

Albert Jeltsch

List of Publications by Year in descending order

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Version: 2024-02-01

280
papers

19,010
citations

13827

67
h-index

15683

125
g-index

298
all docs

298
docs citations

298
times ranked

16946
citing authors

#	ARTICLE	IF	CITATIONS
1	Flanking sequences influence the activity of TET1 and TET2 methylcytosine dioxygenases and affect genomic 5hmC patterns. <i>Communications Biology</i> , 2022, 5, 92.	2.0	15
2	Preferential Self-interaction of DNA Methyltransferase DNMT3A Subunits Containing the R882H Cancer Mutation Leads to Dominant Changes of Flanking Sequence Preferences. <i>Journal of Molecular Biology</i> , 2022, 434, 167482.	2.0	4
3	Special Issue "Structure, Activity, and Function of Protein Methyltransferases". <i>Life</i> , 2022, 12, 405.	1.1	0
4	Methylation of recombinant mononucleosomes by DNMT3A demonstrates efficient linker DNA methylation and a role of H3K36me3. <i>Communications Biology</i> , 2022, 5, 192.	2.0	9
5	The H3.3 G34W oncohistone mutation increases K36 methylation by the protein lysine methyltransferase NSD1. <i>Biochimie</i> , 2022, 198, 86-91.	1.3	3
6	Identification of Chemical Probes Targeting MBD2. <i>ACS Chemical Biology</i> , 2022, 17, 1415-1426.	1.6	1
7	Specificity Analysis of Protein Methyltransferases and Discovery of Novel Substrates Using SPOT Peptide Arrays. <i>Methods in Molecular Biology</i> , 2022, , 313-325.	0.4	7
8	Model-Based Design of a Synthetic Oscillator Based on an Epigenetic Methylation Memory System. <i>ACS Synthetic Biology</i> , 2022, 11, 2445-2455.	1.9	2
9	Genome-wide investigation of the dynamic changes of epigenome modifications after global DNA methylation editing. <i>Nucleic Acids Research</i> , 2021, 49, 158-176.	6.5	20
10	The methyltransferase METTL9 mediates pervasive 1-methylhistidine modification in mammalian proteomes. <i>Nature Communications</i> , 2021, 12, 891.	5.8	54
11	A functional LSD1 coregulator screen reveals a novel transcriptional regulatory cascade connecting R-loop homeostasis with epigenetic regulation. <i>Nucleic Acids Research</i> , 2021, 49, 4350-4370.	6.5	13
12	Model-based robustness and bistability analysis for methylation-based, epigenetic memory systems. <i>FEBS Journal</i> , 2021, 288, 5692-5707.	2.2	4
13	A loss-of-function variant in SUV39H2 identified in autism-spectrum disorder causes altered H3K9 trimethylation and dysregulation of protocadherin β -cluster genes in the developing brain. <i>Molecular Psychiatry</i> , 2021, 26, 7550-7559.	4.1	11
14	Structure, Activity and Function of the Suv39h1 and Suv39h2 Protein Lysine Methyltransferases. <i>Life</i> , 2021, 11, 703.	1.1	17
15	Structural and biochemical insight into the mechanism of dual CpG site binding and methylation by the DNMT3A DNA methyltransferase. <i>Nucleic Acids Research</i> , 2021, 49, 8294-8308.	6.5	9
16	Deep Enzymology Studies on DNA Methyltransferases Reveal Novel Connections between Flanking Sequences and Enzyme Activity. <i>Journal of Molecular Biology</i> , 2021, 433, 167186.	2.0	18
17	Biotechnological Applications of MBD Domain Proteins for DNA Methylation Analysis. <i>Journal of Molecular Biology</i> , 2020, 432, 1816-1823.	2.0	19
18	Analysis of the Substrate Specificity of the SMYD2 Protein Lysine Methyltransferase and Discovery of Novel Non-Histone Substrates. <i>ChemBioChem</i> , 2020, 21, 256-264.	1.3	14

