

Sequence analysis of mutations and translocations across

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Runx1: no longer just for leukemia. EMBO Journal, 2012, 31, 4098-4099.	3.5	31
3	Next-generation sequencing in breast cancer. Current Opinion in Oncology, 2012, 24, 597-604.	1.1	76
4	Functional analysis of receptor tyrosine kinase mutations in lung cancer identifies oncogenic extracellular domain mutations of <i>ERBB2</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14476-14481.	3.3	246
5	Conference Scene: Australia and New Zealand Breast Cancer Trials Group Annual Scientific Meeting. Breast Cancer Management, 2012, 1, 273-275.	0.2	0
6	Medulloblastomics: the end of the beginning. Nature Reviews Cancer, 2012, 12, 818-834.	12.8	560
7	Regulation of mRNA expression in breast cancer - a cis-tematic trans-action. Breast Cancer Research, 2012, 14, 322.	2.2	1
8	Who's driving anyway? Herculean efforts to identify the drivers of breast cancer. Breast Cancer Research, 2012, 14, 323.	2.2	8
10	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. Cell, 2012, 150, 1107-1120.	13.5	1,591
11	Molecular biology in breast cancer: Should molecular classifiers be assessed by conventional tools or by gene expression arrays?. Critical Reviews in Oncology/Hematology, 2012, 84, e58-e69.	2.0	10
12	What are we learning from the cancer genome?. Nature Reviews Clinical Oncology, 2012, 9, 621-630.	12.5	50
13	Evolution of the cancer genome. Nature Reviews Genetics, 2012, 13, 795-806.	7.7	532
14	SnapShot: Breast Cancer. Cancer Cell, 2012, 22, 562-562.e1.	7.7	64
15	Structural analysis of the genome of breast cancer cell line ZR-75-30 identifies twelve expressed fusion genes. BMC Genomics, 2012, 13, 719.	1.2	32
16	Identifying putative breast cancer-associated long intergenic non-coding RNA loci by high density SNP array analysis. Frontiers in Genetics, 2012, 3, 299.	1.1	11
17	The breast cancer landscape. Nature, 2012, 486, 328-329.	13.7	32
18	Genes, genes everywhere.... Nature Reviews Cancer, 2012, 12, 507-507.	12.8	1
19	Cancer Genomics. , 2013, , .		4
20	GATA3 expression in breast carcinoma: utility in triple-negative, sarcomatoid, and metastatic carcinomas. Human Pathology, 2013, 44, 1341-1349.	1.1	192

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21	Next generation sequencing in cancer research and clinical application. Biological Procedures Online, 2013, 15, 4.	1.4	102
22	CoNVEX: copy number variation estimation in exome sequencing data using HMM. BMC Bioinformatics, 2013, 14, S2.	1.2	61
23	Assessment of computational methods for predicting the effects of missense mutations in human cancers. BMC Genomics, 2013, 14, S7.	1.2	153
24	Gene rearrangements in hormone receptor negative breast cancers revealed by mate pair sequencing. BMC Genomics, 2013, 14, 165.	1.2	33
25	Signaling pathway switch in breast cancer. Cancer Cell International, 2013, 13, 66.	1.8	25
26	Luminal breast cancer: from biology to treatment. Nature Reviews Clinical Oncology, 2013, 10, 494-506.	12.5	183
27	Next generation analysis of breast cancer genomes for precision medicine. Cancer Letters, 2013, 339, 1-7.	3.2	19
28	A new genome-driven integrated classification of breast cancer and its implications. EMBO Journal, 2013, 32, 617-628.	3.5	267
29	Personalized therapy for breast cancer: a dream or a reality?. Future Oncology, 2013, 9, 1105-1119.	1.1	27
30	Next Generation Sequencing in Cancer Research. , 2013, , .		5
31	Breast Cancer Metastasis. American Journal of Pathology, 2013, 183, 1084-1095.	1.9	67
32	Endocrine Resistance in Breast Cancer: Focus on the Phosphatidylinositol 3-Kinase/Akt/Mammalian Target of Rapamycin Signaling Pathway. Breast Care, 2013, 8, 248-255.	0.8	40
33	Beyond <i>BRCA1/2</i> : polygenic, "polyfunctional"™ molecular circuitry model to predict breast cancer risk. Biomarkers in Medicine, 2013, 7, 675-678.	0.6	2
34	PIK3CA-AKT pathway mutations in micropapillary breast carcinoma. Human Pathology, 2013, 44, 1320-1327.	1.1	17
35	New insights into the role of Runx1 in epithelial stem cell biology and pathology. Journal of Cellular Biochemistry, 2013, 114, 985-993.	1.2	59
36	Mutational analysis of breast cancer: Guiding personalized treatments. Breast, 2013, 22, S19-S21.	0.9	16
37	Drugdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	9.0	443
38	Latest biopsy approach for suspected metastases in patients with breast cancer. Nature Reviews Clinical Oncology, 2013, 10, 711-719.	12.5	22

#	ARTICLE	IF	CITATIONS
39	Molecular Pathways: PI3K Pathway Targets in Triple-Negative Breast Cancers. <i>Clinical Cancer Research</i> , 2013, 19, 3738-3744.	3.2	53
40	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. <i>Nature Communications</i> , 2013, 4, 2730.	5.8	104
41	From next-generation sequencing to nanopore sequencing technology: paving the way to personalized genomic medicine. <i>Expert Review of Medical Devices</i> , 2013, 10, 1-6.	1.4	76
42	Germline and somatic KLLN alterations in breast cancer dysregulate G2 arrest. <i>Human Molecular Genetics</i> , 2013, 22, 2451-2461.	1.4	20
43	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 409-420.	1.1	120
44	Targeted Sequencing Strategies in Cancer Research. , 2013, , 137-163.		2
47	Integration of Gene Signatures and Genomic Data into Radiation Oncology Practice. <i>Medical Radiology</i> , 2013, , 29-46.	0.0	0
48	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. <i>Breast Cancer Research</i> , 2013, 15, R92.	2.2	320
49	PROGgene: gene expression based survival analysis web application for multiple cancers. <i>Journal of Clinical Bioinformatics</i> , 2013, 3, 22.	1.2	140
50	Emerging patterns of somatic mutations in cancer. <i>Nature Reviews Genetics</i> , 2013, 14, 703-718.	7.7	442
52	Deep sequencing and integrative genome analysis: approaching a new class of biomarkers and therapeutic targets for breast cancer. <i>Pharmacogenomics</i> , 2013, 14, 5-8.	0.6	3
53	A Genome-wide siRNA Screen Identifies Proteasome Addiction as a Vulnerability of Basal-like Triple-Negative Breast Cancer Cells. <i>Cancer Cell</i> , 2013, 24, 182-196.	7.7	147
54	Epigenetic Modifications in Breast Cancer and Their Role in Personalized Medicine. <i>American Journal of Pathology</i> , 2013, 183, 1052-1063.	1.9	75
55	Targeting the PI3-Kinase/Akt/mTOR Signaling Pathway. <i>Surgical Oncology Clinics of North America</i> , 2013, 22, 641-664.	0.6	161
56	Emerging landscape of oncogenic signatures across human cancers. <i>Nature Genetics</i> , 2013, 45, 1127-1133.	9.4	1,190
57	Somatic mutation of CDKN1B in small intestine neuroendocrine tumors. <i>Nature Genetics</i> , 2013, 45, 1483-1486.	9.4	275
59	Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. <i>Molecular Systems Biology</i> , 2013, 9, 637.	3.2	267
60	TACE-dependent TGF β shedding drives triple-negative breast cancer cell invasion. <i>International Journal of Cancer</i> , 2013, 133, n/a-n/a.	2.3	31

#	ARTICLE	IF	CITATIONS
61	Needles in a haystack: finding recurrent genomic changes in breast cancer. <i>Breast Cancer Research</i> , 2013, 14, 304.	2.2	2
62	Activating mutations and senescence secretome: new insights into HER2 activation, drug sensitivity and metastatic progression. <i>Breast Cancer Research</i> , 2013, 15, 309.	2.2	1
63	The genomic map of breast cancer: which roads lead to better targeted therapies?. <i>Breast Cancer Research</i> , 2013, 15, 209.	2.2	10
64	Stochastic profiling of transcriptional regulatory heterogeneities in tissues, tumors and cultured cells. <i>Nature Protocols</i> , 2013, 8, 282-301.	5.5	32
65	Activating HER2 Mutations in HER2 Gene Amplification Negative Breast Cancer. <i>Cancer Discovery</i> , 2013, 3, 224-237.	7.7	697
66	The Genomic Landscape of Breast Cancer as a Therapeutic Roadmap. <i>Cancer Discovery</i> , 2013, 3, 27-34.	7.7	200
67	RUNX2 in mammary gland development and breast cancer. <i>Journal of Cellular Physiology</i> , 2013, 228, 1137-1142.	2.0	66
68	Whole-exome sequencing identifies a recurrent NAB2-STAT6 fusion in solitary fibrous tumors. <i>Nature Genetics</i> , 2013, 45, 131-132.	9.4	500
69	Next-generation sequencing in the clinic: Promises and challenges. <i>Cancer Letters</i> , 2013, 340, 284-295.	3.2	272
70	Prognostic evaluation of the B cell/IL-8 metagene in different intrinsic breast cancer subtypes. <i>Breast Cancer Research and Treatment</i> , 2013, 137, 407-416.	1.1	30
71	Development of PI3K inhibitors: lessons learned from early clinical trials. <i>Nature Reviews Clinical Oncology</i> , 2013, 10, 143-153.	12.5	694
72	RUNX family: Regulation and diversification of roles through interacting proteins. <i>International Journal of Cancer</i> , 2013, 132, 1260-1271.	2.3	162
73	Going Forward with Genetics. <i>American Journal of Pathology</i> , 2013, 182, 1462-1473.	1.9	57
74	Acquired Mutations That Affect Pre-mRNA Splicing in Hematologic Malignancies and Solid Tumors. <i>Journal of the National Cancer Institute</i> , 2013, 105, 1540-1549.	3.0	69
75	Signaling Network Assessment of Mutations and Copy Number Variations Predict Breast Cancer Subtype-Specific Drug Targets. <i>Cell Reports</i> , 2013, 5, 216-223.	2.9	106
76	Building a Genome Analysis Pipeline to Predict Disease Risk and Prevent Disease. <i>Journal of Molecular Biology</i> , 2013, 425, 3993-4005.	2.0	31
77	Integrative deep-sequencing analysis of cancer samples: discoveries and clinical challenges. <i>Pharmacogenomics Journal</i> , 2013, 13, 205-208.	0.9	4
78	High-throughput sequencing for biology and medicine. <i>Molecular Systems Biology</i> , 2013, 9, 640.	3.2	251

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79	Analysis of Circulating Tumor DNA to Monitor Metastatic Breast Cancer. <i>New England Journal of Medicine</i> , 2013, 368, 1199-1209.	13.9	1,884
80	Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. <i>Nature Biotechnology</i> , 2013, 31, 213-219.	9.4	3,934
81	Therapeutic targets in triple negative breast cancer. <i>Journal of Clinical Pathology</i> , 2013, 66, 530-542.	1.0	117
82	Translating Genomics to the Clinic: Implications of Cancer Heterogeneity. <i>Clinical Chemistry</i> , 2013, 59, 127-137.	1.5	25
83	Translating metastasis-related biomarkers to the clinic—progress and pitfalls. <i>Nature Reviews Clinical Oncology</i> , 2013, 10, 169-179.	12.5	40
84	Emerging targeted agents in metastatic breast cancer. <i>Nature Reviews Clinical Oncology</i> , 2013, 10, 191-210.	12.5	158
85	GATA3 Mutations Found in Breast Cancers May Be Associated with Aberrant Nuclear Localization, Reduced Transactivation and Cell Invasiveness. <i>Hormones and Cancer</i> , 2013, 4, 123-139.	4.9	28
86	FOXA1 mutations in hormone-dependent cancers. <i>Frontiers in Oncology</i> , 2013, 3, 20.	1.3	50
87	Lessons from the Cancer Genome. <i>Cell</i> , 2013, 153, 17-37.	13.5	1,133
88	Exome and whole-genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity. <i>Nature Genetics</i> , 2013, 45, 478-486.	9.4	671
89	The war on cancer: are we winning?. <i>Tumor Biology</i> , 2013, 34, 1275-1284.	0.8	42
90	Next-generation sequencing: a powerful tool for the discovery of molecular markers in breast ductal carcinoma <i>in situ</i> . <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 151-165.	1.5	40
91	Cancer genome-sequencing study design. <i>Nature Reviews Genetics</i> , 2013, 14, 321-332.	7.7	100
92	Genomic sequencing in cancer. <i>Cancer Letters</i> , 2013, 340, 161-170.	3.2	28
93	Implementing personalized cancer genomics in clinical trials. <i>Nature Reviews Drug Discovery</i> , 2013, 12, 358-369.	21.5	267
94	Understanding genomic alterations in cancer genomes using an integrative network approach. <i>Cancer Letters</i> , 2013, 340, 261-269.	3.2	70
95	Watching the grin fade: Tracing the effects of polyploidy on different evolutionary time scales. <i>Seminars in Cell and Developmental Biology</i> , 2013, 24, 320-331.	2.3	37
96	The mutational landscape of adenoid cystic carcinoma. <i>Nature Genetics</i> , 2013, 45, 791-798.	9.4	394

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97	Progesterone signalling in breast cancer: a neglected hormone coming into the limelight. <i>Nature Reviews Cancer</i> , 2013, 13, 385-396.	12.8	204
98	Proteomic and bioinformatic analysis of mammalian SWI/SNF complexes identifies extensive roles in human malignancy. <i>Nature Genetics</i> , 2013, 45, 592-601.	9.4	1,082
99	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.	9.4	990
100	Genetic heterogeneity in breast cancer: the road to personalized medicine?. <i>BMC Medicine</i> , 2013, 11, 151.	2.3	47
101	Diverse Mechanisms of Somatic Structural Variations in Human Cancer Genomes. <i>Cell</i> , 2013, 153, 919-929.	13.5	308
102	Identification of driver genes in hepatocellular carcinoma by exome sequencing. <i>Hepatology</i> , 2013, 58, 1693-1702.	3.6	264
103	Genomics-Driven Oncology: Framework for an Emerging Paradigm. <i>Journal of Clinical Oncology</i> , 2013, 31, 1806-1814.	0.8	315
104	Patterns and Mutational Signatures of Tandem Base Substitutions Causing Human Inherited Disease. <i>Human Mutation</i> , 2013, 34, 1119-1130.	1.1	34
105	High-Throughput Gene Expression and Mutation Profiling: Current Methods and Future Perspectives. <i>Breast Care</i> , 2013, 8, 401-406.	0.8	14
106	DNA Repair Gene Patterns as Prognostic and Predictive Factors in Molecular Breast Cancer Subtypes. <i>Oncologist</i> , 2013, 18, 1063-1073.	1.9	75
108	Harnessing massively parallel DNA sequencing for the personalization of cancer management. <i>Personalized Medicine</i> , 2013, 10, 183-190.	0.8	2
109	Cancer heterogeneity and signaling network-based drug target. <i>Pharmacogenomics</i> , 2013, 14, 1243-1246.	0.6	2
110	Fine mapping of breast cancer genome-wide association studies loci in women of African ancestry identifies novel susceptibility markers. <i>Carcinogenesis</i> , 2013, 34, 1520-1528.	1.3	26
112	Integrated clinical genomics: new horizon for diagnostic and biomarker discoveries in cancer. <i>Expert Review of Molecular Diagnostics</i> , 2013, 13, 1-4.	1.5	9
113	Somatic rearrangements across cancer reveal classes of samples with distinct patterns of DNA breakage and rearrangement-induced hypermutability. <i>Genome Research</i> , 2013, 23, 228-235.	2.4	124
114	An evolutionary perspective on anti-tumor immunity. <i>Frontiers in Oncology</i> , 2012, 2, 202.	1.3	15
115	Bringing precision medicine to the clinic: from genomic profiling to the power of clinical observation. <i>Annals of Oncology</i> , 2013, 24, 1956-1957.	0.6	21
116	Overview of diagnostic/targeted treatment combinations in personalized medicine for breast cancer patients. <i>Pharmacogenomics and Personalized Medicine</i> , 2013, 7, 1.	0.4	10

#	ARTICLE	IF	CITATIONS
118	Frequent PIK3CA Mutations in Radial Scars. <i>Diagnostic Molecular Pathology</i> , 2013, 22, 210-214.	2.1	19
119	Research and clinical applications of cancer genome sequencing. <i>Current Opinion in Obstetrics and Gynecology</i> , 2013, 25, 3-10.	0.9	14
120	Low-copy <i>piggyBac</i> transposon mutagenesis in mice identifies genes driving melanoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3640-9.	3.3	28
121	Carboxyl Group Footprinting Mass Spectrometry and Molecular Dynamics Identify Key Interactions in the HER2-HER3 Receptor Tyrosine Kinase Interface. <i>Journal of Biological Chemistry</i> , 2013, 288, 25254-25264.	1.6	29
122	<i>PIK3CA</i> and <i>AKT1</i> Mutations Have Distinct Effects on Sensitivity to Targeted Pathway Inhibitors in an Isogenic Luminal Breast Cancer Model System. <i>Clinical Cancer Research</i> , 2013, 19, 5413-5422.	3.2	84
124	Somatic Mutation Profiling and Associations With Prognosis and Trastuzumab Benefit in Early Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2013, 105, 960-967.	3.0	138
127	Breast Cancer Genomics: From Portraits to Landscapes. , 2013, , 255-294.		0
128	The mutational landscape of chromatin regulatory factors across 4,623 tumor samples. <i>Genome Biology</i> , 2013, 14, r106.	13.9	102
129	Nonequivalent Gene Expression and Copy Number Alterations in High-Grade Serous Ovarian Cancers with <i>BRCA1</i> and <i>BRCA2</i> Mutations. <i>Clinical Cancer Research</i> , 2013, 19, 3474-3484.	3.2	76
130	Clinical Response to a Lapatinib-Based Therapy for a Li-Fraumeni Syndrome Patient with a Novel <i>HER2</i> V659E Mutation. <i>Cancer Discovery</i> , 2013, 3, 1238-1244.	7.7	43
131	Current Challenges for HER2 Testing in Diagnostic Pathology: State of the Art and Controversial Issues. <i>Frontiers in Oncology</i> , 2013, 3, 129.	1.3	73
132	WNT10B/ β -catenin signalling induces HMGA2 and proliferation in metastatic triple-negative breast cancer. <i>EMBO Molecular Medicine</i> , 2013, 5, 264-279.	3.3	163
133	TrAp: a tree approach for fingerprinting subclonal tumor composition. <i>Nucleic Acids Research</i> , 2013, 41, e165-e165.	6.5	113
134	Models of signalling networks – what cell biologists can gain from them and give to them. <i>Journal of Cell Science</i> , 2013, 126, 1913-1921.	1.2	78
135	Functional genomics lead to new therapies in follicular lymphoma. <i>Annals of the New York Academy of Sciences</i> , 2013, 1293, 18-24.	1.8	4
136	New Strategies in Prostate Cancer: Translating Genomics into the Clinic. <i>Clinical Cancer Research</i> , 2013, 19, 517-523.	3.2	50
137	Trastuzumab emtansine for advanced HER2-positive breast cancer and beyond: genome landscape-based targets. <i>Expert Review of Anticancer Therapy</i> , 2013, 13, 5-8.	1.1	11
138	Genome evolution during progression to breast cancer. <i>Genome Research</i> , 2013, 23, 1097-1108.	2.4	98

