

Dirk SchÃ¼beler

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

21,201
citations

18436

62
h-index

37111

96
g-index

102
all docs

102
docs citations

102
times ranked

27975
citing authors

#	ARTICLE	IF	CITATIONS
1	monaLisa: an R/Bioconductor package for identifying regulatory motifs. <i>Bioinformatics</i> , 2022, 38, 2624-2625.	1.8	33
2	Generating specificity in genome regulation through transcription factor sensitivity to chromatin. <i>Nature Reviews Genetics</i> , 2022, 23, 728-740.	7.7	43
3	Molecular Co-occupancy Identifies Transcription Factor Binding Cooperativity In Vivo. <i>Molecular Cell</i> , 2021, 81, 255-267.e6.	4.5	79
4	Mammalian SWI/SNF continuously restores local accessibility to chromatin. <i>Nature Genetics</i> , 2021, 53, 279-287.	9.4	106
5	Systematic dissection of transcriptional regulatory networks by genome-scale and single-cell CRISPR screens. <i>Science Advances</i> , 2021, 7, .	4.7	19
6	BANP opens chromatin and activates CpG-island-regulated genes. <i>Nature</i> , 2021, 596, 133-137.	13.7	49
7	A genome-scale map of DNA methylation turnover identifies site-specific dependencies of DNMT and TET activity. <i>Nature Communications</i> , 2020, 11, 2680.	5.8	97
8	Mechanisms of OCT4-SOX2 motif readout on nucleosomes. <i>Science</i> , 2020, 368, 1460-1465.	6.0	160
9	Targeting neuronal and glial cell types with synthetic promoter AAVs in mice, non-human primates and humans. <i>Nature Neuroscience</i> , 2019, 22, 1345-1356.	7.1	144
10	CG dinucleotides enhance promoter activity independent of DNA methylation. <i>Genome Research</i> , 2019, 29, 554-563.	2.4	49
11	DNA damage detection in nucleosomes involves DNA register shifting. <i>Nature</i> , 2019, 571, 79-84.	13.7	72
12	Mammalian ISWI and SWI/SNF selectively mediate binding of distinct transcription factors. <i>Nature</i> , 2019, 569, 136-140.	13.7	169
13	Non-mendelian Inheritance in Mammals Is Highly Constrained. <i>Cell</i> , 2018, 175, 1179-1181.	13.5	1
14	Cell cycle-resolved chromatin proteomics reveals the extent of mitotic preservation of the genomic regulatory landscape. <i>Nature Communications</i> , 2018, 9, 4048.	5.8	73
15	Genome-wide Single-Molecule Footprinting Reveals High RNA Polymerase II Turnover at Paused Promoters. <i>Molecular Cell</i> , 2017, 67, 411-422.e4.	4.5	168
16	Evidence for Converging DNA Methylation Pathways in Placenta and Cancer. <i>Developmental Cell</i> , 2017, 43, 257-258.	3.1	26
17	Cis-regulatory landscapes of four cell types of the retina. <i>Nucleic Acids Research</i> , 2017, 45, 11607-11621.	6.5	39
18	Multidimensional pooled shRNA screens in human THP-1 cells identify candidate modulators of macrophage polarization. <i>PLoS ONE</i> , 2017, 12, e0183679.	1.1	52