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19	Mechanistic Insights into the Allosteric Regulation of the Clr4 Protein Lysine Methyltransferase by Autoinhibition and Automethylation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8832.	1.8	5
20	DNA sequence-dependent activity and base flipping mechanisms of DNMT1 regulate genome-wide DNA methylation. <i>Nature Communications</i> , 2020, 11, 3723.	5.8	48
21	Complex DNA sequence readout mechanisms of the DNMT3B DNA methyltransferase. <i>Nucleic Acids Research</i> , 2020, 48, 11495-11509.	6.5	16
22	Globally altered epigenetic landscape and delayed osteogenic differentiation in H3.3-G34W-mutant giant cell tumor of bone. <i>Nature Communications</i> , 2020, 11, 5414.	5.8	31
23	Sequence specificity analysis of the SETD2 protein lysine methyltransferase and discovery of a SETD2 super-substrate. <i>Communications Biology</i> , 2020, 3, 511.	2.0	13
24	Development of an epigenetic tetracycline sensor system based on DNA methylation. <i>PLoS ONE</i> , 2020, 15, e0232701.	1.1	8
25	Recognition of nonproline N-terminal residues by the Pro/N-degron pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14158-14167.	3.3	36
26	Comprehensive structure-function characterization of DNMT3B and DNMT3A reveals distinctive de novo DNA methylation mechanisms. <i>Nature Communications</i> , 2020, 11, 3355.	5.8	94
27	Engineering of Effector Domains for Targeted DNA Methylation with Reduced Off-Target Effects. <i>International Journal of Molecular Sciences</i> , 2020, 21, 502.	1.8	34
28	TRAIL receptor signaling: From the basics of canonical signal transduction toward its entanglement with ER stress and the unfolded protein response. <i>International Review of Cell and Molecular Biology</i> , 2020, 351, 57-99.	1.6	22
29	Development of an epigenetic tetracycline sensor system based on DNA methylation. , 2020, 15, e0232701.		0
30	Development of an epigenetic tetracycline sensor system based on DNA methylation. , 2020, 15, e0232701.		0
31	Development of an epigenetic tetracycline sensor system based on DNA methylation. , 2020, 15, e0232701.		0
32	Development of an epigenetic tetracycline sensor system based on DNA methylation. , 2020, 15, e0232701.		0
33	Editorialâ€”Role of DNA Methyltransferases in the Epigenome. <i>Genes</i> , 2019, 10, 574.	1.0	8
34	Somatic Cancer Mutations in the SUV420H1 Protein Lysine Methyltransferase Modulate Its Catalytic Activity. <i>Journal of Molecular Biology</i> , 2019, 431, 3068-3080.	2.0	18
35	Mutations of R882 change flanking sequence preferences of the DNA methyltransferase DNMT3A and cellular methylation patterns. <i>Nucleic Acids Research</i> , 2019, 47, 11355-11367.	6.5	49
36	H3K36me2/3 Binding and DNA Binding of the DNA Methyltransferase DNMT3A PWWP Domain Both Contribute to its Chromatin Interaction. <i>Journal of Molecular Biology</i> , 2019, 431, 5063-5074.	2.0	47

