

John W M Martens

List of Publications by Year in descending order

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Version: 2024-02-01

254
papers

22,504
citations

15880

67
h-index

11946

139
g-index

268
all docs

268
docs citations

268
times ranked

35747
citing authors

#	ARTICLE	IF	CITATIONS
1	Apolipoprotein B mRNA-Editing Catalytic Polypeptide-Like-Induced Protein Changes in Estrogen Receptor-Positive, Human Epidermal Growth Factor Receptor 2-Negative Breast Cancer Throughout Disease Progression. <i>JCO Precision Oncology</i> , 2022, 6, e2100190.	1.5	5
2	Identifying Transcripts with Tandem Duplications from RNA-Sequencing Data to Predict BRCA1-Type Primary Breast Cancer. <i>Cancers</i> , 2022, 14, 753.	1.7	1
3	Prognostic Value of Circulating Tumor Cell Characteristics May Be Biased by Their Quantity. <i>Journal of Clinical Oncology</i> , 2022, 40, 519-520.	0.8	2
4	The prognostic and predictive value of ESR1 fusion gene transcripts in primary breast cancer. <i>BMC Cancer</i> , 2022, 22, 165.	1.1	8
5	Abstract P3-09-18: The association between genomic alterations and body mass index in patients with early breast cancer. <i>Cancer Research</i> , 2022, 82, P3-09-18-P3-09-18.	0.4	0
6	Abstract P2-01-17: Circulating tumor cell count and levels of circulating tumor DNA are complementary prognostic biomarkers in metastatic breast cancer - A pilot study. <i>Cancer Research</i> , 2022, 82, P2-01-17-P2-01-17.	0.4	1
7	Genome-wide aneuploidy detected by mFast-SeqS in circulating cell-free DNA is associated with poor response to pembrolizumab in patients with advanced urothelial cancer. <i>Molecular Oncology</i> , 2022, 16, 2086-2097.	2.1	8
8	Circulating tumour cells to drive the use of neoadjuvant chemotherapy in patients with muscle-invasive bladder cancer. <i>ESMO Open</i> , 2022, 7, 100416.	2.0	10
9	A pipeline for copy number profiling of single circulating tumour cells to assess inpatient tumour heterogeneity. <i>Molecular Oncology</i> , 2022, 16, 2981-3000.	2.1	6
10	Lost by Transcription: Fork Failures, Elevated Expression, and Clinical Consequences Related to Deletions in Metastatic Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5080.	1.8	2
11	ESR1 Methylation Measured in Cell-Free DNA to Evaluate Endocrine Resistance in Metastatic Breast Cancer Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5631.	1.8	4
12	Functional RECAP (REpair CAPacity) assay identifies homologous recombination deficiency undetected by DNA-based BRCAness tests. <i>Oncogene</i> , 2022, 41, 3498-3506.	2.6	9
13	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. <i>Cancers</i> , 2022, 14, 3363.	1.7	2
14	Liquid Biopsies to Select Patients for Perioperative Chemotherapy in Muscle-invasive Bladder Cancer: A Systematic Review. <i>European Urology Oncology</i> , 2021, 4, 204-214.	2.6	20
15	Comparison of variant allele frequency and number of mutant molecules as units of measurement for circulating tumor DNA. <i>Molecular Oncology</i> , 2021, 15, 57-66.	2.1	28
16	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	2.9	5
17	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	5.8	19
18	Differential reprogramming of breast cancer subtypes in 3D cultures and implications for sensitivity to targeted therapy. <i>Scientific Reports</i> , 2021, 11, 7259.	1.6	20

