

Howard Cedar

List of Publications by Year in descending order

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Version: 2024-02-01

107
papers

19,614
citations

19657

61
h-index

27406

106
g-index

107
all docs

107
docs citations

107
times ranked

18703
citing authors

#	ARTICLE	IF	CITATIONS
1	The role of DNA methylation in genome-wide gene regulation during development. <i>Development (Cambridge)</i> , 2022, 149, .	2.5	6
2	Chromosomal coordination and differential structure of asynchronous replicating regions. <i>Nature Communications</i> , 2021, 12, 1035.	12.8	8
3	Asynchronous Replication Timing: A Mechanism for Monoallelic Choice During Development. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 737681.	3.7	2
4	Determining gestational age using genome methylation profile: A novel approach for fetal medicine. <i>Prenatal Diagnosis</i> , 2019, 39, 1005-1010.	2.3	10
5	Role of transcription complexes in the formation of the basal methylation pattern in early development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10387-10391.	7.1	23
6	Postnatal DNA demethylation and its role in tissue maturation. <i>Nature Communications</i> , 2018, 9, 2040.	12.8	56
7	Principles of DNA methylation and their implications for biology and medicine. <i>Lancet, The</i> , 2018, 392, 777-786.	13.7	436
8	Contribution of epigenetic mechanisms to variation in cancer risk among tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2230-2234.	7.1	52
9	Clonally stable V β allelic choice instructs Ig β repertoire. <i>Nature Communications</i> , 2017, 8, 15575.	12.8	17
10	DNA METHYLATION: BRIDGING THE GAP BETWEEN GENES AND FUNCTION. <i>European Neuropsychopharmacology</i> , 2017, 27, S431.	0.7	0
11	Programming asynchronous replication in stem cells. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 1132-1138.	8.2	10
12	Annotating the genome by DNA methylation. <i>International Journal of Developmental Biology</i> , 2017, 61, 137-148.	0.6	4
13	Epigenetic mechanism of FMR1 inactivation in Fragile X syndrome. <i>International Journal of Developmental Biology</i> , 2017, 61, 285-292.	0.6	12
14	Islet cells share promoter hypomethylation independently of expression, but exhibit cell-type-specific methylation in enhancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13525-13530.	7.1	49
15	Tissue-specific DNA demethylation is required for proper B-cell differentiation and function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 5018-5023.	7.1	83
16	Maintenance of Epigenetic Information. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a019372.	5.5	129
17	DNA Methylation in Cancer and Aging. <i>Cancer Research</i> , 2016, 76, 3446-3450.	0.9	646
18	Identification of tissue-specific cell death using methylation patterns of circulating DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1826-34.	7.1	492

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19	Chronic liver inflammation modifies DNA methylation at the precancerous stage of murine hepatocarcinogenesis. <i>Oncotarget</i> , 2015, 6, 11047-11060.	1.8	21
20	Gender-specific postnatal demethylation and establishment of epigenetic memory. <i>Genes and Development</i> , 2015, 29, 923-933.	5.9	83
21	A Novel Pax5-Binding Regulatory Element in the Ig λ Locus. <i>Frontiers in Immunology</i> , 2014, 5, 240.	4.8	6
22	Molecular Rules Governing <i>De Novo</i> Methylation in Cancer. <i>Cancer Research</i> , 2014, 74, 1475-1483.	0.9	55
23	Establishment of methylation patterns in ES cells. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 110-112.	8.2	32
24	Aberrant DNA Methylation in ES Cells. <i>PLoS ONE</i> , 2014, 9, e96090.	2.5	11
25	DNA methylation dynamics in health and disease. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 274-281.	8.2	503
26	Clonal allelic predetermination of immunoglobulin λ rearrangement. <i>Nature</i> , 2012, 490, 561-565.	27.8	42
27	Programming of DNA Methylation Patterns. <i>Annual Review of Biochemistry</i> , 2012, 81, 97-117.	11.1	382
28	Epigenetics of haematopoietic cell development. <i>Nature Reviews Immunology</i> , 2011, 11, 478-488.	22.7	151
29	Reprogramming of DNA Replication Timing. <i>Stem Cells</i> , 2010, 28, 443-449.	3.2	20
30	Epigenetic control of recombination in the immune system. <i>Seminars in Immunology</i> , 2010, 22, 323-329.	5.6	20
31	Allelic inactivation of rDNA loci. <i>Genes and Development</i> , 2009, 23, 2437-2447.	5.9	58
32	Linking DNA methylation and histone modification: patterns and paradigms. <i>Nature Reviews Genetics</i> , 2009, 10, 295-304.	16.3	1,944
33	Developmental programming of CpG island methylation profiles in the human genome. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 564-571.	8.2	345
34	Shifts in Replication Timing Actively Affect Histone Acetylation during Nucleosome Reassembly. <i>Molecular Cell</i> , 2009, 34, 767-774.	9.7	72
35	Choreography of Ig allelic exclusion. <i>Current Opinion in Immunology</i> , 2008, 20, 308-317.	5.5	57
36	De novo DNA methylation promoted by G9a prevents reprogramming of embryonically silenced genes. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1176-1183.	8.2	396

