

Paul A Wade

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

129
papers

13,788
citations

57
h-index

117
g-index

141
ext. papers

15,109
ext. citations

12
avg, IF

6.42
L-index

#	Paper	IF	Citations
129	NLRX1 Deficiency Alters the Gut Microbiome and Is Further Exacerbated by Adherence to a Gluten-Free Diet.. <i>Frontiers in Immunology</i> , 2022 , 13, 882521	8.4	0
128	Epigenetic remodelling upon FGFR inhibition. <i>Nature Cell Biology</i> , 2021 , 23, 1115-1116	23.4	
127	CUT&Tag-BS for simultaneous profiling of histone modification and DNA methylation with high efficiency and low cost.. <i>Cell Reports Methods</i> , 2021 , 1,		1
126	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. <i>Nature Communications</i> , 2021 , 12, 2490	17.4	13
125	A simple and robust method for simultaneous dual-omics profiling with limited numbers of cells. <i>Cell Reports Methods</i> , 2021 , 1,		2
124	Low-input ATAC&mRNA-seq protocol for simultaneous profiling of chromatin accessibility and gene expression. <i>STAR Protocols</i> , 2021 , 2, 100764	1.4	2
123	The estrogen receptor/GATA3/FOXA1 transcriptional network: lessons learned from breast cancer. <i>Current Opinion in Structural Biology</i> , 2021 , 71, 65-70	8.1	2
122	Comprehensive structure-function characterization of DNMT3B and DNMT3A reveals distinctive de novo DNA methylation mechanisms. <i>Nature Communications</i> , 2020 , 11, 3355	17.4	42
121	Alterations in promoter interaction landscape and transcriptional network underlying metabolic adaptation to diet. <i>Nature Communications</i> , 2020 , 11, 962	17.4	14
120	Cancer-specific mutation of GATA3 disrupts the transcriptional regulatory network governed by Estrogen Receptor alpha, FOXA1 and GATA3. <i>Nucleic Acids Research</i> , 2020 , 48, 4756-4768	20.1	12
119	Direct readout of heterochromatic H3K9me3 regulates DNMT1-mediated maintenance DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 18439-18447	11.5	26
118	Interaction of the pioneer transcription factor GATA3 with nucleosomes. <i>Nature Communications</i> , 2020 , 11, 4136	17.4	16
117	The CHD4-related syndrome: a comprehensive investigation of the clinical spectrum, genotype-phenotype correlations, and molecular basis. <i>Genetics in Medicine</i> , 2020 , 22, 389-397	8.1	22
116	DNA methylation in mice is influenced by genetics as well as sex and life experience. <i>Nature Communications</i> , 2019 , 10, 305	17.4	22
115	Maternal Influence and Murine Housing Confound Impact of NLRP1 Inflammasome on Microbiome Composition. <i>Journal of Innate Immunity</i> , 2019 , 11, 416-431	6.9	9
114	DNA methylation and transcriptome aberrations mediated by ER α in mouse seminal vesicles following developmental DES exposure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E4189-E4198	11.5	14
113	Transcriptome and DNA Methylome Analysis in a Mouse Model of Diet-Induced Obesity Predicts Increased Risk of Colorectal Cancer. <i>Cell Reports</i> , 2018 , 22, 624-637	10.6	34

