

G B A Wisman

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,615
citations

147801

31
h-index

189892

50
g-index

55
all docs

55
docs citations

55
times ranked

4152
citing authors

#	ARTICLE	IF	CITATIONS
1	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. <i>Genome Medicine</i> , 2015, 7, 108.	8.2	138
2	Nationwide prevalence of human papillomavirus infection and viral genotype distribution in 37 cities in China. <i>BMC Infectious Diseases</i> , 2015, 15, 257.	2.9	135
3	Genome-Wide Promoter Analysis Uncovers Portions of the Cancer Methylome. <i>Cancer Research</i> , 2008, 68, 2661-2670.	0.9	131
4	CD103 defines intraepithelial CD8+ PD1+ tumour-infiltrating lymphocytes of prognostic significance in endometrial adenocarcinoma. <i>European Journal of Cancer</i> , 2016, 60, 1-11.	2.8	125
5	CD103+ tumor-infiltrating lymphocytes are tumor-reactive intraepithelial CD8+ T cells associated with prognostic benefit and therapy response in cervical cancer. <i>Oncolmmunology</i> , 2017, 6, e1338230.	4.6	116
6	<i>CADM1</i> and <i>MAL</i> promoter methylation levels in hrHPV-positive cervical scrapes increase proportional to degree and duration of underlying cervical disease. <i>International Journal of Cancer</i> , 2013, 133, 1293-1299.	5.1	100
7	Expression of Epidermal Growth Factor Receptor (EGFR) and Activated EGFR Predict Poor Response to (Chemo)radiation and Survival in Cervical Cancer. <i>Clinical Cancer Research</i> , 2009, 15, 7389-7397.	7.0	98
8	Assessment of gene promoter hypermethylation for detection of cervical neoplasia. <i>International Journal of Cancer</i> , 2006, 119, 1908-1914.	5.1	97
9	A four-gene methylation marker panel as triage test in high-risk human papillomavirus positive patients. <i>International Journal of Cancer</i> , 2012, 130, 1861-1869.	5.1	97
10	Platinum-Based Chemotherapy Induces Methylation Changes in Blood DNA Associated with Overall Survival in Patients with Ovarian Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2213-2222.	7.0	83
11	<i>CADM1</i> , <i>MAL</i> and <i>miR124-2</i> methylation analysis in cervical scrapes to detect cervical and endometrial cancer. <i>Journal of Clinical Pathology</i> , 2014, 67, 1067-1071.	2.0	82
12	ARID1A mutation sensitizes most ovarian clear cell carcinomas to BET inhibitors. <i>Oncogene</i> , 2018, 37, 4611-4625.	5.9	72
13	ARID1A mutant ovarian clear cell carcinoma: A clear target for synthetic lethal strategies. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2018, 1870, 176-184.	7.4	69
14	Genome-wide DNA Methylation Profiling Reveals Methylation Markers Associated with 3q Gain for Detection of Cervical Precancer and Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 3813-3822.	7.0	68
15	CD103+ intraepithelial T cells in high-grade serous ovarian cancer are phenotypically diverse TCR ^{hi} CD8 ^{hi} T cells that can be targeted for cancer immunotherapy. <i>Oncotarget</i> , 2016, 7, 75130-75144.	1.8	64
16	Methylation Markers for <i>CCNA1</i> and <i>C13ORF18</i> Are Strongly Associated with High-Grade Cervical Intraepithelial Neoplasia and Cervical Cancer in Cervical Scrapings. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 3000-3007.	2.5	62
17	Discovery of new methylation markers to improve screening for cervical intraepithelial neoplasia grade 2/3. <i>Clinical Epigenetics</i> , 2016, 8, 29.	4.1	53
18	Studying platinum sensitivity and resistance in high-grade serous ovarian cancer: Different models for different questions. <i>Drug Resistance Updates</i> , 2016, 24, 55-69.	14.4	52

