Adrian Peter Bird

List of Publications by Year
in descending order

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Version: 2024-02-01

134 papers	45,958 citations	14124 69 h-index	18400 124 g-index
149 all docs	149 docs citations	149 times ranked	42943 citing authors

#	Article	IF	Citations
1	Genetic therapies for neurological disorders. Human Genetics, 2022, 141, 1085-1091.	1.8	2
2	High-throughput sequencing SELEX for the determination of DNA-binding protein specificities inÂvitro. STAR Protocols, 2022, 3, 101490.	0.5	4
3	SALL4 controls cell fate in response to DNA base composition. Molecular Cell, 2021, 81, 845-858.e8.	4.5	29
4	Neuronal non-CG methylation is an essential target for MeCP2 function. Molecular Cell, 2021, 81, 1260-1275.e12.	4.5	24
5	CDKL5 deficiency disorder: a pathophysiology of neural maintenance. Journal of Clinical Investigation, 2021, 131, .	3.9	4
6	The Selfishness of Law-Abiding Genes. Trends in Genetics, 2020, 36, 8-13.	2.9	11
7	The Molecular Basis of MeCP2 Function in the Brain. Journal of Molecular Biology, 2020, 432, 1602-1623.	2.0	89
8	Quantitative analysis questions the role of MeCP2 as a global regulator of alternative splicing. PLoS Genetics, 2020, 16, e1009087.	1.5	10
9	Absence of MeCP2 binding to non-methylated GT-rich sequences in vivo. Nucleic Acids Research, 2020, 48, 3542-3552.	6.5	10
10	DNA Methylation: Mega-Year Inheritance with the Help of Darwin. Current Biology, 2020, 30, R319-R321.	1.8	4
11	Quantitative analysis questions the role of MeCP2 as a global regulator of alternative splicing. , 2020, 16, e1009087.		0
12	Quantitative analysis questions the role of MeCP2 as a global regulator of alternative splicing. , 2020, 16, e1009087.		0
13	Quantitative analysis questions the role of MeCP2 as a global regulator of alternative splicing. , 2020, 16, e1009087.		0
14	Quantitative analysis questions the role of MeCP2 as a global regulator of alternative splicing. , 2020, 16, e1009087.		0
15	R-Loops Enhance Polycomb Repression at a Subset of Developmental Regulator Genes. Molecular Cell, 2019, 73, 930-945.e4.	4.5	75
16	An Orphan CpG Island Drives Expression of a let-7 miRNA Precursor with an Important Role in Mouse Development. Epigenomes, 2019, 3, 7.	0.8	2
17	CpG Islands: A Historical Perspective. Methods in Molecular Biology, 2018, 1766, 3-13.	0.4	9
18	Toxicity of overexpressed MeCP2 is independent of HDAC3 activity. Genes and Development, 2018, 32, 1514-1524.	2.7	23

