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List of Publications by Year
in descending order

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107	7,150	57758	58581
papers	citations	44 h-index	82 g-index

107	107	107	10411
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Resistance of B-Cell Lymphomas to CAR T-Cell Therapy Is Associated With Genomic Tumor Changes Which Can Result in Transdifferentiation. American Journal of Surgical Pathology, 2022, 46, 742-753.	3.7	9
2	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.	6.3	13
3	Circulating tumor DNA predicts efficacy of a dual AKT/p70S6K inhibitor (LY2780301) plus paclitaxel in metastatic breast cancer: plasma analysis of the TAKTIC phase IB/II study. Molecular Oncology, 2022, 16, 2057-2070.	4.6	4
4	Genomic analysis of paired IDHwt glioblastomas reveals recurrent alterations of MPDZ at relapse after radiotherapy and chemotherapy. Journal of the Neurological Sciences, 2022, 436, 120207.	0.6	6
5	Investigation of Molecular Features Involved in Clinical Responses and Survival in Advanced Endometrial Carcinoma Treated by Hormone Therapy. Journal of Personalized Medicine, 2022, 12, 655.	2.5	2
6	Molecular Profiles of Advanced Urological Cancers in the PERMED-01 Precision Medicine Clinical Trial. Cancers, 2022, 14, 2275.	3.7	0
7	Overcoming Resistance to Antiâ€“Nectin-4 Antibody-Drug Conjugate. Molecular Cancer Therapeutics, 2022, 21, 1227-1235.	4.1	13
8	Case Report: Two Cases of Metastatic Pancreatoblastoma in Adults: Efficacy of Folfirinox and Implication of the Wnt/Î²-Catenin Pathway in Genomic Analysis. Frontiers in Oncology, 2021, 11, 564506.	2.8	6
9	Prospective high-throughput genome profiling of advanced cancers: results of the PERMED-01 clinical trial. Genome Medicine, 2021, 13, 87.	8.2	24
10	High-grade Follicular Lymphomas Exhibit Clinicopathologic, Cytogenetic, and Molecular Diversity Extending Beyond Grades 3A and 3B. American Journal of Surgical Pathology, 2021, 45, 1324-1336.	3.7	15
11	TAKTIC: A prospective, multicentre, uncontrolled, phase IB/II study of LY2780301, a p70S6K/AKT inhibitor, in combination with weekly paclitaxel in HER2-negative advanced breast cancer patients. European Journal of Cancer, 2021, 159, 205-214.	2.8	7
12	Targeted molecular characterization shows differences between primary and secondary myelofibrosis. Genes Chromosomes and Cancer, 2020, 59, 30-39.	2.8	17
13	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.	4.6	23
14	Acute erythroid leukemias have a distinct molecular hierarchy from non-erythroid acute myeloid leukemias. Haematologica, 2020, 105, e340-e342.	3.5	5
15	EBV+ diffuse large B-cell lymphoma associated with chronic inflammation expands the spectrum of breast implant-related lymphomas. Blood, 2020, 135, 2004-2009.	1.4	9
16	A Tyrosine Kinase Expression Signature Predicts the Post-Operative Clinical Outcome in Triple Negative Breast Cancers. Cancers, 2019, 11, 1158.	3.7	6
17	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.	3.7	25
18	High Response to Cetuximab in a Patient With EGFR-Amplified Heavily Pretreated Metastatic Triple-Negative Breast Cancer. JCO Precision Oncology, 2019, 3, 1-8.	3.0	5