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19	Detection of tumor-derived extracellular vesicles in plasma from patients with solid cancer. <i>BMC Cancer</i> , 2021, 21, 315.	1.1	18
20	Splicing factors control triple-negative breast cancer cell mitosis through SUN2 interaction and sororin intron retention. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 82.	3.5	20
21	Circular RNA in Chemonaive Lymph Node Negative Colon Cancer Patients. <i>Cancers</i> , 2021, 13, 1903.	1.7	1
22	A Systematic Review of the Use of Circulating Cell-Free DNA Dynamics to Monitor Response to Treatment in Metastatic Breast Cancer Patients. <i>Cancers</i> , 2021, 13, 1811.	1.7	6
23	Optimizing Nanopore sequencing-based detection of structural variants enables individualized circulating tumor DNA-based disease monitoring in cancer patients. <i>Genome Medicine</i> , 2021, 13, 86.	3.6	14
24	Estrogens and Progestogens in Triple Negative Breast Cancer: Do They Harm?. <i>Cancers</i> , 2021, 13, 2506.	1.7	17
25	A panel of DNA methylation markers for the classification of consensus molecular subtypes 2 and 3 in patients with colorectal cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, 3545-3545.	0.8	0
26	Circulating tumor cell-driven use of neoadjuvant chemotherapy in patients with muscle-invasive bladder cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, 4523-4523.	0.8	2
27	Prospective Evaluation of a Circulating Tumor Cell Sensitivity Profile to Predict Response to Cisplatin Chemotherapy in Metastatic Breast Cancer Patients. <i>Frontiers in Oncology</i> , 2021, 11, 697572.	1.3	0
28	Generating human prostate cancer organoids from leukapheresis enriched circulating tumour cells. <i>European Journal of Cancer</i> , 2021, 150, 179-189.	1.3	47
29	Evaluation of multiple transcriptomic gene risk signatures in male breast cancer. <i>Npj Breast Cancer</i> , 2021, 7, 98.	2.3	4
30	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. <i>Breast Cancer Research</i> , 2021, 23, 86.	2.2	7
31	Transcriptomic Properties of HER2+ Ductal Carcinoma In Situ of the Breast Associate with Absence of Immune Cells. <i>Biology</i> , 2021, 10, 768.	1.3	1
32	Liquid biopsy in esophageal cancer: a case report of false-positive circulating tumor DNA detection due to clonal hematopoiesis. <i>Annals of Translational Medicine</i> , 2021, 9, 1264-1264.	0.7	12
33	Spatial immunophenotypes predict response to anti-PD1 treatment and capture distinct paths of T cell evasion in triple negative breast cancer. <i>Nature Communications</i> , 2021, 12, 5668.	5.8	91
34	A panel of DNA methylation markers for the classification of consensus molecular subtypes 2 and 3 in patients with colorectal cancer. <i>Molecular Oncology</i> , 2021, 15, 3348-3362.	2.1	3
35	Detection of Aneuploidy in Cerebrospinal Fluid from Patients with Breast Cancer Can Improve Diagnosis of Leptomeningeal Metastases. <i>Clinical Cancer Research</i> , 2021, 27, 2798-2806.	3.2	14
36	Whole genome sequencing of metastatic colorectal cancer reveals prior treatment effects and specific metastasis features. <i>Nature Communications</i> , 2021, 12, 574.	5.8	39

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37	High-throughput and affordable genome-wide methylation profiling of circulating cell-free DNA by methylated DNA sequencing (MeD-seq) of LpnPI digested fragments. <i>Clinical Epigenetics</i> , 2021, 13, 196.	1.8	10
38	SPEN is required for Xist upregulation during initiation of X chromosome inactivation. <i>Nature Communications</i> , 2021, 12, 7000.	5.8	16
39	Fusion transcripts and their genomic breakpoints in polyadenylated and ribosomal RNAâ€“minus RNA sequencing data. <i>GigaScience</i> , 2021, 10, .	3.3	10
40	Clonality, Antigen Recognition, and Suppression of CD8+ T Cells Differentially Affect Prognosis of Breast Cancer Subtypes. <i>Clinical Cancer Research</i> , 2020, 26, 505-517.	3.2	26
41	High ctDNA molecule numbers relate with poor outcome in advanced ER+, HER2âˆ“ postmenopausal breast cancer patients treated with everolimus and exemestane. <i>Molecular Oncology</i> , 2020, 14, 490-503.	2.1	14
42	Deubiquitinase Activity Profiling Identifies UCHL1 as a Candidate Oncoprotein That Promotes TGFÎ²-Induced Breast Cancer Metastasis. <i>Clinical Cancer Research</i> , 2020, 26, 1460-1473.	3.2	92
43	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 104-119.	3.0	51
44	Interconnectivity between molecular subtypes and tumor stage in colorectal cancer. <i>BMC Cancer</i> , 2020, 20, 850.	1.1	14
45	Fundamentals of liquid biopsies in metastatic prostate cancer: from characterization to stratification. <i>Current Opinion in Oncology</i> , 2020, 32, 527-534.	1.1	5
46	Intratumoral heterogeneity of second-harmonic generation scattering from tumor collagen and its effects on metastatic risk prediction. <i>BMC Cancer</i> , 2020, 20, 1217.	1.1	10
47	Pan-cancer landscape of homologous recombination deficiency. <i>Nature Communications</i> , 2020, 11, 5584.	5.8	262
48	Estrogen Receptor Pathway Activity Score to Predict Clinical Response or Resistance to Neoadjuvant Endocrine Therapy in Primary Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 680-689.	1.9	44
49	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	1.6	2
50	Loss of Y-Chromosome during Male Breast Carcinogenesis. <i>Cancers</i> , 2020, 12, 631.	1.7	10
51	Integrative analysis of genomic amplification-dependent expression and loss-of-function screen identifies ASAP1 as a driver gene in triple-negative breast cancer progression. <i>Oncogene</i> , 2020, 39, 4118-4131.	2.6	19
52	Transcriptomeâ€“wide association study of breast cancer risk by estrogenâ€“receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
53	ER and PI3K Pathway Activity in Primary ER Positive Breast Cancer Is Associated with Progression-Free Survival of Metastatic Patients under First-Line Tamoxifen. <i>Cancers</i> , 2020, 12, 802.	1.7	20
54	Metabotropic glutamate receptor 1 is associated with unfavorable prognosis in ER-negative and triple-negative breast cancer. <i>Scientific Reports</i> , 2020, 10, 22292.	1.6	11

