Martin Widschwendter

List of Publications by Year
in descending order

105 papers	12,809 citations	36203 51 h-index	29081 104 g-index
108 all docs	108 docs citations	108 times ranked	17805 citing authors

#	Article	IF	Citations
1	CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. Nature Genetics, 2006, 38, 787-793.	9.4	1,715
2	Epigenetic stem cell signature in cancer. Nature Genetics, 2007, 39, 157-158.	9.4	1,023
3	Ovarian cancer screening and mortality in the UK Collaborative Trial of Ovarian Cancer Screening (UKCTOCS): a randomised controlled trial. Lancet, The, 2016, 387, 945-956.	6.3	791
4	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. Genome Research, 2010, 20, 440-446.	2.4	740
5	Osteoclast differentiation factor RANKL controls development of progestin-driven mammary cancer. Nature, 2010, 468, 98-102.	13.7	507
6	DNA methylation and breast carcinogenesis. Oncogene, 2002, 21, 5462-5482.	2.6	435
7	Menopause accelerates biological aging. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9327-9332.	3.3	363
8	Association of Breast Cancer DNA Methylation Profiles with Hormone Receptor Status and Response to Tamoxifen. Cancer Research, 2004, 64, 3807-3813.	0.4	304
9	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. PLoS ONE, 2009, 4, e8274.	1.1	291
10	Dose-Response Association of CD8+ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. JAMA Oncology, 2017, 3, e173290.	3.4	260
11	DNA methylation in serum of breast cancer patients: an independent prognostic marker. Cancer Research, 2003, 63, 7641-5.	0.4	246
12	Independent surrogate variable analysis to deconvolve confounding factors in large-scale microarray profiling studies. Bioinformatics, 2011, 27, 1496-1505.	1.8	232
13	Circulating Tumor-Specific DNA: A Marker for Monitoring Efficacy of Adjuvant Therapy in Cancer Patients. Cancer Research, 2005, 65, 1141-1145.	0.4	225
14	DNA Hypomethylation and Ovarian Cancer Biology. Cancer Research, 2004, 64, 4472-4480.	0.4	221
15	Correlation of an epigenetic mitotic clock with cancer risk. Genome Biology, 2016, 17, 205.	3.8	197
16	DNA methylation outliers in normal breast tissue identify field defects that are enriched in cancer. Nature Communications, 2016, 7, 10478.	5.8	195
17	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	12.5	178
18	Correlation of Smoking-Associated DNA Methylation Changes in Buccal Cells With DNA Methylation Changes in Epithelial Cancer. JAMA Oncology, 2015, 1, 476.	3.4	177

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19	Breast Cancer DNA Methylation Profiles in Cancer Cells and Tumor Stroma: Association with HER-2/neu Status in Primary Breast Cancer. Cancer Research, 2006, 66, 29-33.	0.4	166
20	Risk Algorithm Using Serial Biomarker Measurements Doubles the Number of Screen-Detected Cancers Compared With a Single-Threshold Rule in the United Kingdom Collaborative Trial of Ovarian Cancer Screening. Journal of Clinical Oncology, 2015, 33, 2062-2071.	0.8	166
21	Hypomethylation and hypermethylation of DNA in Wilms tumors. Oncogene, 2002, 21, 6694-6702.	2.6	165
22	Epigenetic variability in cells of normal cytology is associated with the risk of future morphological transformation. Genome Medicine, 2012, 4, 24.	3.6	162
23	The lncRNA HOTAIR impacts on mesenchymal stem cells*via*triple helix formation. Nucleic Acids Research, 2016, 44, 10631-10643.	6.5	141
24	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. Genome Medicine, 2015, 7, 108.	3.6	138
25	Role of DNA Methylation and Epigenetic Silencing of HAND2 in Endometrial Cancer Development. PLoS Medicine, 2013, 10, e1001551.	3.9	135
26	Epigenotyping in Peripheral Blood Cell DNA and Breast Cancer Risk: A Proof of Principle Study. PLoS ONE, 2008, 3, e2656.	1.1	131
27	Epigenome-based cancer risk prediction: rationale, opportunities and challenges. Nature Reviews Clinical Oncology, 2018, 15, 292-309.	12.5	129
28	DNA Methylation in Serum and Tumors of Cervical Cancer Patients. Clinical Cancer Research, 2004, 10, 565-571.	3.2	123
29	The potential of circulating tumor DNA methylation analysis for the early detection and management of ovarian cancer. Genome Medicine, 2017, 9, 116.	3.6	122
30	Differential variability improves the identification of cancer risk markers in DNA methylation studies profiling precursor cancer lesions. Bioinformatics, 2012, 28, 1487-1494.	1.8	119
31	DNA hypomethylation is prevalent even in low-grade breast cancers. Cancer Biology and Therapy, 2004, 3, 1225-1231.	1.5	117
32	A novel cell-type deconvolution algorithm reveals substantial contamination by immune cells in saliva, buccal and cervix. Epigenomics, 2018, 10, 925-940.	1.0	116
33	The Dynamics and Prognostic Potential of DNA Methylation Changes at Stem Cell Gene Loci in Women's Cancer. PLoS Genetics, 2012, 8, e1002517.	1.5	111
34	Association between the cervicovaginal microbiome, BRCA1 mutation status, and risk of ovarian cancer: a case-control study. Lancet Oncology, The, 2019, 20, 1171-1182.	5.1	108
35	Neopterin Is an Independent Prognostic Variable in Females with Breast Cancer. Clinical Chemistry, 1999, 45, 1998-2004.	1.5	101
36	Epigenetic drift, epigenetic clocks and cancer risk. Epigenomics, 2016, 8, 705-719.	1.0	101