112	Base-Resolution Analysis of DNA Methylation Patterns Downstream of in Mouse Naïve B Cells. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 805-813	3.2	5
111	Crosstalk between the microbiome and epigenome: messages from bugs. <i>Journal of Biochemistry</i> , 2018 , 163, 105-112	3.1	104
110	GATA3 zinc finger 2 mutations reprogram the breast cancer transcriptional network. <i>Nature Communications</i> , 2018 , 9, 1059	17.4	45
109	Cryo-EM structure of the nucleosome containing the enhancer DNA sequence. <i>Open Biology</i> , 2018 , 8,	7	16
108	MyD88-dependent dendritic and epithelial cell crosstalk orchestrates immune responses to allergens. <i>Mucosal Immunology</i> , 2018 , 11, 796-810	9.2	14
107	Dosage compensation and DNA methylation landscape of the X chromosome in mouse liver. <i>Scientific Reports</i> , 2018 , 8, 10138	4.9	21
106	An obesity-associated gut microbiome reprograms the intestinal epigenome and leads to altered colonic gene expression. <i>Genome Biology</i> , 2018 , 19, 7	18.3	78
105	CHD4 and the NuRD complex directly control cardiac sarcomere formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 6727-6732	11.5	15
104	CHD3 helicase domain mutations cause a neurodevelopmental syndrome with macrocephaly and impaired speech and language. <i>Nature Communications</i> , 2018 , 9, 4619	17.4	39
103	DNA Methylation Changes in Tbx3 in a Mouse Model Exposed to Polybrominated Diphenyl Ethers. <i>International Journal of Toxicology</i> , 2017 , 36, 229-238	2.4	5
102	Reversing SKI-SMAD4-mediated suppression is essential for T17 cell differentiation. <i>Nature</i> , 2017 , 551, 105-109	50.4	55
101	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. <i>Cell Reports</i> , 2017 , 21, 455-466	10.6	20
100	Rif1 promotes a repressive chromatin state to safeguard against endogenous retrovirus activation. <i>Nucleic Acids Research</i> , 2017 , 45, 12723-12738	20.1	28
99	Proteins That Read DNA Methylation. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 945, 303-320	3.6	28
98	Epigenetic Perturbations by Arg882-Mutated DNMT3A Potentiate Aberrant Stem Cell Gene-Expression Program and Acute Leukemia Development. <i>Cancer Cell</i> , 2016 , 30, 92-107	24.3	96
97	Maternal Age at Delivery Is Associated with an Epigenetic Signature in Both Newborns and Adults. <i>PLoS ONE</i> , 2016 , 11, e0156361	3.7	37
96	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. <i>Genome Biology</i> , 2016 , 17, 36	18.3	74
95	High-quality CHIP-seq analysis of MBD3 in human breast cancer cells. <i>Genomics Data</i> , 2016 , 7, 173-4		3

94	Epigenetics, Obesity, and Colon Cancer. <i>Energy Balance and Cancer</i> , 2016 , 211-233	0.2	
93	BCL-2 family protein, BAD is down-regulated in breast cancer and inhibits cell invasion. <i>Experimental Cell Research</i> , 2015 , 331, 1-10	4.2	20
92	GATA3 in Breast Cancer: Tumor Suppressor or Oncogene?. <i>Gene Expression</i> , 2015 , 16, 163-8	3.4	58
91	Obesity, rather than diet, drives epigenomic alterations in colonic epithelium resembling cancer progression. <i>Cell Metabolism</i> , 2014 , 19, 702-11	24.6	44
90	Epigenetic control of Ccr7 expression in distinct lineages of lung dendritic cells. <i>Journal of Immunology</i> , 2014 , 193, 4904-13	5.3	18
89	Inhibition of histone binding by supramolecular hosts. <i>Biochemical Journal</i> , 2014 , 459, 505-12	3.8	41
88	Breast tumor specific mutation in GATA3 affects physiological mechanisms regulating transcription factor turnover. <i>BMC Cancer</i> , 2014 , 14, 278	4.8	38
87	Genome-wide binding of MBD2 reveals strong preference for highly methylated loci. <i>PLoS ONE</i> , 2014 , 9, e99603	3.7	34
86	Identification of DNA methylation changes in newborns related to maternal smoking during pregnancy. <i>Environmental Health Perspectives</i> , 2014 , 122, 1147-53	8.4	153
85	Diethylstilbestrol (DES)-stimulated hormonal toxicity is mediated by ER α alteration of target gene methylation patterns and epigenetic modifiers (DNMT3A, MBD2, and HDAC2) in the mouse seminal vesicle. <i>Environmental Health Perspectives</i> , 2014 , 122, 262-8	8.4	39
84	Are genomic translocations predictable? (Retrospective on DOI 10.1002/bies.201100122). <i>BioEssays</i> , 2014 , 36, 633	4.1	
83	Fine-tuning of epigenetic regulation with respect to promoter CpG content in a cell type-specific manner. <i>Epigenetics</i> , 2014 , 9, 747-59	5.7	8
82	INO80 facilitates pluripotency gene activation in embryonic stem cell self-renewal, reprogramming, and blastocyst development. <i>Cell Stem Cell</i> , 2014 , 14, 575-91	18	110
81	Serum microRNA expression as an early marker for breast cancer risk in prospectively collected samples from the Sister Study cohort. <i>Breast Cancer Research</i> , 2013 , 15, R42	8.3	81
80	The NuRD architecture. <i>Cellular and Molecular Life Sciences</i> , 2013 , 70, 3513-24	10.3	121
79	DNA methylation profiling in human B cells reveals immune regulatory elements and epigenetic plasticity at Alu elements during B-cell activation. <i>Genome Research</i> , 2013 , 23, 2030-41	9.7	75
78	Chromatin Structure and Gene Expression: Function Follows Form. <i>Epigenetics and Human Health</i> , 2013 , 189-205		
77	Epigenetics and the adaptive immune response. <i>Molecular Aspects of Medicine</i> , 2013 , 34, 813-25	16.7	35