#	ARTICLE	IF	CITATIONS
139	Specific Plasma Autoantibody Reactivity in Myelodysplastic Syndromes. <i>Scientific Reports</i> , 2013, 3, 3311.	1.6	8
140	Genomic Medicine Frontier in Human Solid Tumors: Prospects and Challenges. <i>Journal of Clinical Oncology</i> , 2013, 31, 1874-1884.	0.8	101
141	Triple-negative breast cancer: molecular characterization and targeted therapies. <i>Breast Cancer Management</i> , 2013, 2, 417-430.	0.2	1
143	Prognostic microRNA/mRNA signature from the integrated analysis of patients with invasive breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7413-7417.	3.3	149
144	Incorporating Genomics into Breast Cancer Clinical Trials and Care. <i>Clinical Cancer Research</i> , 2013, 19, 6371-6379.	3.2	15
145	Relapsed Classic E-Cadherin (<i>CDH1</i>) Mutated Invasive Lobular Breast Cancer Shows a High Frequency of <i>HER2</i> (<i>ERBB2</i>) Gene Mutations. <i>Clinical Cancer Research</i> , 2013, 19, 2668-2676.	3.2	122
148	Clinical application of high-throughput genomic technologies for treatment selection in breast cancer. <i>Breast Cancer Research</i> , 2013, 15, R97.	2.2	17
149	Using Multigene Tests to Select Treatment for Early-Stage Breast Cancer. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2013, 11, 174-182.	2.3	44
150	Identification of breast cancer patients based on human signaling network motifs. <i>Scientific Reports</i> , 2013, 3, 3368.	1.6	26
151	Functional Polymorphisms in Xenobiotic Metabolizing Enzymes and Their Impact on the Therapy of Breast Cancer. <i>Frontiers in Genetics</i> , 2013, 3, 329.	1.1	8
152	The Potential Role of Nanotechnology in Therapeutic Approaches for Triple Negative Breast Cancer. <i>Pharmaceutics</i> , 2013, 5, 353-370.	2.0	29
153	Boolean Network Model for Cancer Pathways: Predicting Carcinogenesis and Targeted Therapy Outcomes. <i>PLoS ONE</i> , 2013, 8, e69008.	1.1	148
154	Targeting the Akt Kinase to Modulate Survival, Invasiveness and Drug Resistance of Cancer Cells. <i>Current Medicinal Chemistry</i> , 2013, 20, 1923-1945.	1.2	86
155	Neoadjuvant Therapy in Operable Breast Cancer: Application to Triple Negative Breast Cancer. <i>Journal of Oncology</i> , 2013, 2013, 1-8.	0.6	15
157	Candidate Luminal B Breast Cancer Genes Identified by Genome, Gene Expression and DNA Methylation Profiling. <i>PLoS ONE</i> , 2014, 9, e81843.	1.1	53
158	Expression of RUNX1 Correlates with Poor Patient Prognosis in Triple Negative Breast Cancer. <i>PLoS ONE</i> , 2014, 9, e100759.	1.1	80
159	RUNX1, a transcription factor mutated in breast cancer, controls the fate of ER-positive mammary luminal cells. <i>ELife</i> , 2014, 3, e03881.	2.8	91
160	Loss of the multifunctional RNA-binding protein RBM47 as a source of selectable metastatic traits in breast cancer. <i>ELife</i> , 2014, 3, .	2.8	115

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161	Amplification of Chromosome 1q Genes Encoding the Phosphoinositide Signalling Enzymes <i>PI4KB</i> , <i>AKT3</i> , <i>PIP5K1A</i> and <i>PI3KC2B</i> in Breast Cancer. <i>Journal of Cancer</i> , 2014, 5, 790-796.	1.2	25
162	MYC-driven accumulation of 2-hydroxyglutarate is associated with breast cancer prognosis. <i>Journal of Clinical Investigation</i> , 2014, 124, 398-412.	3.9	348
164	miR-142 regulates the tumorigenicity of human breast cancer stem cells through the canonical WNT signaling pathway. <i>ELife</i> , 2014, 3, .	2.8	153
165	Subtyping of breast cancer using reverse phase protein arrays. <i>Expert Review of Proteomics</i> , 2014, 11, 757-770.	1.3	17
166	Insights into cancer biology through next-generation sequencing. <i>Clinical Medicine</i> , 2014, 14, s71-s77.	0.8	3
167	FOXC1 is a Critical Mediator of EGFR Function in Human Basal-like Breast Cancer. <i>Annals of Surgical Oncology</i> , 2014, 21, 758-766.	0.7	34
168	Understanding the Premalignant Potential of Atypical Hyperplasia through Its Natural History: A Longitudinal Cohort Study. <i>Cancer Prevention Research</i> , 2014, 7, 211-217.	0.7	192
169	Genome-driven integrated classification of breast cancer validated in over 7,500 samples. <i>Genome Biology</i> , 2014, 15, 431.	3.8	178
170	Genome-based approaches for the diagnosis of breast cancer: a review with perspective. <i>Breast Cancer Management</i> , 2014, 3, 173-193.	0.2	0
171	RUNX family members are covalently modified and regulated by PIAS1-mediated sumoylation. <i>Oncogenesis</i> , 2014, 3, e101-e101.	2.1	24
172	The AURORA initiative for metastatic breast cancer. <i>British Journal of Cancer</i> , 2014, 111, 1881-1887.	2.9	77
173	Frequent phosphatidylinositol-3-kinase mutations in proliferative breast lesions. <i>Modern Pathology</i> , 2014, 27, 740-750.	2.9	47
174	Genetic variant rs1058240 at the microRNA-binding site in the GATA3 gene may regulate its mRNA expression. <i>Biomedical Reports</i> , 2014, 2, 404-407.	0.9	6
175	Overexpression of sorcin in multidrug-resistant human breast cancer. <i>Oncology Letters</i> , 2014, 8, 2393-2398.	0.8	18
176	Induction of Wnt-Inducible Signaling Protein-1 Correlates with Invasive Breast Cancer Oncogenesis and Reduced Type 1 Cell-Mediated Cytotoxic Immunity: A Retrospective Study. <i>PLoS Computational Biology</i> , 2014, 10, e1003409.	1.5	43
177	Pathway-Driven Discovery of Rare Mutational Impact on Cancer. <i>BioMed Research International</i> , 2014, 1-10.	0.9	3
178	Predictive value of phosphorylated mammalian target of rapamycin for disease-free survival in breast cancer patients receiving neoadjuvant chemotherapy. <i>Oncology Letters</i> , 2014, 8, 2642-2648.	0.8	1
179	Systems consequences of amplicon formation in human breast cancer. <i>Genome Research</i> , 2014, 24, 1559-1571.	2.4	32

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180	Detecting independent and recurrent copy number aberrations using interval graphs. <i>Bioinformatics</i> , 2014, 30, i195-i203.	1.8	22
181	Integration of Genomic Data Enables Selective Discovery of Breast Cancer Drivers. <i>Cell</i> , 2014, 159, 1461-1475.	13.5	77
182	Evolving techniques for gene fusion detection in soft tissue tumours. <i>Histopathology</i> , 2014, 64, 151-162.	1.6	41
183	The mutational burdens and evolutionary ages of early gastric cancers are comparable to those of advanced gastric cancers. <i>Journal of Pathology</i> , 2014, 234, 365-374.	2.1	33
184	Genome network medicine: innovation to overcome huge challenges in cancer therapy. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014, 6, 201-208.	6.6	8
185	Sequencing HNC: Emergence of Notch Signaling. , 2014, , 303-323.		0
186	Molecular Determinants of Head and Neck Cancer. , 2014, , .		2
187	Polarity gene alterations in pure invasive micropapillary carcinomas of the breast. <i>Breast Cancer Research</i> , 2014, 16, R46.	2.2	40
188	A fine-scale dissection of the DNA double-strand break repair machinery and its implications for breast cancer therapy. <i>Nucleic Acids Research</i> , 2014, 42, 6106-6127.	6.5	72
189	New concepts in breast cancer genomics and genetics. <i>Breast Cancer Research</i> , 2014, 16, 460.	2.2	28
190	Shift in GATA3 functions, and GATA3 mutations, control progression and clinical presentation in breast cancer. <i>Breast Cancer Research</i> , 2014, 16, 464.	2.2	40
191	BRCA1 and BRCA2 Cancer Syndromes and Clinical Significance. , 2014, 19, 43-48.		0
192	Triple-negative breast cancer. <i>Current Opinion in Obstetrics and Gynecology</i> , 2014, 26, 34-40.	0.9	33
193	NCG 4.0: the network of cancer genes in the era of massive mutational screenings of cancer genomes. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau015.	1.4	50
194	Taxonomy of breast cancer based on normal cell phenotype predicts outcome. <i>Journal of Clinical Investigation</i> , 2014, 124, 859-870.	3.9	164
195	The eSNV-detect: a computational system to identify expressed single nucleotide variants from transcriptome sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, e172-e172.	6.5	33
196	Theranostic and Molecular Classification of Breast Cancer. <i>Archives of Pathology and Laboratory Medicine</i> , 2014, 138, 44-56.	1.2	40
197	HER2 Mutation Status in Japanese HER2-negative Breast Cancer Patients. <i>Japanese Journal of Clinical Oncology</i> , 2014, 44, 619-623.	0.6	11

#	ARTICLE	IF	CITATIONS
198	Association of H3K9me3 and H3K27me3 repressive histone marks with breast cancer subtypes in the Nursesâ€™ Health Study. <i>Breast Cancer Research and Treatment</i> , 2014, 147, 639-651.	1.1	45
199	Omics Approaches in Breast Cancer. , 2014, , .		10
200	Breast Cancer Genomics. , 2014, , 53-103.		0
201	MarvelD3 couples tight junctions to the MEK1â€“JNK pathway to regulate cell behavior and survival. <i>Journal of Cell Biology</i> , 2014, 204, 821-838.	2.3	67
202	Performance comparison of SNP detection tools with illumina exome sequencing dataâ€™an assessment using both family pedigree information and sample-matched SNP array data. <i>Nucleic Acids Research</i> , 2014, 42, e101-e101.	6.5	50
203	Whole exome sequencing for cancer – is there evidence of clinical utility?. <i>Advances in Genomics and Genetics</i> , 2014, , 115.	0.8	2
204	Inferring copy number and genotype in tumour exome data. <i>BMC Genomics</i> , 2014, 15, 732.	1.2	102
205	PIK3CA mutations in breast cancer: reconciling findings from preclinical and clinical data. <i>Breast Cancer Research</i> , 2014, 16, 201.	2.2	94
206	Mesenchymal precursor cells maintain the differentiation and proliferation potentials of breast epithelial cells. <i>Breast Cancer Research</i> , 2014, 16, R60.	2.2	18
207	Genomic profile analysis of diffuse-type gastric cancers. <i>Genome Biology</i> , 2014, 15, R55.	13.9	58
208	Clinical value of isoform-specific detection and targeting of AKT1, AKT2 and AKT3 in breast cancer. <i>Breast Cancer Management</i> , 2014, 3, 409-421.	0.2	3
209	Individualizing breast cancer treatmentâ€™The dawn of personalized medicine. <i>Experimental Cell Research</i> , 2014, 320, 1-11.	1.2	26
210	OPG and PgR show similar cohort specific effects as prognostic factors in ER positive breast cancer. <i>Molecular Oncology</i> , 2014, 8, 1196-1207.	2.1	17
211	Sprouty4 interferes with cell proliferation and migration of breast cancer-derived cell lines. <i>Tumor Biology</i> , 2014, 35, 4447-4456.	0.8	26
212	Mutations in EGFR, BRAF and RAS are rare in triple-negative and basal-like breast cancers from Caucasian women. <i>Breast Cancer Research and Treatment</i> , 2014, 143, 385-392.	1.1	54
213	Biallelic <i>DICER1</i> Mutations in Sporadic Pleuropulmonary Blastoma. <i>Cancer Research</i> , 2014, 74, 2742-2749.	0.4	67
214	Emergence of Constitutively Active Estrogen Receptor-Î± Mutations in Pretreated Advanced Estrogen Receptorâ€™Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2014, 20, 1757-1767.	3.2	529
215	Causal Network Models for Predicting Compound Targets and Driving Pathways in Cancer. <i>Journal of Biomolecular Screening</i> , 2014, 19, 791-802.	2.6	23

#	ARTICLE	IF	CITATIONS
216	Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls. <i>Nature Biotechnology</i> , 2014, 32, 246-251.	9.4	722
217	Molecular tests as prognostic factors in breast cancer. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2014, 464, 283-291.	1.4	35
218	Locus-Specific Databases in Cancer: What Future in a Post-Genomic Era? The TP53 LSDB paradigm. <i>Human Mutation</i> , 2014, 35, 643-653.	1.1	15
219	Epistatic interactions and drug response. <i>Journal of Pathology</i> , 2014, 232, 255-263.	2.1	24
220	Novel role of Engrailed 1 as a prosurvival transcription factor in basal-like breast cancer and engineering of interference peptides block its oncogenic function. <i>Oncogene</i> , 2014, 33, 4767-4777.	2.6	76
221	Picking the Point of Inhibition: A Comparative Review of PI3K/AKT/mTOR Pathway Inhibitors. <i>Molecular Cancer Therapeutics</i> , 2014, 13, 1021-1031.	1.9	375
222	The challenge of intratumour heterogeneity in precision medicine. <i>Journal of Internal Medicine</i> , 2014, 276, 41-51.	2.7	66
223	Molecular Testing in Cancer. , 2014, , .		2
224	Characterization of the genomic features and expressed fusion genes in micropapillary carcinomas of the breast. <i>Journal of Pathology</i> , 2014, 232, 553-565.	2.1	88
225	Somatic retrotransposition in human cancer revealed by whole-genome and exome sequencing. <i>Genome Research</i> , 2014, 24, 1053-1063.	2.4	191
226	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. <i>Nature Medicine</i> , 2014, 20, 682-688.	15.2	508
227	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Gene-Environment Interactions. <i>Genetic Epidemiology</i> , 2014, 38, 84-93.	0.6	28
228	An intragenic long noncoding RNA interacts epigenetically with the <i>RUNX1</i> promoter and enhancer chromatin DNA in hematopoietic malignancies. <i>International Journal of Cancer</i> , 2014, 135, 2783-2794.	2.3	82
229	Targeting Akt3 Signaling in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2014, 74, 964-973.	0.4	124
230	DNA Sequencing of Cancer: What Have We Learned?. <i>Annual Review of Medicine</i> , 2014, 65, 63-79.	5.0	41
231	Investigation of molecular alterations of <i>AKT</i> in triple-negative breast cancer. <i>Histopathology</i> , 2014, 64, 660-670.	1.6	20
232	Breast Cancer Genomics. , 2014, , 213-232.		4
233	Landscape of genomic alterations in cervical carcinomas. <i>Nature</i> , 2014, 506, 371-375.	13.7	708

#	ARTICLE	IF	CITATIONS
234	Molecular Homology and Difference between Spontaneous Canine Mammary Cancer and Human Breast Cancer. <i>Cancer Research</i> , 2014, 74, 5045-5056.	0.4	110
235	Identification and use of biomarkers in treatment strategies for triple-negative breast cancer subtypes. <i>Journal of Pathology</i> , 2014, 232, 142-150.	2.1	354
236	mTOR signaling in tumorigenesis. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2014, 1846, 638-654.	3.3	113
237	Regulatory variation: an emerging vantage point for cancer biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014, 6, 37-59.	6.6	6
238	The kinome associated with estrogen receptor-positive status in human breast cancer. <i>Endocrine-Related Cancer</i> , 2014, 21, R357-R370.	1.6	5
239	Luminal B Breast Cancer: Molecular Characterization, Clinical Management, and Future Perspectives. <i>Journal of Clinical Oncology</i> , 2014, 32, 2794-2803.	0.8	298
240	Applications of RNA interference high-throughput screening technology in cancer biology and virology. <i>Protein and Cell</i> , 2014, 5, 805-815.	4.8	17
241	Translating Genomics for Precision Cancer Medicine. <i>Annual Review of Genomics and Human Genetics</i> , 2014, 15, 395-415.	2.5	63
242	A New and More Accurate Estimate of the Rate of Concurrent Tandem-Base Substitution Mutations in the Human Germline: ~1/40.4% of the Single-Nucleotide Substitution Mutation Rate. <i>Human Mutation</i> , 2014, 35, 392-394.	1.1	15
243	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251-1243.	6.0	348
244	WWOX at the crossroads of cancer, metabolic syndrome related traits and CNS pathologies. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2014, 1846, 188-200.	3.3	89
245	Disruption of Runx1 and Runx3 Leads to Bone Marrow Failure and Leukemia Predisposition due to Transcriptional and DNA Repair Defects. <i>Cell Reports</i> , 2014, 8, 767-782.	2.9	80
246	Recurrent ESR1-CCDC170 rearrangements in an aggressive subset of oestrogen receptor-positive breast cancers. <i>Nature Communications</i> , 2014, 5, 4577.	5.8	112
247	PIK3CA Mutations Are Associated With Lower Rates of Pathologic Complete Response to Anti-Human Epidermal Growth Factor Receptor 2 (HER2) Therapy in Primary HER2-Overexpressing Breast Cancer. <i>Journal of Clinical Oncology</i> , 2014, 32, 3212-3220.	0.8	231
248	Next generation sequencing and tumor mutation profiling: are we ready for routine use in the oncology clinic?. <i>BMC Medicine</i> , 2014, 12, 140.	2.3	36
249	DawnRank: discovering personalized driver genes in cancer. <i>Genome Medicine</i> , 2014, 6, 56.	3.6	207
250	JMJD2A contributes to breast cancer progression through transcriptional repression of the tumor suppressor ARHI. <i>Breast Cancer Research</i> , 2014, 16, R56.	2.2	46
251	Toxicogenomics and Cancer Susceptibility: Advances with Next-Generation Sequencing. <i>Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews</i> , 2014, 32, 121-158.	2.9	32

#	ARTICLE	IF	CITATIONS
252	Analysis of interactions between the epigenome and structural mutability of the genome using Genboree workbench tools. BMC Bioinformatics, 2014, 15, S2.	1.2	19
253	Concordance of Genomic Alterations between Primary and Recurrent Breast Cancer. Molecular Cancer Therapeutics, 2014, 13, 1382-1389.	1.9	104
254	Deconvolving tumor purity and ploidy by integrating copy number alterations and loss of heterozygosity. Bioinformatics, 2014, 30, 2121-2129.	1.8	37
255	The 41st David A. Karnofsky Memorial Award Lecture: Academic Research Worldwideâ€”Quo Vadis?. Journal of Clinical Oncology, 2014, 32, 347-354.	0.8	35
256	AbsCN-seq: a statistical method to estimate tumor purity, ploidy and absolute copy numbers from next-generation sequencing data. Bioinformatics, 2014, 30, 1056-1063.	1.8	62
257	Breast tumor PDXs are genetically plastic and correspond to a subset of aggressive cancers prone to relapse. Molecular Oncology, 2014, 8, 431-443.	2.1	48
258	Collection, integration and analysis of cancer genomic profiles: from data to insight. Current Opinion in Genetics and Development, 2014, 24, 92-98.	1.5	22
259	Personalized medicine: Present and future of breast cancer management. Critical Reviews in Oncology/Hematology, 2014, 91, 223-233.	2.0	49
260	The Omics of Triple-Negative Breast Cancers. Clinical Chemistry, 2014, 60, 122-133.	1.5	52
261	Precision medicine and personalized breast cancer: combination pertuzumab therapy. Pharmacogenomics and Personalized Medicine, 2014, 7, 95.	0.4	13
262	Profiling the tyrosine phosphoproteome of different mouse mammary tumour models reveals distinct, model-specific signalling networks and conserved oncogenic pathways. Breast Cancer Research, 2014, 16, 437.	2.2	13
263	Initiation of Metastatic Breast Carcinoma by Targeting of the Ductal Epithelium with Adenovirus-Cre: A Novel Transgenic Mouse Model of Breast Cancer. Journal of Visualized Experiments, 2014, , .	0.2	20
264	Early Biomarkers in Breast Cancer. , 2014, , 569-638.		0
266	Identification of a metabolic and canonical biomarker signature in Mexican HR+/HER2âˆ”, triple positive and triple-negative breast cancer patients. International Journal of Oncology, 2014, 45, 2549-2559.	1.4	5
267	Variation in Sp1 binding sites correlates with expression of survivin in breast cancer. Molecular Medicine Reports, 2014, 10, 1395-1399.	1.1	8
270	Appraisal of the technologies and review of the genomic landscape of ductal carcinoma in situ of the breast. Breast Cancer Research, 2015, 17, 80.	2.2	5
271	Cancer typeâ€”dependent genetic interactions between cancer driver alterations indicate plasticity of epistasis across cell types. Molecular Systems Biology, 2015, 11, 824.	3.2	54
272	Prolonged Response to Trastuzumab in a Patient With HER2-Nonamplified Breast Cancer With Elevated HER2 Dimerization Harboring an ERBB2</i>S310F Mutation. Journal of the National Comprehensive Cancer Network: JNCCN, 2015, 13, 1066-1070.	2.3	31