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19	Binding of high mobility group A proteins to the mammalian genome occurs as a function of AT-content. <i>PLoS Genetics</i> , 2017, 13, e1007102.	1.5	16
20	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
21	Pioneering Activity of the C-Terminal Domain of EBF1 Shapes the Chromatin Landscape for B Cell Programming. <i>Immunity</i> , 2016, 44, 527-541.	6.6	102
22	YAP1 Exerts Its Transcriptional Control via TEAD-Mediated Activation of Enhancers. <i>PLoS Genetics</i> , 2015, 11, e1005465.	1.5	296
23	Competition between DNA methylation and transcription factors determines binding of NRF1. <i>Nature</i> , 2015, 528, 575-579.	13.7	401
24	Function and information content of DNA methylation. <i>Nature</i> , 2015, 517, 321-326.	13.7	1,656
25	Genomic profiling of DNA methyltransferases reveals a role for DNMT3B in genic methylation. <i>Nature</i> , 2015, 520, 243-247.	13.7	566
26	ESCI award lecture: regulation, function and biomarker potential of DNA methylation. <i>European Journal of Clinical Investigation</i> , 2015, 45, 288-293.	1.7	12
27	Ageing-Dependent Demethylation of Regulatory Elements Correlates with Chromatin State and Improved β^2 Cell Function. <i>Cell Metabolism</i> , 2015, 22, 619-632.	7.2	172
28	High-throughput engineering of a mammalian genome reveals building principles of methylation states at CG rich regions. <i>ELife</i> , 2014, 3, e04094.	2.8	66
29	Short sequences can efficiently recruit histone H3 lysine 27 trimethylation in the absence of enhancer activity and DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3415-21.	3.3	121
30	DNA Sequence Explains Seemingly Disordered Methylation Levels in Partially Methylated Domains of Mammalian Genomes. <i>PLoS Genetics</i> , 2014, 10, e1004143.	1.5	64
31	Dynamic DNA methylation orchestrates cardiomyocyte development, maturation and disease. <i>Nature Communications</i> , 2014, 5, 5288.	5.8	272
32	Genomic patterns and context specific interpretation of DNA methylation. <i>Current Opinion in Genetics and Development</i> , 2014, 25, 85-92.	1.5	135
33	DNA methylation is required for the control of stem cell differentiation in the small intestine. <i>Genes and Development</i> , 2014, 28, 652-664.	2.7	159
34	Twisting chromatin in stem cells. <i>EMBO Journal</i> , 2013, 32, 2304-2306.	3.5	1
35	Identification of active regulatory regions from DNA methylation data. <i>Nucleic Acids Research</i> , 2013, 41, e155-e155.	6.5	192
36	Methylation-Dependent and -Independent Genomic Targeting Principles of the MBD Protein Family. <i>Cell</i> , 2013, 153, 480-492.	13.5	312

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37	Molecular determinants of nucleosome retention at CpG-rich sequences in mouse spermatozoa. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 868-875.	3.6	298
38	Sox4 Is a Master Regulator of Epithelial-Mesenchymal Transition by Controlling Ezh2 Expression and Epigenetic Reprogramming. <i>Cancer Cell</i> , 2013, 23, 768-783.	7.7	415
39	Modeling of epigenome dynamics identifies transcription factors that mediate Polycomb targeting. <i>Genome Research</i> , 2013, 23, 60-73.	2.4	108
40	Identification of Dlk1-Dio3 Imprinted Gene Cluster Noncoding RNAs as Novel Candidate Biomarkers for Liver Tumor Promotion. <i>Toxicological Sciences</i> , 2013, 131, 375-386.	1.4	62
41	Transcription Factor Occupancy Can Mediate Active Turnover of DNA Methylation at Regulatory Regions. <i>PLoS Genetics</i> , 2013, 9, e1003994.	1.5	194
42	Protein Complex Interactor Analysis and Differential Activity of KDM3 Subfamily Members Towards H3K9 Methylation. <i>PLoS ONE</i> , 2013, 8, e60549.	1.1	58
43	Chromatin measurements reveal contributions of synthesis and decay to steady-state mRNA levels. <i>Molecular Systems Biology</i> , 2012, 8, 593.	3.2	48
44	Tracking the evolution of cancer methylomes. <i>Nature Genetics</i> , 2012, 44, 1173-1174.	9.4	6
45	Epigenetic Islands in a Genetic Ocean. <i>Science</i> , 2012, 338, 756-757.	6.0	45
46	A chromatin-modifying function of JNK during stem cell differentiation. <i>Nature Genetics</i> , 2012, 44, 94-100.	9.4	113
47	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	9.4	323
48	Target genes of Topoisomerase II ² regulate neuronal survival and are defined by their chromatin state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E934-43.	3.3	142
49	DNA-binding factors shape the mouse methylome at distal regulatory regions. <i>Nature</i> , 2011, 480, 490-495.	13.7	1,203
50	Identification of genetic elements that autonomously determine DNA methylation states. <i>Nature Genetics</i> , 2011, 43, 1091-1097.	9.4	351
51	Phenobarbital Mediates an Epigenetic Switch at the Constitutive Androstane Receptor (CAR) Target Gene <i>Cyp2b10</i> in the Liver of B6C3F1 Mice. <i>PLoS ONE</i> , 2011, 6, e18216.	1.1	75
52	Determinants and dynamics of genome accessibility. <i>Nature Reviews Genetics</i> , 2011, 12, 554-564.	7.7	403
53	Genomic Prevalence of Heterochromatic H3K9me2 and Transcription Do Not Discriminate Pluripotent from Terminally Differentiated Cells. <i>PLoS Genetics</i> , 2011, 7, e1002090.	1.5	119
54	Repressive and active histone methylation mark distinct promoters in human and mouse spermatozoa. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 679-687.	3.6	610