76	MBD3 localizes at promoters, gene bodies and enhancers of active genes. <i>PLoS Genetics</i> , 2013 , 9, e1004028	628	79
75	DNA methylation-mediated silencing of nonsteroidal anti-inflammatory drug-activated gene (NAG-1/GDF15) in glioma cell lines. <i>International Journal of Cancer</i> , 2012 , 130, 267-77	7.5	31
74	R loops: lassoing DNA methylation at CpGi. <i>Molecular Cell</i> , 2012 , 45, 708-9	17.6	2
73	NuRD and pluripotency: a complex balancing act. <i>Cell Stem Cell</i> , 2012 , 10, 497-503	18	83
72	Human tRNA genes function as chromatin insulators. <i>EMBO Journal</i> , 2012 , 31, 330-50	13	99
71	Metastasis-associated protein 3 (MTA3) regulates G2/M progression in proliferating mouse granulosa cells. <i>Biology of Reproduction</i> , 2012 , 86, 1-8	3.9	10
70	Acute depletion of Tet1-dependent 5-hydroxymethylcytosine levels impairs LIF/Stat3 signaling and results in loss of embryonic stem cell identity. <i>Nucleic Acids Research</i> , 2012 , 40, 3364-77	20.1	78
69	Bivalent recognition of nucleosomes by the tandem PHD fingers of the CHD4 ATPase is required for CHD4-mediated repression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 787-92	11.5	85
68	SnapShot: Chromatin remodeling: CHD. <i>Cell</i> , 2011 , 144, 626-626.e1	56.2	24
67	Cancer biology and NuRD: a multifaceted chromatin remodelling complex. <i>Nature Reviews Cancer</i> , 2011 , 11, 588-96	31.3	337
66	Mi-2/NuRD complex function is required for normal S phase progression and assembly of pericentric heterochromatin. <i>Molecular Biology of the Cell</i> , 2011 , 22, 3094-102	3.5	56
65	The transcription factors Snail and Slug activate the transforming growth factor-beta signaling pathway in breast cancer. <i>PLoS ONE</i> , 2011 , 6, e26514	3.7	114
64	DNA methylation prevents CTCF-mediated silencing of the oncogene BCL6 in B cell lymphomas. <i>Journal of Experimental Medicine</i> , 2010 , 207, 1939-50	16.6	72
63	Yin yang 1 regulates the expression of snail through a distal enhancer. <i>Molecular Cancer Research</i> , 2009 , 7, 221-9	6.6	52
62	The Mi-2/NuRD complex associates with pericentromeric heterochromatin during S phase in rapidly proliferating lymphoid cells. <i>Chromosoma</i> , 2009 , 118, 445-57	2.8	31
61	Epstein-Barr virus infection leads to partial phenotypic reversion of terminally differentiated malignant B cells. <i>Cancer Letters</i> , 2009 , 284, 165-74	9.9	22
60	The MBD protein family-reading an epigenetic mark?. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008 , 647, 39-43	3.3	86
59	The BCL6-associated transcriptional co-repressor, MTA3, is selectively expressed by germinal centre B cells and lymphomas of putative germinal centre derivation. <i>Journal of Pathology</i> , 2007 , 213, 106-15	9.4	20

