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List of Publications by Year in Descending Order

250 papers	28,953 citations	70 h-index	168 g-index
270 ext. papers	35,094 ext. citations	9.8 avg, IF	5.9 L-index

#	Paper	IF	Citations
250	Cancer Risks Associated With and Pathogenic Variants.. *Journal of Clinical Oncology*, **2022**, JCO2102112	2.2	7
249	Interval breast cancer is associated with interferon immune response.. *European Journal of Cancer*, **2022**, 162, 194-205	7.5	1
248	Abstract OT2-30-01: Nordictrip, a translational randomized phase-3study exploring the effect of the addition of capecitabine to carboplatinum-based chemotherapy in early triple negative breast cancer, ClinicalTrials.gov Identifier: NCT04335669. *Cancer Research*, **2022**, 82, OT2-30-01-OT2-30-01	10.1	
247	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	10.1	
246	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*, **2021**,	8.1	2
245	Spatial deconvolution of HER2-positive breast cancer delineates tumor-associated cell type interactions. *Nature Communications*, **2021**, 12, 6012	17.4	16
244	Preexisting Somatic Mutations of Estrogen Receptor Alpha () in Early-Stage Primary Breast Cancer. *JNCI Cancer Spectrum*, **2021**, 5, pkab028	4.6	1
243	genetic testing in melanoma-prone families in Sweden in the years 2015-2020: implications for novel national recommendations. *Acta Oncologica*, **2021**, 60, 888-896	3.2	1
242	The predictive ability of the 313 variant-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	8.1	2
241	A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. *Scientific Reports*, **2021**, 11, 14763	4.9	0
240	Association between breast cancer risk and disease aggressiveness: Characterizing underlying gene expression patterns. *International Journal of Cancer*, **2021**, 148, 884-894	7.5	2
239	The spatial RNA integrity number assay for in situ evaluation of transcriptome quality. *Communications Biology*, **2021**, 4, 57	6.7	3
238	Molecular analyses of triple-negative breast cancer in the young and elderly. *Breast Cancer Research*, **2021**, 23, 20	8.3	3
237	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	8.3	2
236	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
235	Breast and Prostate Cancer Risks for Male BRCA1 and BRCA2 Pathogenic Variant Carriers Using Polygenic Risk Scores. *Journal of the National Cancer Institute*, **2021**,	9.7	3
234	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	11.3	5

233	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. *Nature Genetics*, **2020**, 52, 572-581	36.3	76
232	Integrating spatial gene expression and breast tumour morphology via deep learning. *Nature Biomedical Engineering*, **2020**, 4, 827-834	19	64
231	Characterization of the Cancer Spectrum in Men With Germline BRCA1 and BRCA2 Pathogenic Variants: Results From the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). *JAMA Oncology*, **2020**, 6, 1218-1230	13.4	25
230	Analysis of fusion transcripts indicates widespread deregulation of snoRNAs and their host genes in breast cancer. *International Journal of Cancer*, **2020**, 146, 3343-3353	7.5	2
229	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. *Journal of the National Cancer Institute*, **2020**, 112, 1242-1250	9.7	51
228	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
227	Substantial intrinsic variability in chemoradiosensitivity of newly established anaplastic thyroid cancer cell-lines. *Acta Oto-Laryngologica*, **2020**, 140, 337-343	1.6	
226	The Spectrum of Protein Truncating Variants in European Breast Cancer Cases. *Cancers*, **2020**, 12,	6.6	7
225	Association of Genomic Domains in and with Prostate Cancer Risk and Aggressiveness. *Cancer Research*, **2020**, 80, 624-638	10.1	22
224	The mutational landscape of the SCAN-B real-world primary breast cancer transcriptome. *EMBO Molecular Medicine*, **2020**, 12, e12118	12	11
223	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	2.2	
222	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
221	Cancer Risks Associated With Germline Pathogenic Variants: An International Study of 524 Families. *Journal of Clinical Oncology*, **2020**, 38, 674-685	2.2	133
220	Male Breast Carcinoma after Irradiation and Long-Term Phenothiazine Exposure: A Case Report. *Case Reports in Oncology*, **2020**, 13, 956-961	1	1
219	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	8.1	34
218	Clinical Utility of Targeted Sequencing in Lung Cancer: Experience From an Autonomous Swedish Health Care Center. *JTO Clinical and Research Reports*, **2020**, 1, 100013	1.4	2
217	Prognostic implications of the expression levels of different immunoglobulin heavy chain-encoding RNAs in early breast cancer. *Npj Breast Cancer*, **2020**, 6, 28	7.8	8
216	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. *Nature Communications*, **2020**, 11, 3747	17.4	18

