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	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	6.3	19
2	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in BRCA1 and BRCA2 compared with those harboring protein truncating variants. Genetics in Medicine, 2022, 24, 119-129.	2.4	10
3	Interval breast cancer is associated with interferon immune response. European Journal of Cancer, 2022, 162, 194-205.	2.8	3
4	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	1.6	90
5	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
6	Abstract OT2-30-01: Nordictrip, a translational randomized phase-3study exploring the effect of the addition of capecitabine to carboplatinum-based chemotherapy in early â€œtriple negativeâ€•breast cancer, ClinicalTrials.gov Identifier: NCT04335669. Cancer Research, 2022, 82, OT2-30-01-OT2-30-01.	0.9	0
7	Abstract P2-08-11: How reliable are biomarkers assessed on a core needle biopsy? A study of paired core needle biopsies and surgical specimens in early breast cancer. Cancer Research, 2022, 82, P2-08-11-P2-08-11.	0.9	0
8	Merged Testing for Colorectal Cancer Syndromes and Reâ€evaluation of Genetic Variants Improve Diagnostic Yield: results from a nationâ€wide prospective cohort. Genes Chromosomes and Cancer, 2022, , .	2.8	2
9	Association between breast cancer risk and disease aggressiveness: Characterizing underlying gene expression patterns. International Journal of Cancer, 2021, 148, 884-894.	5.1	3
10	The spatial RNA integrity number assay for in situ evaluation of transcriptome quality. Communications Biology, 2021, 4, 57.	4.4	11
11	Molecular analyses of triple-negative breast cancer in the young and elderly. Breast Cancer Research, 2021, 23, 20.	5.0	23
12	Distinct mechanisms of resistance to fulvestrant treatment dictate level of ER independence and selective response to CDK inhibitors in metastatic breast cancer. Breast Cancer Research, 2021, 23, 26.	5.0	19
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	Preexisting Somatic Mutations of Estrogen Receptor Alpha (ESR1) in Early-Stage Primary Breast Cancer. JNCI Cancer Spectrum, 2021, 5, pkab028.	2.9	20
15	CDKN2A genetic testing in melanoma-prone families in Sweden in the years 2015â€“2020: implications for novel national recommendations. Acta OncolÃ³gica, 2021, 60, 888-896.	1.8	9
16	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	2.4	16
17	A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. Scientific Reports, 2021, 11, 14763.	3.3	3
18	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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19	Spatial deconvolution of HER2-positive breast cancer delineates tumor-associated cell type interactions. Nature Communications, 2021, 12, 6012.	12.8	140
20	Sample Preparation Approach Influences PAM50 Risk of Recurrence Score in Early Breast Cancer. Cancers, 2021, 13, 6118.	3.7	10
21	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.9	39
22	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
23	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
24	Male Breast Carcinoma after Irradiation and Long-Term Phenothiazine Exposure: A Case Report. Case Reports in Oncology, 2020, 13, 956-961.	0.7	1
25	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
26	Clinical Utility of Targeted Sequencing in Lung Cancer: Experience From an Autonomous Swedish Health Care Center. JTO Clinical and Research Reports, 2020, 1, 100013.	1.1	4
27	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
28	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. Nature Communications, 2020, 11, 3747.	12.8	53
29	Breast cancer survival in Nordic BRCA2 mutation carriersâ€"unconventional association with oestrogen receptor status. British Journal of Cancer, 2020, 123, 1608-1615.	6.4	8
30	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
31	Integrating spatial gene expression and breast tumour morphology via deep learning. Nature Biomedical Engineering, 2020, 4, 827-834.	22.5	208
32	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	7.1	48
33	Analysis of fusion transcripts indicates widespread deregulation of snoRNAs and their host genes in breast cancer. International Journal of Cancer, 2020, 146, 3343-3353.	5.1	8
34	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
35	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
36	Substantial intrinsic variability in chemoradiosensitivity of newly established anaplastic thyroid cancer cell-lines. Acta Oto-Laryngologica, 2020, 140, 337-343.	0.9	0

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37	The Spectrum of FANCM Protein Truncating Variants in European Breast Cancer Cases. Cancers, 2020, 12, 292.	3.7	11
38	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
39	Defining the mutational landscape of 3,217 primary breast cancer transcriptomes through large-scale RNA-seq within the Sweden Cancerome Analysis Network: Breast Project (SCAN-B; NCT03430492).. Journal of Clinical Oncology, 2020, 38, 518-518.	1.6	2
40	Written pretest information and germline BRCA1/2 pathogenic variant testing in unselected breast cancer patients: predictors of testing uptake. Genetics in Medicine, 2019, 21, 89-96.	2.4	5
41	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
42	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
43	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
44	Agreement between molecular subtyping and surrogate subtype classification: a contemporary population-based study of ER-positive/HER2-negative primary breast cancer. Breast Cancer Research and Treatment, 2019, 178, 459-467.	2.5	23
45	High-definition spatial transcriptomics for in situ tissue profiling. Nature Methods, 2019, 16, 987-990.	19.0	708
46	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
47	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2019, 121, 180-192.	6.4	19
48	Refinement of breast cancer molecular classification by miRNA expression profiles. BMC Genomics, 2019, 20, 503.	2.8	75
49	Functional characterization of novel germline TP53 variants in Swedish families. Clinical Genetics, 2019, 96, 216-225.	2.0	7
50	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
51	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
52	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. Nature Medicine, 2019, 25, 1526-1533.	30.7	218
53	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
54	High patient satisfaction with a simplified BRCA1/2 testing procedure: long-term results of a prospective study. Breast Cancer Research and Treatment, 2019, 173, 313-318.	2.5	11