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19	Affinity for DNA Contributes to NLS Independent Nuclear Localization of MeCP2. Cell Reports, 2018, 24, 2213-2220.	2.9	23
20	A mutation-led search for novel functional domains in MeCP2. Human Molecular Genetics, 2018, 27, 2531-2545.	1.4	22
21	Radically truncated MeCP2 rescues Rett syndrome-like neurological defects. Nature, 2017, 550, 398-401.	13.7	121
22	MeCP2 recognizes cytosine methylated tri-nucleotide and di-nucleotide sequences to tune transcription in the mammalian brain. PLoS Genetics, 2017, 13, e1006793.	1.5	117
23	Genetic determinants of the epigenome in development and cancer. Swiss Medical Weekly, 2017, 147, w14523.	0.8	8
24	The molecular basis of variable phenotypic severity among common missense mutations causing Rett syndrome. Human Molecular Genetics, 2016, 25, 558-570.	1.4	76
25	Exclusive expression of MeCP2 in the nervous system distinguishes between brain and peripheral Rett syndrome-like phenotypes. Human Molecular Genetics, 2016, 25, ddw269.	1.4	57
26	Sequenceâ€specific <scp>DNA</scp> binding by <scp>AT</scp>â€hook motifs in Me<scp>CP</scp>2. FEBS Letters, 2016, 590, 2927-2933.	1.3	26
27	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
28	The Role of Epigenetic Mechanisms in the Regulation of Gene Expression in the Nervous System. Journal of Neuroscience, 2016, 36, 11427-11434.	1.7	109
29	Rett Syndrome: Crossing the Threshold to Clinical Translation. Trends in Neurosciences, 2016, 39, 100-113.	4.2	135
30	Do short, frequent DNA sequence motifs mould the epigenome?. Nature Reviews Molecular Cell Biology, 2016, 17, 257-262.	16.1	30
31	Max Birnstiel 1933â€"2014: Gene pioneer. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 302-303.	3.3	3
32	Rett syndrome: a complex disorder with simple roots. Nature Reviews Genetics, 2015, 16, 261-275.	7.7	277
33	A dominant role for the methyl-CpG-binding protein Mbd2 in controlling Th2 induction by dendritic cells. Nature Communications, 2015, 6, 6920.	5.8	87
34	DNA methylation reader MECP2: cell type- and differentiation stage-specific protein distribution. Epigenetics and Chromatin, 2014, 7, 17.	1.8	55
35	A unique <scp>DNA</scp> methylation signature defines a population of <scp>IFN</scp>â€Î³/<scp>IL</scp>â€4 doubleâ€positive <scp>T</scp> cells during helminth infection. European Journal of Immunology, 2014, 44, 1835-1841.	1.6	26
36	Synthetic CpG islands reveal DNA sequence determinants of chromatin structure. ELife, 2014, 3, e03397.	2.8	95

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37	Systemic Delivery of MeCP2 Rescues Behavioral and Cellular Deficits in Female Mouse Models of Rett Syndrome. Journal of Neuroscience, 2013, 33, 13612-13620.	1.7	194
38	Genome Biology: Not Drowning but Waving. Cell, 2013, 154, 951-952.	13.5	12
39	Epigenetics: Discovery. New Scientist, 2013, 217, ii-iii.	0.0	0
40	Rett syndrome mutations abolish the interaction of MeCP2 with the NCoR/SMRT co-repressor. Nature Neuroscience, 2013, 16, 898-902.	7.1	317
41	Postnatal inactivation reveals enhanced requirement for MeCP2 at distinct age windows. Human Molecular Genetics, 2012, 21, 3806-3814.	1.4	84
42	Morphological and functional reversal of phenotypes in a mouse model of Rett syndrome. Brain, 2012, 135, 2699-2710.	3.7	132
43	Disease Modeling Using Embryonic Stem Cells: MeCP2 Regulates Nuclear Size and RNA Synthesis in Neurons. Stem Cells, 2012, 30, 2128-2139.	1.4	79
44	Cfp1 integrates both CpG content and gene activity for accurate H3K4me3 deposition in embryonic stem cells. Genes and Development, 2012, 26, 1714-1728.	2.7	253
45	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	9.4	323
46	Cell typeâ€"specific DNA methylation at intragenic CpG islands in the immune system. Genome Research, 2011, 21, 1074-1086.	2.4	256
47	Putting the DNA back into DNA methylation. Nature Genetics, 2011, 43, 1050-1051.	9.4	27
48	The Role of MeCP2 in the Brain. Annual Review of Cell and Developmental Biology, 2011, 27, 631-652.	4.0	388
49	The Dinucleotide CG as a Genomic Signalling Module. Journal of Molecular Biology, 2011, 409, 47-53.	2.0	48
50	Embryonic lethal phenotype reveals a function of TDG in maintaining epigenetic stability. Nature, 2011, 470, 419-423.	13.7	323
51	CpG islands and the regulation of transcription. Genes and Development, 2011, 25, 1010-1022.	2.7	2,555
52	Francesca Aran Murphy and Christopher Asprey, eds, Ecumenism Today: The Universal Church in the 21st Century (Aldershot: Ashgate Publishing House, 2008), pp. viii + 220, Â£50.00, ISBN 978-0-7546-5961-7 (hbk).. International Journal of Public Theology, 2011, 5, 499.	0.1	0
53	Christianity as a World Religion. International Journal of Public Theology, 2011, 5, 260-261.	0.1	0
54	Reversibility of functional deficits in experimental models of Rett syndrome. Biochemical Society Transactions, 2010, 38, 498-506.	1.6	59

