

Tomasz K Wojdacz

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

2,754
citations

304368

22
h-index

276539

41
g-index

42
all docs

42
docs citations

42
times ranked

5328
citing authors

#	ARTICLE	IF	CITATIONS
1	ChAMP: 450k Chip Analysis Methylation Pipeline. <i>Bioinformatics</i> , 2014, 30, 428-430.	1.8	757
2	Methylation-sensitive high resolution melting (MS-HRM): a new approach for sensitive and high-throughput assessment of methylation. <i>Nucleic Acids Research</i> , 2007, 35, e41-e41.	6.5	460
3	Methylation-sensitive high-resolution melting. <i>Nature Protocols</i> , 2008, 3, 1903-1908.	5.5	262
4	Comprehensive Genome Methylation Analysis in Bladder Cancer: Identification and Validation of Novel Methylated Genes and Application of These as Urinary Tumor Markers. <i>Clinical Cancer Research</i> , 2011, 17, 5582-5592.	3.2	183
5	Identification and validation of highly frequent CpG island hypermethylation in colorectal adenomas and carcinomas. <i>International Journal of Cancer</i> , 2011, 129, 2855-2866.	2.3	140
6	A new approach to primer design for the control of PCR bias in methylation studies. <i>BMC Research Notes</i> , 2008, 1, 54.	0.6	117
7	Primer design versus PCR bias in methylation independent PCR amplifications. <i>Epigenetics</i> , 2009, 4, 231-234.	1.3	91
8	Reversal of PCR bias for improved sensitivity of the DNA methylation melting curve assay. <i>BioTechniques</i> , 2006, 41, 274-278.	0.8	61
9	Quality assessment of DNA derived from up to 30 years old formalin fixed paraffin embedded (FFPE) tissue for PCR-based methylation analysis using SMART-MSP and MS-HRM. <i>BMC Cancer</i> , 2009, 9, 453.	1.1	61
10	Limitations and advantages of MS-HRM and bisulfite sequencing for single locus methylation studies. <i>Expert Review of Molecular Diagnostics</i> , 2010, 10, 575-580.	1.5	59
11	Identification and validation of candidate epigenetic biomarkers in lung adenocarcinoma. <i>Scientific Reports</i> , 2016, 6, 35807.	1.6	54
12	Rapid detection of methylation change at H19 in human imprinting disorders using methylation-sensitive high-resolution melting. <i>Human Mutation</i> , 2008, 29, 1255-1260.	1.1	51
13	Combining genetic and epigenetic parameters of the serotonin transporter gene in obsessive-compulsive disorder. <i>Journal of Psychiatric Research</i> , 2018, 96, 209-217.	1.5	43
14	Methylation of the BRCA1 promoter in peripheral blood DNA is associated with triple-negative and medullary breast cancer. <i>Breast Cancer Research and Treatment</i> , 2014, 148, 615-622.	1.1	34
15	BRCA1 promoter methylation in peripheral blood is associated with the risk of triple-negative breast cancer. <i>International Journal of Cancer</i> , 2020, 146, 1293-1298.	2.3	33
16	COVID-19 – The Potential Beneficial Therapeutic Effects of Spironolactone during SARS-CoV-2 Infection. <i>Pharmaceuticals</i> , 2021, 14, 71.	1.7	33
17	Prenatal lead exposure is associated with decreased cord blood DNA methylation of the glycoprotein VI gene involved in platelet activation and thrombus formation. <i>Environmental Epigenetics</i> , 2015, 1, dvv007.	0.9	28
18	Transcriptomics and methylomics of CD4-positive T cells in arsenic-exposed women. <i>Archives of Toxicology</i> , 2017, 91, 2067-2078.	1.9	26