#	ARTICLE	IF	CITATIONS
273	Targeting Breast Cancer Metastasis. <i>Breast Cancer: Basic and Clinical Research</i> , 2015, 9s1, BCBCR.S25460.	0.6	145
274	Over expression of hRad9 protein correlates with reduced chemosensitivity in breast cancer with administration of neoadjuvant chemotherapy. <i>Scientific Reports</i> , 2014, 4, 7548.	1.6	12
275	An NGS Workflow Blueprint for DNA Sequencing Data and Its Application in Individualized Molecular Oncology. <i>Cancer Informatics</i> , 2015, 14s5, CIN.S30793.	0.9	10
276	MixClone: a mixture model for inferring tumor subclonal populations. <i>BMC Genomics</i> , 2015, 16, S1.	1.2	10
277	High EGFR protein expression and exon 9 PIK3CA mutations are independent prognostic factors in triple negative breast cancers. <i>BMC Cancer</i> , 2015, 15, 986.	1.1	19
278	A co-culture genome-wide RNAi screen with mammary epithelial cells reveals transmembrane signals required for growth and differentiation. <i>Breast Cancer Research</i> , 2015, 17, 4.	2.2	24
279	Altered regulation of PDK4 expression promotes antiestrogen resistance in human breast cancer cells. <i>SpringerPlus</i> , 2015, 4, 689.	1.2	26
280	GATA family transcriptional factors: emerging suspects in hematologic disorders. <i>Experimental Hematology and Oncology</i> , 2015, 4, 28.	2.0	57
281	Are acinic cell carcinomas of the breast and salivary glands distinct diseases?. <i>Histopathology</i> , 2015, 67, 529-537.	1.6	37
282	Runx1 is associated with breast cancer progression in MMTV- β galactosidase transgenic mice and its depletion in vitro inhibits migration and invasion. <i>Journal of Cellular Physiology</i> , 2015, 230, 2522-2532.	2.0	63
283	The Significance and Therapeutic Potential of GATA3 Expression and Mutation in Breast Cancer: A Systematic Review. <i>Medicinal Research Reviews</i> , 2015, 35, 1300-1315.	5.0	16
284	GATA3 in Breast Cancer: Tumor Suppressor or Oncogene?. <i>Gene Expression</i> , 2015, 16, 163-168.	0.5	90
285	Recurrent fusion transcripts detected by whole-transcriptome sequencing of 120 primary breast cancer samples. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 681-691.	1.5	38
286	mTOR inhibition in breast cancer. <i>Breast Cancer Management</i> , 2015, 4, 67-70.	0.2	0
287	Differential Diagnosis of Benign and Malignant Breast Tumors Using Apparent Diffusion Coefficient Value Measured Through Diffusion-Weighted Magnetic Resonance Imaging. <i>Journal of Computer Assisted Tomography</i> , 2015, 39, 513-522.	0.5	10
288	Clinical Trials of Precision Medicine through Molecular Profiling: Focus on Breast Cancer. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2015, , e183-e190.	1.8	19
289	The Pharmaceutical Applications of Next Generation Sequencing in Oncology Drug Designing and Development. <i>Journal of Next Generation Sequencing & Applications</i> , 2015, 02, .	0.3	1
290	Targeted or whole genome sequencing of formalin fixed tissue samples: potential applications in cancer genomics. <i>Oncotarget</i> , 2015, 6, 25943-25961.	0.8	53

#	ARTICLE	IF	CITATIONS
291	Comparative genomic analysis reveals bilateral breast cancers are genetically independent. <i>Oncotarget</i> , 2015, 6, 31820-31829.	0.8	20
292	Personalized Medicine in Cancer. <i>Journal of Bangladesh College of Physicians & Surgeons</i> , 2015, 32, 153-163.	0.0	0
293	Whole-Exome Sequencing Identifies Novel Somatic Mutations in Chinese Breast Cancer Patients. <i>Journal of Molecular and Genetic Medicine: an International Journal of Biomedical Research</i> , 2015, 09, .	0.1	22
294	Revealing the Molecular Portrait of Triple Negative Breast Tumors in an Understudied Population through Omics Analysis of Formalin-Fixed and Paraffin-Embedded Tissues. <i>PLoS ONE</i> , 2015, 10, e0126762.	1.1	18
295	Significance of PIK3CA Mutations in Patients with Early Breast Cancer Treated with Adjuvant Chemotherapy: A Hellenic Cooperative Oncology Group (HeCOG) Study. <i>PLoS ONE</i> , 2015, 10, e0140293.	1.1	29
296	Somatic mutations in breast and serous ovarian cancer young patients: a systematic review and meta-analysis. <i>Revista Da Associação Médica Brasileira</i> , 2015, 61, 474-483.	0.3	18
297	Hypothesis: Artifacts, Including Spurious Chimeric RNAs with a Short Homologous Sequence, Caused by Consecutive Reverse Transcriptions and Endogenous Random Primers. <i>Journal of Cancer</i> , 2015, 6, 555-567.	1.2	32
298	Triple-Negative Breast Cancer: Molecular Subtypes and New Targets for Therapy. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2015, , e31-e39.	1.8	108
299	Estrogenic gper signaling regulates mir144 expression in cancer cells and cancer-associated fibroblasts (cafs). <i>Oncotarget</i> , 2015, 6, 16573-16587.	0.8	35
300	Genomic profiling of breast cancers. <i>Current Opinion in Obstetrics and Gynecology</i> , 2015, 27, 34-39.	0.9	19
301	Personalized Therapies for Cancer Treatment. , 2015, , 317-346.		0
302	Serial monitoring of circulating tumor <scp>DNA</scp> in patients with primary breast cancer for detection of occult metastatic disease. <i>EMBO Molecular Medicine</i> , 2015, 7, 1034-1047.	3.3	380
303	Targeting ADAM-17 with an inhibitory monoclonal antibody has antitumour effects in triple-negative breast cancer cells. <i>British Journal of Cancer</i> , 2015, 112, 1895-1903.	2.9	52
304	Oncotator: Cancer Variant Annotation Tool. <i>Human Mutation</i> , 2015, 36, E2423-E2429.	1.1	448
305	Genome-wide analysis of alternative transcripts in human breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 151, 295-307.	1.1	26
306	Granulosa Cell-Specific Brca1 Loss Alone or Combined with Trp53 Haploinsufficiency and Transgenic FSH Expression Fails to Induce Ovarian Tumors. <i>Hormones and Cancer</i> , 2015, 6, 142-152.	4.9	1
307	Tracing the footprints of the breast cancer oncogene BRK " Past till present. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2015, 1856, 39-54.	3.3	35
308	Identification of E545k mutation in plasma from a PIK3CA wild-type metastatic breast cancer patient by array-based digital polymerase chain reaction. <i>Translational Research</i> , 2015, 166, 783-787.	2.2	7

#	ARTICLE	IF	CITATIONS
309	Exome Capture and Capturing Technologies in Cancer Research. , 2015, , 279-302.		0
310	Gene-Environment Interactions Target Mitogen-activated Protein 3 Kinase 1 (MAP3K1) Signaling in Eyelid Morphogenesis. Journal of Biological Chemistry, 2015, 290, 19770-19779.	1.6	10
311	Global transcription network incorporating distal regulator binding reveals selective cooperation of cancer drivers and risk genes. Nucleic Acids Research, 2015, 43, 5716-5729.	6.5	6
312	BMX Negatively Regulates BAK Function, Thereby Increasing Apoptotic Resistance to Chemotherapeutic Drugs. Cancer Research, 2015, 75, 1345-1355.	0.4	30
313	Cross-validation and cross-study validation of chronic lymphocytic leukemia with exome sequences and machine learning. , 2015, , .		1
314	Molecular segmentation of luminal breast: Reality in 2015?. Breast, 2015, 24, S41-S43.	0.9	0
315	Molecular characterization of cbf1 ² gene and identification of new transcription variants: Implications for function. Archives of Biochemistry and Biophysics, 2015, 567, 1-12.	1.4	0
316	Runx3 at the interface of immunity, inflammation and cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2015, 1855, 131-143.	3.3	69
317	Genomic aberrations in cervical adenocarcinomas in Hong Kong Chinese women. International Journal of Cancer, 2015, 137, 776-783.	2.3	39
318	Patient-derived xenograft models of breast cancer and their predictive power. Breast Cancer Research, 2015, 17, 17.	2.2	225
319	Evaluating the pharmacokinetics and pharmacodynamics of everolimus for treating breast cancer. Expert Opinion on Drug Metabolism and Toxicology, 2015, 11, 823-834.	1.5	3
320	CLK2 Is an Oncogenic Kinase and Splicing Regulator in Breast Cancer. Cancer Research, 2015, 75, 1516-1526.	0.4	79
321	The enhanced chemotherapeutic effects of doxorubicin loaded PEG coated TiO ₂ nanocarriers in an orthotopic breast tumor bearing mouse model. Journal of Materials Chemistry B, 2015, 3, 1518-1528.	2.9	46
322	The RUNX family: developmental regulators in cancer. Nature Reviews Cancer, 2015, 15, 81-95.	12.8	329
323	Intrinsic cancer subtypes-next steps into personalized medicine. Cellular Oncology (Dordrecht), 2015, 38, 3-16.	2.1	24
324	Pharmacological Profiling of Kinase Dependency in Cell Lines across Triple-Negative Breast Cancer Subtypes. Molecular Cancer Therapeutics, 2015, 14, 298-306.	1.9	14
325	The Molecular Biology of Breast Cancer. , 2015, , 523-530.e3.		0
326	Stem cell state and the epithelial-to-mesenchymal transition: Implications for cancer therapy. Journal of Clinical Pharmacology, 2015, 55, 603-619.	1.0	19

#	ARTICLE	IF	CITATIONS
327	Breast Cancer Genomics From Microarrays to Massively Parallel Sequencing: Paradigms and New Insights. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	80
328	Identification of indels in next-generation sequencing data. <i>BMC Bioinformatics</i> , 2015, 16, 42.	1.2	42
329	Drosophila MAGI interacts with RASSF8 to regulate E-Cadherin-based adherens junctions in the developing eye. <i>Development (Cambridge)</i> , 2015, 142, 1102-12.	1.2	22
330	The Cancer Genomics Resource List 2014. <i>Archives of Pathology and Laboratory Medicine</i> , 2015, 139, 989-1008.	1.2	18
331	The origin of breast tumor heterogeneity. <i>Oncogene</i> , 2015, 34, 5309-5316.	2.6	125
332	Precision Medicine in Breast Cancer: Genes, Genomes, and the Future of Genomically Driven Treatments. <i>Current Oncology Reports</i> , 2015, 17, 15.	1.8	29
333	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. <i>Genome Medicine</i> , 2015, 7, 6.	3.6	6
334	ATM gene mutations in sporadic breast cancer patients from Brazil. <i>SpringerPlus</i> , 2015, 4, 23.	1.2	14
335	Gene-Expression-Based Predictors for Breast Cancer. <i>Annals of Surgical Oncology</i> , 2015, 22, 3418-3432.	0.7	24
336	Robust gene expression and mutation analyses of RNA-sequencing of formalin-fixed diagnostic tumor samples. <i>Scientific Reports</i> , 2015, 5, 12335.	1.6	54
337	Fibroblast growth factor receptor signaling in hereditary and neoplastic disease: biologic and clinical implications. <i>Cancer and Metastasis Reviews</i> , 2015, 34, 479-496.	2.7	101
338	Surgery in the era of the 'omics revolution. <i>British Journal of Surgery</i> , 2015, 102, e29-e40.	0.1	9
339	Anthropometric, Metabolic and Molecular Determinants of Human Epidermal Growth Factor Receptor 2 Expression in Luminal B Breast Cancer. <i>Journal of Cellular Physiology</i> , 2015, 230, 1708-1712.	2.0	5
340	Lipid and Protein Co-Regulation of PI3K Effectors Akt and Itk in Lymphocytes. <i>Frontiers in Immunology</i> , 2015, 6, 117.	2.2	28
341	Estrogen receptor mutations and functional consequences for breast cancer. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 467-476.	3.1	63
342	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. <i>Nature Medicine</i> , 2015, 21, 751-759.	15.2	711
343	The cancer COMPASS: navigating the functions of MLL complexes in cancer. <i>Cancer Genetics</i> , 2015, 208, 178-191.	0.2	122
344	A mass-tolerant database search identifies a large proportion of unassigned spectra in shotgun proteomics as modified peptides. <i>Nature Biotechnology</i> , 2015, 33, 743-749.	9.4	371

#	ARTICLE	IF	CITATIONS
345	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015, 12, 615-621.	9.0	297
346	Genomic Analyses Reveal Mutational Signatures and Frequently Altered Genes in Esophageal Squamous Cell Carcinoma. <i>American Journal of Human Genetics</i> , 2015, 96, 597-611.	2.6	290
347	Recurrent <i>BCAM-AKT2</i> fusion gene leads to a constitutively activated AKT2 fusion kinase in high-grade serous ovarian carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1272-7.	3.3	42
348	Organ-Specific Cancer Metabolism and Its Potential for Therapy. <i>Handbook of Experimental Pharmacology</i> , 2015, 233, 321-353.	0.9	86
349	The Proteomic Landscape of Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2015, 11, 630-644.	2.9	179
350	Therapies for triple negative breast cancer. <i>Expert Opinion on Pharmacotherapy</i> , 2015, 16, 983-998.	0.9	85
351	Clinical management of breast cancer heterogeneity. <i>Nature Reviews Clinical Oncology</i> , 2015, 12, 381-394.	12.5	400
352	An implantable microdevice to perform high-throughput in vivo drug sensitivity testing in tumors. <i>Science Translational Medicine</i> , 2015, 7, 284ra57.	5.8	150
353	<i>MAGI3</i> – <i>AKT3</i> fusion in breast cancer amended. <i>Nature</i> , 2015, 520, E11-E12.	13.7	22
354	Predictive Biomarker Profiling of > 6000 Breast Cancer Patients Shows Heterogeneity in TNBC, With Treatment Implications. <i>Clinical Breast Cancer</i> , 2015, 15, 473-481.e3.	1.1	92
355	Pugh et al. reply. <i>Nature</i> , 2015, 520, E12-E14.	13.7	8
356	Breast cancer risk associated with gene expression and genotype polymorphisms of the folate-metabolizing <i>MTHFR</i> gene: a case-control study in a high altitude Ecuadorian mestizo population. <i>Tumor Biology</i> , 2015, 36, 6451-6461.	0.8	31
357	Genomically amplified <i>Akt3</i> activates DNA repair pathway and promotes glioma progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3421-3426.	3.3	104
358	Next Generation Sequencing in Cancer Research, Volume 2. , 2015, , .		4
359	Is androgen receptor targeting an emerging treatment strategy for triple negative breast cancer?. <i>Cancer Treatment Reviews</i> , 2015, 41, 547-553.	3.4	41
360	<i>Akt1</i> and <i>Akt3</i> Exert Opposing Roles in the Regulation of Vascular Tumor Growth. <i>Cancer Research</i> , 2015, 75, 40-50.	0.4	49
361	Genomic landscapes of breast fibroepithelial tumors. <i>Nature Genetics</i> , 2015, 47, 1341-1345.	9.4	167
362	Targeted Therapies for Triple-Negative Breast Cancer: Combating a Stubborn Disease. <i>Trends in Pharmacological Sciences</i> , 2015, 36, 822-846.	4.0	242

#	ARTICLE	IF	CITATIONS
363	A genome-wide approach to link genotype to clinical outcome by utilizing next generation sequencing and gene chip data of 6,697 breast cancer patients. <i>Genome Medicine</i> , 2015, 7, 104.	3.6	65
364	CSN6 positively regulates c-Jun in a MEKK1-dependent manner. <i>Cell Cycle</i> , 2015, 14, 3079-3087.	1.3	10
365	Mutations in the Kinase Domain of the HER2/ERBB2 Gene Identified in a Wide Variety of Human Cancers. <i>Journal of Molecular Diagnostics</i> , 2015, 17, 487-495.	1.2	53
366	Limited evidence that cancer susceptibility regions are preferential targets for somatic mutation. <i>Genome Biology</i> , 2015, 16, 193.	3.8	19
367	OncoRep: an n-of-1 reporting tool to support genome-guided treatment for breast cancer patients using RNA-sequencing. <i>BMC Medical Genomics</i> , 2015, 8, 24.	0.7	12
368	The mammary stem cell hierarchy: a looking glass into heterogeneous breast cancer landscapes. <i>Endocrine-Related Cancer</i> , 2015, 22, T161-T176.	1.6	45
369	Breast Tumors. , 2015, , 269-302.		0
370	Cancer Genetics and Implications for Clinical Management. <i>Surgical Clinics of North America</i> , 2015, 95, 919-934.	0.5	6
371	<i>De novo</i> resistance biomarkers to anti-HER2 therapies in HER2-positive breast cancer. <i>Pharmacogenomics</i> , 2015, 16, 1411-1426.	0.6	7
372	Spatiotemporal Evolution of the Primary Glioblastoma Genome. <i>Cancer Cell</i> , 2015, 28, 318-328.	7.7	242
373	Droplet digital polymerase chain reaction assay for screening of ESR1 mutations in 325 breast cancer specimens. <i>Translational Research</i> , 2015, 166, 540-553.e2.	2.2	55
374	An ensemble approach to accurately detect somatic mutations using SomaticSeq. <i>Genome Biology</i> , 2015, 16, 197.	3.8	93
375	Breast Tumor Heterogeneity: Source of Fitness, Hurdle for Therapy. <i>Molecular Cell</i> , 2015, 60, 537-546.	4.5	232
376	Endothelial follicle-stimulating hormone receptor expression in invasive breast cancer and vascular remodeling at tumor periphery. <i>Journal of Experimental and Clinical Cancer Research</i> , 2015, 34, 12.	3.5	37
377	The Rho GTPase Rnd1 suppresses mammary tumorigenesis and EMT by restraining Ras-MAPK signalling. <i>Nature Cell Biology</i> , 2015, 17, 81-94.	4.6	97
378	Splicing mutation analysis reveals previously unrecognized pathways in lymph node-invasive breast cancer. <i>Scientific Reports</i> , 2014, 4, 7063.	1.6	41
379	CHIP buffers heterogeneous Bcl-2 expression levels to prevent augmentation of anticancer drug-resistant cell population. <i>Oncogene</i> , 2015, 34, 4656-4663.	2.6	11
380	<i>SF3B1</i> mutations constitute a novel therapeutic target in breast cancer. <i>Journal of Pathology</i> , 2015, 235, 571-580.	2.1	167

#	ARTICLE	IF	CITATIONS
381	Acid ceramidase is associated with an improved prognosis in both DCIS and invasive breast cancer. <i>Molecular Oncology</i> , 2015, 9, 58-67.	2.1	31
382	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. <i>Nature</i> , 2015, 518, 422-426.	13.7	545
383	Clinicopathological significance of androgen receptor, HER2, Ki-67 and EGFR expressions in salivary duct carcinoma. <i>International Journal of Clinical Oncology</i> , 2015, 20, 35-44.	1.0	94
384	IAPP-driven metabolic reprogramming induces regression of p53-deficient tumours in vivo. <i>Nature</i> , 2015, 517, 626-630.	13.7	117
385	The Role of the Microenvironment in Tumor Initiation, Progression, and Metastasis. , 2015, , 239-256.e5.		4
386	Using drug response data to identify molecular effectors, and molecular "omic" data to identify candidate drugs in cancer. <i>Human Genetics</i> , 2015, 134, 3-11.	1.8	27
387	Nanoplasmonic biosensor: Detection and amplification of dual bio-signatures of circulating tumor DNA. <i>Biosensors and Bioelectronics</i> , 2015, 67, 443-449.	5.3	113
388	Breast cancer classification: linking molecular mechanisms to disease prognosis. <i>Briefings in Bioinformatics</i> , 2015, 16, 461-474.	3.2	55
389	Triple-negative breast cancer: investigating potential molecular therapeutic target. <i>Expert Opinion on Therapeutic Targets</i> , 2015, 19, 55-75.	1.5	44
390	Genomic Applications in Pathology. , 2015, , .		1
391	Cross-validation and cross-study validation of chronic lymphocytic leukaemia with exome sequences and machine learning. <i>International Journal of Data Mining and Bioinformatics</i> , 2016, 16, 47.	0.1	2
392	Signaling network analysis of genomic alterations predicts breast cancer drug targets. , 0, , 269-280.		0
393	New generation of breast cancer clinical trials implementing molecular profiling. <i>Cancer Biology and Medicine</i> , 2016, 13, 226-235.	1.4	5
394	Analysis of tumor template from multiple compartments in a blood sample provides complementary access to peripheral tumor biomarkers. <i>Oncotarget</i> , 2016, 7, 26724-26738.	0.8	16
395	Mutations of Chromatin Structure Regulating Genes in Human Malignancies. <i>Current Protein and Peptide Science</i> , 2016, 17, 411-437.	0.7	25
396	Cytotoxic and Apoptotic Activities of Methanolic Subfractions of <i>Scrophularia oxysepala</i> against Human Breast Cancer Cell Line. <i>Evidence-based Complementary and Alternative Medicine</i> , 2016, 2016, 1-10.	0.5	24
397	Post-transcriptional Regulation of BRCA2 through Interactions with miR-19a and miR-19b. <i>Frontiers in Genetics</i> , 2016, 7, 143.	1.1	20
398	A <i>Drosophila</i> Model of HPV E6-Induced Malignancy Reveals Essential Roles for Magi and the Insulin Receptor. <i>PLoS Pathogens</i> , 2016, 12, e1005789.	2.1	12