215	Breast cancer survival in Nordic BRCA2 mutation carriers-unconventional association with oestrogen receptor status. *British Journal of Cancer*, **2020**, 123, 1608-1615	8.7	1
214	Cross comparison and prognostic assessment of breast cancer multigene signatures in a large population-based contemporary clinical series. *Scientific Reports*, **2019**, 9, 12184	4.9	17
213	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	4.4	8
212	High-definition spatial transcriptomics for in situ tissue profiling. *Nature Methods*, **2019**, 16, 987-990	21.6	322
211	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	4.7	52
210	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	8.7	13
209	Refinement of breast cancer molecular classification by miRNA expression profiles. *BMC Genomics*, **2019**, 20, 503	4.5	38
208	Functional characterization of novel germline TP53 variants in Swedish families. *Clinical Genetics*, **2019**, 96, 216-225	4	1
207	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
206	Alternative splicing and ACMG-AMP-2015-based classification of PALB2 genetic variants: an ENIGMA report. *Journal of Medical Genetics*, **2019**, 56, 453-460	5.8	10
205	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	8.1	4
204	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	12.9	14
203	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *Npj Breast Cancer*, **2019**, 5, 38	7.8	12
202	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. *Nature Medicine*, **2019**, 25, 1526-1533	50.5	102
201	Prevalence of BRCA1 and BRCA2 pathogenic variants in a large, unselected breast cancer cohort. *International Journal of Cancer*, **2019**, 144, 1195-1204	7.5	18
200	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	4.4	7
199	The 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	5.8	36
198	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	8.1	44

197	Accuracy of self-reported family history of cancer, mutation status and tumor characteristics in patients with early onset breast cancer. *Acta Oncologica*, **2018**, 57, 595-603	3.2	14
196	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	4.4	9
195	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	2.5	4
194	Clinical Value of RNA Sequencing-Based Classifiers for Prediction of the Five Conventional Breast Cancer Biomarkers: A Report From the Population-Based Multicenter Sweden Cancerome Analysis Network-Breast Initiative. *JCO Precision Oncology*, **2018**, 2,	3.6	45
193	Cytohesin 1 regulates homing and engraftment of human hematopoietic stem and progenitor cells. *Blood*, **2017**, 129, 950-958	2.2	14
192	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
191	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	4.9	10
190	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. *Nature Medicine*, **2017**, 23, 517-525	50.5	444
189	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. *Nature*, **2017**, 543, 714-718	50.4	157
188	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	5.3	39
187	Frequent miRNA-convergent fusion gene events in breast cancer. *Nature Communications*, **2017**, 8, 788	17.4	16
186	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*, **2017**, 10, 1006-1012	1	11
185	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	4.4	17
184	Expanding the genotype-phenotype spectrum in hereditary colorectal cancer by gene panel testing. *Familial Cancer*, **2017**, 16, 195-203	3	40
183	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. *Breast Cancer Research*, **2016**, 18, 112	8.3	25
182	The topography of mutational processes in breast cancer genomes. *Nature Communications*, **2016**, 7, 11383	17.4	172
181	Multiregion Whole-Exome Sequencing Uncovers the Genetic Evolution and Mutational Heterogeneity of Early-Stage Metastatic Melanoma. *Cancer Research*, **2016**, 76, 4765-74	10.1	70
180	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	8.3	51