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37	DNA replication timing of the human β^2 -globin domain is controlled by histone modification at the origin. <i>Genes and Development</i> , 2008, 22, 1319-1324.	5.9	118
38	Role of DNA Methylation in Stable Gene Repression. <i>Journal of Biological Chemistry</i> , 2007, 282, 12194-12200.	3.4	129
39	Polycomb-mediated methylation on Lys27 of histone H3 pre-marks genes for de novo methylation in cancer. <i>Nature Genetics</i> , 2007, 39, 232-236.	21.4	1,062
40	Allelic 'choice' governs somatic hypermutation in vivo at the immunoglobulin β -chain locus. <i>Nature Immunology</i> , 2007, 8, 715-722.	14.5	45
41	C9a-mediated irreversible epigenetic inactivation of Oct-3/4 during early embryogenesis. <i>Nature Cell Biology</i> , 2006, 8, 188-194.	10.3	581
42	Evidence for an instructive mechanism of de novo methylation in cancer cells. <i>Nature Genetics</i> , 2006, 38, 149-153.	21.4	456
43	Fine Tuning of Globin Gene Expression by DNA Methylation. <i>PLoS ONE</i> , 2006, 1, e46.	2.5	43
44	Epigenetic ontogeny of the Igk locus during B cell development. <i>Nature Immunology</i> , 2005, 6, 198-203.	14.5	152
45	Silence of the genes " mechanisms of long-term repression. <i>Nature Reviews Genetics</i> , 2005, 6, 648-654.	16.3	78
46	A stepwise epigenetic process controls immunoglobulin allelic exclusion. <i>Nature Reviews Immunology</i> , 2004, 4, 753-761.	22.7	69
47	CTCF Elements Direct Allele-Specific Undermethylation at the Imprinted H19 Locus. <i>Current Biology</i> , 2004, 14, 1007-1012.	3.9	30
48	Regulation of imprinting: A multi-tiered process. <i>Journal of Cellular Biochemistry</i> , 2003, 88, 400-407.	2.6	26
49	Epigenetic mechanisms that regulate antigen receptor gene expression. <i>Current Opinion in Immunology</i> , 2003, 15, 176-181.	5.5	37
50	The role of DNA methylation in setting up chromatin structure during development. <i>Nature Genetics</i> , 2003, 34, 187-192.	21.4	337
51	Replicating by the clock. <i>Nature Reviews Molecular Cell Biology</i> , 2003, 4, 25-32.	37.0	148
52	Biallelic Germline Transcription at the β Immunoglobulin Locus. <i>Journal of Experimental Medicine</i> , 2003, 197, 743-750.	8.5	48
53	A multistep mechanism for the activation of rearrangement in the immune system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7557-7562.	7.1	24
54	Establishment of transcriptional competence in early and late S phase. <i>Nature</i> , 2002, 420, 198-202.	27.8	163

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55	Differential accessibility at the \hat{I}^{β} chain locus plays a role in allelic exclusion. EMBO Journal, 2002, 21, 5255-5261.	7.8	59
56	The imprinting mechanism of the Prader-Willi/Angelman regional control center. EMBO Journal, 2002, 21, 5807-5814.	7.8	84
57	Epigenetic Crosstalk. Molecular Cell, 2001, 8, 933-935.	9.7	39
58	Asynchronous replication and allelic exclusion in the immune system. Nature, 2001, 414, 221-225.	27.8	222
59	The imprinting box of the Prader-Willi/Angelman syndrome domain. Nature Genetics, 2000, 26, 440-443.	21.4	106
60	Allele-specific expression patterns of interleukin-2 and Pax-5 revealed by a sensitive single-cell RT-PCR analysis. Current Biology, 2000, 10, 789-792.	3.9	72
61	Imprinting: focusing on the center. Current Opinion in Genetics and Development, 2000, 10, 550-554.	3.3	41
62	Developmental regulation of immune system gene rearrangement. Current Opinion in Immunology, 1999, 11, 64-69.	5.5	31
63	The amazing demethylase. Nature, 1999, 397, 568-569.	27.8	68
64	Asynchronous replication of imprinted genes is established in the gametes and maintained during development. Nature, 1999, 401, 929-932.	27.8	163
65	DNA methylation represses transcription in vivo. Nature Genetics, 1999, 22, 203-206.	21.4	341
66	Analysis of putative RNase sensitivity and protease insensitivity of demethylation activity in extracts from rat myoblasts. Nucleic Acids Research, 1998, 26, 5573-5580.	14.5	37
67	DNA methylation: A molecular lock. Current Biology, 1997, 7, R305-R307.	3.9	164
68	The role of DNA demethylation during development. Genes To Cells, 1997, 2, 481-486.	1.2	28
69	DNA Demethylation In Vitro: Involvement of RNA. Cell, 1996, 86, 709-718.	28.9	190
70	A role for nuclear NF- κ B in B-cell-specific demethylation of the Ig \hat{I}^{β} locus. Nature Genetics, 1996, 13, 435-441.	21.4	220
71	Gamete-specific methylation correlates with imprinting of the murine Xist gene. Nature Genetics, 1995, 9, 312-315.	21.4	108
72	Action at a distance. Nature, 1995, 375, 16-17.	27.8	14