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37	Mechanistic Insights into Cytosine-N3 Methylation by DNA Methyltransferase DNMT3A. <i>Journal of Molecular Biology</i> , 2019, 431, 3139-3145.	2.0	17
38	Novel Insights into Peptide Binding and Conformational Dynamics of UHRF1. <i>Structure</i> , 2019, 27, 408-410.	1.6	3
39	Cyclin D1 integrates G9a-mediated histone methylation. <i>Oncogene</i> , 2019, 38, 4232-4249.	2.6	20
40	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	15
41	Application of modified histone peptide arrays in chromatin research. <i>Archives of Biochemistry and Biophysics</i> , 2019, 661, 31-38.	1.4	14
42	Editing the Epigenome: Overview, Open Questions, and Directions of Future Development. <i>Methods in Molecular Biology</i> , 2018, 1767, 3-18.	0.4	19
43	Hijacking DNA methyltransferase transition state analogues to produce chemical scaffolds for PRMT inhibitors. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170072.	1.8	24
44	The DNMT3A R882H mutant displays altered flanking sequence preferences. <i>Nucleic Acids Research</i> , 2018, 46, 3130-3139.	6.5	44
45	Evolutionary analysis indicates that DNA alkylation damage is a byproduct of cytosine DNA methyltransferase activity. <i>Nature Genetics</i> , 2018, 50, 452-459.	9.4	71
46	PWWP-DOMAIN INTERACTOR OF POLYCOMBS1 Interacts with Polycomb-Group Proteins and Histones and Regulates Arabidopsis Flowering and Development. <i>Plant Cell</i> , 2018, 30, 117-133.	3.1	48
47	DNA Methylation Analysis by Bisulfite Conversion Coupled to Double Multiplexed Amplicon-Based Next-Generation Sequencing (NGS). <i>Methods in Molecular Biology</i> , 2018, 1767, 367-382.	0.4	15
48	Allele-Specific Epigenome Editing. <i>Methods in Molecular Biology</i> , 2018, 1767, 137-146.	0.4	3
49	Application of mixed peptide arrays to study combinatorial readout of chromatin modifications. <i>Biochimie</i> , 2018, 146, 14-19.	1.3	6
50	Molecular Processes Connecting DNA Methylation Patterns with DNA Methyltransferases and Histone Modifications in Mammalian Genomes. <i>Genes</i> , 2018, 9, 566.	1.0	55
51	The DNMT3A R882H mutation does not cause dominant negative effects in purified mixed DNMT3A/R882H complexes. <i>Scientific Reports</i> , 2018, 8, 13242.	1.6	26
52	Design and Application of 6mA-Specific Zinc-Finger Proteins for the Readout of DNA Methylation. <i>Methods in Molecular Biology</i> , 2018, 1867, 29-41.	0.4	7
53	Mammalian DNA methyltransferases: new discoveries and open questions. <i>Biochemical Society Transactions</i> , 2018, 46, 1191-1202.	1.6	122
54	From Bioengineering to CRISPR/Cas9 – A Personal Retrospective of 20 Years of Research in Programmable Genome Targeting. <i>Frontiers in Genetics</i> , 2018, 9, 5.	1.1	2

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55	Identification of protein lysine methylation readers with a yeast three-hybrid approach. <i>Epigenetics and Chromatin</i> , 2018, 11, 4.	1.8	1
56	The <i>Legionella pneumophila</i> Methyltransferase RomA Methylates Also Non-histone Proteins during Infection. <i>Journal of Molecular Biology</i> , 2018, 430, 1912-1925.	2.0	13
57	Chromatin-dependent allosteric regulation of DNMT3A activity by MeCP2. <i>Nucleic Acids Research</i> , 2018, 46, 9044-9056.	6.5	34
58	The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates. <i>Nature Communications</i> , 2018, 9, 3411.	5.8	81
59	Mechanism and biological role of Dnmt2 in Nucleic Acid Methylation. <i>RNA Biology</i> , 2017, 14, 1108-1123.	1.5	156
60	Clr4 specificity and catalytic activity beyond H3K9 methylation. <i>Biochimie</i> , 2017, 135, 83-88.	1.3	9
61	The SUV39H1 Protein Lysine Methyltransferase Methylates Chromatin Proteins Involved in Heterochromatin Formation and VDJ Recombination. <i>ACS Chemical Biology</i> , 2017, 12, 958-968.	1.6	26
62	Somatic cancer mutations in the <scp>MLL</scp>1 histone methyltransferase modulate its enzymatic activity and dependence on the <scp>WDR</scp>5/<scp>RBBP</scp>5/<scp>ASH</scp>2L complex. <i>Molecular Oncology</i> , 2017, 11, 373-387.	2.1	16
63	Cocaine-Induced Chromatin Modifications Associate With Increased Expression and Three-Dimensional Looping of <i>Auts2</i> . <i>Biological Psychiatry</i> , 2017, 82, 794-805.	0.7	47
64	Epigenome Editing in the Brain. <i>Advances in Experimental Medicine and Biology</i> , 2017, 978, 409-424.	0.8	7
65	159. The Largest Number of Cocaine-Induced Changes in Chromatin Modifications Are Associated with Increased Expression and 3D Looping of <i>Auts2</i> . <i>Biological Psychiatry</i> , 2017, 81, S66.	0.7	0
66	Design of synthetic epigenetic circuits featuring memory effects and reversible switching based on DNA methylation. <i>Nature Communications</i> , 2017, 8, 15336.	5.8	34
67	Nucleosome stability measured in situ by automated quantitative imaging. <i>Scientific Reports</i> , 2017, 7, 12734.	1.6	15
68	Kinetic Analysis of the Inhibition of the NSD1, NSD2 and SETD2 Protein Lysine Methyltransferases by a K36M Oncohistone Peptide. <i>ChemistrySelect</i> , 2017, 2, 9532-9536.	0.7	7
69	Discovery of Novel and Selective DNA Methyltransferase 1 Inhibitors by Pharmacophore and Docking-Based Virtual Screening. <i>ChemistrySelect</i> , 2017, 2, 8383-8392.	0.7	6
70	Modular fluorescence complementation sensors for live cell detection of epigenetic signals at endogenous genomic sites. <i>Nature Communications</i> , 2017, 8, 649.	5.8	58
71	Methylation of DNA Ligase 1 by G9a/GLP Recruits UHRF1 to Replicating DNA and Regulates DNA Methylation. <i>Molecular Cell</i> , 2017, 67, 550-565.e5.	4.5	151
72	H3K14ac is linked to methylation of H3K9 by the triple Tudor domain of SETDB1. <i>Nature Communications</i> , 2017, 8, 2057.	5.8	72

