

# Balazs Gyorffy

## List of Publications by Year in descending order

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Version: 2024-02-01

254  
papers

20,755  
citations

19608

61  
h-index

12558

132  
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.	1.1	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.	1.1	1,502
3	Validation of miRNA prognostic power in hepatocellular carcinoma using expression data of independent datasets. <i>Scientific Reports</i> , 2018, 8, 9227.	1.6	1,103
4	Cutoff Finder: A Comprehensive and Straightforward Web Application Enabling Rapid Biomarker Cutoff Optimization. <i>PLoS ONE</i> , 2012, 7, e51862.	1.1	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.	2.1	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.	0.8	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.	1.6	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.	1.1	678
9	Pancancer survival analysis of cancer hallmark genes. <i>Scientific Reports</i> , 2021, 11, 6047.	1.6	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.	1.9	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.	1.8	420
12	Determining consistent prognostic biomarkers of overall survival and vascular invasion in hepatocellular carcinoma. <i>Royal Society Open Science</i> , 2018, 5, 181006.	1.1	320
13	Jetset: selecting the optimal microarray probe set to represent a gene. <i>BMC Bioinformatics</i> , 2011, 12, 474.	1.2	277
14	Multigene prognostic tests in breast cancer: past, present, future. <i>Breast Cancer Research</i> , 2015, 17, 11.	2.2	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.	2.3	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.	7.2	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.	1.1	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.	4.3	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.	1.6	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.	3.3	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.	3.3	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.	3.2	141
23	Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. <i>International Journal of Cancer</i> , 2016, 138, 87-97.	2.3	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.	2.3	133
25	miR-34a Silences c-SRC to Attenuate Tumor Growth in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2016, 76, 927-939.	0.4	128
26	Disruption of STAT3 signalling promotes KRAS-induced lung tumorigenesis. <i>Nature Communications</i> , 2015, 6, 6285.	5.8	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.	1.2	123
28	Different mutations in SARS-CoV-2 associate with severe and mild outcome. <i>International Journal of Antimicrobial Agents</i> , 2021, 57, 106272.	1.1	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.	2.1	117
30	Immune Gene Expression Is Associated with Genomic Aberrations in Breast Cancer. <i>Cancer Research</i> , 2017, 77, 3317-3324.	0.4	117
31	Tumor-associated macrophages (TAMs) depend on ZEB1 for their cancer-promoting roles. <i>EMBO Journal</i> , 2017, 36, 3336-3355.	3.5	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.	1.9	111
33	Differential epigenetic reprogramming in response to specific endocrine therapies promotes cholesterol biosynthesis and cellular invasion. <i>Nature Communications</i> , 2015, 6, 10044.	5.8	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.	2.1	107
35	APOBEC3B-Mediated Cytidine Deamination Is Required for Estrogen Receptor Action in Breast Cancer. <i>Cell Reports</i> , 2015, 13, 108-121.	2.9	105
36	Glutamate enrichment as new diagnostic opportunity in breast cancer. <i>International Journal of Cancer</i> , 2015, 136, 1619-1628.	2.3	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.	2.6	102
38	Afatinib restrains K-RAS-driven lung tumorigenesis. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	99
39	Enhancer mapping uncovers phenotypic heterogeneity and evolution in patients with luminal breast cancer. <i>Nature Medicine</i> , 2018, 24, 1469-1480.	15.2	98
40	Inflammation, Adenoma and Cancer: Objective Classification of Colon Biopsy Specimens with Gene Expression Signature. <i>Disease Markers</i> , 2008, 25, 1-16.	0.6	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.	0.8	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.	1.3	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.	3.3	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.	1.1	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.	2.6	81
46	Evaluation of Microarray Preprocessing Algorithms Based on Concordance with RT-PCR in Clinical Samples. <i>PLoS ONE</i> , 2009, 4, e5645.	1.1	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.	1.1	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.	3.3	77
49	FAK activity sustains intrinsic and acquired ovarian cancer resistance to platinum chemotherapy. <i>ELife</i> , 2019, 8, .	2.8	76
50	Predictors of Chemosensitivity in Triple Negative Breast Cancer: An Integrated Genomic Analysis. <i>PLoS Medicine</i> , 2016, 13, e1002193.	3.9	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.	1.9	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.	1.1	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.	0.4	74
54	Leptin as a mediator of tumor-stromal interactions promotes breast cancer stem cell activity. <i>Oncotarget</i> , 2016, 7, 1262-1275.	0.8	74