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55	Characterization of the mechanism by which the RB/E2F pathway controls expression of the cancer genomic DNA deaminase APOBEC3B. <i>ELife</i> , 2020, 9, .	2.8	25
56	Multi-targeted kinase inhibition alleviates mTOR inhibitor resistance in triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 178, 263-274.	1.1	26
57	Uncovering the signaling landscape controlling breast cancer cell migration identifies novel metastasis driver genes. <i>Nature Communications</i> , 2019, 10, 2983.	5.8	58
58	APOBEC3B Gene Expression in Ductal Carcinoma In Situ and Synchronous Invasive Breast Cancer. <i>Cancers</i> , 2019, 11, 1062.	1.7	9
59	A kinase inhibitor screen identifies a dual cdc7/CDK9 inhibitor to sensitise triple-negative breast cancer to EGFR-targeted therapy. <i>Breast Cancer Research</i> , 2019, 21, 77.	2.2	48
60	5-Fluorouracil treatment induces characteristic T>G mutations in human cancer. <i>Nature Communications</i> , 2019, 10, 4571.	5.8	143
61	Circulating Tumor Cell Enumeration and Characterization in Metastatic Castration-Resistant Prostate Cancer Patients Treated with Cabazitaxel. <i>Cancers</i> , 2019, 11, 1212.	1.7	21
62	Cancer-associated fibroblast-derived Gremlin 1 promotes breast cancer progression. <i>Breast Cancer Research</i> , 2019, 21, 109.	2.2	94
63	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. <i>Nature Genetics</i> , 2019, 51, 1450-1458.	9.4	250
64	Associations between AR-V7 status in circulating tumour cells, circulating tumour cell count and survival in men with metastatic castration-resistant prostate cancer. <i>European Journal of Cancer</i> , 2019, 121, 48-54.	1.3	20
65	An increased cell cycle gene network determines MEK and Akt inhibitor double resistance in triple-negative breast cancer. <i>Scientific Reports</i> , 2019, 9, 13308.	1.6	15
66	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019, 29, 356-366.	2.4	85
67	Proteome-wide onco-proteogenomic somatic variant identification in ER-positive breast cancer. <i>Clinical Biochemistry</i> , 2019, 66, 63-75.	0.8	3
68	Incorporating liquid biopsies into treatment decision-making: obstacles and possibilities. <i>Drug Discovery Today</i> , 2019, 24, 1715-1719.	3.2	10
69	<i>AR</i> splice variants in circulating tumor cells of patients with castration-resistant prostate cancer: relation with outcome to cabazitaxel. <i>Molecular Oncology</i> , 2019, 13, 1795-1807.	2.1	23
70	MicroRNAs as possible indicators of drug sensitivity in breast cancer cell lines. <i>PLoS ONE</i> , 2019, 14, e0216400.	1.1	54
71	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	5.8	46
72	The role of mitochondrial DNA in breast tumors. <i>Drug Discovery Today</i> , 2019, 24, 1202-1208.	3.2	15

