

Or Gozani

List of Publications by Year in descending order

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112
papers

14,787
citations

20759

60
h-index

25716

108
g-index

114
all docs

114
docs citations

114
times ranked

15728
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis of nucleosomal H3K36 methylation by NSD methyltransferases. <i>Nature</i> , 2021, 590, 498-503.	13.7	85
2	Epigenetics and beyond: targeting writers of protein lysine methylation to treat disease. <i>Nature Reviews Drug Discovery</i> , 2021, 20, 265-286.	21.5	116
3	Elevated NSD3 histone methylation activity drives squamous cell lung cancer. <i>Nature</i> , 2021, 590, 504-508.	13.7	79
4	Repression of CTSG, ELANE and PRTN3-mediated histone H3 proteolytic cleavage promotes monocyte-to-macrophage differentiation. <i>Nature Immunology</i> , 2021, 22, 711-722.	7.0	36
5	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. <i>Nature Communications</i> , 2021, 12, 2490.	5.8	63
6	Loss-of-function and missense variants in NSD2 cause decreased methylation activity and are associated with a distinct developmental phenotype. <i>Genetics in Medicine</i> , 2021, 23, 1474-1483.	1.1	24
7	Chemical linguistics: Reading the modified proteome. <i>Molecular Cell</i> , 2021, 81, 2501-2503.	4.5	0
8	NSD2 dimethylation at H3K36 promotes lung adenocarcinoma pathogenesis. <i>Molecular Cell</i> , 2021, 81, 4481-4492.e9.	4.5	42
9	Cardioinformatics: the nexus of bioinformatics and precision cardiology. <i>Briefings in Bioinformatics</i> , 2020, 21, 2031-2051.	3.2	15
10	Direct readout of heterochromatic H3K9me3 regulates DNMT1-mediated maintenance DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18439-18447.	3.3	62
11	Multivalent tumor suppressor adenomatous polyposis coli promotes Axin biomolecular condensate formation and efficient β -catenin degradation. <i>Scientific Reports</i> , 2020, 10, 17425.	1.6	12
12	Methyltransferase-like 21C (METTL21C) methylates alanine tRNA synthetase at Lys-943 in muscle tissue. <i>Journal of Biological Chemistry</i> , 2020, 295, 11822-11832.	1.6	11
13	An engineered variant of SETD3 methyltransferase alters target specificity from histidine to lysine methylation. <i>Journal of Biological Chemistry</i> , 2020, 295, 2582-2589.	1.6	15
14	SETD5-Coordinated Chromatin Reprogramming Regulates Adaptive Resistance to Targeted Pancreatic Cancer Therapy. <i>Cancer Cell</i> , 2020, 37, 834-849.e13.	7.7	48
15	Structural basis for the target specificity of actin histidine methyltransferase SETD3. <i>Nature Communications</i> , 2019, 10, 3541.	5.8	27
16	Binding to medium and long chain fatty acyls is a common property of HEAT and ARM repeat modules. <i>Scientific Reports</i> , 2019, 9, 14226.	1.6	3
17	Histone lysine methyltransferases in biology and disease. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 880-889.	3.6	262
18	HeartBioPortal. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002426.	1.6	8