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73	The RNA methyltransferase Dnmt2 methylates DNA in the structural context of a tRNA. <i>RNA Biology</i> , 2017, 14, 1241-1251.	1.5	51
74	Efficient targeted DNA methylation with chimeric dCas9-Dnmt3a-Dnmt3L methyltransferase. <i>Nucleic Acids Research</i> , 2017, 45, 1703-1713.	6.5	224
75	Application of dual reading domains as novel reagents in chromatin biology reveals a new H3K9me3 and H3K36me2/3 bivalent chromatin state. <i>Epigenetics and Chromatin</i> , 2017, 10, 45.	1.8	27
76	Mutations in Histone Lysine Methyltransferases and Demethylases. , 2017, , .		1
77	Correction of aberrant imprinting by allele-specific epigenome editing. <i>Clinical Pharmacology and Therapeutics</i> , 2016, 99, 482-484.	2.3	13
78	Approaches and Guidelines for the Identification of Novel Substrates of Protein Lysine Methyltransferases. <i>Cell Chemical Biology</i> , 2016, 23, 1049-1055.	2.5	19
79	Allosteric control of mammalian DNA methyltransferases - a new regulatory paradigm. <i>Nucleic Acids Research</i> , 2016, 44, 8556-8575.	6.5	156
80	Mechanisms and Biological Roles of DNA Methyltransferases and DNA Methylation: From Past Achievements to Future Challenges. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 1-17.	0.8	32
81	Enzymology of Mammalian DNA Methyltransferases. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 87-122.	0.8	49
82	Specificity of the SUV420H1 and SUV420H2 protein lysine methyltransferases and methylation of novel substrates. <i>Journal of Molecular Biology</i> , 2016, 428, 2344-2358.	2.0	29
83	Conserved motif VIII of murine DNA methyltransferase Dnmt3a is essential for methylation activity. <i>BMC Biochemistry</i> , 2016, 17, 7.	4.4	7
84	Application of recombinant TAF3 PHD domain instead of anti-H3K4me3 antibody. <i>Epigenetics and Chromatin</i> , 2016, 9, 11.	1.8	18
85	Investigation of H2AX methylation by the SUV39H2 protein lysine methyltransferase. <i>FEBS Letters</i> , 2016, 590, 1713-1719.	1.3	8
86	Substrate Specificity of the HEMK2 Protein Glutamine Methyltransferase and Identification of Novel Substrates. <i>Journal of Biological Chemistry</i> , 2016, 291, 6124-6133.	1.6	35
87	Level of tissue differentiation influences the activation of a heat-inducible flower-specific system for genetic containment in poplar (<i>Populus tremula</i> L.). <i>Plant Cell Reports</i> , 2016, 35, 369-384.	2.8	5
88	Epigenome Editing: State of the Art, Concepts, and Perspectives. <i>Trends in Genetics</i> , 2016, 32, 101-113.	2.9	157
89	Investigation of the methylation of Numb by the SET8 protein lysine methyltransferase. <i>Scientific Reports</i> , 2015, 5, 13813.	1.6	6
90	Cytosine methylation of tRNA-Asp by DNMT2 has a role in translation of proteins containing poly-Asp sequences. <i>Cell Discovery</i> , 2015, 1, 15010.	3.1	63