#	ARTICLE	IF	CITATIONS
399	RUNX1 and FOXP3 interplay regulates expression of breast cancer related genes. <i>Oncotarget</i> , 2016, 7, 6552-6565.	0.8	37
400	Cell-specific biomarkers and targeted biopharmaceuticals for breast cancer treatment. <i>Cell Proliferation</i> , 2016, 49, 409-420.	2.4	30
401	Recurrent and pathological gene fusions in breast cancer: current advances in genomic discovery and clinical implications. <i>Breast Cancer Research and Treatment</i> , 2016, 158, 219-232.	1.1	40
402	First-line therapy in HER2 positive metastatic breast cancer: is the mosaic fully completed or are we missing additional pieces?. <i>Journal of Experimental and Clinical Cancer Research</i> , 2016, 35, 104.	3.5	33
403	Discovering potential cancer driver genes by an integrated network-based approach. <i>Molecular BioSystems</i> , 2016, 12, 2921-2931.	2.9	27
404	Community detection from genomic datasets across human cancers. , 2016, , .		3
405	LNDriver: identifying driver genes by integrating mutation and expression data based on gene-gene interaction network. <i>BMC Bioinformatics</i> , 2016, 17, 467.	1.2	28
406	Recent developments and translational aspects in targeted therapy for metastatic breast cancer. <i>ESMO Open</i> , 2016, 1, e000036.	2.0	1
407	The PI3K Pathway: Background and Treatment Approaches. <i>Breast Care</i> , 2016, 11, 398-404.	0.8	28
408	Patient-derived xenograft (PDX) models in basic and translational breast cancer research. <i>Cancer and Metastasis Reviews</i> , 2016, 35, 547-573.	2.7	189
409	Clinical Decision Making. <i>Spine</i> , 2016, 41, S171-S177.	1.0	7
410	Targeting the host immune system: PD-1 and PD-L1 antibodies and breast cancer. <i>Current Opinion in Supportive and Palliative Care</i> , 2016, 10, 336-342.	0.5	9
411	SNooper: a machine learning-based method for somatic variant identification from low-pass next-generation sequencing. <i>BMC Genomics</i> , 2016, 17, 912.	1.2	50
412	Identification of novel candidate drivers connecting different dysfunctional levels for lung adenocarcinoma using protein-protein interactions and a shortest path approach. <i>Scientific Reports</i> , 2016, 6, 29849.	1.6	28
413	Cancer: hunting rare somatic mutations. <i>Nature Methods</i> , 2016, 13, 295-299.	9.0	8
414	Triple-negative breast cancer: challenges and opportunities of a heterogeneous disease. <i>Nature Reviews Clinical Oncology</i> , 2016, 13, 674-690.	12.5	1,938
415	Exploring phenotype patterns of breast cancer within somatic mutations: a modicum in the intrinsic code. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw040.	3.2	2
416	Burden of Nonsynonymous Mutations among TCGA Cancers and Candidate Immune Checkpoint Inhibitor Responses. <i>Cancer Research</i> , 2016, 76, 3767-3772.	0.4	124

#	ARTICLE	IF	CITATIONS
417	Sensitizing Triple-Negative Breast Cancer to PI3K Inhibition by Cotargeting IGF1R. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1545-1556.	1.9	30
418	Analysis of functional germline variants in APOBEC3 and driver genes on breast cancer risk in Moroccan study population. <i>BMC Cancer</i> , 2016, 16, 165.	1.1	20
419	Translocation and deletion breakpoints in cancer genomes are associated with potential non-B DNA-forming sequences. <i>Nucleic Acids Research</i> , 2016, 44, 5673-5688.	6.5	117
420	WeSME: uncovering mutual exclusivity of cancer drivers and beyond. <i>Bioinformatics</i> , 2017, 33, 814-821.	1.8	79
421	PIK3R1 targeting by miR-21 suppresses tumor cell migration and invasion by reducing PI3K/AKT signaling and reversing EMT, and predicts clinical outcome of breast cancer. <i>International Journal of Oncology</i> , 2016, 48, 471-484.	1.4	95
422	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	13.7	1,760
423	Acquired Resistance to Clinical Cancer Therapy: A Twist in Physiological Signaling. <i>Physiological Reviews</i> , 2016, 96, 805-829.	13.1	49
424	Molecular Insights of Pathways Resulting from Two Common PIK3CA Mutations in Breast Cancer. <i>Cancer Research</i> , 2016, 76, 3989-4001.	0.4	27
425	Tumor suppressive actions of the nuclear receptor corepressor 1. <i>Pharmacological Research</i> , 2016, 108, 75-79.	3.1	8
426	Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. <i>Cell Reports</i> , 2016, 17, 249-260.	2.9	21
427	Biosensors for liquid biopsy: circulating nucleic acids to diagnose and treat cancer. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 7255-7264.	1.9	60
428	Deciphering and Targeting Oncogenic Mutations and Pathways in Breast Cancer. <i>Oncologist</i> , 2016, 21, 1063-1078.	1.9	41
429	Protein Tyrosine Phosphatases in Cancer. , 2016, , .		4
430	Role of PTPN11 (SHP2) in Cancer. , 2016, , 115-143.		11
431	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. <i>British Journal of Cancer</i> , 2016, 115, 752-760.	2.9	16
432	Metabolic Reprogramming by the PI3K-Akt-mTOR Pathway in Cancer. <i>Recent Results in Cancer Research</i> , 2016, 207, 39-72.	1.8	143
433	Metabolism in Cancer. <i>Recent Results in Cancer Research</i> , 2016, , .	1.8	5
434	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 1389-1397.	0.9	60

#	ARTICLE	IF	CITATIONS
435	Involvement of Tight Junction Plaque Proteins in Cancer. <i>Current Pathobiology Reports</i> , 2016, 4, 117-133.	1.6	4
436	Global analysis of somatic structural genomic alterations and their impact on gene expression in diverse human cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13768-13773.	3.3	50
437	The molecular landscape of high-risk early breast cancer: comprehensive biomarker analysis of a phase III adjuvant population. <i>Npj Breast Cancer</i> , 2016, 2, 16022.	2.3	21
438	RNAi-mediated downregulation of cyclin Y to attenuate human breast cancer cell growth. <i>Oncology Reports</i> , 2016, 36, 2793-2799.	1.2	14
439	Triple-negative breast cancer: the importance of molecular and histologic subtyping, and recognition of low-grade variants. <i>Npj Breast Cancer</i> , 2016, 2, 16036.	2.3	127
440	Comment on "The incidence of leukaemia in women with BRCA1 and BRCA2 mutations: an International Prospective Cohort Study". <i>British Journal of Cancer</i> , 2016, 115, e2-e2.	2.9	3
441	Preliminary Application of Precision Genomic Medicine Detecting Gene Variation in Patients with Multifocal Osteosarcoma. <i>Orthopaedic Surgery</i> , 2016, 8, 129-138.	0.7	2
442	Transposon mutagenesis identifies genes that cooperate with mutant Pten in breast cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7749-E7758.	3.3	48
443	One microenvironment does not fit all: heterogeneity beyond cancer cells. <i>Cancer and Metastasis Reviews</i> , 2016, 35, 601-629.	2.7	58
444	A microscopic landscape of the invasive breast cancer genome. <i>Scientific Reports</i> , 2016, 6, 27545.	1.6	33
445	Whole genome sequencing of 51 breast cancers reveals that tumors are devoid of bovine leukemia virus DNA. <i>Retrovirology</i> , 2016, 13, 75.	0.9	42
446	Progress in the clinical detection of heterogeneity in breast cancer. <i>Cancer Medicine</i> , 2016, 5, 3475-3488.	1.3	50
447	Big Data Analytics in Genomics. , 2016, , .		7
448	The stepwise evolution of the exome during acquisition of docetaxel resistance in breast cancer cells. <i>BMC Genomics</i> , 2016, 17, 442.	1.2	25
449	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	5.8	119
450	Glycosyltransferase Gene Expression Profiles Classify Cancer Types and Propose Prognostic Subtypes. <i>Scientific Reports</i> , 2016, 6, 26451.	1.6	63
451	Whole-exome sequencing identifies recurrent <i>AKT1</i> mutations in sclerosing hemangioma of lung. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10672-10677.	3.3	42
452	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. <i>Nature Communications</i> , 2016, 7, 11479.	5.8	1,221

#	ARTICLE	IF	CITATIONS
453	A Bioinformatics Approach for Understanding Genotype-Phenotype Correlation in Breast Cancer. , 2016, , 397-428.		1
454	Emerging Role of Genomic Rearrangements in Breast Cancer: Applying Knowledge from Other Cancers. Biomarkers in Cancer, 2016, 8s1, B1C.S34417.	3.6	27
455	Precision Oncology: The UC San Diego Moores Cancer Center PREDICT Experience. Molecular Cancer Therapeutics, 2016, 15, 743-752.	1.9	144
456	Comprehensive Gene Mutation Profiling of Breast Tumors: Is It Ready for Prime Time Use?. Current Breast Cancer Reports, 2016, 8, 53-59.	0.5	0
457	High prevalence of luminal B breast cancer intrinsic subtype in Colombian women. Carcinogenesis, 2016, 37, 669-676.	1.3	39
458	Small Molecule Inhibitor of CBF β -RUNX Binding for RUNX Transcription Factor Driven Cancers. EBioMedicine, 2016, 8, 117-131.	2.7	84
459	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. Cancer Letters, 2016, 376, 104-109.	3.2	22
460	Modeling the integration of bacterial rRNA fragments into the human cancer genome. BMC Bioinformatics, 2016, 17, 134.	1.2	5
461	Targeted Pten deletion plus p53-R270H mutation in mouse mammary epithelium induces aggressive claudin-low and basal-like breast cancer. Breast Cancer Research, 2016, 18, 9.	2.2	20
462	Variation in the Incidence and Magnitude of Tumor-Infiltrating Lymphocytes in Breast Cancer Subtypes. JAMA Oncology, 2016, 2, 1354.	3.4	426
463	SOX1 inhibits breast cancer cell growth and invasion through suppressing the Wnt/ β -catenin signaling pathway. Apms, 2016, 124, 547-555.	0.9	29
464	Clinicopathological features and prognosis of triple-negative breast cancer: a comparison between younger (<60) and elderly (\geq 60) patients. European Journal of Cancer Care, 2016, 25, 1065-1075.	0.7	14
465	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. Cell, 2016, 164, 293-309.	13.5	399
466	Mutation Profiling of Usual Ductal Hyperplasia of the Breast Reveals Activating Mutations Predominantly at Different Levels of the PI3K/AKT/mTOR Pathway. American Journal of Pathology, 2016, 186, 15-23.	1.9	20
467	BRCAness revisited. Nature Reviews Cancer, 2016, 16, 110-120.	12.8	976
468	Circulating tumor DNA for triple-negative breast cancer diagnosis and treatment decisions. Expert Review of Molecular Diagnostics, 2016, 16, 39-50.	1.5	11
469	MiRNA-21 induces epithelial to mesenchymal transition and gemcitabine resistance via the PTEN/AKT pathway in breast cancer. Tumor Biology, 2016, 37, 7245-7254.	0.8	81
470	HER2 mutation status in Japanese HER2-positive breast cancer patients. Breast Cancer, 2016, 23, 902-907.	1.3	7

#	ARTICLE	IF	CITATIONS
471	AKT signaling in ERBB2-amplified breast cancer. , 2016, 158, 63-70.		49
472	Ductal carcinoma in situ of the breast: the importance of morphologic and molecular interactions. Human Pathology, 2016, 49, 114-123.	1.1	48
473	The Role of PIWIL4, an Argonaute Family Protein, in Breast Cancer. Journal of Biological Chemistry, 2016, 291, 10646-10658.	1.6	56
475	Targeted capture massively parallel sequencing analysis of LCIS and invasive lobular cancer: Repertoire of somatic genetic alterations and clonal relationships. Molecular Oncology, 2016, 10, 360-370.	2.1	41
476	Crossroad between linear and nonlinear transcription concepts in the discovery of next-generation sequencing systems-based anticancer therapies. Drug Discovery Today, 2016, 21, 663-673.	3.2	16
477	Whole exome sequencing of rare aggressive breast cancer histologies. Breast Cancer Research and Treatment, 2016, 156, 21-32.	1.1	38
478	Catalog of genetic progression of human cancers: breast cancer. Cancer and Metastasis Reviews, 2016, 35, 49-62.	2.7	18
479	A Multiplexed Amplicon Approach for Detecting Gene Fusions by Next-Generation Sequencing. Journal of Molecular Diagnostics, 2016, 18, 165-175.	1.2	66
480	MicroRNA-378-mediated suppression of Runx1 alleviates the aggressive phenotype of triple-negative MDA-MB-231 human breast cancer cells. Tumor Biology, 2016, 37, 8825-8839.	0.8	41
481	Autoregulatory loop of nuclear corepressor 1 expression controls invasion, tumor growth, and metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E328-37.	3.3	41
482	BreCAN-DB: a repository cum browser of personalized DNA breakpoint profiles of cancer genomes. Nucleic Acids Research, 2016, 44, D952-D958.	6.5	2
483	A Systems Oncology Approach Identifies NT5E as a Key Metabolic Regulator in Tumor Cells and Modulator of Platinum Sensitivity. Journal of Proteome Research, 2016, 15, 280-290.	1.8	26
484	Treatment of Triple-Negative Breast Cancer with TORC1/2 Inhibitors Sustains a Drug-Resistant and Notch-Dependent Cancer Stem Cell Population. Cancer Research, 2016, 76, 440-452.	0.4	93
485	FOXO factors and breast cancer: outfoxing endocrine resistance. Endocrine-Related Cancer, 2016, 23, R113-R130.	1.6	39
486	Targeting p300 Addiction in <i>CBP</i> -Deficient Cancers Causes Synthetic Lethality by Apoptotic Cell Death due to Abrogation of <i>MYC</i> Expression. Cancer Discovery, 2016, 6, 430-445.	7.7	129
487	The role of GATA3 in breast carcinomas: a review. Human Pathology, 2016, 48, 37-47.	1.1	101
488	APOBEC3B high expression status is associated with aggressive phenotype in Japanese breast cancers. Breast Cancer, 2016, 23, 780-788.	1.3	34
489	Evaluation of targeted therapies in advanced breast cancer: the need for large-scale molecular screening and transformative clinical trial designs. Oncogene, 2016, 35, 1743-1749.	2.6	13

#	ARTICLE	IF	CITATIONS
491	Relationship between RUNX1 and AXIN1 in ER-negative versus ER-positive Breast Cancer. <i>Cell Cycle</i> , 2017, 16, 312-318.	1.3	18
492	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
493	Exploring the pharmacological mechanism of Yanghe Decoction on HER2-positive breast cancer by a network pharmacology approach. <i>Journal of Ethnopharmacology</i> , 2017, 199, 68-85.	2.0	98
494	Inhibition of Ubc13-mediated Ubiquitination by GPS2 Regulates Multiple Stages of B Cell Development. <i>Journal of Biological Chemistry</i> , 2017, 292, 2754-2772.	1.6	30
495	Functional germline variants in driver genes of breast cancer. <i>Cancer Causes and Control</i> , 2017, 28, 259-271.	0.8	12
496	A Transposon-based Analysis Reveals <i>RASA1</i> Is Involved in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2017, 77, 1357-1368.	0.4	34
497	Transposon insertional mutagenesis in mice identifies human breast cancer susceptibility genes and signatures for stratification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2215-E2224.	3.3	34
498	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. <i>Cancer Discovery</i> , 2017, 7, 410-423.	7.7	121
499	Lateral gene transfer between prokaryotes and eukaryotes. <i>Experimental Cell Research</i> , 2017, 358, 421-426.	1.2	65
500	Transcriptomic and genomic features of invasive lobular breast cancer. <i>Seminars in Cancer Biology</i> , 2017, 44, 98-105.	4.3	34
501	<i>HER2</i> somatic mutations are associated with poor survival in <i>HER2</i> -negative breast cancers. <i>Cancer Science</i> , 2017, 108, 671-677.	1.7	53
502	Effect of <i>Momordica charantia</i> protein on proliferation, apoptosis and the AKT signal transduction pathway in the human endometrial carcinoma Ishikawa H cell line in vitro. <i>Oncology Letters</i> , 2017, 13, 3032-3038.	0.8	6
503	RUNX transcription factors at the interface of stem cells and cancer. <i>Biochemical Journal</i> , 2017, 474, 1755-1768.	1.7	38
504	Single-cell RNA-seq enables comprehensive tumour and immune cell profiling in primary breast cancer. <i>Nature Communications</i> , 2017, 8, 15081.	5.8	743
505	Landscape of Combination Immunotherapy and Targeted Therapy to Improve Cancer Management. <i>Cancer Research</i> , 2017, 77, 3666-3671.	0.4	93
506	Novel therapeutic strategies in the treatment of triple-negative breast cancer. <i>Therapeutic Advances in Medical Oncology</i> , 2017, 9, 493-511.	1.4	58
507	Insulin Receptor Isoforms in Physiology and Disease: An Updated View. <i>Endocrine Reviews</i> , 2017, 38, 379-431.	8.9	270
508	Molecular genetics complexity impeding research progress in breast and ovarian cancers. <i>Molecular and Clinical Oncology</i> , 2017, 7, 3-14.	0.4	12

#	ARTICLE	IF	CITATIONS
509	Inhibition of long non-coding RNA ROR reverses resistance to Tamoxifen by inducing autophagy in breast cancer. <i>Tumor Biology</i> , 2017, 39, 101042831770579.	0.8	67
510	Genomic profiling of breast secretory carcinomas reveals distinct genetics from other breast cancers and similarity to mammary analog secretory carcinomas. <i>Modern Pathology</i> , 2017, 30, 1086-1099.	2.9	63
511	Translational Genomics: Practical Applications of the Genomic Revolution in Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2630-2639.	3.2	30
512	Mutational Signatures in Breast Cancer: The Problem at the DNA Level. <i>Clinical Cancer Research</i> , 2017, 23, 2617-2629.	3.2	102
513	Oncogenic Roles of the PI3K/AKT/mTOR Axis. <i>Current Topics in Microbiology and Immunology</i> , 2017, 407, 153-189.	0.7	242
514	Role of Aspirin in Breast Cancer Survival. <i>Current Oncology Reports</i> , 2017, 19, 48.	1.8	62
515	Cross-talk between the CK2 and AKT signaling pathways in cancer. <i>Advances in Biological Regulation</i> , 2017, 64, 1-8.	1.4	51
516	Tumor burden monitoring using cell-free tumor DNA could be limited by tumor heterogeneity in advanced breast cancer and should be evaluated together with radiographic imaging. <i>BMC Cancer</i> , 2017, 17, 210.	1.1	59
518	Runx Genes in Breast Cancer and the Mammary Lineage. <i>Advances in Experimental Medicine and Biology</i> , 2017, 962, 353-368.	0.8	16
519	Breast ductal carcinoma in situ carry mutational driver events representative of invasive breast cancer. <i>Modern Pathology</i> , 2017, 30, 952-963.	2.9	50
520	<i>In vivo</i> models in breast cancer research: progress, challenges and future directions. <i>DMM Disease Models and Mechanisms</i> , 2017, 10, 359-371.	1.2	131
521	New Developments in Breast Cancer and Their Impact on Daily Practice in Pathology. <i>Archives of Pathology and Laboratory Medicine</i> , 2017, 141, 490-498.	1.2	40
522	CTCs and ctDNA: Two Tales of a Complex Biology. <i>Cancer Drug Discovery and Development</i> , 2017, , 119-137.	0.2	1
523	Roles of RUNX in Solid Tumors. <i>Advances in Experimental Medicine and Biology</i> , 2017, 962, 299-320.	0.8	21
524	Runx3 in Immunity, Inflammation and Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2017, 962, 369-393.	0.8	43
525	The Emerging Roles of RUNX Transcription Factors in Epithelial-Mesenchymal Transition. <i>Advances in Experimental Medicine and Biology</i> , 2017, 962, 471-489.	0.8	8
526	Pathologic diagnosis of breast cancer patients: evolution of the traditional clinical-pathologic paradigm toward "precision" cancer therapy. <i>Biotechnic and Histochemistry</i> , 2017, 92, 175-200.	0.7	10
527	The enigmatic role of <i>RUNX1</i> in female-related cancers " current knowledge & future perspectives. <i>FEBS Journal</i> , 2017, 284, 2345-2362.	2.2	22

