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List of Publications by Citations

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	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
249	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
248	Gene-expression profiles in hereditary breast cancer. *New England Journal of Medicine*, **2001**, 344, 539-48	59.2	1462
247	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
246	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	50.4	1193
245	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979
244	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. *Science*, **2016**, 353, 78-82	33.3	944
243	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, 2554-9	10.1	726
242	Recruitment of HIF-1alpha and HIF-2alpha to common target genes is differentially regulated in neuroblastoma: HIF-2alpha promotes an aggressive phenotype. *Cancer Cell*, **2006**, 10, 413-23	24.3	532
241	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. *Nature Medicine*, **2017**, 23, 517-525	50.5	444
240	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
239	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
238	The CD44+/CD24- phenotype is enriched in basal-like breast tumors. *Breast Cancer Research*, **2008**, 10, R53	8.3	408
237	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, 7564-9	11.5	397
236	Amplification and deletion of topoisomerase IIalpha associate with ErbB-2 amplification and affect sensitivity to topoisomerase II inhibitor doxorubicin in breast cancer. *American Journal of Pathology* , **2000**, 156, 839-47	5.8	333
235	High-definition spatial transcriptomics for in situ tissue profiling. *Nature Methods*, **2019**, 16, 987-990	21.6	322
234	GOBO: gene expression-based outcome for breast cancer online. *PLoS ONE*, **2011**, 6, e17911	3.7	295

233	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
232	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
231	Variation of breast cancer risk among BRCA1/2 carriers. *JAMA - Journal of the American Medical Association*, **2008**, 299, 194-201	27.4	213
230	ERBB2 amplification is associated with tamoxifen resistance in steroid-receptor positive breast cancer. *Cancer Letters*, **1994**, 81, 137-44	9.9	207
229	Denaturing high-performance liquid chromatography detects reliably BRCA1 and BRCA2 mutations. *Genomics*, **1999**, 62, 369-76	4.3	192
228	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
227	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
226	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
225	The topography of mutational processes in breast cancer genomes. *Nature Communications*, **2016**, 7, 11383	17.4	172
224	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
223	Characterization of topoisomerase II gene amplification and deletion in breast cancer. *Genes Chromosomes and Cancer*, **1999**, 26, 142-150	5	166
222	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
221	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
220	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. *Nature*, **2017**, 543, 714-718	50.4	157
219	Molecular classification of familial non-BRCA1/BRCA2 breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 2532-7	11.5	157
218	Cytokeratin 5/14-positive breast cancer: true basal phenotype confined to BRCA1 tumors. *Modern Pathology*, **2005**, 18, 1321-8	9.8	153
217	Steroid receptors in hereditary breast carcinomas associated with BRCA1 or BRCA2 mutations or unknown susceptibility genes. *Cancer*, **1998**, 83, 310-319	6.4	152
216	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

215	Estrogen receptor beta expression is associated with tamoxifen response in ERalpha-negative breast carcinoma. *Clinical Cancer Research*, **2007**, 13, 1987-94	12.9	147
214	RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. *Carcinogenesis*, **2006**, 27, 1593-9	4.6	145
213	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
212	Distinct genomic profiles in hereditary breast tumors identified by array-based comparative genomic hybridization. *Cancer Research*, **2005**, 65, 7612-21	10.1	141
211	Haplotype and phenotype analysis of nine recurrent BRCA2 mutations in 111 families: results of an international study. *American Journal of Human Genetics*, **1998**, 62, 1381-8	11	138
210	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
209	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		135
208	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, 71-5	5	135
207	Cancer Risks Associated With Germline Pathogenic Variants: An International Study of 524 Families. *Journal of Clinical Oncology*, **2020**, 38, 674-685	2.2	133
206	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
205	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
204	Amplification and overexpression of p40 subunit of eukaryotic translation initiation factor 3 in breast and prostate cancer. *American Journal of Pathology*, **1999**, 154, 1777-83	5.8	124
203	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	10.1	116
202	Global H3K27 trimethylation and EZH2 abundance in breast tumor subtypes. *Molecular Oncology*, **2012**, 6, 494-506	7.9	114
201	The contribution of the hereditary nonpolyposis colorectal cancer syndrome to the development of ovarian cancer. *Gynecologic Oncology*, **2006**, 101, 238-43	4.9	112
200	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
199	Human neuroblastoma cells exposed to hypoxia: induction of genes associated with growth, survival, and aggressive behavior. *Experimental Cell Research*, **2004**, 295, 469-87	4.2	103
198	Nonsense mutations in the shelterin complex genes ACD and TERF2IP in familial melanoma. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	102

