

Balazs Gyorffy

List of Publications by Year in descending order

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Version: 2024-02-01

254
papers

20,755
citations

19657

61
h-index

12272

133
g-index

283
all docs

283
docs citations

283
times ranked

31897
citing authors

#	ARTICLE	IF	CITATIONS
1	An online survival analysis tool to rapidly assess the effect of 22,277 genes on breast cancer prognosis using microarray data of 1,809 patients. <i>Breast Cancer Research and Treatment</i> , 2010, 123, 725-731.	2.5	2,480
2	Online Survival Analysis Software to Assess the Prognostic Value of Biomarkers Using Transcriptomic Data in Non-Small-Cell Lung Cancer. <i>PLoS ONE</i> , 2013, 8, e82241.	2.5	1,502
3	Validation of miRNA prognostic power in hepatocellular carcinoma using expression data of independent datasets. <i>Scientific Reports</i> , 2018, 8, 9227.	3.3	1,103
4	Cutoff Finder: A Comprehensive and Straightforward Web Application Enabling Rapid Biomarker Cutoff Optimization. <i>PLoS ONE</i> , 2012, 7, e51862.	2.5	983
5	Web-Based Survival Analysis Tool Tailored for Medical Research (KMplot): Development and Implementation. <i>Journal of Medical Internet Research</i> , 2021, 23, e27633.	4.3	852
6	Cross-validation of survival associated biomarkers in gastric cancer using transcriptomic data of 1,065 patients. <i>Oncotarget</i> , 2016, 7, 49322-49333.	1.8	821
7	Implementing an online tool for genome-wide validation of survival-associated biomarkers in ovarian-cancer using microarray data from 1287 patients. <i>Endocrine-Related Cancer</i> , 2012, 19, 197-208.	3.1	738
8	miRpower: a web-tool to validate survival-associated miRNAs utilizing expression data from 2178 breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2016, 160, 439-446.	2.5	678
9	Pancancer survival analysis of cancer hallmark genes. <i>Scientific Reports</i> , 2021, 11, 6047.	3.3	620
10	Survival analysis across the entire transcriptome identifies biomarkers with the highest prognostic power in breast cancer. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4101-4109.	4.1	436
11	TNMplot.com: A Web Tool for the Comparison of Gene Expression in Normal, Tumor and Metastatic Tissues. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2622.	4.1	420
12	Determining consistent prognostic biomarkers of overall survival and vascular invasion in hepatocellular carcinoma. <i>Royal Society Open Science</i> , 2018, 5, 181006.	2.4	320
13	Jetset: selecting the optimal microarray probe set to represent a gene. <i>BMC Bioinformatics</i> , 2011, 12, 474.	2.6	277
14	Multigene prognostic tests in breast cancer: past, present, future. <i>Breast Cancer Research</i> , 2015, 17, 11.	5.0	209
15	ROCplot.org: Validating predictive biomarkers of chemotherapy/hormonal therapy/anti-HER2 therapy using transcriptomic data of 3,104 breast cancer patients. <i>International Journal of Cancer</i> , 2019, 145, 3140-3151.	5.1	197
16	Iron Uptake via DMT1 Integrates Cell Cycle with JAK-STAT3 Signaling to Promote Colorectal Tumorigenesis. <i>Cell Metabolism</i> , 2016, 24, 447-461.	16.2	168
17	A meta-analysis of gene expression-based biomarkers predicting outcome after tamoxifen treatment in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 140, 219-232.	2.5	162
18	ADIPOQ/adiponectin induces cytotoxic autophagy in breast cancer cells through STK11/LKB1-mediated activation of the AMPK-ULK1 axis. <i>Autophagy</i> , 2017, 13, 1386-1403.	9.1	156

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19	Tumor-selective proteotoxicity of verteporfin inhibits colon cancer progression independently of YAP1. <i>Science Signaling</i> , 2015, 8, ra98.	3.6	152
20	Genome-wide reprogramming of the chromatin landscape underlies endocrine therapy resistance in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1490-9.	7.1	149
21	Cyclin-dependent kinase 8 mediates chemotherapy-induced tumor-promoting paracrine activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13799-13804.	7.1	146
22	Infiltrating T Cells Increase IDO1 Expression in Glioblastoma and Contribute to Decreased Patient Survival. <i>Clinical Cancer Research</i> , 2017, 23, 6650-6660.	7.0	141
23	Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. <i>International Journal of Cancer</i> , 2016, 138, 87-97.	5.1	136
24	Gene expression profiling of 30 cancer cell lines predicts resistance towards 11 anticancer drugs at clinically achieved concentrations. <i>International Journal of Cancer</i> , 2006, 118, 1699-1712.	5.1	133
25	miR-34a Silences c-SRC to Attenuate Tumor Growth in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2016, 76, 927-939.	0.9	128
26	Disruption of STAT3 signalling promotes KRAS-induced lung tumorigenesis. <i>Nature Communications</i> , 2015, 6, 6285.	12.8	124
27	Remodeling of central metabolism in invasive breast cancer compared to normal breast tissue – a GC-TOFMS based metabolomics study. <i>BMC Genomics</i> , 2012, 13, 334.	2.8	123
28	Different mutations in SARS-CoV-2 associate with severe and mild outcome. <i>International Journal of Antimicrobial Agents</i> , 2021, 57, 106272.	2.5	122
29	Systematic evaluation of the miRNAome and its downstream effects on mRNA expression identifies gastric cancer progression. <i>Journal of Pathology</i> , 2010, 222, 310-319.	4.5	117
30	Immune Gene Expression Is Associated with Genomic Aberrations in Breast Cancer. <i>Cancer Research</i> , 2017, 77, 3317-3324.	0.9	117
31	Tumor-associated macrophages (TAMs) depend on ZEB1 for their cancer-promoting roles. <i>EMBO Journal</i> , 2017, 36, 3336-3355.	7.8	112
32	Multi-omics approaches in cancer research with applications in tumor subtyping, prognosis, and diagnosis. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 949-960.	4.1	111
33	Differential epigenetic reprogramming in response to specific endocrine therapies promotes cholesterol biosynthesis and cellular invasion. <i>Nature Communications</i> , 2015, 6, 10044.	12.8	108
34	A prognostic gene expression index in ovarian cancer – validation across different independent data sets. <i>Journal of Pathology</i> , 2009, 218, 273-280.	4.5	107
35	APOBEC3B-Mediated Cytidine Deamination Is Required for Estrogen Receptor Action in Breast Cancer. <i>Cell Reports</i> , 2015, 13, 108-121.	6.4	105
36	Glutamate enrichment as new diagnostic opportunity in breast cancer. <i>International Journal of Cancer</i> , 2015, 136, 1619-1628.	5.1	103