#	ARTICLE	IF	CITATIONS
528	The genetic landscape of breast carcinomas with neuroendocrine differentiation. <i>Journal of Pathology</i> , 2017, 241, 405-419.	2.1	52
529	DNA damage repair in breast cancer and its therapeutic implications. <i>Pathology</i> , 2017, 49, 156-165.	0.3	47
530	Whole-exome sequencing predicted cancer epitope trees of 23 early cervical cancers in Chinese women. <i>Cancer Medicine</i> , 2017, 6, 207-219.	1.3	12
531	Delayed Sequential Co-Delivery of Gefitinib and Doxorubicin for Targeted Combination Chemotherapy. <i>Molecular Pharmaceutics</i> , 2017, 14, 4551-4559.	2.3	30
532	Mapping genomic and transcriptomic alterations spatially in epithelial cells adjacent to human breast carcinoma. <i>Nature Communications</i> , 2017, 8, 1245.	5.8	14
533	Sample Size Calculation for Differential Expression Analysis of RNA-Seq Data. , 2017, , 359-379.		0
535	Onco-proteogenomics: Multi-omics level data integration for accurate phenotype prediction. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2017, 54, 414-432.	2.7	16
536	Piecing together the puzzle: nanopore technology in detection and quantification of cancer biomarkers. <i>RSC Advances</i> , 2017, 7, 42653-42666.	1.7	13
537	Basal-A Triple-Negative Breast Cancer Cells Selectively Rely on RNA Splicing for Survival. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 2849-2861.	1.9	41
538	Genomic comparison of esophageal squamous cell carcinoma and its precursor lesions by multi-region whole-exome sequencing. <i>Nature Communications</i> , 2017, 8, 524.	5.8	103
539	Mixed invasive ductal and lobular carcinoma has distinct clinical features and predicts worse prognosis when stratified by estrogen receptor status. <i>Scientific Reports</i> , 2017, 7, 10380.	1.6	20
540	Identifying DNase I hypersensitive sites as driver distal regulatory elements in breast cancer. <i>Nature Communications</i> , 2017, 8, 436.	5.8	22
541	The Evolving Role of Companion Diagnostics for Breast Cancer in an Era of Next-Generation Omics. <i>American Journal of Pathology</i> , 2017, 187, 2185-2198.	1.9	17
542	A functional BRCA1 coding sequence genetic variant contributes to prognosis of triple-negative breast cancer, especially after radiotherapy. <i>Breast Cancer Research and Treatment</i> , 2017, 166, 109-116.	1.1	12
543	Novel applications of next-generation sequencing in breast cancer research. <i>Genes and Diseases</i> , 2017, 4, 149-153.	1.5	6
544	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017, 32, 169-184.e7.	7.7	534
545	New Views into the Genetic Landscape of Metastatic Breast Cancer. <i>Cancer Cell</i> , 2017, 32, 131-133.	7.7	2
546	Mouse Models of Breast Cancer: Deceptions that Reveal the Truth. , 2017, , 49-60.		0

#	ARTICLE	IF	CITATIONS
547	Recurrent and functional regulatory mutations in breast cancer. <i>Nature</i> , 2017, 547, 55-60.	13.7	269
548	Posttranslationally modified progesterone receptors direct ligand-specific expression of breast cancer stem cell-associated gene programs. <i>Journal of Hematology and Oncology</i> , 2017, 10, 89.	6.9	60
549	Identification of Stem Cells in the Epithelium of the Stomach Corpus and Antrum of Mice. <i>Gastroenterology</i> , 2017, 152, 218-231.e14.	0.6	121
550	Transcriptional Regulation by Wild-Type and Cancer-Related Mutant Forms of p53. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017, 7, a026054.	2.9	94
551	The Role of Genetic Testing in the Selection of Therapy for Breast Cancer. <i>JAMA Oncology</i> , 2017, 3, 262.	3.4	11
552	Intratumor and circulating clonal heterogeneity shape the basis of precision breast cancer therapy. <i>Future Oncology</i> , 2017, 13, 113-116.	1.1	4
553	Pathology and Molecular Pathology of Breast Cancer. , 2017, , 173-231.		1
554	<i>GATA3</i> rs3824662 gene polymorphism as possible risk factor in a cohort of Egyptian patients with pediatric acute lymphoblastic leukemia and its prognostic impact. <i>Leukemia and Lymphoma</i> , 2017, 58, 689-698.	0.6	9
555	Bioinformatics exploration of PAK1 (P21-activated kinase-1) revealed potential network gene elements in breast invasive carcinoma. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 2269-2279.	2.0	7
556	Predicting and Overcoming Chemotherapeutic Resistance in Breast Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1026, 59-104.	0.8	46
557	Human Mutations Associated With Brain Malformations Resulting in Hyperexcitability in Rodents. , 2017, , 827-844.		1
558	Role of Î²-Interferon Inducer (DEAE-Dextran) in Tumorigenesis by VEGF and NOTCH1 Inhibition along with Apoptosis Induction. <i>Frontiers in Pharmacology</i> , 2017, 8, 930.	1.6	6
559	Alternative Splicing in Breast Cancer and the Potential Development of Therapeutic Tools. <i>Genes</i> , 2017, 8, 217.	1.0	24
560	Integrated MicroRNA-mRNA Profiling Identifies Oncostatin M as a Marker of Mesenchymal-Like ER-Negative/HER2-Negative Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2017, 18, 194.	1.8	18
561	Overexpression of p53 protein is a marker of poor prognosis in Mexican women with breast cancer. <i>Oncology Reports</i> , 2017, 37, 3026-3036.	1.2	17
562	Insulin Resistance: Any Role in the Changing Epidemiology of Thyroid Cancer?. <i>Frontiers in Endocrinology</i> , 2017, 8, 314.	1.5	42
563	Tumor Heterogeneity in Breast Cancer. <i>Frontiers in Medicine</i> , 2017, 4, 227.	1.2	379
564	Ductal Carcinoma In Situ Biology, Biomarkers, and Diagnosis. <i>Frontiers in Oncology</i> , 2017, 7, 248.	1.3	88

#	ARTICLE	IF	CITATIONS
565	Signal Transduction Networks Analysis: The Reverse Phase Protein Array. , 2017, , .		0
566	Integrated analysis of promoter mutation, methylation and expression of AKT1 gene in Chinese breast cancer patients. PLoS ONE, 2017, 12, e0174022.	1.1	12
567	Identification of cell proliferation, immune response and cell migration as critical pathways in a prognostic signature for HER2+:ER1±- breast cancer. PLoS ONE, 2017, 12, e0179223.	1.1	9
568	Integrative analysis of genomic alterations in triple-negative breast cancer in association with homologous recombination deficiency. PLoS Genetics, 2017, 13, e1006853.	1.5	39
569	Characterization of potential driver mutations involved in human breast cancer by computational approaches. Oncotarget, 2017, 8, 50252-50272.	0.8	50
570	Risk Reduction Strategies in Breast Cancer Prevention. The Journal of Breast Health, 2017, 13, 103-112.	0.4	20
571	Response of a Metastatic Breast Carcinoma With a Previously Uncharacterized ERBB2 G776V Mutation to Human Epidermal Growth Factor Receptor 2â€œTargeted Therapy. JCO Precision Oncology, 2017, 1, 1-9.	1.5	0
572	Novel Targeted Agents and Immunotherapy in Breast Cancer. American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting, 2017, 37, 65-75.	1.8	8
573	Isoform expression patterns of EPHA10 protein mediate breast cancer progression by regulating the E-Cadherin and Î²-catenin complex. Oncotarget, 2017, 8, 30344-30356.	0.8	15
574	Developing DNA methylation-based diagnostic biomarkers. Journal of Genetics and Genomics, 2018, 45, 87-97.	1.7	41
575	MicroRNA-34a Inhibition of the TLR Signaling Pathway Via CXCL10 Suppresses Breast Cancer Cell Invasion and Migration. Cellular Physiology and Biochemistry, 2018, 46, 1286-1304.	1.1	30
576	Clinically actionable mutation profiles in patients with cancer identified by whole-genome sequencing. Journal of Physical Education and Sports Management, 2018, 4, a002279.	0.5	21
577	Genetic alterations crossing the borders of distinct hematopoietic lineages and solid tumors: Diagnostic challenges in the era of high-throughput sequencing in hemato-oncology. Critical Reviews in Oncology/Hematology, 2018, 126, 64-79.	2.0	12
578	Fusion genes: A promising tool combating against cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2018, 1869, 149-160.	3.3	36
579	Development of a personalized therapeutic strategy for ERBB-gene-mutated cancers. Therapeutic Advances in Medical Oncology, 2018, 10, 175883401774604.	1.4	11
580	Biomarkers for assessing the effectiveness of immunotherapy in breast cancer. Biomarkers in Medicine, 2018, 12, 97-100.	0.6	1
581	Endobronchial Ultrasound-Guided Transbronchial Needle Aspiration for Diagnosis and Staging of Lung Cancer. Clinics in Chest Medicine, 2018, 39, 111-123.	0.8	12
582	Biomarkers in breast cancer: A consensus statement by the Spanish Society of Medical Oncology and the Spanish Society of Pathology. Clinical and Translational Oncology, 2018, 20, 815-826.	1.2	57

#	ARTICLE	IF	CITATIONS
583	Network science in clinical trials: A patient-centered approach. <i>Seminars in Cancer Biology</i> , 2018, 52, 135-150.	4.3	9
584	Genome profile in a extremely rare case of pulmonary sclerosing pneumocytoma presenting with diffusely-scattered nodules in the right lung. <i>Cancer Biology and Therapy</i> , 2018, 19, 13-19.	1.5	16
585	Mechanisms of resistance in estrogen receptor positive breast cancer: overcoming resistance to tamoxifen/aromatase inhibitors. <i>Current Opinion in Pharmacology</i> , 2018, 41, 59-65.	1.7	105
586	A homologous mapping method for three-dimensional reconstruction of protein networks reveals disease-associated mutations. <i>BMC Systems Biology</i> , 2018, 12, 13.	3.0	1
587	Multi-omics profiling of younger Asian breast cancers reveals distinctive molecular signatures. <i>Nature Communications</i> , 2018, 9, 1725.	5.8	122
588	HER2 Activating Mutations in Estrogen Receptor Positive Breast Cancer. <i>Current Breast Cancer Reports</i> , 2018, 10, 41-47.	0.5	3
589	An integrative bioinformatics approach reveals coding and non-coding gene variants associated with gene expression profiles and outcome in breast cancer molecular subtypes. <i>British Journal of Cancer</i> , 2018, 118, 1107-1114.	2.9	26
590	Mutation screening of 10 cancer susceptibility genes in unselected breast cancer patients. <i>Clinical Genetics</i> , 2018, 93, 41-51.	1.0	15
591	Breast Cancer Risk Associated with Genotype Polymorphisms of the Aurora Kinase a Gene (AURKA): a Case-Control Study in a High Altitude Ecuadorian Mestizo Population. <i>Pathology and Oncology Research</i> , 2018, 24, 457-465.	0.9	11
592	Breast Cancer in Latinas: A Focus on Intrinsic Subtypes Distribution. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 3-10.	1.1	26
593	An Akt3 Splice Variant Lacking the Serine 472 Phosphorylation Site Promotes Apoptosis and Suppresses Mammary Tumorigenesis. <i>Cancer Research</i> , 2018, 78, 103-114.	0.4	13
594	Analysis of clonal expansions through the normal and premalignant human breast epithelium reveals the presence of luminal stem cells. <i>Journal of Pathology</i> , 2018, 244, 61-70.	2.1	13
595	Emerging Innovative Therapeutic Approaches Leveraging Cyclin-Dependent Kinase Inhibitors to Treat Advanced Breast Cancer. <i>Clinical Pharmacology and Therapeutics</i> , 2018, 103, 1009-1019.	2.3	5
596	Genome-Wide Transcriptome Analysis of Estrogen Receptor-Positive and Human Epithelial Growth Factor Receptor 2-Positive Breast Cancers by Ribonucleic Acid Sequencing. <i>Gynecologic and Obstetric Investigation</i> , 2018, 83, 338-348.	0.7	1
597	Expressed Gene Fusions as Frequent Drivers of Poor Outcomes in Hormone Receptor-Positive Breast Cancer. <i>Cancer Discovery</i> , 2018, 8, 336-353.	7.7	32
598	Breast Cancers Activate Stromal Fibroblast-Induced Suppression of Progenitors in Adjacent Normal Tissue. <i>Stem Cell Reports</i> , 2018, 10, 196-211.	2.3	21
599	A Living Biobank of Breast Cancer Organoids Captures Disease Heterogeneity. <i>Cell</i> , 2018, 172, 373-386.e10.	13.5	1,201
600	Phosphatidylinositol 3-Kinase Selective Inhibition With Alpelisib (BYL719) in PIK3CA-Altered Solid Tumors: Results From the First-in-Human Study. <i>Journal of Clinical Oncology</i> , 2018, 36, 1291-1299.	0.8	298

#	ARTICLE	IF	CITATIONS
601	Tumor <i>PIK3CA</i> Genotype and Prognosis in Early-Stage Breast Cancer: A Pooled Analysis of Individual Patient Data. <i>Journal of Clinical Oncology</i> , 2018, 36, 981-990.	0.8	95
602	Teneurins: An Integrative Molecular, Functional, and Biomedical Overview of Their Role in Cancer. <i>Frontiers in Neuroscience</i> , 2018, 12, 937.	1.4	12
603	Inference of protein-protein networks for triple-negative breast cancer using single-patient proteomic data. , 2018, , .		0
604	Differentiating breast cancer molecular subtypes using a DNA aptamer selected against MCF-7 cells. <i>Biomaterials Science</i> , 2018, 6, 3152-3159.	2.6	43
605	Gene prioritization, communality analysis, networking and metabolic integrated pathway to better understand breast cancer pathogenesis. <i>Scientific Reports</i> , 2018, 8, 16679.	1.6	29
606	Overexpression of MUC1 predicts poor prognosis in patients with breast cancer. <i>Oncology Reports</i> , 2019, 41, 801-810.	1.2	76
607	Targeting BRCA Deficiency in Breast Cancer: What are the Clinical Evidences and the Next Perspectives?. <i>Cancers</i> , 2018, 10, 506.	1.7	40
608	Detection of PIK3/AKT pathway in Moroccan population with triple negative breast cancer. <i>BMC Cancer</i> , 2018, 18, 900.	1.1	15
609	Avelumab, an IgG1 anti-PD-L1 Immune Checkpoint Inhibitor, Triggers NK Cell-Mediated Cytotoxicity and Cytokine Production Against Triple Negative Breast Cancer Cells. <i>Frontiers in Immunology</i> , 2018, 9, 2140.	2.2	92
610	De Novo Myelodysplastic Syndrome and Subsequent Diagnosis of Primary Solid Tumors: Evidence from the National Cancer Institute 2001-2011. <i>Anticancer Research</i> , 2018, 38, 5819-5823.	0.5	1
611	Characterization of Nigerian breast cancer reveals prevalent homologous recombination deficiency and aggressive molecular features. <i>Nature Communications</i> , 2018, 9, 4181.	5.8	77
612	Hierarchical HotNet: identifying hierarchies of altered subnetworks. <i>Bioinformatics</i> , 2018, 34, i972-i980.	1.8	102
613	miR-3178 inhibits cell proliferation and metastasis by targeting Notch1 in triple-negative breast cancer. <i>Cell Death and Disease</i> , 2018, 9, 1059.	2.7	41
614	Prevalence and spectrum of AKT1, PIK3CA, PTEN and TP53 somatic mutations in Chinese breast cancer patients. <i>PLoS ONE</i> , 2018, 13, e0203495.	1.1	30
615	Quantitative Proteomic Analysis Reveals Caffeineâ€ Perturbed Proteomic Profiles in Normal Bladder Epithelial Cells. <i>Proteomics</i> , 2018, 18, e1800190.	1.3	7
616	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. <i>Cancer Cell</i> , 2018, 34, 427-438.e6.	7.7	633
617	The prognostic effects of somatic mutations in ER-positive breast cancer. <i>Nature Communications</i> , 2018, 9, 3476.	5.8	89
618	In vivo phosphoproteomics reveals kinase activity profiles that predict treatment outcome in triple-negative breast cancer. <i>Nature Communications</i> , 2018, 9, 3501.	5.8	45

#	ARTICLE	IF	CITATIONS
619	MAP3K1 and MAP2K4 mutations are associated with sensitivity to MEK inhibitors in multiple cancer models. <i>Cell Research</i> , 2018, 28, 719-729.	5.7	105
620	How shall we treat early triple-negative breast cancer (TNBC): from the current standard to upcoming immuno-molecular strategies. <i>ESMO Open</i> , 2018, 3, e000357.	2.0	112
621	Loss of c-KIT expression in breast cancer correlates with malignant transformation of breast epithelium and is mediated by KIT gene promoter DNA hypermethylation. <i>Experimental and Molecular Pathology</i> , 2018, 105, 41-49.	0.9	28
622	The cJUN NH2-terminal kinase (JNK) signaling pathway promotes genome stability and prevents tumor initiation. <i>ELife</i> , 2018, 7, .	2.8	28
623	Mutational Analysis of Oncogenic AKT1 Gene Associated with Breast Cancer Risk in the High Altitude Ecuadorian Mestizo Population. <i>BioMed Research International</i> , 2018, 2018, 1-10.	0.9	28
624	Genetic Markers in Triple-Negative Breast Cancer. <i>Clinical Breast Cancer</i> , 2018, 18, e841-e850.	1.1	148
625	Introduction to Molecular Mechanisms in Notch Signal Transduction and Disease Pathogenesis. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1066, 3-30.	0.8	12
626	Global trends in nanomedicine research on triple negative breast cancer: a bibliometric analysis. <i>International Journal of Nanomedicine</i> , 2018, Volume 13, 2321-2336.	3.3	53
627	Wnt Signalling in Gastrointestinal Epithelial Stem Cells. <i>Genes</i> , 2018, 9, 178.	1.0	64
628	Applying Expression Profile Similarity for Discovery of Patient-Specific Functional Mutations. <i>High-Throughput</i> , 2018, 7, 6.	4.4	3
629	Long non-coding RNAs: implications in targeted diagnoses, prognosis, and improved therapeutic strategies in human non- and triple-negative breast cancer. <i>Clinical Epigenetics</i> , 2018, 10, 88.	1.8	49
630	Therapeutic landscape in mutational triple negative breast cancer. <i>Molecular Cancer</i> , 2018, 17, 99.	7.9	70
631	AKT isoform-specific expression and activation across cancer lineages. <i>BMC Cancer</i> , 2018, 18, 742.	1.1	32
632	The Impact of ESR1 Mutations on the Treatment of Metastatic Breast Cancer. <i>Hormones and Cancer</i> , 2018, 9, 215-228.	4.9	36
633	Applications of RNA Indexes for Precision Oncology in Breast Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 108-119.	3.0	16
634	Knockdown of LncRNA MAPT-AS1 inhibites proliferation and migration and sensitizes cancer cells to paclitaxel by regulating MAPT expression in ER-negative breast cancers. <i>Cell and Bioscience</i> , 2018, 8, 7.	2.1	37
635	Suppression of Breast Cancer Stem Cells and Tumor Growth by the RUNX1 Transcription Factor. <i>Molecular Cancer Research</i> , 2018, 16, 1952-1964.	1.5	48
636	Breast cancer patients suggestive of Li-Fraumeni syndrome: mutational spectrum, candidate genes, and unexplained heredity. <i>Breast Cancer Research</i> , 2018, 20, 87.	2.2	9

