Daniel Birnbaum

List of Publications by Year
in descending order

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229 papers	23,377 citations	10351 72 h-index	8370 147 g-index
237 all docs	237 docs citations	237 times ranked	28905 citing authors

#	ARTICLE	IF	CITATIONS
1	ALDH1 Is a Marker of Normal and Malignant Human Mammary Stem Cells and a Predictor of Poor Clinical Outcome. Cell Stem Cell, 2007, 1, 555-567.	5.2	3,550
2	Breast Cancer Cell Lines Contain Functional Cancer Stem Cells with Metastatic Capacity and a Distinct Molecular Signature. Cancer Research, 2009, 69, 1302-1313.	0.4	1,067
3	Breast Cancer Stem Cells Transition between Epithelial and Mesenchymal States Reflective of their Normal Counterparts. Stem Cell Reports, 2014, 2, 78-91.	2.3	854
4	CXCR1 blockade selectively targets human breast cancer stem cells in vitro and in xenografts. Journal of Clinical Investigation, 2010, 120, 485-497.	3.9	658
5	Aldehyde Dehydrogenase 1â€“Positive Cancer Stem Cells Mediate Metastasis and Poor Clinical Outcome in Inflammatory Breast Cancer. Clinical Cancer Research, 2010, 16, 45-55.	3.2	646
6	Mutations of polycombâ€·associated gene <i>ASXL1</i> in myelodysplastic syndromes and chronic myelomonocytic leukaemia. British Journal of Haematology, 2009, 145, 788-800.	1.2	537
7	Human breast cancer cells enhance self tolerance by promoting evasion from NK cell antitumor immunity. Journal of Clinical Investigation, 2011, 121, 3609-3622.	3.9	524
8	Gene expression profiling of breast cell lines identifies potential new basal markers. Oncogene, 2006, 25, 2273-2284.	2.6	494
9	Prognostic Score Including Gene Mutations in Chronic Myelomonocytic Leukemia. Journal of Clinical Oncology, 2013, 31, 2428-2436.	0.8	462
10	Genomic characterization of metastatic breast cancers. Nature, 2019, 569, 560-564.	13.7	448
11	Prognostic and predictive value of PDL1 expression in breast cancer. Oncotarget, 2015, 6, 5449-5464.	0.8	424
12	Salinomycin kills cancer stem cells by sequestering iron in lysosomes. Nature Chemistry, 2017, 9, 1025-1033.	6.6	423
13	How basal are tripleâ€·negative breast cancers?. International Journal of Cancer, 2008, 123, 236-240.	2.3	384
14	Mutations of ASXL1 gene in myeloproliferative neoplasms. Leukemia, 2009, 23, 2183-2186.	3.3	301
15	Gene Expression Profiling Shows Medullary Breast Cancer Is a Subgroup of Basal Breast Cancers. Cancer Research, 2006, 66, 4636-4644.	0.4	273
16	TET2 mutation is an independent favorable prognostic factor in myelodysplastic syndromes (MDSs). Blood, 2009, 114, 3285-3291.	0.6	264
17	Integrated Profiling of Basal and Luminal Breast Cancers. Cancer Research, 2007, 67, 11565-11575.	0.4	254
18	TET2 gene mutation is a frequent and adverse event in chronic myelomonocytic leukemia. Haematologica, 2009, 94, 1676-1681.	1.7	234

#	ARTICLE	IF	CITATIONS
19	A gene expression signature identifies two prognostic subgroups of basal breast cancer. Breast Cancer Research and Treatment, 2011, 126, 407-420.	1.1	231
20	Gene Expression Profiling Identifies Molecular Subtypes of Inflammatory Breast Cancer. Cancer Research, 2005, 65, 2170-2178.	0.4	229
21	Mutations in ASXL1 are associated with poor prognosis across the spectrum of malignant myeloid diseases. Journal of Hematology and Oncology, 2012, 5, 12.	6.9	226
