

Paul A Wade

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5287594/publications.pdf>

Version: 2024-02-01

133
papers

16,284
citations

19636

61
h-index

16164

124
g-index

141
all docs

141
docs citations

141
times ranked

18529
citing authors

#	ARTICLE	IF	CITATIONS
1	Methylated DNA and MeCP2 recruit histone deacetylase to repress transcription. <i>Nature Genetics</i> , 1998, 19, 187-191.	9.4	2,484
2	DNMT1 forms a complex with Rb, E2F1 and HDAC1 and represses transcription from E2F-responsive promoters. <i>Nature Genetics</i> , 2000, 25, 338-342.	9.4	884
3	Mi-2 complex couples DNA methylation to chromatin remodelling and histone deacetylation. <i>Nature Genetics</i> , 1999, 23, 62-66.	9.4	720
4	Rhythmic histone acetylation underlies transcription in the mammalian circadian clock. <i>Nature</i> , 2003, 421, 177-182.	13.7	600
5	MTA3, a Mi-2/NuRD Complex Subunit, Regulates an Invasive Growth Pathway in Breast Cancer. <i>Cell</i> , 2003, 113, 207-219.	13.5	483
6	Histone acetylation: chromatin in action. <i>Trends in Biochemical Sciences</i> , 1997, 22, 128-132.	3.7	441
7	Cancer biology and NuRD: a multifaceted chromatin remodelling complex. <i>Nature Reviews Cancer</i> , 2011, 11, 588-596.	12.8	435
8	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, 843-848.	1.8	416
9	The human Mi-2/NuRD complex and gene regulation. <i>Oncogene</i> , 2007, 26, 5433-5438.	2.6	409
10	Methyl CpG-binding proteins and transcriptional repression. <i>BioEssays</i> , 2001, 23, 1131-1137.	1.2	315
11	Aberrant Expression of the Transcription Factors Snail and Slug Alters the Response to Genotoxic Stress. <i>Molecular and Cellular Biology</i> , 2004, 24, 7559-7566.	1.1	305
12	MTA3 and the Mi-2/NuRD Complex Regulate Cell Fate during B Lymphocyte Differentiation. <i>Cell</i> , 2004, 119, 75-86.	13.5	298
13	Transcriptional control at regulatory checkpoints by histone deacetylases: molecular connections between cancer and chromatin. <i>Human Molecular Genetics</i> , 2001, 10, 693-698.	1.4	272
14	Mi-2/NuRD: multiple complexes for many purposes. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1677, 52-57.	2.4	261
15	Chromatin Compaction by Human MeCP2. <i>Journal of Biological Chemistry</i> , 2003, 278, 32181-32188.	1.6	259
16	Generation of Superhelical Torsion by ATP-Dependent Chromatin Remodeling Activities. <i>Cell</i> , 2000, 103, 1133-1142.	13.5	241
17	Active Remodeling of Somatic Nuclei in Egg Cytoplasm by the Nucleosomal ATPase ISWI. <i>Science</i> , 2000, 289, 2360-2362.	6.0	211
18	The affinity of different MBD proteins for a specific methylated locus depends on their intrinsic binding properties. <i>Nucleic Acids Research</i> , 2003, 31, 1765-1774.	6.5	202