58	Structure of the SANT domain from the <i>Xenopus</i> chromatin remodeling factor ISWI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 67, 1198-202	4.2	15
57	The human Mi-2/NuRD complex and gene regulation. <i>Oncogene</i> , 2007 , 26, 5433-8	9.2	354
56	Intrinsic disorder and autonomous domain function in the multifunctional nuclear protein, MeCP2. <i>Journal of Biological Chemistry</i> , 2007 , 282, 15057-64	5.4	97
55	A 3Tenhancer controls snail expression in melanoma cells. <i>Cancer Research</i> , 2007 , 67, 6113-20	10.1	27
54	The transcription factor snail mediates epithelial to mesenchymal transitions by repression of estrogen receptor-alpha. <i>Molecular Endocrinology</i> , 2007 , 21, 2907-18		151
53	MeCP2 in Rett syndrome: transcriptional repressor or chromatin architectural protein?. <i>Current Opinion in Genetics and Development</i> , 2007 , 17, 121-5	4.9	41
52	MBD family proteins: reading the epigenetic code. <i>Journal of Cell Science</i> , 2006 , 119, 3033-7	5.3	93
51	Nuclear Akt associates with PKC-phosphorylated Ebp1, preventing DNA fragmentation by inhibition of caspase-activated DNase. <i>EMBO Journal</i> , 2006 , 25, 2083-95	13	102
50	Nucleophosmin/B23, a nuclear PI(3,4,5)P(3) receptor, mediates the antiapoptotic actions of NGF by inhibiting CAD. <i>Molecular Cell</i> , 2005 , 18, 435-45	17.6	104
49	Hormonal regulation of metastasis-associated protein 3 transcription in breast cancer cells. <i>Molecular Endocrinology</i> , 2004 , 18, 2937-49		53
48	Aberrant expression of the transcription factors snail and slug alters the response to genotoxic stress. <i>Molecular and Cellular Biology</i> , 2004 , 24, 7559-66	4.8	265
47	Mi-2/NuRD: multiple complexes for many purposes. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004 , 1677, 52-7		240
46	Chromosomal regulation by MeCP2: structural and enzymatic considerations. <i>Cellular and Molecular Life Sciences</i> , 2004 , 61, 2163-7	10.3	29
45	Dynamic regulation of DNA methylation coupled transcriptional repression: BDNF regulation by MeCP2. <i>BioEssays</i> , 2004 , 26, 217-20	4.1	11
44	Methods for preparation and assays for <i>Xenopus</i> ISWI complexes. <i>Methods in Enzymology</i> , 2004 , 377, 364-75	1.7	
43	MTA3 and the Mi-2/NuRD complex regulate cell fate during B lymphocyte differentiation. <i>Cell</i> , 2004 , 119, 75-86	56.2	269
42	Use of bifunctional cross-linking reagents in mapping genomic distribution of chromatin remodeling complexes. <i>Methods</i> , 2004 , 33, 81-5	4.6	31
41	Chromatin compaction by human MeCP2. Assembly of novel secondary chromatin structures in the absence of DNA methylation. <i>Journal of Biological Chemistry</i> , 2003 , 278, 32181-8	5.4	229

40	Nucleosome sliding induced by the xMi-2 complex does not occur exclusively via a simple twist-diffusion mechanism. <i>Journal of Biological Chemistry</i> , 2003 , 278, 30562-8	5.4	16
39	Rhythmic histone acetylation underlies transcription in the mammalian circadian clock. <i>Nature</i> , 2003 , 421, 177-82	50.4	545
38	MTA3, a Mi-2/NuRD complex subunit, regulates an invasive growth pathway in breast cancer. <i>Cell</i> , 2003 , 113, 207-19	56.2	426
37	The affinity of different MBD proteins for a specific methylated locus depends on their intrinsic binding properties. <i>Nucleic Acids Research</i> , 2003 , 31, 1765-74	20.1	184
36	Mi-2 beta associates with BRG1 and RET finger protein at the distinct regions with transcriptional activating and repressing abilities. <i>Journal of Biological Chemistry</i> , 2003 , 278, 51638-45	5.4	61
35	Chromatin remodeling in nuclear cloning. <i>FEBS Journal</i> , 2002 , 269, 2284-7		42
34	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , 2002 , 9, 263-7		148
33	WSTF-ISWI chromatin remodeling complex targets heterochromatic replication foci. <i>EMBO Journal</i> , 2002 , 21, 2231-41	13	175
32	The barrier function of an insulator couples high histone acetylation levels with specific protection of promoter DNA from methylation. <i>Genes and Development</i> , 2002 , 16, 1540-54	12.6	143
31	Specific targeting and constitutive association of histone deacetylase complexes during transcriptional repression. <i>Genes and Development</i> , 2002 , 16, 687-92	12.6	104
30	Purification of MeCP2-containing deacetylase from <i>Xenopus laevis</i> . <i>Methods in Molecular Biology</i> , 2002 , 200, 131-41	1.4	1
29	A <i>Drosophila</i> MBD family member is a transcriptional corepressor associated with specific genes. <i>FEBS Journal</i> , 2001 , 268, 5397-406		35
28	Methyl CpG-binding proteins and transcriptional repression. <i>BioEssays</i> , 2001 , 23, 1131-7	4.1	279
27	Methyl CpG binding proteins: coupling chromatin architecture to gene regulation. <i>Oncogene</i> , 2001 , 20, 3166-73	9.2	166
26	Multiple N-CoR complexes contain distinct histone deacetylases. <i>Journal of Biological Chemistry</i> , 2001 , 276, 8807-11	5.4	80
25	Transcriptional control at regulatory checkpoints by histone deacetylases: molecular connections between cancer and chromatin. <i>Human Molecular Genetics</i> , 2001 , 10, 693-8	5.6	239
24	Purification of the MeCP2/histone deacetylase complex from <i>Xenopus laevis</i> . <i>Methods in Molecular Biology</i> , 2001 , 181, 297-307	1.4	7
23	DNMT1 forms a complex with Rb, E2F1 and HDAC1 and represses transcription from E2F-responsive promoters. <i>Nature Genetics</i> , 2000 , 25, 338-42	36.3	807