22	Mutations of IDH1 and IDH2 genes in early and accelerated phases of myelodysplastic syndromes and MDS/myeloproliferative neoplasms. Leukemia, 2010, 24, 1094-1096.	3.3	225
23	A refined molecular taxonomy of breast cancer. Oncogene, 2012, 31, 1196-1206.	2.6	221
24	Mutations affecting mRNA splicing define distinct clinical phenotypes and correlate with patient outcome in myelodysplastic syndromes. Blood, 2012, 119, 3211-3218.	0.6	220
25	Comprehensive Profiling of 8p11-12 Amplification in Breast Cancer. Molecular Cancer Research, 2005, 3, 655-667.	1.5	201
26	ASXL1 mutation is associated with poor prognosis and acute transformation in chronic myelomonocytic leukaemia. British Journal of Haematology, 2010, 151, 365-375.	1.2	199
27	Retinoid signaling regulates breast cancer stem cell differentiation. Cell Cycle, 2009, 8, 3297-3302.	1.3	193
28	The t(6;8)(q27;p11) Translocation in a Stem Cell Myeloproliferative Disorder Fuses a Novel Gene, FOP, to Fibroblast Growth Factor Receptor 1. Blood, 1999, 93, 1381-1389.	0.6	187
29	A Recurrent Chromosome Breakpoint in Breast Cancer at the NRG1/Neuregulin 1/Heregulin Gene. Cancer Research, 2004, 64, 6840-6844.	0.4	185
30	Immunophenotypic analysis of inflammatory breast cancers: identification of anâ€˜inflammatory signatureâ€™. Journal of Pathology, 2004, 202, 265-273.	2.1	180
31	Gene Expression Profiling for Molecular Characterization of Inflammatory Breast Cancer and Prediction of Response to Chemotherapy. Cancer Research, 2004, 64, 8558-8565.	0.4	177
32	Basal Breast Cancer: A Complex and Deadly Molecular Subtype. Current Molecular Medicine, 2012, 12, 96-110.	0.6	173
33	Cancer Stem Cells in Breast: Current Opinion and Future Challenges. Pathobiology, 2008, 75, 75-84.	1.9	169
34	BCOR and BCORL1 mutations in myelodysplastic syndromes and related disorders. Blood, 2013, 122, 3169-3177.	0.6	169
35	FGFRI andPLAT genes and DNA amplification at 8p 12 in breast and ovarian cancers. Genes Chromosomes and Cancer, 1993, 7, 219-226.	1.5	158
36	MOZ is fused top300 in an acute monocytic leukemia with t(8;22). , 2000, 28, 138-144.		157

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37	MicroRNA93 Regulates Proliferation and Differentiation of Normal and Malignant Breast Stem Cells. PLoS Genetics, 2012, 8, e1002751.	1.5	150
38	Protein expression profiling identifies subclasses of breast cancer and predicts prognosis. Cancer Research, 2005, 65, 767-79.	0.4	148
39	Distinct and Complementary Information Provided by Use of Tissue and DNA Microarrays in the Study of Breast Tumor Markers. American Journal of Pathology, 2002, 161, 1223-1233.	1.9	144
40	Down-Regulation of ECRG4, a Candidate Tumor Suppressor Gene, in Human Breast Cancer. PLoS ONE, 2011, 6, e27656.	1.1	143
41	Combined mutations of ASXL1, CBL, FLT3, IDH1, IDH2, JAK2, KRAS, NPM1, NRAS, RUNX1, TET2 and WT1 genes in myelodysplastic syndromes and acute myeloid leukemias. BMC Cancer, 2010, 10, 401.	1.1	140
42	Mutation analysis of <i>ASXL1, CBL, DNMT3A, IDH1, IDH2, JAK2, MPL, NF1, SF3B1, SUZ12,</i> and <i>TET2</i> in myeloproliferative neoplasms. Genes Chromosomes and Cancer, 2012, 51, 743-755.	1.5	139
43	Genome profiling of ERBB2-amplified breast cancers. BMC Cancer, 2010, 10, 539.	1.1	136
44	Nectin-4 is a new histological and serological tumor associated marker for breast cancer. BMC Cancer, 2007, 7, 73.	1.1	134
45	A stemness-related ZEB1â€"MSRB3 axis governs cellular pliancy and breast cancer genome stability. Nature Medicine, 2017, 23, 568-578.	15.2	131