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19	Enterovirus pathogenesis requires the host methyltransferase SETD3. <i>Nature Microbiology</i> , 2019, 4, 2523-2537.	5.9	51
20	METTL13 Methylation of eEF1A Increases Translational Output to Promote Tumorigenesis. <i>Cell</i> , 2019, 176, 491-504.e21.	13.5	117
21	SETD3 is an actin histidine methyltransferase that prevents primary dystocia. <i>Nature</i> , 2019, 565, 372-376.	13.7	116
22	Reading the future of leukaemia. <i>Nature</i> , 2017, 543, 186-187.	13.7	10
23	Histone modifications for chromatin dynamics and cellular plasticity. <i>Journal of Molecular Biology</i> , 2017, 429, 1921-1923.	2.0	2
24	Characterization of H3.3K36M as a tool to study H3K36 methylation in cancer cells. <i>Epigenetics</i> , 2017, 12, 917-922.	1.3	13
25	RBM25 is a global splicing factor promoting inclusion of alternatively spliced exons and is itself regulated by lysine mono-methylation. <i>Journal of Biological Chemistry</i> , 2017, 292, 13381-13390.	1.6	37
26	Systematic Analysis of Known and Candidate Lysine Demethylases in the Regulation of Myoblast Differentiation. <i>Journal of Molecular Biology</i> , 2017, 429, 2055-2065.	2.0	20
27	ASH1L Links Histone H3 Lysine 36 Dimethylation to MLL Leukemia. <i>Cancer Discovery</i> , 2016, 6, 770-783.	7.7	122
28	Nonhistone Lysine Methylation in the Regulation of Cancer Pathways. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2016, 6, a026435.	2.9	98
29	Molecular and Neural Functions of Rai1 , the Causal Gene for Smith-Magenis Syndrome. <i>Neuron</i> , 2016, 92, 392-406.	3.8	51
30	Structural Basis for the Unique Multivalent Readout of Unmodified H3 Tail by Arabidopsis ORC1b BAH-PHD Cassette. <i>Structure</i> , 2016, 24, 486-494.	1.6	19
31	Coordination of stress signals by the lysine methyltransferase SMYD2 promotes pancreatic cancer. <i>Genes and Development</i> , 2016, 30, 772-785.	2.7	68
32	A PWWP Domain of Histone-Lysine N-Methyltransferase NSD2 Binds to Dimethylated Lys-36 of Histone H3 and Regulates NSD2 Function at Chromatin. <i>Journal of Biological Chemistry</i> , 2016, 291, 8465-8474.	1.6	71
33	Histone H4 Lysine 20 (H4K20) Methylation, Expanding the Signaling Potential of the Proteome One Methyl Moiety at a Time. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 755-764.	2.5	53
34	Novel insights into the oncogenic function of the SMYD3 lysine methyltransferase. <i>Translational Cancer Research</i> , 2016, 5, 330-333.	0.4	8
35	A Meier-Gorlin Syndrome Mutation Impairs the ORC1-Nucleosome Association. <i>ACS Chemical Biology</i> , 2015, 10, 1176-1180.	1.6	9
36	A Proteomic Strategy Identifies Lysine Methylation of Splicing Factor snRNP70 by the SETMAR Enzyme. <i>Journal of Biological Chemistry</i> , 2015, 290, 12040-12047.	1.6	30

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37	The PZP Domain of AF10 Senses Unmodified H3K27 to Regulate DOT1L-Mediated Methylation of H3K79. <i>Molecular Cell</i> , 2015, 60, 319-327.	4.5	78
38	Set5 and Set1 cooperate to repress gene expression at telomeres and retrotransposons. <i>Epigenetics</i> , 2014, 9, 513-522.	1.3	28
39	An unexpected journey: Lysine methylation across the proteome. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1395-1403.	0.9	83
40	Emerging Technologies to Map the Protein Methyloome. <i>Journal of Molecular Biology</i> , 2014, 426, 3350-3362.	2.0	64
41	Proteome-wide enrichment of proteins modified by lysine methylation. <i>Nature Protocols</i> , 2014, 9, 37-50.	5.5	71
42	A molecular threading mechanism underlies Jumonji lysine demethylase KDM2A regulation of methylated H3K36. <i>Genes and Development</i> , 2014, 28, 1758-1771.	2.7	83
43	Histone-binding domains: Strategies for discovery and characterization. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 669-675.	0.9	19
44	SMYD3 links lysine methylation of MAP3K2 to Ras-driven cancer. <i>Nature</i> , 2014, 510, 283-287.	13.7	331
45	Nuclear PI5P, Uhrf1, and the Road Not Taken. <i>Molecular Cell</i> , 2014, 54, 901-903.	4.5	2
46	Histone Methylation in Chromatin Signaling. , 2014, , 213-256.		4
47	A General Molecular Affinity Strategy for Global Detection and Proteomic Analysis of Lysine Methylation. <i>Molecular Cell</i> , 2013, 50, 444-456.	4.5	143
48	Chd5 Requires PHD-Mediated Histone 3 Binding for Tumor Suppression. <i>Cell Reports</i> , 2013, 3, 92-102.	2.9	47
49	Nuclear phosphatidylinositol-5-phosphate regulates ING2 stability at discrete chromatin targets in response to DNA damage. <i>Scientific Reports</i> , 2013, 3, 2137.	1.6	51
50	New marks on the block. <i>Nucleus</i> , 2012, 3, 335-339.	0.6	11
51	Smyd3 regulates cancer cell phenotypes and catalyzes histone H4 lysine 5 methylation. <i>Epigenetics</i> , 2012, 7, 340-343.	1.3	158
52	The BAH domain of ORC1 links H4K20me2 to DNA replication licensing and Meierâ€™Gorlin syndrome. <i>Nature</i> , 2012, 484, 115-119.	13.7	314
53	Structureâ€™activity relationships of methyl-lysine reader antagonists. <i>MedChemComm</i> , 2012, 3, 45-51.	3.5	33
54	SIRT7 links H3K18 deacetylation to maintenance of oncogenic transformation. <i>Nature</i> , 2012, 487, 114-118.	13.7	503