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55	Accessibility of the <i>Drosophila</i> genome discriminates PcG repression, H4K16 acetylation and replication timing. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 894-900.	3.6	100
56	Tackling the epigenome: challenges and opportunities for collaboration. <i>Nature Biotechnology</i> , 2010, 28, 1039-1044.	9.4	82
57	Targets and dynamics of promoter DNA methylation during early mouse development. <i>Nature Genetics</i> , 2010, 42, 1093-1100.	9.4	527
58	Heterochromatin protein 1 (HP1) modulates replication timing of the <i>Drosophila</i> genome. <i>Genome Research</i> , 2010, 20, 771-780.	2.4	77
59	Characterizing Light-Regulated Retinal MicroRNAs Reveals Rapid Turnover as a Common Property of Neuronal MicroRNAs. <i>Cell</i> , 2010, 141, 618-631.	13.5	431
60	Chromatin in Multicolor. <i>Cell</i> , 2010, 143, 183-184.	13.5	3
61	Relics of repeat-induced point mutation direct heterochromatin formation in <i>Neurospora crassa</i> . <i>Genome Research</i> , 2009, 19, 427-437.	2.4	137
62	Chromatin state marks cell-type- and gender-specific replication of the <i>Drosophila</i> genome. <i>Genes and Development</i> , 2009, 23, 589-601.	2.7	141
63	Genetics and epigenetics: stability and plasticity during cellular differentiation. <i>Trends in Genetics</i> , 2009, 25, 129-136.	2.9	271
64	Chromatin: Sub Out the Replacement. <i>Current Biology</i> , 2009, 19, R545-R547.	1.8	5
65	Methylation matters. <i>Nature</i> , 2009, 462, 296-297.	13.7	23
66	H3K64 trimethylation marks heterochromatin and is dynamically remodeled during developmental reprogramming. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 777-781.	3.6	125
67	Methylated DNA Immunoprecipitation (MeDIP). <i>Methods in Molecular Biology</i> , 2009, 507, 55-64.	0.4	203
68	New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. <i>Blood</i> , 2009, 113, 2488-2497.	0.6	133
69	DNA methylation in ES cells requires the lysine methyltransferase G9a but not its catalytic activity. <i>EMBO Journal</i> , 2008, 27, 2691-2701.	3.5	207
70	Lineage-Specific Polycomb Targets and De Novo DNA Methylation Define Restriction and Potential of Neuronal Progenitors. <i>Molecular Cell</i> , 2008, 30, 755-766.	4.5	802
71	Transcription-Coupled Methylation of Histone H3 at Lysine 36 Regulates Dosage Compensation by Enhancing Recruitment of the MSL Complex in <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Biology</i> , 2008, 28, 3401-3409.	1.1	64
72	Global Reorganization of Replication Domains During Embryonic Stem Cell Differentiation. <i>PLoS Biology</i> , 2008, 6, e245.	2.6	496