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37	The PI3K inhibitor LY294002 blocks drug export from resistant colon carcinoma cells overexpressing MRP1. <i>Oncogene</i> , 2006, 25, 1743-1752.	5.9	102
38	Afatinib restrains K-RAS-driven lung tumorigenesis. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	99
39	Enhancer mapping uncovers phenotypic heterogeneity and evolution in patients with luminal breast cancer. <i>Nature Medicine</i> , 2018, 24, 1469-1480.	30.7	98
40	Inflammation, Adenoma and Cancer: Objective Classification of Colon Biopsy Specimens with Gene Expression Signature. <i>Disease Markers</i> , 2008, 25, 1-16.	1.3	92
41	Inhibition of CDK8 mediator kinase suppresses estrogen dependent transcription and the growth of estrogen receptor positive breast cancer. <i>Oncotarget</i> , 2017, 8, 12558-12575.	1.8	92
42	Classical pathology and mutational load of breast cancer – integration of two worlds. <i>Journal of Pathology: Clinical Research</i> , 2015, 1, 225-238.	3.0	91
43	Guidelines for the selection of functional assays to evaluate the hallmarks of cancer. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2016, 1866, 300-319.	7.4	89
44	RecurrenceOnline: an online analysis tool to determine breast cancer recurrence and hormone receptor status using microarray data. <i>Breast Cancer Research and Treatment</i> , 2012, 132, 1025-1034.	2.5	85
45	Activation of tumor suppressor LKB1 by honokiol abrogates cancer stem-like phenotype in breast cancer via inhibition of oncogenic Stat3. <i>Oncogene</i> , 2017, 36, 5709-5721.	5.9	81
46	Evaluation of Microarray Preprocessing Algorithms Based on Concordance with RT-PCR in Clinical Samples. <i>PLoS ONE</i> , 2009, 4, e5645.	2.5	80
47	Meta-analysis of gene expression profiles related to relapse-free survival in 1,079 breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2009, 118, 433-441.	2.5	78
48	Quantitative proteomics identifies STEAP4 as a critical regulator of mitochondrial dysfunction linking inflammation and colon cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9608-E9617.	7.1	77
49	FAK activity sustains intrinsic and acquired ovarian cancer resistance to platinum chemotherapy. <i>ELife</i> , 2019, 8, .	6.0	76
50	Predictors of Chemosensitivity in Triple Negative Breast Cancer: An Integrated Genomic Analysis. <i>PLoS Medicine</i> , 2016, 13, e1002193.	8.4	75
51	Gender-specific association of vitamin D receptor polymorphism combinations with type 1 diabetes mellitus. <i>European Journal of Endocrinology</i> , 2002, 147, 803-808.	3.7	74
52	Correlations of Differentially Expressed Gap Junction Connexins Cx26, Cx30, Cx32, Cx43 and Cx46 with Breast Cancer Progression and Prognosis. <i>PLoS ONE</i> , 2014, 9, e112541.	2.5	74
53	Systematic Analysis of AU-Rich Element Expression in Cancer Reveals Common Functional Clusters Regulated by Key RNA-Binding Proteins. <i>Cancer Research</i> , 2016, 76, 4068-4080.	0.9	74
54	Leptin as a mediator of tumor-stromal interactions promotes breast cancer stem cell activity. <i>Oncotarget</i> , 2016, 7, 1262-1275.	1.8	74

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55	HOXB7 Is an ER \pm Cofactor in the Activation of HER2 and Multiple ER Target Genes Leading to Endocrine Resistance. <i>Cancer Discovery</i> , 2015, 5, 944-959.	9.4	72
56	Prediction of doxorubicin sensitivity in breast tumors based on gene expression profiles of drug-resistant cell lines correlates with patient survival. <i>Oncogene</i> , 2005, 24, 7542-7551.	5.9	69
57	Gene signature of the metastatic potential of cutaneous melanoma: too much for too little?. <i>Clinical and Experimental Metastasis</i> , 2010, 27, 371-387.	3.3	69
58	Expression of CDK8 and CDK8-interacting Genes as Potential Biomarkers in Breast Cancer. <i>Current Cancer Drug Targets</i> , 2015, 15, 739-749.	1.6	67
59	Acquired cisplatin resistance in the head&neck cancer cell line Cal27 is associated with decreased DKK1 expression and can partially be reversed by overexpression of DKK1. <i>International Journal of Cancer</i> , 2008, 123, 2013-2019.	5.1	66
60	Combined Wnt/ β -Catenin, Met, and CXCL12/CXCR4 Signals Characterize Basal Breast Cancer and Predict Disease Outcome. <i>Cell Reports</i> , 2013, 5, 1214-1227.	6.4	66
61	Expression of CDK7, Cyclin H, and MAT1 Is Elevated in Breast Cancer and Is Prognostic in Estrogen Receptor&Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 5929-5938.	7.0	66
62	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.	8.2	65
63	<i>HUWE</i> 1 is a critical colonic tumour suppressor gene that prevents <i>MYC</i> signalling, <i>DNA</i> damage accumulation and tumour initiation. <i>EMBO Molecular Medicine</i> , 2017, 9, 181-197.	6.9	63
64	MultipleTesting.com: A tool for life science researchers for multiple hypothesis testing correction. <i>PLoS ONE</i> , 2021, 16, e0245824.	2.5	63
65	Integrated analysis of the immunological and genetic status in and across cancer types: impact of mutational signatures beyond tumor mutational burden. <i>Oncolmmunology</i> , 2018, 7, e1526613.	4.6	60
66	<i>TP53</i> mutation&correlated genes predict the risk of tumor relapse and identify <i>MPS1</i> as a potential therapeutic kinase in <i>TP53</i> &mutated breast cancers. <i>Molecular Oncology</i> , 2014, 8, 508-519.	4.6	59
67	Synaptic mitochondria: A brain mitochondria cluster with a specific proteome. <i>Journal of Proteomics</i> , 2015, 120, 142-157.	2.4	59
68	BCL9/ β -catenin Signaling is Associated With Poor Outcome in Colorectal Cancer. <i>EBioMedicine</i> , 2015, 2, 1932-1943.	6.1	58
69	Low level of exosomal long non-coding RNA <i>HOTTIP</i> is a prognostic biomarker in colorectal cancer. <i>RNA Biology</i> , 2019, 16, 1339-1345.	3.1	58
70	Expression and Function of Phosphodiesterase Type 5 in Human Breast Cancer Cell Lines and Tissues: Implications for Targeted Therapy. <i>Clinical Cancer Research</i> , 2016, 22, 2271-2282.	7.0	55
71	JAK&STAT inhibition impairs <i>KRAS</i> &driven lung adenocarcinoma progression. <i>International Journal of Cancer</i> , 2019, 145, 3376-3388.	5.1	54
72	<i>muTarget</i> : A platform linking gene expression changes and mutation status in solid tumors. <i>International Journal of Cancer</i> , 2021, 148, 502-511.	5.1	53