#	ARTICLE	IF	CITATIONS
19	WSTF-ISWI chromatin remodeling complex targets heterochromatic replication foci. <i>EMBO Journal</i> , 2002, 21, 2231-2241.	3.5	201
20	Methyl CpG binding proteins: coupling chromatin architecture to gene regulation. <i>Oncogene</i> , 2001, 20, 3166-3173.	2.6	181
21	Identification of DNA Methylation Changes in Newborns Related to Maternal Smoking during Pregnancy. <i>Environmental Health Perspectives</i> , 2014, 122, 1147-1153.	2.8	171
22	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, 1540-1554.	2.7	169
23	The Transcription Factor Snail Mediates Epithelial to Mesenchymal Transitions by Repression of Estrogen Receptor- β . <i>Molecular Endocrinology</i> , 2007, 21, 2907-2918.	3.7	166
24	Crosstalk between the microbiome and epigenome: messages from bugs. <i>Journal of Biochemistry</i> , 2018, 163, 105-112.	0.9	163
25	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , 2002, 9, 263-267.	9.7	160
26	DNA demethylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 5894-5896.	3.3	153
27	The NuRD architecture. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 3513-3524.	2.4	153
28	INO80 Facilitates Pluripotency Gene Activation in Embryonic Stem Cell Self-Renewal, Reprogramming, and Blastocyst Development. <i>Cell Stem Cell</i> , 2014, 14, 575-591.	5.2	148
29	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, 1160-1169.	1.1	142
30	The Transcription Factors Snail and Slug Activate the Transforming Growth Factor-Beta Signaling Pathway in Breast Cancer. <i>PLoS ONE</i> , 2011, 6, e26514.	1.1	137
31	Chromatin: Histone acetyltransferases in control. <i>Current Biology</i> , 1997, 7, R82-R84.	1.8	136
32	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.	7.7	130
33	Human tRNA genes function as chromatin insulators. <i>EMBO Journal</i> , 2012, 31, 330-350.	3.5	129
34	DNA methylation prevents CTCF-mediated silencing of the oncogene <i>BCL6</i> in B cell lymphomas. <i>Journal of Experimental Medicine</i> , 2010, 207, 1939-1950.	4.2	124
35	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. <i>Genome Biology</i> , 2016, 17, 36.	3.8	121
36	An obesity-associated gut microbiome reprograms the intestinal epigenome and leads to altered colonic gene expression. <i>Genome Biology</i> , 2018, 19, 7.	3.8	117

#	ARTICLE	IF	CITATIONS
37	Intrinsic Disorder and Autonomous Domain Function in the Multifunctional Nuclear Protein, MeCP2. <i>Journal of Biological Chemistry</i> , 2007, 282, 15057-15064.	1.6	115
38	Nucleophosmin/B23, a Nuclear PI(3,4,5)P3 Receptor, Mediates the Antiapoptotic Actions of NGF by Inhibiting CAD. <i>Molecular Cell</i> , 2005, 18, 435-445.	4.5	114
39	Specific targeting and constitutive association of histone deacetylase complexes during transcriptional repression. <i>Genes and Development</i> , 2002, 16, 687-692.	2.7	112
40	MBD family proteins: reading the epigenetic code. <i>Journal of Cell Science</i> , 2006, 119, 3033-3037.	1.2	108
41	Nuclear Akt associates with PKC-phosphorylated Ebp1, preventing DNA fragmentation by inhibition of caspase-activated DNase. <i>EMBO Journal</i> , 2006, 25, 2083-2095.	3.5	108
42	NuRD and Pluripotency: A Complex Balancing Act. <i>Cell Stem Cell</i> , 2012, 10, 497-503.	5.2	99
43	MBD3 Localizes at Promoters, Gene Bodies and Enhancers of Active Genes. <i>PLoS Genetics</i> , 2013, 9, e1004028.	1.5	97
44	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, 787-792.	3.3	96
45	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.	2.2	96
46	Transcriptional activation in an improved whole-cell extract from <i>Saccharomyces cerevisiae</i> .. <i>Molecular and Cellular Biology</i> , 1991, 11, 4555-4560.	1.1	95
47	Functional Delineation of Three Groups of the ATP-dependent Family of Chromatin Remodeling Enzymes. <i>Journal of Biological Chemistry</i> , 2000, 275, 18864-18870.	1.6	95
48	A Novel Collection of Accessory Factors Associated with Yeast RNA Polymerase II. <i>Protein Expression and Purification</i> , 1996, 8, 85-90.	0.6	94
49	The MBD protein familyâ€”Reading an epigenetic mark?. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 647, 39-43.	0.4	94
50	Comprehensive structure-function characterization of DNMT3B and DNMT3A reveals distinctive de novo DNA methylation mechanisms. <i>Nature Communications</i> , 2020, 11, 3355.	5.8	94
51	DNA methylation profiling in human B cells reveals immune regulatory elements and epigenetic plasticity at <i>Alu</i> elements during B-cell activation. <i>Genome Research</i> , 2013, 23, 2030-2041.	2.4	93
52	GATA3 in Breast Cancer: Tumor Suppressor or Oncogene?. <i>Gene Expression</i> , 2015, 16, 163-168.	0.5	90
53	Reversing SKIâ€”SMAD4-mediated suppression is essential for TH17 cell differentiation. <i>Nature</i> , 2017, 551, 105-109.	13.7	88
54	Multiple N-CoR Complexes Contain Distinct Histone Deacetylases. <i>Journal of Biological Chemistry</i> , 2001, 276, 8807-8811.	1.6	86