46	Uncovering the Molecular Secrets of Inflammatory Breast Cancer Biology: An Integrated Analysis of Three Distinct Affymetrix Gene Expression Datasets. Clinical Cancer Research, 2013, 19, 4685-4696.	3.2	130
47	<i>ZNF703</i> gene amplification at 8p12 specifies luminal B breast cancer. EMBO Molecular Medicine, 2011, 3, 153-166.	3.3	126
48	The Histone Deacetylase Inhibitor Abexinostat Induces Cancer Stem Cells Differentiation in Breast Cancer with Low <i>Xist</i> Expression. Clinical Cancer Research, 2013, 19, 6520-6531.	3.2	122
49	Prognosis and Gene Expression Profiling of 20q13-Amplified Breast Cancers. Clinical Cancer Research, 2006, 12, 4533-4544.	3.2	121
50	Mevalonate Metabolism Regulates Basal Breast Cancer Stem Cells and Is a Potential Therapeutic Target. Stem Cells, 2012, 30, 1327-1337.	1.4	120
51	Identification and validation of an ERBB2 gene expression signature in breast cancers. Oncogene, 2004, 23, 2564-2575.	2.6	117
52	Myeloid malignancies: mutations, models and management. BMC Cancer, 2012, 12, 304.	1.1	116
53	Human Breast Tumor Cells Induce Self-Tolerance Mechanisms to Avoid NKG2D-Mediated and DNAM-Mediated NK Cell Recognition. Cancer Research, 2011, 71, 6621-6632.	0.4	114
54	A whole-genome sequence and transcriptome perspective on HER2-positive breast cancers. Nature Communications, 2016, 7, 12222.	5.8	113

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55	Postoperative serum proteomic profiles may predict metastatic relapse in high-risk primary breast cancer patients receiving adjuvant chemotherapy. Oncogene, 2006, 25, 981-989.	2.6	112
56	miR-600 Acts as a Bimodal Switch that Regulates Breast Cancer Stem Cell Fate through WNT Signaling. Cell Reports, 2017, 18, 2256-2268.	2.9	111
57	Genome profiling of chronic myelomonocytic leukemia: frequent alterations of RAS and RUNX1genes. BMC Cancer, 2008, 8, 299.	1.1	109
58	Lobular and ductal carcinomas of the breast have distinct genomic and expression profiles. Oncogene, 2008, 27, 5359-5372.	2.6	107
59	Genome profiling of pancreatic adenocarcinoma. Genes Chromosomes and Cancer, 2011, 50, 456-465.	1.5	107
60	Mutual exclusion of ASXL1 and NPM1 mutations in a series of acute myeloid leukemias. Leukemia, 2010, 24, 469-473.	3.3	106
61	Sixteenâ€“Kinase Gene Expression Identifies Luminal Breast Cancers with Poor Prognosis. Cancer Research, 2008, 68, 767-776.	0.4	105
62	Breast cancer stem cells: tools and models to rely on. BMC Cancer, 2009, 9, 202.	1.1	105
63	<i>PDL1</i> expression in inflammatory breast cancer is frequent and predicts for the pathological response to chemotherapy. Oncotarget, 2015, 6, 13506-13519.	0.8	105
64	ALDH1-Positive Cancer Stem Cells Predict Engraftment of Primary Breast Tumors and Are Governed by a Common Stem Cell Program. Cancer Research, 2013, 73, 7290-7300.	0.4	103
65	SETBP1 mutations in 658 patients with myelodysplastic syndromes, chronic myelomonocytic leukemia and secondary acute myeloid leukemias. Leukemia, 2013, 27, 1401-1403.	3.3	102
66	TACC1â€“chTOGâ€“Aurora A protein complex in breast cancer. Oncogene, 2003, 22, 8102-8116.	2.6	99
67	Identification of p62/SQSTM1 as a component of non-canonical Wnt VANGL2â€“JNK signalling in breast cancer. Nature Communications, 2016, 7, 10318.	5.8	85
