Annika Lindblom

List of Publications by Year
in descending order

170 papers	20,106 citations	29994 54 h-index	12558 132 g-index
176 all docs	176 docs citations	176 times ranked	19944 citing authors

#	Article	IF	Citations
1	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
2	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
3	A Swedish Genome-Wide Haplotype Association Analysis Identifies a Novel Breast Cancer Susceptibility Locus in 8p21.2 and Characterizes Three Loci on Chromosomes 10, 11 and 16. Cancers, 2022, 14, 1206.	1.7	1
4	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
5	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	2.3	35
6	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	0.6	36
7	Genetically predicted circulating concentrations of micronutrients and risk of colorectal cancer among individuals of European descent: a Mendelian randomization study. American Journal of Clinical Nutrition, 2021, 113, 1490-1502.	2.2	27
8	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
9	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
10	Identification of known and novel familial cancer genes in Swedish colorectal cancer families. International Journal of Cancer, 2021, 149, 627-634.	2.3	0
11	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529.	2.6	5
12	Massive parallel sequencing in a family with rectal cancer. Hereditary Cancer in Clinical Practice, 2021, 19, 23.	0.6	3
13	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	1.7	4
14	No Difference in Penetrance between Truncating and Missense/Aberrant Splicing Pathogenic Variants in MLH1 and MSH2: A Prospective Lynch Syndrome Database Study. Journal of Clinical Medicine, 2021, 10, 2856.	1.0	11
15	Sequencing for germline mutations in Swedish breast cancer families reveals novel breast cancer risk genes. Scientific Reports, 2021, 11, 14737.	1.6	2
16	A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. Scientific Reports, 2021, 11, 14763.	1.6	3
17	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	2.2	7
18	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183

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19	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	1.1	19
20	A Combined Proteomics and Mendelian Randomization Approach to Investigate the Effects of Aspirin-Targeted Proteins on Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 564-575.	1.1	10
21	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
22	Salicylic Acid and Risk of Colorectal Cancer: A Two-Sample Mendelian Randomization Study. Nutrients, 2021, 13, 4164.	1.7	3
23	Colorectal cancer risk susceptibility loci in a Swedish population. Molecular Carcinogenesis, 2021, , .	1.3	2
24	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
25	Cancer risks by gene, age, and gender in 6350 carriers of pathogenic mismatch repair variants: findings from the Prospective Lynch Syndrome Database. Genetics in Medicine, 2020, 22, 15-25.	1.1	365
26	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
27	Cumulative Burden of Colorectal Cancerâ€“Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	0.6	110
28	Circulating Levels of Insulin-like Growth Factor 1 and Insulin-like Growth Factor Binding Protein 3 Associate With Risk of Colorectal Cancer Based on Serologic and Mendelian Randomization Analyses. Gastroenterology, 2020, 158, 1300-1312.e20.	0.6	90
29	Identification of Novel Loci and New Risk Variant in Known Loci for Colorectal Cancer Risk in East Asians. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 477-486.	1.1	25
30	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	2.6	124
31	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
32	Circulating bilirubin levels and risk of colorectal cancer: serological and Mendelian randomization analyses. BMC Medicine, 2020, 18, 229.	2.3	28
33	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. BMC Medicine, 2020, 18, 396.	2.3	76
34	Hemochromatosis risk genotype is not associated with colorectal cancer or age at its diagnosis. Human Genetics and Genomics Advances, 2020, 1, 100010.	1.0	3
35	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
36	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2