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55	CpG islands influence chromatin structure via the CpG-binding protein Cfp1. Nature, 2010, 464, 1082-1086.	13.7	577
56	Targeting of De Novo DNA Methylation Throughout the Oct-4 Gene Regulatory Region in Differentiating Embryonic Stem Cells. PLoS ONE, 2010, 5, e9937.	1.1	65
57	God and Human Dignity. International Journal of Public Theology, 2009, 3, 503-504.	0.1	0
58	A Temporal Threshold for Formaldehyde Crosslinking and Fixation. PLoS ONE, 2009, 4, e4636.	1.1	110
59	DNA methylation landscapes: provocative insights from epigenomics. Nature Reviews Genetics, 2008, 9, 465-476.	7.7	2,619
60	A Novel CpG Island Set Identifies Tissue-Specific Methylation at Developmental Gene Loci. PLoS Biology, 2008, 6, e22.	2.6	533
61	The methyl-CpG-binding protein MeCP2 and neurological disease. Biochemical Society Transactions, 2008, 36, 575-583.	1.6	63
62	MBD2-Mediated Transcriptional Repression of the <i>p14</i>^{ARF} Tumor Suppressor Gene in Human Colon Cancer Cells. Pathobiology, 2008, 75, 281-287.	1.9	30
63	Michael Amaladoss. 2006. <i>The Asian Jesus</i>. New York: Orbis Books, pp. 180, Pb, Â£11.99.. Studies in World Christianity, 2008, 14, 182-182.	0.1	0
64	MBD2 Is Required for Correct Spatial Gene Expression in the Gut. Molecular and Cellular Biology, 2007, 27, 4049-4057.	1.1	29
65	Mbd2 Contributes to DNA Methylation-Directed Repression of the Xist Gene. Molecular and Cellular Biology, 2007, 27, 3750-3757.	1.1	57
66	Interaction between chromatin proteins MECP2 and ATRX is disrupted by mutations that cause inherited mental retardation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2709-2714.	3.3	231
67	Reversal of Neurological Defects in a Mouse Model of Rett Syndrome. Science, 2007, 315, 1143-1147.	6.0	1,093
68	CpG methylation is targeted to transcription units in an invertebrate genome. Genome Research, 2007, 17, 625-631.	2.4	217
69	Perceptions of epigenetics. Nature, 2007, 447, 396-398.	13.7	2,465
70	Kaiso-Deficient Mice Show Resistance to Intestinal Cancer. Molecular and Cellular Biology, 2006, 26, 199-208.	1.1	146
71	Gene Expression Analysis Exposes Mitochondrial Abnormalities in a Mouse Model of Rett Syndrome. Molecular and Cellular Biology, 2006, 26, 5033-5042.	1.1	182
72	MBD2 deficiency does not accelerate p53 mediated lymphomagenesis. Oncogene, 2005, 24, 2430-2432.	2.6	18

