Ãke Borg

List of Publications by Year
in descending order

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255 papers	39,393 citations	7096 78 h-index	3182 186 g-index
270 all docs	270 docs citations	270 times ranked	48980 citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
2	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
3	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. Science, 2016, 353, 78-82.	12.6	1,983
4	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
5	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
6	Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 539-548.	27.0	1,669
7	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
8	PIK3CA Mutations Correlate with Hormone Receptors, Node Metastasis, and ERBB2, and Are Mutually Exclusive with PTEN Loss in Human Breast Carcinoma. Cancer Research, 2005, 65, 2554-2559.	0.9	813
9	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	30.7	769
10	High-definition spatial transcriptomics for in situ tissue profiling. Nature Methods, 2019, 16, 987-990.	19.0	708
11	Recruitment of HIF-1Î± and HIF-2Î± to common target genes is differentially regulated in neuroblastoma: HIF-2Î± promotes an aggressive phenotype. Cancer Cell, 2006, 10, 413-423.	16.8	624
12	Association Between <emph type="ital">BRCA1</emph> and <emph type="ital">BRCA2</emph> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. JAMA - Journal of the American Medical Association, 2012, 307, 382.	7.4	546
13	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
14	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
15	The CD44+/CD24-phenotype is enriched in basal-like breast tumors. Breast Cancer Research, 2008, 10, R53.	5.0	464
16	Poor prognosis in carcinoma is associated with a gene expression signature of aberrant PTEN tumor suppressor pathway activity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7564-7569.	7.1	445
17	Serial monitoring of circulating tumor <scp>DNA</scp> in patients with primary breast cancer for detection of occult metastatic disease. EMBO Molecular Medicine, 2015, 7, 1034-1047.	6.9	380
18	Amplification and Deletion of Topoisomerase IIÎ± Associate with ErbB-2 Amplification and Affect Sensitivity to Topoisomerase II Inhibitor Doxorubicin in Breast Cancer. American Journal of Pathology, 2000, 156, 839-847.	3.8	361

#	Article	IF	Citations
19	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. PLoS ONE, 2011, 6, e17911.	2.5	361
20	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
21	Recurrent gross mutations of the PTEN tumor suppressor gene in breast cancers with deficient DSB repair. Nature Genetics, 2008, 40, 102-107.	21.4	316
22	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	1.6	270
23	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
24	Variation of Breast Cancer Risk Among BRCA1/2 Carriers. JAMA - Journal of the American Medical Association, 2008, 299, 194-201.	7.4	244
25	Gene Expression Profilingâ€"Based Identification of Molecular Subtypes in Stage IV Melanomas with Different Clinical Outcome. Clinical Cancer Research, 2010, 16, 3356-3367.	7.0	235
26	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	12.8	235
27	ERBB2 amplification is associated with tamoxifen resistance in steroid-receptor positive breast cancer. Cancer Letters, 1994, 81, 137-144.	7.2	230
28	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	27.8	229
29	MiRNA expression in urothelial carcinomas: Important roles of miRâ€10a, miRâ€222, miRâ€125b, miRâ€7 and miRâ€452 for tumor stage and metastasis, and frequent homozygous losses of miRâ€31. International Journal of Cancer, 2009, 124, 2236-2242.	5.1	222
30	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. Nature Medicine, 2019, 25, 1526-1533.	30.7	218