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55	HOXB7 Is an ER± Cofactor in the Activation of HER2 and Multiple ER Target Genes Leading to Endocrine Resistance. <i>Cancer Discovery</i> , 2015, 5, 944-959.	7.7	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.	2.6	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.	1.7	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.	0.8	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.	2.3	66
60	Combined Wnt/β2-Catenin, Met, and CXCL12/CXCR4 Signals Characterize Basal Breast Cancer and Predict Disease Outcome. <i>Cell Reports</i> , 2013, 5, 1214-1227.	2.9	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.	3.2	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.	3.6	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.	3.3	63
64	MultipleTesting.com: A tool for life science researchers for multiple hypothesis testing correction. <i>PLoS ONE</i> , 2021, 16, e0245824.	1.1	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.	2.1	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.	2.1	59
67	Synaptic mitochondria: A brain mitochondria cluster with a specific proteome. <i>Journal of Proteomics</i> , 2015, 120, 142-157.	1.2	59
68	BCL9/9L-β2-catenin Signaling is Associated With Poor Outcome in Colorectal Cancer. <i>EBioMedicine</i> , 2015, 2, 1932-1943.	2.7	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.	1.5	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.	3.2	55
71	JAK&STAT inhibition impairs <i>KRAS</i> &driven lung adenocarcinoma progression. <i>International Journal of Cancer</i> , 2019, 145, 3376-3388.	2.3	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.	2.3	53

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73	MEK1 is associated with carboplatin resistance and is a prognostic biomarker in epithelial ovarian cancer. <i>BMC Cancer</i> , 2014, 14, 837.	1.1	52
74	HOXC10 Expression Supports the Development of Chemotherapy Resistance by Fine Tuning DNA Repair in Breast Cancer Cells. <i>Cancer Research</i> , 2016, 76, 4443-4456.	0.4	52
75	Predictive biomarkers of platinum and taxane resistance using the transcriptomic data of 1816 ovarian cancer patients. <i>Gynecologic Oncology</i> , 2020, 156, 654-661.	0.6	51
76	Identification of a claudin-4 and E-cadherin score to predict prognosis in breast cancer. <i>Cancer Science</i> , 2011, 102, 2248-2254.	1.7	50
77	A Comprehensive Overview of Targeted Therapy in Metastatic Renal Cell Carcinoma. <i>Current Cancer Drug Targets</i> , 2012, 12, 857-872.	0.8	49
78	Discovery of a Glucocorticoid Receptor (GR) Activity Signature Using Selective GR Antagonism in ER-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 3433-3446.	3.2	49
79	Multivariate analysis of oestrogen receptor alpha, pS2, metallothionein and CD24 expression in invasive breast cancers. <i>British Journal of Cancer</i> , 2006, 95, 339-346.	2.9	47
80	New network topology approaches reveal differential correlation patterns in breast cancer. <i>BMC Systems Biology</i> , 2013, 7, 78.	3.0	47
81	TP53 mutation hits energy metabolism and increases glycolysis in breast cancer. <i>Oncotarget</i> , 2016, 7, 67183-67195.	0.8	46
82	Elevated HOX gene expression in acute myeloid leukemia is associated with NPM1 mutations and poor survival. <i>Journal of Advanced Research</i> , 2019, 20, 105-116.	4.4	45
83	The pioneer factor PBX1 is a novel driver of metastatic progression in ER±-positive breast cancer. <i>Oncotarget</i> , 2015, 6, 21878-21891.	0.8	45
84	DNA methylation-based diagnostic, prognostic, and predictive biomarkers in colorectal cancer. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2022, 1877, 188722.	3.3	45
85	Parallel Evolution under Chemotherapy Pressure in 29 Breast Cancer Cell Lines Results in Dissimilar Mechanisms of Resistance. <i>PLoS ONE</i> , 2012, 7, e30804.	1.1	44
86	Predictive biomarker discovery through the parallel integration of clinical trial and functional genomics datasets. <i>Genome Medicine</i> , 2010, 2, 53.	3.6	43
87	MLL-fusion-driven leukemia requires SETD2 to safeguard genomic integrity. <i>Nature Communications</i> , 2018, 9, 1983.	5.8	43
88	A Comprehensive Outline of Trastuzumab Resistance Biomarkers in HER2 Overexpressing Breast Cancer. <i>Current Cancer Drug Targets</i> , 2015, 15, 665-683.	0.8	42
89	The critical role of the ZNF217 oncogene in promoting breast cancer metastasis to the bone. <i>Journal of Pathology</i> , 2017, 242, 73-89.	2.1	42
90	SREBP1 drives Keratin-80-dependent cytoskeletal changes and invasive behavior in endocrine-resistant ER± breast cancer. <i>Nature Communications</i> , 2019, 10, 2115.	5.8	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.	4.6	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.	2.7	42
93	Survival analysis in breast cancer using proteomic data from four independent datasets. <i>Scientific Reports</i> , 2021, 11, 16787.	1.6	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.	2.9	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.	2.3	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.	1.1	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.	3.3	41
98	Deciphering and Targeting Oncogenic Mutations and Pathways in Breast Cancer. <i>Oncologist</i> , 2016, 21, 1063-1078.	1.9	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.	2.3	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.	6.9	41
101	A Web-Based Data Warehouse on Gene Expression in Human Malignant Melanoma. <i>Journal of Investigative Dermatology</i> , 2007, 127, 394-399.	0.3	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.	1.6	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.	0.5	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.	0.9	37
105	BRD4 Regulates Metastatic Potential of Castration-Resistant Prostate Cancer through AHNAK. <i>Molecular Cancer Research</i> , 2019, 17, 1627-1638.	1.5	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.	1.4	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.	2.1	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.	0.5	34

