Esa1 Suggests a Unified Mechanism for Catalysis and Substrate Binding by Histone Acetyltransferases. <i>Molecular Cell</i> , 2000, 6, 1195-1205.	9.7	151
92	Catalytic Mechanism and Function of Invariant Glutamic Acid 173 from the Histone Acetyltransferase GCN5 Transcriptional Coactivator. <i>Journal of Biological Chemistry</i> , 1999, 274, 18157-18160.	3.4	198
93	Structure of Tetrahymena GCN5 bound to coenzyme A and a histone H3 peptide. <i>Nature</i> , 1999, 401, 93-98.	27.8	258
94	Structure of HAP1-18-DNA implicates direct allosteric effect of protein-DNA interactions on transcriptional activation. <i>Nature Structural Biology</i> , 1999, 6, 22-27.	9.7	26
95	Structure of a HAP1-DNA complex reveals dramatically asymmetric DNA binding by a homodimeric protein. <i>Nature Structural Biology</i> , 1999, 6, 64-71.	9.7	81
96	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, 751-759.	9.7	87