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91	Editorial: Alfred Pingoud (1945–2015). <i>Nucleic Acids Research</i> , 2015, 43, 7661-7663.	6.5	0
92	Targeted epigenome editing of an endogenous locus with chromatin modifiers is not stably maintained. <i>Epigenetics and Chromatin</i> , 2015, 8, 12.	1.8	77
93	Identification, cloning and heterologous expression of active [NiFe]-hydrogenase 2 from <i>Citrobacter</i> sp. SG in <i>Escherichia coli</i> . <i>Journal of Biotechnology</i> , 2015, 199, 1-8.	1.9	5
94	DNMT1-associated DNA methylation changes in cancer. <i>Cell Cycle</i> , 2015, 14, 5-5.	1.3	12
95	Somatic cancer mutations in the DNMT2 tRNA methyltransferase alter its catalytic properties. <i>Biochimie</i> , 2015, 112, 66-72.	1.3	41
96	Somatic cancer mutations in the MLL3-SET domain alter the catalytic properties of the enzyme. <i>Clinical Epigenetics</i> , 2015, 7, 36.	1.8	36
97	An ATPase-Deficient Variant of the SNF2 Family Member HELLS Shows Altered Dynamics at Pericentromeric Heterochromatin. <i>Journal of Molecular Biology</i> , 2015, 427, 1903-1915.	2.0	14
98	Investigation of the C-terminal domain of the bacterial DNA-(adenine N6)-methyltransferase CcrM. <i>Biochimie</i> , 2015, 119, 60-67.	1.3	5
99	COMT gene polymorphisms, cognitive performance, and physical fitness in older adults. <i>Psychology of Sport and Exercise</i> , 2015, 20, 20-28.	1.1	12
100	Affinity reagents for studying histone modifications & guidelines for their quality control. <i>Epigenomics</i> , 2015, 7, 1185-1196.	1.0	12
101	Activity and specificity of the human SUV39H2 protein lysine methyltransferase. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 55-63.	0.9	45
102	Specificity Analysis of Histone Modification-Specific Antibodies or Reading Domains on Histone Peptide Arrays. <i>Methods in Molecular Biology</i> , 2015, 1348, 275-284.	0.4	7
103	Quality of histone modification antibodies undermines chromatin biology research. <i>F1000Research</i> , 2015, 4, 1160.	0.8	7
104	Quality of histone modification antibodies undermines chromatin biology research. <i>F1000Research</i> , 2015, 4, 1160.	0.8	5
105	The Role of Electrostatic Interactions in Binding of Histone H3K4me2/3 to the Sgf29 Tandem Tudor Domain. <i>PLoS ONE</i> , 2015, 10, e0139205.	1.1	5
106	The Inhibition of the Mammalian DNA Methyltransferase 3a (Dnmt3a) by Dietary Black Tea and Coffee Polyphenols. , 2015, , 213-231.		0
107	The Dnmt2 RNA methyltransferase homolog of <i>Geobacter sulfurreducens</i> specifically methylates tRNA-Glu. <i>Nucleic Acids Research</i> , 2014, 42, 6487-6496.	6.5	27
108	Non-radioactive Protein Lysine Methyltransferase Microplate Assay Based on Reading Domains. <i>ChemMedChem</i> , 2014, 9, 554-559.	1.6	7