31	Denaturing High-Performance Liquid Chromatography Detects Reliably BRCA1 and BRCA2 Mutations. Genomics, 1999, 62, 369-376.	2.9	214
32	Integrating spatial gene expression and breast tumour morphology via deep learning. Nature Biomedical Engineering, 2020, 4, 827-834.	22.5	208
33	CXCL14 is an autocrine growth factor for fibroblasts and acts as a multi-modal stimulator of prostate tumor growth. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3414-3419.	7.1	204
34	Identification of New MicroRNAs in Paired Normal and Tumor Breast Tissue Suggests a Dual Role for the ERBB2/Her2 Gene. Cancer Research, 2011, 71, 78-86.	0.9	191
35	Molecular classification of familial non- BRCA1/BRCA2 breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2532-2537.	7.1	182
36	RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. Carcinogenesis, 2005, 27, 1593-1599.	2.8	179

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37	Highâ€resolution genomic profiles of breast cancer cell lines assessed by tiling BAC array comparative genomic hybridization. Genes Chromosomes and Cancer, 2007, 46, 543-558.	2.8	176
38	Characterization of topoisomerase II? gene amplification and deletion in breast cancer. Genes Chromosomes and Cancer, 1999, 26, 142-150.	2.8	172
39	Steroid receptors in hereditary breast carcinomas associated with BRCA1 or BRCA2 mutations or unknown susceptibility genes. Cancer, 1998, 83, 310-319.	4.1	170
40	Common Breast Cancer Susceptibility Alleles and the Risk of Breast Cancer for BRCA1 and BRCA2 Mutation Carriers: Implications for Risk Prediction. Cancer Research, 2010, 70, 9742-9754.	0.9	169
41	Cytokeratin 5/14-positive breast cancer: true basal phenotype confined to BRCA1 tumors. Modern Pathology, 2005, 18, 1321-1328.	5.5	167
42	Population-Based Study of the Risk of Second Primary Contralateral Breast Cancer Associated With Carrying a Mutation inBRCA1orBRCA2. Journal of Clinical Oncology, 2010, 28, 2404-2410.	1.6	166
43	Amplification of cyclin D1 in squamous cell carcinoma of the head and neck and the prognostic value of chromosomal abnormalities and cyclin D1 overexpression. , 1997, 79, 380-389.		164
44	Estrogen Receptor Î² Expression Is Associated with Tamoxifen Response in ERÎ±-Negative Breast Carcinoma. Clinical Cancer Research, 2007, 13, 1987-1994.	7.0	160
45	TP53 mutations and breast cancer prognosis: Particularly poor survival rates for cases with mutations in the zinc-binding domains. Genes Chromosomes and Cancer, 1995, 14, 71-75.	2.8	154
46	Haplotype and Phenotype Analysis of Nine Recurrent BRCA2 Mutations in 111 Families: Results of an International Study. American Journal of Human Genetics, 1998, 62, 1381-1388.	6.2	150
47	Molecular stratification of metastatic melanoma using gene expression profiling : Prediction of survival outcome and benefit from molecular targeted therapy. Oncotarget, 2015, 6, 12297-12309.	1.8	148
48	Distinct Genomic Profiles in Hereditary Breast Tumors Identified by Array-Based Comparative Genomic Hybridization. Cancer Research, 2005, 65, 7612-7621.	0.9	147
49	The non-coding RNA of the multidrug resistance-linked vault particle encodes multiple regulatory small RNAs. Nature Cell Biology, 2009, 11, 1268-1271.	10.3	147
50	Identification of Subtypes in Human Epidermal Growth Factor Receptor 2â€“Positive Breast Cancer Reveals a Gene Signature Prognostic of Outcome. Journal of Clinical Oncology, 2010, 28, 1813-1820.	1.6	145
51	Spatial deconvolution of HER2-positive breast cancer delineates tumor-associated cell type interactions. Nature Communications, 2021, 12, 6012.	12.8	140
52	Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. Molecular Oncology, 2012, 6, 494-506.	4.6	136
53	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	6.3	134
