G B A Wisman

List of Publications by Year
in descending order

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	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
2	<scp>DNA</scp> methylation markers as triage test for the early identification of cervical lesions in a Chinese population. International Journal of Cancer, 2021, 148, 1768-1777.	5.1	13
3	Prognostic image-based quantification of CD8CD103 T cell subsets in high-grade serous ovarian cancer patients. OncoImmunology, 2021, 10, 1935104.	4.6	10
4	Combined STING levels and CD103+ T cell infiltration have significant prognostic implications for patients with cervical cancer. OncoImmunology, 2021, 10, 1936391.	4.6	9
5	Association of homozygous variants of STING1 with outcome in human cervical cancer. Cancer Science, 2021, 112, 61-71.	3.9	11
6	Evaluation of six methylation markers derived from genome-wide screens for detection of cervical precancer and cancer. Epigenomics, 2020, 12, 1569-1578.	2.1	15
7	Kinome capture sequencing of high-grade serous ovarian carcinoma reveals novel mutations in the JAK3 gene. PLoS ONE, 2020, 15, e0235766.	2.5	2
8	Low-dose triple drug combination targeting the PI3K/AKT/mTOR pathway and the MAPK pathway is an effective approach in ovarian clear cell carcinoma. Cancer Letters, 2019, 461, 102-111.	7.2	40
9	DNA methylation markers as a triage test for identification of cervical lesions in a high risk human papillomavirus positive screening cohort. International Journal of Cancer, 2019, 144, 746-754.	5.1	37
10	Integrative Kinome Profiling Identifies mTORC1/2 Inhibition as Treatment Strategy in Ovarian Clear Cell Carcinoma. Clinical Cancer Research, 2018, 24, 3928-3940.	7.0	35
11	ARID1A mutation sensitizes most ovarian clear cell carcinomas to BET inhibitors. Oncogene, 2018, 37, 4611-4625.	5.9	72
12	Integrated transcriptomic and epigenomic analysis of ovarian cancer reveals epigenetically silenced GULP1. Cancer Letters, 2018, 433, 242-251.	7.2	16
13	Host-cell DNA methylation patterns during high-risk HPV-induced carcinogenesis reveal a heterogeneous nature of cervical pre-cancer. Epigenetics, 2018, 13, 769-778.	2.7	43
14	ARID1A mutant ovarian clear cell carcinoma: A clear target for synthetic lethal strategies. Biochimica Et Biophysica Acta: Reviews on Cancer, 2018, 1870, 176-184.	7.4	69
15	HER2 immunohistochemistry in endometrial and ovarian clear cell carcinoma: discordance between antibodies and with <i>inâ€situ</i> hybridisation. Histopathology, 2018, 73, 852-863.	2.9	24
16	Proteomic alterations in early stage cervical cancer. Oncotarget, 2018, 9, 18128-18147.	1.8	20
17	Genome-wide DNA Methylation Profiling Reveals Methylation Markers Associated with 3q Gain for Detection of Cervical Precancer and Cancer. Clinical Cancer Research, 2017, 23, 3813-3822.	7.0	68
18	A Complex Network of Tumor Microenvironment in Human High-Grade Serous Ovarian Cancer. Clinical Cancer Research, 2017, 23, 7621-7632.	7.0	31

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19	CD103+ tumor-infiltrating lymphocytes are tumor-reactive intraepithelial CD8+ T cells associated with prognostic benefit and therapy response in cervical cancer. OncoImmunology, 2017, 6, e1338230.	4.6	116
20	Methylome analysis of extreme chemoresponsive patients identifies novel markers of platinum sensitivity in high-grade serous ovarian cancer. BMC Medicine, 2017, 15, 116.	5.5	44
21	Platinum-Based Chemotherapy Induces Methylation Changes in Blood DNA Associated with Overall Survival in Patients with Ovarian Cancer. Clinical Cancer Research, 2017, 23, 2213-2222.	7.0	83
22	Nuclear COMMD1 Is Associated with Cisplatin Sensitivity in Ovarian Cancer. PLoS ONE, 2016, 11, e0165385.	2.5	13
23	RAB25 expression is epigenetically downregulated in oral and oropharyngeal squamous cell carcinoma with lymph node metastasis. Epigenetics, 2016, 11, 653-663.	2.7	18
24	Genome-wide methylation profiling of ovarian cancer patient-derived xenografts treated with the demethylating agent decitabine identifies novel epigenetically regulated genes and pathways. Genome Medicine, 2016, 8, 107.	8.2	31
25	CD103 defines intraepithelial CD8+ PD1+ tumour-infiltrating lymphocytes of prognostic significance in endometrial adenocarcinoma. European Journal of Cancer, 2016, 60, 1-11.	2.8	125
26	Discovery of new methylation markers to improve screening for cervical intraepithelial neoplasia grade 2/3. Clinical Epigenetics, 2016, 8, 29.	4.1	53
27	Identification and validation of <scp><i>WISP</i></scp><i>1</i> as an epigenetic regulator of metastasis in oral squamous cell carcinoma. Genes Chromosomes and Cancer, 2016, 55, 45-59.	2.8	28
28	Re-expression of Selected Epigenetically Silenced Candidate Tumor Suppressor Genes in Cervical Cancer by TET2-directed Demethylation. Molecular Therapy, 2016, 24, 536-547.	8.2	33
29	Studying platinum sensitivity and resistance in high-grade serous ovarian cancer: Different models for different questions. Drug Resistance Updates, 2016, 24, 55-69.	14.4	52
30	Treatment Regimen, Surgical Outcome, and T-cell Differentiation Influence Prognostic Benefit of Tumor-Infiltrating Lymphocytes in High-Grade Serous Ovarian Cancer. Clinical Cancer Research, 2016, 22, 714-724.	7.0	51
31	CD103+ intraepithelial T cells in high-grade serous ovarian cancer are phenotypically diverse TCRÎ±Î²+ CD8Î±Î²+ T cells that can be targeted for cancer immunotherapy. Oncotarget, 2016, 7, 75130-75144.	1.8	64
32	Genome-wide methylome analysis using MethylCap-seq uncovers 4 hypermethylated markers with high sensitivity for both adeno- and squamous-cell cervical carcinoma. Oncotarget, 2016, 7, 80735-80750.	1.8	15
33	Markers of fibroblast-rich tumor stroma and perivascular cells in serous ovarian cancer: Inter- and intra-patient heterogeneity and impact on survival. Oncotarget, 2016, 7, 18573-18584.	1.8	40
34	Biobanking of patient and patient-derived xenograft ovarian tumour tissue: efficient preservation with low and high fetal calf serum based methods. Scientific Reports, 2015, 5, 14495.	3.3	41
35	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. Genome Medicine, 2015, 7, 108.	8.2	138
36	Mining for viral fragments in methylation enriched sequencing data. Frontiers in Genetics, 2015, 6, 16.	2.3	5