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73	MEK1 is associated with carboplatin resistance and is a prognostic biomarker in epithelial ovarian cancer. BMC Cancer, 2014, 14, 837.	2.6	52
74	HOXC10 Expression Supports the Development of Chemotherapy Resistance by Fine Tuning DNA Repair in Breast Cancer Cells. Cancer Research, 2016, 76, 4443-4456.	0.9	52
75	Predictive biomarkers of platinum and taxane resistance using the transcriptomic data of 1816 ovarian cancer patients. Gynecologic Oncology, 2020, 156, 654-661.	1.4	51
76	Identification of a claudin-4 and E-cadherin score to predict prognosis in breast cancer. Cancer Science, 2011, 102, 2248-2254.	3.9	50
77	A Comprehensive Overview of Targeted Therapy in Metastatic Renal Cell Carcinoma. Current Cancer Drug Targets, 2012, 12, 857-872.	1.6	49
78	Discovery of a Glucocorticoid Receptor (GR) Activity Signature Using Selective GR Antagonism in ER-Negative Breast Cancer. Clinical Cancer Research, 2018, 24, 3433-3446.	7.0	49
79	Multivariate analysis of oestrogen receptor alpha, pS2, metallothionein and CD24 expression in invasive breast cancers. British Journal of Cancer, 2006, 95, 339-346.	6.4	47
80	New network topology approaches reveal differential correlation patterns in breast cancer. BMC Systems Biology, 2013, 7, 78.	3.0	47
81	TP53 mutation hits energy metabolism and increases glycolysis in breast cancer. Oncotarget, 2016, 7, 67183-67195.	1.8	46
82	Elevated HOX gene expression in acute myeloid leukemia is associated with NPM1 mutations and poor survival. Journal of Advanced Research, 2019, 20, 105-116.	9.5	45
83	The pioneer factor PBX1 is a novel driver of metastatic progression in ER \pm -positive breast cancer. Oncotarget, 2015, 6, 21878-21891.	1.8	45
84	DNA methylation-based diagnostic, prognostic, and predictive biomarkers in colorectal cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2022, 1877, 188722.	7.4	45
85	Parallel Evolution under Chemotherapy Pressure in 29 Breast Cancer Cell Lines Results in Dissimilar Mechanisms of Resistance. PLoS ONE, 2012, 7, e30804.	2.5	44
86	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. Genome Medicine, 2010, 2, 53.	8.2	43
87	MLL-fusion-driven leukemia requires SETD2 to safeguard genomic integrity. Nature Communications, 2018, 9, 1983.	12.8	43
88	A Comprehensive Outline of Trastuzumab Resistance Biomarkers in HER2 Overexpressing Breast Cancer. Current Cancer Drug Targets, 2015, 15, 665-683.	1.6	42
89	The critical role of the ZNF217 oncogene in promoting breast cancer metastasis to the bone. Journal of Pathology, 2017, 242, 73-89.	4.5	42
90	SREBP1 drives Keratin-80-dependent cytoskeletal changes and invasive behavior in endocrine-resistant ER \pm breast cancer. Nature Communications, 2019, 10, 2115.	12.8	42