179	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. *Science*, **2016**, 353, 78-82	33.3	944
178	Genome-wide RNAi Screen Identifies Cohesin Genes as Modifiers of Renewal and Differentiation in Human HSCs. *Cell Reports*, **2016**, 14, 2988-3000	10.6	48
177	BRCA1/BRCA2 founder mutations and cancer risks: impact in the western Danish population. *Familial Cancer*, **2016**, 15, 507-12	3	8
176	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. *Nature Genetics*, **2016**, 48, 374-86	36.3	93
175	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	8.3	8
174	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	4.9	14
173	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	50.4	1193
172	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. *Cell Reports*, **2016**, 16, 2032-	46.6	30
171	Nonsense mutations in the shelterin complex genes ACD and TERF2IP in familial melanoma. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	102
170	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	14.4	70
169	Passenger strand loading in overexpression experiments using microRNA mimics. *RNA Biology*, **2015**, 12, 787-91	4.8	25
168	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. *Genome Research*, **2015**, 25, 814-24	9.7	52
167	The Life History of 21 Breast Cancers. *Cell*, **2015**, 162, 924	56.2	7
166	Candidate genetic modifiers for breast and ovarian cancer risk in BRCA1 and BRCA2 mutation carriers. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 308-16	4	20
165	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	5	5
164	Mutation Screening of 1,237 Cancer Genes across Six Model Cell Lines of Basal-Like Breast Cancer. *PLoS ONE*, **2015**, 10, e0144528	3.7	5
163	Mutational and gene fusion analyses of primary large cell and large cell neuroendocrine lung cancer. *Oncotarget*, **2015**, 6, 22028-37	3.3	51
162	Genome-Wide DNA Methylation Analysis in Melanoma Reveals the Importance of CpG Methylation in MITF Regulation. *Journal of Investigative Dermatology*, **2015**, 135, 1820-1828	4.3	39

161	Serial monitoring of circulating tumor DNA in patients with primary breast cancer for detection of occult metastatic disease. *EMBO Molecular Medicine*, **2015**, 7, 1034-47	12	284
160	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, 193-8	2.5	18
159	Molecular characterization of melanoma cases in Denmark suspected of genetic predisposition. *PLoS ONE*, **2015**, 10, e0122662	3.7	16
158	Molecular stratification of metastatic melanoma using gene expression profiling: Prediction of survival outcome and benefit from molecular targeted therapy. *Oncotarget*, **2015**, 6, 12297-309	3.3	102
157	Remarkable similarities of chromosomal rearrangements between primary human breast cancers and matched distant metastases as revealed by whole-genome sequencing. *Oncotarget*, **2015**, 6, 37169-84	3.3	19
156	Loss of CITED1, an MITF regulator, drives a phenotype switch in vitro and can predict clinical outcome in primary melanoma tumours. *PeerJ*, **2015**, 3, e788	3.1	14
155	Aberrant Activation of the PI3K/mTOR Pathway Promotes Resistance to Sorafenib in AML. *Blood*, **2015**, 126, 2472-2472	2.2	
154	High risk of in-breast tumor recurrence after BRCA1/2-associated breast cancer. *Breast Cancer Research and Treatment*, **2014**, 147, 571-8	4.4	34
153	The HER2-encoded miR-4728-3p regulates ESR1 through a non-canonical internal seed interaction. *PLoS ONE*, **2014**, 9, e97200	3.7	20
152	Cancer-associated fibroblasts expressing CXCL14 rely upon NOS1-derived nitric oxide signaling for their tumor-supporting properties. *Cancer Research*, **2014**, 74, 2999-3010	10.1	86
151	Germline rearrangements in families with strong family history of glioma and malignant melanoma, colon, and breast cancer. *Neuro-Oncology*, **2014**, 16, 1333-40	1	9
150	High risk of tobacco-related cancers in CDKN2A mutation-positive melanoma families. *Journal of Medical Genetics*, **2014**, 51, 545-52	5.8	55
149	Genome-wide DNA methylation analysis of lung carcinoma reveals one neuroendocrine and four adenocarcinoma epitypes associated with patient outcome. *Clinical Cancer Research*, **2014**, 20, 6127-40	12.9	72
148	Cohesin Genes Are Negative Regulators of HSC Renewal. *Blood*, **2014**, 124, 605-605	2.2	
147	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
146	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
145	Detecting EGFR alterations in clinical specimens-pitfalls and necessities. *Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin*, **2013**, 463, 755-64	5.1	4
144	Mutual exclusivity analysis of genetic and epigenetic drivers in melanoma identifies a link between p14 ARF and RAR signaling. *Molecular Cancer Research*, **2013**, 11, 1166-78	6.6	19