68	Fifteen years of research on oralâ€“facialâ€“digital syndromes: from 1 to 16 causal genes. Journal of Medical Genetics, 2017, 54, 371-380.	1.5	85
69	Peripheral Blood NK Cells from Breast Cancer Patients Are Tumor-Induced Composite Subsets. Journal of Immunology, 2013, 190, 2424-2436.	0.4	84
70	Gene expression profiles of inflammatory breast cancer: correlation with response to neoadjuvant chemotherapy and metastasis-free survival. Annals of Oncology, 2014, 25, 358-365.	0.6	82
71	Correlated break at PARK2/FRA6E and loss of AF-6/Afadin protein expression are associated with poor outcome in breast cancer. Oncogene, 2007, 26, 298-307.	2.6	81
72	Prognostic value of <i>PDL1</i> expression in pancreatic cancer. Oncotarget, 2016, 7, 71198-71210.	0.8	81

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73	The ERBB2/HER2 Receptor Differentially Interacts with ERBIN and PICK1 PSD-95/DLG/ZO-1 Domain Proteins. Journal of Biological Chemistry, 2001, 276, 15256-15263.	1.6	80
74	Nectin-4: a new prognostic biomarker for efficient therapeutic targeting of primary and metastatic triple-negative breast cancer. Annals of Oncology, 2017, 28, 769-776.	0.6	77
75	Protein Profiling of Human Breast Tumor Cells Identifies Novel Biomarkers Associated with Molecular Subtypes. Molecular and Cellular Proteomics, 2008, 7, 1420-1433.	2.5	74
76	Association of GATA3, P53, Ki67 status and vascular peritumoral invasion are strongly prognostic in luminal breast cancer. Breast Cancer Research, 2009, 11, R23.	2.2	74
77	Carcinogenesis and translational controls: TACC1 is down-regulated in human cancers and associates with mRNA regulators. Oncogene, 2002, 21, 5619-5630.	2.6	73
78	Proteomics of Breast Cancer. Molecular and Cellular Proteomics, 2006, 5, 1772-1786.	2.5	72
79	Gene expression profiling of cancer by use of DNA arrays: how far from the clinic?. Lancet Oncology, The, 2001, 2, 674-682.	5.1	69
80	Role of <i>ASXL1</i> and <i>TP53</i> mutations in the molecular classification and prognosis of acute myeloid leukemias with myelodysplasia-related changes. Oncotarget, 2015, 6, 8388-8396.	0.8	69
81	Comparative genomic analysis of primary tumors and metastases in breast cancer. Oncotarget, 2016, 7, 27208-27219.	0.8	69
82	Reasons for breast cancer heterogeneity. Journal of Biology, 2008, 7, 6.	2.7	67
83	The Functional Landscape of Hsp27 Reveals New Cellular Processes such as DNA Repair and Alternative Splicing and Proposes Novel Anticancer Targets. Molecular and Cellular Proteomics, 2014, 13, 3585-3601.	2.5	65
84	Acute myeloid leukaemia with 8p11 (MYST3) rearrangement: an integrated cytologic, cytogenetic and molecular study by the groupe francophone de cytogÃ©nÃ©tique hÃ©matologique. Leukemia, 2008, 22, 1567-1575.	3.3	64
85	A 25-gene classifier predicts overall survival in resectable pancreatic cancer. BMC Medicine, 2017, 15, 170.	2.3	64
86	PRICKLE1 Contributes to Cancer Cell Dissemination through Its Interaction with mTORC2. Developmental Cell, 2016, 37, 311-325.	3.1	63
87	Control of ciliogenesis by FOR20, a novel centrosome and pericentriolar satellite protein. Journal of Cell Science, 2010, 123, 2391-2401.	1.2	61
88	Head and Body/Tail Pancreatic Carcinomas Are Not the Same Tumors. Cancers, 2019, 11, 497.	1.7	61
89	Gene Expression Profiling and Clinical Outcome in Breast Cancer. OMICS A Journal of Integrative Biology, 2006, 10, 429-443.	1.0	60