22	Functional delineation of three groups of the ATP-dependent family of chromatin remodeling enzymes. <i>Journal of Biological Chemistry</i> , 2000 , 275, 18864-70	5.4	87
21	Multiple ISWI ATPase complexes from xenopus laevis. Functional conservation of an ACF/CHRAC homolog. <i>Journal of Biological Chemistry</i> , 2000 , 275, 35248-55	5.4	64
20	Generation of superhelical torsion by ATP-dependent chromatin remodeling activities. <i>Cell</i> , 2000 , 103, 1133-42	56.2	233
19	Active remodeling of somatic nuclei in egg cytoplasm by the nucleosomal ATPase ISWI. <i>Science</i> , 2000 , 289, 2360-2	33.3	192
18	ATP-Dependent histone octamer mobilization and histone deacetylation mediated by the Mi-2 chromatin remodeling complex. <i>Biochemistry</i> , 2000 , 39, 5238-45	3.2	76
17	Purification of a histone deacetylase complex from <i>Xenopus laevis</i> : preparation of substrates and assay procedures. <i>Methods in Enzymology</i> , 1999 , 304, 715-25	1.7	14
16	DNA demethylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 5894-6	11.5	135
15	Mi-2 complex couples DNA methylation to chromatin remodelling and histone deacetylation. <i>Nature Genetics</i> , 1999 , 23, 62-6	36.3	639
14	Transcriptional regulation: SWItching circuitry. <i>Current Biology</i> , 1999 , 9, R221-4	6.3	37
13	Characterization of a chromatin remodelling activity in <i>Xenopus</i> oocytes. <i>FEBS Journal</i> , 1999 , 262, 426-34		19
12	Functional analysis of the SIN3-histone deacetylase RPD3-RbAp48-histone H4 connection in the <i>Xenopus</i> oocyte. <i>Molecular and Cellular Biology</i> , 1999 , 19, 5847-60	4.8	63
11	Methylated DNA and MeCP2 recruit histone deacetylase to repress transcription. <i>Nature Genetics</i> , 1998 , 19, 187-91	36.3	2246
10	A multiple subunit Mi-2 histone deacetylase from <i>Xenopus laevis</i> cofractionates with an associated Snf2 superfamily ATPase. <i>Current Biology</i> , 1998 , 8, 843-6	6.3	382
9	Histone deacetylase directs the dominant silencing of transcription in chromatin: association with MeCP2 and the Mi-2 chromodomain SWI/SNF ATPase. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1998 , 63, 435-45	3.9	55
8	Cdc73p and Paf1p are found in a novel RNA polymerase II-containing complex distinct from the Srbp-containing holoenzyme. <i>Molecular and Cellular Biology</i> , 1997 , 17, 1160-9	4.8	125
7	Histone acetyltransferases in control. <i>Current Biology</i> , 1997 , 7, R82-4	6.3	126
6	Histone acetylation: chromatin in action. <i>Trends in Biochemical Sciences</i> , 1997 , 22, 128-32	10.3	402
5	A novel collection of accessory factors associated with yeast RNA polymerase II. <i>Protein Expression and Purification</i> , 1996 , 8, 85-90	2	79

4	Isolation of yeast transcription factor IIA using a functional transcription assay. <i>Protein Expression and Purification</i> , 1994 , 5, 577-82	2	2
3	Resolution of transcription factors from a transcriptionally active whole-cell extract from yeast: purification of TFIIB, TBP, and RNA polymerase Ila. <i>Protein Expression and Purification</i> , 1993 , 4, 290-7	2	6
2	Transcriptional activation in an improved whole-cell extract from <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1991 , 11, 4555-60	4.8	94
1	DNA Demethylation1-5		