#	ARTICLE	IF	CITATIONS
637	CRISPR Technology for Breast Cancer: Diagnostics, Modeling, and Therapy. <i>Advanced Biology</i> , 2018, 2, 1800132.	3.0	11
638	Whole exome sequencing of breast cancer (TNBC) cases from India: association of MSH6 and BRIP1 variants with TNBC risk and oxidative DNA damage. <i>Molecular Biology Reports</i> , 2018, 45, 1413-1419.	1.0	6
639	Flightless-I Blocks p62-Mediated Recognition of LC3 to Impede Selective Autophagy and Promote Breast Cancer Progression. <i>Cancer Research</i> , 2018, 78, 4853-4864.	0.4	19
640	Whole-Genome Sequencing in Cancer. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a034579.	2.9	38
641	Metallic air pollutants and breast cancer heterogeneity. <i>Environmental Research</i> , 2019, 177, 108639.	3.7	34
642	A Spontaneous Aggressive ER ⁺ Mammary Tumor Model Is Driven by Kras Activation. <i>Cell Reports</i> , 2019, 28, 1526-1537.e4.	2.9	19
643	Integrative genomic analysis identifies associations of molecular alterations to APOBEC and BRCA1/2 mutational signatures in breast cancer. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e810.	0.6	7
644	A 23 gene-based molecular prognostic score precisely predicts overall survival of breast cancer patients. <i>EBioMedicine</i> , 2019, 46, 150-159.	2.7	64
645	Long noncoding RNA CASC2 promotes paclitaxel resistance in breast cancer through regulation of miR-18a-5p/CDK19. <i>Histochemistry and Cell Biology</i> , 2019, 152, 281-291.	0.8	45
646	miR-29b-3p promotes progression of MDA-MB-231 triple-negative breast cancer cells through downregulating TRAF3. <i>Biological Research</i> , 2019, 52, 38.	1.5	58
647	Emerging Role of Genomics and Cell-Free DNA in Breast Cancer. <i>Current Treatment Options in Oncology</i> , 2019, 20, 68.	1.3	9
648	Epidemiological characterization, genetic alterations of <i>Helicobacter pylori</i> infection in chronic gastric disorder and prognostic values of heterozygosity loss in chromosome 3p. <i>Molecular Biology Reports</i> , 2019, 46, 4323-4332.	1.0	0
649	Targeting DNA repair in breast cancer. <i>Breast</i> , 2019, 47, 33-42.	0.9	11
650	Double PIK3CA mutations in cis increase oncogenicity and sensitivity to PI3K inhibitors. <i>Science</i> , 2019, 366, 714-723.	6.0	185
651	Cytokeratin 7-negative and GATA binding protein 3-negative breast cancers: Clinicopathological features and prognostic significance. <i>BMC Cancer</i> , 2019, 19, 1085.	1.1	17
652	The HER2 S310F Mutant Can Form an Active Heterodimer with the EGFR, Which Can Be Inhibited by Cetuximab but Not by Trastuzumab as well as Pertuzumab. <i>Biomolecules</i> , 2019, 9, 629.	1.8	10
653	The splicing factor RBM25 controls MYC activity in acute myeloid leukemia. <i>Nature Communications</i> , 2019, 10, 172.	5.8	42
654	Breast Cancer Heterogeneity in Primary and Metastatic Disease. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1152, 75-104.	0.8	27

#	ARTICLE	IF	CITATIONS
655	High expression of the vacuole membrane protein 1 (VMP1) is a potential marker of poor prognosis in HER2 positive breast cancer. PLoS ONE, 2019, 14, e0221413.	1.1	9
656	Estrogen receptor 1 mutations in 260 cervical cancer samples from Chinese patients. Oncology Letters, 2019, 18, 2771-2776.	0.8	4
657	Available and emerging molecular markers in the clinical management of breast cancer. Expert Review of Molecular Diagnostics, 2019, 19, 919-928.	1.5	9
658	PIK3CA and MAP3K1 alterations imply luminal A status and are associated with clinical benefit from pan-PI3K inhibitor buparlisib and letrozole in ER+ metastatic breast cancer. Npj Breast Cancer, 2019, 5, 31.	2.3	31
659	Precision medicine for locally advanced breast cancer: frontiers and challenges in Latin America. Ecancermedalscience, 2019, 13, 896.	0.6	8
660	Association between histone lysine methyltransferase KMT2C mutation and clinicopathological factors in breast cancer. Biomedicine and Pharmacotherapy, 2019, 116, 108997.	2.5	21
661	Endocrine Resistance in Hormone Receptor Positive Breast Cancer—From Mechanism to Therapy. Frontiers in Endocrinology, 2019, 10, 245.	1.5	150
662	RUNX family: Oncogenes or tumor suppressors (Review). Oncology Reports, 2019, 42, 3-19.	1.2	60
663	Cytoplasmic HAX1 Is an Independent Risk Factor for Breast Cancer Metastasis. Journal of Oncology, 2019, 2019, 1-13.	0.6	8
664	The transcription factor CBFB suppresses breast cancer through orchestrating translation and transcription. Nature Communications, 2019, 10, 2071.	5.8	60
665	Interchromosomal Translocations as a Means to Map Chromosome Territories in Breast Cancer. Cancer Informatics, 2019, 18, 117693511984257.	0.9	2
666	Biomarkers to diagnose metastatic breast carcinoma to the pancreas: A case report and update. Diagnostic Cytopathology, 2019, 47, 912-917.	0.5	6
667	Upregulation of AKT1 and downregulation of AKT3 caused by dysregulation of microRNAs contributes to pathogenesis of hemangioma by promoting proliferation of endothelial cells. Journal of Cellular Physiology, 2019, 234, 21342-21351.	2.0	5
668	A breast one-patient panel of heterogeneous genomes reveals genetic alterations driving DCIS into invasive lesions. Future Oncology, 2019, 15, 1565-1576.	1.1	6
670	De Novo HER2 S310Y mutation associates with poor response to EGFR tyrosine kinase inhibitor in activating EGFR-mutant NSCLC patient: A case report. European Journal of Inflammation, 2019, 17, 205873921982716.	0.2	0
671	Patient-Driven Discovery, Therapeutic Targeting, and Post-Clinical Validation of a Novel <i>AKT1</i> Fusion—Driven Cancer. Cancer Discovery, 2019, 9, 605-616.	7.7	11
672	Prevalence and role of HER2 mutations in cancer. , 2019, 199, 188-196.		44
673	Differential effects of the Akt inhibitor MK-2206 on migration and radiation sensitivity of glioblastoma cells. BMC Cancer, 2019, 19, 299.	1.1	28

#	ARTICLE	IF	CITATIONS
674	Non-invasive analysis of tumor mutation profiles and druggable mutations by sequencing of cell free DNA of Chinese metastatic breast cancer patients. <i>Thoracic Cancer</i> , 2019, 10, 807-814.	0.8	7
675	Patterns of Genomic Instability in Breast Cancer. <i>Trends in Pharmacological Sciences</i> , 2019, 40, 198-211.	4.0	68
676	Tumor suppressor MCPH1 regulates gene expression profiles related to malignant conversion and chromosomal assembly. <i>International Journal of Cancer</i> , 2019, 145, 2070-2081.	2.3	5
677	Recent therapeutic trends and promising targets in triple negative breast cancer. , 2019, 199, 30-57.		164
678	Reactive oxygen species modulate macrophage immunosuppressive phenotype through the up-regulation of PD-L1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4326-4335.	3.3	137
679	Identifying driver genes involving gene dysregulated expression, tissue-specific expression and gene-gene network. <i>BMC Medical Genomics</i> , 2019, 12, 168.	0.7	11
680	Deciphering HER2 Breast Cancer Disease: Biological and Clinical Implications. <i>Frontiers in Oncology</i> , 2019, 9, 1124.	1.3	52
681	Distinct functions of AKT isoforms in breast cancer: a comprehensive review. <i>Cell Communication and Signaling</i> , 2019, 17, 154.	2.7	192
682	Identification of Breast Cancer Subtype Specific MicroRNAs Using Survival Analysis to Find Their Role in Transcriptomic Regulation. <i>Frontiers in Genetics</i> , 2019, 10, 1047.	1.1	16
683	Identification of two novel breast cancer loci through large-scale genome-wide association study in the Japanese population. <i>Scientific Reports</i> , 2019, 9, 17332.	1.6	9
684	Prospective Decision Analysis Study of Clinical Genomic Testing in Metastatic Breast Cancer: Impact on Outcomes and Patient Perceptions. <i>JCO Precision Oncology</i> , 2019, 3, 1-11.	1.5	8
685	Genomic Alterations Associated with Recurrence and TNBC Subtype in High-Risk Early Breast Cancers. <i>Molecular Cancer Research</i> , 2019, 17, 97-108.	1.5	17
686	Genomic Applications in Breast Carcinoma. , 2019, , 347-361.		0
687	KLP-PI: a new prognostic index for luminal B HER-2-negative breast cancer. <i>Human Cell</i> , 2019, 32, 172-184.	1.2	2
688	Dynamic genome and transcriptional network-based biomarkers and drugs: precision in breast cancer therapy. <i>Medicinal Research Reviews</i> , 2019, 39, 1205-1227.	5.0	21
689	Overexpression of novel lncRNA NLIPMT inhibits metastasis by reducing phosphorylated glycogen synthase kinase 3 β in breast cancer. <i>Journal of Cellular Physiology</i> , 2019, 234, 10698-10708.	2.0	21
690	Crosstalk between Estrogen Signaling and Breast Cancer Metabolism. <i>Trends in Endocrinology and Metabolism</i> , 2019, 30, 25-38.	3.1	93
691	The RUNX Transcriptional Coregulator, CBF β , Suppresses Migration of ER+ Breast Cancer Cells by Repressing ER α -Mediated Expression of the Migratory Factor TFF1. <i>Molecular Cancer Research</i> , 2019, 17, 1015-1023.	1.5	10

#	ARTICLE	IF	CITATIONS
692	Down-regulated expression of LINC00518 prevents epithelial cell growth and metastasis in breast cancer through the inhibition of CDX2 methylation and the Wnt signaling pathway. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 708-723.	1.8	23
693	Potential of Liquid Biopsies for Breast Cancer Screening, Diagnosis, and Response to Treatment. <i>Oncology</i> , 2019, 96, 115-124.	0.9	11
694	Ductal Carcinoma in Situ Biomarkers in a Precision Medicine Era. <i>American Journal of Pathology</i> , 2019, 189, 956-965.	1.9	15
695	<i>CRTC1</i> – <i>MAML2</i> fusion in mucoepidermoid carcinoma of the breast. <i>Histopathology</i> , 2019, 74, 463-473.	1.6	33
696	<i>RUNX1</i> –dependent mechanisms in biological control and dysregulation in cancer. <i>Journal of Cellular Physiology</i> , 2019, 234, 8597-8609.	2.0	48
697	Functional Role of miRNAs in the Progression of Breast Ductal Carcinoma in Situ. <i>American Journal of Pathology</i> , 2019, 189, 966-974.	1.9	11
698	A Novel Method for Identifying the Potential Cancer Driver Genes Based on Molecular Data Integration. <i>Biochemical Genetics</i> , 2020, 58, 16-39.	0.8	13
699	<i>Fbxl17</i> is rearranged in breast cancer and loss of its activity leads to increased global O-GlcNAcylation. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 2605-2620.	2.4	10
700	Using R and Bioconductor in Clinical Genomics and Transcriptomics. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 3-20.	1.2	77
701	Know your enemy: Genetics, aging, exposomic and inflammation in the war against triple negative breast cancer. <i>Seminars in Cancer Biology</i> , 2020, 60, 285-293.	4.3	16
702	Mechanisms of resistance to estrogen receptor modulators in ER+/HER2 ⁺ advanced breast cancer. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 559-572.	2.4	19
703	<i>RUNX2/CBFB</i> modulates the response to MEK inhibitors through activation of receptor tyrosine kinases in KRAS-mutant colorectal cancer. <i>Translational Oncology</i> , 2020, 13, 201-211.	1.7	7
704	Construction of an immune-related genes nomogram for the preoperative prediction of axillary lymph node metastasis in triple-negative breast cancer. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2020, 48, 288-297.	1.9	30
705	NOTCH and DNA repair pathways are more frequently targeted by genomic alterations in inflammatory than in non-inflammatory breast cancers. <i>Molecular Oncology</i> , 2020, 14, 504-519.	2.1	23
706	A phase 2 clinical trial—assessing the efficacy and safety of pembrolizumab and radiotherapy in patients with metastatic triple-negative breast cancer. <i>Cancer</i> , 2020, 126, 850-860.	2.0	116
707	Molecular Classification of Breast Cancer. <i>Advances in Anatomic Pathology</i> , 2020, 27, 27-35.	2.4	283
708	The immunologic aspects in hormone receptor positive breast cancer. <i>Cancer Treatment and Research Communications</i> , 2020, 25, 100207.	0.7	4
709	Genetic and clinical landscape of breast cancers with germline BRCA1/2 variants. <i>Communications Biology</i> , 2020, 3, 578.	2.0	20

#	ARTICLE	IF	CITATIONS
710	Identification of new driver and passenger mutations within APOBEC-induced hotspot mutations in bladder cancer. <i>Genome Medicine</i> , 2020, 12, 85.	3.6	39
711	In vivo CRISPR/Cas9 targeting of fusion oncogenes for selective elimination of cancer cells. <i>Nature Communications</i> , 2020, 11, 5060.	5.8	60
713	Predictive Role of TP53, PIK3CA and MLL2 in ER+ HER2+ Breast Bancer: Biomarker Analysis of Neo-ALL-IN [NCT 01275859]. <i>Anticancer Research</i> , 2020, 40, 5883-5893.	0.5	1
714	Prostate cancer reactivates developmental epigenomic programs during metastatic progression. <i>Nature Genetics</i> , 2020, 52, 790-799.	9.4	174
715	Utility of Circulating Tumor Cells for Detection of Early-Stage Luminal A Breast Cancer. <i>American Journal of the Medical Sciences</i> , 2020, 360, 543-551.	0.4	6
716	Mitochondrial DNA Mutation Analysis in Breast Cancer: Shifting From Germline Heteroplasmy Toward Homoplasmy in Tumors. <i>Frontiers in Oncology</i> , 2020, 10, 572954.	1.3	19
717	Weighted gene co-expression network analysis identified underlying hub genes and mechanisms in the occurrence and development of viral myocarditis. <i>Annals of Translational Medicine</i> , 2020, 8, 1348-1348.	0.7	7
718	Multi-Omics Characterization of the 4T1 Murine Mammary Gland Tumor Model. <i>Frontiers in Oncology</i> , 2020, 10, 1195.	1.3	94
719	Comprehensive Cohort Analysis of Mutational Spectrum in Early Onset Breast Cancer Patients. <i>Cancers</i> , 2020, 12, 2089.	1.7	9
720	The transcription factor CBFB mutations indicate an improved survival in HR+ /HER2- breast cancer. <i>Gene</i> , 2020, 759, 144970.	1.0	5
721	Clinicopathological and genomic features of breast mucinous carcinoma. <i>Breast</i> , 2020, 53, 130-137.	0.9	11
722	Akt3 induces oxidative stress and DNA damage by activating the NADPH oxidase via phosphorylation of p47 ^{phox} . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28806-28815.	3.3	18
723	Stage-specific protein-domain mutational profile of invasive ductal breast cancer. <i>BMC Medical Genomics</i> , 2020, 13, 150.	0.7	0
724	Immunotherapy in Breast Cancer: Current Practice and Clinical Challenges. <i>BioDrugs</i> , 2020, 34, 611-623.	2.2	38
725	FOXA1 Mutations Reveal Distinct Chromatin Profiles and Influence Therapeutic Response in Breast Cancer. <i>Cancer Cell</i> , 2020, 38, 534-550.e9.	7.7	67
726	The biological function and clinical significance of SF3B1 mutations in cancer. <i>Biomarker Research</i> , 2020, 8, 38.	2.8	47
727	A validated lineage-derived somatic truth data set enables benchmarking in cancer genome analysis. <i>Communications Biology</i> , 2020, 3, 744.	2.0	1
728	Adipocytes promote breast tumorigenesis through TAZ-dependent secretion of Resistin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33295-33304.	3.3	37

#	ARTICLE	IF	CITATIONS
729	Regulation of Canonical Oncogenic Signaling Pathways in Cancer via DNA Methylation. <i>Cancers</i> , 2020, 12, 3199.	1.7	13
730	Therapeutic Efficacy of GC1118, a Novel Anti-EGFR Antibody, against Glioblastoma with High EGFR Amplification in Patient-Derived Xenografts. <i>Cancers</i> , 2020, 12, 3210.	1.7	10
731	Frequency and spectrum of PIK3CA somatic mutations in breast cancer. <i>Breast Cancer Research</i> , 2020, 22, 45.	2.2	175
732	<i>Osb1r8</i> orchestrates intrachromosomal loop structure required for maintaining stem cell pluripotency. <i>International Journal of Biological Sciences</i> , 2020, 16, 1861-1875.	2.6	6
733	Impact of TP53 mutations in breast cancer: Clinicopathological features and prognosisImpact of TP53 mutations in breast CA. <i>Thoracic Cancer</i> , 2020, 11, 1861-1868.	0.8	8
734	Subtype-specific characterization of breast cancer invasionUsing a microfluidic tumor platform. <i>PLoS ONE</i> , 2020, 15, e0234012.	1.1	17
735	Biology of the Triple-Negative Breast Cancer: Immunohistochemical, RNA, and DNA Features. <i>Breast Care</i> , 2020, 15, 208-216.	0.8	6
736	Discovery of 3-Quinazolin-4(3 <i>H</i>)-on-3-yl-2, <i>N</i> -dimethylpropanamides as Orally Active and Selective PI3K± Inhibitors. <i>ACS Medicinal Chemistry Letters</i> , 2020, 11, 1463-1469.	1.3	4
737	RUNX1 and RUNX2 transcription factors function in opposing roles to regulate breast cancer stem cells. <i>Journal of Cellular Physiology</i> , 2020, 235, 7261-7272.	2.0	34
738	Methylome Variation Predicts Exemestane Resistance in Advanced ER ⁺ Breast Cancer. <i>Technology in Cancer Research and Treatment</i> , 2020, 19, 153303381989633.	0.8	5
739	OncoOmics approaches to reveal essential genes in breast cancer: a panoramic view from pathogenesis to precision medicine. <i>Scientific Reports</i> , 2020, 10, 5285.	1.6	36
740	Breast Cancer: A Molecularly Heterogenous Disease Needing Subtype-Specific Treatments. <i>Medical Sciences (Basel, Switzerland)</i> , 2020, 8, 18.	1.3	72
741	Adaptive Molecular Evolution of <i>AKT3</i> Gene for Positive Diversifying Selection in Mammals. <i>BioMed Research International</i> , 2020, 2020, 1-13.	0.9	3
742	Flaming the fight against cancer cells: the role of microRNA-93. <i>Cancer Cell International</i> , 2020, 20, 277.	1.8	9
743	Age-related mutational signature negatively associated with immune activity and survival outcome in triple-negative breast cancer. <i>Oncolmmunology</i> , 2020, 9, 1788252.	2.1	20
744	Response of metastatic mouse invasive lobular carcinoma to mTOR inhibition is partly mediated by the adaptive immune system. <i>Oncolmmunology</i> , 2020, 9, 1724049.	2.1	12
745	Ret Receptor Has Distinct Alterations and Functions in Breast Cancer. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2020, 25, 13-26.	1.0	12
746	Current concepts in breast cancer genomics: An evidence based review by the CGC breast cancer working group. <i>Cancer Genetics</i> , 2020, 244, 11-20.	0.2	4

#	ARTICLE	IF	CITATIONS
747	ARID1A determines luminal identity and therapeutic response in estrogen-receptor-positive breast cancer. <i>Nature Genetics</i> , 2020, 52, 198-207.	9.4	140
748	Germline Variants in Driver Genes of Breast Cancer and Their Association with Familial and Early-Onset Breast Cancer Risk in a Chilean Population. <i>Cancers</i> , 2020, 12, 249.	1.7	4
749	Single-molecule detection of cancer mutations using a novel PCR-LDR-qPCR assay. <i>Human Mutation</i> , 2020, 41, 1051-1068.	1.1	8
750	Next generation sequencing can be helpful in histologic diagnosis: A case report of metastatic breast cancer mimicking atypical carcinoid tumor of lung. <i>Pathology Research and Practice</i> , 2020, 216, 152835.	1.0	0
751	Hypoxia-sensitive supramolecular nanogels for the cytosolic delivery of ribonuclease A as a breast cancer therapeutic. <i>Journal of Controlled Release</i> , 2020, 320, 83-95.	4.8	54
752	A role for CBF β in maintaining the metastatic phenotype of breast cancer cells. <i>Oncogene</i> , 2020, 39, 2624-2637.	2.6	11
753	Landscape analysis of adjacent gene rearrangements reveals BCL2L1-ETV6 gene fusions in more aggressive triple-negative breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9912-9921.	3.3	17
754	Targeted next generation sequencing identifies somatic mutations in a cohort of Egyptian breast cancer patients. <i>Journal of Advanced Research</i> , 2020, 24, 149-157.	4.4	13
755	Sporadic activation of an oxidative stress-dependent NRF2-p53 signaling network in breast epithelial spheroids and premalignancies. <i>Science Signaling</i> , 2020, 13, .	1.6	25
756	Oncolytic vesicular stomatitis virus-based cellular vaccine improves triple-negative breast cancer outcome by enhancing natural killer and CD8 ⁺ T-cell functionality. , 2020, 8, e000465.		28
757	RUNX1 Is a Driver of Renal Cell Carcinoma Correlating with Clinical Outcome. <i>Cancer Research</i> , 2020, 80, 2325-2339.	0.4	21
758	New Advances in Molecular Breast Cancer Pathology. <i>Seminars in Cancer Biology</i> , 2021, 72, 102-113.	4.3	37
759	Expression pattern, regulation, and clinical significance of TOX in breast cancer. <i>Cancer Immunology, Immunotherapy</i> , 2021, 70, 349-363.	2.0	13
760	Problematic breast tumors reassessed in light of novel molecular data. <i>Modern Pathology</i> , 2021, 34, 38-47.	2.9	25
761	Multi-color clonal tracking reveals intra-stage proliferative heterogeneity during mammary tumor progression. <i>Oncogene</i> , 2021, 40, 12-27.	2.6	17
762	Role of GATA3 exon 6 germline mutations in breast cancer progression in Egyptian female patients. <i>Experimental Biology and Medicine</i> , 2021, 246, 40-47.	1.1	3
763	Insulin-Induced Gene 2 Expression Is Associated with Breast Cancer Metastasis. <i>American Journal of Pathology</i> , 2021, 191, 385-395.	1.9	2
764	Molecular intrinsic versus clinical subtyping in breast cancer: A comprehensive review. <i>Clinical Genetics</i> , 2021, 99, 613-637.	1.0	42