54	Patterns of chromosomal imbalances defines subgroups of breast cancer with distinct clinical features and prognosis. A study of 305 tumors by comparative genomic hybridization. Cancer Research, 2003, 63, 8861-8.	0.9	134

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55	Amplification and Overexpression of p40 Subunit of Eukaryotic Translation Initiation Factor 3 in Breast and Prostate Cancer. American Journal of Pathology, 1999, 154, 1777-1783.	3.8	132
56	The Sweden Cancerome Analysis Network - Breast (SCAN-B) Initiative: a large-scale multicenter infrastructure towards implementation of breast cancer genomic analyses in the clinical routine. Genome Medicine, 2015, 7, 20.	8.2	129
57	The contribution of the hereditary nonpolyposis colorectal cancer syndrome to the development of ovarian cancer. Gynecologic Oncology, 2006, 101, 238-243.	1.4	125
58	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
59	Cancer-Associated Fibroblasts Expressing CXCL14 Rely upon NOS1-Derived Nitric Oxide Signaling for Their Tumor-Supporting Properties. Cancer Research, 2014, 74, 2999-3010.	0.9	120
60	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
61	Human neuroblastoma cells exposed to hypoxia: induction of genes associated with growth, survival, and aggressive behavior. Experimental Cell Research, 2004, 295, 469-487.	2.6	114
62	Pregnancy-associated breast cancer in BRCA1 and BRCA2 germline mutation carriers. Lancet, The, 1998, 352, 1359-1360.	13.7	111
63	Screening for copyâ€number alterations and loss of heterozygosity in chronic lymphocytic leukemiaâ€"A comparative study of four differently designed, high resolution microarray platforms. Genes Chromosomes and Cancer, 2008, 47, 697-711.	2.8	111
64	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. Journal of the National Cancer Institute, 2020, 112, 1242-1250.	6.3	106
65	Characterization ofBRCA1andBRCA2deleterious mutations and variants of unknown clinical significance in unilateral and bilateral breast cancer: the WECARE study. Human Mutation, 2010, 31, E1200-E1240.	2.5	103
66	c-myc amplification is an independent prognostic factor in postmenopausal breast cancer. International Journal of Cancer, 1992, 51, 687-691.	5.1	102
67	Large scale multifactorial likelihood quantitative analysis of BRCA1 and BRCA2 variants: An ENIGMA resource to support clinical variant classification. Human Mutation, 2019, 40, 1557-1578.	2.5	102
68	Recurrent 10q22-q23 Deletions: A Genomic Disorder on 10q Associated with Cognitive and Behavioral Abnormalities. American Journal of Human Genetics, 2007, 80, 938-947.	6.2	101
69	Clinical Value of RNA Sequencingâ€"Based Classifiers for Prediction of the Five Conventional Breast Cancer Biomarkers: A Report From the Population-Based Multicenter Sweden Cancerome Analysis Networkâ€"Breast Initiative. JCO Precision Oncology, 2018, 2, 1-18.	3.0	101
70	Survival in prospectively ascertained familial breast cancer: Analysis of a series stratified by tumour characteristics,BRCAmutations and oophorectomy. International Journal of Cancer, 2002, 101, 555-559.	5.1	99
71	BRCA1 R1699Q variant displaying ambiguous functional abrogation confers intermediate breast and ovarian cancer risk. Journal of Medical Genetics, 2012, 49, 525-532.	3.2	97
72	Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. Clinical Cancer Research, 2012, 18, 4026-4036.	7.0	96

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73	Genome-wide DNA Methylation Analysis of Lung Carcinoma Reveals One Neuroendocrine and Four Adenocarcinoma Epitypes Associated with Patient Outcome. Clinical Cancer Research, 2014, 20, 6127-6140.	7.0	91
74	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
75	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	1.6	90