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73	Co-regulated gene expression of splicing factors as drivers of cancer progression. <i>Scientific Reports</i> , 2019, 9, 5484.	1.6	22
74	Polyomavirus T Antigen Induces APOBEC3B Expression Using an LXCXE-Dependent and TP53-Independent Mechanism. <i>MBio</i> , 2019, 10, .	1.8	35
75	Androgen receptor expression in circulating tumor cells of patients with metastatic breast cancer. <i>International Journal of Cancer</i> , 2019, 145, 1083-1089.	2.3	27
76	The genomic landscape of metastatic castration-resistant prostate cancers reveals multiple distinct genotypes with potential clinical impact. <i>Nature Communications</i> , 2019, 10, 5251.	5.8	130
77	JNK-Dependent cJun Phosphorylation Mitigates TGF β ² - and EGF-Induced Pre-Malignant Breast Cancer Cell Invasion by Suppressing AP-1-Mediated Transcriptional Responses. <i>Cells</i> , 2019, 8, 1481.	1.8	11
78	Characterizing the invasion of different breast cancer cell lines with distinct E-cadherin status in 3D using a microfluidic system. <i>Biomedical Microdevices</i> , 2019, 21, 101.	1.4	17
79	Comprehensive evaluation of methods to assess overall and cell-specific immune infiltrates in breast cancer. <i>Breast Cancer Research</i> , 2019, 21, 151.	2.2	30
80	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
81	Novel methods to diagnose leptomeningeal metastases in breast cancer. <i>Neuro-Oncology</i> , 2019, 21, 428-439.	0.6	10
82	High-throughput isolation of circulating tumor DNA: a comparison of automated platforms. <i>Molecular Oncology</i> , 2019, 13, 392-402.	2.1	37
83	An Optimized Workflow to Evaluate Estrogen Receptor Gene Mutations in Small Amounts of Cell-Free DNA. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 123-137.	1.2	15
84	PIK3CA mutations in ductal carcinoma in situ and adjacent invasive breast cancer. <i>Endocrine-Related Cancer</i> , 2019, 26, 471-482.	1.6	17
85	The molecular genetic make-up of male breast cancer. <i>Endocrine-Related Cancer</i> , 2019, 26, 779-794.	1.6	27
86	An In-Depth Evaluation of the Validity and Logistics Surrounding the Testing of AR-V7 mRNA Expression in Circulating Tumor Cells. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 316-325.	1.2	15
87	Interferon-Stimulated Genes Are Involved in Cross-resistance to Radiotherapy in Tamoxifen-Resistant Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 3397-3408.	3.2	68
88	Characterizing steroid hormone receptor chromatin binding landscapes in male and female breast cancer. <i>Nature Communications</i> , 2018, 9, 482.	5.8	50
89	Sensitive detection of mitochondrial DNA variants for analysis of mitochondrial DNA-enriched extracts from frozen tumor tissue. <i>Scientific Reports</i> , 2018, 8, 2261.	1.6	12
90	T lymphocytes facilitate brain metastasis of breast cancer by inducing Guanylate-Binding Protein 1 expression. <i>Acta Neuropathologica</i> , 2018, 135, 581-599.	3.9	63