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19	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. <i>Blood Advances</i> , 2019, 3, 2474-2481.	2.5	25
20	Identification and characterization of locus-specific methylation patterns within novel loci undergoing hypermethylation during breast cancer pathogenesis. <i>Breast Cancer Research</i> , 2014, 16, R17.	2.2	24
21	Techniques Used in Studies of Age-Related DNA Methylation Changes. <i>Annals of the New York Academy of Sciences</i> , 2006, 1067, 479-487.	1.8	23
22	Challenges for the application of DNA methylation biomarkers in molecular diagnostic testing for cancer. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 283-294.	1.5	22
23	The influence of DNA degradation in formalin-fixed, paraffin-embedded (FFPE) tissue on locus-specific methylation assessment by MS-HRM. <i>Experimental and Molecular Pathology</i> , 2015, 99, 632-640.	0.9	22
24	No difference in the frequency of locus-specific methylation in the peripheral blood DNA of women diagnosed with breast cancer and age-matched controls. <i>Future Oncology</i> , 2011, 7, 1451-1455.	1.1	19
25	Methylation-sensitive high-resolution melting in the context of legislative requirements for validation of analytical procedures for diagnostic applications. <i>Expert Review of Molecular Diagnostics</i> , 2012, 12, 39-47.	1.5	19
26	Melting Curve Assays for DNA Methylation Analysis. <i>Methods in Molecular Biology</i> , 2009, 507, 229-240.	0.4	18
27	Methylation of cancer related genes in tumor and peripheral blood DNA from the same breast cancer patient as two independent events. <i>Diagnostic Pathology</i> , 2011, 6, 116.	0.9	17
28	Alterations of telomere length and <sc>DNA</sc> methylation in hairdressers: A cross-sectional study. <i>Environmental and Molecular Mutagenesis</i> , 2016, 57, 159-167.	0.9	15
29	The Limitations of Locus Specific Methylation Qualification and Quantification in Clinical Material. <i>Frontiers in Genetics</i> , 2012, 3, 21.	1.1	10
30	Short history of 5-methylcytosine: from discovery to clinical applications. <i>Journal of Clinical Pathology</i> , 2021, 74, 692-696.	1.0	8
31	Chronic lymphocytic leukemia patients with heterogeneously or fully methylated <i>LPL</i> promotor display longer time to treatment. <i>Epigenomics</i> , 2018, 10, 1155-1166.	1.0	7
32	Bortezomib induces methylation changes in neuroblastoma cells that appear to play a significant role in resistance development to this compound. <i>Scientific Reports</i> , 2021, 11, 9846.	1.6	7
33	IGHV-associated methylation signatures more accurately predict clinical outcomes of chronic lymphocytic leukemia patients than IGHV mutation load. <i>Haematologica</i> , 2022, 107, 877-886.	1.7	5
34	Epigenetic activation of antiviral sensors and effectors of interferon response pathways during SARS-CoV-2 infection. <i>Biomedicine and Pharmacotherapy</i> , 2022, 153, 113396.	2.5	5
35	MS-HRM assay identifies high levels of epigenetic heterogeneity in human immortalized cell lines. <i>Gene</i> , 2015, 560, 165-172.	1.0	3
36	Gene silencing of Nox4 by CpG island methylation during hepatocarcinogenesis in rats. <i>Biology Open</i> , 2016, 6, 59-70.	0.6	3

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37	The transcriptional coregulator MAML1 affects DNA methylation and gene expression patterns in human embryonic kidney cells. <i>Molecular Biology Reports</i> , 2016, 43, 141-150.	1.0	3
38	Long-Term Treatment with Bortezomib Induces Specific Methylation Changes in Differentiated Neuronal Cells. <i>Cancers</i> , 2022, 14, 3402.	1.7	2
39	Current methylation screening methods. <i>Epigenomics</i> , 2009, 1, 223-226.	1.0	1
40	Exposure to arsenic and intra-chromosomal instability in blood. <i>Metallomics</i> , 2014, 6, 1387-1389.	1.0	1
41	Discordant pattern of <i>BRCA1</i> gene epimutation in blood between mothers and daughters. <i>Journal of Clinical Pathology</i> , 2015, 68, 575-577.	1.0	1
42	Methylation biomarker development in the context of the EU regulations for clinical use of in-vitro diagnostic devices. <i>Expert Review of Molecular Diagnostics</i> , 2019, 19, 439-441.	1.5	1