#	ARTICLE	IF	CITATIONS
765	Donatelli et al. combined apoptotic body analogues for efficient targeted therapy of triple-negative breast cancer. <i>Journal of Materials Chemistry B</i> , 2021, 9, 8472-8479.	2.9	4
766	Defining Breast Cancer. , 2021, , 1-31.		0
767	3D Functional Genomics Screens Identify CREBBP as a Targetable Driver in Aggressive Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2021, 81, 847-859.	0.4	7
768	p66ShcA potentiates the cytotoxic response of triple negative breast cancers to PARP inhibitors. <i>JCI Insight</i> , 2021, 6, .	2.3	0
769	A Lipid Targeting, pH-Responsive Nanoemulsion Encapsulating a DNA Intercalating Agent and HDAC Inhibitor Reduces TNBC Tumor Burden. <i>Advanced Therapeutics</i> , 2021, 4, 2000211.	1.6	4
770	Nexus between PI3K/AKT and Estrogen Receptor Signaling in Breast Cancer. <i>Cancers</i> , 2021, 13, 369.	1.7	35
771	Autophagy Blockade Limits HER2+ Breast Cancer Tumorigenesis by Perturbing HER2 Trafficking and Promoting Release Via Small Extracellular Vesicles. <i>Developmental Cell</i> , 2021, 56, 341-355.e5.	3.1	25
773	Teneurin3: Role in Cancer and Potential Role as Diagnostic Biomarkers and Targets for Therapy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2321.	1.8	16
774	Immunotherapy for breast cancer using EpCAM aptamer tumor-targeted gene knockdown. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	38
775	Effect of Capivasertib in Patients With an <i>AKT1 E17K</i> -Mutated Tumor. <i>JAMA Oncology</i> , 2021, 7, 271.	3.4	49
776	AKT3 Expression in Mesenchymal Colorectal Cancer Cells Drives Growth and Is Associated with Epithelial-Mesenchymal Transition. <i>Cancers</i> , 2021, 13, 801.	1.7	16
777	Breast Cancer Patient Prognosis Is Determined by the Interplay between TP53 Mutation and Alternative Transcript Expression: Insights from TP53 Long Amplicon Digital PCR Assays. <i>Cancers</i> , 2021, 13, 1531.	1.7	5
778	Identification of Hub Genes and Pathways of Triple Negative Breast Cancer by Expression Profiles Analysis. <i>Cancer Management and Research</i> , 2021, Volume 13, 2095-2104.	0.9	6
779	Aberrations of Chromosomes 1 and 16 in Breast Cancer: A Framework for Cooperation of Transcriptionally Dysregulated Genes. <i>Cancers</i> , 2021, 13, 1585.	1.7	10
780	6-lncRNA Assessment Model for Monitoring and Prognosis of HER2-Positive Breast Cancer: Based on Transcriptome Data. <i>Pathology and Oncology Research</i> , 2021, 27, 609083.	0.9	6
782	Oncogenic mutation or overexpression of oncogenic KRAS or BRAF is not sufficient to confer oncogene addiction. <i>PLoS ONE</i> , 2021, 16, e0249388.	1.1	2
783	Breast cancer as an example of tumour heterogeneity and tumour cell plasticity during malignant progression. <i>British Journal of Cancer</i> , 2021, 125, 164-175.	2.9	177
784	Comprehensive omic characterization of breast cancer in Mexican-Hispanic women. <i>Nature Communications</i> , 2021, 12, 2245.	5.8	14

#	ARTICLE	IF	CITATIONS
785	Functional Characterization of Circulating Tumor Cells (CTCs) from Metastatic ER+/HER2 ⁻ Breast Cancer Reveals Dependence on HER2 and FOXM1 for Endocrine Therapy Resistance and Tumor Cell Survival: Implications for Treatment of ER+/HER2 ⁻ Breast Cancer. <i>Cancers</i> , 2021, 13, 1810.	1.7	13
786	CircRNA circTRAF3 promotes nasopharyngeal carcinoma metastasis through targeting miR-203a-3p/AKT3 axis. <i>Pathology Research and Practice</i> , 2021, 221, 153438.	1.0	6
787	Identification of driver genes based on gene mutational effects and network centrality. <i>BMC Bioinformatics</i> , 2021, 22, 457.	1.2	3
788	Signatures of Discriminative Copy Number Aberrations in 31 Cancer Subtypes. <i>Frontiers in Genetics</i> , 2021, 12, 654887.	1.1	6
789	HDAC6 inhibitors sensitize non-mesenchymal triple-negative breast cancer cells to cysteine deprivation. <i>Scientific Reports</i> , 2021, 11, 10956.	1.6	17
790	CBFB cooperates with p53 to maintain TAp73 expression and suppress breast cancer. <i>PLoS Genetics</i> , 2021, 17, e1009553.	1.5	8
791	Discovery and biological evaluation of a small-molecule inhibitor of CRM1 that suppresses the growth of triple-negative breast cancer cells. <i>Traffic</i> , 2021, 22, 221-229.	1.3	2
792	Transcription Factors: The Fulcrum Between Cell Development and Carcinogenesis. <i>Frontiers in Oncology</i> , 2021, 11, 681377.	1.3	25
793	MAG11, a Scaffold Protein with Tumor Suppressive and Vascular Functions. <i>Cells</i> , 2021, 10, 1494.	1.8	10
795	Checkpoint inhibitor therapy for metastatic triple-negative breast cancer. <i>Cancer and Metastasis Reviews</i> , 2021, 40, 537-547.	2.7	58
796	The temporal mutational and immune tumour microenvironment remodelling of HER2-negative primary breast cancers. <i>Npj Breast Cancer</i> , 2021, 7, 73.	2.3	2
797	Attacking the PI3K/Akt/mTOR signaling pathway for targeted therapeutic treatment in human cancer. <i>Seminars in Cancer Biology</i> , 2022, 85, 69-94.	4.3	140
798	A supersensitive silicon nanowire array biosensor for quantitating tumor marker ctDNA. <i>Biosensors and Bioelectronics</i> , 2021, 181, 113147.	5.3	36
799	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 32-39.	4.3	35
800	NGS in Lung, Breast, and Unknown Primary Cancer in Colombia: A Multidisciplinary Consensus on Challenges and Opportunities. <i>JCO Global Oncology</i> , 2021, 7, 1012-1023.	0.8	7
801	Akt Isoforms: A Family Affair in Breast Cancer. <i>Cancers</i> , 2021, 13, 3445.	1.7	31
802	Stem cell therapy: A paradigm shift in breast cancer treatment. <i>World Journal of Stem Cells</i> , 2021, 13, 841-860.	1.3	8
803	DIF-1 inhibits growth and metastasis of triple-negative breast cancer through AMPK-mediated inhibition of the mTORC1-S6K signaling pathway. <i>Oncogene</i> , 2021, 40, 5579-5589.	2.6	18

#	ARTICLE	IF	CITATIONS
804	Multi-Gene Testing Overview with a Clinical Perspective in Metastatic Triple-Negative Breast Cancer. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7154.	1.8	5
806	Comprehensive Analysis of Metabolic Genes in Breast Cancer Based on Multi-Omics Data. <i>Pathology and Oncology Research</i> , 2021, 27, 1609789.	0.9	2
807	Predictive biomarkers for 5-fluorouracil and oxaliplatin-based chemotherapy in gastric cancers via profiling of patient-derived xenografts. <i>Nature Communications</i> , 2021, 12, 4840.	5.8	27
808	Why proper characterization of breast cancer subtypes makes a difference in patient care. <i>Breast Journal</i> , 2021, 27, 689-690.	0.4	0
809	A New Story of the Three Magi: Scaffolding Proteins and lncRNA Suppressors of Cancer. <i>Cancers</i> , 2021, 13, 4264.	1.7	6
810	A Fourâ€ Gene-Based Risk Score With High Prognostic Value in Gastric Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 584213.	1.3	6
811	Genetic and immune characteristics of sentinel lymph node metastases and multiple lymph node metastases compared to their matched primary breast tumours. <i>EBioMedicine</i> , 2021, 71, 103542.	2.7	6
812	Targeted Sequencing Revealed Distinct Mutational Profiles of Ocular and Extraocular Sebaceous Carcinomas. <i>Cancers</i> , 2021, 13, 4810.	1.7	5
813	FBXL16 modulates the proliferation and autophagy in breast cancer cells via activating SRC-3-AKT signaling pathway. <i>Reproductive Biology</i> , 2021, 21, 100538.	0.9	5
814	Abscopal Effect of Radiotherapy Enhanced with Immune Checkpoint Inhibitors of Triple Negative Breast Cancer in 4T1 Mammary Carcinoma Model. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10476.	1.8	16
815	Circular RNA: A potential diagnostic, prognostic, and therapeutic biomarker for human triple-negative breast cancer. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 63-80.	2.3	34
816	A sensitive HPLC-FLD method for the quantification of alpelisib, a novel phosphatidylinositol 3-kinase inhibitor, in rat plasma: Drug metabolism and pharmacokinetic evaluation in vitro and in vivo. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2021, 1163, 122508.	1.2	11
817	Quadruple-responsive nanoparticle-mediated targeted combination chemotherapy for metastatic breast cancer. <i>Nanoscale</i> , 2021, 13, 5765-5779.	2.8	15
818	Hsa_circ_0000199 facilitates chemo-tolerance of triple-negative breast cancer by interfering with miR-206/613-led PI3K/Akt/mTOR signaling. <i>Aging</i> , 2021, 13, 4522-4551.	1.4	40
819	Biology and Treatment of Basal-Like Breast Cancer. , 2013, , 91-109.		2
820	Metronomic Chemotherapy in Breast Cancers. , 2014, , 93-110.		2
821	Identifying Driver Mutations in Cancer. <i>Translational Bioinformatics</i> , 2013, , 33-56.	0.0	4
822	Molecular Profiling of Breast Cancer in Clinical Trials: A Perspective. , 2020, , 313-332.		4

#	ARTICLE	IF	CITATIONS
823	Somatic mutations of triple-negative breast cancer: a comparison between Black and White women. <i>Breast Cancer Research and Treatment</i> , 2020, 182, 503-509.	1.1	11
824	Genetic alterations and their association with clinicopathologic characteristics in advanced breast carcinomas: focusing on clinically actionable genetic alterations. <i>Human Pathology</i> , 2020, 102, 94-103.	1.1	16
826	RUNX1 prevents oestrogen-mediated AXIN1 suppression and β -catenin activation in ER-positive breast cancer. <i>Nature Communications</i> , 2016, 7, 10751.	5.8	61
827	The molecular landscape of Asian breast cancers reveals clinically relevant population-specific differences. <i>Nature Communications</i> , 2020, 11, 6433.	5.8	37
828	Inhibitors in AKTion: ATP-competitive vs allosteric. <i>Biochemical Society Transactions</i> , 2020, 48, 933-943.	1.6	27
830	Death-associated protein kinase 1 promotes growth of p53-mutant cancers. <i>Journal of Clinical Investigation</i> , 2015, 125, 2707-2720.	3.9	49
831	Role of steroid receptor and coregulator mutations in hormone-dependent cancers. <i>Journal of Clinical Investigation</i> , 2017, 127, 1126-1135.	3.9	42
832	Translating Genomic Research into Clinical Practice: Promise and Pitfalls. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2013, 33, 15-23.	1.8	7
834	Gain- and Loss-of-Function Mutations in the Breast Cancer Gene GATA3 Result in Differential Drug Sensitivity. <i>PLoS Genetics</i> , 2016, 12, e1006279.	1.5	43
835	Circulating tumour DNA in metastatic breast cancer to guide clinical trial enrolment and precision oncology: A cohort study. <i>PLoS Medicine</i> , 2020, 17, e1003363.	3.9	18
836	Deep Clonal Profiling of Formalin Fixed Paraffin Embedded Clinical Samples. <i>PLoS ONE</i> , 2012, 7, e50586.	1.1	42
837	The Relative Timing of Mutations in a Breast Cancer Genome. <i>PLoS ONE</i> , 2013, 8, e64991.	1.1	22
838	Genomic Instability: A Stronger Prognostic Marker Than Proliferation for Early Stage Luminal Breast Carcinomas. <i>PLoS ONE</i> , 2013, 8, e76496.	1.1	16
839	Massively Parallel Sequencing Reveals an Accumulation of De Novo Mutations and an Activating Mutation of LPAR1 in a Patient with Metastatic Neuroblastoma. <i>PLoS ONE</i> , 2013, 8, e77731.	1.1	24
840	The Genome of Polymorphonuclear Neutrophils Maintains Normal Coding Sequences. <i>PLoS ONE</i> , 2013, 8, e78685.	1.1	1
841	Association between PARP-1 V762A Polymorphism and Breast Cancer Susceptibility in Saudi Population. <i>PLoS ONE</i> , 2013, 8, e85541.	1.1	43
842	NCI-60 Whole Exome Sequencing and Pharmacological CellMiner Analyses. <i>PLoS ONE</i> , 2014, 9, e101670.	1.1	38
843	Exome Analysis Reveals Differentially Mutated Gene Signatures of Stage, Grade and Subtype in Breast Cancers. <i>PLoS ONE</i> , 2015, 10, e0119383.	1.1	19

#	ARTICLE	IF	CITATIONS
844	Analysis of Paired Primary-Metastatic Hormone-Receptor Positive Breast Tumors (HRPBC) Uncovers Potential Novel Drivers of Hormonal Resistance. PLoS ONE, 2016, 11, e0155840.	1.1	20
845	Mutant PIK3CA Induces EMT in a Cell Type Specific Manner. PLoS ONE, 2016, 11, e0167064.	1.1	5
846	Identification of Post-Transcriptional Modulators of Breast Cancer Transcription Factor Activity Using MINDy. PLoS ONE, 2016, 11, e0168770.	1.1	4
847	Genomic comparison of early-passage conditionally reprogrammed breast cancer cells to their corresponding primary tumors. PLoS ONE, 2017, 12, e0186190.	1.1	24
848	RUNX1 Dosage in Development and Cancer. Molecules and Cells, 2020, 43, 126-138.	1.0	16
849	Complex Interplay between the RUNX Transcription Factors and Wnt/ β -Catenin Pathway in Cancer: A Tango in the Night. Molecules and Cells, 2020, 43, 188-197.	1.0	15
850	The Immunobiology of Cancer: An Update Review. Indonesian Biomedical Journal, 2017, 9, 53.	0.2	2
851	Narrowing the focus: a toolkit to systematically connect oncogenic signaling pathways with cancer phenotypes. Genes and Cancer, 2016, 7, 218-228.	0.6	5
852	DNA-damage related genes and clinical outcome in hormone receptor positive breast cancer. Oncotarget, 2017, 8, 62834-62841.	0.8	13
853	A microRNA/Runx1/Runx2 network regulates prostate tumor progression from onset to adenocarcinoma in TRAMP mice. Oncotarget, 2016, 7, 70462-70474.	0.8	21
854	The nuclear corepressor 1 and the thyroid hormone receptor β 2 suppress breast tumor lymphangiogenesis. Oncotarget, 2016, 7, 78971-78984.	0.8	15
855	Targeting oncogenic vulnerabilities in triple negative breast cancer: biological bases and ongoing clinical studies. Oncotarget, 2017, 8, 22218-22234.	0.8	46
856	Runx1 stabilizes the mammary epithelial cell phenotype and prevents epithelial to mesenchymal transition. Oncotarget, 2017, 8, 17610-17627.	0.8	53
857	Regulatory network of <i>GATA3</i> in pediatric acute lymphoblastic leukemia. Oncotarget, 2017, 8, 36040-36053.	0.8	30
858	Characterization of CADD522, a small molecule that inhibits RUNX2-DNA binding and exhibits antitumor activity. Oncotarget, 2017, 8, 70916-70940.	0.8	16
859	RUNX1 promote invasiveness in pancreatic ductal adenocarcinoma through regulating miR-93. Oncotarget, 2017, 8, 99567-99579.	0.8	22
860	RUNX1 and RUNX3 protect against YAP-mediated EMT, stem-ness and shorter survival outcomes in breast cancer. Oncotarget, 2018, 9, 14175-14192.	0.8	59
861	Somatic mutations in early onset luminal breast cancer. Oncotarget, 2018, 9, 22460-22479.	0.8	25

#	ARTICLE	IF	CITATIONS
862	A Phase Ib, open-label, dose-finding study of alpelisib in combination with paclitaxel in patients with advanced solid tumors. <i>Oncotarget</i> , 2018, 9, 31709-31718.	0.8	32
863	Inhibition of the RUNX1-CBF β transcription factor complex compromises mammary epithelial cell identity: a phenotype potentially stabilized by mitotic gene bookmarking. <i>Oncotarget</i> , 2020, 11, 2512-2530.	0.8	8
864	Genomic differences between pure ductal carcinoma <i>in situ</i> and synchronous ductal carcinoma <i>in situ</i> with invasive breast cancer. <i>Oncotarget</i> , 2015, 6, 7597-7607.	0.8	67
865	Cell type of origin as well as genetic alterations contribute to breast cancer phenotypes. <i>Oncotarget</i> , 2015, 6, 9018-9030.	0.8	19
866	Oncogenic AKT1(E17K) mutation induces mammary hyperplasia but prevents HER2-driven tumorigenesis. <i>Oncotarget</i> , 2016, 7, 17301-17313.	0.8	22
867	A new view of the mammary epithelial hierarchy and its implications for breast cancer initiation and metastasis. <i>Journal of Cancer Metastasis and Treatment</i> , 2019, 2019, .	0.5	9
868	Lectin-like transcript 1 as an natural killer cell-mediated immunotherapeutic target for triple negative breast cancer and prostate cancer. <i>Journal of Cancer Metastasis and Treatment</i> , 2019, 2019, .	0.5	2
869	Characterization of frequently mutated cancer genes in Chinese breast tumors: a comparison of Chinese and TCGA cohorts. <i>Annals of Translational Medicine</i> , 2019, 7, 179-179.	0.7	56
870	Therapeutic Targeting of Cancers with Loss of PTEN Function. <i>Current Drug Targets</i> , 2014, 15, 65-79.	1.0	194
871	BRCA Mutational Status is a Promising Predictive Biomarker for Platinum-based Chemotherapy in Triple-Negative Breast Cancer. <i>Current Drug Targets</i> , 2020, 21, 962-973.	1.0	8
872	Computational Approaches to Predict the Non-canonical DNAs. <i>Current Bioinformatics</i> , 2019, 14, 470-479.	0.7	7
873	Human Cancer Modeling: Recapitulating Tumor Heterogeneity Towards Personalized Medicine. <i>Multidisciplinary Cancer Investigation</i> , 2017, 1, 3-12.	0.1	3
874	DNA Methylation in Breast Tumor from High-risk Women in the Breast Cancer Family Registry. <i>Anticancer Research</i> , 2017, 37, 659-664.	0.5	7
875	BRAF, KRAS and PIK3CA Mutation and Sensitivity to Trastuzumab in Breast Cancer Cell Line Model. <i>Asian Pacific Journal of Cancer Prevention</i> , 2017, 18, 2209-2213.	0.5	16
876	Mediator kinase module and human tumorigenesis. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2015, 50, 393-426.	2.3	88
877	Revealing the Complexity of Breast Cancer by Next Generation Sequencing. <i>Cancers</i> , 2015, 7, 2183-2200.	1.7	28
878	Clinical applications of next-generation sequencing in colorectal cancers. <i>World Journal of Gastroenterology</i> , 2013, 19, 6784.	1.4	29
879	Comprehensive identification and characterization of somatic copy number alterations in triple-negative breast cancer. <i>International Journal of Oncology</i> , 2020, 56, 522-530.	1.4	12