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91	IGF1R signaling drives antiestrogen resistance through PAK2/PIX activation in luminal breast cancer. <i>Oncogene</i> , 2018, 37, 1869-1884.	2.6	34
92	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. <i>Scientific Reports</i> , 2018, 8, 6574.	1.6	51
93	Confirmation of a metastasis-specific microRNA signature in primary colon cancer. <i>Scientific Reports</i> , 2018, 8, 5242.	1.6	33
94	Performance of <i>BRCA1</i> 2 mutation prediction models in male breast cancer patients. <i>Clinical Genetics</i> , 2018, 93, 52-59.	1.0	5
95	Estrogen receptor mutations and splice variants determined in liquid biopsies from metastatic breast cancer patients. <i>Molecular Oncology</i> , 2018, 12, 48-57.	2.1	52
96	Steps forward for cancer precision medicine. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 1-2.	21.5	37
97	Breast cancer genomics and immuno-oncological markers to guide immune therapies. <i>Seminars in Cancer Biology</i> , 2018, 52, 178-188.	4.3	111
98	Clinical performance of an analytically validated assay in comparison to microarray technology to assess PITX2 DNA-methylation in breast cancer. <i>Scientific Reports</i> , 2018, 8, 16861.	1.6	10
99	Mitochondrial RNA Expression and Single Nucleotide Variants in Association with Clinical Parameters in Primary Breast Cancers. <i>Cancers</i> , 2018, 10, 500.	1.7	7
100	Clinical Validation of PITX2 DNA Methylation to Predict Outcome in High-Risk Breast Cancer Patients Treated with Anthracycline-Based Chemotherapy. <i>Breast Care</i> , 2018, 13, 425-433.	0.8	8
101	Elucidating the Underlying Functional Mechanisms of Breast Cancer Susceptibility Through Post-GWAS Analyses. <i>Frontiers in Genetics</i> , 2018, 9, 280.	1.1	11
102	Tumor-Specific Mitochondrial DNA Variants Are Rarely Detected in Cell-Free DNA. <i>Neoplasia</i> , 2018, 20, 687-696.	2.3	28
103	Association of microRNA-7 and its binding partner CDR1-AS with the prognosis and prediction of 1st-line tamoxifen therapy in breast cancer. <i>Scientific Reports</i> , 2018, 8, 9657.	1.6	32
104	Gene length corrected trimmed mean of M-values (GeTMM) processing of RNA-seq data performs similarly in intersample analyses while improving intrasample comparisons. <i>BMC Bioinformatics</i> , 2018, 19, 236.	1.2	105
105	Dendritic Cells Actively Limit Interleukin-10 Production Under Inflammatory Conditions via DC-SCRIPT and Dual-Specificity Phosphatase 4. <i>Frontiers in Immunology</i> , 2018, 9, 1420.	2.2	16
106	The Prevalence of CD146 Expression in Breast Cancer Subtypes and Its Relation to Outcome. <i>Cancers</i> , 2018, 10, 134.	1.7	18
107	Functional <i>Ex Vivo</i> Assay Reveals Homologous Recombination Deficiency in Breast Cancer Beyond BRCA Gene Defects. <i>Clinical Cancer Research</i> , 2018, 24, 6277-6287.	3.2	53
108	Interrogation of transcriptomic changes associated with drug-induced hepatic sinusoidal dilatation in colorectal cancer. <i>PLoS ONE</i> , 2018, 13, e0198099.	1.1	9

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109	MicroRNA expression in pre-treatment plasma of patients with benign breast diseases and breast cancer. <i>Oncotarget</i> , 2018, 9, 24335-24346.	0.8	11
110	The complete genomic landscape of metastatic prostate cancer pinpoints clinically targetable subgroups.. <i>Journal of Clinical Oncology</i> , 2018, 36, 5014-5014.	0.8	0
111	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , 2017, 49, 341-348.	9.4	75
112	Proteomic characterization of microdissected breast tissue environment provides a protein-level overview of malignant transformation. <i>Proteomics</i> , 2017, 17, 1600213.	1.3	7
113	Male breast cancer precursor lesions: analysis of the EORTC 10085/TBCRC/BIG/NABCG International Male Breast Cancer Program. <i>Modern Pathology</i> , 2017, 30, 509-518.	2.9	32
114	Application of circulating tumor DNA in prospective clinical oncology trials – standardization of preanalytical conditions. <i>Molecular Oncology</i> , 2017, 11, 295-304.	2.1	123
115	Low Tumor Mitochondrial DNA Content Is Associated with Better Outcome in Breast Cancer Patients Receiving Anthracycline-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2017, 23, 4735-4743.	3.2	14
116	A Systematic Analysis of Oncogenic Gene Fusions in Primary Colon Cancer. <i>Cancer Research</i> , 2017, 77, 3814-3822.	0.4	76
117	Somatic Tumor Mutations Detected by Targeted Next Generation Sequencing in Minute Amounts of Serum-Derived Cell-Free DNA. <i>Scientific Reports</i> , 2017, 7, 2136.	1.6	7
118	Improved diagnosis and prognostication of patients with pleural malignant mesothelioma using biomarkers in pleural effusions and peripheral blood samples – a short report. <i>Cellular Oncology (Dordrecht)</i> , 2017, 40, 511-519.	2.1	5
119	Phosphoserine aminotransferase 1 is associated to poor outcome on tamoxifen therapy in recurrent breast cancer. <i>Scientific Reports</i> , 2017, 7, 2099.	1.6	33
120	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. <i>Nature Medicine</i> , 2017, 23, 517-525.	15.2	769
121	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017, 543, 714-718.	13.7	229
122	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. <i>Oncogene</i> , 2017, 36, 2737-2749.	2.6	34
123	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
124	Increased MAPK1/3 Phosphorylation in Luminal Breast Cancer Related with PIK3CA Hotspot Mutations and Prognosis. <i>Translational Oncology</i> , 2017, 10, 854-866.	1.7	5
125	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017, 32, 169-184.e7.	7.7	534
126	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67