76	Cancer predisposing BARD1 mutations in breastâ€“ovarian cancer families. Breast Cancer Research and Treatment, 2012, 131, 89-97.	2.5	88
77	Endothelial Induced EMT in Breast Epithelial Cells with Stem Cell Properties. PLoS ONE, 2011, 6, e23833.	2.5	87
78	Multiregion Whole-Exome Sequencing Uncovers the Genetic Evolution and Mutational Heterogeneity of Early-Stage Metastatic Melanoma. Cancer Research, 2016, 76, 4765-4774.	0.9	86
79	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	3.5	85
80	BRCA1 andBRCA2 mutations among breast cancer patients from the Philippines. International Journal of Cancer, 2002, 98, 596-603.	5.1	83
81	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	2.4	82
82	BRCA1-related breast cancer in Austrian breast and ovarian cancer families: SpecificBRCA1 mutations and pathological characteristics. , 1998, 77, 354-360.		81
83	Chromosome I alterations in breast cancer: Allelic loss on Ip and Iq Is related to lymphogenic metastases and poor prognosis. Genes Chromosomes and Cancer, 1992, 5, 311-320.	2.8	80
84	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. European Journal of Human Genetics, 2000, 8, 757-763.	2.8	75
85	Genome-wide RNAi Screen Identifies Cohesin Genes as Modifiers of Renewal and Differentiation in Human HSCs. Cell Reports, 2016, 14, 2988-3000.	6.4	75
86	Refinement of breast cancer molecular classification by miRNA expression profiles. BMC Genomics, 2019, 20, 503.	2.8	75
87	Multiple splicing variants of the estrogen receptor are present in individual human breast tumors. Journal of Steroid Biochemistry and Molecular Biology, 1996, 59, 251-260.	2.5	73
88	High risk of tobacco-related cancers inCDKN2Amutation-positive melanoma families. Journal of Medical Genetics, 2014, 51, 545-552.	3.2	73
89	High-resolution genomic profiling of male breast cancer reveals differences hidden behind the similarities with female breast cancer. Breast Cancer Research and Treatment, 2011, 129, 747-760.	2.5	70
90	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69

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91	An integrated genomics analysis of epigenetic subtypes in human breast tumors links DNA methylation patterns to chromatin states in normal mammary cells. Breast Cancer Research, 2016, 18, 27.	5.0	67
92	A genomic map of a 6-Mb region at 13q21-q22 implicated in cancer development: identification and characterization of candidate genes. Human Genetics, 2002, 110, 111-121.	3.8	66
93	Staf50 is a novel p53 target gene conferring reduced clonogenic growth of leukemic U-937 cells. Oncogene, 2004, 23, 4050-4059.	5.9	66
94	Mapping of a Novel Ocular and Cutaneous Malignant Melanoma Susceptibility Locus to Chromosome 9q21.32. Journal of the National Cancer Institute, 2005, 97, 1377-1382.	6.3	63
95	Genetic Aberrations in Hypodiploid Breast Cancer. American Journal of Pathology, 1998, 153, 191-199.	3.8	62
96	Mutational and gene fusion analyses of primary large cell and large cell neuroendocrine lung cancer. Oncotarget, 2015, 6, 22028-22037.	1.8	61
97	Chromosome 5 imbalance mapping in breast tumors from BRCA1 and BRCA2 mutation carriers and sporadic breast tumors. International Journal of Cancer, 2006, 119, 1052-1060.	5.1	59
98	Individuals with FANCM biallelic mutations do not develop Fanconi anemia, but show risk for breast cancer, chemotherapy toxicity and may display chromosome fragility. Genetics in Medicine, 2018, 20, 452-457.	2.4	59
99	Gene products of chromosome 11q and their association with CCND1gene amplification and tamoxifen resistance in premenopausal breast cancer. Breast Cancer Research, 2008, 10, R81.	5.0	58