#	ARTICLE	IF	CITATIONS
55	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, 3364-3377.	6.5	84
56	Mi-2 ^{Δ2} 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, 51638-51645.	1.6	82
57	ATP-Dependent Histone Octamer Mobilization and Histone Deacetylation Mediated by the Mi-2 Chromatin Remodeling Complex. <i>Biochemistry</i> , 2000, 39, 5238-5245.	1.2	79
58	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, 3094-3102.	0.9	74
59	GATA3 zinc finger 2 mutations reprogram the breast cancer transcriptional network. <i>Nature Communications</i> , 2018, 9, 1059.	5.8	72
60	CHD3 helicase domain mutations cause a neurodevelopmental syndrome with macrocephaly and impaired speech and language. <i>Nature Communications</i> , 2018, 9, 4619.	5.8	70
61	Multiple ISWI ATPase Complexes from <i>Xenopus laevis</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 35248-35255.	1.6	67
62	Yin Yang 1 Regulates the Expression of <i>Snail</i> through a Distal Enhancer. <i>Molecular Cancer Research</i> , 2009, 7, 221-229.	1.5	67
63	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, 5847-5860.	1.1	64
64	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. <i>Nature Communications</i> , 2021, 12, 2490.	5.8	63
65	Maternal Age at Delivery Is Associated with an Epigenetic Signature in Both Newborns and Adults. <i>PLoS ONE</i> , 2016, 11, e0156361.	1.1	62
66	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.	3.3	62
67	Obesity, Rather Than Diet, Drives Epigenomic Alterations in Colonic Epithelium Resembling Cancer Progression. <i>Cell Metabolism</i> , 2014, 19, 702-711.	7.2	61
68	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, 435-446.	2.0	61
69	Interaction of the pioneer transcription factor GATA3 with nucleosomes. <i>Nature Communications</i> , 2020, 11, 4136.	5.8	60
70	Hormonal Regulation of Metastasis-Associated Protein 3 Transcription in Breast Cancer Cells. <i>Molecular Endocrinology</i> , 2004, 18, 2937-2949.	3.7	59
71	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.	2.9	53
72	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.	1.1	53