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19	Major Response to Carboplatin in a Patient With Metastatic Triple-Negative Breast Cancer With Somatic Mutation of BRCA1 and Loss of RAD51B. JCO Precision Oncology, 2019, 3, 1-9.	3.0	0
20	Mutation patterns in essential thrombocythemia, polycythemia vera and secondary myelofibrosis. Leukemia and Lymphoma, 2019, 60, 1289-1293.	1.3	4
21	Common origin of sequential cutaneous CD30+ lymphoproliferations with nodal involvement evidenced by genomeâ€wide clonal evolution. Histopathology, 2019, 74, 654-662.	2.9	6
22	CDKN2A/B Deletion and Double-hit Mutations of the MAPK Pathway Underlie the Aggressive Behavior of Langerhans Cell Tumors. American Journal of Surgical Pathology, 2018, 42, 150-159.	3.7	23
23	Poly (ADP-Ribose) Polymerase Inhibitors for De Novo BRCA2-Null Small-Cell Prostate Cancer. JCO Precision Oncology, 2018, 2, 1-8.	3.0	2
24	Development of parallel reaction monitoring (PRM)-based quantitative proteomics applied to HER2-Positive breast cancer. Oncotarget, 2018, 9, 33762-33777.	1.8	17
25	Genomic analysis of myeloproliferative neoplasms in chronic and acute phases. Haematologica, 2017, 102, e11-e14.	3.5	42
26	Epigenetically centered evolution in an example of myeloid malignancy. American Journal of Hematology, 2016, 91, E361-2.	4.1	0
27	Targeted NGS, array-CGH, and patient-derived tumor xenografts for precision medicine in advanced breast cancer: a single-center prospective study. Oncotarget, 2016, 7, 79428-79441.	1.8	11
28	Comparative genomic analysis of primary tumors and metastases in breast cancer. Oncotarget, 2016, 7, 27208-27219.	1.8	69
29	Prognostic and predictive value of PDL1 expression in breast cancer. Oncotarget, 2015, 6, 5449-5464.	1.8	424
30	Candidate Luminal B Breast Cancer Genes Identified by Genome, Gene Expression and DNA Methylation Profiling. PLoS ONE, 2014, 9, e81843.	2.5	53
31	Claudin-low breast cancers: clinical, pathological, molecular and prognostic characterization. Molecular Cancer, 2014, 13, 228.	19.2	91
32	Brief Reports: A Distinct DNA Methylation Signature Defines Breast Cancer Stem Cells and Predicts Cancer Outcome. Stem Cells, 2014, 32, 3031-3036.	3.2	33
33	ESPL1 is a candidate oncogene of luminal B breast cancers. Breast Cancer Research and Treatment, 2014, 147, 51-59.	2.5	51
34	Early lesions of follicular lymphoma: a genetic perspective. Haematologica, 2014, 99, 481-488.	3.5	91
35	Comparative genomic hybridisation array and DNA sequencing to direct treatment of metastatic breast cancer: a multicentre, prospective trial (SAFIR01/UNICANCER). Lancet Oncology, The, 2014, 15, 267-274.	10.7	351
36	Array comparative genomic hybridization and sequencing of 23 genes in 80 patients with myelofibrosis at chronic or acute phase. Haematologica, 2014, 99, 37-45.	3.5	38

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37	Abstract 3881: A distinct DNA methylation signature defines breast cancer stem cells and predict cancer outcome. , 2014, , .		1
38	Abstract 3020: Patient-derived xenograft (PDX) models to study the role of breast cancer stem cells in metastasis formation. , 2014, , .		0
39	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.	0.9	103
40	A new case with 10q23 interstitial deletion encompassing both PTEN and BMPR1A narrows the genetic region deleted in juvenile polyposis syndrome. Journal of Applied Genetics, 2013, 54, 43-47.	1.9	9
41	Comprehensive genome characterization of solitary fibrous tumors using highâ€resolution arrayâ€based comparative genomic hybridization. Genes Chromosomes and Cancer, 2013, 52, 156-164.	2.8	6
42	Gene Expression Profiling of Solitary Fibrous Tumors. PLoS ONE, 2013, 8, e64497.	2.5	21
43	Alterations of polycomb gene BMI1 in human myeloproliferative neoplasms. Cell Cycle, 2012, 11, 3141-3142.	2.6	4
44	Cortical and Subventricular Zone Glioblastoma-Derived Stem-Like Cells Display Different Molecular Profiles and Differential In Vitro and In Vivo Properties. Annals of Surgical Oncology, 2012, 19, 608-619.	1.5	32
45	8q24 Cancer Risk Allele Associated with Major Metastatic Risk in Inflammatory Breast Cancer. PLoS ONE, 2012, 7, e37943.	2.5	34
46	Search for Distinctive Markers in DNT and Cortical Grade II Glioma in Children: Same Clinicopathological and Molecular Entities?. Current Topics in Medicinal Chemistry, 2012, 12, 1683-1692.	2.1	9
47	Poly(ADP-ribose) polymerase-1 mRNA expression in human breast cancer: a meta-analysis. Breast Cancer Research and Treatment, 2011, 127, 273-281.	2.5	66
48	ZNF703 gene amplification at 8p12 specifies luminal B breast cancer. EMBO Molecular Medicine, 2011, 3, 153-166.	6.9	126
49	Genome profiling of pancreatic adenocarcinoma. Genes Chromosomes and Cancer, 2011, 50, 456-465.	2.8	107
50	High-Resolution Comparative Genomic Hybridization of Inflammatory Breast Cancer and Identification of Candidate Genes. PLoS ONE, 2011, 6, e16950.	2.5	57
51	Down-Regulation of ECRG4, a Candidate Tumor Suppressor Gene, in Human Breast Cancer. PLoS ONE, 2011, 6, e27656.	2.5	143
52	Absence of R140Q mutation of isocitrate dehydrogenase 2 in gliomas and breast cancers. Oncology Letters, 2010, 1, 883-884.	1.8	7
53	Genome profiling of ERBB2-amplified breast cancers. BMC Cancer, 2010, 10, 539.	2.6	136
54	BARD1 homozygous deletion, a possible alternative to BRCA1 mutation in basal breast cancer. Genes Chromosomes and Cancer, 2010, 49, 1143-1151.	2.8	23