143	High expression of ZNF703 independent of amplification indicates worse prognosis in patients with luminal B breast cancer. *Cancer Medicine*, **2013**, 2, 437-46	4.8	33
142	Histological specificity of alterations and expression of KIT and KITLG in non-small cell lung carcinoma. *Genes Chromosomes and Cancer*, **2013**, 52, 1088-96	5	12
141	Distinct gene expression signatures in lynch syndrome and familial colorectal cancer type x. *PLoS ONE*, **2013**, 8, e71755	3.7	26
140	A BAP1 mutation in a Danish family predisposes to uveal melanoma and other cancers. *PLoS ONE*, **2013**, 8, e72144	3.7	48
139	Cancer predisposing BARD1 mutations in breast-ovarian cancer families. *Breast Cancer Research and Treatment*, **2012**, 131, 89-97	4.4	68
138	Association between BRCA1 and BRCA2 mutations and survival in women with invasive epithelial ovarian cancer. *JAMA - Journal of the American Medical Association*, **2012**, 307, 382-90	27.4	427
137	Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. *Molecular Oncology*, **2012**, 6, 494-506	7.9	114
136	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
135	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979
134	Prevalence of germline TP53 mutations and history of Li-Fraumeni syndrome in families with childhood adrenocortical tumors, choroid plexus tumors, and rhabdomyosarcoma: a population-based survey. *Pediatric Blood and Cancer*, **2012**, 59, 846-53	3	14
133	Amplification and overexpression of the ABCC3 (MRP3) gene in primary breast cancer. *Genes Chromosomes and Cancer*, **2012**, 51, 832-40	5	21
132	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, 583-94	4.4	37
131	BRCA1 R1699Q variant displaying ambiguous functional abrogation confers intermediate breast and ovarian cancer risk. *Journal of Medical Genetics*, **2012**, 49, 525-32	5.8	82
130	The retinoblastoma gene undergoes rearrangements in BRCA1-deficient basal-like breast cancer. *Cancer Research*, **2012**, 72, 4028-36	10.1	37
129	Molecular profiling reveals low- and high-grade forms of primary melanoma. *Clinical Cancer Research*, **2012**, 18, 4026-36	12.9	81
128	GOBO: gene expression-based outcome for breast cancer online. *PLoS ONE*, **2011**, 6, e17911	3.7	295
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, 747-60	4.4	63
126	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, 179-85	4.4	4

125	Common variants of the BRCA1 wild-type allele modify the risk of breast cancer in BRCA1 mutation carriers. *Human Molecular Genetics*, **2011**, 20, 4732-47	5.6	21
124	Genetic variation at 9p22.2 and ovarian cancer risk for BRCA1 and BRCA2 mutation carriers. *Journal of the National Cancer Institute*, **2011**, 103, 105-16	9.7	37
123	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	10.1	160
122	Endothelial induced EMT in breast epithelial cells with stem cell properties. *PLoS ONE*, **2011**, 6, e23833	3.7	71
121	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
120	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, 9742-54	10.1	147
119	Gene expression profiling-based identification of molecular subtypes in stage IV melanomas with different clinical outcome. *Clinical Cancer Research*, **2010**, 16, 3356-67	12.9	185
118	Identification of subtypes in human epidermal growth factor receptor 2--positive breast cancer reveals a gene signature prognostic of outcome. *Journal of Clinical Oncology*, **2010**, 28, 1813-20	2.2	130
117	Population-based study of the risk of second primary contralateral breast cancer associated with carrying a mutation in BRCA1 or BRCA2. *Journal of Clinical Oncology*, **2010**, 28, 2404-10	2.2	137
116	Common genetic variants and modification of penetrance of BRCA2-associated breast cancer. *PLoS Genetics*, **2010**, 6, e1001183	6	74
115	Swedish CDKN2A mutation carriers do not present the atypical mole syndrome phenotype. *Melanoma Research*, **2010**, 20, 266-72	3.3	6
114	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, 175-83	4.4	20
113	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, 491-8	4.4	50
112	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, 839-46	2.8	11
111	Frequent alterations of the PI3K/AKT/mTOR pathways in hereditary nonpolyposis colorectal cancer. *Familial Cancer*, **2010**, 9, 125-9	3	44
110	Genetic profiles of gastroesophageal cancer: combined analysis using expression array and tiling array--comparative genomic hybridization. *Cancer Genetics and Cytogenetics*, **2010**, 200, 120-6		26
109	Characterization of BRCA1 and BRCA2 deleterious mutations and variants of unknown clinical significance in unilateral and bilateral breast cancer: the WECARE study. *Human Mutation*, **2010**, 31, E1200-40	4.7	80
108	Genetic profiles distinguish different types of hereditary ovarian cancer. *Oncology Reports*, **2010**, 24, 885-95	3.5	9