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55	On silico peptide microarrays for high-resolution mapping of antibody epitopes and diverse protein-protein interactions. <i>Nature Medicine</i> , 2012, 18, 1434-1440.	15.2	97
56	Everybody's welcome: the big tent approach to epigenetic drug discovery. <i>Drug Discovery Today: Therapeutic Strategies</i> , 2012, 9, e75-e81.	0.5	3
57	Phf19 links methylated Lys36 of histone H3 to regulation of Polycomb activity. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1257-1265.	3.6	229
58	Methylation of H4 lysines 5, 8 and 12 by yeast Set5 calibrates chromatin stress responses. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 361-363.	3.6	49
59	Methylation by Set9 modulates FoxO3 stability and transcriptional activity. <i>Aging</i> , 2012, 4, 462-479.	1.4	76
60	Lysine Methylation and Regulation of Gene Expression Programs. <i>FASEB Journal</i> , 2012, 26, 467.2.	0.2	0
61	Regulation of p53 function by lysine methylation. <i>Epigenomics</i> , 2011, 3, 361-369.	1.0	55
62	CUL4B: Trash Talking at Chromatin. <i>Molecular Cell</i> , 2011, 43, 321-323.	4.5	0
63	NSD2 Links Dimethylation of Histone H3 at Lysine 36 to Oncogenic Programming. <i>Molecular Cell</i> , 2011, 44, 609-620.	4.5	356
64	Lysine methylation of the NF- κ B subunit RelA by SETD6 couples activity of the histone methyltransferase GLP at chromatin to tonic repression of NF- κ B signaling. <i>Nature Immunology</i> , 2011, 12, 29-36.	7.0	230
65	A proteomic approach for the identification of novel lysine methyltransferase substrates. <i>Epigenetics and Chromatin</i> , 2011, 4, 19.	1.8	55
66	A Chemical Method for Labeling Lysine Methyltransferase Substrates. <i>ChemBioChem</i> , 2011, 12, 330-334.	1.3	67
67	Structural basis of SETD6-mediated regulation of the NF- κ B network via methyl-lysine signaling. <i>Nucleic Acids Research</i> , 2011, 39, 6380-6389.	6.5	61
68	Hypoxia-induced methylation of a pontin chromatin remodeling factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13510-13515.	3.3	100
69	Members of the H3K4 trimethylation complex regulate lifespan in a germline-dependent manner in <i>C. elegans</i> . <i>Nature</i> , 2010, 466, 383-387.	13.7	468
70	TRIM24 links a non-canonical histone signature to breast cancer. <i>Nature</i> , 2010, 468, 927-932.	13.7	374
71	The MBT Repeats of L3MBTL1 Link SET8-mediated p53 Methylation at Lysine 382 to Target Gene Repression. <i>Journal of Biological Chemistry</i> , 2010, 285, 37725-37732.	1.6	86
72	Methylation of the Retinoblastoma Tumor Suppressor by SMYD2. <i>Journal of Biological Chemistry</i> , 2010, 285, 37733-37740.	1.6	188