90	Chromosome arm 8p and cancer: a fragile hypothesis. Lancet Oncology, The, 2003, 4, 639-642.	5.1	57

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91	NCOA3, a new fusion partner for MOZ/MYST3 in M5 acute myeloid leukemia. Leukemia, 2008, 22, 663-665.	3.3	57
92	High-Resolution Comparative Genomic Hybridization of Inflammatory Breast Cancer and Identification of Candidate Genes. PLoS ONE, 2011, 6, e16950.	1.1	57
93	A recurrent chromosome translocation breakpoint in breast and pancreatic cancer cell lines targets the neuregulin/NRG1gene. Genes Chromosomes and Cancer, 2003, 37, 333-345.	1.5	56
94	The immunologic constant of rejection classification refines the prognostic value of conventional prognostic signatures in breast cancer. British Journal of Cancer, 2018, 119, 1383-1391.	2.9	54
95	Candidate Luminal B Breast Cancer Genes Identified by Genome, Gene Expression and DNA Methylation Profiling. PLoS ONE, 2014, 9, e81843.	1.1	53
96	Loss of AF6/afadin, a marker of poor outcome in breast cancer, induces cell migration, invasiveness and tumor growth. Oncogene, 2011, 30, 3862-3874.	2.6	52
97	Mutations and deletions of ARID1A in breast tumors. Oncogene, 2012, 31, 4255-4256.	2.6	52
98	Simvastatin prevents triple-negative breast cancer metastasis in pre-clinical models through regulation of FOXO3a. Breast Cancer Research and Treatment, 2015, 154, 495-508.	1.1	52
99	How different are luminal A and basal breast cancers?. International Journal of Cancer, 2009, 124, 1338-1348.	2.3	51
100	ESPL1 is a candidate oncogene of luminal B breast cancers. Breast Cancer Research and Treatment, 2014, 147, 51-59.	1.1	51
101	Genome profiling of acute myelomonocytic leukemia: alteration of the MYB locus in MYST3-linked cases. Leukemia, 2009, 23, 85-94.	3.3	49
102	Impact of gene mutations on treatment response and prognosis of acute myeloid leukemia secondary to myeloproliferative neoplasms. American Journal of Hematology, 2018, 93, 330-338.	2.0	49
103	Alteration of cohesin genes in myeloid diseases. American Journal of Hematology, 2010, 85, 717-719.	2.0	46
104	Kinome expression profiling and prognosis of basal breast cancers. Molecular Cancer, 2011, 10, 86.	7.9	46
105	Genomic profiling of inflammatory breast cancer: A review. Breast, 2014, 23, 538-545.	0.9	46
106	Gene expression profiling of inflammatory breast cancer. Cancer, 2010, 116, 2783-2793.	2.0	45
107	Aurora B -TACC1 protein complex in cytokinesis. Oncogene, 2004, 23, 4516-4522.	2.6	43
108	Poly(ADP-Ribose) Polymerase 1 (PARP1) Overexpression in Human Breast Cancer Stem Cells and Resistance to Olaparib. PLoS ONE, 2014, 9, e104302.	1.1	43

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109	OFIP/KIAA0753 forms a complex with OFD1 and FOR20 at pericentriolar satellites and centrosomes and is mutated in one individual with oral-facial-digital syndrome. Human Molecular Genetics, 2016, 25, 497-513.	1.4	42
110	Genomic analysis of myeloproliferative neoplasms in chronic and acute phases. Haematologica, 2017, 102, e11-e14.	1.7	42
111	SLX4 interacts with RTEL1 to prevent transcription-mediated DNA replication perturbations. Nature Structural and Molecular Biology, 2020, 27, 438-449.	3.6	39
112	Myelodysplastic syndromes: lost between two states?. Leukemia, 2010, 24, 1-5.	3.3	38
113	Array comparative genomic hybridization and sequencing of 23 genes in 80 patients with myelofibrosis at chronic or acute phase. Haematologica, 2014, 99, 37-45.	1.7	38
