

# 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.

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 | p53 sites acetylated in vitro by PCAF and p300 are acetylated in vivo in response to DNA damage. <i>Molecular and Cellular Biology</i> , <b>1999</b> , 19, 1202-9  | 4.8  | 660       |
| 78 | DNA recognition by GAL4: structure of a protein-DNA complex. <i>Nature</i> , <b>1992</b> , 356, 408-14   | 50.4 | 617       |
| 77 | Acetylation of the p53 DNA-binding domain regulates apoptosis induction. <i>Molecular Cell</i> , <b>2006</b> , 24, 841-516   | 51.6 | 562       |
| 76 | Virtual ligand screening of the p300/CBP histone acetyltransferase: identification of a selective small molecule inhibitor. <i>Chemistry and Biology</i> , <b>2010</b> , 17, 471-82  |      | 463       |
| 75 | 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> , <b>2000</b> , 5, 917-26  | 17.6 | 455       |
| 74 | The structural basis of protein acetylation by the p300/CBP transcriptional coactivator. <i>Nature</i> , <b>2008</b> , 451, 846-50   | 50.4 | 323       |
| 73 | Histone acetyltransferases: function, structure, and catalysis. <i>Current Opinion in Genetics and Development</i> , <b>2001</b> , 11, 155-61  | 4.9  | 304       |
| 72 | Discovery of a selective catalytic p300/CBP inhibitor that targets lineage-specific tumours. <i>Nature</i> , <b>2017</b> , 550, 128-132  | 50.4 | 303       |
| 71 | Writers and readers of histone acetylation: structure, mechanism, and inhibition. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2014</b> , 6, a018762   | 10.2 | 287       |
| 70 | Structure of Tetrahymena GCN5 bound to coenzyme A and a histone H3 peptide. <i>Nature</i> , <b>1999</b> , 401, 93-8  | 50.4 | 244       |
| 69 | Histone modifying enzymes: structures, mechanisms, and specificities. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2009</b> , 1789, 58-68  | 6    | 231       |
| 68 | Catalytic mechanism and function of invariant glutamic acid 173 from the histone acetyltransferase GCN5 transcriptional coactivator. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 18157-60                                    | 5.4  | 181       |
| 67 | Protein modules that manipulate histone tails for chromatin regulation. <i>Nature Reviews Molecular Cell Biology</i> , <b>2001</b> , 2, 422-32   | 48.7 | 161       |
| 66 | Structure of the human Papillomavirus E7 oncoprotein and its mechanism for inactivation of the retinoblastoma tumor suppressor. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 578-86   | 5.4  | 154       |
| 65 | 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> , <b>2004</b> , 101, 8563-8 | 11.5 | 148       |
| 64 | Crystal structure of yeast Esa1 suggests a unified mechanism for catalysis and substrate binding by histone acetyltransferases. <i>Molecular Cell</i> , <b>2000</b> , 6, 1195-205  | 17.6 | 141       |
| 63 | Structure of histone acetyltransferases. <i>Journal of Molecular Biology</i> , <b>2001</b> , 311, 433-44   | 6.5  | 132       |

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|----|---|------|-----|
| 62 | 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> , <b>2008</b> , 18, 741-7                    | 8.1  | 130 |
| 61 | Structural basis for histone and phosphohistone binding by the GCN5 histone acetyltransferase. <i>Molecular Cell</i> , <b>2003</b> , 12, 461-73   | 17.6 | 123 |
| 60 | Solution structure of the DNA-binding domain of Cd2-GAL4 from <i>S. cerevisiae</i> . <i>Nature</i> , <b>1992</b> , 356, 450-3   | 50.4 | 122 |
| 59 | Structure and substrate binding properties of cobB, a Sir2 homolog protein deacetylase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , <b>2004</b> , 337, 731-41   | 6.5  | 111 |
| 58 | 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> , <b>2003</b> , 100, 2363-8 | 11.5 | 109 |
| 57 | Molecular basis for N-terminal acetylation by the heterodimeric NatA complex. <i>Nature Structural and Molecular Biology</i> , <b>2013</b> , 20, 1098-105   | 17.6 | 107 |
| 56 | Structure of the yeast Hst2 protein deacetylase in ternary complex with 2FO-acetyl ADP ribose and histone peptide. <i>Structure</i> , <b>2003</b> , 11, 1403-11   | 5.2  | 101 |
| 55 | Structure and activity of enzymes that remove histone modifications. <i>Current Opinion in Structural Biology</i> , <b>2005</b> , 15, 673-80  | 8.1  | 97  |
| 54 | Characterization of histone acylations links chromatin modifications with metabolism. <i>Nature Communications</i> , <b>2017</b> , 8, 1141  | 17.4 | 95  |
| 53 | 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> , <b>2002</b> , 99, 14065-70                                       | 11.5 | 95  |
| 52 | Structures of SAP-1 bound to DNA targets from the E74 and c-fos promoters: insights into DNA sequence discrimination by Ets proteins. <i>Molecular Cell</i> , <b>1998</b> , 2, 201-12   | 17.6 | 94  |
| 51 | Fungal Rtt109 histone acetyltransferase is an unexpected structural homolog of metazoan p300/CBP. <i>Nature Structural and Molecular Biology</i> , <b>2008</b> , 15, 738-45   | 17.6 | 93  |
| 50 | The catalytic mechanism of the ESA1 histone acetyltransferase involves a self-acetylated intermediate. <i>Nature Structural Biology</i> , <b>2002</b> , 9, 862-9  |      | 93  |
| 49 | Structure and autoregulation of the yeast Hst2 homolog of Sir2. <i>Nature Structural and Molecular Biology</i> , <b>2003</b> , 10, 864-71   | 17.6 | 89  |
| 48 | MYST protein acetyltransferase activity requires active site lysine autoacetylation. <i>EMBO Journal</i> , <b>2012</b> , 31, 58-70  | 13   | 87  |
| 47 | Structure of SET domain proteins: a new twist on histone methylation. <i>Trends in Biochemical Sciences</i> , <b>2003</b> , 28, 59-62   | 10.3 | 84  |
| 46 | Application of a fluorescent histone acetyltransferase assay to probe the substrate specificity of the human p300/CBP-associated factor. <i>Analytical Biochemistry</i> , <b>2000</b> , 287, 319-28   | 3.1  | 79  |
| 45 | Crystal structure of a PUT3-DNA complex reveals a novel mechanism for DNA recognition by a protein containing a Zn <sub>2</sub> Cys <sub>6</sub> binuclear cluster. <i>Nature Structural Biology</i> , <b>1997</b> , 4, 751-9               |      | 76  |