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109	Application of histone modification-specific interaction domains as an alternative to antibodies. <i>Genome Research</i> , 2014, 24, 1842-1853.	2.4	52
110	Specificity Analysis of Protein Lysine Methyltransferases Using SPOT Peptide Arrays. <i>Journal of Visualized Experiments</i> , 2014, , e52203.	0.2	25
111	The Tudor Domain of the PHD Finger Protein 1 Is a Dual Reader of Lysine Trimethylation at Lysine 36 of Histone H3 and Lysine 27 of Histone Variant H3t. <i>Journal of Molecular Biology</i> , 2014, 426, 1651-1660.	2.0	24
112	Substrate Specificity Analysis and Novel Substrates of the Protein Lysine Methyltransferase NSD1. <i>Chemistry and Biology</i> , 2014, 21, 226-237.	6.2	52
113	Design, Synthesis and Biological Evaluation of 4- <i>N</i> -(4-aminophenyl)benzamide Analogues of Quinoline-Based SGI-1027 as Inhibitors of DNA Methylation. <i>ChemMedChem</i> , 2014, 9, 590-601.	1.6	49
114	Label-free measurement of histone lysine methyltransferases activity by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Analytical Biochemistry</i> , 2014, 456, 25-31.	1.1	22
115	Synthesis and Evaluation of Analogues of <i>N</i> -Phthaloyl-tryptophan (RG108) as Inhibitors of DNA Methyltransferase 1. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 421-434.	2.9	80
116	Cooperative DNA Binding and Protein/DNA Fiber Formation Increases the Activity of the Dnmt3a DNA Methyltransferase. <i>Journal of Biological Chemistry</i> , 2014, 289, 29602-29613.	1.6	44
117	Targeted Mutagenesis Results in an Activation of DNA Methyltransferase 1 and Confirms an Autoinhibitory Role of its RFTS Domain. <i>ChemBioChem</i> , 2014, 15, 743-748.	1.3	31
118	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. <i>Cell Reports</i> , 2014, 8, 743-753.	2.9	66
119	New concepts in DNA methylation. <i>Trends in Biochemical Sciences</i> , 2014, 39, 310-318.	3.7	361
120	Role of somatic cancer mutations in human protein lysine methyltransferases. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2014, 1846, 366-379.	3.3	34
121	The UHRF1 Protein Stimulates the Activity and Specificity of the Maintenance DNA Methyltransferase DNMT1 by an Allosteric Mechanism. <i>Journal of Biological Chemistry</i> , 2014, 289, 4106-4115.	1.6	107
122	Targeted Methylation of the Epithelial Cell Adhesion Molecule (EpCAM) Promoter to Silence Its Expression in Ovarian Cancer Cells. <i>PLoS ONE</i> , 2014, 9, e87703.	1.1	60
123	Genomic Imprinting—The Struggle of the Genders at the Molecular Level. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 13524-13536.	7.2	8
124	Targeted Methylation and Gene Silencing of VEGF-A in Human Cells by Using a Designed Dnmt3a-Dnmt3L Single-Chain Fusion Protein with Increased DNA Methylation Activity. <i>Journal of Molecular Biology</i> , 2013, 425, 479-491.	2.0	138
125	Identification of Novel Inhibitors of DNA Methylation by Screening of a Chemical Library. <i>ACS Chemical Biology</i> , 2013, 8, 543-548.	1.6	51
126	Oxygen, epigenetic signaling, and the evolution of early life. <i>Trends in Biochemical Sciences</i> , 2013, 38, 172-176.	3.7	29