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37	Cancer prevention with aspirin in hereditary colorectal cancer (Lynch syndrome), 10-year follow-up and registry-based 20-year data in the CAPP2 study: a double-blind, randomised, placebo-controlled trial. Lancet, The, 2020, 395, 1855-1863.	6.3	220
38	Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 860-870.	1.1	26
39	Increased risk for uterine cancer among first-degree relatives to Swedish gastric cancer patients. Hereditary Cancer in Clinical Practice, 2020, 18, 12.	0.6	0
40	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
41	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	1.1	14
42	Systematic meta-analyses, field synopsis and global assessment of the evidence of genetic association studies in colorectal cancer. Gut, 2020, 69, 1460-1471.	6.1	27
43	Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. Nature Communications, 2020, 11, 597.	5.8	193
44	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129
45	Genetic analyses supporting colorectal, gastric, and prostate cancer syndromes. Genes Chromosomes and Cancer, 2019, 58, 775-782.	1.5	6
46	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
47	Linkage analysis revealed risk loci on 6p21 and 18p11.2-q11.2 in familial colon and rectal cancer, respectively. European Journal of Human Genetics, 2019, 27, 1286-1295.	1.4	4
48	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
49	Exome sequencing in 51 early onset nonâ€familial CRC cases. Molecular Genetics & Genomic Medicine, 2019, 7, e605.	0.6	17
50	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. Human Genetics, 2019, 138, 307-326.	1.8	44
51	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	2.2	24
52	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
53	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. International Journal of Epidemiology, 2019, 48, 767-780.	0.9	35
54	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377

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55	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19
56	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	1.3	62
57	Haplotype analysis suggest that the MLH1 c.2059Câ€‰>â€‰T mutation is a Swedish founder mutation. Familial Cancer, 2018, 17, 531-537.	0.9	3
58	Cancer risk and survival in path_MMR carriers by gene and gender up to 75 years of age: a report from the Prospective Lynch Syndrome Database. Gut, 2018, 67, 1306-1316.	6.1	410
59	Cancer Risks for PMS2-Associated Lynch Syndrome. Journal of Clinical Oncology, 2018, 36, 2961-2968.	0.8	147
60	Testing strategies to reduce morbidity and mortality from Lynch syndrome. Scandinavian Journal of Gastroenterology, 2018, 53, 1535-1540.	0.6	4
61	A retrospective study of extracolonic, non-endometrial cancer in Swedish Lynch syndrome families. Hereditary Cancer in Clinical Practice, 2018, 16, 16.	0.6	11
62	Mendelian randomisation study of age at menarche and age at menopause and the risk of colorectal cancer. British Journal of Cancer, 2018, 118, 1639-1647.	2.9	16
63	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
64	Genome-wide scan of the effect of common nsSNPs on colorectal cancer survival outcome. British Journal of Cancer, 2018, 119, 988-993.	2.9	10
65	Recurrent, low-frequency coding variants contributing to colorectal cancer in the Swedish population. PLoS ONE, 2018, 13, e0193547.	1.1	10
66	Two novel colorectal cancer risk loci in the region on chromosome 9q22.32. Oncotarget, 2018, 9, 11170-11179.	0.8	4
67	Cancer incidence and survival in Lynch syndrome patients receiving colonoscopic and gynaecological surveillance: first report from the prospective Lynch syndrome database. Gut, 2017, 66, 464-472.	6.1	411
68	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for BRCA1 pathogenic variant carriers. European Journal of Human Genetics, 2017, 25, 432-438.	1.4	26
69	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
70	Incidence of and survival after subsequent cancers in carriers of pathogenic MMR variants with previous cancer: a report from the prospective Lynch syndrome database. Gut, 2017, 66, 1657-1664.	6.1	127
71	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
72	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289

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73	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
74	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
75	Genetic anticipation in Swedish Lynch syndrome families. PLoS Genetics, 2017, 13, e1007012.	1.5	14
76	Colorectal cancer incidence in path_MLH1 carriers subjected to different follow-up protocols: a Prospective Lynch Syndrome Database report. Hereditary Cancer in Clinical Practice, 2017, 15, 18.	0.6	49
77	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	2.2	43
78	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	0.8	14
79	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
80	Cancer risk susceptibility loci in a Swedish population. Oncotarget, 2017, 8, 110300-110310.	0.8	7
81	Defining New Colorectal Cancer Syndromes in a Population-based Cohort of the Disease. Anticancer Research, 2017, 37, 1831-1835.	0.5	9
82	Parent of Origin and Prognosis in Familial Breast Cancer in Sweden. Anticancer Research, 2017, 37, 1257-1262.	0.5	0
83	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	0.8	31
84	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	3.9	118
85	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
86	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
87	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
88	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	2.2	31
89	Mismatch repair gene mutation spectrum in the Swedish Lynch syndrome population. Oncology Reports, 2016, 36, 2823-2835.	1.2	43
90	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43