#	ARTICLE	IF	CITATIONS
880	Bioinformatics analysis of the expression of HOXC13 and its role in the prognosis of breast cancer. <i>Oncology Letters</i> , 2020, 19, 899-907.	0.8	13
881	ZW10 interacting kinetochore protein may serve as a prognostic biomarker for human breast cancer: An integrated bioinformatics analysis. <i>Oncology Letters</i> , 2020, 19, 2163-2174.	0.8	12
882	Many Breast Cancer Mutations Parallel Mutations in Known Viral Cancers. <i>Journal of Genomes and Exomes</i> , 0, 3, 17-35.	0.0	2
883	The Role of Genomic Profiling in Advanced Breast Cancer: The Two Faces of Janus. <i>Translational Oncogenomics</i> , 2016, Suppl. 1, 1-7.	1.7	2
884	Clinical Targeted Next-Generation sequencing Panels for Detection of Somatic Variants in Gliomas. <i>Cancer Research and Treatment</i> , 2020, 52, 41-50.	1.3	14
885	An Exploration of Mutation Status of Cancer Genes in Breast Cancers. <i>Journal of Next Generation Sequencing & Applications</i> , 2014, 01, .	0.3	2
886	The False Paradigm of RUNX3 Function as Tumor Suppressor in Gastric Cancer. <i>Journal of Cancer Therapy</i> , 2013, 04, 16-25.	0.1	4
887	Preventive and Risk Reduction Strategies for Women at High Risk of Developing Breast Cancer: a Review. <i>Asian Pacific Journal of Cancer Prevention</i> , 2016, 17, 895-904.	0.5	7
888	Premature polyadenylation of MAGI3 produces a dominantly-acting oncogene in human breast cancer. <i>ELife</i> , 2016, 5, .	2.8	20
889	Novel insights into breast cancer copy number genetic heterogeneity revealed by single-cell genome sequencing. <i>ELife</i> , 2020, 9, .	2.8	47
890	Small Molecule Kinase Inhibitor Drugs (1995â€“2021): Medical Indication, Pharmacology, and Synthesis. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 1047-1131.	2.9	114
891	An Introduction to Molecular Pathology. , 2002, , 15-36.		0
892	MAGI Scaffolding Molecules Involved in Cancer Cell Signaling. <i>Journal of Carcinogenesis & Mutagenesis</i> , 0, , .	0.3	1
894	Breast: Ductal carcinoma. <i>Atlas of Genetics and Cytogenetics in Oncology and Haematology</i> , 2013, , .	0.1	2
895	Abstract 549: MAGI3-Akt3, a novel fusion protein in the PI 3-K pathway in cancer.. , 2013, , .		0
896	Translating Genomic Research into Clinical Practice: Promise and Pitfalls. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2013, , 15-23.	1.8	4
897	Molecular Testing in Breast Cancer. , 2014, , 169-188.		0
898	Omics of Hereditary Breast Cancer. , 2014, , 17-40.		0

#	ARTICLE	IF	CITATIONS
899	Are mutations in K-RAS, BRAF and PIK3CA genes critical for response to adjuvant trastuzumab treatment in patients with HER-2 positive breast cancer?. Journal of Cancer Therapeutics & Research, 2014, 3, 3.	1.2	2
900	Next Generation Sequencing in Cancer Research and Clinical Application. , 2014, , 71-94.		1
901	Genomic Applications in Breast Carcinoma. , 2015, , 359-382.		0
903	Early Biomarkers in Breast Cancer. , 2015, , 61-142.		0
904	Next-Generation Sequencing Applications in Head and Neck Oncology. , 2015, , 401-422.		0
906	Molecular Pathology of Lobular Carcinoma. Molecular Pathology Library, 2015, , 95-105.	0.1	0
907	Critical Roles of the AKT Substrate Girdin in Disease Initiation and Progression. , 2015, , 233-250.		0
909	Genomic Markers in ER-Negative Breast Cancer. , 2016, , 283-298.		0
910	Next-Generation Sequencing Based Testing for Breast Cancer. , 2016, , 299-328.		0
916	The Unfolded Protein Response in Triple-Negative Breast Cancer. Cancer Drug Discovery and Development, 2019, , 133-161.	0.2	0
921	Expression of MTERF3 gene in breast carcinoma and the relationship with clinicopathological characteristics. Translational Cancer Research, 2020, 9, 173-186.	0.4	2
925	Novel temporal and spatial patterns of metastatic colonization from breast cancer rapid-autopsy tumor biopsies. Genome Medicine, 2021, 13, 170.	3.6	5
926	Current and Emerging Molecular Therapies for Head and Neck Squamous Cell Carcinoma. Cancers, 2021, 13, 5471.	1.7	18
927	Molecular-Genetic Portrait of Breast Cancer with Triple Negative Phenotype. Cancers, 2021, 13, 5348.	1.7	4
928	The Multiple Interactions of RUNX with the Hippo-YAP Pathway. Cells, 2021, 10, 2925.	1.8	16
931	Dissecting the heterogeneity and tumorigenesis of BRCA1 deficient mammary tumors via single cell RNA sequencing. Theranostics, 2021, 11, 9967-9987.	4.6	6
933	PHENOTYPIC CHARACTERISTIC OF THE DENDRITIC CELLS GENERATED FROM PERIPHERAL BLOOD MONOCYTES IN PATIENTS WITH TRIPLE-NEGATIVE BREAST CANCER. Bulletin of Problems Biology and Medicine, 2020, 2, 124.	0.0	0
935	Effects of Long-Term In Vitro Expansion on Genetic Stability and Tumor Formation Capacity of Stem Cells. Stem Cell Reviews and Reports, 2021, , 1.	1.7	1

#	ARTICLE	IF	CITATIONS
936	Discovery of a novel potentially transforming somatic mutation in <i>CSF2RB</i> gene in breast cancer. <i>Cancer Medicine</i> , 2021, 10, 8138-8150.	1.3	6
937	mRNA Expressions of Specific Gamma-Glutamyl Transferases in Molecular Subtypes of Breast Cancer. <i>Athens Journal of Health & Medical Sciences</i> , 2020, 7, 157-170.	0.1	0
940	Correlation of Notch1, pAKT and nuclear NF- κ B expression in triple negative breast cancer. <i>American Journal of Cancer Research</i> , 2013, 3, 230-9.	1.4	22
941	Monitoring response to therapy in patients with cancer: is circulating DNA the answer?. <i>Annals of Translational Medicine</i> , 2013, 1, 24.	0.7	2
943	Special suppressive role of miR-29b in HER2-positive breast cancer cells by targeting Stat3. <i>American Journal of Translational Research (discontinued)</i> , 2015, 7, 878-90.	0.0	19
944	Frequency of Human Papillomavirus Genotypes 6, 11, 16, 18 And 31 in Paraffin-Embedded Tissue Samples of Invasive Breast Carcinoma, North- East of Iran. <i>Iranian Journal of Pathology</i> , 2015, 10, 192-8.	0.2	10
945	Knockdown of eIF3D inhibits breast cancer cell proliferation and invasion through suppressing the Wnt/ β 2-catenin signaling pathway. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 10420-7.	0.5	18
946	ING5 inhibits epithelial-mesenchymal transition in breast cancer by suppressing PI3K/Akt pathway. <i>International Journal of Clinical and Experimental Medicine</i> , 2015, 8, 15498-505.	1.3	20
947	Profiling the epigenetic interplay of lncRNA RUNXOR and oncogenic RUNX1 in breast cancer cells by gene in situ cis-activation. <i>American Journal of Cancer Research</i> , 2019, 9, 1635-1649.	1.4	8
948	Differential distribution of immune cells in breast invasive carcinoma vs. breast carcinoma and its significance in interpretation of immune surveillance. <i>International Journal of Clinical and Experimental Pathology</i> , 2017, 10, 7743-7749.	0.5	1
949	The Role of RUNX1 in NF1-Related Tumors and Blood Disorders. <i>Molecules and Cells</i> , 2020, 43, 153-159.	1.0	0
950	Detection of Genetic Polymorphism of HER2 Gene in HER2 Positive Breast Cancer Women in Iraq. <i>Iraqi Journal of Science</i> , 0, , 3507-3520.	0.3	0
951	Nuclear Morphological Characteristics in Breast Cancer: Correlation with Hormone Receptor and Human Epidermal Growth Factor Receptor 2. <i>Analytical Cellular Pathology</i> , 2021, 2021, 1-10.	0.7	1
952	Mutational signatures in GATA3 transcription factor and its DNA binding domain that stimulate breast cancer and HDR syndrome. <i>Scientific Reports</i> , 2021, 11, 22762.	1.6	1
954	A Runx1-enhancer Element eR1 Identified Lineage Restricted Mammary Luminal Stem Cells. <i>Stem Cells</i> , 2022, 40, 112-122.	1.4	6
955	The role of mediator subunit 12 in tumorigenesis and cancer therapeutics (Review). <i>Oncology Letters</i> , 2022, 23, 74.	0.8	6
956	p21 activated kinase-1 and tamoxifen “ A deadly nexus impacting breast cancer outcomes. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2022, 1877, 188668.	3.3	8
957	The SF3B1R625H mutation promotes prolactinoma tumor progression through aberrant splicing of DLG1. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 26.	3.5	11

#	ARTICLE	IF	CITATIONS
958	Retinoblastoma protein regulates carcinogen susceptibility at heterochromatic cancer driver loci. <i>Life Science Alliance</i> , 2022, 5, e202101134.	1.3	4
959	Role and Involvement of TENM4 and miR-708 in Breast Cancer Development and Therapy. <i>Cells</i> , 2022, 11, 172.	1.8	4
960	Blood Circulating Non-Coding RNAs for the Clinical Management of Triple-Negative Breast Cancer. <i>Cancers</i> , 2022, 14, 803.	1.7	5
961	Toxicogenomics for the prediction of carcinogenicity of xenobiotic substances. , 2022, , 283-306.		0
962	Discovering the Triad between Nav1.5, Breast Cancer, and the Immune System: A Fundamental Review and Future Perspectives. <i>Biomolecules</i> , 2022, 12, 310.	1.8	2
963	Systematic review and meta-analysis of genomic alterations in acral melanoma. <i>Pigment Cell and Melanoma Research</i> , 2022, 35, 369-386.	1.5	6
964	Zero-Inflated Poisson Models with Measurement Error in the Response. <i>Biometrics</i> , 2023, 79, 1089-1102.	0.8	1
965	The Novel Role of Cytomorphology from Ultrasound-Guided Fine Needle Aspiration Cytology in Evaluating the Status of Prognostic Factors including Estrogen Receptor, Progesterone Receptor and HER2 in Breast Cancer. <i>Analytical Cellular Pathology</i> , 2022, 2022, 1-8.	0.7	1
966	A Comprehensive Survey of Genomic Mutations in Breast Cancer Reveals Recurrent Neoantigens as Potential Therapeutic Targets. <i>Frontiers in Oncology</i> , 2022, 12, 786438.	1.3	6
967	Rearrangement processes and structural variations show evidence of selection in oesophageal adenocarcinomas. <i>Communications Biology</i> , 2022, 5, 335.	2.0	8
969	Subclonal heterogeneity and evolution in breast cancer. <i>Npj Breast Cancer</i> , 2021, 7, 155.	2.3	23
970	Somatic Mutational Profile of High-Grade Serous Ovarian Carcinoma and Triple-Negative Breast Carcinoma in Young and Elderly Patients: Similarities and Divergences. <i>Cells</i> , 2021, 10, 3586.	1.8	6
971	Panel Informativity Optimizer. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 697-709.	1.2	2
972	Response of Leptomeningeal Metastasis of Breast Cancer With a HER2/neu Activating Variant to Tucatinib: A Case Report. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2022, 20, 745-752.	2.3	7
1012	RASGRF1 Fusions Activate Oncogenic RAS Signaling and Confer Sensitivity to MEK Inhibition. <i>Clinical Cancer Research</i> , 2022, 28, 3091-3103.	3.2	8
1014	From genomic data analysis to drug development: a new generation of trials using molecular marker assessment in breast cancer. <i>Chinese Clinical Oncology</i> , 2014, 3, 16.	0.4	3
1016	Targeting biologically specific molecules in triple negative breast cancer (TNBC). , 2022, , 177-200.		7
1017	Novel biomarkers in triple-negative breast cancer - role and perspective. , 2022, , 29-60.		1

#	ARTICLE	IF	CITATIONS
1018	Current situation of programmed cell death protein 1/programmed cell death ligand 1 inhibitors in advanced triple-negative breast cancer. Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research, 2022, 34, 117-130.	0.7	2
1019	RUNX1 as a Novel Molecular Target for Breast Cancer. Clinical Breast Cancer, 2022, 22, 499-506.	1.1	7
1020	Dynamic Meta-data Network Sparse PCA for Cancer Subtype Biomarker Screening. Frontiers in Genetics, 2022, 13, .	1.1	0
1021	Single-cell analysis reveals the Comma-1D cell line as a unique model for mammary gland development and breast cancer. Journal of Cell Science, 2022, 135, .	1.2	2
1022	Mutational landscape of nasopharyngeal carcinoma based on targeted next-generation sequencing: implications for predicting clinical outcomes. Molecular Medicine, 2022, 28, 55.	1.9	2
1023	OMEN: network-based driver gene identification using mutual exclusivity. Bioinformatics, 2022, 38, 3245-3251.	1.8	4
1024	Frequent 4EBP1 Amplification Induces Synthetic Dependence on FGFR Signaling in Cancer. Cancers, 2022, 14, 2397.	1.7	1
1025	Heritable genomic diversity in breast cancer driver genes and associations with risk in a Chilean population. Biological Research, 2022, 55, .	1.5	1
1026	Promising Therapeutic Impact of a Selective Estrogen Receptor Downregulator, Fulvestrant, as Demonstrated In Vitro upon Low-Grade Serous Ovarian Carcinoma Cell Lines. Current Oncology, 2022, 29, 4020-4033.	0.9	0
1027	Serial Tumor Molecular Profiling of Newly Diagnosed HER2-Negative Breast Cancers During Chemotherapy in Combination with Angiogenesis Inhibitors. Targeted Oncology, 2022, 17, 355-368.	1.7	1
1028	Update on prognostic and predictive biomarkers of breast cancer. Seminars in Diagnostic Pathology, 2022, 39, 322-332.	1.0	20
1029	MUC1 expressing tumor growth was retarded after human mucin 1 (MUC1) plasmid DNA immunization. International Journal of Immunopathology and Pharmacology, 2022, 36, 039463202211123.	1.0	0
1030	Biological Random Walks: multi-omics integration for disease gene prioritization. Bioinformatics, 2022, 38, 4145-4152.	1.8	4
1031	Association of Pathway Mutations With Survival in Taiwanese Breast Cancers. Frontiers in Oncology, 0, 12, .	1.3	2
1032	Emerging Trends in Bioinformatics for Breast Cancer Molecular Research. , 2022, , 86-108.		0
1033	Immunology and immunotherapy in breast cancer. Cancer Biology and Medicine, 2022, 19, 609-618.	1.4	10
1034	Design and Validation of Nanofibers Made of Self-Assembled Peptides to Become Multifunctional Stimuli-Sensitive Nanovectors of Anticancer Drug Doxorubicin. Pharmaceutics, 2022, 14, 1544.	2.0	14
1035	Prevalence of Estrogen Receptor Alpha (<i>ESR1</i>) Somatic Mutations in Breast Cancer. JNCI Cancer Spectrum, 0, , .	1.4	0

#	ARTICLE	IF	CITATIONS
1037	PI3K/AKT/mTOR-Targeted Therapy for Breast Cancer. <i>Cells</i> , 2022, 11, 2508.	1.8	42
1038	ABL kinases regulate translation in HER2+ cells through Y-box-binding protein 1 to facilitate colonization of the brain. <i>Cell Reports</i> , 2022, 40, 111268.	2.9	5
1040	Crosstalk between CXCR4/ACKR3 and EGFR Signaling in Breast Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11887.	1.8	1
1041	A Case Series Exploration of Multi-Regional Expression Heterogeneity in Triple-Negative Breast Cancer Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13322.	1.8	2
1042	Voltage imaging reveals the dynamic electrical signatures of human breast cancer cells. <i>Communications Biology</i> , 2022, 5, .	2.0	12
1043	Designing a humanized immunotoxin based on DELTA-stichotoxin-Hmg2a toxin: an in silico study. <i>Journal of Molecular Modeling</i> , 2022, 28, .	0.8	1
1044	RUNX Proteins as Epigenetic Modulators in Cancer. <i>Cells</i> , 2022, 11, 3687.	1.8	5
1045	Using ensemble learning and genetic algorithm on magnetic resonance imaging radiomics to classify molecular subtypes of breast cancer. <i>Precision Medical Sciences</i> , 0, .	0.1	0
1046	SETD7 Expression Is Associated with Breast Cancer Survival Outcomes for Specific Molecular Subtypes: A Systematic Analysis of Publicly Available Datasets. <i>Cancers</i> , 2022, 14, 6029.	1.7	2
1047	An integrated investigation of structural and pathway alteration caused by PIK3CA and TP53 mutations identified in cfDNA of metastatic breast cancer. <i>Journal of Cellular Biochemistry</i> , 2023, 124, 188-204.	1.2	2
1048	Targeting the PI3K/AKT/mTOR and RAF/MEK/ERK pathways for cancer therapy. <i>Molecular Biomedicine</i> , 2022, 3, .	1.7	29
1049	Characterization of triple negative breast cancer gene expression profiles in Mexican patients. <i>Molecular and Clinical Oncology</i> , 2022, 18, .	0.4	1
1050	LncRNA Osilr9 coordinates promoter DNA demethylation and the intrachromosomal loop structure required for maintaining stem cell pluripotency. <i>Molecular Therapy</i> , 2023, 31, 1791-1806.	3.7	2
1051	DeteX: A highly accurate software for detecting SNV and InDel in single and paired NGS data in cancer research. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
1052	Early Triple-Negative Breast Cancers in a Singapore Cohort Exhibit High PIK3CA Mutation Rates Associated With Low PD-L1 Expression. <i>Modern Pathology</i> , 2023, 36, 100056.	2.9	2
1053	Predicting Tumor Mutation Burden of TNBC Based on Nuclei Scores of Histopathological Images. , 2022, , .		1
1054	A Bayesian model for identifying cancer subtypes from paired methylation profiles. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	0
1055	Genome-wide association studies demonstrate the genes associated with perimysial thickness in ducks. <i>Animal Genetics</i> , 2023, 54, 363-374.	0.6	3

#	ARTICLE	IF	CITATIONS
1056	RUNX3 in Stem Cell and Cancer Biology. <i>Cells</i> , 2023, 12, 408.	1.8	6
1057	HER2-driven breast cancer suppression by the JNK signaling pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	4
1058	Deciphering breast cancer: from biology to the clinic. <i>Cell</i> , 2023, 186, 1708-1728.	13.5	72
1059	A Rapid, Shallow Whole Genome Sequencing Workflow Applicable to Limiting Amounts of Cell-Free DNA. <i>Clinical Chemistry</i> , 2023, 69, 510-518.	1.5	2
1061	Heterologous prime-boost cellular vaccination induces potent antitumor immunity against triple negative breast cancer. <i>Frontiers in Immunology</i> , 0, 14, .	2.2	2
1062	The RUNX/CBF β Complex in Breast Cancer: A Conundrum of Context. <i>Cells</i> , 2023, 12, 641.	1.8	2
1063	Dysregulation of Mitochondrial Translation Caused by CBF β Deficiency Cooperates with Mutant PIK3CA and Is a Vulnerability in Breast Cancer. <i>Cancer Research</i> , 2023, 83, 1280-1298.	0.4	1
1064	Genetics, Treatment, and New Technologies of Hormone Receptor-Positive Breast Cancer. <i>Cancers</i> , 2023, 15, 1303.	1.7	2
1065	The complex nature of heterogeneity and its roles in breast cancer biology and therapeutic responsiveness. <i>Frontiers in Endocrinology</i> , 0, 14, .	1.5	4
1066	POP1 promotes the progression of breast cancer through maintaining telomere integrity. <i>Carcinogenesis</i> , 2023, 44, 252-262.	1.3	2
1067	The Role of Genetic Mutations in Mitochondrial-Driven Cancer Growth in Selected Tumors: Breast and Gynecological Malignancies. <i>Life</i> , 2023, 13, 996.	1.1	1
1082	Prediction of Cancer Driver Genes Based on Pyramidal Dynamic Mapping Algorithm. <i>Lecture Notes in Computer Science</i> , 2023, , 77-86.	1.0	0
1084	Protein-Protein Interactions in Cancer. , 2023, , 43-100.		0
1087	Molecular Mechanisms of Environmental Oncogenesis. , 2023, , 3-60.		0
1090	Consequences of gaining an extra chromosome. <i>Chromosome Research</i> , 2023, 31, .	1.0	3
1101	Mechanisms of Endocrine Resistance in Hormone Receptor-Positive Breast Cancer. <i>Cancer Treatment and Research</i> , 2023, , 219-235.	0.2	1