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37	The sex hormone system in carriers of BRCA1/2 mutations: a case-control study. Lancet Oncology, The, 2013, 14, 1226-1232.	5.1	98
38	<i>HOXA11</i> DNA methylation—A novel prognostic biomarker in ovarian cancer. International Journal of Cancer, 2008, 123, 725-729.	2.3	97
39	A comparison of feature selection and classification methods in DNA methylation studies using the Illumina Infinium platform. BMC Bioinformatics, 2012, 13, 59.	1.2	95
40	Genome-wide DNA methylation analysis of archival formalin-fixed paraffin-embedded tissue using the Illumina Infinium HumanMethylation27 BeadChip. Methods, 2010, 52, 248-254.	1.9	92
41	Testing breast cancer serum biomarkers for early detection and prognosis in pre-diagnosis samples. British Journal of Cancer, 2017, 116, 501-508.	2.9	86
42	CDH1 and CDH13 methylation in serum is an independent prognostic marker in cervical cancer patients. International Journal of Cancer, 2004, 109, 163-166.	2.3	85
43	Prognostic DNA Methylation Marker in Serum of Cancer Patients. Annals of the New York Academy of Sciences, 2004, 1022, 44-49.	1.8	77
44	DNA methylation markers for early detection of women's cancer: promise and challenges. Epigenomics, 2014, 6, 311-327.	1.0	76
45	Toll-like receptor 9 expression in breast and ovarian cancer is associated with poorly differentiated tumors. Cancer Science, 2010, 101, 1059-1066.	1.7	72
46	Analysis of Aberrant DNA Methylation and Human Papillomavirus DNA in Cervicovaginal Specimens to Detect Invasive Cervical Cancer and Its Precursors. Clinical Cancer Research, 2004, 10, 3396-3400.	3.2	65
47	Genome-Scale Screen for DNA Methylation-Based Detection Markers for Ovarian Cancer. PLoS ONE, 2011, 6, e28141.	1.1	65
48	An integrative pan-cancer-wide analysis of epigenetic enzymes reveals universal patterns of epigenomic deregulation in cancer. Genome Biology, 2015, 16, 140.	3.8	60
49	HOXA methylation in normal endometrium from premenopausal women is associated with the presence of ovarian cancer: A proof of principle study. International Journal of Cancer, 2009, 125, 2214-2218.	2.3	59
50	Epigenetic reprogramming of fallopian tube fimbriae in BRCA mutation carriers defines early ovarian cancer evolution. Nature Communications, 2016, 7, 11620.	5.8	56
51	A BRCA1-mutation associated DNA methylation signature in blood cells predicts sporadic breast cancer incidence and survival. Genome Medicine, 2014, 6, 47.	3.6	53
52	The Dynamics of DNA Methylation Covariation Patterns in Carcinogenesis. PLoS Computational Biology, 2014, 10, e1003709.	1.5	52
53	Pre-eclampsia: a disorder of placental mitochondria?. Trends in Molecular Medicine, 1998, 4, 286-291.	2.6	51
54	Distinctive topology of age-associated epigenetic drift in the human interactome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14138-14143.	3.3	49