197	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
196	Whole-genome sequencing of triple-negative breast cancers in a population-based clinical study. *Nature Medicine*, **2019**, 25, 1526-1533	50.5	102
195	Pregnancy-associated breast cancer in BRCA1 and BRCA2 germline mutation carriers. *Lancet, The*, **1998**, 352, 1359-60	40	99
194	c-myc amplification is an independent prognostic factor in postmenopausal breast cancer. *International Journal of Cancer*, **1992**, 51, 687-91	7.5	95
193	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
192	Survival in prospectively ascertained familial breast cancer: analysis of a series stratified by tumour characteristics, BRCA mutations and oophorectomy. *International Journal of Cancer*, **2002**, 101, 555-9	7.5	91
191	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
190	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
189	Molecular profiling reveals low- and high-grade forms of primary melanoma. *Clinical Cancer Research*, **2012**, 18, 4026-36	12.9	81
188	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
187	Recurrent 10q22-q23 deletions: a genomic disorder on 10q associated with cognitive and behavioral abnormalities. *American Journal of Human Genetics*, **2007**, 80, 938-47	11	79
186	Chromosome 1 alterations in breast cancer: allelic loss on 1p and 1q is related to lymphogenic metastases and poor prognosis. *Genes Chromosomes and Cancer*, **1992**, 5, 311-20	5	77
185	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
184	Common genetic variants and modification of penetrance of BRCA2-associated breast cancer. *PLoS Genetics*, **2010**, 6, e1001183	6	74
183	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
182	BRCA1 and BRCA2 mutations among breast cancer patients from the Philippines. *International Journal of Cancer*, **2002**, 98, 596-603	7.5	71
181	Endothelial induced EMT in breast epithelial cells with stem cell properties. *PLoS ONE*, **2011**, 6, e23833	3.7	71
180	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

179	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
178	Cancer predisposing BARD1 mutations in breast-ovarian cancer families. *Breast Cancer Research and Treatment*, **2012**, 131, 89-97	4.4	68
177	Multiple splicing variants of the estrogen receptor are present in individual human breast tumors. *Journal of Steroid Biochemistry and Molecular Biology*, **1996**, 59, 251-60	5.1	67
176	Integrating spatial gene expression and breast tumour morphology via deep learning. *Nature Biomedical Engineering*, **2020**, 4, 827-834	19	64
175	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. *European Journal of Human Genetics*, **2000**, 8, 757-63	5.3	64
174	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
173	BRCA1-related breast cancer in Austrian breast and ovarian cancer families: specific BRCA1 mutations and pathological characteristics. *International Journal of Cancer*, **1998**, 77, 354-60	7.5	63
172	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, 111-21	6.3	63
171	Genetic aberrations in hypodiploid breast cancer: frequent loss of chromosome 4 and amplification of cyclin D1 oncogene. *American Journal of Pathology*, **1998**, 153, 191-9	5.8	61
170	Mapping of a novel ocular and cutaneous malignant melanoma susceptibility locus to chromosome 9q21.32. *Journal of the National Cancer Institute*, **2005**, 97, 1377-82	9.7	60
169	Staf50 is a novel p53 target gene conferring reduced clonogenic growth of leukemic U-937 cells. *Oncogene*, **2004**, 23, 4050-9	9.2	59
168	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
167	High risk of tobacco-related cancers in CDKN2A mutation-positive melanoma families. *Journal of Medical Genetics*, **2014**, 51, 545-52	5.8	55
166	Chromosome 5 imbalance mapping in breast tumors from BRCA1 and BRCA2 mutation carriers and sporadic breast tumors. *International Journal of Cancer*, **2006**, 119, 1052-60	7.5	55
165	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
164	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. *Genome Research*, **2015**, 25, 814-24	9.7	52
163	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
162	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