#	ARTICLE	IF	CITATIONS
73	Rif1 promotes a repressive chromatin state to safeguard against endogenous retrovirus activation. <i>Nucleic Acids Research</i> , 2017, 45, 12723-12738.	6.5	49
74	Inhibition of histone binding by supramolecular hosts. <i>Biochemical Journal</i> , 2014, 459, 505-512.	1.7	48
75	Chromatin remodeling in nuclear cloning. <i>FEBS Journal</i> , 2002, 269, 2284-2287.	0.2	47
76	Breast tumor specific mutation in GATA3 affects physiological mechanisms regulating transcription factor turnover. <i>BMC Cancer</i> , 2014, 14, 278.	1.1	47
77	MeCP2 in Rett syndrome: transcriptional repressor or chromatin architectural protein?. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 121-125.	1.5	46
78	Epigenetics and the adaptive immune response. <i>Molecular Aspects of Medicine</i> , 2013, 34, 813-825.	2.7	44
79	Genome-Wide Binding of MBD2 Reveals Strong Preference for Highly Methylated Loci. <i>PLoS ONE</i> , 2014, 9, e99603.	1.1	44
80	Proteins That Read DNA Methylation. <i>Advances in Experimental Medicine and Biology</i> , 2016, 945, 303-320.	0.8	42
81	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.	3.3	42
82	Transcriptional regulation: SWItching circuitry. <i>Current Biology</i> , 1999, 9, R221-R224.	1.8	40
83	Diethylstilbestrol (DES)-Stimulated Hormonal Toxicity is Mediated by ER \pm 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, 262-268.	2.8	40
84	Epigenetic Control of <i>Ccr7</i> Expression in Distinct Lineages of Lung Dendritic Cells. <i>Journal of Immunology</i> , 2014, 193, 4904-4913.	0.4	40
85	DNA methylation in mice is influenced by genetics as well as sex and life experience. <i>Nature Communications</i> , 2019, 10, 305.	5.8	40
86	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.	6.5	40
87	Dosage compensation and DNA methylation landscape of the X chromosome in mouse liver. <i>Scientific Reports</i> , 2018, 8, 10138.	1.6	38
88	A Drosophila MBD family member is a transcriptional corepressor associated with specific genes. <i>FEBS Journal</i> , 2001, 268, 5397-5406.	0.2	37
89	The Mi-2/NuRD complex associates with pericentromeric heterochromatin during S phase in rapidly proliferating lymphoid cells. <i>Chromosoma</i> , 2009, 118, 445-457.	1.0	37
90	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, 267-277.	2.3	36

#	ARTICLE	IF	CITATIONS
91	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. <i>Cell Reports</i> , 2017, 21, 455-466.	2.9	36
92	ReCoGnizing methylated DNA. , 2001, 8, 575-577.		34
93	DNA damage repair and transcription. <i>Cellular and Molecular Life Sciences</i> , 2004, 61, 2163-7.	2.4	32
94	Use of bifunctional cross-linking reagents in mapping genomic distribution of chromatin remodeling complexes. <i>Methods</i> , 2004, 33, 81-85.	1.9	32
95	Guest Editorial: Epigenetics: Environmental Instructions for the Genome. <i>Environmental Health Perspectives</i> , 2006, 114, A140-1.	2.8	32
96	SnapShot: Chromatin Remodeling: CHD. <i>Cell</i> , 2011, 144, 626-626.e1.	13.5	31
97	Cryo-EM structure of the nucleosome containing the <i>ALB1</i> enhancer DNA sequence. <i>Open Biology</i> , 2018, 8, .	1.5	31
98	Alterations in promoter interaction landscape and transcriptional network underlying metabolic adaptation to diet. <i>Nature Communications</i> , 2020, 11, 962.	5.8	31
99	A 3â€² Enhancer Controls Snail Expression in Melanoma Cells. <i>Cancer Research</i> , 2007, 67, 6113-6120.	0.4	30
100	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, 106-115.	2.1	25
101	BCL-2 family protein, BAD is down-regulated in breast cancer and inhibits cell invasion. <i>Experimental Cell Research</i> , 2015, 331, 1-10.	1.2	25
102	Epsteinâ€™Barr virus infection leads to partial phenotypic reversion of terminally differentiated malignant B cells. <i>Cancer Letters</i> , 2009, 284, 165-174.	3.2	24
103	Characterization of a chromatin remodelling activity in <i>Xenopus</i> oocytes. <i>FEBS Journal</i> , 1999, 262, 426-434.	0.2	22
104	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, 30562-30568.	1.6	19
105	DNA methylation and transcriptome aberrations mediated by ERÎ± 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.	3.3	18
106	MyD88-dependent dendritic and epithelial cell crosstalk orchestrates immune responses to allergens. <i>Mucosal Immunology</i> , 2018, 11, 796-810.	2.7	18
107	Structure of the SANT domain from the <i>Xenopus</i> chromatin remodeling factor ISWI. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 1198-1202.	1.5	16
108	Maternal Influence and Murine Housing Confound Impact of NLRP1 Inflammasome on Microbiome Composition. <i>Journal of Innate Immunity</i> , 2019, 11, 416-431.	1.8	15