100	Adjuvant systemic therapy for breast cancer in BRCA1/BRCA2 mutation carriers in a population-based study of risk of contralateral breast cancer. Breast Cancer Research and Treatment, 2010, 123, 491-498.	2.5	57
101	Expanding the genotypeâ€“phenotype spectrum in hereditary colorectal cancer by gene panel testing. Familial Cancer, 2017, 16, 195-203.	1.9	55
102	Flow Cytometric DNA Index and S-Phase Fraction in Breast Cancer in Relation to Other Prognostic Variables and to Clinical Outcome. Acta OncolÃ³gica, 1992, 31, 157-165.	1.8	53
103	Array-CGH identifies cyclin D1 and UBCH10 amplicons in anaplastic thyroid carcinoma. Endocrine-Related Cancer, 2008, 15, 801-815.	3.1	53
104	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. Nature Communications, 2020, 11, 3747.	12.8	53
105	Gene expression profiles relate to SS18/SSX fusion type in synovial sarcoma. International Journal of Cancer, 2006, 118, 1165-1172.	5.1	52
106	Frequent alterations of the PI3K/AKT/mTOR pathways in hereditary nonpolyposis colorectal cancer. Familial Cancer, 2010, 9, 125-129.	1.9	52
107	Characterisation of dic(9;20)(p11â€“13;q11) in childhood Bâ€cell precursor acute lymphoblastic leukaemia by tiling resolution arrayâ€based comparative genomic hybridisation reveals clustered breakpoints at 9p13.2 and 20q11.2. British Journal of Haematology, 2006, 135, 492-499.	2.5	51
108	A BAP1 Mutation in a Danish Family Predisposes to Uveal Melanoma and Other Cancers. PLoS ONE, 2013, 8, e72144.	2.5	51

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109	BRCA1 and BRCA2 point mutations and large rearrangements in breast and ovarian cancer families in Northern Poland. Oncology Reports, 2008, 19, 263-8.	2.6	51
110	Somatic genetic alterations inBRCA2-associated and sporadic male breast cancer. Genes Chromosomes and Cancer, 1999, 24, 56-61.	2.8	50
111	Tiling resolution array comparative genomic hybridization, expression and methylation analyses of dup(1q) in Burkitt lymphomas and pediatric high hyperdiploid acute lymphoblastic leukemias reveal clustered near-centromeric breakpoints and overexpression of genes in 1q22-32.3. Human Molecular Genetics, 2007, 16, 2215-2225.	2.9	50
112	The BRCA1 c. 5096G>A p.Arg1699Gln (R1699Q) intermediate risk variant: breast and ovarian cancer risk estimation and recommendations for clinical management from the ENIGMA consortium. Journal of Medical Genetics, 2018, 55, 15-20.	3.2	50
113	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	7.1	48
114	High risk of in-breast tumor recurrence after BRCA1/2-associated breast cancer. Breast Cancer Research and Treatment, 2014, 147, 571-578.	2.5	47
115	BRCA1 and BRCA2 mutations in Danish families with hereditary breast and/or ovarian cancer. Acta OncolÃ³gica, 2008, 47, 772-777.	1.8	46
116	Genome-Wide DNA Methylation Analysis in Melanoma Reveals the Importance of CpG Methylation in MITF Regulation. Journal of Investigative Dermatology, 2015, 135, 1820-1828.	0.7	46
117	Clinical framework for next generation sequencing based analysis of treatment predictive mutations and multiplexed gene fusion detection in non-small cell lung cancer. Oncotarget, 2017, 8, 34796-34810.	1.8	45
118	Characterisation of amplification patterns and target genes at chromosome 11q13 in CCND1-amplified sporadic and familial breast tumours. Breast Cancer Research and Treatment, 2012, 133, 583-594.	2.5	44
119	Characterization of a Novel Breast Carcinoma Xenograft and Cell Line Derived from a BRCA1 Germ-Line Mutation Carrier. Laboratory Investigation, 2003, 83, 387-396.	3.7	43
120	Detection and precise mapping of germline rearrangements inBRCA1, BRCA2, MSH2, andMLH1using zoom-in array comparative genomic hybridization (aCGH). Human Mutation, 2008, 29, 555-564.	2.5	42