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19	Treatment Regimen, Surgical Outcome, and T-cell Differentiation Influence Prognostic Benefit of Tumor-Infiltrating Lymphocytes in High-Grade Serous Ovarian Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 714-724.	7.0	51
20	Detection of cervical neoplasia by DNA methylation analysis in cervico-vaginal lavages, a feasibility study. <i>Gynecologic Oncology</i> , 2011, 120, 280-283.	1.4	50
21	Methylome analysis of extreme chemoresponsive patients identifies novel markers of platinum sensitivity in high-grade serous ovarian cancer. <i>BMC Medicine</i> , 2017, 15, 116.	5.5	44
22	DNA methylation analysis in self-sampled brush material as a triage test in hrHPV-positive women. <i>British Journal of Cancer</i> , 2014, 111, 1095-1101.	6.4	43
23	Host-cell DNA methylation patterns during high-risk HPV-induced carcinogenesis reveal a heterogeneous nature of cervical pre-cancer. <i>Epigenetics</i> , 2018, 13, 769-778.	2.7	43
24	Biobanking of patient and patient-derived xenograft ovarian tumour tissue: efficient preservation with low and high fetal calf serum based methods. <i>Scientific Reports</i> , 2015, 5, 14495.	3.3	41
25	Low-dose triple drug combination targeting the PI3K/AKT/mTOR pathway and the MAPK pathway is an effective approach in ovarian clear cell carcinoma. <i>Cancer Letters</i> , 2019, 461, 102-111.	7.2	40
26	Markers of fibroblast-rich tumor stroma and perivascular cells in serous ovarian cancer: Inter- and intra-patient heterogeneity and impact on survival. <i>Oncotarget</i> , 2016, 7, 18573-18584.	1.8	40
27	Gene promoter methylation patterns throughout the process of cervical carcinogenesis. <i>Cellular Oncology</i> , 2010, 32, 131-43.	1.9	40
28	Functional validation of putative tumor suppressor gene <i>C13ORF18</i> in cervical cancer by Artificial Transcription Factors. <i>Molecular Oncology</i> , 2013, 7, 669-679.	4.6	39
29	DNA methylation markers as a triage test for identification of cervical lesions in a high risk human papillomavirus positive screening cohort. <i>International Journal of Cancer</i> , 2019, 144, 746-754.	5.1	37
30	The role of ATM and 53BP1 as predictive markers in cervical cancer. <i>International Journal of Cancer</i> , 2012, 131, 2056-2066.	5.1	35
31	Integrative Kinome Profiling Identifies mTORC1/2 Inhibition as Treatment Strategy in Ovarian Clear Cell Carcinoma. <i>Clinical Cancer Research</i> , 2018, 24, 3928-3940.	7.0	35
32	Re-expression of Selected Epigenetically Silenced Candidate Tumor Suppressor Genes in Cervical Cancer by TET2-directed Demethylation. <i>Molecular Therapy</i> , 2016, 24, 536-547.	8.2	33
33	Discovery of DNA methylation markers in cervical cancer using relaxation ranking. <i>BMC Medical Genomics</i> , 2008, 1, 57.	1.5	32
34	Genome-wide methylation profiling of ovarian cancer patient-derived xenografts treated with the demethylating agent decitabine identifies novel epigenetically regulated genes and pathways. <i>Genome Medicine</i> , 2016, 8, 107.	8.2	31
35	A Complex Network of Tumor Microenvironment in Human High-Grade Serous Ovarian Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 7621-7632.	7.0	31
36	Checkpoint kinase 2 (Chk2) supports sensitivity to platinum-based treatment in high grade serous ovarian cancer. <i>Gynecologic Oncology</i> , 2014, 133, 591-598.	1.4	28

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37	Prolonged re-expression of the hypermethylated gene <i>EPB41L3</i> using artificial transcription factors and epigenetic drugs. <i>Epigenetics</i> , 2015, 10, 384-396.	2.7	28
38	Identification and validation of <i>WISP1</i> as an epigenetic regulator of metastasis in oral squamous cell carcinoma. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 45-59.	2.8	28
39	HER2 immunohistochemistry in endometrial and ovarian clear cell carcinoma: discordance between antibodies and with <i>in situ</i> hybridisation. <i>Histopathology</i> , 2018, 73, 852-863.	2.9	24
40	DNA hypermethylation biomarkers to predict response to cisplatin treatment, radiotherapy or chemoradiation: the present state of art. <i>Cellular Oncology (Dordrecht)</i> , 2012, 35, 231-241.	4.4	20
41	Clinical Validation of the Cervista HPV HR Test According to the International Guidelines for Human Papillomavirus Test Requirements for Cervical Cancer Screening. <i>Journal of Clinical Microbiology</i> , 2014, 52, 4391-4393.	3.9	20
42	Proteomic alterations in early stage cervical cancer. <i>Oncotarget</i> , 2018, 9, 18128-18147.	1.8	20
43	RAB25 expression is epigenetically downregulated in oral and oropharyngeal squamous cell carcinoma with lymph node metastasis. <i>Epigenetics</i> , 2016, 11, 653-663.	2.7	18
44	Integrated transcriptomic and epigenomic analysis of ovarian cancer reveals epigenetically silenced GULP1. <i>Cancer Letters</i> , 2018, 433, 242-251.	7.2	16
45	Evaluation of six methylation markers derived from genome-wide screens for detection of cervical precancer and cancer. <i>Epigenomics</i> , 2020, 12, 1569-1578.	2.1	15
46	Genome-wide methylome analysis using MethylCap-seq uncovers 4 hypermethylated markers with high sensitivity for both adeno- and squamous-cell cervical carcinoma. <i>Oncotarget</i> , 2016, 7, 80735-80750.	1.8	15
47	Nuclear COMMD1 Is Associated with Cisplatin Sensitivity in Ovarian Cancer. <i>PLoS ONE</i> , 2016, 11, e0165385.	2.5	13
48	DNA methylation markers as triage test for the early identification of cervical lesions in a Chinese population. <i>International Journal of Cancer</i> , 2021, 148, 1768-1777.	5.1	13
49	Comparing the Cervista HPV HR Test and Hybrid Capture 2 Assay in a Dutch Screening Population: Improved Specificity of the Cervista HPV HR Test by Changing the Cut-Off. <i>PLoS ONE</i> , 2014, 9, e101930.	2.5	11
50	Association of homozygous variants of STING1 with outcome in human cervical cancer. <i>Cancer Science</i> , 2021, 112, 61-71.	3.9	11
51	Prognostic image-based quantification of CD8CD103 T cell subsets in high-grade serous ovarian cancer patients. <i>Oncolmmunology</i> , 2021, 10, 1935104.	4.6	10
52	Combined STING levels and CD103+ T cell infiltration have significant prognostic implications for patients with cervical cancer. <i>Oncolmmunology</i> , 2021, 10, 1936391.	4.6	9
53	Mining for viral fragments in methylation enriched sequencing data. <i>Frontiers in Genetics</i> , 2015, 6, 16.	2.3	5
54	Kinome capture sequencing of high-grade serous ovarian carcinoma reveals novel mutations in the JAK3 gene. <i>PLoS ONE</i> , 2020, 15, e0235766.	2.5	2

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55	Preferences and Experiences Regarding the Use of the Self-Sampling Device in hrHPV Screening for Cervical Cancer. Patient, 2022, 15, 245-253.	2.7	2