114	Systems biology analysis reveals NFAT5 as a novel biomarker and master regulator of inflammatory breast cancer. Journal of Translational Medicine, 2015, 13, 138.	1.8	38
115	Validation and comparison of the molecular classifications of pancreatic carcinomas. Molecular Cancer, 2017, 16, 168.	7.9	38
116	MMP2 and MMP9 serum levels are associated with favorable outcome in patients with inflammatory breast cancer treated with bevacizumab-based neoadjuvant chemotherapy in the BEVERLY-2 study. Oncotarget, 2016, 7, 18531-18540.	0.8	38
117	Mutations and deletions of the SUZ12 polycomb gene in myeloproliferative neoplasms. Blood Cancer Journal, 2011, 1, e33-e33.	2.8	36
118	Gene mutations differently impact the prognosis of the myelodysplastic and myeloproliferative classes of chronic myelomonocytic leukemia. American Journal of Hematology, 2014, 89, 604-609.	2.0	36
119	The centrosomal FOP protein is required for cell cycle progression and survival. Cell Cycle, 2009, 8, 1217-1227.	1.3	34
120	8q24 Cancer Risk Allele Associated with Major Metastatic Risk in Inflammatory Breast Cancer. PLoS ONE, 2012, 7, e37943.	1.1	34
121	Brief Reports: A Distinct DNA Methylation Signature Defines Breast Cancer Stem Cells and Predicts Cancer Outcome. Stem Cells, 2014, 32, 3031-3036.	1.4	33
122	Molecular characterization of acute erythroid leukemia (M6-AML) using targeted next-generation sequencing. Leukemia, 2016, 30, 966-970.	3.3	31
123	Sensitive and easy screening for circulating tumor cells by flow cytometry. JCI Insight, 2019, 4, .	2.3	31
124	Comparison of the prognostic value of genomic grade index, Ki67 expression and mitotic activity index in early node-positive breast cancer patients. Annals of Oncology, 2013, 24, 625-632.	0.6	28
125	Human erythroleukemia genetics and transcriptomes identify master transcription factors as functional disease drivers. Blood, 2020, 136, 698-714.	0.6	28
126	A Negative Feedback Regulatory Loop Associates the Tyrosine Kinase Receptor ERBB2 and the Transcription Factor GATA4 in Breast Cancer Cells. Molecular Cancer Research, 2009, 7, 402-414.	1.5	27

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127	A genomeâ€•wide <scp>RNA</scp> i screen reveals essential therapeutic targets of breast cancer stem cells. EMBO Molecular Medicine, 2019, 11, e9930.	3.3	27
128	The therapeutic response of ER+/HER2âˆ’ breast cancers differs according to the molecular Basal or Luminal subtype. Npj Breast Cancer, 2020, 6, 8.	2.3	27
129	MARCKS protein overexpression in inflammatory breast cancer. Oncotarget, 2017, 8, 6246-6257.	0.8	27
130	Rearrangements involving 12q in myeloproliferative disorders: possible role of HMGA2 and SOCS2 genes. Cancer Genetics and Cytogenetics, 2007, 176, 80-88.	1.0	26
131	A case of inv(8)(p11q24) associated with acute myeloid leukemia involves theMOZ andCBP genes in a masked t(8;16)., 1999, 26, 161-165.		25
132	Signaling pathway switch in breast cancer. Cancer Cell International, 2013, 13, 66.	1.8	25
133	EFA6B Antagonizes Breast Cancer. Cancer Research, 2014, 74, 5493-5506.	0.4	25
134	Characterization and Targeting of Platelet-Derived Growth Factor Receptor alpha (PDGFRA) in Inflammatory Breast Cancer (IBC). Neoplasia, 2017, 19, 564-573.	2.3	25