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127	ESR1 mutations: Moving towards guiding treatment decision-making in metastatic breast cancer patients. <i>Cancer Treatment Reviews</i> , 2017, 52, 33-40.	3.4	75
128	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
129	The Predictive Value of <i>PITX2</i> DNA Methylation for High-Risk Breast Cancer Therapy: Current Guidelines, Medical Needs, and Challenges. <i>Disease Markers</i> , 2017, 2017, 1-14.	0.6	18
130	High mRNA expression of splice variant SYK short correlates with hepatic disease progression in chemonaive lymph node negative colon cancer patients. <i>PLoS ONE</i> , 2017, 12, e0185607.	1.1	14
131	Prospects of Targeting the Gastrin Releasing Peptide Receptor and Somatostatin Receptor 2 for Nuclear Imaging and Therapy in Metastatic Breast Cancer. <i>PLoS ONE</i> , 2017, 12, e0170536.	1.1	8
132	Progressive APOBEC3B mRNA expression in distant breast cancer metastases. <i>PLoS ONE</i> , 2017, 12, e0171343.	1.1	31
133	Cell-free DNA mutations as biomarkers in breast cancer patients receiving tamoxifen. <i>Oncotarget</i> , 2016, 7, 43412-43418.	0.8	30
134	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	1.1	12
135	The 29.5 kb APOBEC3B Deletion Polymorphism Is Not Associated with Clinical Outcome of Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0161731.	1.1	15
136	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	2.3	51
137	The advantage of laser-capture microdissection over whole tissue analysis in proteomic profiling studies. <i>Proteomics</i> , 2016, 16, 1474-1485.	1.3	38
138	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
139	Recurrent HOXB13 mutations in the Dutch population do not associate with increased breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 30026.	1.6	3
140	A novel independence test for somatic alterations in cancer shows that biology drives mutual exclusivity but chance explains most co-occurrence. <i>Genome Biology</i> , 2016, 17, 261.	3.8	114
141	BRCA1-deficient breast cancer cell lines are resistant to MEK inhibitors and show distinct sensitivities to 6-thioguanine. <i>Scientific Reports</i> , 2016, 6, 28217.	1.6	23
142	Endocrine therapy resistance in estrogen receptor (ER)-positive breast cancer. <i>Drug Discovery Today</i> , 2016, 21, 1181-1188.	3.2	53
143	Molecular characterization of irinotecan (SN-38) resistant human breast cancer cell lines. <i>BMC Cancer</i> , 2016, 16, 34.	1.1	35
144	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	13.7	1,760

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145	mRNA expression profiles of colorectal liver metastases as a novel biomarker for early recurrence after partial hepatectomy. <i>Molecular Oncology</i> , 2016, 10, 1542-1550.	2.1	9
146	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 36874.	1.6	2
147	Prognostic significance of nuclear expression of UMP-CMP kinase in triple negative breast cancer patients. <i>Scientific Reports</i> , 2016, 6, 32027.	1.6	19
148	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
149	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , 2016, 7, 11383.	5.8	235
150	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	5.8	119
151	Somatic mutation detection using various targeted detection assays in paired samples of circulating tumor DNA, primary tumor and metastases from patients undergoing resection of colorectal liver metastases. <i>Molecular Oncology</i> , 2016, 10, 1575-1584.	2.1	61
152	Prognostic value of automated Ki67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , 2016, 18, 104.	2.2	56
153	The DNA cytosine deaminase APOBEC3B promotes tamoxifen resistance in ER-positive breast cancer. <i>Science Advances</i> , 2016, 2, e1601737.	4.7	175
154	GATA3 mRNA expression, but not mutation, associates with longer progression-free survival in ER-positive breast cancer patients treated with first-line tamoxifen for recurrent disease. <i>Cancer Letters</i> , 2016, 376, 104-109.	3.2	22
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