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73	Trimethylation of histone H3 lysine 4 impairs methylation of histone H3 lysine 9. <i>Epigenetics</i> , 2010, 5, 767-775.	1.3	64
74	A Functional Link between the Histone Demethylase PHF8 and the Transcription Factor ZNF711 in X-Linked Mental Retardation. <i>Molecular Cell</i> , 2010, 38, 165-178.	4.5	186
75	Negative Regulation of Hypoxic Responses via Induced Reptin Methylation. <i>Molecular Cell</i> , 2010, 39, 71-85.	4.5	152
76	Structural Insight into p53 Recognition by the 53BP1 Tandem Tudor Domain. <i>Journal of Molecular Biology</i> , 2010, 398, 489-496.	2.0	50
77	Molecular Mechanism of MLL PHD3 and RNA Recognition by the Cyp33 RRM Domain. <i>Journal of Molecular Biology</i> , 2010, 400, 145-154.	2.0	40
78	Binding of the MLL PHD3 Finger to Histone H3K4me3 Is Required for MLL-Dependent Gene Transcription. <i>Journal of Molecular Biology</i> , 2010, 400, 137-144.	2.0	88
79	Decoding Chromatin Goes High Tech. <i>Cell</i> , 2010, 142, 844-846.	13.5	7
80	Epigenome Microarray Platform for Proteome-Wide Dissection of Chromatin-Signaling Networks. <i>PLoS ONE</i> , 2009, 4, e6789.	1.1	91
81	SIRT6 stabilizes DNA-dependent Protein Kinase at chromatin for DNA double-strand break repair. <i>Aging</i> , 2009, 1, 109-121.	1.4	270
82	Cell cycle-dependent deacetylation of telomeric histone H3 lysine K56 by human SIRT6. <i>Cell Cycle</i> , 2009, 8, 2664-2666.	1.3	339
83	The Target of the NSD Family of Histone Lysine Methyltransferases Depends on the Nature of the Substrate. <i>Journal of Biological Chemistry</i> , 2009, 284, 34283-34295.	1.6	257
84	NMR assignments and histone specificity of the ING2 PHD finger. <i>Magnetic Resonance in Chemistry</i> , 2009, 47, 352-358.	1.1	9
85	ING4 Mediates Crosstalk between Histone H3 K4 Trimethylation and H3 Acetylation to Attenuate Cellular Transformation. <i>Molecular Cell</i> , 2009, 33, 248-256.	4.5	191
86	HBO1 HAT Complexes Target Chromatin throughout Gene Coding Regions via Multiple PHD Finger Interactions with Histone H3 Tail. <i>Molecular Cell</i> , 2009, 33, 257-265.	4.5	163
87	SIRT6 is a histone H3 lysine 9 deacetylase that modulates telomeric chromatin. <i>Nature</i> , 2008, 452, 492-496.	13.7	945
88	Histone H3K4me3 Binding Is Required for the DNA Repair and Apoptotic Activities of ING1 Tumor Suppressor. <i>Journal of Molecular Biology</i> , 2008, 380, 303-312.	2.0	115
89	Role for 53BP1 Tudor Domain Recognition of p53 Dimethylated at Lysine 382 in DNA Damage Signaling. <i>Journal of Biological Chemistry</i> , 2008, 283, 34660-34666.	1.6	71
90	Aire employs a histone-binding module to mediate immunological tolerance, linking chromatin regulation with organ-specific autoimmunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15878-15883.	3.3	155