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55	Osteoprotegerin (OPG), The Endogenous Inhibitor of Receptor Activator of NF-κB Ligand (RANKL), is Dysregulated in BRCA Mutation Carriers. EBioMedicine, 2015, 2, 1331-1339.	2.7	49
56	Methylation patterns in serum DNA for early identification of disseminated breast cancer. Genome Medicine, 2017, 9, 115.	3.6	49
57	DNA methylation analysis in liquid‐based cytology for cervical cancer screening. International Journal of Cancer, 2009, 125, 2995-3002.	2.3	47
58	Methylome analysis of extreme chemoresponsive patients identifies novel markers of platinum sensitivity in high-grade serous ovarian cancer. BMC Medicine, 2017, 15, 116.	2.3	44
59	<i>PPM1D</i>Mosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. Journal of the National Cancer Institute, 2016, 108, djv347.	3.0	43
60	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	3.2	43
61	Methylated DNA as a possible screening marker for neoplastic disease in several body fluids. Expert Review of Molecular Diagnostics, 2003, 3, 443-458.	1.5	41
62	The potential prognostic, predictive, and therapeutic values of DNA methylation in cancer. Commentary re: J. Kwong et al., Promoter hypermethylation of multiple genes in nasopharyngeal carcinoma. Clin. Cancer Res., 8: 131-137, 2002, and H-Z. Zou et al., Detection of aberrant p16 methylation in the serum of colorectal cancer patients. Clin. Cancer Res., 8: 188-191, 2002. Clinical Cancer Research, 2002, 8, 17-21.	3.2	39
63	Underlying mechanisms of ovarian cancer risk reduction after tubal ligation. Acta Obstetricia Et Gynecologica Scandinavica, 2011, 90, 559-563.	1.3	38
64	Analysis of Methylated Genes in Peritoneal Fluids of Ovarian Cancer Patients: A New Prognostic Tool. Clinical Chemistry, 2004, 50, 2171-2173.	1.5	37
65	Methylated <i>NEUROD1</i> Promoter is a Marker for Chemosensitivity in Breast Cancer. Clinical Cancer Research, 2008, 14, 3494-3502.	3.2	37
66	Association of serum sex steroid receptor bioactivity and sex steroid hormones with breast cancer risk in postmenopausal women. Endocrine-Related Cancer, 2012, 19, 137-147.	1.6	36
67	Stochastic epigenetic outliers can define field defects in cancer. BMC Bioinformatics, 2016, 17, 178.	1.2	36
68	Circulating Methylated DNA: A New Generation of Tumor Markers: Fig. 1.. Clinical Cancer Research, 2006, 12, 7205-7208.	3.2	29
69	Targeting progesterone signaling prevents metastatic ovarian cancer. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31993-32004.	3.3	29
70	DNA Methylation Patterns in Normal Tissue Correlate more Strongly with Breast Cancer Status than Copy-Number Variants. EBioMedicine, 2018, 31, 243-252.	2.7	27
71	The multi-omic landscape of transcription factor inactivation in cancer. Genome Medicine, 2016, 8, 89.	3.6	26
72	Emerging promise of epigenetics and DNA methylation for the diagnosis and management of women's cancers. Epigenomics, 2010, 2, 9-38.	1.0	25