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91	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	0.8	21
92	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
93	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
94	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
95	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1503-1510.	1.1	64
96	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
97	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
98	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
99	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	1.6	19
100	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
101	Exome sequencing in one family with gastric- and rectal cancer. BMC Genetics, 2016, 17, 41.	2.7	31
102	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
103	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. Human Molecular Genetics, 2016, 25, 2256-2268.	1.4	106
104	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
105	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
106	The effect of genotypes and parent of origin on cancer risk and age of cancer development in PMS2 mutation carriers. Genetics in Medicine, 2016, 18, 405-409.	1.1	15
107	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
108	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26

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109	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. Scientific Reports, 2015, 5, 17369.	1.6	35
110	Tumour spectrum in non-BRCA hereditary breast cancer families in Sweden. Hereditary Cancer in Clinical Practice, 2015, 13, 15.	0.6	11
111	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	2.2	26
112	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
113	Regulator of Chromosome Condensation 2 Identifies High-Risk Patients within Both Major Phenotypes of Colorectal Cancer. Clinical Cancer Research, 2015, 21, 3759-3770.	3.2	32
114	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	2.6	76
115	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
116	Screening for germline phosphatase and tensin homolog-mutations in suspected Cowden syndrome and Cowden syndrome-like families among uterine cancer patients. Oncology Letters, 2015, 9, 1782-1786.	0.8	3
117	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	2.6	37
118	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
119	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	1.6	25
120	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	1.1	24
121	The gynecological surveillance of women with Lynch syndrome in Sweden. Gynecologic Oncology, 2015, 138, 717-722.	0.6	20
122	Lynch Syndrome Caused by Germline PMS2 Mutations: Delineating the Cancer Risk. Journal of Clinical Oncology, 2015, 33, 319-325.	0.8	177
123	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	0.8	15
124	Whole-genome Linkage Analysis and Sequence Analysis of Candidate Loci in Familial Breast Cancer. Anticancer Research, 2015, 35, 3155-65.	0.5	4
125	Predicting Outcome in Colonoscopic High-risk Surveillance. Anticancer Research, 2015, 35, 4813-9.	0.5	5
126	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49

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127	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
128	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
129	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
130	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. Human Molecular Genetics, 2014, 23, 4729-4737.	1.4	128
131	Genome-wide association study yields variants at 20p12.2 that associate with urinary bladder cancer. Human Molecular Genetics, 2014, 23, 5545-5557.	1.4	46
132	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
133	Familial cancer among consecutive uterine cancer patients in Sweden. Hereditary Cancer in Clinical Practice, 2014, 12, 14.	0.6	6
134	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
135	The MLH1 c.1852_1853delinsGC (p.K618A) Variant in Colorectal Cancer: Genetic Association Study in 18,723 Individuals. PLoS ONE, 2014, 9, e95022.	1.1	7
136	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	2.6	98
137	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	2.6	201
138	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
139	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
140	Linkage Analysis in Familial Non-Lynch Syndrome Colorectal Cancer Families from Sweden. PLoS ONE, 2013, 8, e83936.	1.1	9
141	Variants of the PPARD Gene and Their Clinicopathological Significance in Colorectal Cancer. PLoS ONE, 2013, 8, e83952.	1.1	5
142	CHEK2*1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancerâ€“Specific Death, and Increased Risk of a Second Breast Cancer. Journal of Clinical Oncology, 2012, 30, 4308-4316.	0.8	162
143	Bioinformatics for Human Genetics: Promises and Challenges. Human Mutation, 2011, 32, 495-500.	1.1	21
144	Fine scale mapping of the breast cancer 16q12 locus. Human Molecular Genetics, 2010, 19, 2507-2515.	1.4	68