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55	Metachronous and Synchronous Occurrence of 5 Primary Malignancies in a Female Patient between 1997 and 2013: A Case Report with Germline and Somatic Genetic Analysis. Case Reports in Oncology, 2018, 10, 1006-1012.	0.7	14
56	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
57	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
58	Accuracy of self-reported family history of cancer, mutation status and tumor characteristics in patients with early onset breast cancer. Acta OncolÃ³gica, 2018, 57, 595-603.	1.8	19
59	BRCAsearch: written pre-test information and BRCA1/2 germline mutation testing in unselected patients with newly diagnosed breast cancer. Breast Cancer Research and Treatment, 2018, 168, 117-126.	2.5	14
60	Germline mutations in BRCA1 and BRCA2 incidentally revealed in a biobank research study: experiences from re-contacting mutation carriers and relatives. Journal of Community Genetics, 2018, 9, 201-208.	1.2	5
61	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
62	Cytohesin 1 regulates homing and engraftment of human hematopoietic stem and progenitor cells. Blood, 2017, 129, 950-958.	1.4	17
63	MA12.01 Next Generation Sequencing Based Clinical Framework for Analyses of Treatment Predictive Mutations and Gene Fusions in Lung Cancer. Journal of Thoracic Oncology, 2017, 12, S409-S410.	1.1	0
64	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
65	Case-control analysis of truncating mutations in DNA damage response genes connects TEX15 and FANCD2 with hereditary breast cancer susceptibility. Scientific Reports, 2017, 7, 681.	3.3	20
66	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	30.7	769
67	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	27.8	229
68	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
69	Expanding the genotypeâ€“phenotype spectrum in hereditary colorectal cancer by gene panel testing. Familial Cancer, 2017, 16, 195-203.	1.9	55
70	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
71	Frequent miRNA-convergent fusion gene events in breast cancer. Nature Communications, 2017, 8, 788.	12.8	24
72	Proteomic analysis of breast tumors confirms the mRNA intrinsic molecular subtypes using different classifiers: a large-scale analysis of fresh frozen tissue samples. Breast Cancer Research, 2016, 18, 69.	5.0	9

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73	HER2-encoded mir-4728 forms a receptor-independent circuit with miR-21-5p through the non-canonical poly(A) polymerase PAPD5. Scientific Reports, 2016, 6, 35664.	3.3	17
74	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
75	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	6.4	36
76	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
77	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	12.8	235
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	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
80	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. Science, 2016, 353, 78-82.	12.6	1,983
81	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
82	BRCA1/BRCA2 founder mutations and cancer risks: impact in the western Danish population. Familial Cancer, 2016, 15, 507-512.	1.9	9
83	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
84	Mutation Screening of 1,237 Cancer Genes across Six Model Cell Lines of Basal-Like Breast Cancer. PLoS ONE, 2015, 10, e0144528.	2.5	6
85	Mutational and gene fusion analyses of primary large cell and large cell neuroendocrine lung cancer. Oncotarget, 2015, 6, 22028-22037.	1.8	61
86	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
87	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
88	Mutational analysis of BRCA1/2 in a group of 134 consecutive ovarian cancer patients. Novel and recurrent BRCA1/2 alterations detected by next generation sequencing. Journal of Applied Genetics, 2015, 56, 193-198.	1.9	19
89	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	6.3	134
90	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

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91	Passenger strand loading in overexpression experiments using microRNA mimics. RNA Biology, 2015, 12, 787-791.	3.1	39
92	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69
93	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	2.5	22
94	Impact of a paternal origin of germline BRCA1/2 mutations on the age at breast and ovarian cancer diagnosis in a Southern Swedish cohort. Genes Chromosomes and Cancer, 2015, 54, 39-50.	2.8	6
95	Molecular Characterization of Melanoma Cases in Denmark Suspected of Genetic Predisposition. PLoS ONE, 2015, 10, e0122662.	2.5	21
96	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
97	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
98	Loss of CITED1, an MITF regulator, drives a phenotype switchin vitroand can predict clinical outcome in primary melanoma tumours. PeerJ, 2015, 3, e788.	2.0	20
99	Aberrant Activation of the PI3K/mTOR Pathway Promotes Resistance to Sorafenib in AML. Blood, 2015, 126, 2472-2472.	1.4	0
100	The HER2-Encoded miR-4728-3p Regulates ESR1 through a Non-Canonical Internal Seed Interaction. PLoS ONE, 2014, 9, e97200.	2.5	27
101	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
102	Germline rearrangements in families with strong family history of glioma and malignant melanoma, colon, and breast cancer. Neuro-Oncology, 2014, 16, 1333-1340.	1.2	11
103	High risk of tobacco-related cancers inCDKN2Amutation-positive melanoma families. Journal of Medical Genetics, 2014, 51, 545-552.	3.2	73
104	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
105	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
106	Cohesin Genes Are Negative Regulators of HSC Renewal. Blood, 2014, 124, 605-605.	1.4	0
107	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	27.8	8,060
108	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