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| 44 | Structure of a HAP1-DNA complex reveals dramatically asymmetric DNA binding by a homodimeric protein. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 64-71  |      | 73 |
| 43 | 14-3-3 interaction with histone H3 involves a dual modification pattern of phosphoacetylation. <i>Molecular and Cellular Biology</i> , <b>2008</b> , 28, 2840-9  | 4.8  | 72 |
| 42 | Crystal structure of the mouse p53 core DNA-binding domain at 2.7 Å resolution. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 12120-7  | 5.4  | 70 |
| 41 | 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> , <b>2011</b> , 286, 37002-10   | 5.4  | 68 |
| 40 | 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> , <b>2007</b> , 21, 2711-6  | 12.6 | 65 |
| 39 | Molecular basis for Gcn5/PCAF histone acetyltransferase selectivity for histone and nonhistone substrates. <i>Biochemistry</i> , <b>2003</b> , 42, 14366-74  | 3.2  | 61 |
| 38 | Structure of the $\beta$ -tubulin acetyltransferase, $\beta$ TAT1, and implications for tubulin-specific acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 19655-60                     | 11.5 | 59 |
| 37 | Structural basis for dimerization in DNA recognition by Gal4. <i>Structure</i> , <b>2008</b> , 16, 1019-26   | 5.2  | 55 |
| 36 | Histone acetyltransferases: Rising ancient counterparts to protein kinases. <i>Biopolymers</i> , <b>2013</b> , 99, 98-111  | 12.2 | 54 |
| 35 | Structure and mechanism of non-histone protein acetyltransferase enzymes. <i>FEBS Journal</i> , <b>2013</b> , 280, 5570-81   | 5.7  | 49 |
| 34 | Structure of a Sir2 substrate, Alba, reveals a mechanism for deacetylation-induced enhancement of DNA binding. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 26071-7   | 5.4  | 49 |
| 33 | Structure of the p300 histone acetyltransferase bound to acetyl-coenzyme A and its analogues. <i>Biochemistry</i> , <b>2014</b> , 53, 3415-22  | 3.2  | 47 |
| 32 | The molecular basis for histone H4- and H2A-specific amino-terminal acetylation by NatD. <i>Structure</i> , <b>2015</b> , 23, 332-41   | 5.2  | 46 |
| 31 | Structure of the Rtt109-AcCoA/Vps75 complex and implications for chaperone-mediated histone acetylation. <i>Structure</i> , <b>2011</b> , 19, 221-31   | 5.2  | 40 |
| 30 | Oligomerization properties of the viral oncoproteins adenovirus E1A and human papillomavirus E7 and their complexes with the retinoblastoma protein. <i>Biochemistry</i> , <b>2000</b> , 39, 16033-45  | 3.2  | 40 |
| 29 | Discovery of Spiro Oxazolidinones as Selective, Orally Bioavailable Inhibitors of p300/CBP Histone Acetyltransferases. <i>ACS Medicinal Chemistry Letters</i> , <b>2018</b> , 9, 28-33   | 4.3  | 40 |
| 28 | 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> , <b>2018</b> , 115, 4405-4410 | 11.5 | 38 |
| 27 | The human monocytic leukemia zinc finger histone acetyltransferase domain contains DNA-binding activity implicated in chromatin targeting. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 36603-13  | 5.4  | 37 |