161	Mutational and gene fusion analyses of primary large cell and large cell neuroendocrine lung cancer. *Oncotarget*, **2015**, 6, 22028-37	3.3	51
160	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
159	Flow cytometric DNA index and S-phase fraction in breast cancer in relation to other prognostic variables and to clinical outcome. *Acta Oncologica*, **1992**, 31, 157-65	3.2	50
158	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
157	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
156	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
155	Characterisation of dic(9;20)(p11-13;q11) in childhood B-cell precursor acute lymphoblastic leukaemia by tiling resolution array-based comparative genomic hybridisation reveals clustered breakpoints at 9p13.2 and 20q11.2. *British Journal of Haematology*, **2006**, 135, 492-9	4.5	48
154	A BAP1 mutation in a Danish family predisposes to uveal melanoma and other cancers. *PLoS ONE*, **2013**, 8, e72144	3.7	48
153	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
152	Somatic genetic alterations in BRCA2-associated and sporadic male breast cancer. *Genes Chromosomes and Cancer*, **1999**, 24, 56-61	5	47
151	Gene expression profiles relate to SS18/SSX fusion type in synovial sarcoma. *International Journal of Cancer*, **2006**, 118, 1165-72	7.5	45
150	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
149	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
148	Frequent alterations of the PI3K/AKT/mTOR pathways in hereditary nonpolyposis colorectal cancer. *Familial Cancer*, **2010**, 9, 125-9	3	44
147	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
146	Expanding the genotype-phenotype spectrum in hereditary colorectal cancer by gene panel testing. *Familial Cancer*, **2017**, 16, 195-203	3	40
145	BRCA1 and BRCA2 mutations in Danish families with hereditary breast and/or ovarian cancer. *Acta Oncologica*, **2008**, 47, 772-7	3.2	40
144	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	3.3	39

143	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
142	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
141	Characterization of a novel breast carcinoma xenograft and cell line derived from a BRCA1 germ-line mutation carrier. *Laboratory Investigation*, **2003**, 83, 387-96	5.9	39
140	Refinement of breast cancer molecular classification by miRNA expression profiles. *BMC Genomics*, **2019**, 20, 503	4.5	38
139	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
138	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
137	The retinoblastoma gene undergoes rearrangements in BRCA1-deficient basal-like breast cancer. *Cancer Research*, **2012**, 72, 4028-36	10.1	37
136	Array-CGH identifies cyclin D1 and UBCH10 amplicons in anaplastic thyroid carcinoma. *Endocrine-Related Cancer*, **2008**, 15, 801-15	5.7	37
135	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
134	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
133	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
132	BRCA1 and BRCA2 mutation analysis in breast-ovarian cancer families from northeastern Poland. *Human Mutation*, **2003**, 21, 553-4	4.7	35
131	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
130	Increased CpG methylation of the estrogen receptor gene in BRCA1-linked estrogen receptor-negative breast cancers. *Oncogene*, **2002**, 21, 7034-41	9.2	34
129	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
128	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
127	Haplotype analysis and age estimation of the 113insR CDKN2A founder mutation in Swedish melanoma families. *Genes Chromosomes and Cancer*, **2001**, 31, 107-16	5	33
126	p53 mutation and cyclin D1 amplification correlate with cisplatin sensitivity in xenografted human squamous cell carcinomas from head and neck. *Acta Oncologica*, **2006**, 45, 300-5	3.2	31