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55	Alteration of cohesin genes in myeloid diseases. American Journal of Hematology, 2010, 85, 717-719.	4.1	46
56	ASXL1 mutation is associated with poor prognosis and acute transformation in chronic myelomonocytic leukaemia. British Journal of Haematology, 2010, 151, 365-375.	2.5	199
57	Loss, mutation and deregulation of L3MBTL4 in breast cancers. Molecular Cancer, 2010, 9, 213.	19.2	63
58	Germline APC mutation spectrum derived from 863 genomic variations identified through a 15-year medical genetics service to French patients with FAP. Journal of Medical Genetics, 2010, 47, 721-722.	3.2	32
59	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.	3.4	27
60	Mutations of polycombâ€associated gene ASXL1 in myelodysplastic syndromes and chronic myelomonocytic leukaemia. British Journal of Haematology, 2009, 145, 788-800.	2.5	537
61	Absence of ESR1 amplification in a series of breast cancers. International Journal of Cancer, 2008, 123, 2970-2972.	5.1	23
62	Genome profiling of chronic myelomonocytic leukemia: frequent alterations of RAS and RUNX1genes. BMC Cancer, 2008, 8, 299.	2.6	109
63	Expression of the tachykinin receptor mRNAs in healthy human colon. European Journal of Pharmacology, 2008, 599, 121-125.	3.5	17
64	Integrated Profiling of Basal and Luminal Breast Cancers. Cancer Research, 2007, 67, 11565-11575.	0.9	254
65	New types of MYST3-CBP and CBP-MYST3 fusion transcripts in t(8;16)(p11;p13) acute myeloid leukemias. Haematologica, 2007, 92, 262-263.	3.5	12
66	Comparison of a Selection of Rapid Automated DNA and RNA Extraction Technologies for Detection of Somatic or Constitutional Gene Abnormalities in Cancer Diagnosis. Cell Preservation Technology, 2007, 5, 2-15.	0.6	2
67	Nectin-4 is a new histological and serological tumor associated marker for breast cancer. BMC Cancer, 2007, 7, 73.	2.6	134
68	Combined translocation with ZNF198-FGFR1 gene fusion and deletion of potential tumor suppressors in a myeloproliferative disorder. Cancer Genetics and Cytogenetics, 2007, 173, 154-158.	1.0	24
69	Rearrangements involving 12q in myeloproliferative disorders: possible role of HMGA2 and SOCS2 genes. Cancer Genetics and Cytogenetics, 2007, 176, 80-88.	1.0	26
70	High Frequency of Chromosome 14 Deletion in Early-Onset Colon Cancer. Diseases of the Colon and Rectum, 2007, 50, 1881-1886.	1.3	22
71	Gene Expression Profiling Shows Medullary Breast Cancer Is a Subgroup of Basal Breast Cancers. Cancer Research, 2006, 66, 4636-4644.	0.9	273
72	Prognosis and Gene Expression Profiling of 20q13-Amplified Breast Cancers. Clinical Cancer Research, 2006, 12, 4533-4544.	7.0	121

