

Arie B Brinkman

List of Publications by Year in descending order

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38
papers

7,089
citations

147801

31
h-index

302126

39
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41
all docs

41
docs citations

41
times ranked

13988
citing authors

#	ARTICLE	IF	CITATIONS
1	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
2	Dynamic Readers for 5-(Hydroxy)Methylcytosine and Its Oxidized Derivatives. <i>Cell</i> , 2013, 152, 1146-1159.	28.9	888
3	Quantitative comparison of genome-wide DNA methylation mapping technologies. <i>Nature Biotechnology</i> , 2010, 28, 1106-1114.	17.5	534
4	Whole-Genome Bisulfite Sequencing of Two Distinct Interconvertible DNA Methylomes of Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2013, 13, 360-369.	11.1	424
5	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , 2012, 22, 1128-1138.	5.5	344
6	MBD2/NuRD and MBD3/NuRD, Two Distinct Complexes with Different Biochemical and Functional Properties. <i>Molecular and Cellular Biology</i> , 2006, 26, 843-851.	2.3	290
7	PML-RAR $\hat{\pm}$ /RXR Alters the Epigenetic Landscape in Acute Promyelocytic Leukemia. <i>Cancer Cell</i> , 2010, 17, 173-185.	16.8	276
8	The Lrp family of transcriptional regulators. <i>Molecular Microbiology</i> , 2003, 48, 287-294.	2.5	252
9	Whole-genome DNA methylation profiling using MethylCap-seq. <i>Methods</i> , 2010, 52, 232-236.	3.8	243
10	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , 2016, 7, 11383.	12.8	235
11	Dynamic binding of RBPJ is determined by Notch signaling status. <i>Genes and Development</i> , 2013, 27, 1059-1071.	5.9	218
12	Crystal structure of the Lrp-like transcriptional regulator from the archaeon <i>Pyrococcus furiosus</i> . <i>EMBO Journal</i> , 2001, 20, 990-997.	7.8	135
13	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	12.8	119
14	Structural insight into gene transcriptional regulation and effector binding by the Lrp/AsnC family. <i>Nucleic Acids Research</i> , 2006, 34, 1439-1449.	14.5	106
15	The <i>Sulfolobus solfataricus</i> Lrp-like Protein LysM Regulates Lysine Biosynthesis in Response to Lysine Availability. <i>Journal of Biological Chemistry</i> , 2002, 277, 29537-29549.	3.4	98
16	Histone modification patterns associated with the human X chromosome. <i>EMBO Reports</i> , 2006, 7, 628-634.	4.5	94
17	Temporal uncoupling of the DNA methylome and transcriptional repression during embryogenesis. <i>Genome Research</i> , 2011, 21, 1313-1327.	5.5	92
18	Integrative Proteomic Profiling Reveals PRC2-Dependent Epigenetic Crosstalk Maintains Ground-State Pluripotency. <i>Cell Stem Cell</i> , 2019, 24, 123-137.e8.	11.1	90

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19	The archaeal TFIIE \pm homologue facilitates transcription initiation by enhancing TATA \hat{c} box recognition. <i>EMBO Reports</i> , 2001, 2, 133-138.	4.5	86
20	An Lrp-like Transcriptional Regulator from the Archaeon <i>Pyrococcus furiosus</i> Is Negatively Autoregulated. <i>Journal of Biological Chemistry</i> , 2000, 275, 38160-38169.	3.4	79
21	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , 2017, 49, 341-348.	21.4	75
22	A Novel Ligand-binding Domain Involved in Regulation of Amino Acid Metabolism in Prokaryotes. <i>Journal of Biological Chemistry</i> , 2002, 277, 37464-37468.	3.4	72
23	Comparative genome-wide DNA methylation analysis of colorectal tumor and matched normal tissues. <i>Epigenetics</i> , 2012, 7, 1355-1367.	2.7	67
24	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. <i>Cell Reports</i> , 2014, 8, 743-753.	6.4	66
25	Explaining the Bias in the 23S rRNA Gene Mutations Associated with Clarithromycin Resistance in Clinical Isolates of <i>Helicobacter pylori</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 1998, 42, 2749-2751.	3.2	57
26	CDK2AP1/DOC-1 is a bona fide subunit of the Mi-2/NuRD complex. <i>Molecular BioSystems</i> , 2010, 6, 1700.	2.9	54
27	Transcription of the Rod-Shaped Viruses SIRV1 and SIRV2 of the Hyperthermophilic Archaeon <i>Sulfolobus</i> . <i>Journal of Bacteriology</i> , 2004, 186, 7745-7753.	2.2	52
28	Molecular characterization of a conserved archaeal copper resistance (<i>cop</i>) gene cluster and its copper-responsive regulator in <i>Sulfolobus solfataricus</i> P2. <i>Microbiology (United Kingdom)</i> , 2006, 152, 1969-1979.	1.8	49
29	A SILAC-Based Screen for Methyl-CpG Binding Proteins Identifies RBP-J as a DNA Methylation and Sequence-Specific Binding Protein. <i>PLoS ONE</i> , 2011, 6, e25884.	2.5	49
30	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	12.8	46
31	Genome-Wide Binding of MBD2 Reveals Strong Preference for Highly Methylated Loci. <i>PLoS ONE</i> , 2014, 9, e99603.	2.5	44
32	Comprehensive evaluation of methods to assess overall and cell-specific immune infiltrates in breast cancer. <i>Breast Cancer Research</i> , 2019, 21, 151.	5.0	30
33	DNA methylation immediately adjacent to active histone marking does not silence transcription. <i>Nucleic Acids Research</i> , 2007, 35, 801-811.	14.5	24
34	Targeted discovery tools: proteomics and chromatin immunoprecipitation-on-chip. <i>BJU International</i> , 2005, 96, 16-22.	2.5	8
35	Terminal keratinocyte differentiation in vitro is associated with a stable DNA methylome. <i>Experimental Dermatology</i> , 2021, 30, 1023-1032.	2.9	8
36	Crystallization and quaternary structure analysis of an Lrp-like regulatory protein from the hyperthermophile <i>Pyrococcus furiosus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 886-888.	2.5	2

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37	Structural insight into gene transcriptional regulation and effector binding by the Lrp/AsnC family. Nucleic Acids Research, 2006, 34, 1944-1944.	14.5	1
38	Abstract P6-08-10: Mutational signatures impact the breast cancer transcriptome and distinguish mitotic from immune response pathways. Cancer Research, 2016, 76, P6-08-10-P6-08-10.	0.9	1