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91	RNA-binding protein NONO contributes to cancer cell growth and confers drug resistance as a theranostic target in TNBC. <i>Theranostics</i> , 2020, 10, 7974-7992.	10.0	42
92	Molecular stratifications, biomarker candidates and new therapeutic options in current medulloblastoma treatment approaches. <i>Cancer and Metastasis Reviews</i> , 2020, 39, 211-233.	5.9	42
93	Survival analysis in breast cancer using proteomic data from four independent datasets. <i>Scientific Reports</i> , 2021, 11, 16787.	3.3	42
94	PSMB7 is associated with anthracycline resistance and is a prognostic biomarker in breast cancer. <i>British Journal of Cancer</i> , 2010, 102, 361-368.	6.4	41
95	Meta-analysis of gene expression profiles associated with histological classification and survival in 829 ovarian cancer samples. <i>International Journal of Cancer</i> , 2012, 131, 95-105.	5.1	41
96	Current composite-feature classification methods do not outperform simple single-genes classifiers in breast cancer prognosis. <i>Frontiers in Genetics</i> , 2013, 4, 289.	2.3	41
97	Type I IFN induces protein ISGylation to enhance cytokine expression and augments colonic inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14313-14318.	7.1	41
98	Deciphering and Targeting Oncogenic Mutations and Pathways in Breast Cancer. <i>Oncologist</i> , 2016, 21, 1063-1078.	3.7	41
99	AXL-associated tumor inflammation as a poor prognostic signature in chemotherapy-treated triple-negative breast cancer patients. <i>Npj Breast Cancer</i> , 2016, 2, 16033.	5.2	41
100	Molecular markers and potential therapeutic targets in non-WNT/non-SHH (group 3 and group 4) medulloblastomas. <i>Journal of Hematology and Oncology</i> , 2019, 12, 29.	17.0	41
101	A Web-Based Data Warehouse on Gene Expression in Human Malignant Melanoma. <i>Journal of Investigative Dermatology</i> , 2007, 127, 394-399.	0.7	40
102	<i>Helicobacter pylori</i> and Antrum Erosion-Specific Gene Expression Patterns: The Discriminative Role of CXCL13 and VCAM1 Transcripts. <i>Helicobacter</i> , 2008, 13, 112-126.	3.5	40
103	Association of PDCD1 and CTLA-4 Gene Expression with Clinicopathological Factors and Survival in Non-Small-Cell Lung Cancer: Results from a Large and Pooled Microarray Database. <i>Journal of Thoracic Oncology</i> , 2015, 10, 1020-1026.	1.1	38
104	ABCC2 (MRP2, cMOAT) Localized in the Nuclear Envelope of Breast Carcinoma Cells Correlates with Poor Clinical Outcome. <i>Pathology and Oncology Research</i> , 2012, 18, 331-342.	1.9	37
105	BRD4 Regulates Metastatic Potential of Castration-Resistant Prostate Cancer through AHNK. <i>Molecular Cancer Research</i> , 2019, 17, 1627-1638.	3.4	37
106	Research funding: past performance is a stronger predictor of future scientific output than reviewer scores. <i>Journal of Informetrics</i> , 2020, 14, 101050.	2.9	36
107	Expression of MHC class I, HLA-A and HLA-B identifies immune-activated breast tumors with favorable outcome. <i>Oncolimmunology</i> , 2019, 8, e1629780.	4.6	34
108	Loss of estrogen receptor beta expression correlates with shorter overall survival and lack of clinical response to chemotherapy in ovarian cancer patients. <i>Anticancer Research</i> , 2011, 31, 711-8.	1.1	34

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109	ZEB1-induced tumourigenesis requires senescence inhibition via activation of DKK1/mutant p53/Mdm2/CtBP and repression of macroH2A1. <i>Gut</i> , 2017, 66, 666-682.	12.1	33
110	Stromal myofibroblasts in breast cancer: relations between their occurrence, tumor grade and expression of some tumour markers. <i>Folia Histochemica Et Cytobiologica</i> , 2006, 44, 111-6.	1.5	33
111	A functional interplay between ZNF217 and Estrogen Receptor alpha exists in luminal breast cancers. <i>Molecular Oncology</i> , 2014, 8, 1441-1457.	4.6	32
112	Proteomic identification of prognostic tumour biomarkers, using chemotherapy-induced cancer-associated fibroblasts. <i>Aging</i> , 2015, 7, 816-838.	3.1	32
113	Prognostic value of DLGAP5 in colorectal cancer. <i>International Journal of Colorectal Disease</i> , 2019, 34, 1455-1465.	2.2	32
114	FOXM1 functions collaboratively with PLAU to promote gastric cancer progression. <i>Journal of Cancer</i> , 2020, 11, 788-794.	2.5	32
115	Shp2 signaling suppresses senescence in <i>PyMT</i> -induced mammary gland cancer in mice. <i>EMBO Journal</i> , 2015, 34, 1493-1508.	7.8	31
116	Acid ceramidase is associated with an improved prognosis in both DCIS and invasive breast cancer. <i>Molecular Oncology</i> , 2015, 9, 58-67.	4.6	31
117	Identifying Cancers Impacted by CDK8/19. <i>Cells</i> , 2019, 8, 821.	4.1	31
118	Single-nucleotide polymorphisms of VEGF gene are associated with risk of congenital valvuloseptal heart defects. <i>American Heart Journal</i> , 2006, 151, 878-881.	2.7	30
119	Expression of classical NF- κ B pathway effectors in human ovarian carcinoma. <i>Histopathology</i> , 2010, 56, 727-739.	2.9	30
120	Demographic shift disproportionately increases cancer burden in an aging nation: current and expected incidence and mortality in Hungary up to 2030. <i>Clinical Epidemiology</i> , 2018, Volume 10, 1093-1108.	3.0	30
121	DUSP4 is associated with increased resistance against anti-HER2 therapy in breast cancer. <i>Oncotarget</i> , 2017, 8, 77207-77218.	1.8	30
122	Elevated BUBR1 Expression Is Associated with Poor Survival in Early Breast Cancer Patients. <i>Journal of Histochemistry and Cytochemistry</i> , 2013, 61, 330-339.	2.5	28
123	KRAS driven expression signature has prognostic power superior to mutation status in non-small cell lung cancer. <i>International Journal of Cancer</i> , 2017, 140, 930-937.	5.1	28
124	The CIN4 Chromosomal Instability qPCR Classifier Defines Tumor Aneuploidy and Stratifies Outcome in Grade 2 Breast Cancer. <i>PLoS ONE</i> , 2013, 8, e56707.	2.5	28
125	Transcriptomic immunologic signature associated with favorable clinical outcome in basal-like breast tumors. <i>PLoS ONE</i> , 2017, 12, e0175128.	2.5	28
126	Benzyl Isothiocyanate potentiates p53 signaling and antitumor effects against breast cancer through activation of p53-LKB1 and p73-LKB1 axes. <i>Scientific Reports</i> , 2017, 7, 40070.	3.3	27