107	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. *Melanoma Research*, **2010**, 20, 381-91	3.3	22
106	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, 3414-9	11.5	169
105	MiRNA expression in urothelial carcinomas: important roles of miR-10a, miR-222, miR-125b, miR-7 and miR-452 for tumor stage and metastasis, and frequent homozygous losses of miR-31. *International Journal of Cancer*, **2009**, 124, 2236-42	7.5	190
104	Indistinguishable genomic profiles and shared prognostic markers in undifferentiated pleomorphic sarcoma and leiomyosarcoma: different sides of a single coin?. *Laboratory Investigation*, **2009**, 89, 668-75	5.9	36
103	The non-coding RNA of the multidrug resistance-linked vault particle encodes multiple regulatory small RNAs. *Nature Cell Biology*, **2009**, 11, 1268-71	23.4	127
102	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, 786-92	5.3	28
101	Recurrent gross mutations of the PTEN tumor suppressor gene in breast cancers with deficient DSB repair. *Nature Genetics*, **2008**, 40, 102-7	36.3	289
100	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, 572-7	4.5	20
99	Gene products of chromosome 11q and their association with CCND1 gene amplification and tamoxifen resistance in premenopausal breast cancer. *Breast Cancer Research*, **2008**, 10, R81	8.3	48
98	The CD44+/CD24- phenotype is enriched in basal-like breast tumors. *Breast Cancer Research*, **2008**, 10, R53	8.3	408
97	Transcriptional adaptation of neuroblastoma cells to hypoxia. *Biochemical and Biophysical Research Communications*, **2008**, 366, 1054-60	3.4	21
96	Array-CGH identifies cyclin D1 and UBCH10 amplicons in anaplastic thyroid carcinoma. *Endocrine-Related Cancer*, **2008**, 15, 801-15	5.7	37
95	Variation of breast cancer risk among BRCA1/2 carriers. *JAMA - Journal of the American Medical Association*, **2008**, 299, 194-201	27.4	213
94	BRCA1 and BRCA2 mutations in Danish families with hereditary breast and/or ovarian cancer. *Acta Oncologica*, **2008**, 47, 772-7	3.2	40
93	Higher occurrence of childhood cancer in families with germline mutations in BRCA2, MMR and CDKN2A genes. *Familial Cancer*, **2008**, 7, 331-7	3	26
92	Detection and precise mapping of germline rearrangements in BRCA1, BRCA2, MSH2, and MLH1 using zoom-in array comparative genomic hybridization (aCGH). *Human Mutation*, **2008**, 29, 555-64	4.7	39
91	Screening for copy-number alterations and loss of heterozygosity in chronic lymphocytic leukemia--a comparative study of four differently designed, high resolution microarray platforms. *Genes Chromosomes and Cancer*, **2008**, 47, 697-711	5	109
90	BRCA1 and BRCA2 point mutations and large rearrangements in breast and ovarian cancer families in Northern Poland. *Oncology Reports*, **2008**, 19, 263-8	3.5	49

89	Tumor Genome Wide DNA Alterations Assessed by Array CGH in Patients with Poor and Excellent Survival following Operation for Colorectal Cancer. *Cancer Informatics*, **2007**, 3, 117693510700300	2.4	13
88	High-resolution genomic profiles of breast cancer cell lines assessed by tiling BAC array comparative genomic hybridization. *Genes Chromosomes and Cancer*, **2007**, 46, 543-58	5	162
87	Comprehensive mutational analysis of a cohort of Swedish Cornelia de Lange syndrome patients. *European Journal of Human Genetics*, **2007**, 15, 143-9	5.3	36
86	Cytogenetic characterization and gene expression profiling of the trastuzumab-resistant breast cancer cell line JIMT-1. *Cancer Genetics and Cytogenetics*, **2007**, 172, 95-106		18
85	Microarray analysis of gliomas reveals chromosomal position-associated gene expression patterns and identifies potential immunotherapy targets. *Journal of Neuro-Oncology*, **2007**, 85, 11-24	4.8	23
84	Absence of the common IGF1 19 CA-repeat allele is more common among BRCA1 mutation carriers than among non-carriers from BRCA1 families. *Familial Cancer*, **2007**, 6, 445-52	3	6
83	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, 2215-25	5.6	41
82	Estrogen receptor beta expression is associated with tamoxifen response in ERalpha-negative breast carcinoma. *Clinical Cancer Research*, **2007**, 13, 1987-94	12.9	147
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