

Tomasz K Wojdacz

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/480032/tomasz-k-wojdacz-publications-by-year.pdf>

Version: 2024-04-20

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.

39
papers

2,134
citations

19
h-index

42
g-index

42
ext. papers

2,499
ext. citations

5.4
avg, IF

4.92
L-index

#	Paper	IF	Citations
39	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	4.9	1
38	-associated methylation signatures more accurately predict clinical outcomes of chronic lymphocytic leukemia patients than mutation load. <i>Haematologica</i> , 2021 ,	6.6	1
37	COVID-19-The Potential Beneficial Therapeutic Effects of Spironolactone during SARS-CoV-2 Infection. <i>Pharmaceuticals</i> , 2021 , 14,	5.2	17
36	Short history of 5-methylcytosine: from discovery to clinical applications. <i>Journal of Clinical Pathology</i> , 2021 , 74, 692-696	3.9	0
35	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	7.5	12
34	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	3.8	1
33	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. <i>Blood Advances</i> , 2019 , 3, 2474-2481	7.8	13
32	Combining genetic and epigenetic parameters of the serotonin transporter gene in obsessive-compulsive disorder. <i>Journal of Psychiatric Research</i> , 2018 , 96, 209-217	5.2	30
31	Chronic lymphocytic leukemia patients with heterogeneously or fully methylated LPL promotor display longer time to treatment. <i>Epigenomics</i> , 2018 , 10, 1155-1166	4.4	6
30	Transcriptomics and methylomics of CD4-positive T cells in arsenic-exposed women. <i>Archives of Toxicology</i> , 2017 , 91, 2067-2078	5.8	20
29	Gene silencing of Nox4 by CpG island methylation during hepatocarcinogenesis in rats. <i>Biology Open</i> , 2017 , 6, 59-70	2.2	3
28	Identification and validation of candidate epigenetic biomarkers in lung adenocarcinoma. <i>Scientific Reports</i> , 2016 , 6, 35807	4.9	41
27	The transcriptional coregulator MAML1 affects DNA methylation and gene expression patterns in human embryonic kidney cells. <i>Molecular Biology Reports</i> , 2016 , 43, 141-50	2.8	3
26	Alterations of telomere length and DNA methylation in hairdressers: A cross-sectional study. <i>Environmental and Molecular Mutagenesis</i> , 2016 , 57, 159-67	3.2	12
25	MS-HRM assay identifies high levels of epigenetic heterogeneity in human immortalized cell lines. <i>Gene</i> , 2015 , 560, 165-72	3.8	3
24	Discordant pattern of BRCA1 gene epimutation in blood between mothers and daughters. <i>Journal of Clinical Pathology</i> , 2015 , 68, 575-7	3.9	1
23	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	2.4	20

22	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, 632-40	4.4	19
21	ChAMP: 450k Chip Analysis Methylation Pipeline. <i>Bioinformatics</i> , 2014 , 30, 428-30	7.2	497
20	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, 615-22	4.4	28
19	Exposure to arsenic and intra-chromosomal instability in blood. <i>Metallomics</i> , 2014 , 6, 1387-9	4.5	0
18	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	8.3	22
17	Challenges for the application of DNA methylation biomarkers in molecular diagnostic testing for cancer. <i>Expert Review of Molecular Diagnostics</i> , 2013 , 13, 283-94	3.8	19
16	The limitations of locus specific methylation qualification and quantification in clinical material. <i>Frontiers in Genetics</i> , 2012 , 3, 21	4.5	9
15	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	3.8	19
14	Identification and validation of highly frequent CpG island hypermethylation in colorectal adenomas and carcinomas. <i>International Journal of Cancer</i> , 2011 , 129, 2855-66	7.5	123
13	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	3	15
12	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, 5582-92	12.9	146
11	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, 1451-5	3.6	18
10	Limitations and advantages of MS-HRM and bisulfite sequencing for single locus methylation studies. <i>Expert Review of Molecular Diagnostics</i> , 2010 , 10, 575-80	3.8	50
9	Primer design versus PCR bias in methylation independent PCR amplifications. <i>Epigenetics</i> , 2009 , 4, 231-4	4.7	76
8	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	4.8	56
7	Melting curve assays for DNA methylation analysis. <i>Methods in Molecular Biology</i> , 2009 , 507, 229-40	1.4	18
6	Methylation-sensitive high-resolution melting. <i>Nature Protocols</i> , 2008 , 3, 1903-8	18.8	217
5	A new approach to primer design for the control of PCR bias in methylation studies. <i>BMC Research Notes</i> , 2008 , 1, 54	2.3	103

4	Rapid detection of methylation change at H19 in human imprinting disorders using methylation-sensitive high-resolution melting. <i>Human Mutation</i> , 2008 , 29, 1255-60	4.7	46
3	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	20.1	390
2	Reversal of PCR bias for improved sensitivity of the DNA methylation melting curve assay. <i>BioTechniques</i> , 2006 , 41, 274, 276, 278	2.5	55
1	Techniques used in studies of age-related DNA methylation changes. <i>Annals of the New York Academy of Sciences</i> , 2006 , 1067, 479-87	6.5	23