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109	ZEB1-induced tumorigenesis requires senescence inhibition via activation of DKK1/mutant p53/Mdm2/CtBP and repression of macroH2A1. <i>Gut</i> , 2017, 66, 666-682.	6.1	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.	0.6	33
111	A functional interplay between ZNF217 and Estrogen Receptor alpha exists in luminal breast cancers. <i>Molecular Oncology</i> , 2014, 8, 1441-1457.	2.1	32
112	Proteomic identification of prognostic tumour biomarkers, using chemotherapy-induced cancer-associated fibroblasts. <i>Aging</i> , 2015, 7, 816-838.	1.4	32
113	Prognostic value of DLGAP5 in colorectal cancer. <i>International Journal of Colorectal Disease</i> , 2019, 34, 1455-1465.	1.0	32
114	FOXM1 functions collaboratively with PLAU to promote gastric cancer progression. <i>Journal of Cancer</i> , 2020, 11, 788-794.	1.2	32
115	Shp2 signaling suppresses senescence in <i>PyMT</i> -induced mammary gland cancer in mice. <i>EMBO Journal</i> , 2015, 34, 1493-1508.	3.5	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.	2.1	31
117	Identifying Cancers Impacted by CDK8/19. <i>Cells</i> , 2019, 8, 821.	1.8	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.	1.2	30
119	Expression of classical NF- $\kappa$ B pathway effectors in human ovarian carcinoma. <i>Histopathology</i> , 2010, 56, 727-739.	1.6	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.	1.5	30
121	DUSP4 is associated with increased resistance against anti-HER2 therapy in breast cancer. <i>Oncotarget</i> , 2017, 8, 77207-77218.	0.8	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.	1.3	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.	2.3	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.	1.1	28
125	Transcriptomic immunologic signature associated with favorable clinical outcome in basal-like breast tumors. <i>PLoS ONE</i> , 2017, 12, e0175128.	1.1	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.	1.6	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.	3.2	27
128	Comprehensive Outline of Whole Exome Sequencing Data Analysis Tools Available in Clinical Oncology. <i>Cancers</i> , 2019, 11, 1725.	1.7	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.	2.6	26
130	Biomarkers Downstream of RAS: A Search for Robust Transcriptional Targets. <i>Current Cancer Drug Targets</i> , 2010, 10, 858-868.	0.8	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.	2.9	26
132	Phosphodiesterase 5 (PDE5) Is Highly Expressed in Cancer-Associated Fibroblasts and Enhances Breast Tumor Progression. <i>Cancers</i> , 2019, 11, 1740.	1.7	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.	1.6	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.	2.2	24
135	BRD4 regulates key transcription factors that drive epithelial-mesenchymal transition in castration-resistant prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 268-277.	2.0	24
136	HIF-3 $\beta$ promotes colorectal tumor cell growth by activation of JAK-STAT3 signaling. <i>Oncotarget</i> , 2016, 7, 11567-11579.	0.8	24
137	Colon cancer subtypes: concordance, effect on survival and selection of the most representative preclinical models. <i>Scientific Reports</i> , 2016, 6, 37169.	1.6	23
138	Mutations Defining Patient Cohorts With Elevated PD-L1 Expression in Gastric Cancer. <i>Frontiers in Pharmacology</i> , 2018, 9, 1522.	1.6	23
139	Use of Routinely Collected Amniotic Fluid for Whole-Genome Expression Analysis of Polygenic Disorders. <i>Clinical Chemistry</i> , 2006, 52, 2013-2020.	1.5	22
140	Transcription Factor ZBP-89 Drives a Feedforward Loop of $\beta$ -Catenin Expression in Colorectal Cancer. <i>Cancer Research</i> , 2016, 76, 6877-6887.	0.4	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.	1.6	22
142	<i>linc00673</i> (ERLR01) is a prognostic indicator of overall survival in breast cancer. <i>Transcription</i> , 2018, 9, 17-29.	1.7	22
143	Genomic Mapping Identifies Mutations in RYR2 and AHNAK as Associated with Favorable Outcome in Basal-Like Breast Tumors Expressing PD1/PD-L1. <i>Cancers</i> , 2020, 12, 2243.	1.7	22
144	Evidence for Enhanced Exosome Production in Aromatase Inhibitor-Resistant Breast Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5841.	1.8	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.	1.1	21
147	Gene expression-based biomarkers designating glioblastomas resistant to multiple treatment strategies. <i>Carcinogenesis</i> , 2021, 42, 804-813.	1.3	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.	2.0	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.	1.3	20
150	Dynamin impacts homology-directed repair and breast cancer response to chemotherapy. <i>Journal of Clinical Investigation</i> , 2018, 128, 5307-5321.	3.9	20
151	Oncogene-mediated metabolic gene signature predicts breast cancer outcome. <i>Npj Breast Cancer</i> , 2021, 7, 141.	2.3	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.	0.8	19
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