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| 26 | Nonenzymatic Protein Acetylation Detected by NAPPA Protein Arrays. <i>ACS Chemical Biology</i> , <b>2015</b> , 10, 2034-47   | 4.9  | 36 |
| 25 | Multiple roles for acetylation in the interaction of p300 HAT with ATF-2. <i>Biochemistry</i> , <b>2007</b> , 46, 8207-16  | 3.2  | 36 |
| 24 | Molecular Basis for Histone Acetyltransferase Regulation by Binding Partners, Associated Domains, and Autoacetylation. <i>ACS Chemical Biology</i> , <b>2016</b> , 11, 632-42              | 4.9  | 35 |
| 23 | Crystal Structure of the Golgi-Associated Human NEAcetyltransferase 60 Reveals the Molecular Determinants for Substrate-Specific Acetylation. <i>Structure</i> , <b>2016</b> , 24, 1044-56 | 5.2  | 33 |
| 22 | Structure of Human NatA and Its Regulation by the Huntingtin Interacting Protein HYPK. <i>Structure</i> , <b>2018</b> , 26, 925-935.e8   | 5.2  | 33 |
| 21 | The N-terminal Acetyltransferase Naa10/ARD1 Does Not Acetylate Lysine Residues. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 5270-7   | 5.4  | 31 |
| 20 | Identification and characterization of novel sirtuin inhibitor scaffolds. <i>Bioorganic and Medicinal Chemistry</i> , <b>2009</b> , 17, 7031-41  | 3.4  | 30 |
| 19 | Catalytic mechanism of histone acetyltransferase p300: from the proton transfer to acetylation reaction. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 2009-19               | 3.4  | 25 |
| 18 | Structure of HAP1-18-DNA implicates direct allosteric effect of protein-DNA interactions on transcriptional activation. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 22-7           |      | 23 |
| 17 | Identification and characterization of small molecule antagonists of pRb inactivation by viral oncoproteins. <i>Chemistry and Biology</i> , <b>2012</b> , 19, 518-28                       |      | 22 |
| 16 | Modulation of DNA-binding domains for sequence-specific DNA recognition. <i>Gene</i> , <b>2003</b> , 304, 1-12   | 3.8  | 22 |
| 15 | Probing the interaction between NatA and the ribosome for co-translational protein acetylation. <i>PLoS ONE</i> , <b>2017</b> , 12, e0186278   | 3.7  | 19 |
| 14 | Chaperone-mediated acetylation of histones by Rtt109 identified by quantitative proteomics. <i>Journal of Proteomics</i> , <b>2013</b> , 81, 80-90   | 3.9  | 17 |
| 13 | Structure and biochemical characterization of protein acetyltransferase from <i>Sulfolobus solfataricus</i> . <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 19412-9          | 5.4  | 17 |
| 12 | When viral oncoprotein meets tumor suppressor: a structural view. <i>Genes and Development</i> , <b>2006</b> , 20, 2332-7  | 12.6 | 16 |
| 11 | Biochemical and structural characterization of recombinant histone acetyltransferase proteins. <i>Methods in Enzymology</i> , <b>2004</b> , 376, 106-19                                    | 1.7  | 16 |
| 10 | Structure of a Leu3-DNA complex: recognition of everted CGG half-sites by a Zn <sub>2</sub> Cys <sub>6</sub> binuclear cluster protein. <i>Structure</i> , <b>2006</b> , 14, 725-35        | 5.2  | 14 |
| 9  | Structural and Functional Role of Acetyltransferase hMOF K274 Autoacetylation. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 18190-8   | 5.4  | 14 |

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| 8 | Molecular Basis for Cohesin Acetylation by Establishment of Sister Chromatid Cohesion N-Acetyltransferase ESCO1. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 26468-26477                    | 5.4  | 12 |
| 7 | 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> , <b>2012</b> , 51, 9524-34 | 3.2  | 11 |
| 6 | Structural and Chemical Basis of Histone Acetylation. <i>Novartis Foundation Symposium</i> , <b>2008</b> , 78-101   |      | 11 |
| 5 | The scaffolding protein JADE1 physically links the acetyltransferase subunit HBO1 with its histone H3-H4 substrate. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 4498-4509                   | 5.4  | 10 |
| 4 | Insights into structure and function of GCN5/PCAF and yEsa 1 histone acetyltransferase domains. <i>Methods in Enzymology</i> , <b>2003</b> , 371, 545-64  | 1.7  | 9  |
| 3 | Molecular basis for acetyl-CoA production by ATP-citrate lyase. <i>Nature Structural and Molecular Biology</i> , <b>2020</b> , 27, 33-41  | 17.6 | 8  |
| 2 | Molecular basis for chromatin assembly and modification by multiprotein complexes. <i>Protein Science</i> , <b>2019</b> , 28, 329-343   | 6.3  | 7  |
| 1 | Discovery of spirohydantoin as selective, orally bioavailable inhibitors of p300/CBP histone acetyltransferases. <i>Bioorganic and Medicinal Chemistry Letters</i> , <b>2021</b> , 39, 127854               | 2.9  | 4  |