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145	The Clinical Phenotype of Lynch Syndrome Due to Germ-Line PMS2 Mutations. Gastroenterology, 2008, 135, 419-428.e1.	0.6	480
146	BRCA1 Mutations in a Population-based Study of Breast Cancer in Stockholm County. Genetic Testing and Molecular Biomarkers, 2004, 8, 127-132.	1.7	21
147	Colorectal cancer as a complex disease: defining at-risk subjects in the general population â€“ a preventive strategy. Expert Review of Anticancer Therapy, 2004, 4, 377-385.	1.1	6
148	Germline mutation screening of the STK11/LKB1 gene in familial breast cancer with LOH on 19p. Clinical Genetics, 2001, 57, 394-397.	1.0	28
149	Microsatellite Instability and hMLH1 and hMSH2 Expression Analysis in Familial and Sporadic Colorectal Cancer. Laboratory Investigation, 2001, 81, 535-541.	1.7	97
150	GermlineBRCA1 andHMLH1 mutations in a family with male and female breast carcinoma. , 2000, 85, 796-800.		29
151	Microsatellite instability as a predictor of a mutation in a DNA mismatch repair gene in familial colorectal cancer. , 2000, 27, 17-25.		74
152	Enhanced detection of mutations in BRCA1 exon 11 using restriction endonuclease fingerprinting-single-strand conformation polymorphism. Journal of Molecular Medicine, 2000, 78, 580-587.	1.7	3
153	Hereditary Cancer. Acta OncolÃ³gica, 1999, 38, 439-447.	0.8	11
154	Colorectal cancer with and without microsatellite instability involves different genes. , 1999, 26, 247-252.		118
155	BRCA2 germline mutations in Swedish breast cancer families. European Journal of Human Genetics, 1998, 6, 134-139.	1.4	20
156	A widely expressed transcription factor with multiple DNA sequence specificity,CTCF, is localized at chromosome segment 16q22.1 within one of the smallest regions of overlap for common deletions in breast and prostate cancers. , 1998, 22, 26-36.		121
157	DGGE screening of mutations in mismatch repair genes (hMSH2 and hMLH1) in 34 Swedish families with colorectal cancer. Clinical Genetics, 1998, 53, 131-135.	1.0	19
158	A human compound heterozygote for two MLH1 missense mutations. Nature Genetics, 1997, 17, 135-136.	9.4	47
159	Molecular basis of HNPCC: Mutations of MMR genes. Human Mutation, 1997, 10, 89-99.	1.1	166
160	Low frequency of hMSH2 mutations in Swedish HNPCC families. , 1997, 74, 134-137.		20
161	Mapping of a new MAP kinase activated protein kinase gene (3PK) to human chromosome band 3p21.2 and ordering of 3PK and two cosmid markers in the 3p22â€“p21 tumour-suppressor region by two-colour fluorescencein situ hybridization. Chromosome Research, 1996, 4, 310-313.	1.0	11
162	Familial breast cancer and genes involved in breast carcinogenesis. Breast Cancer Research and Treatment, 1995, 34, 171-183.	1.1	11

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163	Finnish mutations in Swedish HNPCC families. Nature Medicine, 1995, 1, 1104-1104.	15.2	12
164	Sublocalization of a locus at 3p21.3?23 predisposing to hereditary nonpolyposis colon cancer. Human Genetics, 1994, 94, 210-4.	1.8	10
165	Mutation in the DNA mismatch repair gene homologue hMLH 1 is associated with hereditary non-polyposis colon cancer. Nature, 1994, 368, 258-261.	13.7	2,001
166	Four separate regions on chromosome 17 show loss of heterozygosity in familial breast carcinomas. Human Genetics, 1993, 91, 6-12.	1.8	25
167	Genetic mapping of a second locus predisposing to hereditary nonâ€“polyposis colon cancer. Nature Genetics, 1993, 5, 279-282.	9.4	408
168	Hereditary breast cancer in sweden: a predominance of maternally inherited cases. Breast Cancer Research and Treatment, 1992, 24, 159-165.	1.1	12
169	Molecular basis of HNPCC: Mutations of MMR genes. , 0, .		2
170	A widely expressed transcription factor with multiple DNA sequence specificity, CTCF, is localized at chromosome segment 16q22.1 within one of the smallest regions of overlap for common deletions in breast and prostate cancers. , 0, .		1