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73	Developmental changes in methylation of spermatogenesis-specific genes include reprogramming in the epididymis. <i>Nature Genetics</i> , 1994, 7, 59-63.	21.4	149
74	Spl elements protect a CpG island from de novo methylation. <i>Nature</i> , 1994, 371, 435-438.	27.8	698
75	DNA methylation and genomic imprinting. <i>Cell</i> , 1994, 77, 473-476.	28.9	356
76	B cell-specific demethylation: A novel role for the intronic β chain enhancer sequence. <i>Cell</i> , 1994, 76, 913-923.	28.9	185
77	Role of DNA methylation in the regulation of transcription. <i>Current Opinion in Genetics and Development</i> , 1994, 4, 255-259.	3.3	302
78	Allelic inactivation regulates olfactory receptor gene expression. <i>Cell</i> , 1994, 78, 823-834.	28.9	985
79	Dynamics of DNA methylation during development. <i>BioEssays</i> , 1993, 15, 709-713.	2.5	121
80	Chromosome structure and eukaryotic gene organization. <i>Current Opinion in Genetics and Development</i> , 1991, 1, 534-537.	3.3	10
81	Demethylation of CpG islands in embryonic cells. <i>Nature</i> , 1991, 351, 239-241.	27.8	153
82	Dynamics of demethylation and activation of the β -actin gene in myoblasts. <i>Cell</i> , 1990, 63, 1229-1237.	28.9	164
83	Mapping replication units in animal cells. <i>Cell</i> , 1989, 57, 909-920.	28.9	241
84	A temperature-sensitive mutation in asparaginyl-tRNA synthetase causes cell-cycle arrest in early S phase. <i>Experimental Cell Research</i> , 1989, 184, 53-60.	2.6	6
85	DNA methylation and gene activity. <i>Cell</i> , 1988, 53, 3-4.	28.9	894
86	5-aza-C-induced changes in the time of replication of the X chromosomes of <i>Microtus agrestis</i> are followed by non-random reversion to a late pattern of replication. <i>Chromosoma</i> , 1987, 95, 81-88.	2.2	19
87	Muscle-specific activation of a methylated chimeric actin gene. <i>Cell</i> , 1986, 46, 409-416.	28.9	138
88	DNA methylation affects the formation of active chromatin. <i>Cell</i> , 1986, 44, 535-543.	28.9	578
89	DNA hypomethylation causes an increase in DNase-I sensitivity and an advance in the time of replication of the entire inactive X chromosome. <i>Chromosoma</i> , 1985, 93, 152-156.	2.2	80
90	DNase I sensitivity in facultative and constitutive heterochromatin. <i>Chromosoma</i> , 1985, 93, 38-42.	2.2	50

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91	Regulated expression of an introduced MHC Hâ€“2Kbm1 gene in murine embryonal carcinoma cells. Nature, 1984, 310, 415-418.	27.8	61
92	Mapping of DNAase I sensitive regions on mitotic chromosomes. Cell, 1984, 38, 493-499.	28.9	146
93	DNA Methylation in Eukaryotic Cells. International Review of Cytology, 1984, 92, 159-185.	6.2	78
94	In situ nick-translation distinguishes between active and inactive X chromosomes. Nature, 1983, 304, 88-90.	27.8	92
95	Effect of CpG methylation onMspI. Nucleic Acids Research, 1983, 11, 3571-3580.	14.5	67
96	Substrate and sequence specificity of a eukaryotic DNA methylase. Nature, 1982, 295, 620-622.	27.8	448
97	Methylation of CpG sequences in eukaryotic DNA. FEBS Letters, 1981, 124, 67-71.	2.8	273
98	Sequence specificity of methylation in higher plant DNA. Nature, 1981, 292, 860-862.	27.8	727
99	In vitro methylation of DNA with Hpa II methylase. Nucleic Acids Research, 1981, 9, 633-646.	14.5	56
100	Restriction enzyme digestion of hemimethylated DNA. Nucleic Acids Research, 1981, 9, 2509-2515.	14.5	105
101	Nuclease sensitivity of active chromatin. Nucleic Acids Research, 1980, 8, 5143-5156.	14.5	27
102	Direct detection of methylated cytosine in DNA by use of the restriction enzyme MspI. Nucleic Acids Research, 1979, 6, 2125-2132.	14.5	187
103	Nick translation of active genes in intact nuclei. Developmental Biology, 1979, 69, 496-505.	2.0	54
104	Organization of 5-methylcytosine in chromosomal DNA. Biochemistry, 1978, 17, 2934-2938.	2.5	105
105	Selective degradation of integrated murine leukemia proviral DNA by deoxyribonucleases. Cell, 1977, 11, 933-940.	28.9	101
106	Transcription of DNA and chromatin with calf thymus RNA polymerase B in vitro. Journal of Molecular Biology, 1975, 95, 257-269.	4.2	46
107	Transcription of chromatin in vitro. Journal of Molecular Biology, 1973, 77, 237-254.	4.2	146