

Paul A Wade

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5287594/paul-a-wade-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Methylated DNA and MeCP2 recruit histone deacetylase to repress transcription. <i>Nature Genetics</i> , 1998 , 19, 187-91	36.3	2246
128	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
127	Mi-2 complex couples DNA methylation to chromatin remodelling and histone deacetylation. <i>Nature Genetics</i> , 1999 , 23, 62-6	36.3	639
126	Rhythmic histone acetylation underlies transcription in the mammalian circadian clock. <i>Nature</i> , 2003 , 421, 177-82	50.4	545
125	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
124	Histone acetylation: chromatin in action. <i>Trends in Biochemical Sciences</i> , 1997 , 22, 128-32	10.3	402
123	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
122	The human Mi-2/NuRD complex and gene regulation. <i>Oncogene</i> , 2007 , 26, 5433-8	9.2	354
121	Cancer biology and NuRD: a multifaceted chromatin remodelling complex. <i>Nature Reviews Cancer</i> , 2011 , 11, 588-96	31.3	337
120	Methyl CpG-binding proteins and transcriptional repression. <i>BioEssays</i> , 2001 , 23, 1131-7	4.1	279
119	MTA3 and the Mi-2/NuRD complex regulate cell fate during B lymphocyte differentiation. <i>Cell</i> , 2004 , 119, 75-86	56.2	269
118	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
117	Mi-2/NuRD: multiple complexes for many purposes. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004 , 1677, 52-7		240
116	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
115	Generation of superhelical torsion by ATP-dependent chromatin remodeling activities. <i>Cell</i> , 2000 , 103, 1133-42	56.2	233
114	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
113	Active remodeling of somatic nuclei in egg cytoplasm by the nucleosomal ATPase ISWI. <i>Science</i> , 2000 , 289, 2360-2	33.3	192

112	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
111	WSTF-ISWI chromatin remodeling complex targets heterochromatic replication foci. <i>EMBO Journal</i> , 2002 , 21, 2231-41	13	175
110	Methyl CpG binding proteins: coupling chromatin architecture to gene regulation. <i>Oncogene</i> , 2001 , 20, 3166-73	9.2	166
109	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
108	The transcription factor snail mediates epithelial to mesenchymal transitions by repression of estrogen receptor-alpha. <i>Molecular Endocrinology</i> , 2007 , 21, 2907-18		151
107	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , 2002 , 9, 263-7		148
106	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
105	DNA demethylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 5894-6	11.5	135
104	Histone acetyltransferases in control. <i>Current Biology</i> , 1997 , 7, R82-4	6.3	126
103	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
102	The NuRD architecture. <i>Cellular and Molecular Life Sciences</i> , 2013 , 70, 3513-24	10.3	121
101	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
100	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
99	Crosstalk between the microbiome and epigenome: messages from bugs. <i>Journal of Biochemistry</i> , 2018 , 163, 105-112	3.1	104
98	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
97	Specific targeting and constitutive association of histone deacetylase complexes during transcriptional repression. <i>Genes and Development</i> , 2002 , 16, 687-92	12.6	104
96	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
95	Human tRNA genes function as chromatin insulators. <i>EMBO Journal</i> , 2012 , 31, 330-50	13	99

94	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
93	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
92	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
91	MBD family proteins: reading the epigenetic code. <i>Journal of Cell Science</i> , 2006 , 119, 3033-7	5.3	93
90	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
89	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
88	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
87	NuRD and pluripotency: a complex balancing act. <i>Cell Stem Cell</i> , 2012 , 10, 497-503	18	83
86	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
85	Multiple N-CoR complexes contain distinct histone deacetylases. <i>Journal of Biological Chemistry</i> , 2001 , 276, 8807-11	5.4	80
84	MBD3 localizes at promoters, gene bodies and enhancers of active genes. <i>PLoS Genetics</i> , 2013 , 9, e1004028	10.28	79
83	A novel collection of accessory factors associated with yeast RNA polymerase II. <i>Protein Expression and Purification</i> , 1996 , 8, 85-90	2	79
82	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
81	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
80	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
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	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. <i>Genome Biology</i> , 2016 , 17, 36	18.3	74
77	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

76	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
75	Functional analysis of the SIN3-histone deacetylase RPD3-RbAp48-histone H4 connection in the <i>Xenopus oocyte</i> . <i>Molecular and Cellular Biology</i> , 1999 , 19, 5847-60	4.8	63
74	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
73	GATA3 in Breast Cancer: Tumor Suppressor or Oncogene?. <i>Gene Expression</i> , 2015 , 16, 163-8	3.4	58
72	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
71	Reversing SKI-SMAD4-mediated suppression is essential for T17 cell differentiation. <i>Nature</i> , 2017 , 551, 105-109	5.4	55
70	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
69	Hormonal regulation of metastasis-associated protein 3 transcription in breast cancer cells. <i>Molecular Endocrinology</i> , 2004 , 18, 2937-49		53
68	Yin yang 1 regulates the expression of snail through a distal enhancer. <i>Molecular Cancer Research</i> , 2009 , 7, 221-9	6.6	52
67	GATA3 zinc finger 2 mutations reprogram the breast cancer transcriptional network. <i>Nature Communications</i> , 2018 , 9, 1059	17.4	45
66	Obesity, rather than diet, drives epigenomic alterations in colonic epithelium resembling cancer progression. <i>Cell Metabolism</i> , 2014 , 19, 702-11	24.6	44
65	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
64	Chromatin remodeling in nuclear cloning. <i>FEBS Journal</i> , 2002 , 269, 2284-7		42
63	Inhibition of histone binding by supramolecular hosts. <i>Biochemical Journal</i> , 2014 , 459, 505-12	3.8	41
62	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
61	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
60	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
59	Breast tumor specific mutation in GATA3 affects physiological mechanisms regulating transcription factor turnover. <i>BMC Cancer</i> , 2014 , 14, 278	4.8	38