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109	Detecting EGFR alterations in clinical specimensâ€"pitfalls and necessities. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2013, 463, 755-764.	2.8	7
110	Mutual Exclusivity Analysis of Genetic and Epigenetic Drivers in Melanoma Identifies a Link Between p14ARF and RARÎ² Signaling. Molecular Cancer Research, 2013, 11, 1166-1178.	3.4	23
111	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
112	Histological specificity of alterations and expression of KIT and KITLG in nonâ€small cell lung carcinoma. Genes Chromosomes and Cancer, 2013, 52, 1088-1096.	2.8	17
113	Distinct Gene Expression Signatures in Lynch Syndrome and Familial Colorectal Cancer Type X. PLoS ONE, 2013, 8, e71755.	2.5	28
114	A BAP1 Mutation in a Danish Family Predisposes to Uveal Melanoma and Other Cancers. PLoS ONE, 2013, 8, e72144.	2.5	51
115	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
116	The Retinoblastoma Gene Undergoes Rearrangements in BRCA1-Deficient Basal-like Breast Cancer. Cancer Research, 2012, 72, 4028-4036.	0.9	41
117	Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. Clinical Cancer Research, 2012, 18, 4026-4036.	7.0	96
118	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
119	Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. Molecular Oncology, 2012, 6, 494-506.	4.6	136
120	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
121	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
122	Prevalence of germline TP53 mutations and history of Liâ€"Fraumeni syndrome in families with childhood adrenocortical tumors, choroid plexus tumors, and rhabdomyosarcoma: A populationâ€based survey. Pediatric Blood and Cancer, 2012, 59, 846-853.	1.5	17
123	Amplification and overexpression of the ABCC3 (MRP3) gene in primary breast cancer. Genes Chromosomes and Cancer, 2012, 51, 832-840.	2.8	23
124	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
125	Cancer predisposing BARD1 mutations in breastâ€"ovarian cancer families. Breast Cancer Research and Treatment, 2012, 131, 89-97.	2.5	88
126	GOBO: Gene Expression-Based Outcome for Breast Cancer Online. PLoS ONE, 2011, 6, e17911.	2.5	361

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127	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
128	A BRCA2 mutation incorrectly mapped in the original BRCA2 reference sequence, is a common West Danish founder mutation disrupting mRNA splicing. Breast Cancer Research and Treatment, 2011, 128, 179-185.	2.5	4
129	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
130	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
131	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
132	Endothelial Induced EMT in Breast Epithelial Cells with Stem Cell Properties. PLoS ONE, 2011, 6, e23833.	2.5	87
133	Swedish CDKN2A mutation carriers do not present the atypical mole syndrome phenotype. Melanoma Research, 2010, 20, 266-272.	1.2	8
134	Oral contraceptives and postmenopausal hormones and risk of contralateral breast cancer among BRCA1 and BRCA2 mutation carriers and noncarriers: the WECARE Study. Breast Cancer Research and Treatment, 2010, 120, 175-183.	2.5	22
135	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
136	Reproductive factors and risk of contralateral breast cancer by BRCA1 and BRCA2 mutation status: results from the WECARE study. Cancer Causes and Control, 2010, 21, 839-846.	1.8	12
137	Frequent alterations of the PI3K/AKT/mTOR pathways in hereditary nonpolyposis colorectal cancer. Familial Cancer, 2010, 9, 125-129.	1.9	52
138	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
139	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
140	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
141	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
142	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
143	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
144	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

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145	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	3.5	85
146	Genetic profiles distinguish different types of hereditary ovarian cancer. Oncology Reports, 2010, 24, 885-95.	2.6	9
147	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. Melanoma Research, 2010, 20, 381-91.	1.2	22
148	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
149	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
150	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
151	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
152	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
153	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
154	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
155	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
156	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
157	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
158	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
159	The CD44+/CD24-phenotype is enriched in basal-like breast tumors. Breast Cancer Research, 2008, 10, R53.	5.0	464
160	Transcriptional adaptation of neuroblastoma cells to hypoxia. Biochemical and Biophysical Research Communications, 2008, 366, 1054-1060.	2.1	23
161	Array-CGH identifies cyclin D1 and UBCH10 amplicons in anaplastic thyroid carcinoma. Endocrine-Related Cancer, 2008, 15, 801-815.	3.1	53
162	Variation of Breast Cancer Risk Among BRCA1/2 Carriers. JAMA - Journal of the American Medical Association, 2008, 299, 194-201.	7.4	244

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163	BRCA1 and BRCA2 mutations in Danish families with hereditary breast and/or ovarian cancer. Acta OncolÃ³gica, 2008, 47, 772-777.	1.8	46
164	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
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