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127	Multimerization of the Dnmt3a DNA Methyltransferase and Its Functional Implications. <i>Progress in Molecular Biology and Translational Science</i> , 2013, 117, 445-464.	0.9	16
128	Target recognition, RNA methylation activity and transcriptional regulation of the Dictyostelium discoideum Dnmt2-homologue (DnmA). <i>Nucleic Acids Research</i> , 2013, 41, 8615-8627.	6.5	56
129	The <i>Caulobacter crescentus</i> DNA-(adenine-N6)-methyltransferase CcrM methylates DNA in a distributive manner. <i>Nucleic Acids Research</i> , 2012, 40, 1708-1716.	6.5	22
130	Function and disruption of DNA Methyltransferase 3a cooperative DNA binding and nucleoprotein filament formation. <i>Nucleic Acids Research</i> , 2012, 40, 569-580.	6.5	124
131	Pmt1, a Dnmt2 homolog in <i>Schizosaccharomyces pombe</i> , mediates tRNA methylation in response to nutrient signaling. <i>Nucleic Acids Research</i> , 2012, 40, 11648-11658.	6.5	70
132	DNA methyltransferase inhibitors in cancer: a chemical and therapeutic patent overview and selected clinical studies. <i>Expert Opinion on Therapeutic Patents</i> , 2012, 22, 1427-1442.	2.4	90
133	Mapping the tRNA Binding Site on the Surface of Human DNMT2 Methyltransferase. <i>Biochemistry</i> , 2012, 51, 4438-4444.	1.2	17
134	The SET8 H4K20 protein lysine methyltransferase has a long recognition sequence covering seven amino acid residues. <i>Biochimie</i> , 2012, 94, 2212-2218.	1.3	35
135	DNA Interaction of the CcrM DNA Methyltransferase: A Mutational and Modeling Study. <i>ChemBioChem</i> , 2012, 13, 1304-1311.	1.3	9
136	A Fluorescence-Based Supramolecular Tandem Assay for Monitoring Lysine Methyltransferase Activity in Homogeneous Solution. <i>Chemistry - A European Journal</i> , 2012, 18, 3521-3528.	1.7	74
137	Specificity of Dnmt1 for Methylation of Hemimethylated CpG Sites Resides in Its Catalytic Domain. <i>Chemistry and Biology</i> , 2012, 19, 572-578.	6.2	73
138	Mechanistic details of the DNA recognition by the Dnmt1 DNA methyltransferase. <i>FEBS Letters</i> , 2012, 586, 1821-1823.	1.3	24
139	Using the fluorescence decay of 2-aminopurine to investigate conformational change in the recognition sequence of the EcoRV DNA-(adenine-N6)-methyltransferase on enzyme binding. <i>Biophysical Chemistry</i> , 2012, 160, 28-34.	1.5	11
140	Identification of ICAD-derived peptides capable of inhibiting caspase-activated DNase. <i>FEBS Journal</i> , 2012, 279, 2917-2928.	2.2	4
141	Rapid Synthesis of New DNMT Inhibitors Derivatives of Procainamide. <i>ChemBioChem</i> , 2012, 13, 157-165.	1.3	51
142	Oligomerization and Binding of the Dnmt3a DNA Methyltransferase to Parallel DNA Molecules. <i>Journal of Biological Chemistry</i> , 2011, 286, 24200-24207.	1.6	89
143	Auto-methylation of the mouse DNA-(cytosine C5)-methyltransferase Dnmt3a at its active site cysteine residue. <i>FEBS Journal</i> , 2011, 278, 2055-2063.	2.2	16
144	The inhibition of the mammalian DNA methyltransferase 3a (Dnmt3a) by dietary black tea and coffee polyphenols. <i>BMC Biochemistry</i> , 2011, 12, 16.	4.4	56

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145	Application of Cellspots peptide arrays for the analysis of the binding specificity of epigenetic reading domains to modified histone tails. <i>BMC Biochemistry</i> , 2011, 12, 48.	4.4	72
146	Structure and Function of Mammalian DNA Methyltransferases. <i>ChemBioChem</i> , 2011, 12, 206-222.	1.3	561
147	Approaches to Enzyme and Substrate Design of the Murine Dnmt3a DNA Methyltransferase. <i>ChemBioChem</i> , 2011, 12, 1589-1594.	1.3	29
148	Editorial: Molecular Epigenetics: Connecting Human Biology and Disease with Little Marks. <i>ChemBioChem</i> , 2011, 12, 183-184.	1.3	2
149	C5â€DNA Methyltransferase Inhibitors: From Screening to Effects on Zebrafish Embryo Development. <i>ChemBioChem</i> , 2011, 12, 1337-1345.	1.3	69
150	Burning off DNA Methylation: New Evidence for Oxygenâ€Dependent DNA Demethylation. <i>ChemBioChem</i> , 2011, 12, 2543-2545.	1.3	18
151	Specificity Analysis-Based Identification of New Methylation Targets of the SET7/9 Protein Lysine Methyltransferase. <i>Chemistry and Biology</i> , 2011, 18, 111-120.	6.2	149
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