125	BRCA2 mutations in 154 finnish male breast cancer patients. *Neoplasia*, **2004**, 6, 541-5	6.4	31
124	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	5	31
123	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. *Cell Reports*, **2016**, 16, 2032-46	8.6	30
122	Chromosomal aberrations in breast cancer: A comparison between cytogenetics and comparative genomic hybridization **1999**, 25, 115-122		29
121	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, 507-16	1.6	28
120	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**, Suppl 1, S195-7	4.7	28
119	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
118	BRCA2 mutation in a family with hereditary prostate cancer. *Genes Chromosomes and Cancer*, **2001**, 30, 299-301	5	28
117	Somatic frameshift alterations in mononucleotide repeat-containing genes in different tumor types from an HNPCC family with germline MSH2 mutation. *Genes Chromosomes and Cancer*, **2000**, 29, 33-9	5	28
116	Intratumor versus intertumor heterogeneity in gene expression profiles of soft-tissue sarcomas. *Genes Chromosomes and Cancer*, **2005**, 43, 302-8	5	27
115	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	3.2	27
114	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
113	Higher occurrence of childhood cancer in families with germline mutations in BRCA2, MMR and CDKN2A genes. *Familial Cancer*, **2008**, 7, 331-7	3	26
112	Multiple copies of mutant BRCA1 and BRCA2 alleles in breast tumors from germ-line mutation carriers. *Genes Chromosomes and Cancer*, **2000**, 28, 432-42	5	26
111	Distinct gene expression signatures in lynch syndrome and familial colorectal cancer type x. *PLoS ONE*, **2013**, 8, e71755	3.7	26
110	Passenger strand loading in overexpression experiments using microRNA mimics. *RNA Biology*, **2015**, 12, 787-91	4.8	25
109	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
108	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

107	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
106	hMLH1, hMSH2 and hMSH6 mutations in hereditary non-polyposis colorectal cancer families from southern Sweden. *International Journal of Cancer*, **1999**, 83, 197-202	7.5	23
105	Association of Genomic Domains in and with Prostate Cancer Risk and Aggressiveness. *Cancer Research*, **2020**, 80, 624-638	10.1	22
104	Germline BRCA1 and HMLH1 mutations in a family with male and female breast carcinoma. *International Journal of Cancer*, **2000**, 85, 796-800	7.5	22
103	Chromosome aberrations in prophylactic mastectomies from women belonging to breast cancer families. *Genes Chromosomes and Cancer*, **1996**, 16, 185-8	5	22
102	Predicting continuous values of prognostic markers in breast cancer from microarray gene expression profiles. *Molecular Cancer Therapeutics*, **2004**, 3, 161-8	6.1	22
101	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. *Melanoma Research*, **2010**, 20, 381-91	3.3	22
100	Amplification and overexpression of the ABCC3 (MRP3) gene in primary breast cancer. *Genes Chromosomes and Cancer*, **2012**, 51, 832-40	5	21
99	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
98	Transcriptional adaptation of neuroblastoma cells to hypoxia. *Biochemical and Biophysical Research Communications*, **2008**, 366, 1054-60	3.4	21
97	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
96	The HER2-encoded miR-4728-3p regulates ESR1 through a non-canonical internal seed interaction. *PLoS ONE*, **2014**, 9, e97200	3.7	20
95	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
94	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
93	A somatic BRCA2 mutation in RER+ endometrial carcinomas that specifically deletes the amino-terminal transactivation domain. *Genes Chromosomes and Cancer*, **1999**, 24, 207-12	5	20
92	Mutual exclusivity analysis of genetic and epigenetic drivers in melanoma identifies a link between p14 ARF and RARβ signaling. *Molecular Cancer Research*, **2013**, 11, 1166-78	6.6	19
91	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
90	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

89	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
88	Genetic predisposition to breast cancer. *Acta Oncologica*, **1996**, 35, 1-8	3.2	18
87	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. *Nature Communications*, **2020**, 11, 3747	17.4	18
86	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
85	Lack of HIN-1 methylation in BRCA1-linked and "BRCA1-like" breast tumors. *Cancer Research*, **2003**, 63, 2024-7	10.1	18
84	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
83	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
82	Duplication 16q12.1-q22.1 characterized by array CGH in a girl with spina bifida. *European Journal of Medical Genetics*, **2007**, 50, 237-41	2.6	17
81	Deletion mapping of chromosome segment 11q24-q25, exhibiting extensive allelic loss in early onset breast cancer. *International Journal of Cancer*, **2001**, 92, 208-13	7.5	17
80	Frequent miRNA-convergent fusion gene events in breast cancer. *Nature Communications*, **2017**, 8, 788	17.4	16
79	Detection and delineation of an unusual 17p11.2 deletion by array-CGH and refinement of the Smith-Magenis syndrome minimum deletion to approximately 650 kb. *European Journal of Medical Genetics*, **2005**, 48, 290-300	2.6	16
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