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73	ETV6 gene rearrangements in invasive breast carcinoma. Genes Chromosomes and Cancer, 2005, 44, 103-108.	2.8	30
74	Comprehensive Profiling of 8p11-12 Amplification in Breast Cancer. Molecular Cancer Research, 2005, 3, 655-667.	3.4	201
75	Dual lympho-myeloproliferative disorder in a patient with t(8;22) with BCR-FGFR1 gene fusion. International Journal of Oncology, 2005, 26, 1485.	3.3	8
76	Protein expression profiling identifies subclasses of breast cancer and predicts prognosis. Cancer Research, 2005, 65, 767-79.	0.9	148
77	A Recurrent Chromosome Breakpoint in Breast Cancer at the NRG1/Neuregulin 1/Heregulin Gene. Cancer Research, 2004, 64, 6840-6844.	0.9	185
78	Variant MYST4-CBP gene fusion in a t(10;16) acute myeloid leukaemia. British Journal of Haematology, 2004, 125, 601-604.	2.5	24
79	Identification and validation of an ERBB2 gene expression signature in breast cancers. Oncogene, 2004, 23, 2564-2575.	5.9	117
80	Comparative multi-methodological measurement of ERBB2 status in breast cancer. Journal of Pathology, 2004, 202, 286-298.	4.5	61
81	A recurrent chromosome translocation breakpoint in breast and pancreatic cancer cell lines targets the neuregulin/NRG1 gene. Genes Chromosomes and Cancer, 2003, 37, 333-345.	2.8	56
82	Loss of FHIT protein expression is a marker of adverse evolution in good prognosis localized breast cancer. International Journal of Cancer, 2003, 107, 854-862.	5.1	19
83	Chromosome arm 8p and cancer: a fragile hypothesis. Lancet Oncology, The, 2003, 4, 639-642.	10.7	57
84	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.	4.0	5
85	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.	4.0	14
86	Interaction between Two Ubiquitin-Protein Isopeptide Ligases of Different Classes, CBLC and AIP4/ITCH. Journal of Biological Chemistry, 2002, 277, 45267-45275.	3.4	78
87	Gene expression profiles of poor-prognosis primary breast cancer correlate with survival. Human Molecular Genetics, 2002, 11, 863-872.	2.9	117
88	Loss of heterozygosity at microsatellite markers from region p11-21 of chromosome 8 in microdissected breast tumor but not in peritumoral cells. International Journal of Oncology, 2002, 21, 989.	3.3	7
89	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.	3.8	144
90	Reciprocal translocations in breast tumor cell lines: Cloning of a t(3;20) that targets theFHITgene. Genes Chromosomes and Cancer, 2002, 35, 204-218.	2.8	30

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91	Carcinogenesis and translational controls: TACC1 is down-regulated in human cancers and associates with mRNA regulators. Oncogene, 2002, 21, 5619-5630.	5.9	73
92	WNT pathway and mammary carcinogenesis: Loss of expression of candidate tumor suppressor gene SFRP1 in most invasive carcinomas except of the medullary type. Oncogene, 2001, 20, 5810-5817.	5.9	169
93	Novel, Soluble Isoform of the Herpes Simplex Virus (HSV) Receptor Nectin1 (or PRR1-HIgR-HveC) Modulates Positively and Negatively Susceptibility to HSV Infection. Journal of Virology, 2001, 75, 5684-5691.	3.4	46
94	VEGFc and VEGFR3 expression in human thyroid pathologies. , 2000, 86, 47-52.		41
95	ERBIN: a basolateral PDZ protein that interacts with the mammalian ERBB2/HER2 receptor. Nature Cell Biology, 2000, 2, 407-414.	10.3	273
96	Human nectin3/PRR3: a novel member of the PVR/PRR/nectin family that interacts with afadin. Gene, 2000, 255, 347-355.	2.2	68
97	Differential expression assay of chromosome arm 8p genes identifies Frizzled-related (FRP1/FRZB) and Fibroblast Growth Factor Receptor 1 (FGFR1) as candidate breast cancer genes. Oncogene, 1999, 18, 1903-1910.	5.9	118
98	t(6;8), t(8;9) and t(8;13) translocations associated with stem cell myeloproliferative disorders have close or identical breakpoints in chromosome region 8p11-12. Oncogene, 1998, 16, 945-949.	5.9	68
99	FGF7 protein expression in human breast carcinomas. , 1998, 186, 269-274.		15
100	Chromosome region 8p11-p21: Refined mapping and molecular alterations in breast cancer. , 1998, 22, 186-199.		55
101	Expression offgf andfgf receptor genes in human breast cancer. International Journal of Cancer, 1995, 61, 170-176.	5.1	213
102	Patterns of loss of heterozygosity at loci from chromosome arm 13q suggest a possible involvement ofBRCA2 in sporadic breast tumors. Genes Chromosomes and Cancer, 1995, 13, 291-294.	2.8	37
103	Optimization of immunohistochemical detection of ERBB2 in human breast cancer: Impact of fixation. Journal of Pathology, 1994, 173, 65-75.	4.5	114
104	Expression of the FGFR1 gene in human breast-carcinoma cells. International Journal of Cancer, 1994, 59, 373-378.	5.1	88
105	Unrestricted T-cell receptor V-region gene repertoire in tumor-infiltrating lymphocytes from human breast carcinomas. Cancer, 1993, 72, 506-510.	4.1	12
106	FGFRI andPLAT genes and DNA amplification at 8p 12 in breast and ovarian cancers. Genes Chromosomes and Cancer, 1993, 7, 219-226.	2.8	158
107	Antiestrogen binding within different pituitary cell populations. Comparison with androgen and estrogen receptors. The Journal of Steroid Biochemistry, 1986, 24, 395-399.	1.1	1