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73	Genomic Approaches Reveal Unexpected Genetic Divergence Within Ciona intestinalis. Journal of Molecular Evolution, 2005, 61, 627-635.	0.8	72
74	Up-regulation of glucocorticoid-regulated genes in a mouse model of Rett syndrome. Human Molecular Genetics, 2005, 14, 2247-2256.	1.4	174
75	The effect of interspecific oocytes on demethylation of sperm DNA. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7636-7640.	3.3	112
76	The major form of MeCP2 has a novel N-terminus generated by alternative splicing. Nucleic Acids Research, 2004, 32, 1818-1823.	6.5	217
77	Oxidative damage to methyl-CpG sequences inhibits the binding of the methyl-CpG binding domain (MBD) of methyl-CpG binding protein 2 (MeCP2). Nucleic Acids Research, 2004, 32, 4100-4108.	6.5	660
78	MBD4 deficiency does not increase mutation or accelerate tumorigenesis in mice lacking MMR. Oncogene, 2004, 23, 5693-5696.	2.6	16
79	MBD4 deficiency reduces the apoptotic response to DNA-damaging agents in the murine small intestine. Oncogene, 2003, 22, 7130-7136.	2.6	85
80	Epigenetic regulation of gene expression: how the genome integrates intrinsic and environmental signals. Nature Genetics, 2003, 33, 245-254.	9.4	5,434
81	Deficiency of Mbd2 suppresses intestinal tumorigenesis. Nature Genetics, 2003, 34, 145-147.	9.4	181
82	Il2 transcription unleashed by active DNA demethylation. Nature Immunology, 2003, 4, 208-209.	7.0	27
83	Fas-associated death domain protein interacts with methyl-CpG binding domain protein 4: A potential link between genome surveillance and apoptosis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5211-5216.	3.3	134
84	MOLECULAR BIOLOGY: MeCP2 Repression Goes Nonglobal. Science, 2003, 302, 793-795.	6.0	66
85	Enhanced CpG Mutability and Tumorigenesis in MBD4-Deficient Mice. Science, 2002, 297, 403-405.	6.0	294
86	DNA methylation patterns and epigenetic memory. Genes and Development, 2002, 16, 6-21.	2.7	5,932
87	MeCP2 and other methyl-cpg binding proteins. Mental Retardation and Developmental Disabilities Research Reviews, 2002, 8, 87-93.	3.5	64
88	dSIR2 and dHDAC6: Two Novel, Inhibitor-Resistant Deacetylases in Drosophila melanogaster. Experimental Cell Research, 2001, 265, 90-103.	1.2	64
89	The p120 catenin partner Kaiso is a DNA methylation-dependent transcriptional repressor. Genes and Development, 2001, 15, 1613-1618.	2.7	431
90	A mouse Mecp2-null mutation causes neurological symptoms that mimic Rett syndrome. Nature Genetics, 2001, 27, 322-326.	9.4	1,401

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91	Closely related proteins MBD2 and MBD3 play distinctive but interacting roles in mouse development. Genes and Development, 2001, 15, 710-723.	2.7	453
92	Mutant weed breaks silence. Nature, 2000, 405, 137-138.	13.7	7
93	Histone deacetylases: silencers for hire. Trends in Biochemical Sciences, 2000, 25, 121-126.	3.7	400
94	Sequence Analysis of Transposable Elements in the Sea Squirt, Ciona intestinalis. Molecular Biology and Evolution, 2000, 17, 1685-1694.	3.5	41
95	Active Repression of Methylated Genes by the Chromosomal Protein MBD1. Molecular and Cellular Biology, 2000, 20, 1394-1406.	1.1	238
96	MBD2 is a transcriptional repressor belonging to the MeCP1 histone deacetylase complex. Nature Genetics, 1999, 23, 58-61.	9.4	783
97	Absence of genome-wide changes in DNA methylation during development of the zebrafish. Nature Genetics, 1999, 23, 139-140.	9.4	130
98	The thymine glycosylase MBD4 can bind to the product of deamination at methylated CpG sites. Nature, 1999, 401, 301-304.	13.7	576
99	Vestiges of a DNA methylation system in Drosophila melanogaster?. Nature Genetics, 1999, 23, 389-390.	9.4	124
100	Somatic frameshift mutations in the MBD4 gene of sporadic colon cancers with mismatch repair deficiency. Oncogene, 1999, 18, 8044-8047.	2.6	127
101	Genomic structure and chromosomal mapping of the murine and human Mbd1, Mbd2, Mbd3, and Mbd4 genes. Mammalian Genome, 1999, 10, 906-912.	1.0	100
102	CpG islands as genomic footprints of promoters that are associated with replication origins. Current Biology, 1999, 9, R661-R667.	1.8	206
103	Nonmethylated Transposable Elements and Methylated Genes in a Chordate Genome. Science, 1999, 283, 1164-1167.	6.0	134
104	Densely methylated sequences that are preferentially localized at telomere-proximal regions of human chromosomes. Gene, 1999, 240, 269-277.	1.0	72
105	Transcriptional repression by the methyl-CpG-binding protein MeCP2 involves a histone deacetylase complex. Nature, 1998, 393, 386-389.	13.7	3,102
106	Identification and Characterization of a Family of Mammalian Methyl-CpG Binding Proteins. Molecular and Cellular Biology, 1998, 18, 6538-6547.	1.1	1,216
107	An Alternative Promoter in the Mouse Major Histocompatibility Complex Class II I-AÎ² Gene: Implications for the Origin of CpG Islands. Molecular and Cellular Biology, 1998, 18, 4433-4443.	1.1	65
108	Identification and characterization of a family of mammalian methyl CpG-binding proteins. Genetical Research, 1998, 72, 59-72.	0.3	10