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91	The plant homeodomain finger of RAG2 recognizes histone H3 methylated at both lysine-4 and arginine-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18993-18998.	3.3	186
92	Proteome-wide Analysis in <i>Saccharomyces cerevisiae</i> Identifies Several PHD Fingers as Novel Direct and Selective Binding Modules of Histone H3 Methylated at Either Lysine 4 or Lysine 36. <i>Journal of Biological Chemistry</i> , 2007, 282, 2450-2455.	1.6	218
93	Modulation of p53 Function by SET8-Mediated Methylation at Lysine 382. <i>Molecular Cell</i> , 2007, 27, 636-646.	4.5	375
94	Stabilized Phosphatidylinositol-5-Phosphate Analogues as Ligands for the Nuclear Protein ING2. <i>Journal of Chemistry, Biology, and Molecular Modeling</i> . <i>Journal of the American Chemical Society</i> , 2007, 129, 6498-6506.	6.6	39
95	Recognition of unmethylated histone H3 lysine 4 links BHC80 to LSD1-mediated gene repression. <i>Nature</i> , 2007, 448, 718-722.	13.7	386
96	RAG2 PHD finger couples histone H3 lysine 4 trimethylation with V(D)J recombination. <i>Nature</i> , 2007, 450, 1106-1110.	13.7	429
97	Structures and function of PHD fingers of ING tumor suppressors. <i>FASEB Journal</i> , 2007, 21, A283.	0.2	0
98	Molecular mechanism of histone H3K4me3 recognition by plant homeodomain of ING2. <i>Nature</i> , 2006, 442, 100-103.	13.7	609
99	ING2 PHD domain links histone H3 lysine 4 methylation to active gene repression. <i>Nature</i> , 2006, 442, 96-99.	13.7	851
100	PtdIns(5)P activates the host cell PI3-kinase/Akt pathway during <i>Shigella flexneri</i> infection. <i>EMBO Journal</i> , 2006, 25, 1024-1034.	3.5	208
101	The Yng1p Plant Homeodomain Finger Is a Methyl-Histone Binding Module That Recognizes Lysine 4-Methylated Histone H3. <i>Molecular and Cellular Biology</i> , 2006, 26, 7871-7879.	1.1	142
102	Modification of protein sub-nuclear localization by synthetic phosphoinositides: Evidence for nuclear phosphoinositide signaling mechanisms. <i>Advances in Enzyme Regulation</i> , 2005, 45, 171-185.	2.9	12
103	The fellowships of the ING2s. <i>Journal of Cellular Biochemistry</i> , 2005, 96, 1127-1136.	1.2	40
104	A PHD Finger Motif in the C Terminus of RAG2 Modulates Recombination Activity. <i>Journal of Biological Chemistry</i> , 2005, 280, 28701-28710.	1.6	58
105	The PHD Finger of the Chromatin-Associated Protein ING2 Functions as a Nuclear Phosphoinositide Receptor. <i>Cell</i> , 2003, 114, 99-111.	13.5	467
106	The Peutz-Jegher Gene Product LKB1 Is a Mediator of p53-Dependent Cell Death. <i>Molecular Cell</i> , 2001, 7, 1307-1319.	4.5	293
107	Characterization of a Protein Complex Containing Spliceosomal Proteins SAPs 49, 130, 145, and 155. <i>Molecular and Cellular Biology</i> , 1999, 19, 6796-6802.	1.1	128
108	Phosphorylation of spliceosomal protein SAP 155 coupled with splicing catalysis. <i>Genes and Development</i> , 1998, 12, 1409-1414.	2.7	164

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109	A Potential Role for U2AF-SAP 155 Interactions in Recruiting U2 snRNP to the Branch Site. <i>Molecular and Cellular Biology</i> , 1998, 18, 4752-4760.	1.1	247
110	Cyclin E Associates with Components of the Pre-mRNA Splicing Machinery in Mammalian Cells. <i>Molecular and Cellular Biology</i> , 1998, 18, 4526-4536.	1.1	91
111	Identification of Proteins That Interact with Exon Sequences, Splice Sites, and the Branchpoint Sequence during Each Stage of Spliceosome Assembly. <i>Molecular and Cellular Biology</i> , 1996, 16, 3317-3326.	1.1	107
112	Evidence that sequence-independent binding of highly conserved U2 snRNP proteins upstream of the branch site is required for assembly of spliceosomal complex A.. <i>Genes and Development</i> , 1996, 10, 233-243.	2.7	210