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37	Prolonged re-expression of the hypermethylated gene *EPB41L3* using artificial transcription factors and epigenetic drugs. Epigenetics, 2015, 10, 384-396.	2.7	28
38	Nationwide prevalence of human papillomavirus infection and viral genotype distribution in 37 cities in China. BMC Infectious Diseases, 2015, 15, 257.	2.9	135
39	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. PLoS ONE, 2014, 9, e101930.	2.5	11
40	*CADM1*, *MAL* and *miR124-2* methylation analysis in cervical scrapes to detect cervical and endometrial cancer. Journal of Clinical Pathology, 2014, 67, 1067-1071.	2.0	82
41	Clinical Validation of the Cervista HPV HR Test According to the International Guidelines for Human Papillomavirus Test Requirements for Cervical Cancer Screening. Journal of Clinical Microbiology, 2014, 52, 4391-4393.	3.9	20
42	DNA methylation analysis in self-sampled brush material as a triage test in hrHPV-positive women. British Journal of Cancer, 2014, 111, 1095-1101.	6.4	43
43	Checkpoint kinase 2 (Chk2) supports sensitivity to platinum-based treatment in high grade serous ovarian cancer. Gynecologic Oncology, 2014, 133, 591-598.	1.4	28
44	Functional validation of putative tumor suppressor gene *C13ORF18* in cervical cancer by Artificial Transcription Factors. Molecular Oncology, 2013, 7, 669-679.	4.6	39
45	*CADM1* and *MAL* promoter methylation levels in hrHPV-positive cervical scrapes increase proportional to degree and duration of underlying cervical disease. International Journal of Cancer, 2013, 133, 1293-1299.	5.1	100
46	DNA hypermethylation biomarkers to predict response to cisplatin treatment, radiotherapy or chemoradiation: the present state of art. Cellular Oncology (Dordrecht), 2012, 35, 231-241.	4.4	20
47	The role of ATM and 53BP1 as predictive markers in cervical cancer. International Journal of Cancer, 2012, 131, 2056-2066.	5.1	35
48	A four‐gene methylation marker panel as triage test in high‐risk human papillomavirus positive patients. International Journal of Cancer, 2012, 130, 1861-1869.	5.1	97
49	Detection of cervical neoplasia by DNA methylation analysis in cervico-vaginal lavages, a feasibility study. Gynecologic Oncology, 2011, 120, 280-283.	1.4	50
50	Gene promoter methylation patterns throughout the process of cervical carcinogenesis. Cellular Oncology, 2010, 32, 131-43.	1.9	40
51	Expression of Epidermal Growth Factor Receptor (EGFR) and Activated EGFR Predict Poor Response to (Chemo)radiation and Survival in Cervical Cancer. Clinical Cancer Research, 2009, 15, 7389-7397.	7.0	98
52	Methylation Markers for *CCNA1* and *C13ORF18* Are Strongly Associated with High-Grade Cervical Intraepithelial Neoplasia and Cervical Cancer in Cervical Scrapings. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3000-3007.	2.5	62
53	Discovery of DNA methylation markers in cervical cancer using relaxation ranking. BMC Medical Genomics, 2008, 1, 57.	1.5	32
54	Genome-Wide Promoter Analysis Uncovers Portions of the Cancer Methylome. Cancer Research, 2008, 68, 2661-2670.	0.9	131

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55	Assessment of gene promoter hypermethylation for detection of cervical neoplasia. International Journal of Cancer, 2006, 119, 1908-1914.	5.1	97