#	ARTICLE	IF	CITATIONS
109	Purification of a histone deacetylase complex from <i>Xenopus laevis</i> : Preparation of substrates and assay procedures. <i>Methods in Enzymology</i> , 1999, 304, 715-725.	0.4	14
110	Metastasis-Associated Protein 3 (MTA3) Regulates G2/M Progression in Proliferating Mouse Granulosa Cells. <i>Biology of Reproduction</i> , 2012, 86, 1-8.	1.2	14
111	The estrogen receptor/GATA3/FOXA1 transcriptional network: lessons learned from breast cancer. <i>Current Opinion in Structural Biology</i> , 2021, 71, 65-70.	2.6	14
112	Dynamic regulation of DNA methylation coupled transcriptional repression: BDNF regulation by MeCP2. <i>BioEssays</i> , 2004, 26, 217-220.	1.2	11
113	Fine-tuning of epigenetic regulation with respect to promoter CpG content in a cell type-specific manner. <i>Epigenetics</i> , 2014, 9, 747-759.	1.3	11
114	Purification of the MeCP2/Histone Deacetylase Complex from <i>Xenopus laevis</i> . , 2002, 181, 297-307.		9
115	SWitching off methylated DNA. <i>Nature Genetics</i> , 2005, 37, 212-213.	9.4	8
116	Base-Resolution Analysis of DNA Methylation Patterns Downstream of <i>Dnmt3a</i> in Mouse Na ⁺ ve B Cells. <i>Genes, Genomes, Genetics</i> , 2018, 8, 805-813.	0.8	8
117	DNA Methylation Changes in <i>Tbx3</i> in a Mouse Model Exposed to Polybrominated Diphenyl Ethers. <i>International Journal of Toxicology</i> , 2017, 36, 229-238.	0.6	7
118	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, 290-297.	0.6	6
119	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, 100118.	1.4	6
120	Nuclear transfer: Epigenetics pays a visit. <i>Nature Cell Biology</i> , 2004, 6, 920-922.	4.6	5
121	High-quality ChIP-seq analysis of MBD3 in human breast cancer cells. <i>Genomics Data</i> , 2016, 7, 173-174.	1.3	5
122	Low-input ATAC&mRNA-seq protocol for simultaneous profiling of chromatin accessibility and gene expression. <i>STAR Protocols</i> , 2021, 2, 100764.	0.5	5
123	R Loops: Lassoing DNA Methylation at CpG. <i>Molecular Cell</i> , 2012, 45, 708-709.	4.5	4
124	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.	2.2	4
125	A simple and robust method for simultaneous dual-omics profiling with limited numbers of cells. <i>Cell Reports Methods</i> , 2021, 1, 100041.	1.4	3
126	Isolation of Yeast Transcription Factor IIA Using a Functional Transcription Assay. <i>Protein Expression and Purification</i> , 1994, 5, 577-582.	0.6	2

#	ARTICLE	IF	CITATIONS
127	Purification of MeCP2-Containing Deacetylase from <i>Xenopus laevis</i> . , 2002, 200, 131-141.		1
128	Epigenetic remodelling upon FGFR inhibition. <i>Nature Cell Biology</i> , 2021, 23, 1115-1116.	4.6	1
129	Methods for Preparation and Assays for <i>Xenopus</i> ISWI Complexes. <i>Methods in Enzymology</i> , 2003, 377, 364-375.	0.4	0
130	Chromatin Structure and Gene Expression: Function Follows Form. <i>Epigenetics and Human Health</i> , 2013, , 189-205.	0.2	0
131	Are genomic translocations predictable? (Retrospective on DOI 10.1002/bies.201100122). <i>BioEssays</i> , 2014, 36, 633-633.	1.2	0
132	Epigenetics, Obesity, and Colon Cancer. <i>Energy Balance and Cancer</i> , 2016, , 211-233.	0.2	0
133	Integrated Analysis of Colonic DNA Methylome and Transcriptome Predicts Increased Risk of Colorectal Cancer in the Obese. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0