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127	Activation of Farnesoid X Receptor impairs the tumor-promoting function of breast cancer-associated fibroblasts. <i>Cancer Letters</i> , 2018, 437, 89-99.	7.2	27
128	Comprehensive Outline of Whole Exome Sequencing Data Analysis Tools Available in Clinical Oncology. <i>Cancers</i> , 2019, 11, 1725.	3.7	27
129	Examination of Hardy-Weinberg equilibrium in papers of <i>Kidney International</i> : An underused tool. <i>Kidney International</i> , 2004, 65, 1956-1958.	5.2	26
130	Biomarkers Downstream of RAS: A Search for Robust Transcriptional Targets. <i>Current Cancer Drug Targets</i> , 2010, 10, 858-868.	1.6	26
131	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.	6.4	26
132	Phosphodiesterase 5 (PDE5) Is Highly Expressed in Cancer-Associated Fibroblasts and Enhances Breast Tumor Progression. <i>Cancers</i> , 2019, 11, 1740.	3.7	26
133	SETD3 acts as a prognostic marker in breast cancer patients and modulates the viability and invasion of breast cancer cells. <i>Scientific Reports</i> , 2020, 10, 2262.	3.3	26
134	A Transcriptomic Immunologic Signature Predicts Favorable Outcome in Neoadjuvant Chemotherapy Treated Triple Negative Breast Tumors. <i>Frontiers in Immunology</i> , 2019, 10, 2802.	4.8	24
135	BRD4 regulates key transcription factors that drive epithelialâ€mesenchymal transition in castration-resistant prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 268-277.	3.9	24
136	HIF-3Î±1 promotes colorectal tumor cell growth by activation of JAK-STAT3 signaling. <i>Oncotarget</i> , 2016, 7, 11567-11579.	1.8	24
137	Colon cancer subtypes: concordance, effect on survival and selection of the most representative preclinical models. <i>Scientific Reports</i> , 2016, 6, 37169.	3.3	23
138	Mutations Defining Patient Cohorts With Elevated PD-L1 Expression in Gastric Cancer. <i>Frontiers in Pharmacology</i> , 2018, 9, 1522.	3.5	23
139	Use of Routinely Collected Amniotic Fluid for Whole-Genome Expression Analysis of Polygenic Disorders. <i>Clinical Chemistry</i> , 2006, 52, 1013-1020.	3.2	22
140	Transcription Factor ZBP-89 Drives a Feedforward Loop of Î²-Catenin Expression in Colorectal Cancer. <i>Cancer Research</i> , 2016, 76, 6877-6887.	0.9	22
141	Integrated molecular analysis of Tamoxifen-resistant invasive lobular breast cancer cells identifies MAPK and GRM/mGluR signaling as therapeutic vulnerabilities. <i>Molecular and Cellular Endocrinology</i> , 2018, 471, 105-117.	3.2	22
142	<i>linc00673 (ERLR01)</i> is a prognostic indicator of overall survival in breast cancer. <i>Transcription</i> , 2018, 9, 17-29.	3.1	22
143	Genomic Mapping Identifies Mutations in RYR2 and AHNK as Associated with Favorable Outcome in Basal-Like Breast Tumors Expressing PD1/PD-L1. <i>Cancers</i> , 2020, 12, 2243.	3.7	22
144	Evidence for Enhanced Exosome Production in Aromatase Inhibitor-Resistant Breast Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5841.	4.1	22

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145	Improving Pathological Assessment of Breast Cancer by Employing Array-Based Transcriptome Analysis. <i>Microarrays</i> (Basel, Switzerland), 2013, 2, 228-242.	1.4	21
146	Identifying Resistance Mechanisms against Five Tyrosine Kinase Inhibitors Targeting the ERBB/RAS Pathway in 45 Cancer Cell Lines. <i>PLoS ONE</i> , 2013, 8, e59503.	2.5	21
147	Gene expression-based biomarkers designating glioblastomas resistant to multiple treatment strategies. <i>Carcinogenesis</i> , 2021, 42, 804-813.	2.8	21
148	Brain protein expression changes in WAG/Rij rats, a genetic rat model of absence epilepsy after peripheral lipopolysaccharide treatment. <i>Brain, Behavior, and Immunity</i> , 2014, 35, 86-95.	4.1	20
149	Genomic Signatures of Immune Activation Predict Outcome in Advanced Stages of Ovarian Cancer and Basal-Like Breast Tumors. <i>Frontiers in Oncology</i> , 2019, 9, 1486.	2.8	20
150	Dynamin impacts homology-directed repair and breast cancer response to chemotherapy. <i>Journal of Clinical Investigation</i> , 2018, 128, 5307-5321.	8.2	20
151	Oncogene-mediated metabolic gene signature predicts breast cancer outcome. <i>Npj Breast Cancer</i> , 2021, 7, 141.	5.2	20
152	Effects of RAL signal transduction in KRAS- and BRAF-mutated cells and prognostic potential of the RAL signature in colorectal cancer. <i>Oncotarget</i> , 2015, 6, 13334-13346.	1.8	19
153	Immunohistochemical Ki67 after short-term hormone therapy identifies low-risk breast cancers as reliably as genomic markers. <i>Oncotarget</i> , 2017, 8, 26122-26128.	1.8	19
154	The cell cycle-related genes RHAMM, AURKA, TPX2, PLK1, and PLK4 are associated with the poor prognosis of breast cancer patients. <i>Journal of Cellular Biochemistry</i> , 2022, 123, 581-600.	2.6	19
155	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.	4.1	18
156	Induction of cell cycle arrest and inflammatory genes by combined treatment with epigenetic, differentiating, and chemotherapeutic agents in triple-negative breast cancer. <i>Breast Cancer Research</i> , 2018, 20, 145.	5.0	18
157	Induction of APOBEC3B expression by chemotherapy drugs is mediated by DNA-PK-directed activation of NF- κ B. <i>Oncogene</i> , 2021, 40, 1077-1090.	5.9	18
158	Mitotic read-out genes confer poor outcome in luminal A breast cancer tumors. <i>Oncotarget</i> , 2017, 8, 21733-21740.	1.8	18
159	Enhanced Immunoreactivity of TIMP-2 in the Stromal Compartment of Tumor as a Marker of Favorable Prognosis in Ovarian Cancer Patients. <i>Journal of Histochemistry and Cytochemistry</i> , 2012, 60, 491-501.	2.5	17
160	Cancer heterogeneity determined by functional proteomics. <i>Seminars in Cell and Developmental Biology</i> , 2017, 64, 132-142.	5.0	17
161	Principles of tumorigenesis and emerging molecular drivers of SHH-activated medulloblastomas. <i>Annals of Clinical and Translational Neurology</i> , 2019, 6, 990-1005.	3.7	17
162	COVIDOUTCOME-estimating COVID severity based on mutation signatures in the SARS-CoV-2 genome. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	17