135	A Comparison of DNA Mutation and Copy Number Profiles of Primary Breast Cancers and Paired Brain Metastases for Identifying Clinically Relevant Genetic Alterations in Brain Metastases. Cancers, 2019, 11, 665.	1.7	25
136	Variant MYST4-CBP gene fusion in a t(10;16) acute myeloid leukaemia. British Journal of Haematology, 2004, 125, 601-604.	1.2	24
137	Protein expression, survival and docetaxel benefit in node-positive breast cancer treated with adjuvant chemotherapy in the FNCLCC - PACS 01 randomized trial. Breast Cancer Research, 2011, 13, R109.	2.2	24
138	The Genomic Grade Index predicts postoperative clinical outcome in patients with soft-tissue sarcoma. Annals of Oncology, 2018, 29, 459-465.	0.6	24
139	Prospective high-throughput genome profiling of advanced cancers: results of the PERMED-01 clinical trial. Genome Medicine, 2021, 13, 87.	3.6	24
140	Liquid Biopsies for Ovarian Carcinoma: How Blood Tests May Improve the Clinical Management of a Deadly Disease. Cancers, 2019, 11, 774.	1.7	23
141	XPO1 Expression Is a Poor-Prognosis Marker in Pancreatic Adenocarcinoma. Journal of Clinical Medicine, 2019, 8, 596.	1.0	23
142	NOTCH and DNA repair pathways are more frequently targeted by genomic alterations in inflammatory than in nonâ€•inflammatory breast cancers. Molecular Oncology, 2020, 14, 504-519.	2.1	23
143	Immune landscape of inflammatory breast cancer suggests vulnerability to immune checkpoint inhibitors. OncoImmunology, 2021, 10, 1929724.	2.1	22
144	p53 and cancer stem cells: The mevalonate connexion. Cell Cycle, 2012, 11, 2583-2584.	1.3	21

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145	Gene Expression Profiling of Solitary Fibrous Tumors. PLoS ONE, 2013, 8, e64497.	1.1	21
146	Drug response profiling can predict response to ponatinib in a patient with t(1;9)(q24;q34)-associated B-cell acute lymphoblastic leukemia. Blood Cancer Journal, 2015, 5, e292-e292.	2.8	21
147	Identification of a YAC spanning the translocation breakpoint t(8;22) associated with acute monocytic leukemia. , 1996, 15, 191-194.		20
148	Molecular classification as prognostic factor and guide for treatment decision of pancreatic cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2018, 1869, 248-255.	3.3	20
149	Genomic Grade Index predicts postoperative clinical outcome of GIST. British Journal of Cancer, 2012, 107, 1433-1441.	2.9	19
150	A chemogenomic approach to identify personalized therapy for patients with relapse or refractory acute myeloid leukemia: results of a prospective feasibility study. Blood Cancer Journal, 2020, 10, 64.	2.8	18
151	How to best classify breast cancer: Conventional and novel classifications (Review). International Journal of Oncology, 2005, 27, 1307.	1.4	17
152	Alterations of NFIA in chronic malignant myeloid diseases. Leukemia, 2009, 23, 583-585.	3.3	17
153	Ajuba: a new microtubuleâ€•associated protein that interacts with BUBR1 and Aurora B at kinetochores in metaphase. Biology of the Cell, 2009, 101, 221-240.	0.7	17
154	Rare mutations in DNMT3A in myeloproliferative neoplasms and myelodysplastic syndromes. Blood Cancer Journal, 2011, 1, e18-e18.	2.8	17
155	Development of parallel reaction monitoring (PRM)-based quantitative proteomics applied to HER2-Positive breast cancer. Oncotarget, 2018, 9, 33762-33777.	0.8	17
156	Targeted molecular characterization shows differences between primary and secondary myelofibrosis. Genes Chromosomes and Cancer, 2020, 59, 30-39.	1.5	17