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109	Gene Silencing by Methylâ€CPGâ€Binding Proteins. Novartis Foundation Symposium, 1998, 214, 6-21.	1.2	84
110	MeCP2 Is a Transcriptional Repressor with Abundant Binding Sites in Genomic Chromatin. Cell, 1997, 88, 471-481.	13.5	1,165
111	Human Genome Evolution. Edited by M. Jackson, T. Strachan and G. Dover. BIOS Scientific Publishers, 1996. 306 + x pages. Price Â£60.00 ($120). ISBN 1 859960 95 2.. Genetical Research, 1997, 69, 75-78.	0.3	0
112	A component of the transcriptional represser MeCP1 shares a motif with DNA methyltransferase and HRX proteins. Nature Genetics, 1997, 16, 256-259.	9.4	222
113	The methyl-CpG binding protein MeCP2 is essential for embryonic development in the mouse. Nature Genetics, 1996, 12, 205-208.	9.4	227
114	Studies of DNA methylation in animals. Journal of Cell Science, 1995, 1995, 37-39.	1.2	50
115	Binding of Histone H1 to DNA Is Indifferent to Methylation at CpG Sequences. Journal of Biological Chemistry, 1995, 270, 26473-26481.	1.6	44
116	Themajor transitions in evolution. Trends in Ecology and Evolution, 1995, 10, 385.	4.2	2
117	Predicting the total number of human genes. Nature Genetics, 1994, 8, 114-114.	9.4	35
118	Dissection of the methyl-CpG binding domain from the chromosomal protein MeCP2. Nucleic Acids Research, 1993, 21, 4886-4892.	6.5	561
119	Transcriptional repression by methylation of CpG. Journal of Cell Science, 1992, 1992, 9-14.	1.2	78
120	The essentials of DNA methylation. Cell, 1992, 70, 5-8.	13.5	972
121	Purification, sequence, and cellular localization of a novel chromosomal protein that binds to Methylated DNA. Cell, 1992, 69, 905-914.	13.5	1,253
122	DNA methylation and chromatin structure. FEBS Letters, 1991, 285, 155-159.	1.3	167
123	DNA methylation inhibits transcription indirectly via a methyl-CpG binding protein. Cell, 1991, 64, 1123-1134.	13.5	708
124	Non-methylated islands in fish genomes are GC-poor. Nucleic Acids Research, 1991, 19, 1469-1474.	6.5	43
125	High levels of De Novo methylation and altered chromatin structure at CpG islands in cell lines. Cell, 1990, 62, 503-514.	13.5	671
126	A fraction of the mouse genome that is derived from islands of nonmethylated, CpG-rich DNA. Cell, 1985, 40, 91-99.	13.5	661

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127	Transcription in oocytes of highly methylated rDNA from Xenopus laevis sperm. Nature, 1983, 306, 200-203.	13.7	54
128	DNaseI-hypersensitive sites at promoter-like sequences in the spacer ofXenopus laevisandXenopus borealisribosomal DNA. Nucleic Acids Research, 1983, 11, 5361-5380.	6.5	33
129	The origin of the rRNA precursor fromXenopus borealis, analysedin vivoandin vitro. Nucleic Acids Research, 1983, 11, 8167-8181.	6.5	15
130	DNAase I sensitivity and methylation of active versus inactive rRNA genes in Xenopus species hybrids. Cell, 1982, 29, 211-218.	13.5	60
131	Loss of rDNA methylation accompanies the onset of ribosomal gene activity in early development of X. laevis. Cell, 1981, 26, 381-390.	13.5	111
132	Ribosomal RNA gene amplification by rolling circles. Journal of Molecular Biology, 1974, 87, 473-487.	2.0	106
133	Is Gene Amplification RNA-directed?. Nature: New Biology, 1973, 242, 226-230.	4.5	26
134	Comparative analysis of potential broad-spectrum neuronal Cre drivers. Wellcome Open Research, 0, 7, 185.	0.9	1