58	Transcriptional regulation: SWItching circuitry. <i>Current Biology</i> , 1999 , 9, R221-4	6.3	37
57	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
56	Epigenetics and the adaptive immune response. <i>Molecular Aspects of Medicine</i> , 2013 , 34, 813-25	16.7	35
55	A Drosophila MBD family member is a transcriptional corepressor associated with specific genes. <i>FEBS Journal</i> , 2001 , 268, 5397-406		35
54	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
53	Genome-wide binding of MBD2 reveals strong preference for highly methylated loci. <i>PLoS ONE</i> , 2014 , 9, e99603	3.7	34
52	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
51	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
50	Use of bifunctional cross-linking reagents in mapping genomic distribution of chromatin remodeling complexes. <i>Methods</i> , 2004 , 33, 81-5	4.6	31
49	Chromosomal regulation by MeCP2: structural and enzymatic considerations. <i>Cellular and Molecular Life Sciences</i> , 2004 , 61, 2163-7	10.3	29
48	Rif1 promotes a repressive chromatin state to safeguard against endogenous retrovirus activation. <i>Nucleic Acids Research</i> , 2017 , 45, 12723-12738	20.1	28
47	Proteins That Read DNA Methylation. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 945, 303-320	3.6	28
46	A 3Tenhancer controls snail expression in melanoma cells. <i>Cancer Research</i> , 2007 , 67, 6113-20	10.1	27
45	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
44	SnapShot: Chromatin remodeling: CHD. <i>Cell</i> , 2011 , 144, 626-626.e1	56.2	24
43	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
42	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
41	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

40	Dosage compensation and DNA methylation landscape of the X chromosome in mouse liver. <i>Scientific Reports</i> , 2018 , 8, 10138	4.9	21
39	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. <i>Cell Reports</i> , 2017 , 21, 455-466	10.6	20
38	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
37	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
36	Characterization of a chromatin remodelling activity in <i>Xenopus</i> oocytes. <i>FEBS Journal</i> , 1999 , 262, 426-34		19
35	Epigenetic control of <i>Ccr7</i> expression in distinct lineages of lung dendritic cells. <i>Journal of Immunology</i> , 2014 , 193, 4904-13	5.3	18
34	Cryo-EM structure of the nucleosome containing the enhancer DNA sequence. <i>Open Biology</i> , 2018 , 8,	7	16
33	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
32	Interaction of the pioneer transcription factor GATA3 with nucleosomes. <i>Nature Communications</i> , 2020 , 11, 4136	17.4	16
31	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
30	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
29	Alterations in promoter interaction landscape and transcriptional network underlying metabolic adaptation to diet. <i>Nature Communications</i> , 2020 , 11, 962	17.4	14
28	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
27	MyD88-dependent dendritic and epithelial cell crosstalk orchestrates immune responses to allergens. <i>Mucosal Immunology</i> , 2018 , 11, 796-810	9.2	14
26	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
25	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. <i>Nature Communications</i> , 2021 , 12, 2490	17.4	13
24	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
23	Dynamic regulation of DNA methylation coupled transcriptional repression: BDNF regulation by MeCP2. <i>BioEssays</i> , 2004 , 26, 217-20	4.1	11

22	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
21	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
20	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
19	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
18	Resolution of transcription factors from a transcriptionally active whole-cell extract from yeast: purification of TFIIB, TBP, and RNA polymerase IIa. <i>Protein Expression and Purification</i> , 1993 , 4, 290-7	2	6
17	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
16	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
15	High-quality CHIP-seq analysis of MBD3 in human breast cancer cells. <i>Genomics Data</i> , 2016 , 7, 173-4		3
14	R loops: lassoing DNA methylation at CpGi. <i>Molecular Cell</i> , 2012 , 45, 708-9	17.6	2
13	Isolation of yeast transcription factor IIA using a functional transcription assay. <i>Protein Expression and Purification</i> , 1994 , 5, 577-82	2	2
12	A simple and robust method for simultaneous dual-omics profiling with limited numbers of cells. <i>Cell Reports Methods</i> , 2021 , 1,		2
11	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
10	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
9	Purification of MeCP2-containing deacetylase from <i>Xenopus laevis</i> . <i>Methods in Molecular Biology</i> , 2002 , 200, 131-41	1.4	1
8	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
7	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
6	Chromatin Structure and Gene Expression: Function Follows Form. <i>Epigenetics and Human Health</i> , 2013 , 189-205		
5	Are genomic translocations predictable? (Retrospective on DOI 10.1002/bies.201100122). <i>BioEssays</i> , 2014 , 36, 633	4.1	

- 4 Methods for preparation and assays for Xenopus ISWI complexes. *Methods in Enzymology*, **2004**, 377, 364-75 1.7
- 3 Epigenetic remodelling upon FGFR inhibition. *Nature Cell Biology*, **2021**, 23, 1115-1116 23.4
- 2 DNA Demethylation1-5
- 1 Epigenetics, Obesity, and Colon Cancer. *Energy Balance and Cancer*, **2016**, 211-233 0.2