157	Distant metastasis: not out of reach any more. Journal of Biology, 2009, 8, 28.	2.7	16
158	Mutation of FOP/FGFR1OP in mice recapitulates human short rib-polydactyly ciliopathy. Human Molecular Genetics, 2018, 27, 3377-3391.	1.4	15
159	PARP1 expression in soft tissue sarcomas is a poorâ€•prognosis factor and a new potential therapeutic target. Molecular Oncology, 2019, 13, 1577-1588.	2.1	15
160	Immunologic constant of rejection signature is prognostic in soft-tissue sarcoma and refines the CINSARC signature. , 2022, 10, e003687.		15
161	Endometriosis-Associated Ovarian Carcinomas. New England Journal of Medicine, 2011, 364, 482-485.	13.9	14
162	â€œStealthâ€•tumors. OncoImmunology, 2012, 1, 366-368.	2.1	14

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163	Gene expression profiling of breast tumor cell lines to predict for therapeutic response to microtubule-stabilizing agents. Breast Cancer Research and Treatment, 2012, 132, 1035-1047.	1.1	14
164	Revisiting the Concept of Stress in the Prognosis of Solid Tumors: A Role for Stress Granules Proteins?. Cancers, 2020, 12, 2470.	1.7	14
165	A further case of acute myelomonocytic leukemia with inv(8) chromosomal rearrangement and MOZ-NCOA2 gene fusion. International Journal of Molecular Medicine, 2003, 12, 423-8.	1.8	14
166	A reason why the ERBB2 gene is amplified and not mutated in breast cancer. Cancer Cell International, 2009, 9, 5.	1.8	13
167	ECT2 associated to PRICKLE1 are poor-prognosis markers in triple-negative breast cancer. British Journal of Cancer, 2019, 120, 931-940.	2.9	13
168	BMI1 nuclear location is critical for RAD51-dependent response to replication stress and drives chemoresistance in breast cancer stem cells. Cell Death and Disease, 2022, 13, 96.	2.7	13
169	Overcoming Resistance to Antiâ€“Nectin-4 Antibody-Drug Conjugate. Molecular Cancer Therapeutics, 2022, 21, 1227-1235.	1.9	13
170	New types of MYST3-CBP and CBP-MYST3 fusion transcripts in t(8;16)(p11;p13) acute myeloid leukemias. Haematologica, 2007, 92, 262-263.	1.7	12
171	The CINSARC signature: Prognostic and predictive of response to chemotherapy?. Cell Cycle, 2010, 9, 4025-4027.	1.3	12
172	The emerging role of the TGFÎ² tumor suppressor pathway in pancreatic cancer. Cell Cycle, 2012, 11, 683-686.	1.3	12
173	De-repression of the RAC activator ELMO1 in cancer stem cells drives progression of TGFÎ²-deficient squamous cell carcinoma from transition zones. ELife, 2017, 6, .	2.8	12
174	RAS activation induces synthetic lethality of MEK inhibition with mitochondrial oxidative metabolism in acute myeloid leukemia. Leukemia, 2022, 36, 1237-1252.	3.3	12
175	Gene expression profiling separates chronic myelomonocytic leukemia in two molecular subtypes. Leukemia, 2007, 21, 2359-2362.	3.3	11
176	Targeting breast cancer stem cells: fishing season open!. Breast Cancer Research, 2010, 12, 312.	2.2	11
177	Gene expression profile predicts outcome after anthracycline-based adjuvant chemotherapy in early breast cancer. Breast Cancer Research and Treatment, 2011, 127, 363-373.	1.1	11
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179	Epigenetic down-regulation of the HIST1 locus predicts better prognosis in acute myeloid leukemia with NPM1 mutation. Clinical Epigenetics, 2019, 11, 141.	1.8	11
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