#	ARTICLE	IF	CITATIONS
163	Comparison of 5 Ki-67 antibodies regarding reproducibility and capacity to predict prognosis in breast cancer: does the antibody matter?. Human Pathology, 2017, 65, 31-40.	2.0	16
164	Genetic mutational status of genes regulating epigenetics: Role of the histone methyltransferase KMT2D in triple negative breast tumors. PLoS ONE, 2019, 14, e0209134.	2.5	16
165	In silico transcriptomic mapping of integrins and immune activation in Basal-like and HER2+ breast cancer. Cellular Oncology (Dordrecht), 2021, 44, 569-580.	4.4	16
166	TGF- β 1 potentiates V β 9V β 2 T cell adoptive immunotherapy of cancer. Cell Reports Medicine, 2021, 2, 100473.	6.5	16
167	Factors influencing the scientific performance of Momentum grant holders: an evaluation of the first 117 research groups. Scientometrics, 2018, 117, 409-426.	3.0	15
168	Challenging the heterogeneity of disease presentation in malignant melanoma—impact on patient treatment. Cell Biology and Toxicology, 2019, 35, 1-14.	5.3	15
169	Mini-Factor H Modulates Complement-Dependent IL-6 and IL-10 Release in an Immune Cell Culture (PBMC) Model: Potential Benefits Against Cytokine Storm. Frontiers in Immunology, 2021, 12, 642860.	4.8	15
170	Missed Calculations and New Conclusions: Re-Calculation of Genotype Distribution Data Published in Journal of Investigative Dermatology, 1998–2003. Journal of Investigative Dermatology, 2004, 122, 644-646.	0.7	14
171	Re-calculated Hardy–Weinberg values in papers published in Atherosclerosis between 1995 and 2003. Atherosclerosis, 2004, 173, 141-143.	0.8	14
172	Uncovering Potential Therapeutic Targets in Colorectal Cancer by Deciphering Mutational Status and Expression of Druggable Oncogenes. Cancers, 2019, 11, 983.	3.7	14
173	Gene Expression Indicates Altered Immune Modulation and Signaling Pathway Activation in Ovarian Cancer Patients Resistant to Topotecan. International Journal of Molecular Sciences, 2019, 20, 2750.	4.1	14
174	Prognostic significance of hedgehog signaling network-related gene expression in breast cancer patients. Journal of Cellular Biochemistry, 2021, 122, 577-597.	2.6	14
175	Clinical Correlations of Polycomb Repressive Complex 2 in Different Tumor Types. Cancers, 2021, 13, 3155.	3.7	14
176	<i>LDB1</i> overexpression is a negative prognostic factor in colorectal cancer. Oncotarget, 2016, 7, 84258-84270.	1.8	14
177	Potential options for managing LOX+ ER α breast cancer patients. Oncotarget, 2016, 7, 32893-32901.	1.8	14
178	Analysis of gene expression profiles in melanoma cells with acquired resistance against antineoplastic drugs. Melanoma Research, 2006, 16, 147-155.	1.2	13
179	The FOXC2 Transcription Factor Promotes Melanoma Outgrowth and Regulates Expression of Genes Associated With Drug Resistance and Interferon Responsiveness. Cancer Genomics and Proteomics, 2019, 16, 491-503.	2.0	13
180	Long-Term Exposure of Early-Transformed Human Mammary Cells to Low Doses of Benzo[a]pyrene and/or Bisphenol A Enhances Their Cancerous Phenotype via an AhR/GPR30 Interplay. Frontiers in Oncology, 2020, 10, 712.	2.8	13

#	ARTICLE	IF	CITATIONS
181	Is there a golden age in publication activity?â€”an analysis of age-related scholarly performance across all scientific disciplines. <i>Scientometrics</i> , 2020, 124, 1081-1097.	3.0	13
182	The prognostic association of SPAG5 gene expression in breast cancer patients with systematic therapy. <i>BMC Cancer</i> , 2019, 19, 1046.	2.6	12
183	Targeting RICTOR Sensitizes SMAD4-Negative Colon Cancer to Irinotecan. <i>Molecular Cancer Research</i> , 2020, 18, 414-423.	3.4	12
184	PDGFRA, HSD17B4 and HMGB2 are potential therapeutic targets in polycystic ovarian syndrome and breast cancer. <i>Oncotarget</i> , 2017, 8, 69520-69526.	1.8	12
185	Dynamic classification using caseâ€”specific training cohorts outperforms static gene expression signatures in breast cancer. <i>International Journal of Cancer</i> , 2015, 136, 2091-2098.	5.1	11
186	Evaluation of transcriptionally regulated genes identifies NCOR1 in hormone receptor negative breast tumors and lung adenocarcinomas as a potential tumor suppressor gene. <i>PLoS ONE</i> , 2018, 13, e0207776.	2.5	11
187	Transcriptome evolution from breast epithelial cells to basal-like tumors. <i>Oncotarget</i> , 2018, 9, 453-463.	1.8	11
188	Mapping Bromodomains in breast cancer and association with clinical outcome. <i>Scientific Reports</i> , 2019, 9, 5734.	3.3	11
189	Evaluating ZNF217 mRNA Expression Levels as a Predictor of Response to Endocrine Therapy in ER+ Breast Cancer. <i>Frontiers in Pharmacology</i> , 2018, 9, 1581.	3.5	11
190	Differential impact of classical and non-canonical NF-Î²B pathway-related gene expression on the survival of breast cancer patients. <i>Journal of Cancer</i> , 2019, 10, 5191-5211.	2.5	11
191	Identification of a stemness-related gene panel associated with BET inhibition in triple negative breast cancer. <i>Cellular Oncology (Dordrecht)</i> , 2020, 43, 431-444.	4.4	11
192	Mapping of Genomic Vulnerabilities in the Post-Translational Ubiquitination, SUMOylation and Neddylation Machinery in Breast Cancer. <i>Cancers</i> , 2021, 13, 833.	3.7	11
193	Gene Expression Profiling in Early Breast Cancerâ€”Patient Stratification Based on Molecular and Tumor Microenvironment Features. <i>Biomedicines</i> , 2022, 10, 248.	3.2	11
194	A Network-Based Target Overlap Score for Characterizing Drug Combinations: High Correlation with Cancer Clinical Trial Results. <i>PLoS ONE</i> , 2015, 10, e0129267.	2.5	10
195	Validation of RNAi Silencing Efficiency Using Gene Array Data shows 18.5% Failure Rate across 429 Independent Experiments. <i>Molecular Therapy - Nucleic Acids</i> , 2016, 5, e366.	5.1	10
196	Alterations in SCAI Expression during Cell Plasticity, Fibrosis and Cancer. <i>Pathology and Oncology Research</i> , 2018, 24, 641-651.	1.9	10
197	Down-regulation of A20 promotes immune escape of lung adenocarcinomas. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	10
198	RIP140 inhibits glycolysis-dependent proliferation of breast cancer cells by regulating GLUT3 expression through transcriptional crosstalk between hypoxia induced factor and p53. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 270.	5.4	10