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73	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	1.2	24
74	The integrative epigenomic-transcriptomic landscape of ER positive breast cancer. Clinical Epigenetics, 2015, 7, 126.	1.8	24
75	DNA Methylation Changes in Sera of Women in Early Pregnancy Are Similar to Those in Advanced Breast Cancer Patients. Clinical Chemistry, 2004, 50, 1065-1068.	1.5	23
76	Prediction models for endometrial cancer for the general population or symptomatic women: A systematic review. Critical Reviews in Oncology/Hematology, 2018, 126, 92-99.	2.0	23
77	A DNA methylation pattern similar to normal tissue is associated with better prognosis in human cervical cancer. Cancer Letters, 2004, 209, 231-236.	3.2	22
78	GALR1 Methylation in Vaginal Swabs Is Highly Accurate in Identifying Women With Endometrial Cancer. International Journal of Gynecological Cancer, 2013, 23, 1050-1055.	1.2	21
79	Integration of genetic and epigenetic markers for risk stratification: opportunities and challenges. Personalized Medicine, 2016, 13, 93-95.	0.8	21
80	The WID-BC-index identifies women with primary poor prognostic breast cancer based on DNA methylation in cervical samples. Nature Communications, 2022, 13, 449.	5.8	21
81	The DNA methylome of cervical cells can predict the presence of ovarian cancer. Nature Communications, 2022, 13, 448.	5.8	20
82	Corruption of the Intra-Gene DNA Methylation Architecture Is a Hallmark of Cancer. PLoS ONE, 2013, 8, e68285.	1.1	19
83	Intra-Gene DNA Methylation Variability Is a Clinically Independent Prognostic Marker in Women's Cancers. PLoS ONE, 2015, 10, e0143178.	1.1	14
84	Epigenetics makes its mark on women-specific cancers—an opportunity to redefine oncological approaches?. Gynecologic Oncology, 2013, 128, 134-143.	0.6	13
85	Comparison of two protocols for the management of asymptomatic postmenopausal women with adnexal tumours – a randomised controlled trial of RMI/RCOG vs Simple Rules. British Journal of Cancer, 2017, 116, 584-591.	2.9	13
86	What do European women know about their female cancer risks and cancer screening? A cross-sectional online intervention survey in five European countries. BMJ Open, 2018, 8, e023789.	0.8	13
87	Ethical, Legal, and Regulatory Issues for the Implementation of Omics-Based Risk Prediction of Women's Cancer: Points to Consider. Public Health Genomics, 2018, 21, 37-44.	0.6	13
88	Outcome of patients with advanced ovarian cancer who do not undergo debulking surgery: A single institution retrospective review. Gynecologic Oncology, 2017, 144, 57-60.	0.6	11
89	DNA methylation of polycomb group target genes in cores taken from breast cancer centre and periphery. Breast Cancer Research and Treatment, 2010, 120, 345-355.	1.1	10
90	Accounting for differential variability in detecting differentially methylated regions. Briefings in Bioinformatics, 2019, 20, 47-57.	3.2	10

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91	A Systematic Review on Cost-effectiveness Studies Evaluating Ovarian Cancer Early Detection and Prevention Strategies. Cancer Prevention Research, 2020, 13, 429-442.	0.7	10
92	Antiprogestins reduce epigenetic field cancerization in breast tissue of young healthy women. Genome Medicine, 2022, 14, .	3.6	10
93	Cost-Effectiveness of Early Detection and Prevention Strategies for Endometrial Cancerâ€"A Systematic Review. Cancers, 2020, 12, 1874.	1.7	9
94	A Mouse Model That Reproduces the Developmental Pathways and Site Specificity of the Cancers Associated With the Human BRCA1 Mutation Carrier State. EBioMedicine, 2015, 2, 1318-1330.	2.7	8
95	Susceptibility to hormone-mediated cancer is reflected by different tick rates of the epithelial and general epigenetic clock. Genome Biology, 2022, 23, 52.	3.8	8
96	A donor-specific epigenetic classifier for acute graft-versus-host disease severity in hematopoietic stem cell transplantation. Genome Medicine, 2015, 7, 128.	3.6	7
97	Mechanism of cytokinesis failure in ovarian cystadenomas with defective BRCA1 and P53 pathways. International Journal of Cancer, 2018, 143, 2932-2942.	2.3	6
98	DNA methylation signatures to predict the cervicovaginal microbiome status. Clinical Epigenetics, 2020, 12, 180.	1.8	3
99	Non-Surgical Cancer Risk Reduction in BRCA1 Mutation Carriers: Disabling the Remote Control. Cancers, 2020, 12, 547.	1.7	3
100	Brca1 Mutations Enhance Mouse Reproductive Functions by Increasing Responsiveness to Male-Derived Scent. PLoS ONE, 2015, 10, e0139013.	1.1	3
101	The Dark Side of Antihormonal Action in Breast Cancer. , 2009, , 63-84.		1
102	A Network Systems Approach to Identify Functional Epigenetic Drivers in Cancer. Translational Bioinformatics, 2013, , 131-152.	0.0	1
103	Author Correction: Susceptibility to hormone-mediated cancer is reflected by different tick rates of the epithelial and general epigenetic clock. Genome Biology, 2022, 23, .	3.8	1
104	Pregnancy and breast cancer. , 0, , 229-242.		0
105	Feasibility of circulating tumour cell (CTC) enumeration and molecular profiling (MP) as a biomarker in advanced endometrial cancer (aEC).. Journal of Clinical Oncology, 2014, 32, 5600-5600.	0.8	0