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73	RNA Polymerase II: Just Stopping By. <i>Cell</i> , 2007, 130, 16-18.	13.5	12
74	Enhancing genome annotation with chromatin. <i>Nature Genetics</i> , 2007, 39, 284-285.	9.4	9
75	Distribution, silencing potential and evolutionary impact of promoter DNA methylation in the human genome. <i>Nature Genetics</i> , 2007, 39, 457-466.	9.4	1,922
76	Localized H3K36 methylation states define histone H4K16 acetylation during transcriptional elongation in <i>Drosophila</i> . <i>EMBO Journal</i> , 2007, 26, 4974-4984.	3.5	153
77	Genomic patterns of DNA methylation: targets and function of an epigenetic mark. <i>Current Opinion in Cell Biology</i> , 2007, 19, 273-280.	2.6	338
78	Dosage compensation in high resolution: global up-regulation through local recruitment. <i>Genes and Development</i> , 2006, 20, 749-753.	2.7	8
79	A question of timing: emerging links between transcription and replication. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 177-183.	1.5	65
80	Chromosome-wide and promoter-specific analyses identify sites of differential DNA methylation in normal and transformed human cells. <i>Nature Genetics</i> , 2005, 37, 853-862.	9.4	1,591
81	Methylation of histones: playing memory with DNA. <i>Current Opinion in Cell Biology</i> , 2005, 17, 230-238.	2.6	110
82	Variant histone H3.3 is deposited at sites of nucleosomal displacement throughout transcribed genes while active histone modifications show a promoter-proximal bias. <i>Genes and Development</i> , 2005, 19, 1761-1766.	2.7	152
83	A New Map for Navigating the Yeast Epigenome. <i>Cell</i> , 2005, 122, 489-492.	13.5	9
84	DNA replication-timing analysis of human chromosome 22 at high resolution and different developmental states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 17771-17776.	3.3	121
85	The histone modification pattern of active genes revealed through genome-wide chromatin analysis of a higher eukaryote. <i>Genes and Development</i> , 2004, 18, 1263-1271.	2.7	706
86	A Complex Chromatin Landscape Revealed by Patterns of Nuclease Sensitivity and Histone Modification within the Mouse β -Globin Locus. <i>Molecular and Cellular Biology</i> , 2003, 23, 5234-5244.	1.1	143
87	DNA Methylation Density Influences the Stability of an Epigenetic Imprint and Dnmt3a/b-Independent De Novo Methylation. <i>Molecular and Cellular Biology</i> , 2002, 22, 7572-7580.	1.1	120
88	ChIPs of the β -globin locus: unraveling gene regulation within an active domain. <i>Current Opinion in Genetics and Development</i> , 2002, 12, 170-177.	1.5	84
89	Genome-wide DNA replication profile for <i>Drosophila melanogaster</i> : a link between transcription and replication timing. <i>Nature Genetics</i> , 2002, 32, 438-442.	9.4	310
90	Nuclear compartmentalization and gene activity. <i>Nature Reviews Molecular Cell Biology</i> , 2000, 1, 137-143.	16.1	276

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91	Stabilized, long-term expression of heterodimeric proteins from tricistronic mRNA. <i>Gene</i> , 2000, 254, 1-8.	1.0	44
92	Nuclear localization and histone acetylation: a pathway for chromatin opening and transcriptional activation of the human β -globin locus. <i>Genes and Development</i> , 2000, 14, 940-950.	2.7	261
93	A sensitive transcription assay based on a simplified nuclear runon protocol. <i>Technical Tips Online</i> , 1997, 2, 140-142.	0.2	5