#	ARTICLE	IF	CITATIONS
199	A unified platform enabling biomarker ranking and validation for 1562 drugs using transcriptomic data of 1250 cancer cell lines. Computational and Structural Biotechnology Journal, 2022, 20, 2885-2894.	4.1	10
200	Lower risk for Down syndrome associated with longer oral contraceptive use: a case-control study of women of advanced maternal age presenting for prenatal diagnosis. Contraception, 2013, 87, 455-458.	1.5	9
201	BRCA Mutation-Related and Claudin-Low Breast Cancer: Blood Relatives or Stepsisters?. Pathobiology, 2016, 83, 1-12.	3.8	9
202	Epigenetic modulation of FOXM1-gene interacting network by BET inhibitors in breast cancer. Breast Cancer Research and Treatment, 2018, 172, 725-732.	2.5	9
203	GAS2L1 Is a Potential Biomarker of Circulating Tumor Cells in Pancreatic Cancer. Cancers, 2020, 12, 3774.	3.7	9
204	Identification of a neural development gene expression signature in colon cancer stem cells reveals a role for EGR2 in tumorigenesis. IScience, 2022, 25, 104498.	4.1	9
205	Identification of Consensus Genes and Key Regulatory Elements in 5-Fluorouracil Resistance in Gastric and Colon Cancer. Oncology Research and Treatment, 2007, 30, 421-426.	1.2	8
206	Cell Dispersal Influences Tumor Heterogeneity and Introduces a Bias in NGS Data Interpretation. Scientific Reports, 2017, 7, 7358.	3.3	8
207	A snapshot of 3649 Web-based services published between 1994 and 2017 shows a decrease in availability after 2 years. Briefings in Bioinformatics, 2019, 20, 1004-1010.	6.5	8
208	The orphan nuclear receptor estrogen-related receptor beta (ERR β) in triple-negative breast cancer. Breast Cancer Research and Treatment, 2020, 179, 585-604.	2.5	8
209	Prognostic impact of the glypican family of heparan sulfate proteoglycans on the survival of breast cancer patients. Journal of Cancer Research and Clinical Oncology, 2021, 147, 1937-1955.	2.5	8
210	HKG promotes metastatic dissemination in prostate cancer. Scientific Reports, 2021, 11, 12287.	3.3	8
211	miRNA Expression Signatures of Therapy Response in Squamous Cell Carcinomas. Cancers, 2021, 13, 63.	3.7	8
212	Highly expressed genes are associated with inverse antisense transcription in mouse. Journal of Genetics, 2007, 86, 103-109.	0.7	7
213	Serum PlGF and EGF are independent prognostic markers in non-metastatic colorectal cancer. Scientific Reports, 2019, 9, 10921.	3.3	7
214	Characterization of Stem-like Circulating Tumor Cells in Pancreatic Cancer. Diagnostics, 2020, 10, 305.	2.6	7
215	A bioinformatic analysis of the inhibin-betaglycan-endoglin/CD105 network reveals prognostic value in multiple solid tumors. PLoS ONE, 2021, 16, e0249558.	2.5	7
216	Complement-mediated hypersensitivity reactions to an amphotericin B-containing lipid complex (Abelcet) in pediatric patients and anesthetized rats: Benefits of slow infusion. Nanomedicine: Nanotechnology, Biology, and Medicine, 2021, 34, 102366.	3.3	7