121	Indistinguishable genomic profiles and shared prognostic markers in undifferentiated pleomorphic sarcoma and leiomyosarcoma: different sides of a single coin?. Laboratory Investigation, 2009, 89, 668-675.	3.7	42
122	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	5.0	42
123	Comprehensive mutational analysis of a cohort of Swedish Cornelia de Lange syndrome patients. European Journal of Human Genetics, 2007, 15, 143-149.	2.8	41
124	The Retinoblastoma Gene Undergoes Rearrangements in BRCA1-Deficient Basal-like Breast Cancer. Cancer Research, 2012, 72, 4028-4036.	0.9	41
125	Genetic Variation at 9p22.2 and Ovarian Cancer Risk for BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2011, 103, 105-116.	6.3	40
126	Serum selenium, selenoprotein P and glutathione peroxidase 3 as predictors of mortality and recurrence following breast cancer diagnosis: A multicentre cohort study. Redox Biology, 2021, 47, 102145.	9.0	40

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127	Haplotype analysis and age estimation of the 113insRCDKN2A founder mutation in Swedish melanoma families. Genes Chromosomes and Cancer, 2001, 31, 107-116.	2.8	39
128	Increased CpG methylation of the estrogen receptor gene in BRCA1-linked estrogen receptor-negative breast cancers. Oncogene, 2002, 21, 7034-7041.	5.9	39
129	BRCA1 and BRCA2 mutation analysis in breast-ovarian cancer families from northeastern Poland. Human Mutation, 2003, 21, 553-554.	2.5	39
130	High expression of <scp>ZNF703</scp> independent of amplification indicates worse prognosis in patients with luminal B breast cancer. Cancer Medicine, 2013, 2, 437-446.	2.8	39
131	Passenger strand loading in overexpression experiments using microRNA mimics. RNA Biology, 2015, 12, 787-791.	3.1	39
132	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.9	39
133	Cross comparison and prognostic assessment of breast cancer multigene signatures in a large population-based contemporary clinical series. Scientific Reports, 2019, 9, 12184.	3.3	39
134	Chromosomal aberrations in breast cancer: A comparison between cytogenetics and comparative genomic hybridization. , 1999, 25, 115-122.		37
135	Prediction of Lymph Node Metastasis in Breast Cancer by Gene Expression and Clinicopathological Models: Development and Validation within a Population-Based Cohort. Clinical Cancer Research, 2019, 25, 6368-6381.	7.0	37
136	Intratumor versus intertumor heterogeneity in gene expression profiles of soft-tissue sarcomas. Genes Chromosomes and Cancer, 2005, 43, 302-308.	2.8	36
137	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	6.4	36
138	The mutational landscape of the <scp>SCAN</scp> â€B realâ€world primary breast cancer transcriptome. EMBO Molecular Medicine, 2020, 12, e12118.	6.9	36
139	Loss of heterozygosity at 11q23.1 and survival in breast cancer: Results of a large European study. Genes Chromosomes and Cancer, 1999, 25, 212-221.	2.8	34
140	BRCA2 Mutations in 154 Finnish Male Breast Cancer Patients. Neoplasia, 2004, 6, 541-545.	5.3	33
141	p53 mutation and cyclin D1 amplification correlate with cisplatin sensitivity in xenografted human squamous cell carcinomas from head and neck. Acta OncolÃ³gica, 2006, 45, 300-305.	1.8	33
142	Higher occurrence of childhood cancer in families with germline mutations in BRCA2, MMR and CDKN2A genes. Familial Cancer, 2008, 7, 331-337.	1.9	32
143	Common variants of the BRCA1 wild-type allele modify the risk of breast cancer in BRCA1 mutation carriers. Human Molecular Genetics, 2011, 20, 4732-4747.	2.9	32
144	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32

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145	Prevalence of BRCA1 and BRCA2 pathogenic variants in a large, unselected breast cancer cohort. International Journal of Cancer, 2019, 144, 1195-1204.	5.1	31
146	Transcription of Human Endogenous Retroviral Sequences Related to Mouse Mammary Tumor Virus in Human Breast and Placenta: Similar Pattern in Most Malignant and Nonmalignant Breast Tissues*. AIDS Research and Human Retroviruses, 1997, 13, 507-516.	1.1	30
147	Identification of a novel splice-site mutation of the BRCA1 gene in two breast cancer families: Screening reveals low frequency in Icelandic breast cancer patients. Human Mutation, 1998, 11, S195-S197.	2.5	30
148	BRCA1 1675delA and 1135insA Account for One Third of Norwegian Familial Breast-Ovarian Cancer and Are Associated with Later Disease Onset than Less Frequent Mutations. Disease Markers, 1999, 15, 79-84.	1.3	30
149	Somatic frameshift alterations in mononucleotide repeatâ€containing genes in different tumor types from an HNPCC family with germline MSH2 mutation. Genes Chromosomes and Cancer, 2000, 29, 33-39.	2.8	30
150	BRCA2 mutation in a family with hereditary prostate cancer. Genes Chromosomes and Cancer, 2001, 30, 299-301.	2.8	30
151	Detection of submicroscopic constitutional chromosome aberrations in clinical diagnostics: a validation of the practical performance of different array platforms. European Journal of Human Genetics, 2008, 16, 786-792.	2.8	30
152	Alternative splicing and ACMG-AMP-2015-based classification of PALB2 genetic variants: an ENIGMA report. Journal of Medical Genetics, 2019, 56, 453-460.	3.2	30
153	GermlineBRCA1 andHMLH1 mutations in a family with male and female breast carcinoma. , 2000, 85, 796-800.		29
154	Multiple copies of mutantBRCA1 andBRCA2 alleles in breast tumors from germ-line mutation carriers. Genes Chromosomes and Cancer, 2000, 28, 432-442.	2.8	28
155	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
156	Distinct Gene Expression Signatures in Lynch Syndrome and Familial Colorectal Cancer Type X. PLoS ONE, 2013, 8, e71755.	2.5	28
157	The HER2-Encoded miR-4728-3p Regulates ESR1 through a Non-Canonical Internal Seed Interaction. PLoS ONE, 2014, 9, e97200.	2.5	27
158	hMLH1, hMSH2 andhMSH6 mutations in hereditary non-polyposis colorectal cancer families from Southern Sweden. , 1999, 83, 197-202.		26
159	Genetic profiles of gastroesophageal cancer: combined analysis using expression array and tiling arrayâ€“comparative genomic hybridization. Cancer Genetics and Cytogenetics, 2010, 200, 120-126.	1.0	26
160	FANCM mutation c.5791C>T is a risk factor for triple-negative breast cancer in the Finnish population. Breast Cancer Research and Treatment, 2017, 166, 217-226.	2.5	26
161	Chromosome aberrations in prophylactic mastectomies from women belonging to breast cancer families. , 1996, 16, 185-188.		25
162	Microarray analysis of gliomas reveals chromosomal position-associated gene expression patterns and identifies potential immunotherapy targets. Journal of Neuro-Oncology, 2007, 85, 11-24.	2.9	25

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163	Prognostic implications of the expression levels of different immunoglobulin heavy chain-encoding RNAs in early breast cancer. Npj Breast Cancer, 2020, 6, 28.	5.2	25
164	Remarkable similarities of chromosomal rearrangements between primary human breast cancers and matched distant metastases as revealed by whole-genome sequencing. Oncotarget, 2015, 6, 37169-37184.	1.8	25
165	Frequent miRNA-convergent fusion gene events in breast cancer. Nature Communications, 2017, 8, 788.	12.8	24
166	Array-CGH reveals hidden gene dose changes in children with acute lymphoblastic leukaemia and a normal or failed karyotype by G-banding. British Journal of Haematology, 2008, 140, 572-577.	2.5	23
167	Transcriptional adaptation of neuroblastoma cells to hypoxia. Biochemical and Biophysical Research Communications, 2008, 366, 1054-1060.	2.1	23
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