#	ARTICLE	IF	CITATIONS
217	Genomic Mapping of Splicing-Related Genes Identify Amplifications in LSM1, CLNS1A, and ILF2 in Luminal Breast Cancer. <i>Cancers</i> , 2021, 13, 4118.	3.7	7
218	Transcriptomic Mapping of Non-Small Cell Lung Cancer K-RAS p.G12C Mutated Tumors: Identification of Surfaceome Targets and Immunologic Correlates. <i>Frontiers in Immunology</i> , 2021, 12, 786069.	4.8	7
219	A novel mesenchymal-associated transcriptomic signature for risk-stratification and therapeutic response prediction in colorectal cancer. <i>International Journal of Cancer</i> , 2020, 147, 3250-3261.	5.1	6
220	Currently favored sampling practices for tumor sequencing can produce optimal results in the clinical setting. <i>Scientific Reports</i> , 2020, 10, 14403.	3.3	6
221	RNA sequencing of long-term label-retaining colon cancer stem cells identifies novel regulators of quiescence. <i>IScience</i> , 2021, 24, 102618.	4.1	6
222	A qPCR-based method for molecular subtype classification of urinary bladder cancer-stromal gene expressions show higher prognostic values than intrinsic tumor genes. <i>International Journal of Cancer</i> , 2021, , .	5.1	6
223	Biomarkers for Systemic Therapy in Ovarian Cancer. <i>Current Cancer Drug Targets</i> , 2014, 14, 259-273.	1.6	6
224	Exploratory Analysis of Single-Gene Predictive Biomarkers in HERA DASL Cohort Reveals That C8A mRNA Expression Is Prognostic of Outcome and Predictive of Benefit of Trastuzumab. <i>JCO Precision Oncology</i> , 2018, 2, 1-12.	3.0	5
225	Histotype-specific analysis of acid ceramidase expression in ovarian cancer. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2020, 476, 855-862.	2.8	5
226	Concomitant activation of GLI1 and Notch1 contributes to racial disparity of human triple negative breast cancer progression. <i>ELife</i> , 2021, 10, .	6.0	5
227	Combined analysis of gene expression, DNA copy number, and mutation profiling data to display biological process anomalies in individual breast cancers. <i>Breast Cancer Research and Treatment</i> , 2014, 144, 561-568.	2.5	4
228	Independent validation of induced overexpression efficiency across 242 experiments shows a success rate of 39%. <i>Scientific Reports</i> , 2019, 9, 343.	3.3	4
229	The prognostic significance of FOXC2 gene expression in cancer: A comprehensive analysis of RNA-seq data from the cancer genome atlas. <i>Cancer Genetics</i> , 2021, 254-255, 58-64.	0.4	4
230	RIP140 Represses Intestinal Paneth Cell Differentiation and Interplays with SOX9 Signaling in Colorectal Cancer. <i>Cancers</i> , 2021, 13, 3192.	3.7	4
231	Novel Insights into the Antagonistic Effects of Losartan against Angiotensin II/AGTR1 Signaling in Glioblastoma Cells. <i>Cancers</i> , 2021, 13, 4555.	3.7	4
232	The Prognostic Relevance of PMCA4 Expression in Melanoma: Gender Specificity and Implications for Immune Checkpoint Inhibition. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3324.	4.1	4
233	The hyaluronan-related genes HAS2, HYAL1-4, PH20 and HYALP1 are associated with prognosis, cell viability and spheroid formation capacity in ovarian cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2022, 148, 3399-3419.	2.5	4
234	Computational analysis reveals 43% antisense transcription in 1182 transcripts in mouse muscle. <i>DNA Sequence</i> , 2006, 17, 422-430.	0.7	3

#	ARTICLE	IF	CITATIONS
235	Effect of extended oral contraception use on the prevalence of fetal trisomy 21 in women aged at least 35 years. International Journal of Gynecology and Obstetrics, 2017, 138, 261-266.	2.3	3
236	Transcriptomic Correlates of Immunologic Activation in Head and Neck and Cervical Cancer. Frontiers in Oncology, 2021, 11, 714550.	2.8	3
237	Identification of a Tumor Cell Associated Type I IFN Resistance Gene Expression Signature of Human Melanoma, the Components of Which Have a Predictive Potential for Immunotherapy. International Journal of Molecular Sciences, 2022, 23, 2704.	4.1	3
238	Predicting effective drug combinations via network propagation. , 2013, , .		2
239	Predicting the chance of relapse after tamoxifen treatment in breast cancer. Biomarkers in Medicine, 2014, 8, 77-79.	1.4	2
240	Signal Transduction Pathways of TNAP: Molecular Network Analyses. Sub-Cellular Biochemistry, 2015, 76, 185-205.	2.4	2
241	Propagation on Molecular Interaction Networks: Prediction of Effective Drug Combinations and Biomarkers in Cancer Treatment. Current Pharmaceutical Design, 2016, 22, 1-1.	1.9	2
242	Association of Sperm-Associated Antigen 5 and Treatment Response in Patients With Estrogen Receptorâ€“Positive Breast Cancer. JAMA Network Open, 2020, 3, e209486.	5.9	2
243	Transcriptomic Profiles of CD47 in Breast Tumors Predict Outcome and Are Associated with Immune Activation. International Journal of Molecular Sciences, 2021, 22, 3836.	4.1	2
244	Exploring the Significance of the Exon 4-Skipping Isoform of the ZNF217 Oncogene in Breast Cancer. Frontiers in Oncology, 2021, 11, 647269.	2.8	2
245	Primary Founder Mutations in the PRKDC Gene Increase Tumor Mutation Load in Colorectal Cancer. International Journal of Molecular Sciences, 2022, 23, 633.	4.1	2
246	Evidence for the Oocyte Mosaicism Selection model on the origin of Patau syndrome (trisomy 13). Acta Obstetricia Et Gynecologica Scandinavica, 2019, 98, 1558-1564.	2.8	1
247	Functional transcriptomics: An experimental basis for understanding the systems biology for cancer cells. Advances in Enzyme Regulation, 2007, 47, 41-62.	2.6	0
248	Editorial (Thematic Issue: Cancer Biomarkers from Bench to Bedside). Current Cancer Drug Targets, 2015, 15, 642-642.	1.6	0
249	Meta-analysis of 59 gene expression based biomarker candidates predicting survival after tamoxifen treatment in breast cancer.. Journal of Clinical Oncology, 2013, 31, e11564-e11564.	1.6	0
250	Inhibition of MEK1 increases carboplatin sensitivity in ovarian cancer.. Journal of Clinical Oncology, 2014, 32, 5557-5557.	1.6	0
251	Application of a dynamic retraining for each patient using case-specific training cohorts to predict survival in breast cancer patients.. Journal of Clinical Oncology, 2014, 32, 1065-1065.	1.6	0
252	Resistance-Associated Signatures in Breast Cancer. , 2007, 176, 37-50.		0

#	ARTICLE	IF	CITATIONS
253	Could tivozanib be a new potent pan-VEGF inhibitor in RCC therapy?. Translational Andrology and Urology, 2012, 1, 192-3.	1.4	0
254	Application of Microarrays for the Prediction of Therapy Response in Breast Cancer. Cancer Genomics and Proteomics, 2005, 2, 255-263.	2.0	0